



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 11:02 AM EDT

PDB ID : 8G6W / pdb_00008g6w
EMDB ID : EMD-29786
Title : Structure of WT E.coli 70S ribosome complexed with mRNA, P-site fMet-NH-tRNA^{fMet} and A-site ortho-aminobenzoic acid charged NH-tRNA^{Phe}
Authors : Majumdar, C.; Cate, J.H.D.
Deposited on : 2023-02-16
Resolution : 2.02 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

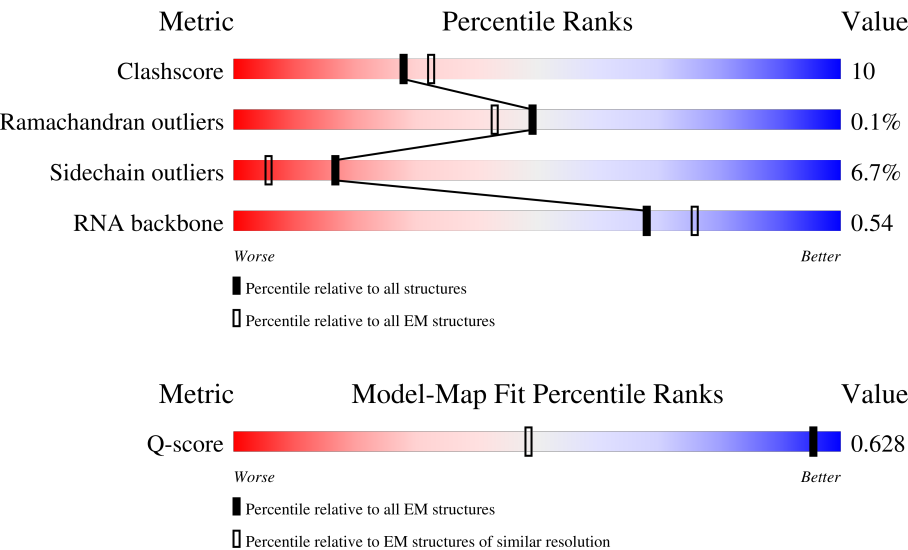
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.02 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	1728 (1.52 - 2.52)

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

Mol	Chain	Length	Quality of chain
1	0	55	13% 71% 22% 7%
2	1	46	93% 7%
3	2	65	86% 11% ••

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	A	1542	
7	B	241	
8	C	233	
9	D	206	
10	E	167	
11	F	135	
12	G	179	
13	H	130	
14	I	130	
15	J	103	
16	K	129	
17	L	124	
18	M	118	
19	N	101	
20	O	89	
21	P	82	
22	Q	84	
23	R	75	
24	S	92	
25	T	87	
26	U	71	
27	X	28	
28	Y	76	

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Mol	Chain	Length	Quality of chain
29	Z	76	
30	a	2904	
31	b	120	
32	c	273	
33	d	209	
34	e	201	
35	f	179	
36	g	177	
37	h	149	
38	i	142	
39	j	123	
40	k	144	
41	l	136	
42	m	127	
43	n	117	
44	o	115	
45	p	118	
46	q	103	
47	r	110	
48	s	100	
49	t	104	
50	u	94	
51	v	85	
52	w	78	
53	x	63	

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Mol	Chain	Length	Quality of chain
54	y	59	
55	z	57	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
63	SPD	d	301	-	-	X	-

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 145749 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called 50S ribosomal protein L34.

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

- Molecule 3 is a protein called 50S ribosomal protein L35.

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

- Molecule 4 is a protein called 50S ribosomal protein L36.

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

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called 16S rRNA.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

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

- Molecule 8 is a protein called 30S ribosomal protein S3.

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

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

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

- Molecule 11 is a protein called 30S ribosomal protein S6.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	98	Total	C	N	O	S	0	0
			785	493	149	142	1		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	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	conflict	UNP A0A0H3PWX2

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

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

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

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

- Molecule 24 is a protein called 30S ribosomal protein S19.

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

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

- Molecule 26 is a protein called 30S ribosomal protein S21.

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

- Molecule 27 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	15	Total	C	N	O	P	0	0
			317	143	56	103	15		

- Molecule 28 is a RNA chain called A-site oABZ-tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	74	Total	C	N	O	P	0	0
			1578	705	285	515	73		

- Molecule 29 is a RNA chain called P-site fMet-tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	75	Total	C	N	O	P	0	0
			1601	713	289	524	75		

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2753	Total	C	N	O	P	2	0
			59170	26402	10901	19112	2755		

- Molecule 31 is a RNA chain called 5S rRNA.

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

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

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

- Molecule 34 is a protein called 50S ribosomal protein L4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

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

- Molecule 37 is a protein called 50S ribosomal protein L9.

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

- Molecule 38 is a protein called 50S ribosomal protein L13.

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

- Molecule 39 is a protein called 50S ribosomal protein L14.

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

- Molecule 40 is a protein called 50S ribosomal protein L15.

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

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	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
l	82	MS6	MET	conflict	UNP E6BI61

- Molecule 42 is a protein called 50S ribosomal protein L17.

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

- Molecule 43 is a protein called 50S ribosomal protein L18.

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

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

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

- Molecule 46 is a protein called Ribosomal protein L21.

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

- Molecule 47 is a protein called 50S ribosomal protein L22.

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

- Molecule 48 is a protein called 50S ribosomal protein L23.

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

- Molecule 49 is a protein called 50S ribosomal protein L24.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	77	Total	C	N	O	S	0	0
			582	360	115	106	1		

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

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

- Molecule 54 is a protein called 50S ribosomal protein L30.

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

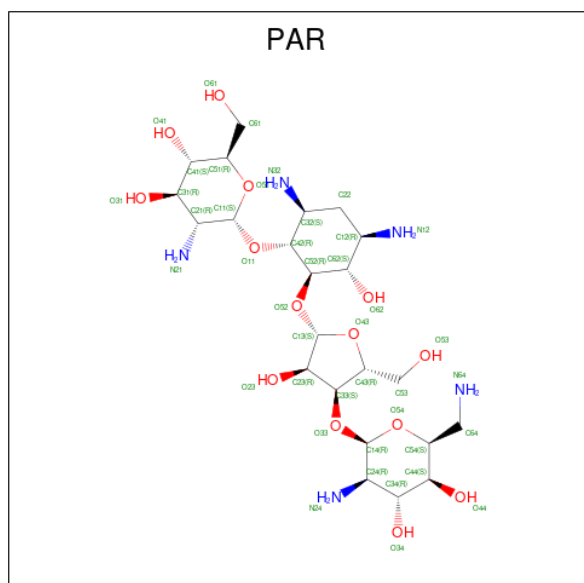
- Molecule 55 is a protein called 50S ribosomal protein L32.

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

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	
56	4	1	Total	Zn	0
			1	1	

- Molecule 57 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄).

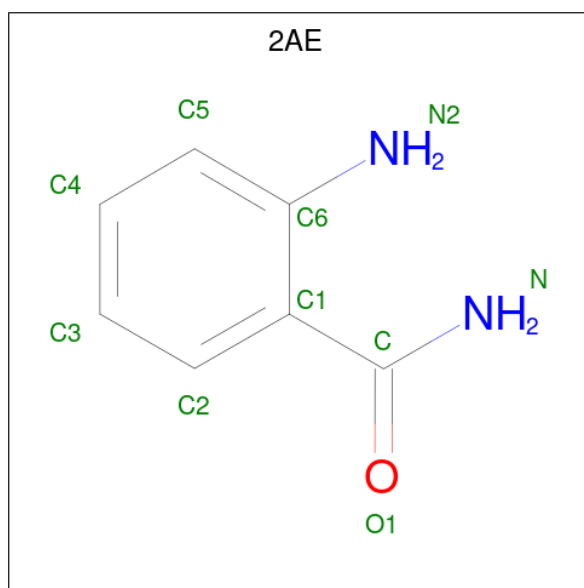


Mol	Chain	Residues	Atoms				AltConf
57	A	1	Total	C	N	O	0
			42	23	5	14	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

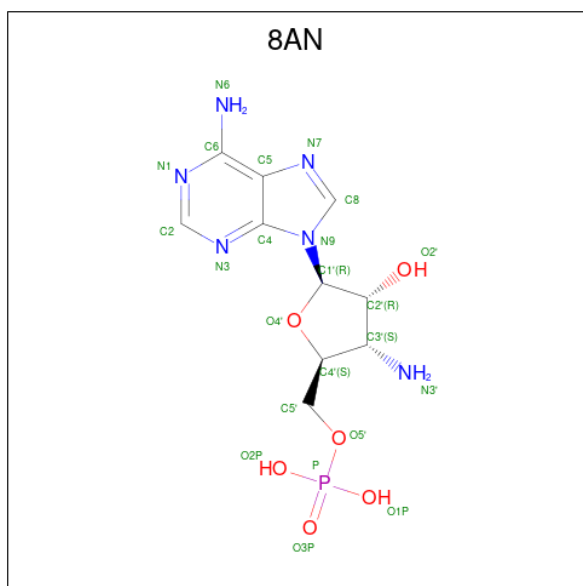
Mol	Chain	Residues	Atoms		AltConf
58	A	89	Total 89	Mg 89	0
58	M	1	Total 1	Mg 1	0
58	O	1	Total 1	Mg 1	0
58	X	1	Total 1	Mg 1	0
58	Z	1	Total 1	Mg 1	0
58	a	217	Total 217	Mg 217	0
58	b	5	Total 5	Mg 5	0
58	c	1	Total 1	Mg 1	0
58	d	1	Total 1	Mg 1	0
58	m	1	Total 1	Mg 1	0
58	p	1	Total 1	Mg 1	0
58	z	1	Total 1	Mg 1	0

- Molecule 59 is 2-AMINO-BENZAMIDE (CCD ID: 2AE) (formula: $C_7H_8N_2O$) (labeled as "Ligand of Interest" by depositor).



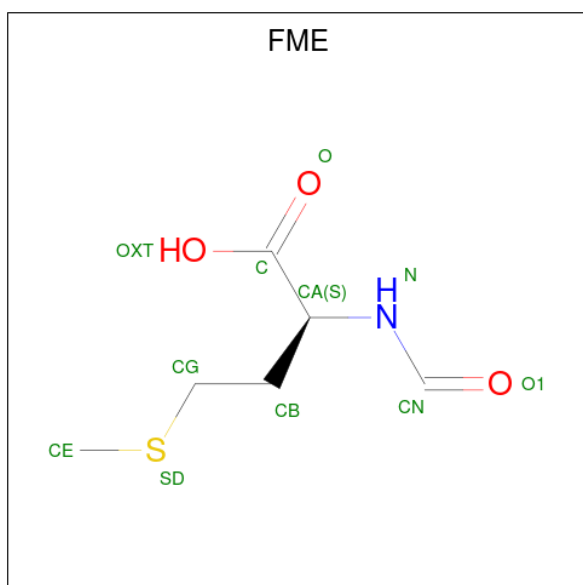
Mol	Chain	Residues	Atoms				AltConf
59	Y	1	Total	C	N	O	0
			10	7	2	1	

- Molecule 60 is 3'-amino-3'-deoxyadenosine 5'-(dihydrogen phosphate) (CCD ID: 8AN) (formula: $C_{10}H_{15}N_6O_6P$).



Mol	Chain	Residues	Atoms					AltConf
60	Z	1	Total	C	N	O	P	0
			22	10	6	5	1	

- Molecule 61 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).

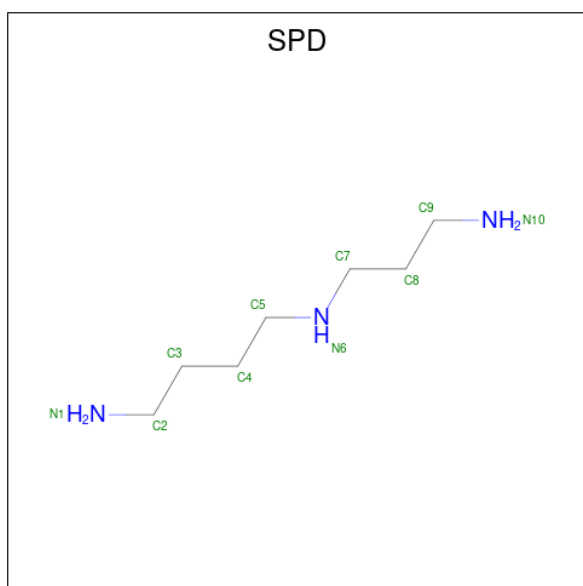


Mol	Chain	Residues	Atoms					AltConf
61	Z	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
62	a	13	Total	K	0
			13	13	
62	c	1	Total	K	0
			1	1	

- Molecule 63 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



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

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Mol	Chain	Residues	Atoms			AltConf
63	d	1	Total	C	N	0
			10	7	3	

- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	1	16	Total	O	0
			16	16	
64	2	19	Total	O	0
			19	19	
64	3	2	Total	O	0
			2	2	
64	A	10	Total	O	0
			10	10	
64	a	3197	Total	O	0
			3197	3197	
64	b	41	Total	O	0
			41	41	
64	c	86	Total	O	0
			86	86	
64	d	34	Total	O	0
			34	34	
64	e	34	Total	O	0
			34	34	
64	h	1	Total	O	0
			1	1	
64	i	14	Total	O	0
			14	14	
64	j	11	Total	O	0
			11	11	
64	k	32	Total	O	0
			32	32	
64	l	22	Total	O	0
			22	22	
64	m	20	Total	O	0
			20	20	
64	o	8	Total	O	0
			8	8	
64	p	16	Total	O	0
			16	16	
64	q	15	Total	O	0
			15	15	

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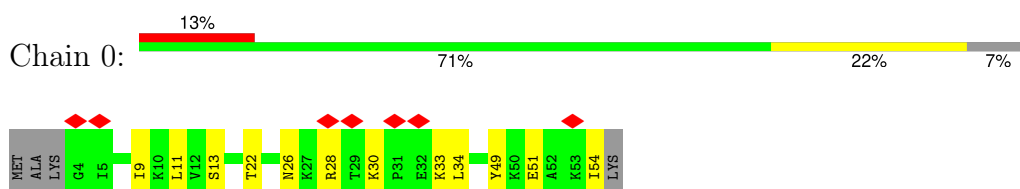
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Mol	Chain	Residues	Atoms		AltConf
64	r	25	Total 25	O 25	0
64	s	6	Total 6	O 6	0
64	t	1	Total 1	O 1	0
64	u	4	Total 4	O 4	0
64	v	11	Total 11	O 11	0
64	w	7	Total 7	O 7	0
64	x	1	Total 1	O 1	0
64	y	2	Total 2	O 2	0
64	z	24	Total 24	O 24	0

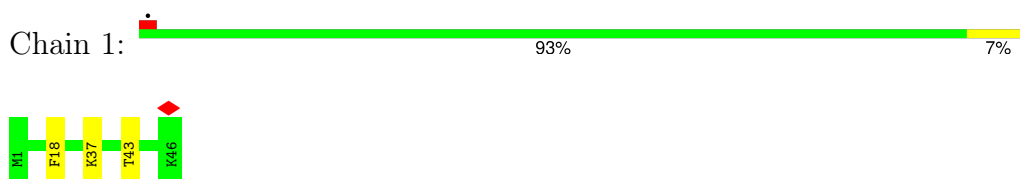
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

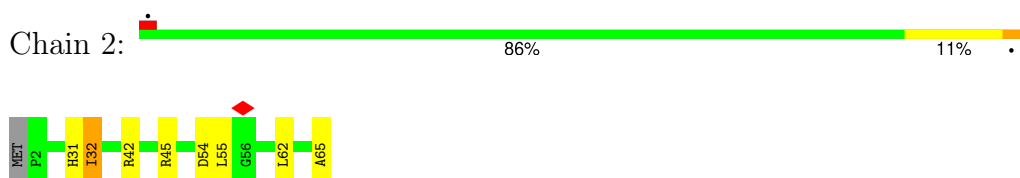
- Molecule 1: 50S ribosomal protein L33



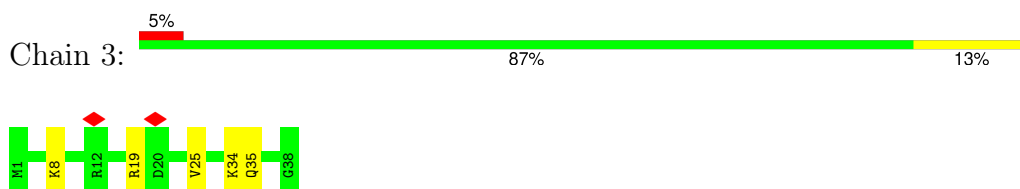
- Molecule 2: 50S ribosomal protein L34



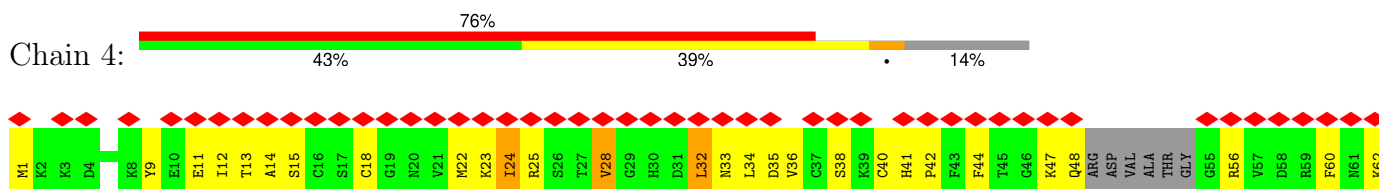
- Molecule 3: 50S ribosomal protein L35

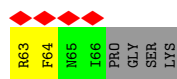


- Molecule 4: 50S ribosomal protein L36

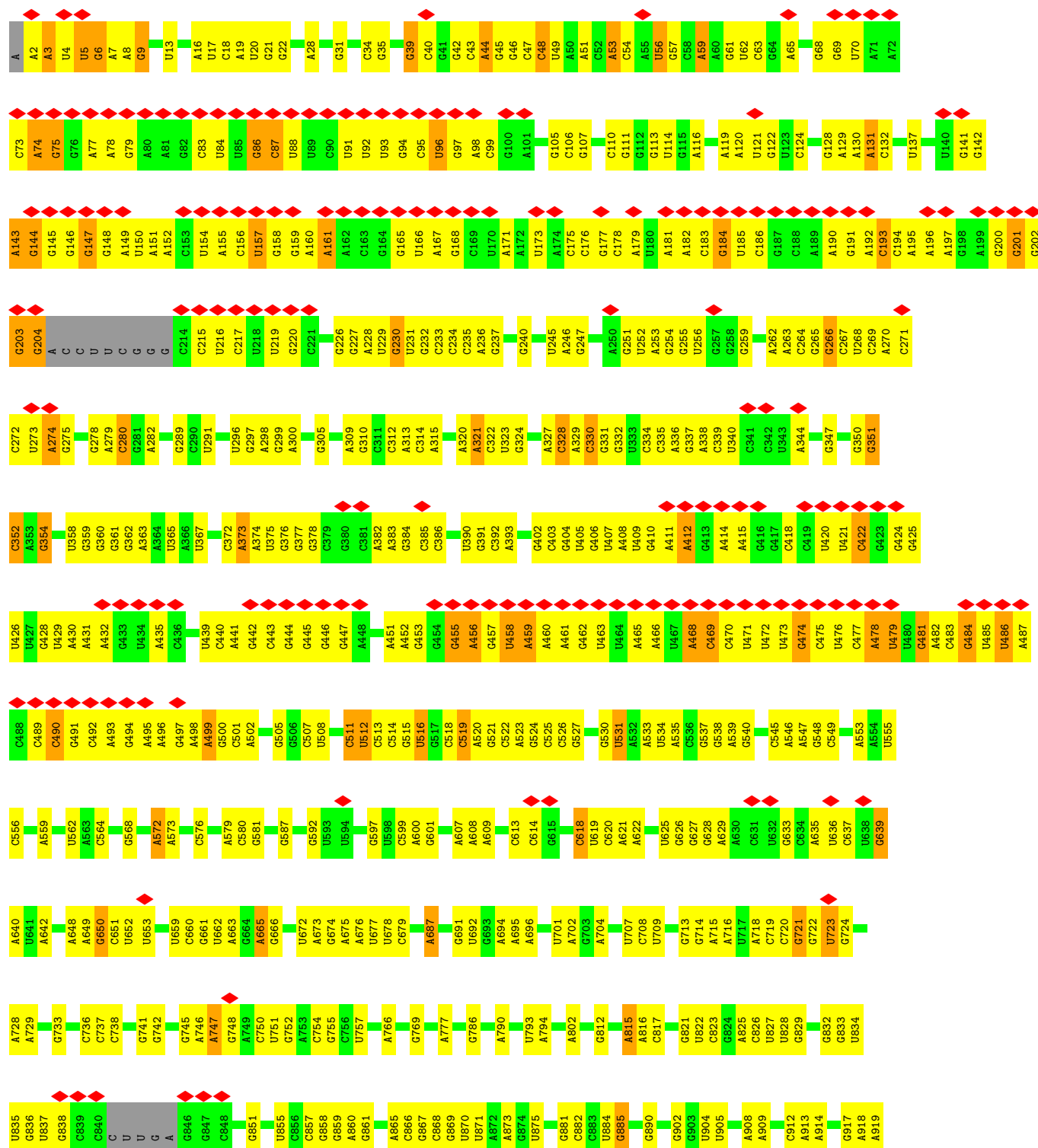


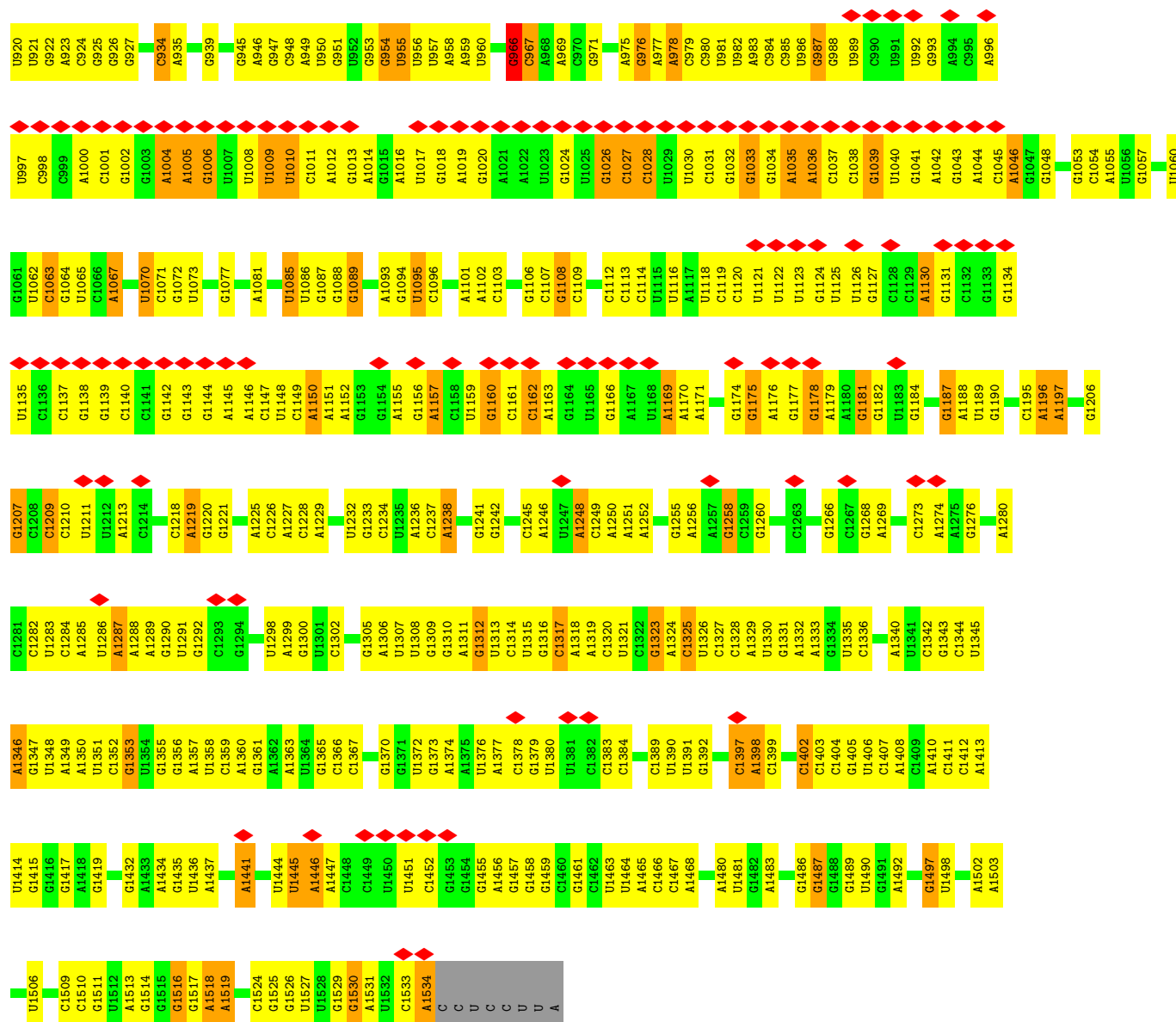
- Molecule 5: 50S ribosomal protein L31



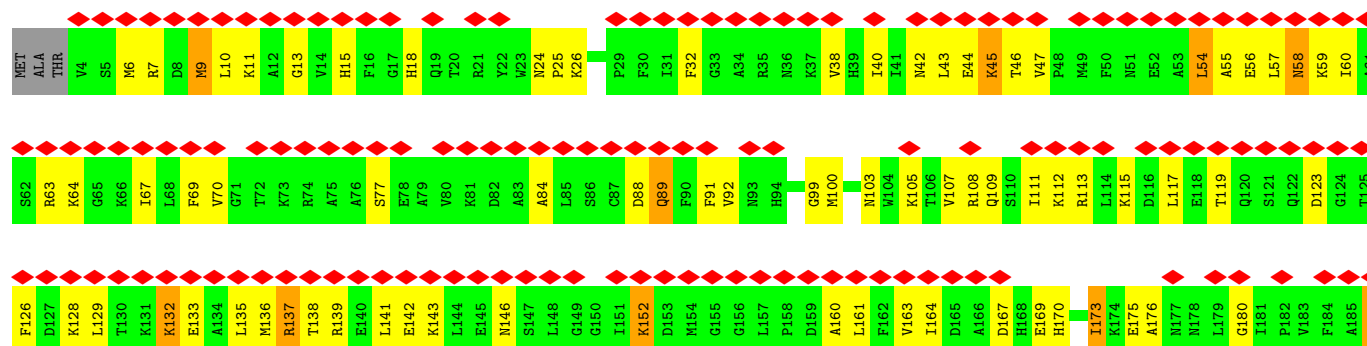


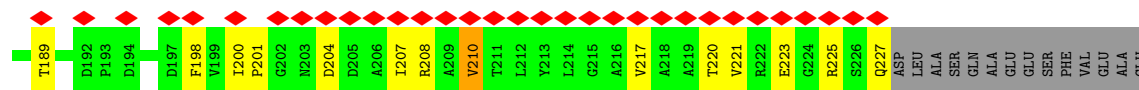
● Molecule 6: 16S rRNA



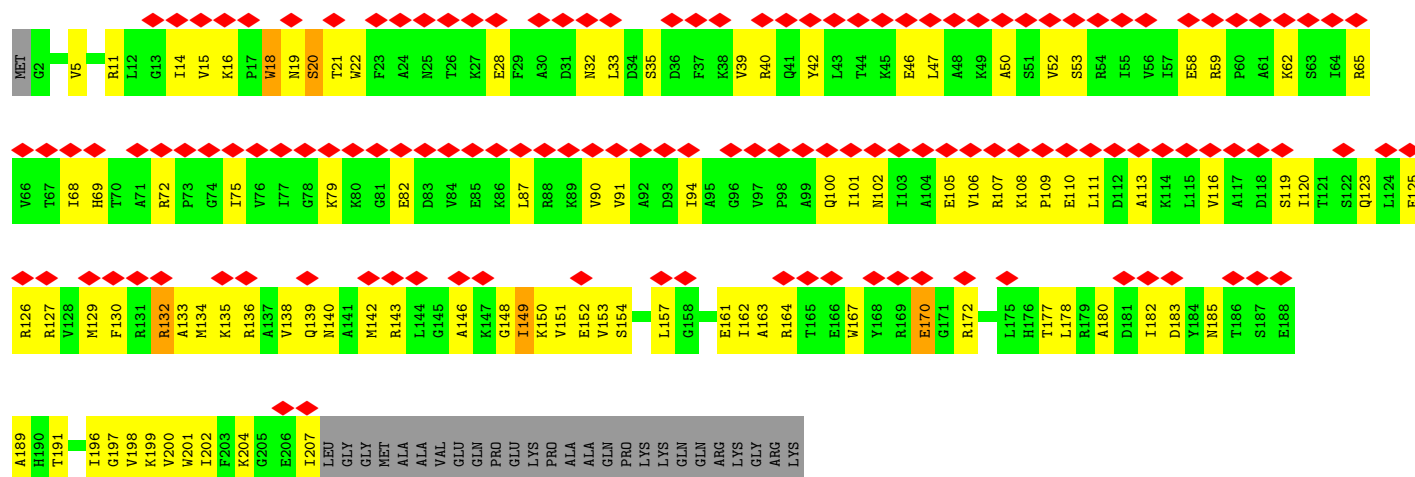


• Molecule 7: 30S ribosomal protein S2





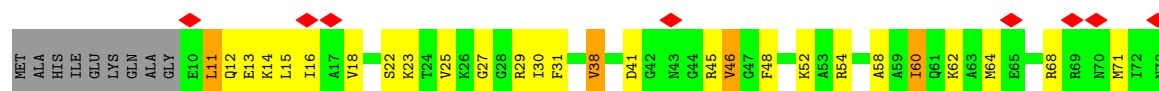
• Molecule 8: 30S ribosomal protein S3

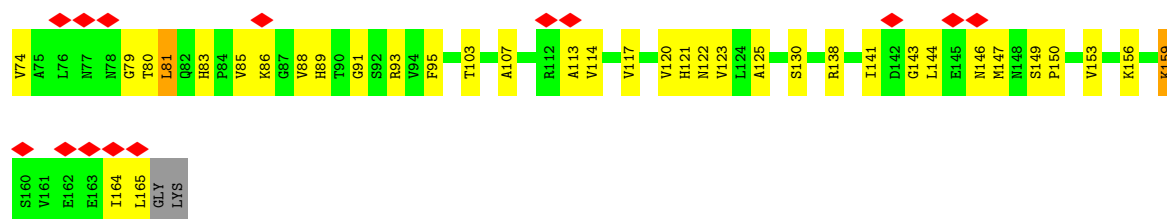


• Molecule 9: 30S ribosomal protein S4

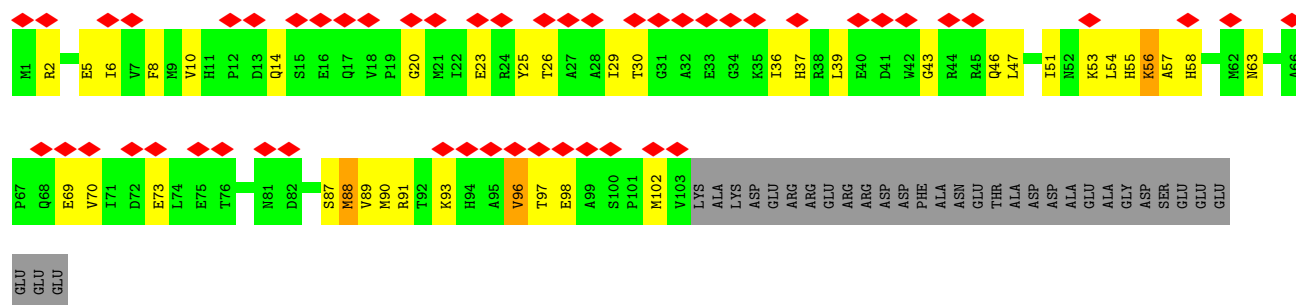
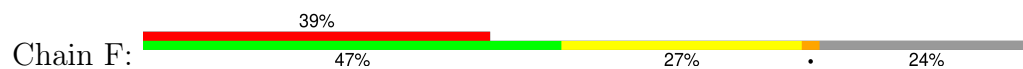


• Molecule 10: 30S ribosomal protein S5

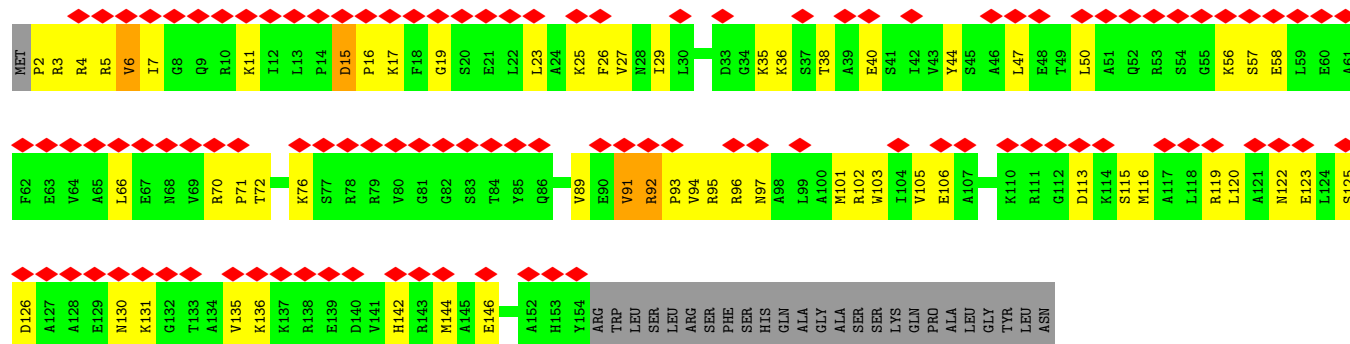




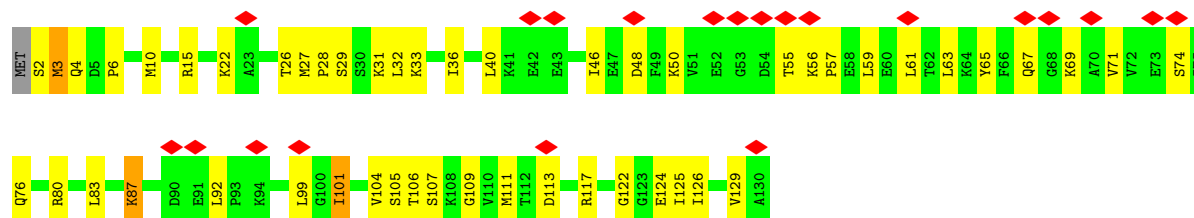
• Molecule 11: 30S ribosomal protein S6



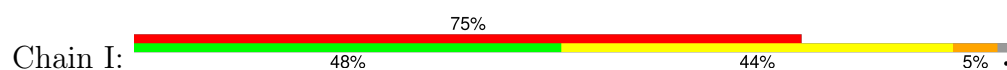
• Molecule 12: 30S ribosomal protein S7

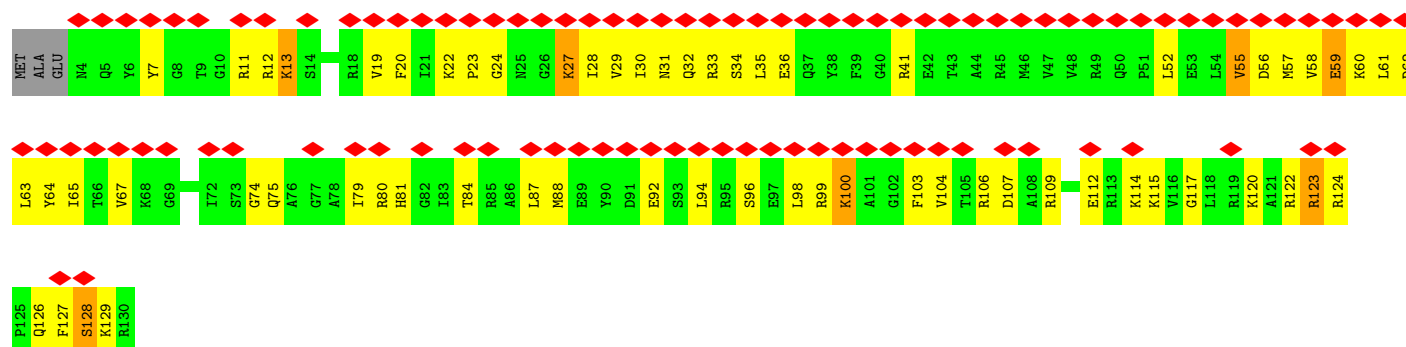


• Molecule 13: 30S ribosomal protein S8

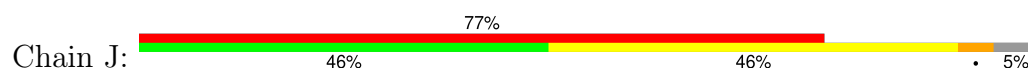


• Molecule 14: 30S ribosomal protein S9

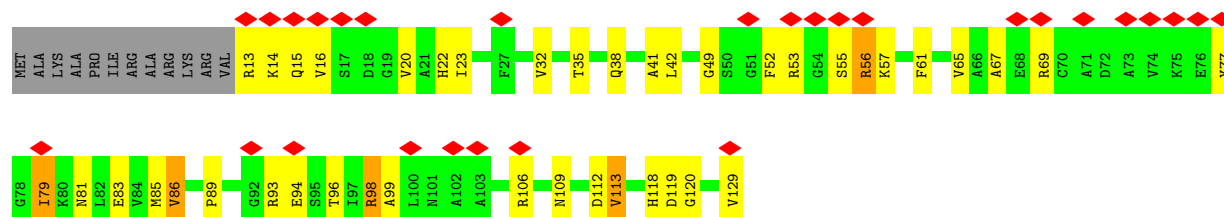




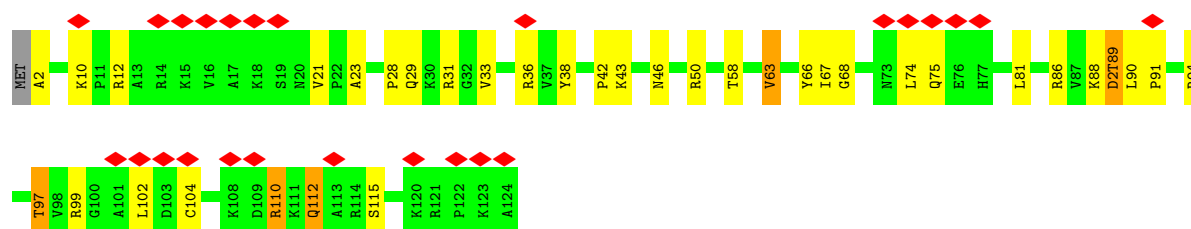
• Molecule 15: 30S ribosomal protein S10



• Molecule 16: 30S ribosomal protein S11

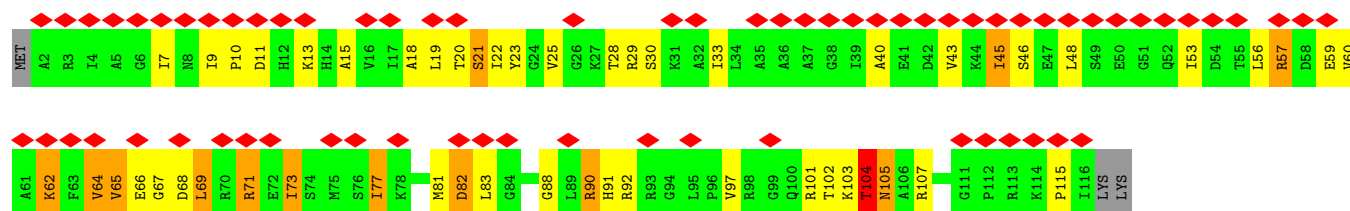


• Molecule 17: 30S ribosomal protein S12

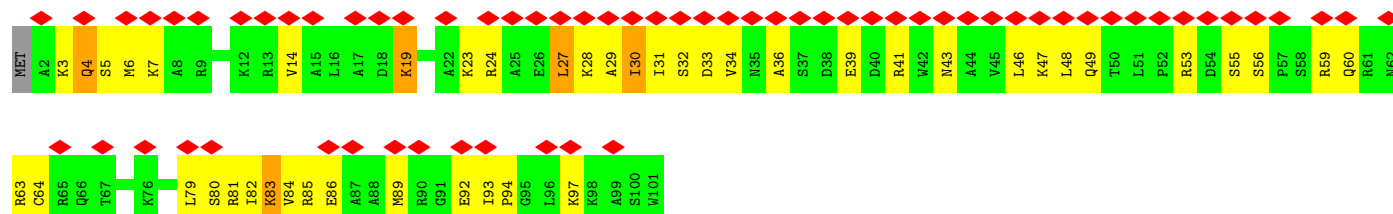


• Molecule 18: 30S ribosomal protein S13

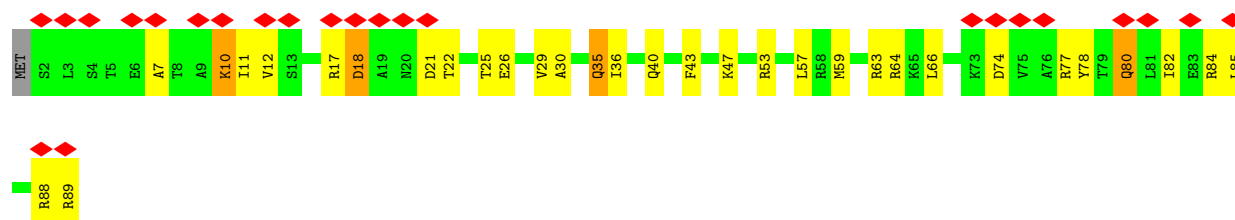




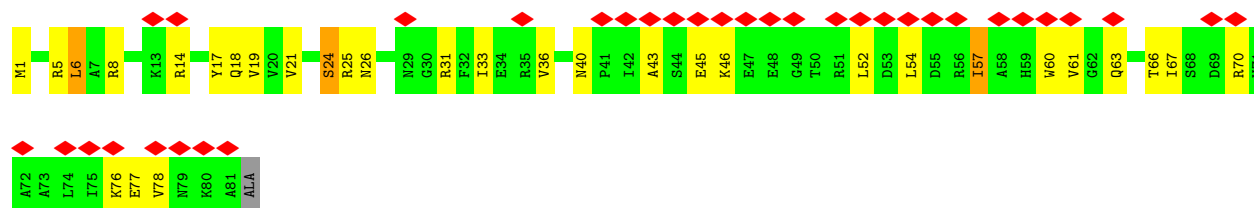
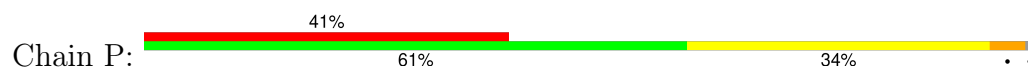
• Molecule 19: 30S ribosomal protein S14



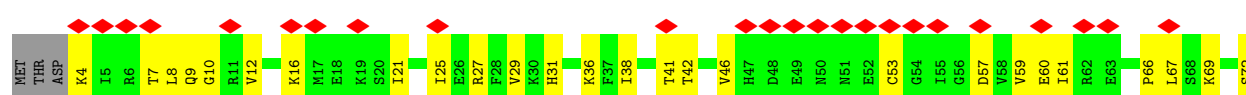
• Molecule 20: 30S ribosomal protein S15

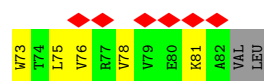


• Molecule 21: 30S ribosomal protein S16

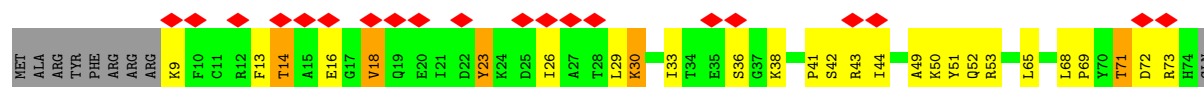


• Molecule 22: 30S ribosomal protein S17

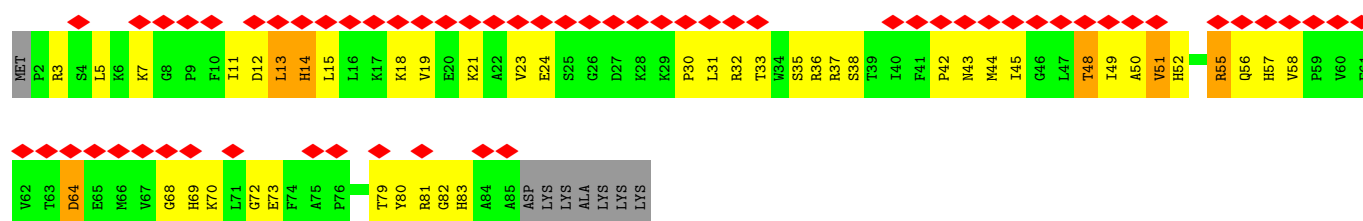




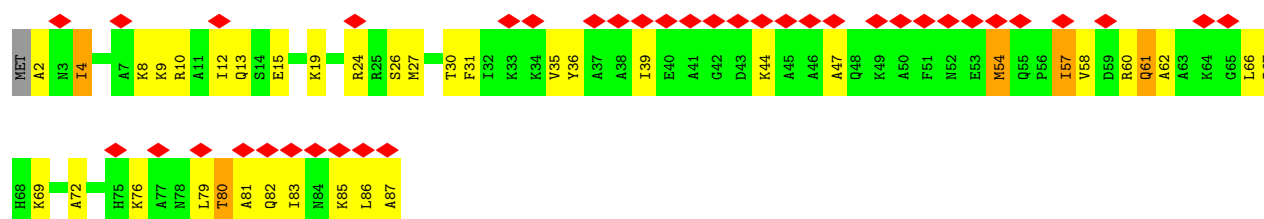
- Molecule 23: 30S ribosomal protein S18



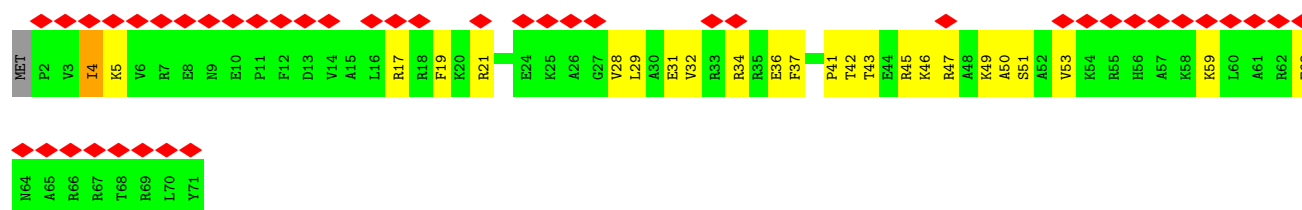
- Molecule 24: 30S ribosomal protein S19



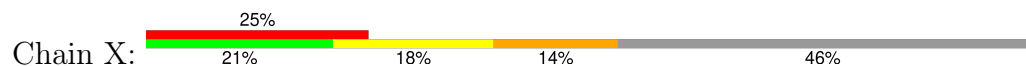
- Molecule 25: 30S ribosomal protein S20

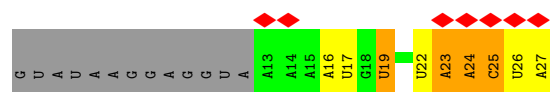


- Molecule 26: 30S ribosomal protein S21

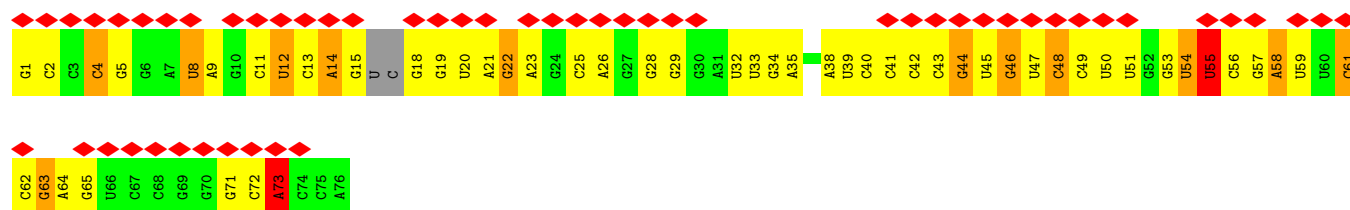


- Molecule 27: mRNA

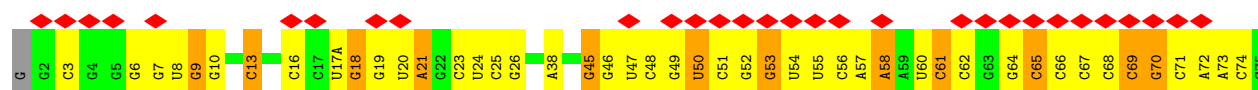




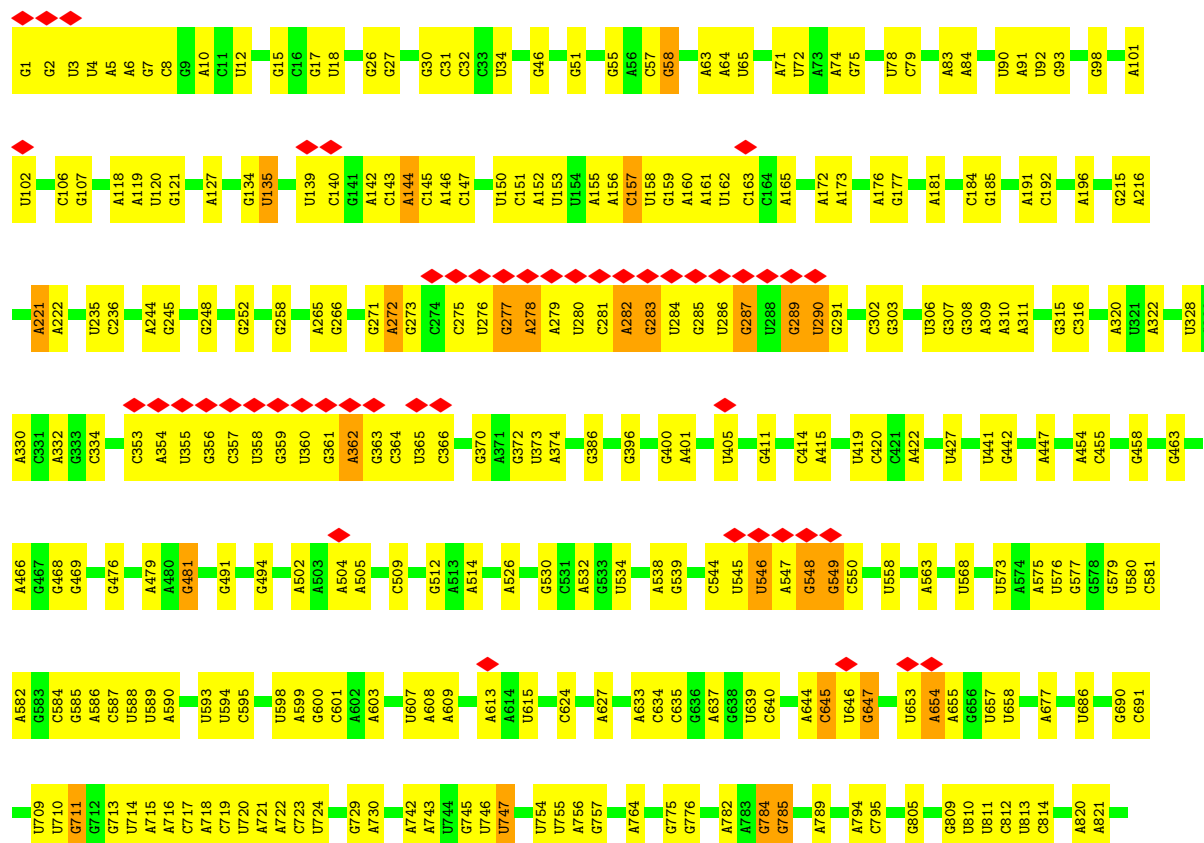
• Molecule 28: A-site oABZ-tRNAPhe

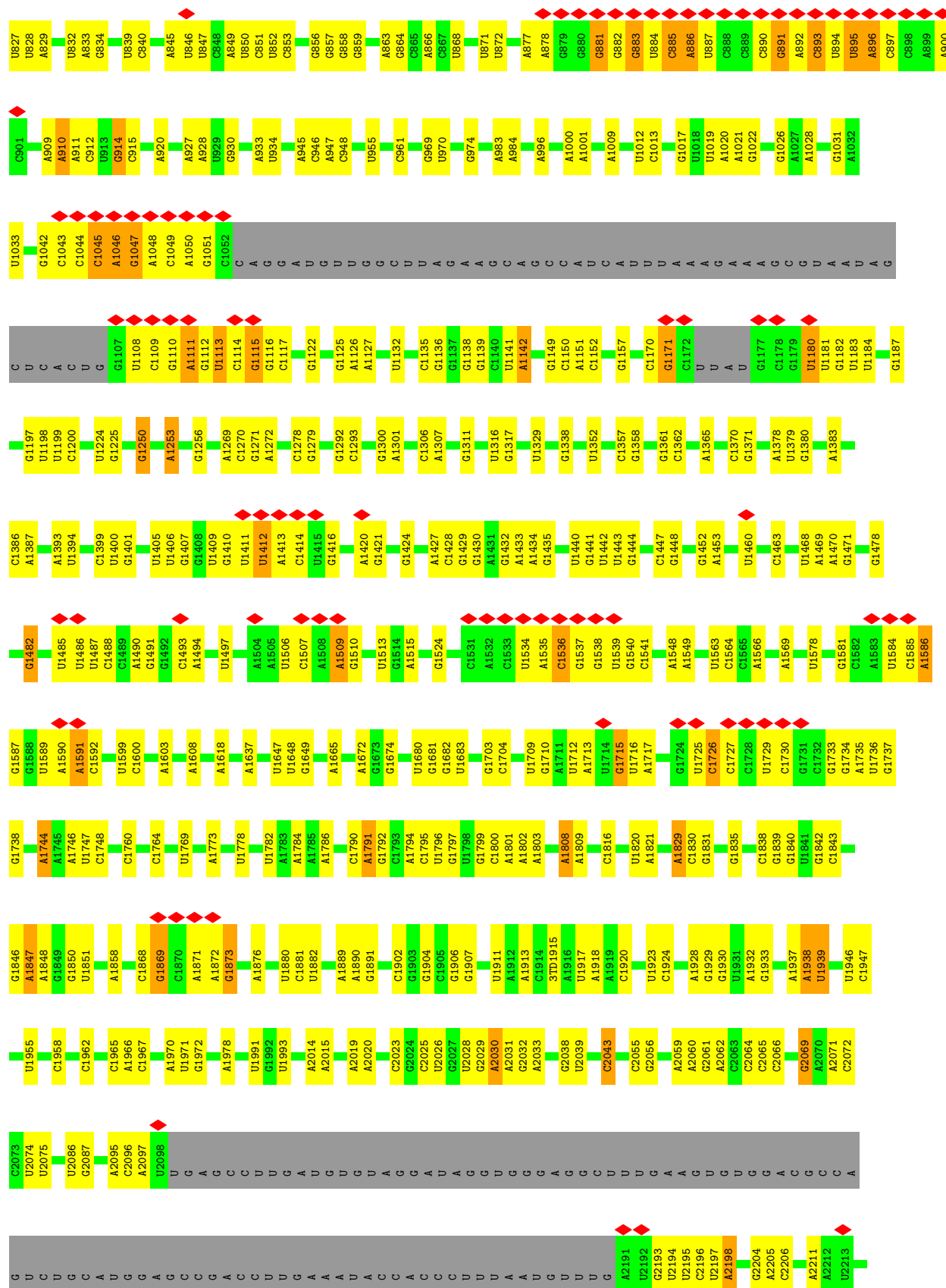


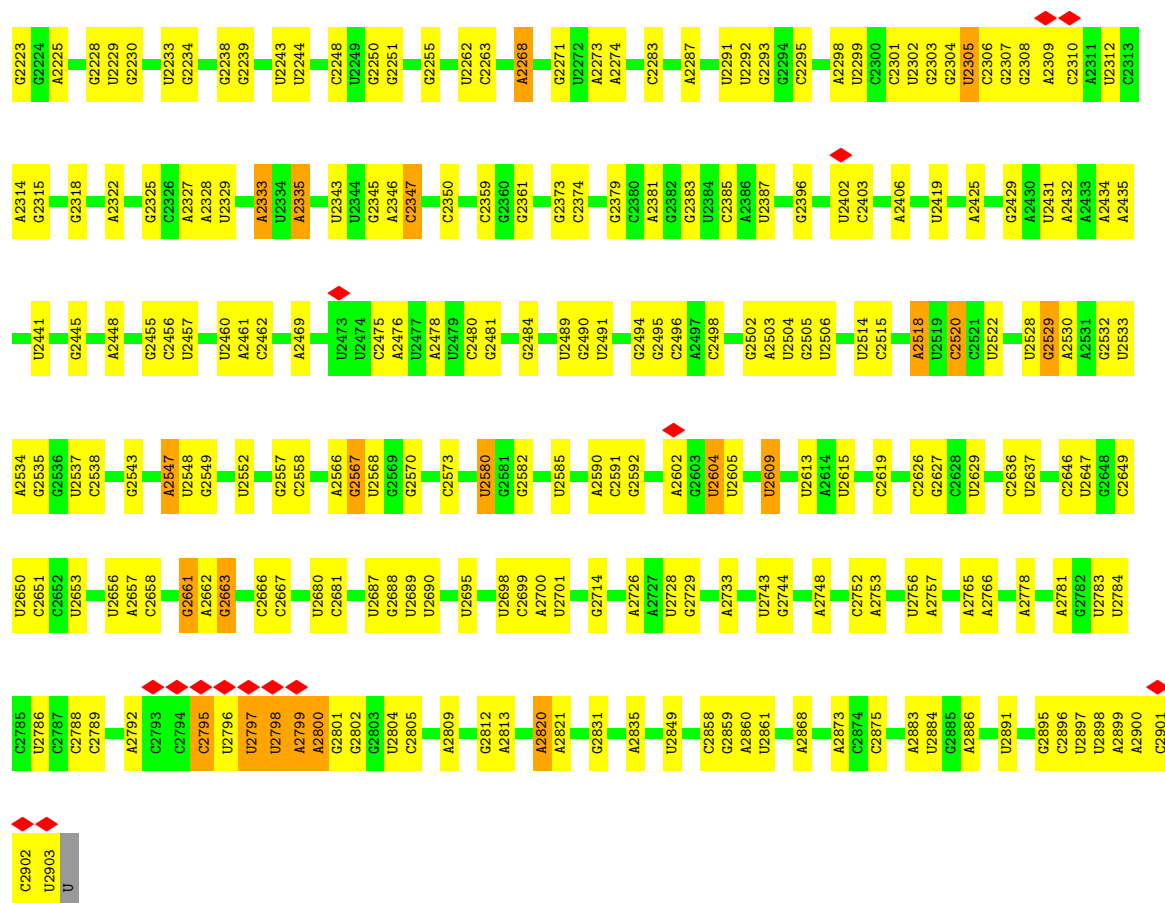
• Molecule 29: P-site fMet-tRNAfMet



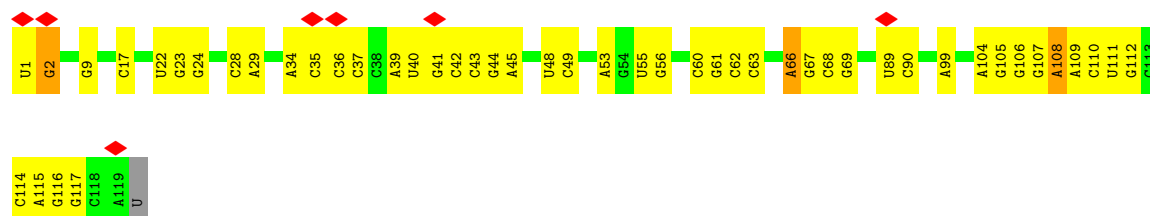
• Molecule 30: 23S rRNA



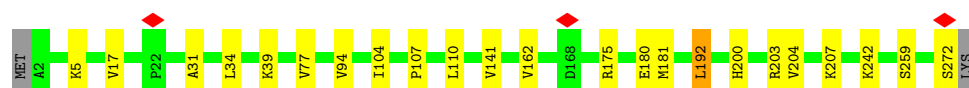
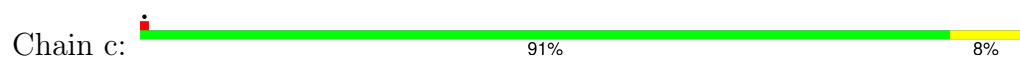




• Molecule 31: 5S rRNA

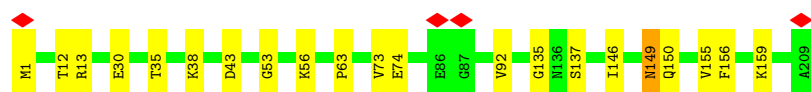


• Molecule 32: 50S ribosomal protein L2

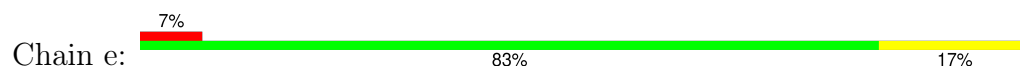


• Molecule 33: 50S ribosomal protein L3

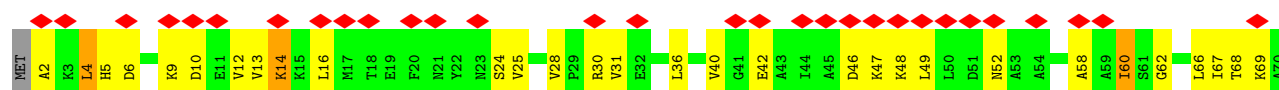




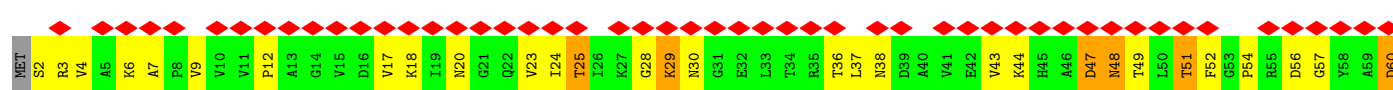
- Molecule 34: 50S ribosomal protein L4



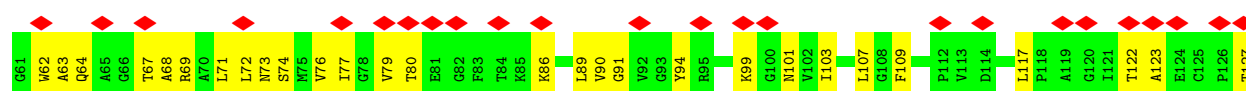
- Molecule 35: 50S ribosomal protein L5



- Molecule 36: 50S ribosomal protein L6



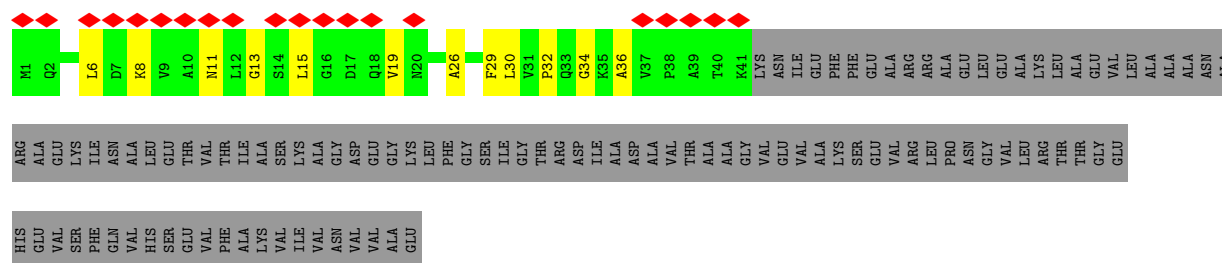
- Molecule 37: 50S ribosomal protein L9



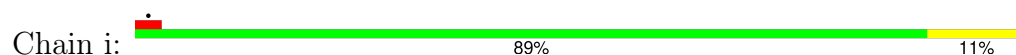
- Molecule 38: 50S ribosomal protein L10



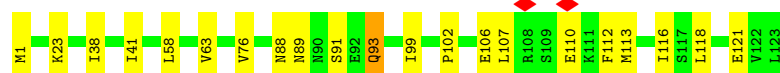
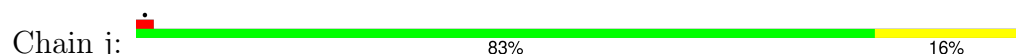
- Molecule 39: 50S ribosomal protein L11



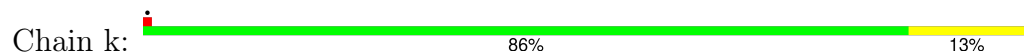
- Molecule 38: 50S ribosomal protein L13



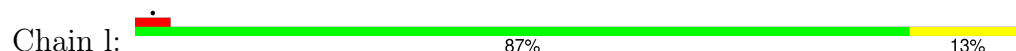
- Molecule 39: 50S ribosomal protein L14



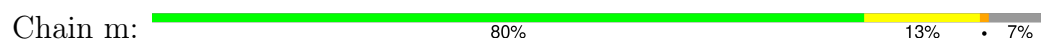
- Molecule 40: 50S ribosomal protein L15



- Molecule 41: 50S ribosomal protein L16



- Molecule 42: 50S ribosomal protein L17

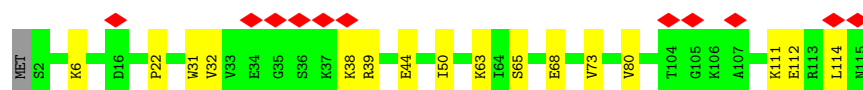
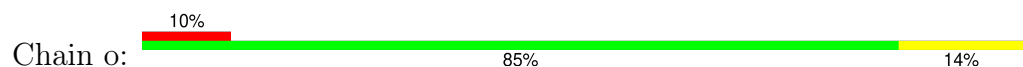


- Molecule 43: 50S ribosomal protein L18

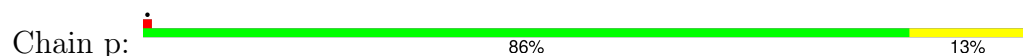




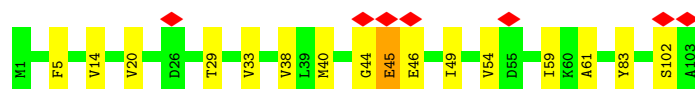
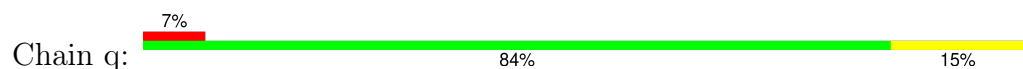
- Molecule 44: 50S ribosomal protein L19



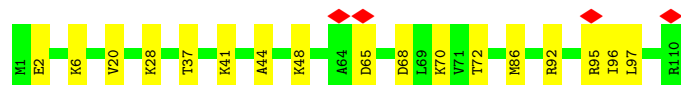
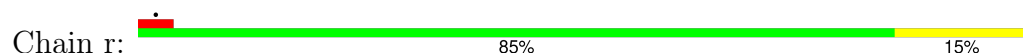
- Molecule 45: 50S ribosomal protein L20



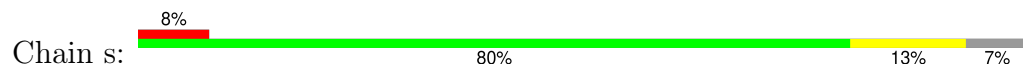
- Molecule 46: Ribosomal protein L21



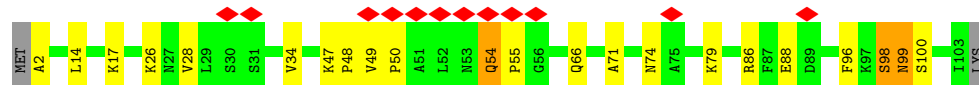
- Molecule 47: 50S ribosomal protein L22



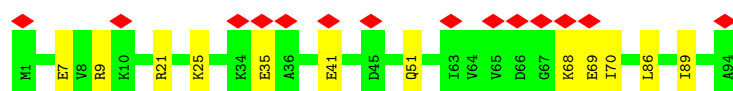
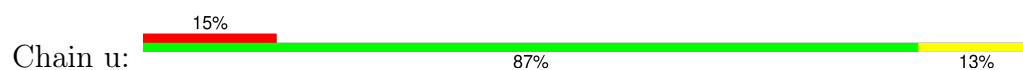
- Molecule 48: 50S ribosomal protein L23



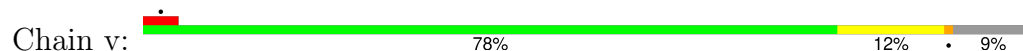
- Molecule 49: 50S ribosomal protein L24



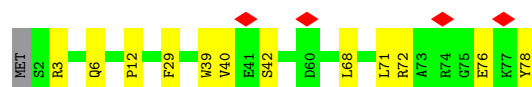
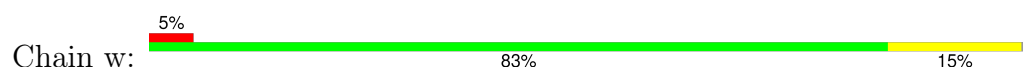
- Molecule 50: 50S ribosomal protein L25



- Molecule 51: 50S ribosomal protein L27



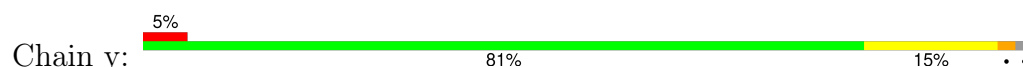
- Molecule 52: 50S ribosomal protein L28



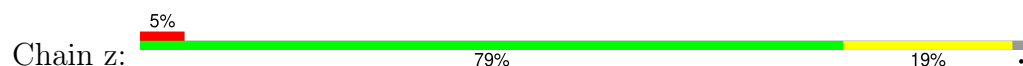
- Molecule 53: 50S ribosomal protein L29



- Molecule 54: 50S ribosomal protein L30



- Molecule 55: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	339543	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.218	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0169	Depositor
Map size (Å)	381.96478, 381.96478, 381.96478	wwPDB
Map dimensions	464, 464, 464	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8232, 0.8232, 0.8232	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, PAR, D2T, OMC, 4D4, 5MU, 3TD, OMG, MG, UR3, IAS, 5MC, FME, 1MG, 2MA, 2MG, K, 2AE, 4OC, PSU, ZN, 6MZ, MA6, MS6, SPD, MEQ, 8AN, OMU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.19	0/424	0.44	0/565
2	1	0.23	0/380	0.50	0/498
3	2	0.23	0/513	0.47	0/676
4	3	0.21	0/303	0.41	0/397
5	4	0.19	0/488	0.54	0/649
6	A	0.17	0/36236	0.36	0/56520
7	B	0.19	0/1784	0.51	0/2403
8	C	0.21	0/1651	0.49	0/2225
9	D	0.20	0/1665	0.53	0/2227
10	E	0.20	0/1165	0.48	0/1568
11	F	0.21	0/858	0.49	0/1160
12	G	0.20	0/1219	0.50	0/1635
13	H	0.19	0/989	0.51	0/1326
14	I	0.19	0/1034	0.55	0/1375
15	J	0.52	1/795 (0.1%)	0.66	4/1075 (0.4%)
16	K	0.19	0/884	0.44	0/1191
17	L	0.20	0/960	0.50	0/1286
18	M	0.22	0/900	0.58	0/1204
19	N	0.20	0/817	0.54	0/1088
20	O	0.18	0/722	0.48	0/964
21	P	0.21	0/653	0.51	0/877
22	Q	0.20	0/650	0.50	0/871
23	R	0.19	0/553	0.52	0/742
24	S	0.19	0/685	0.47	0/922
25	T	0.22	0/676	0.46	0/895
26	U	0.21	0/597	0.55	0/792
27	X	0.32	0/354	0.61	1/548 (0.2%)
28	Y	0.34	0/1763	0.61	6/2745 (0.2%)
29	Z	0.22	0/1788	0.45	1/2786 (0.0%)
30	a	0.24	0/65717	0.41	2/102515 (0.0%)
31	b	0.18	0/2850	0.34	0/4444

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.22	0/2121	0.47	0/2852
33	d	0.21	0/1576	0.45	0/2119
34	e	0.21	0/1571	0.47	0/2113
35	f	0.20	0/1434	0.52	0/1926
36	g	0.20	0/1343	0.57	0/1816
37	h	0.23	0/306	0.73	1/413 (0.2%)
38	i	0.21	0/1152	0.42	0/1551
39	j	0.23	0/955	0.46	0/1279
40	k	0.24	0/1062	0.54	0/1413
41	l	0.21	0/1073	0.43	0/1433
42	m	0.24	0/958	0.53	0/1281
43	n	0.20	0/902	0.54	0/1209
44	o	0.24	0/929	0.46	0/1242
45	p	0.23	0/960	0.47	0/1278
46	q	0.22	0/829	0.47	0/1107
47	r	0.24	0/864	0.46	0/1156
48	s	0.21	0/744	0.45	0/994
49	t	0.22	0/787	0.56	0/1051
50	u	0.20	0/766	0.46	0/1025
51	v	0.40	1/589 (0.2%)	0.48	0/780
52	w	0.23	0/635	0.48	0/848
53	x	0.17	0/502	0.49	0/667
54	y	0.21	0/453	0.50	0/605
55	z	0.22	0/450	0.48	0/599
All	All	0.22	2/153034 (0.0%)	0.42	15/228926 (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
3	2	0	1
18	M	0	1
36	g	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	J	31	ARG	N-CA	-12.61	1.29	1.46
51	v	9	SER	C-N	7.10	1.43	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	Z	72	A	P-O3'-C3'	-8.04	108.13	120.20
30	a	2064	C	P-O3'-C3'	-7.12	109.52	120.20
30	a	2549	G	P-O3'-C3'	-6.88	109.87	120.20
28	Y	13	C	P-O3'-C3'	-6.79	110.01	120.20
37	h	13	GLY	N-CA-C	6.63	120.43	110.75
15	J	30	LYS	O-C-N	-6.37	112.22	122.41
28	Y	55	U	P-O3'-C3'	-5.91	111.34	120.20
28	Y	54	U	P-O3'-C3'	-5.86	111.41	120.20
15	J	31	ARG	N-CA-C	5.70	119.33	112.38
27	X	19	U	P-O3'-C3'	-5.43	112.06	120.20
28	Y	73	A	P-O3'-C3'	-5.41	112.08	120.20
15	J	30	LYS	CA-C-N	5.04	128.67	120.60
15	J	30	LYS	C-N-CA	5.04	128.67	120.60
28	Y	12	U	P-O3'-C3'	-5.03	112.65	120.20
28	Y	71	G	P-O3'-C3'	-5.00	112.69	120.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	31	HIS	Peptide
18	M	104	THR	Peptide
36	g	47	ASP	Peptide
36	g	48	ASN	Peptide

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	0	417	0	451	7	0
2	1	377	0	418	3	0
3	2	504	0	572	5	0
4	3	302	0	340	4	0
5	4	480	0	478	23	0
6	A	32612	0	16432	671	0
7	B	1753	0	1780	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	1624	0	1696	74	0
9	D	1643	0	1707	62	0
10	E	1152	0	1196	43	0
11	F	839	0	833	27	0
12	G	1203	0	1254	37	0
13	H	979	0	1031	31	0
14	I	1022	0	1070	64	0
15	J	785	0	826	40	0
16	K	877	0	883	31	0
17	L	957	0	1017	22	0
18	M	891	0	952	36	0
19	N	805	0	844	38	0
20	O	714	0	734	19	0
21	P	643	0	661	22	0
22	Q	641	0	682	24	0
23	R	544	0	565	23	0
24	S	668	0	693	46	0
25	T	670	0	719	28	0
26	U	589	0	629	18	0
27	X	317	0	161	9	0
28	Y	1578	0	800	46	0
29	Z	1601	0	813	34	0
30	a	59170	0	29783	548	0
31	b	2549	0	1291	29	0
32	c	2082	0	2154	12	0
33	d	1566	0	1618	18	0
34	e	1552	0	1619	26	0
35	f	1410	0	1444	67	0
36	g	1323	0	1371	44	0
37	h	303	0	327	8	0
38	i	1129	0	1162	9	0
39	j	946	0	1023	16	0
40	k	1053	0	1129	13	0
41	l	1075	0	1146	11	0
42	m	945	0	989	10	0
43	n	892	0	923	14	0
44	o	917	0	962	9	0
45	p	947	0	1019	14	0
46	q	816	0	839	8	0
47	r	857	0	922	12	0
48	s	738	0	807	6	0
49	t	779	0	831	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	u	753	0	780	5	0
51	v	582	0	593	8	0
52	w	625	0	652	7	0
53	x	501	0	531	9	0
54	y	449	0	488	7	0
55	z	444	0	458	9	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
57	A	42	0	45	2	0
58	A	89	0	0	0	0
58	M	1	0	0	0	0
58	O	1	0	0	0	0
58	X	1	0	0	0	0
58	Z	1	0	0	0	0
58	a	217	0	0	0	0
58	b	5	0	0	0	0
58	c	1	0	0	0	0
58	d	1	0	0	0	0
58	m	1	0	0	0	0
58	p	1	0	0	0	0
58	z	1	0	0	0	0
59	Y	10	0	7	0	0
60	Z	22	0	12	1	0
61	Z	10	0	10	0	0
62	a	13	0	0	1	0
62	c	1	0	0	0	0
63	a	70	0	133	6	0
63	d	10	0	18	13	0
64	1	16	0	0	0	0
64	2	19	0	0	0	0
64	3	2	0	0	0	0
64	A	10	0	0	0	0
64	a	3197	0	0	35	0
64	b	41	0	0	0	0
64	c	86	0	0	0	0
64	d	34	0	0	0	0
64	e	34	0	0	0	0
64	h	1	0	0	0	0
64	i	14	0	0	0	0
64	j	11	0	0	0	0
64	k	32	0	0	0	0
64	l	22	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	m	20	0	0	0	0
64	o	8	0	0	0	0
64	p	16	0	0	1	0
64	q	15	0	0	0	0
64	r	25	0	0	1	0
64	s	6	0	0	0	0
64	t	1	0	0	0	0
64	u	4	0	0	0	0
64	v	11	0	0	0	0
64	w	7	0	0	0	0
64	x	1	0	0	1	0
64	y	2	0	0	0	0
64	z	24	0	0	0	0
All	All	145749	0	95323	2240	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 10.

All (2240) 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)
33:d:135:GLY:O	63:d:301:SPD:N10	1.60	1.34
62:a:6214:K:K	64:a:9425:HOH:O	1.65	1.06
28:Y:19:G:C2	30:a:896:A:C6	2.43	1.06
6:A:458:U:H3	6:A:474:G:H1	1.09	0.99
28:Y:19:G:N3	30:a:896:A:C6	2.32	0.97
28:Y:19:G:N2	30:a:896:A:C5	2.33	0.96
29:Z:50:U:H3	29:Z:64:G:H1	1.01	0.94
6:A:1009:U:H3	6:A:1020:G:H1	1.10	0.91
30:a:2096:C:O2	30:a:2193:G:N2	2.04	0.90
35:f:142:ASP:HB3	35:f:145:LYS:HG2	1.54	0.90
30:a:1868:C:O2	30:a:1873:G:N2	2.06	0.88
9:D:11:LEU:HD23	9:D:63:ARG:HE	1.39	0.88
25:T:39:ILE:HD11	25:T:83:ILE:HG13	1.56	0.88
30:a:1045:C:O2	30:a:1111:A:N6	2.08	0.86
12:G:27:VAL:HG11	12:G:40:GLU:HG2	1.56	0.86
6:A:1318:A:H5''	24:S:3:ARG:HH12	1.39	0.86
28:Y:51:U:H3	28:Y:63:G:H1	1.24	0.85
33:d:135:GLY:O	63:d:301:SPD:C9	2.24	0.85
28:Y:19:G:C4	30:a:896:A:N6	2.45	0.84
6:A:677:U:H3	6:A:713:G:H22	1.24	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:18:CYS:SG	5:4:40:CYS:HB3	2.19	0.83
28:Y:19:G:C2	30:a:896:A:C5	2.66	0.82
9:D:172:GLU:HG3	9:D:183:LYS:HD2	1.60	0.82
30:a:2518:A:OP2	63:a:6212:SPD:N1	2.12	0.82
30:a:284:U:H3	30:a:356:G:H1	1.28	0.82
24:S:50:ALA:HB1	24:S:57:HIS:HB3	1.60	0.81
30:a:2658:C:O2	30:a:2663:G:N2	2.14	0.81
5:4:63:ARG:NH2	6:A:1312:G:OP2	2.13	0.80
30:a:1047:G:HO2'	30:a:1110:G:H1	0.84	0.80
6:A:107:G:N7	25:T:10:ARG:NH2	2.29	0.80
30:a:2658:C:N3	30:a:2663:G:N1	2.25	0.80
35:f:69:LYS:HA	35:f:84:PRO:HA	1.63	0.80
6:A:673:A:H2'	6:A:674:G:C8	2.17	0.80
30:a:283:G:N2	30:a:357:C:O2	2.15	0.79
6:A:492:C:H2'	6:A:493:A:C8	2.17	0.79
9:D:15:GLU:OE2	9:D:63:ARG:NH1	2.16	0.79
7:B:167:ASP:O	7:B:170:HIS:ND1	2.16	0.78
6:A:1032:G:H2'	6:A:1033:G:H4'	1.64	0.78
6:A:979:C:O2	19:N:59:ARG:NH1	2.16	0.78
12:G:130:ASN:HA	12:G:135:VAL:HG21	1.65	0.77
6:A:1009:U:O2	6:A:1020:G:N2	2.18	0.77
35:f:74:VAL:HB	35:f:79:ILE:HG12	1.67	0.76
63:a:6208:SPD:N1	64:a:6307:HOH:O	2.16	0.76
15:J:7:ARG:HB2	15:J:101:SER:HB2	1.67	0.76
28:Y:19:G:C2	30:a:896:A:N6	2.54	0.75
28:Y:4:C:H2'	28:Y:5:G:H8	1.50	0.75
35:f:134:GLU:HG2	35:f:136:ILE:HG22	1.69	0.75
10:E:81:LEU:HD12	10:E:147:MET:HE1	1.67	0.75
30:a:215:G:OP2	64:a:6303:HOH:O	2.05	0.74
11:F:93:LYS:H	11:F:93:LYS:HD3	1.50	0.74
35:f:129:SER:HB3	35:f:155:THR:HG23	1.68	0.74
30:a:370:G:OP2	64:a:6302:HOH:O	2.03	0.74
6:A:946:A:H2'	6:A:947:G:C8	2.21	0.74
8:C:35:SER:OG	8:C:59:ARG:NH2	2.20	0.74
18:M:23:TYR:HB3	18:M:66:GLU:HG2	1.69	0.74
33:d:135:GLY:C	63:d:301:SPD:N10	2.44	0.74
6:A:1127:G:H1	6:A:1145:A:H61	1.36	0.74
19:N:24:ARG:NH1	19:N:55:SER:OG	2.21	0.73
19:N:46:LEU:HA	19:N:49:GLN:HG3	1.69	0.73
30:a:2532:G:O2'	30:a:2657:A:N1	2.21	0.73
30:a:2255:G:H21	51:v:9:SER:HB2	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:324:G:N1	6:A:327:A:OP2	2.22	0.72
28:Y:26:A:H61	28:Y:44:G:H1	1.33	0.72
28:Y:53:G:H2'	28:Y:54:U:O4'	1.90	0.72
6:A:297:G:N2	6:A:300:A:OP2	2.22	0.72
6:A:1441:A:H62	6:A:1461:G:H21	1.35	0.72
6:A:358:U:H2'	6:A:359:G:H8	1.54	0.72
28:Y:15:G:H22	28:Y:48:C:H42	1.38	0.72
6:A:203:G:N2	6:A:204:G:O6	2.23	0.72
6:A:73:C:HO2'	6:A:74:A:H8	1.36	0.72
30:a:1534:U:O2'	30:a:1537:G:O6	2.04	0.72
30:a:2255:G:N2	51:v:9:SER:HB2	2.05	0.71
15:J:8:ILE:HD11	15:J:76:ILE:HG12	1.71	0.71
6:A:143:A:H5'	6:A:144:G:H5'	1.72	0.71
30:a:1868:C:N3	30:a:1873:G:N1	2.30	0.71
12:G:113:ASP:HB2	12:G:119:ARG:HG3	1.73	0.71
8:C:127:ARG:HH12	8:C:191:THR:HB	1.55	0.71
36:g:89:LEU:HD23	36:g:94:TYR:HB3	1.71	0.71
17:L:46:ASN:ND2	17:L:89:D2T:SB	2.64	0.71
27:X:24:A:H5''	27:X:25:C:H6	1.56	0.71
6:A:1349:A:H5''	14:I:123:ARG:HG2	1.71	0.70
7:B:43:LEU:HA	7:B:46:THR:HG22	1.72	0.70
10:E:25:VAL:HG23	10:E:27:GLY:H	1.56	0.70
23:R:36:SER:HA	23:R:72:ASP:HB3	1.72	0.70
6:A:455:G:H2'	6:A:456:A:C8	2.26	0.70
6:A:1347:G:O6	14:I:12:ARG:NH2	2.24	0.70
6:A:147:G:H2'	6:A:148:G:C8	2.26	0.70
15:J:52:LEU:HB2	19:N:81:ARG:HD2	1.73	0.70
30:a:155:A:H2'	30:a:156:A:C8	2.27	0.70
30:a:1799:G:O2'	32:c:180:GLU:OE2	2.09	0.70
11:F:63:ASN:HD22	11:F:96:VAL:HB	1.56	0.70
20:O:26:GLU:OE1	20:O:77:ARG:NH2	2.25	0.70
30:a:945:A:H1'	63:a:6211:SPD:H81	1.73	0.70
6:A:1124:G:H5''	15:J:37:ARG:HG3	1.72	0.70
35:f:136:ILE:HG12	35:f:143:TYR:HD1	1.55	0.70
30:a:1434:A:H2'	30:a:1435:G:C8	2.25	0.70
31:b:66:A:OP2	31:b:108:A:N6	2.24	0.70
6:A:600:A:H2'	6:A:601:G:H8	1.57	0.70
22:Q:9:GLN:NE2	22:Q:59:VAL:O	2.25	0.70
24:S:11:ILE:HD11	24:S:15:LEU:HD12	1.73	0.70
6:A:6:G:H1	10:E:103:THR:HG21	1.55	0.69
12:G:4:ARG:HB3	12:G:6:VAL:HG23	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:823:C:HO2'	13:H:2:SER:N	1.88	0.69
30:a:422:A:OP2	64:a:6302:HOH:O	2.09	0.69
18:M:71:ARG:HH12	35:f:113:ASP:HB3	1.57	0.69
32:c:31:ALA:HA	32:c:34:LEU:HD12	1.74	0.69
6:A:181:A:N6	6:A:195:A:OP2	2.26	0.69
14:I:20:PHE:HB2	14:I:64:TYR:HB3	1.74	0.69
6:A:458:U:O2	6:A:474:G:N2	2.21	0.69
30:a:568:U:H1'	30:a:2030:6MZ:H9C1	1.74	0.69
30:a:2529:G:H4'	36:g:175:LYS:HD3	1.74	0.69
29:Z:51:C:H2'	29:Z:52:G:C8	2.26	0.69
17:L:86:ARG:HA	17:L:94:ARG:HA	1.75	0.69
19:N:3:LYS:HB2	19:N:6:MET:HG2	1.75	0.69
30:a:283:G:N1	30:a:357:C:N3	2.35	0.69
15:J:54:SER:O	19:N:81:ARG:NH1	2.25	0.69
30:a:2609:U:OP1	63:d:301:SPD:N1	2.26	0.68
30:a:252:G:N7	64:a:6333:HOH:O	2.26	0.68
7:B:46:THR:HB	7:B:201:PRO:HG2	1.76	0.68
25:T:10:ARG:HD3	25:T:13:GLN:HE21	1.57	0.68
28:Y:72:C:H2'	28:Y:73:A:C8	2.27	0.68
30:a:2580:PSU:H5'	63:d:301:SPD:N10	2.09	0.68
6:A:1323:G:H2'	6:A:1324:A:H8	1.58	0.68
36:g:12:PRO:HG2	36:g:80:THR:HG21	1.74	0.68
42:m:30:ARG:NH1	42:m:74:GLU:OE1	2.26	0.68
16:K:89:PRO:HB3	26:U:32:VAL:HG21	1.75	0.68
6:A:539:A:OP2	17:L:112:GLN:NE2	2.27	0.68
35:f:28:VAL:O	35:f:30:ARG:NH1	2.27	0.68
6:A:1238:A:OP1	6:A:1335:U:O2'	2.12	0.68
19:N:79:LEU:HB2	19:N:84:VAL:HG23	1.75	0.68
6:A:993:G:H22	6:A:996:A:H62	1.42	0.67
20:O:17:ARG:HH11	20:O:18:ASP:HB3	1.58	0.67
39:j:102:PRO:HD2	44:o:68:GLU:HG3	1.76	0.67
50:u:9:ARG:HG2	50:u:41:GLU:HG2	1.75	0.67
16:K:20:VAL:HG22	16:K:83:GLU:HB2	1.75	0.67
30:a:1932:A:OP2	64:a:6304:HOH:O	2.11	0.67
30:a:2291:U:H2'	30:a:2292:U:C6	2.29	0.67
35:f:111:ILE:HG12	35:f:137:ILE:HG21	1.76	0.67
12:G:116:MET:HA	12:G:119:ARG:HE	1.59	0.67
20:O:43:PHE:HB3	20:O:53:ARG:HH21	1.59	0.67
30:a:549:G:H2'	30:a:550:C:C6	2.30	0.67
31:b:1:U:H2'	31:b:2:G:C8	2.30	0.67
6:A:1157:A:H61	6:A:1178:G:H1'	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:23:ILE:HG21	16:K:96:THR:HG21	1.77	0.67
28:Y:4:C:H2'	28:Y:5:G:C8	2.28	0.67
28:Y:19:G:N3	30:a:896:A:N6	2.41	0.67
30:a:892:A:H2'	30:a:893:C:C6	2.29	0.67
35:f:36:LEU:HB2	35:f:89:VAL:HG23	1.76	0.67
6:A:553:A:H5''	17:L:21:VAL:HG21	1.76	0.67
18:M:64:VAL:HG13	18:M:68:ASP:HB3	1.76	0.67
28:Y:43:C:H2'	28:Y:44:G:C8	2.29	0.67
30:a:258:G:N7	64:a:6341:HOH:O	2.27	0.67
9:D:105:MET:HG3	9:D:171:LEU:HD13	1.77	0.67
13:H:22:LYS:O	13:H:65:TYR:OH	2.12	0.67
45:p:11:ARG:NH1	64:p:301:HOH:O	2.26	0.67
30:a:1478:G:H1	30:a:1513:U:H3	1.41	0.67
8:C:151:VAL:HG22	8:C:200:VAL:HG22	1.76	0.66
8:C:28:GLU:OE1	8:C:32:ASN:ND2	2.28	0.66
24:S:32:ARG:HE	24:S:57:HIS:CD2	2.13	0.66
9:D:56:ARG:HH21	9:D:63:ARG:HH12	1.42	0.66
30:a:2432:A:OP2	64:a:6306:HOH:O	2.13	0.66
7:B:6:MET:HE3	7:B:43:LEU:HB2	1.75	0.66
9:D:26:ARG:HH21	9:D:31:LYS:HZ3	1.43	0.66
30:a:2543:G:OP2	64:a:6305:HOH:O	2.12	0.66
6:A:6:G:H4'	6:A:298:A:H4'	1.77	0.66
6:A:155:A:H2'	6:A:156:C:C6	2.30	0.66
53:x:9:LYS:O	64:x:101:HOH:O	2.14	0.66
12:G:91:VAL:HG12	12:G:95:ARG:HB3	1.78	0.66
30:a:401:A:N1	64:a:6351:HOH:O	2.29	0.66
33:d:137:SER:OG	63:d:301:SPD:H92	1.94	0.66
12:G:119:ARG:O	12:G:123:GLU:HB2	1.96	0.66
6:A:235:C:H2'	6:A:236:A:C8	2.30	0.66
6:A:268:U:H2'	6:A:269:C:C6	2.30	0.66
30:a:549:G:H2'	30:a:550:C:H6	1.61	0.66
30:a:920:A:OP1	54:y:19:LYS:NZ	2.29	0.66
6:A:489:C:H2'	6:A:490:C:C6	2.31	0.65
9:D:91:LEU:HD12	9:D:188:ARG:HD3	1.77	0.65
30:a:494:G:H4'	47:r:6:LYS:HB2	1.78	0.65
6:A:216:U:H2'	6:A:217:C:C6	2.31	0.65
9:D:91:LEU:HG	9:D:197:GLU:HG3	1.78	0.65
6:A:1380:U:O2'	12:G:3:ARG:NH1	2.28	0.65
6:A:167:A:H2'	6:A:168:G:H8	1.62	0.65
6:A:269:C:H2'	6:A:270:A:H8	1.61	0.65
28:Y:18:G:H1	28:Y:55:U:H1'	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:f:47:LYS:NZ	35:f:84:PRO:HG2	2.11	0.65
39:j:121:GLU:OE1	44:o:65:SER:OG	2.15	0.65
6:A:692:U:O2'	6:A:694:A:N7	2.26	0.65
30:a:2096:C:H2'	30:a:2097:A:C8	2.31	0.65
30:a:2495:G:N7	64:a:6347:HOH:O	2.28	0.65
37:h:26:ALA:HA	37:h:30:LEU:HB2	1.77	0.65
30:a:358:U:H2'	30:a:359:G:H8	1.61	0.65
6:A:259:G:OP1	25:T:36:TYR:OH	2.15	0.65
6:A:337:G:H2'	6:A:338:A:C8	2.32	0.65
7:B:138:THR:O	7:B:142:GLU:HG3	1.97	0.65
30:a:1434:A:H2'	30:a:1435:G:H8	1.61	0.65
6:A:1402:4OC:HM22	6:A:1403:C:H5'	1.78	0.64
30:a:46:G:OP2	64:a:6303:HOH:O	2.15	0.64
30:a:2886:A:N1	64:a:6352:HOH:O	2.29	0.64
51:v:25:ARG:HH11	51:v:31:VAL:HG12	1.61	0.64
6:A:1318:A:H5''	24:S:3:ARG:NH1	2.12	0.64
29:Z:18:G:N2	29:Z:58:A:OP2	2.30	0.64
31:b:48:U:H2'	31:b:49:C:C6	2.33	0.64
6:A:56:U:H2'	6:A:57:G:C8	2.32	0.64
7:B:67:ILE:HD13	7:B:160:ALA:HB3	1.80	0.64
6:A:713:G:H2'	6:A:714:G:C8	2.33	0.64
20:O:17:ARG:NH1	20:O:18:ASP:HB3	2.13	0.64
24:S:36:ARG:NH1	24:S:52:HIS:O	2.28	0.64
30:a:639:U:H2'	30:a:640:C:C6	2.32	0.64
6:A:405:U:O4	9:D:2:ALA:N	2.30	0.64
13:H:104:VAL:HG22	13:H:125:ILE:HD13	1.80	0.64
29:Z:9:G:H21	29:Z:45:G:H3'	1.62	0.64
6:A:253:A:OP1	22:Q:69:LYS:NZ	2.31	0.63
6:A:701:U:OP1	6:A:702:A:O2'	2.11	0.63
30:a:585:G:N7	45:p:6:ARG:NH1	2.43	0.63
16:K:52:PHE:HB3	16:K:56:ARG:HB2	1.79	0.63
47:r:41:LYS:HZ1	55:z:22:LEU:HD11	1.64	0.63
9:D:60:LYS:O	9:D:64:ILE:HG13	1.98	0.63
51:v:59:LEU:HD12	51:v:80:ILE:HD12	1.79	0.63
6:A:1162:C:H2'	6:A:1163:A:H8	1.62	0.63
6:A:147:G:H2'	6:A:148:G:H8	1.64	0.63
6:A:1397:C:OP2	10:E:29:ARG:NH2	2.31	0.63
29:Z:66:C:H2'	29:Z:67:C:C6	2.33	0.63
47:r:28:LYS:HD2	47:r:70:LYS:HG2	1.79	0.63
9:D:62:ARG:HH21	9:D:68:LEU:HA	1.63	0.63
35:f:108:VAL:HG13	35:f:109:PRO:HD3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:y:6:LYS:HE3	54:y:37:GLU:HB2	1.80	0.63
6:A:201:G:H2'	6:A:202:G:C8	2.34	0.63
6:A:231:U:H2'	6:A:232:G:H8	1.64	0.63
30:a:594:U:H2'	30:a:595:C:C6	2.34	0.63
9:D:8:LYS:HG3	9:D:21:LEU:HD23	1.79	0.63
23:R:41:PRO:HB2	23:R:44:ILE:HG13	1.79	0.63
6:A:674:G:H2'	6:A:675:A:H8	1.64	0.63
6:A:1157:A:N6	6:A:1178:G:H1'	2.13	0.63
30:a:1939:5MU:OP1	30:a:2604:PSU:O2'	2.17	0.63
10:E:153:VAL:HA	10:E:156:LYS:HD2	1.79	0.62
28:Y:63:G:H2'	28:Y:64:A:C8	2.33	0.62
6:A:790:A:OP1	29:Z:38:A:O2'	2.17	0.62
29:Z:66:C:H2'	29:Z:67:C:H6	1.63	0.62
19:N:29:ALA:O	19:N:33:ASP:HB2	1.99	0.62
30:a:743:A:OP1	63:d:301:SPD:H82	1.99	0.62
30:a:2328:A:H2'	30:a:2329:U:C6	2.34	0.62
6:A:1062:U:H2'	6:A:1063:C:C6	2.35	0.62
6:A:1356:G:H2'	6:A:1357:A:C8	2.34	0.62
9:D:91:LEU:HD13	9:D:191:LEU:HD12	1.80	0.62
9:D:198:HIS:O	9:D:202:GLU:HG2	1.99	0.62
13:H:105:SER:HB2	13:H:126:ILE:HD11	1.81	0.62
30:a:2788:C:H2'	30:a:2789:C:C6	2.34	0.62
9:D:7:PRO:HB2	9:D:10:LYS:HG3	1.82	0.62
6:A:219:U:H2'	6:A:220:G:H8	1.65	0.62
6:A:867:G:O2'	6:A:873:A:N1	2.29	0.62
18:M:105:ASN:O	18:M:107:ARG:HD2	2.00	0.62
29:Z:51:C:H2'	29:Z:52:G:H8	1.64	0.62
6:A:1355:G:H2'	6:A:1356:G:H8	1.65	0.62
9:D:150:LYS:HZ1	9:D:178:MET:HB2	1.63	0.61
14:I:55:VAL:HG21	14:I:87:LEU:HD21	1.81	0.61
19:N:79:LEU:HD22	19:N:83:LYS:HB3	1.82	0.61
31:b:1:U:H2'	31:b:2:G:H8	1.63	0.61
47:r:37:THR:OG1	47:r:48:LYS:NZ	2.31	0.61
6:A:17:U:H2'	6:A:18:C:C6	2.35	0.61
6:A:334:C:HO2'	6:A:1434:A:HO2'	1.46	0.61
6:A:1027:C:H2'	6:A:1028:C:C6	2.35	0.61
30:a:711:G:H1	30:a:720:U:H3	1.46	0.61
30:a:2728:U:HO2'	30:a:2729:G:H8	1.48	0.61
6:A:1162:C:H2'	6:A:1163:A:C8	2.36	0.61
6:A:1323:G:H2'	6:A:1324:A:C8	2.35	0.61
30:a:1250:G:H5''	45:p:6:ARG:HD3	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:115:SER:O	12:G:119:ARG:NE	2.34	0.61
15:J:11:LYS:HB2	15:J:97:ASP:HB2	1.81	0.61
6:A:600:A:H2'	6:A:601:G:C8	2.35	0.61
6:A:976:G:OP2	6:A:1358:U:O2'	2.18	0.61
6:A:1149:C:H2'	6:A:1150:A:C8	2.35	0.61
8:C:69:HIS:HB3	8:C:106:VAL:HG23	1.81	0.61
25:T:44:LYS:HE3	25:T:87:ALA:HB2	1.82	0.61
28:Y:58:A:O2'	28:Y:61:C:N4	2.33	0.61
6:A:235:C:H2'	6:A:236:A:H8	1.64	0.61
14:I:52:LEU:O	14:I:56:ASP:N	2.33	0.61
30:a:362:A:H3'	30:a:363:G:H8	1.66	0.61
33:d:35:THR:HG22	33:d:73:VAL:HG21	1.81	0.61
30:a:2431:U:OP1	64:a:6306:HOH:O	2.15	0.61
6:A:299:G:H2'	6:A:300:A:C8	2.36	0.61
29:Z:18:G:H21	29:Z:58:A:H5'	1.64	0.61
30:a:1412:U:H2'	30:a:1413:A:H8	1.66	0.61
6:A:1367:C:OP2	14:I:114:LYS:NZ	2.27	0.61
34:e:51:GLU:OE1	34:e:88:ARG:NH1	2.33	0.61
6:A:859:G:H2'	6:A:860:A:C8	2.35	0.61
6:A:1095:U:H2'	6:A:1096:C:C6	2.34	0.61
30:a:2609:U:OP1	63:d:301:SPD:H21	2.01	0.61
6:A:157:U:H1'	6:A:165:G:N2	2.15	0.60
6:A:628:G:H2'	6:A:629:A:H8	1.66	0.60
30:a:155:A:H2'	30:a:156:A:H8	1.64	0.60
6:A:1345:U:OP1	14:I:122:ARG:NH1	2.34	0.60
8:C:100:GLN:NE2	8:C:102:ASN:OD1	2.33	0.60
10:E:13:GLU:OE2	10:E:68:ARG:NE	2.31	0.60
30:a:856:G:H2'	30:a:857:G:C8	2.36	0.60
30:a:1311:G:OP2	30:a:1311:G:N2	2.27	0.60
6:A:460:A:H2'	6:A:461:A:C8	2.36	0.60
9:D:48:LEU:HD21	9:D:56:ARG:HG3	1.83	0.60
33:d:135:GLY:O	63:d:301:SPD:H92	2.01	0.60
6:A:113:G:H1'	6:A:354:G:H5'	1.81	0.60
6:A:272:C:H2'	6:A:273:U:C6	2.37	0.60
6:A:362:G:N2	6:A:365:U:OP2	2.34	0.60
18:M:101:ARG:NE	18:M:104:THR:OG1	2.31	0.60
14:I:12:ARG:HG3	14:I:13:LYS:H	1.66	0.60
27:X:24:A:H5''	27:X:25:C:C6	2.34	0.60
30:a:1412:U:H2'	30:a:1413:A:C8	2.36	0.60
1:O:33:LYS:HD2	1:O:51:GLU:OE1	2.01	0.60
6:A:1218:C:H2'	6:A:1219:A:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1513:A:H2'	6:A:1514:G:C8	2.36	0.60
9:D:126:ASN:OD1	9:D:142:VAL:N	2.34	0.60
35:f:163:ASP:HB3	35:f:167:ARG:HH21	1.67	0.60
6:A:447:G:N2	6:A:487:A:H62	1.99	0.60
30:a:1126:A:H5''	63:a:6212:SPD:H102	1.66	0.60
31:b:66:A:H5'	31:b:108:A:H61	1.66	0.60
6:A:34:C:H2'	6:A:35:G:H8	1.67	0.60
6:A:1010:U:H2'	6:A:1011:C:C6	2.37	0.60
6:A:1287:A:H2'	6:A:1288:A:C8	2.35	0.60
6:A:1516:2MG:N2	6:A:1519:MA6:OP2	2.33	0.60
9:D:137:VAL:HG23	9:D:141:ASP:HB3	1.82	0.60
10:E:31:PHE:O	10:E:54:ARG:NH1	2.35	0.60
12:G:26:PHE:HZ	12:G:120:LEU:HD11	1.67	0.60
20:O:29:VAL:HG13	20:O:63:ARG:HG3	1.84	0.60
21:P:5:ARG:NH1	21:P:24:SER:HA	2.16	0.60
8:C:134:MET:O	8:C:138:VAL:HG23	2.02	0.59
16:K:67:ALA:HB2	16:K:96:THR:OG1	2.02	0.59
30:a:1386:C:H2'	30:a:1387:A:C8	2.36	0.59
5:4:41:HIS:HB3	5:4:44:PHE:HB2	1.84	0.59
6:A:628:G:H2'	6:A:629:A:C8	2.37	0.59
23:R:9:LYS:NZ	23:R:43:ARG:O	2.34	0.59
51:v:38:VAL:HG12	51:v:59:LEU:HB2	1.84	0.59
6:A:1040:U:H2'	6:A:1041:G:H8	1.66	0.59
14:I:84:THR:HG22	14:I:98:LEU:HD13	1.84	0.59
25:T:35:VAL:HG21	25:T:54:MET:HG2	1.83	0.59
30:a:1043:C:H2'	30:a:1044:C:O4'	2.03	0.59
1:0:13:SER:HB2	1:0:49:TYR:CZ	2.38	0.59
6:A:154:U:O4	6:A:155:A:N6	2.35	0.59
6:A:451:A:N6	6:A:481:G:H5'	2.17	0.59
6:A:1314:C:H2'	6:A:1315:U:C6	2.37	0.59
12:G:126:ASP:OD1	12:G:131:LYS:NZ	2.32	0.59
24:S:70:LYS:N	24:S:73:GLU:OE1	2.34	0.59
28:Y:15:G:N2	28:Y:48:C:H42	1.99	0.59
31:b:66:A:H61	31:b:107:G:H2'	1.67	0.59
6:A:1004:A:H2'	6:A:1005:A:O4'	2.02	0.59
8:C:110:GLU:HG3	8:C:140:ASN:HB3	1.85	0.59
11:F:8:PHE:HA	11:F:87:SER:HA	1.85	0.59
19:N:4:GLN:HA	19:N:7:LYS:HD2	1.83	0.59
30:a:593:U:H2'	30:a:594:U:C6	2.38	0.59
12:G:25:LYS:HB3	12:G:101:MET:HE1	1.85	0.59
7:B:223:GLU:O	7:B:227:GLN:HG3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:27:MET:HE1	13:H:61:LEU:HD12	1.85	0.59
28:Y:39:U:H2'	28:Y:40:C:C6	2.38	0.59
30:a:2796:U:H3	30:a:2799:A:H61	1.50	0.59
36:g:7:ALA:O	36:g:69:ARG:NE	2.36	0.59
6:A:358:U:H2'	6:A:359:G:C8	2.36	0.59
6:A:745:G:H2'	6:A:746:A:C8	2.37	0.59
10:E:74:VAL:HG11	10:E:144:LEU:HD22	1.85	0.59
30:a:1136:G:N7	64:a:6371:HOH:O	2.32	0.59
31:b:48:U:OP1	43:n:30:ARG:NH2	2.36	0.58
35:f:13:VAL:HG13	35:f:14:LYS:HD2	1.84	0.58
39:j:91:SER:OG	39:j:93:GLN:NE2	2.36	0.58
44:o:111:LYS:NZ	44:o:112:GLU:O	2.36	0.58
50:u:68:LYS:HE2	50:u:70:ILE:HG12	1.85	0.58
6:A:1196:A:O4'	27:X:24:A:N6	2.36	0.58
26:U:46:LYS:HG2	26:U:47:ARG:HH21	1.68	0.58
34:e:21:ARG:HD3	34:e:106:LYS:HB3	1.83	0.58
6:A:452:A:H2'	6:A:453:G:O4'	2.03	0.58
6:A:546:A:P	9:D:69:GLU:HB2	2.43	0.58
11:F:63:ASN:ND2	11:F:96:VAL:HB	2.18	0.58
14:I:75:GLN:O	14:I:79:ILE:HG12	2.04	0.58
24:S:32:ARG:HA	24:S:50:ALA:HB3	1.84	0.58
36:g:60:ASP:OD1	36:g:60:ASP:N	2.31	0.58
49:t:47:LYS:HG3	49:t:48:PRO:HD2	1.85	0.58
6:A:335:C:H2'	6:A:336:A:H8	1.67	0.58
6:A:461:A:H2'	6:A:462:G:H8	1.67	0.58
6:A:515:G:H2'	6:A:516:PSU:H6	1.67	0.58
30:a:12:U:O2	30:a:2626:C:H4'	2.02	0.58
6:A:68:G:H21	6:A:152:A:H1'	1.68	0.58
6:A:1245:C:H2'	6:A:1246:A:C8	2.38	0.58
8:C:72:ARG:HB3	8:C:75:ILE:HD11	1.84	0.58
30:a:2205:A:H2'	30:a:2206:C:C6	2.38	0.58
21:P:5:ARG:HH12	21:P:24:SER:HA	1.68	0.58
30:a:414:C:H2'	30:a:415:A:C8	2.39	0.58
34:e:168:ASP:OD2	34:e:170:ARG:NE	2.36	0.58
30:a:871:U:H2'	30:a:872:U:C6	2.38	0.58
9:D:37:ALA:HB3	9:D:42:GLY:HA2	1.84	0.58
23:R:16:GLU:HG3	23:R:18:VAL:HG23	1.86	0.58
40:k:29:LYS:O	40:k:29:LYS:HG2	2.04	0.58
6:A:447:G:H21	6:A:487:A:N6	2.02	0.58
6:A:1187:G:H5'	14:I:115:LYS:HD3	1.85	0.58
26:U:17:ARG:O	26:U:21:ARG:HG2	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:f:4:LEU:HB3	35:f:173:PHE:HE1	1.68	0.58
7:B:129:LEU:HD22	7:B:133:GLU:HB2	1.86	0.57
12:G:93:PRO:HA	12:G:96:ARG:HG3	1.85	0.57
16:K:86:VAL:HG21	26:U:19:PHE:HZ	1.68	0.57
30:a:833:A:H2'	30:a:834:G:C8	2.38	0.57
30:a:1047:G:O2'	30:a:1109:C:N4	2.37	0.57
5:4:1:MET:HG3	31:b:43:C:H5''	1.86	0.57
6:A:407:U:H2'	6:A:408:A:H8	1.69	0.57
6:A:1463:U:H2'	6:A:1464:U:C6	2.39	0.57
7:B:139:ARG:HA	7:B:142:GLU:CD	2.30	0.57
8:C:130:PHE:O	8:C:134:MET:HG3	2.04	0.57
14:I:84:THR:HG21	14:I:103:PHE:HB2	1.86	0.57
30:a:236:C:OP2	64:a:6308:HOH:O	2.17	0.57
30:a:635:C:OP2	40:k:126:ARG:NH2	2.37	0.57
30:a:2065:C:H2'	30:a:2066:C:H6	1.68	0.57
6:A:131:A:H2'	6:A:132:C:C6	2.39	0.57
6:A:447:G:H21	6:A:487:A:H62	1.52	0.57
9:D:59:GLN:OE1	9:D:62:ARG:NH1	2.37	0.57
20:O:12:VAL:HG11	20:O:22:THR:HG22	1.86	0.57
30:a:355:U:H2'	30:a:356:G:H8	1.68	0.57
30:a:882:G:H2'	30:a:883:G:H5''	1.86	0.57
33:d:12:THR:HG22	33:d:13:ARG:H	1.66	0.57
34:e:194:LYS:HA	34:e:197:GLU:HG3	1.86	0.57
51:v:37:ILE:HG21	51:v:80:ILE:HG21	1.87	0.57
6:A:728:A:H2'	6:A:729:A:C8	2.39	0.57
6:A:1329:A:H5''	18:M:25:VAL:HA	1.85	0.57
22:Q:59:VAL:HG12	22:Q:78:VAL:HA	1.87	0.57
30:a:2243:U:H2'	30:a:2244:U:C6	2.39	0.57
6:A:45:G:H2'	6:A:46:G:C8	2.39	0.57
6:A:1266:G:N2	6:A:1269:A:OP2	2.27	0.57
28:Y:15:G:H22	28:Y:48:C:N4	2.03	0.57
30:a:2695:U:OP2	64:a:6309:HOH:O	2.18	0.57
35:f:46:ASP:HB3	35:f:49:LEU:HB2	1.87	0.57
10:E:143:GLY:HA2	10:E:146:ASN:ND2	2.20	0.57
36:g:24:ILE:HG21	36:g:72:LEU:HD11	1.85	0.57
6:A:215:C:H2'	6:A:216:U:C6	2.40	0.57
6:A:636:U:H2'	6:A:637:C:C6	2.40	0.57
36:g:24:ILE:HD11	36:g:43:VAL:HG21	1.87	0.57
7:B:161:LEU:HD22	7:B:176:ALA:HB2	1.86	0.57
30:a:2233:U:H2'	30:a:2234:G:C8	2.39	0.57
39:j:106:GLU:N	39:j:106:GLU:OE1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:451:A:H61	6:A:481:G:H5'	1.70	0.57
6:A:489:C:H2'	6:A:490:C:H6	1.68	0.57
6:A:950:U:H2'	6:A:951:G:H8	1.70	0.57
6:A:1130:A:H2'	6:A:1131:G:H8	1.69	0.57
6:A:1220:G:O3'	24:S:36:ARG:HD3	2.05	0.57
8:C:58:GLU:HB2	8:C:65:ARG:HB2	1.86	0.57
30:a:881:G:H2'	30:a:882:G:C8	2.40	0.57
30:a:2799:A:O2'	30:a:2800:A:H5''	2.05	0.57
42:m:24:MET:HE1	42:m:40:LYS:HD3	1.86	0.57
42:m:103:ARG:HG3	42:m:110:MET:SD	2.45	0.57
6:A:1436:U:H2'	6:A:1437:A:H8	1.70	0.57
8:C:22:TRP:HB3	8:C:59:ARG:HB2	1.85	0.57
9:D:115:ARG:O	9:D:119:SER:HB3	2.05	0.57
15:J:53:ILE:HD11	15:J:63:ASP:HB2	1.87	0.57
30:a:2298:A:OP1	35:f:71:ARG:NH2	2.38	0.57
1:0:9:ILE:HD12	1:0:51:GLU:HG3	1.85	0.56
30:a:1405:U:H2'	30:a:1406:U:C6	2.39	0.56
6:A:350:G:H2'	6:A:351:G:C8	2.40	0.56
6:A:1085:U:H3'	6:A:1086:U:H5	1.68	0.56
6:A:1144:G:N2	6:A:1146:A:H62	2.03	0.56
6:A:1228:C:H4'	18:M:115:PRO:HA	1.87	0.56
6:A:1530:G:H2'	6:A:1531:A:C8	2.39	0.56
28:Y:19:G:N3	30:a:896:A:N1	2.52	0.56
28:Y:72:C:H2'	28:Y:73:A:H8	1.69	0.56
36:g:37:LEU:HD13	36:g:68:ALA:HB1	1.87	0.56
6:A:149:A:H1'	6:A:1446:A:H2	1.70	0.56
6:A:310:G:H5''	21:P:31:ARG:HB2	1.88	0.56
6:A:714:G:H2'	6:A:715:A:C8	2.40	0.56
6:A:950:U:H2'	6:A:951:G:C8	2.40	0.56
6:A:1155:A:H2'	6:A:1156:G:O4'	2.06	0.56
8:C:150:LYS:HG2	8:C:201:TRP:CE3	2.40	0.56
16:K:42:LEU:HD12	16:K:79:ILE:HD11	1.87	0.56
27:X:25:C:H2'	27:X:26:U:C6	2.40	0.56
30:a:64:A:H2'	30:a:65:U:C6	2.40	0.56
30:a:927:A:H2'	30:a:928:A:C8	2.40	0.56
30:a:1141:U:H4'	30:a:1142:A:O4'	2.06	0.56
30:a:2547:A:H2'	30:a:2548:U:C6	2.40	0.56
32:c:107:PRO:HD2	32:c:110:LEU:HD22	1.87	0.56
36:g:73:ASN:O	36:g:77:ILE:HG13	2.05	0.56
6:A:335:C:H2'	6:A:336:A:C8	2.41	0.56
6:A:460:A:H2'	6:A:461:A:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:674:G:H21	16:K:118:HIS:HB2	1.71	0.56
6:A:958:A:C5	24:S:55:ARG:HD3	2.41	0.56
11:F:70:VAL:O	11:F:73:GLU:HG3	2.05	0.56
21:P:40:ASN:HB3	21:P:43:ALA:HB2	1.87	0.56
30:a:813:U:H2'	30:a:814:C:C6	2.41	0.56
4:3:8:LYS:HE3	30:a:1031:G:H5''	1.86	0.56
13:H:29:SER:HB2	13:H:59:LEU:N	2.21	0.56
24:S:69:HIS:HB3	24:S:73:GLU:OE1	2.05	0.56
6:A:131:A:O2'	6:A:262:A:N3	2.32	0.56
6:A:459:A:H2'	6:A:460:A:C8	2.41	0.56
6:A:538:G:H2'	6:A:539:A:C8	2.41	0.56
6:A:538:G:H2'	6:A:539:A:H8	1.71	0.56
6:A:745:G:H2'	6:A:746:A:H8	1.70	0.56
7:B:115:LYS:HE3	7:B:152:LYS:HB2	1.88	0.56
30:a:414:C:H2'	30:a:415:A:H8	1.69	0.56
30:a:784:G:H5'	30:a:785:G:OP1	2.06	0.56
30:a:1796:U:H2'	30:a:1797:G:H8	1.70	0.56
30:a:2831:G:OP1	33:d:56:LYS:NZ	2.39	0.56
41:l:41:LEU:HD11	41:l:102:LEU:HD13	1.88	0.56
11:F:69:GLU:OE1	11:F:69:GLU:N	2.36	0.56
15:J:84:VAL:O	15:J:88:MET:HG2	2.06	0.56
6:A:982:U:H5''	19:N:6:MET:HE2	1.87	0.56
6:A:1455:G:H2'	6:A:1456:A:C8	2.41	0.56
8:C:79:LYS:HG2	8:C:82:GLU:HG2	1.86	0.56
9:D:56:ARG:HH21	9:D:63:ARG:NH1	2.04	0.56
10:E:11:LEU:HD22	10:E:71:MET:HE1	1.88	0.56
23:R:23:TYR:HA	23:R:29:LEU:HD11	1.87	0.56
30:a:5:A:H2'	30:a:6:A:C8	2.40	0.56
30:a:851:C:H2'	30:a:852:U:C6	2.41	0.56
31:b:111:U:H2'	31:b:112:G:H8	1.71	0.56
38:i:111:LYS:HD2	38:i:111:LYS:N	2.21	0.56
39:j:99:ILE:HD13	39:j:118:LEU:HB2	1.88	0.56
4:3:34:LYS:NZ	30:a:2743:U:OP1	2.33	0.56
6:A:587:G:H4'	13:H:4:GLN:HB3	1.87	0.56
6:A:954:G:H2'	6:A:955:U:C6	2.41	0.56
7:B:58:ASN:HD22	7:B:58:ASN:C	2.14	0.56
14:I:24:GLY:HA3	14:I:62:ASP:OD1	2.06	0.56
30:a:1045:C:OP1	30:a:1046:A:H5''	2.06	0.56
6:A:263:A:H2'	6:A:264:C:C6	2.41	0.56
6:A:328:C:H4'	6:A:329:A:H5'	1.87	0.56
8:C:142:MET:SD	8:C:170:GLU:HB3	2.44	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2327:A:H2'	30:a:2328:A:C8	2.42	0.56
36:g:43:VAL:HG13	36:g:52:PHE:HE1	1.71	0.56
6:A:142:G:O2'	6:A:196:A:N1	2.31	0.55
6:A:1060:U:H5''	15:J:53:ILE:HG22	1.88	0.55
6:A:1330:U:H4'	18:M:23:TYR:CE1	2.40	0.55
30:a:185:G:N7	64:a:6377:HOH:O	2.33	0.55
30:a:594:U:H2'	30:a:595:C:H6	1.71	0.55
34:e:117:ARG:NH2	34:e:183:PHE:O	2.39	0.55
49:t:54:GLN:CD	49:t:54:GLN:H	2.13	0.55
8:C:68:ILE:O	8:C:68:ILE:HG13	2.06	0.55
11:F:6:ILE:HG12	11:F:89:VAL:HG22	1.87	0.55
30:a:191:A:H2'	30:a:192:C:C6	2.41	0.55
34:e:188:MET:HE2	34:e:193:VAL:HG22	1.87	0.55
43:n:79:ALA:HB2	43:n:110:ALA:HA	1.87	0.55
54:y:45:ARG:HH22	54:y:59:GLU:CD	2.15	0.55
6:A:149:A:H2'	6:A:150:U:C6	2.41	0.55
10:E:79:GLY:O	10:E:121:HIS:N	2.37	0.55
30:a:2314:A:H2'	30:a:2315:G:C8	2.41	0.55
30:a:2609:U:OP1	63:d:301:SPD:C2	2.55	0.55
35:f:118:SER:O	35:f:128:TYR:OH	2.17	0.55
36:g:44:LYS:NZ	36:g:51:THR:O	2.37	0.55
6:A:1436:U:H2'	6:A:1437:A:C8	2.41	0.55
6:A:1518:MA6:H103	6:A:1519:MA6:H102	1.89	0.55
7:B:13:GLY:HA3	7:B:208:ARG:HH12	1.71	0.55
8:C:163:ALA:O	8:C:164:ARG:NE	2.39	0.55
18:M:29:ARG:O	18:M:33:ILE:HG12	2.07	0.55
6:A:1001:C:H2'	6:A:1002:G:H8	1.72	0.55
6:A:1093:A:N3	6:A:1109:C:O2'	2.37	0.55
18:M:65:VAL:O	18:M:69:LEU:N	2.29	0.55
30:a:909:A:H2'	30:a:912:C:C5	2.42	0.55
30:a:2194:U:H2'	30:a:2195:U:C6	2.42	0.55
6:A:269:C:H2'	6:A:270:A:C8	2.42	0.55
6:A:512:U:H2'	6:A:513:C:C6	2.42	0.55
6:A:627:G:H2'	6:A:628:G:H8	1.70	0.55
6:A:1348:U:H4'	14:I:122:ARG:HD2	1.87	0.55
15:J:9:ARG:HB2	15:J:99:GLN:HB3	1.89	0.55
30:a:3:U:H2'	30:a:4:U:C6	2.42	0.55
12:G:76:LYS:NZ	12:G:89:VAL:HG21	2.21	0.55
14:I:28:ILE:HD13	14:I:35:LEU:HD22	1.88	0.55
29:Z:61:C:H2'	29:Z:62:C:C6	2.42	0.55
6:A:2:A:H1'	6:A:613:C:O2'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:185:U:H2'	6:A:186:C:C6	2.42	0.55
6:A:618:C:H5'	6:A:619:U:H5''	1.89	0.55
16:K:35:THR:HA	16:K:41:ALA:HA	1.89	0.55
28:Y:19:G:O6	30:a:881:G:O2'	2.25	0.55
30:a:849:A:H2'	30:a:850:U:C6	2.42	0.55
30:a:2801:G:H2'	30:a:2802:G:H8	1.72	0.55
53:x:10:SER:N	53:x:13:GLU:OE2	2.38	0.55
6:A:958:A:C6	24:S:55:ARG:HD3	2.42	0.55
23:R:26:ILE:O	23:R:30:LYS:N	2.36	0.55
28:Y:64:A:H2'	28:Y:65:G:H8	1.72	0.55
30:a:1703:G:H2'	30:a:1704:C:C6	2.42	0.55
36:g:30:ASN:HB2	36:g:79:VAL:HA	1.89	0.55
43:n:53:THR:HB	43:n:65:THR:HB	1.87	0.55
3:2:54:ASP:HB3	40:k:57:LEU:HD22	1.88	0.54
6:A:769:G:H4'	6:A:1513:A:H4'	1.89	0.54
9:D:55:LEU:O	9:D:59:GLN:HG2	2.07	0.54
11:F:5:GLU:OE1	23:R:23:TYR:OH	2.22	0.54
12:G:113:ASP:OD2	12:G:122:ASN:ND2	2.40	0.54
25:T:72:ALA:O	25:T:76:LYS:HG2	2.06	0.54
30:a:1357:C:H2'	30:a:1358:G:O4'	2.07	0.54
30:a:1734:G:H2'	30:a:1735:A:H8	1.72	0.54
36:g:23:VAL:HA	36:g:36:THR:HA	1.89	0.54
6:A:407:U:H2'	6:A:408:A:C8	2.42	0.54
6:A:642:A:N7	13:H:107:SER:HA	2.22	0.54
6:A:1005:A:H3'	6:A:1006:G:H8	1.72	0.54
30:a:1746:A:H2'	30:a:1747:U:C6	2.42	0.54
14:I:106:ARG:NH1	14:I:107:ASP:O	2.40	0.54
6:A:1513:A:H2'	6:A:1514:G:H8	1.72	0.54
21:P:1:MET:O	21:P:24:SER:OG	2.26	0.54
30:a:1734:G:H2'	30:a:1735:A:C8	2.43	0.54
9:D:29:ASP:OD1	9:D:29:ASP:N	2.40	0.54
34:e:48:THR:HG23	34:e:88:ARG:HH11	1.73	0.54
6:A:310:G:OP1	21:P:31:ARG:N	2.40	0.54
6:A:511:C:O2'	6:A:512:U:OP2	2.21	0.54
6:A:1064:G:H1'	6:A:1190:G:H21	1.73	0.54
30:a:364:C:H2'	30:a:365:U:C6	2.43	0.54
6:A:236:A:H2'	6:A:237:G:H8	1.72	0.54
6:A:859:G:H2'	6:A:860:A:H8	1.73	0.54
6:A:923:A:H2'	6:A:924:C:C6	2.43	0.54
6:A:1326:U:H2'	6:A:1327:C:C6	2.42	0.54
6:A:1463:U:H2'	6:A:1464:U:H6	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:717:C:H3'	30:a:718:A:H8	1.72	0.54
34:e:175:ILE:HD11	34:e:199:MET:HE1	1.90	0.54
35:f:101:GLU:O	35:f:105:THR:HG23	2.07	0.54
36:g:38:ASN:ND2	36:g:64:GLN:OE1	2.31	0.54
6:A:264:C:O2'	22:Q:66:PRO:O	2.23	0.54
6:A:444:G:H2'	6:A:445:G:C8	2.43	0.54
6:A:993:G:H2'	6:A:993:G:N3	2.23	0.54
6:A:993:G:N2	6:A:996:A:H62	2.04	0.54
6:A:1032:G:H3'	6:A:1032:G:N3	2.23	0.54
6:A:1085:U:H3'	6:A:1086:U:C5	2.43	0.54
6:A:1251:A:H2'	6:A:1252:A:C8	2.42	0.54
19:N:53:ARG:HH21	24:S:37:ARG:NH2	2.05	0.54
28:Y:63:G:H2'	28:Y:64:A:H8	1.69	0.54
29:Z:10:G:N2	29:Z:26:G:H1'	2.23	0.54
30:a:1715:G:N2	30:a:1744:A:OP2	2.35	0.54
42:m:44:LEU:O	42:m:48:VAL:HG12	2.08	0.54
6:A:142:G:H3'	6:A:143:A:H8	1.73	0.54
6:A:374:A:N1	6:A:390:U:O2'	2.38	0.54
8:C:183:ASP:N	8:C:202:ILE:O	2.40	0.54
30:a:1808:A:H3'	30:a:1809:A:C8	2.42	0.54
6:A:231:U:H2'	6:A:232:G:C8	2.43	0.54
6:A:377:G:H2'	6:A:378:G:H8	1.73	0.54
6:A:445:G:H2'	6:A:446:G:H8	1.73	0.54
6:A:470:C:H2'	6:A:471:U:C6	2.43	0.54
6:A:613:C:H2'	6:A:614:C:C6	2.42	0.54
6:A:918:A:H2'	6:A:919:A:C8	2.43	0.54
6:A:1291:U:H2'	6:A:1292:G:C8	2.43	0.54
7:B:32:PHE:HB3	7:B:40:ILE:HG22	1.89	0.54
8:C:153:VAL:HG22	8:C:198:VAL:HG22	1.90	0.54
30:a:1548:A:H2'	30:a:1549:A:C8	2.43	0.54
38:i:9:GLU:HG2	38:i:10:THR:HG23	1.90	0.54
6:A:309:A:O2'	6:A:607:A:N1	2.41	0.53
6:A:445:G:H2'	6:A:446:G:C8	2.43	0.53
10:E:46:VAL:HG21	10:E:114:VAL:HG13	1.88	0.53
17:L:68:GLY:O	17:L:99:ARG:NH1	2.34	0.53
39:j:38:ILE:HD11	39:j:112:PHE:HZ	1.72	0.53
29:Z:67:C:H2'	29:Z:68:C:C6	2.43	0.53
45:p:50:ARG:O	45:p:54:LYS:NZ	2.39	0.53
53:x:18:LEU:HB2	53:x:53:VAL:HG11	1.90	0.53
6:A:946:A:H2'	6:A:947:G:H8	1.68	0.53
6:A:1268:G:H2'	6:A:1269:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:14:ILE:HD13	8:C:178:LEU:HB3	1.89	0.53
30:a:151:C:H2'	30:a:152:A:H8	1.73	0.53
30:a:1028:A:N6	30:a:1125:G:H2'	2.23	0.53
30:a:1796:U:H2'	30:a:1797:G:C8	2.43	0.53
30:a:1978:A:OP2	64:a:6311:HOH:O	2.18	0.53
38:i:140:LEU:HG	38:i:142:ILE:HG13	1.91	0.53
55:z:29:SER:OG	55:z:40:ARG:HD3	2.07	0.53
5:4:32:LEU:HD21	35:f:139:PRO:HG2	1.91	0.53
6:A:1377:A:OP1	12:G:92:ARG:NH2	2.42	0.53
8:C:32:ASN:HA	8:C:59:ARG:HH21	1.72	0.53
17:L:74:LEU:HD21	17:L:104:CYS:HA	1.90	0.53
21:P:60:TRP:HA	21:P:63:GLN:HG3	1.89	0.53
30:a:1637:A:H5'	30:a:1760:C:O2'	2.09	0.53
6:A:181:A:O2'	6:A:194:C:N4	2.39	0.53
6:A:268:U:H2'	6:A:269:C:H6	1.74	0.53
6:A:455:G:H2'	6:A:456:A:H8	1.72	0.53
7:B:57:LEU:HD22	7:B:67:ILE:HD12	1.89	0.53
9:D:152:GLN:HB2	9:D:155:VAL:HG23	1.90	0.53
19:N:28:LYS:HA	19:N:31:ILE:HD12	1.89	0.53
6:A:236:A:H2'	6:A:237:G:C8	2.43	0.53
6:A:266:G:H3'	22:Q:69:LYS:HB2	1.90	0.53
29:Z:6:G:H2'	29:Z:7:G:C8	2.44	0.53
30:a:851:C:H2'	30:a:852:U:H6	1.74	0.53
30:a:1199:U:H2'	30:a:1200:C:H6	1.73	0.53
46:q:40:MET:HE2	46:q:49:ILE:HG12	1.90	0.53
6:A:219:U:H2'	6:A:220:G:C8	2.43	0.53
6:A:384:G:H2'	6:A:385:C:C6	2.44	0.53
6:A:834:U:H2'	6:A:835:U:C6	2.44	0.53
6:A:1372:U:H2'	6:A:1373:G:O4'	2.08	0.53
7:B:60:ILE:HD13	7:B:160:ALA:HB2	1.91	0.53
10:E:113:ALA:O	10:E:117:VAL:HG22	2.09	0.53
17:L:50:ARG:HB3	17:L:66:TYR:HE1	1.72	0.53
26:U:31:GLU:HA	26:U:34:ARG:HG2	1.89	0.53
29:Z:50:U:H2'	29:Z:51:C:O4'	2.08	0.53
30:a:1506:U:H2'	30:a:1507:C:C6	2.44	0.53
6:A:491:G:H2'	6:A:492:C:C6	2.44	0.53
6:A:746:A:H2'	6:A:747:A:C8	2.44	0.53
30:a:2198:A:C4	37:h:29:PHE:HB2	2.44	0.53
30:a:2491[B]:U:OP2	64:a:6310:HOH:O	2.18	0.53
31:b:55:U:H4'	35:f:24:SER:HB2	1.91	0.53
5:4:56:ARG:O	5:4:60:PHE:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:186:ILE:HG13	7:B:204:ASP:HB3	1.90	0.53
10:E:86:LYS:HE2	10:E:95:PHE:HB2	1.91	0.53
13:H:32:LEU:O	13:H:36:ILE:HG12	2.08	0.53
22:Q:25:ILE:HB	22:Q:42:THR:HG22	1.90	0.53
30:a:1747:U:H2'	30:a:1748:C:C6	2.44	0.53
30:a:2591:C:H2'	30:a:2592:G:C8	2.44	0.53
41:l:41:LEU:HG	41:l:96:ILE:HG13	1.89	0.53
6:A:948:C:H2'	6:A:949:A:H8	1.74	0.53
6:A:957:U:H4'	24:S:79:THR:OG1	2.09	0.53
6:A:1125:U:O2'	6:A:1126:U:O5'	2.23	0.53
9:D:147:GLU:HA	9:D:150:LYS:HD2	1.89	0.53
11:F:37:HIS:HB3	11:F:97:THR:HG22	1.91	0.53
11:F:93:LYS:HD3	11:F:93:LYS:N	2.23	0.53
24:S:11:ILE:HD12	24:S:38:SER:HB2	1.91	0.53
28:Y:26:A:N6	28:Y:44:G:H1	2.05	0.53
30:a:78:U:OP1	53:x:7:ARG:NH2	2.42	0.53
30:a:1794:A:H2'	30:a:1795:C:C6	2.44	0.53
30:a:2567:G:H2'	30:a:2568:U:C6	2.44	0.53
41:l:53:MET:HE1	41:l:103:TYR:CG	2.43	0.53
6:A:1127:G:H1	6:A:1145:A:N6	2.06	0.52
8:C:19:ASN:O	8:C:40:ARG:NH2	2.43	0.52
10:E:88:VAL:HG22	10:E:93:ARG:HG2	1.89	0.52
18:M:45:ILE:HA	18:M:48:LEU:HG	1.91	0.52
30:a:644:A:H2'	30:a:645:C:O4'	2.09	0.52
30:a:1181:U:H2'	30:a:1182:G:C8	2.44	0.52
31:b:111:U:H2'	31:b:112:G:C8	2.44	0.52
6:A:116:A:H61	6:A:313:A:H1'	1.73	0.52
6:A:934:C:O2'	6:A:1344:C:OP2	2.27	0.52
6:A:1018:G:H2'	6:A:1019:A:C8	2.44	0.52
6:A:1250:A:H2'	6:A:1251:A:C8	2.44	0.52
6:A:1497:G:H1'	6:A:1518:MA6:H2	1.92	0.52
8:C:189:ALA:HB3	8:C:196:ILE:HB	1.92	0.52
9:D:105:MET:HG2	9:D:173:VAL:HG22	1.89	0.52
14:I:120:LYS:HB2	14:I:123:ARG:HB2	1.92	0.52
30:a:2455:G:H2'	30:a:2456:C:C6	2.44	0.52
35:f:135:GLN:OE1	35:f:150:ARG:N	2.34	0.52
6:A:86:G:O2'	6:A:87:C:O5'	2.26	0.52
6:A:377:G:H2'	6:A:378:G:C8	2.44	0.52
6:A:958:A:N3	6:A:985:C:O2'	2.38	0.52
10:E:58:ALA:O	10:E:62:LYS:HG3	2.09	0.52
15:J:14:ASP:N	15:J:14:ASP:OD1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:881:G:O6	30:a:895:U:O2	2.28	0.52
6:A:580:C:H2'	6:A:581:G:O4'	2.09	0.52
6:A:716:A:N3	16:K:120:GLY:N	2.57	0.52
7:B:221:VAL:O	7:B:225:ARG:HG3	2.08	0.52
16:K:86:VAL:HG21	26:U:19:PHE:CZ	2.44	0.52
25:T:26:SER:O	25:T:30:THR:OG1	2.25	0.52
36:g:28:GLY:HA3	36:g:79:VAL:HB	1.91	0.52
6:A:312:C:H2'	6:A:313:A:C8	2.44	0.52
6:A:1312:G:H2'	6:A:1313:U:C6	2.44	0.52
20:O:47:LYS:O	20:O:53:ARG:NH1	2.34	0.52
29:Z:67:C:H2'	29:Z:68:C:H6	1.75	0.52
30:a:909:A:H2'	30:a:912:C:H5	1.73	0.52
55:z:40:ARG:HG2	55:z:40:ARG:HH11	1.74	0.52
6:A:323:U:H2'	6:A:324:G:O4'	2.10	0.52
6:A:1343:G:H2'	6:A:1344:C:C6	2.44	0.52
8:C:138:VAL:HG13	8:C:149:ILE:HG23	1.91	0.52
22:Q:8:LEU:HD23	22:Q:25:ILE:HG21	1.92	0.52
30:a:2096:C:N3	30:a:2193:G:N1	2.49	0.52
31:b:106:G:H2'	31:b:107:G:O4'	2.10	0.52
35:f:47:LYS:HZ1	35:f:84:PRO:HG2	1.75	0.52
5:4:38:SER:HB3	35:f:105:THR:HA	1.90	0.52
7:B:115:LYS:O	7:B:119:THR:HG23	2.09	0.52
9:D:177:LYS:O	9:D:177:LYS:HD3	2.10	0.52
10:E:86:LYS:HG2	10:E:95:PHE:HA	1.90	0.52
13:H:36:ILE:O	13:H:40:LEU:HG	2.10	0.52
29:Z:50:U:O4	29:Z:64:G:O6	2.27	0.52
30:a:635:C:O2'	30:a:639:U:OP1	2.27	0.52
30:a:742:A:H2'	30:a:743:A:C8	2.44	0.52
31:b:28:C:OP1	43:n:36:TYR:OH	2.25	0.52
32:c:175:ARG:NH2	32:c:181:MET:HE1	2.24	0.52
54:y:40:ASP:OD2	54:y:45:ARG:NH1	2.28	0.52
6:A:1328:C:OP1	18:M:28:THR:OG1	2.27	0.52
6:A:1408:A:N1	57:A:1601:PAR:O61	2.40	0.52
9:D:105:MET:HE3	9:D:171:LEU:HD22	1.91	0.52
22:Q:61:ILE:HG22	22:Q:75:LEU:HA	1.91	0.52
28:Y:19:G:N2	30:a:896:A:C4	2.75	0.52
29:Z:21:A:N6	29:Z:46:G:H2'	2.24	0.52
30:a:581:C:H2'	30:a:582:A:C8	2.45	0.52
39:j:38:ILE:HD11	39:j:112:PHE:CZ	2.44	0.52
6:A:313:A:H2'	6:A:314:C:C6	2.44	0.52
6:A:459:A:H2'	6:A:460:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:904:U:H2'	6:A:905:U:C6	2.45	0.52
6:A:1116:U:O2	6:A:1184:G:O6	2.28	0.52
6:A:1119:C:H2'	6:A:1120:C:H6	1.75	0.52
8:C:14:ILE:HG13	8:C:15:VAL:H	1.75	0.52
14:I:88:MET:HE2	14:I:88:MET:HA	1.92	0.52
18:M:81:MET:HE2	18:M:91:HIS:HB3	1.92	0.52
27:X:24:A:H4'	27:X:25:C:OP2	2.09	0.52
30:a:839:U:H2'	30:a:840:C:C6	2.44	0.52
35:f:143:TYR:HA	35:f:146:VAL:HG23	1.91	0.52
49:t:86:ARG:NH2	49:t:88:GLU:OE2	2.43	0.52
6:A:39:G:H2'	6:A:40:C:C6	2.44	0.52
8:C:123:GLN:OE1	8:C:136:ARG:NH1	2.43	0.52
11:F:20:GLY:O	11:F:23:GLU:HG3	2.10	0.52
12:G:15:ASP:OD1	12:G:19:GLY:N	2.42	0.52
14:I:12:ARG:NH1	14:I:107:ASP:OD2	2.43	0.52
30:a:2194:U:H2'	30:a:2195:U:H6	1.75	0.52
16:K:14:LYS:HG2	16:K:15:GLN:H	1.74	0.51
30:a:2096:C:H2'	30:a:2097:A:H8	1.73	0.51
34:e:10:SER:OG	34:e:11:ALA:N	2.42	0.51
6:A:501:C:H1'	6:A:549:C:H1'	1.91	0.51
6:A:1004:A:O2'	6:A:1036:A:N6	2.43	0.51
6:A:1273:C:H2'	6:A:1274:A:O4'	2.10	0.51
6:A:1317:C:OP1	19:N:56:SER:OG	2.22	0.51
30:a:633:A:H5''	40:k:70:LYS:HD2	1.92	0.51
30:a:709:U:H2'	30:a:710:U:C6	2.45	0.51
30:a:2783:U:H2'	30:a:2784:U:C6	2.43	0.51
33:d:30:GLU:OE2	33:d:53:GLY:HA2	2.10	0.51
6:A:264:C:H2'	6:A:265:G:O4'	2.11	0.51
6:A:816:A:OP1	6:A:1526:G:O2'	2.22	0.51
6:A:1004:A:C6	6:A:1026:G:H1'	2.45	0.51
6:A:1255:G:O2'	6:A:1258:G:N3	2.33	0.51
7:B:67:ILE:HB	7:B:89:GLN:HG3	1.92	0.51
16:K:49:GLY:O	16:K:69:ARG:NH2	2.39	0.51
24:S:13:LEU:HD23	24:S:13:LEU:H	1.75	0.51
25:T:2:ALA:O	25:T:8:LYS:NZ	2.35	0.51
30:a:2537:U:H2'	30:a:2538:C:C6	2.45	0.51
1:0:11:LEU:HD21	1:0:34:LEU:HD23	1.92	0.51
6:A:539:A:H2'	6:A:540:G:C8	2.45	0.51
15:J:18:ILE:HG12	15:J:72:ARG:HG3	1.93	0.51
30:a:1463:C:OP2	64:a:6312:HOH:O	2.19	0.51
49:t:14:LEU:HD11	49:t:71:ALA:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:253:A:H2'	6:A:254:G:C8	2.46	0.51
6:A:1286:U:H2'	6:A:1287:A:H5'	1.91	0.51
8:C:129:MET:O	8:C:132:ARG:HB2	2.10	0.51
12:G:92:ARG:O	12:G:96:ARG:HG2	2.11	0.51
18:M:59:GLU:OE2	18:M:62:LYS:NZ	2.39	0.51
23:R:30:LYS:HE3	23:R:33:ILE:HD11	1.93	0.51
23:R:73:ARG:HB3	23:R:73:ARG:CZ	2.39	0.51
24:S:31:LEU:HD12	24:S:49:ILE:HG22	1.93	0.51
30:a:1482:G:H1'	30:a:1509:A:H61	1.76	0.51
30:a:2065:C:H2'	30:a:2066:C:C6	2.44	0.51
30:a:2469:A:N6	30:a:2481:G:O2'	2.43	0.51
30:a:2580:PSU:OP1	63:d:301:SPD:H91	2.11	0.51
48:s:2:ILE:HD13	48:s:42:GLU:HA	1.93	0.51
6:A:149:A:H1'	6:A:1446:A:C2	2.45	0.51
6:A:545:C:P	9:D:59:GLN:HE22	2.34	0.51
6:A:639:G:O6	6:A:640:A:N6	2.43	0.51
6:A:653:U:C2	13:H:56:LYS:HG2	2.45	0.51
6:A:1347:G:H5''	14:I:109:ARG:HB3	1.92	0.51
30:a:1149:G:H2'	30:a:1150:C:C6	2.45	0.51
30:a:1269:A:H2'	30:a:1270:C:C6	2.45	0.51
14:I:19:VAL:HG12	14:I:65:ILE:HG12	1.92	0.51
30:a:580:U:H2'	30:a:581:C:C6	2.45	0.51
6:A:1527:U:OP2	26:U:42:THR:OG1	2.21	0.51
35:f:108:VAL:HG23	35:f:111:ILE:HD12	1.92	0.51
30:a:2301:C:H2'	30:a:2302:U:C6	2.45	0.51
30:a:2801:G:H2'	30:a:2802:G:C8	2.46	0.51
6:A:627:G:H2'	6:A:628:G:C8	2.45	0.51
21:P:57:ILE:O	21:P:61:VAL:HG23	2.11	0.51
29:Z:56:C:H2'	29:Z:57:A:C8	2.45	0.51
30:a:1682:G:H2'	30:a:1683:U:C6	2.46	0.51
37:h:34:GLY:O	37:h:36:ALA:N	2.42	0.51
10:E:107:ALA:HB2	10:E:125:ALA:HB3	1.93	0.50
55:z:43:ILE:HG22	55:z:49:TYR:HB2	1.94	0.50
6:A:31:G:O2'	6:A:48:C:N4	2.42	0.50
30:a:55:G:O2'	30:a:127:A:N1	2.44	0.50
30:a:1839:G:OP2	64:a:6313:HOH:O	2.19	0.50
30:a:2698:U:H2'	30:a:2699:C:C6	2.45	0.50
6:A:1149:C:P	14:I:11:ARG:HH21	2.34	0.50
6:A:1319:A:O2'	6:A:1323:G:N7	2.41	0.50
8:C:138:VAL:HA	8:C:149:ILE:HD13	1.93	0.50
11:F:25:TYR:O	11:F:29:ILE:HG13	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:101:ILE:HG13	13:H:129:VAL:HB	1.93	0.50
18:M:48:LEU:HD12	18:M:53:ILE:HG12	1.94	0.50
18:M:67:GLY:O	18:M:71:ARG:HG2	2.11	0.50
29:Z:69:C:H2'	29:Z:70:G:C8	2.47	0.50
30:a:30:G:H2'	30:a:31:C:C6	2.46	0.50
30:a:1534:U:N3	30:a:1536:C:N3	2.59	0.50
30:a:2859:G:H2'	30:a:2860:A:C8	2.46	0.50
35:f:2:ALA:N	35:f:94:GLU:OE2	2.44	0.50
35:f:103:LEU:O	35:f:108:VAL:HG12	2.11	0.50
6:A:359:G:H2'	6:A:360:G:C8	2.47	0.50
6:A:404:G:O6	9:D:2:ALA:N	2.44	0.50
6:A:461:A:H2'	6:A:462:G:C8	2.45	0.50
6:A:519:C:H2'	6:A:520:A:O4'	2.12	0.50
6:A:920:U:H2'	6:A:921:U:C6	2.45	0.50
7:B:70:VAL:HG12	7:B:169:GLU:HG2	1.94	0.50
28:Y:19:G:C5	30:a:896:A:N6	2.80	0.50
30:a:1361:G:H2'	30:a:1362:C:C6	2.46	0.50
30:a:1413:A:H2'	30:a:1414:C:C6	2.46	0.50
30:a:2292:U:H2'	30:a:2293:G:C8	2.47	0.50
30:a:2752:C:H2'	30:a:2753:A:O4'	2.12	0.50
6:A:736:C:H2'	6:A:737:C:H6	1.77	0.50
6:A:1160:G:O6	6:A:1182:G:O6	2.30	0.50
6:A:1355:G:H2'	6:A:1356:G:C8	2.46	0.50
25:T:62:ALA:HA	25:T:67:ILE:O	2.11	0.50
28:Y:64:A:H2'	28:Y:65:G:C8	2.46	0.50
30:a:32:C:N4	30:a:447:A:OP2	2.45	0.50
30:a:2071:A:H2'	30:a:2072:C:C6	2.47	0.50
6:A:815:A:N7	6:A:1509:C:O2'	2.35	0.50
29:Z:55:U:H2'	29:Z:57:A:OP2	2.12	0.50
30:a:26:G:H1'	30:a:514:A:N6	2.27	0.50
30:a:161:A:OP2	30:a:162:U:O2'	2.27	0.50
30:a:1199:U:H2'	30:a:1200:C:C6	2.46	0.50
30:a:1712:U:OP2	30:a:1713:A:O2'	2.27	0.50
5:4:9:TYR:OH	35:f:102:ARG:NH2	2.45	0.50
6:A:546:A:O2'	6:A:548:G:O2'	2.25	0.50
6:A:1533:C:H4'	6:A:1534:A:C8	2.47	0.50
11:F:30:THR:HG23	11:F:36:ILE:HD13	1.92	0.50
30:a:2205:A:H2'	30:a:2206:C:H6	1.77	0.50
30:a:2271:G:OP1	51:v:18:ALA:HB1	2.12	0.50
35:f:4:LEU:HB3	35:f:173:PHE:CE1	2.46	0.50
6:A:1112:C:C4	8:C:178:LEU:HD12	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:90:VAL:O	8:C:94:ILE:HG13	2.11	0.50
22:Q:12:VAL:HG22	22:Q:21:ILE:HD12	1.94	0.50
30:a:1842:G:H2'	30:a:1843:C:C6	2.45	0.50
36:g:48:ASN:O	36:g:48:ASN:ND2	2.45	0.50
39:j:63:VAL:HG12	39:j:107:LEU:HD11	1.93	0.50
6:A:1071:C:H2'	6:A:1072:G:H8	1.77	0.50
6:A:1238:A:H2	6:A:1241:G:N3	2.09	0.50
10:E:149:SER:O	10:E:153:VAL:HG23	2.11	0.50
29:Z:73:A:H5''	29:Z:74:C:H5'	1.93	0.50
30:a:279:A:H2'	30:a:280:U:O4'	2.12	0.50
30:a:883:G:H2'	30:a:884:U:C6	2.46	0.50
30:a:885:C:H3'	30:a:886:A:H8	1.77	0.50
30:a:2615:U:C2	55:z:4:GLN:HA	2.47	0.50
51:v:68:LYS:NZ	51:v:69:PHE:O	2.41	0.50
6:A:43:C:H2'	6:A:44:A:O4'	2.12	0.49
7:B:163:VAL:HG11	7:B:173:ILE:HD11	1.94	0.49
8:C:16:LYS:NZ	8:C:182:ILE:O	2.34	0.49
25:T:54:MET:O	25:T:58:VAL:HG23	2.11	0.49
60:Z:101:8AN:H1'	64:a:6414:HOH:O	2.12	0.49
30:a:1443:U:H2'	30:a:1444:G:H8	1.77	0.49
30:a:2795:C:H2'	30:a:2796:U:C6	2.47	0.49
42:m:86:ARG:NH2	42:m:117:ASP:OD1	2.27	0.49
6:A:178:C:OP2	25:T:60:ARG:NH1	2.45	0.49
6:A:1067:A:O2'	6:A:1108:G:N2	2.44	0.49
8:C:116:VAL:O	8:C:120:ILE:HG13	2.12	0.49
8:C:123:GLN:HG2	8:C:126:ARG:HH21	1.76	0.49
12:G:5:ARG:NH1	12:G:7:ILE:O	2.46	0.49
14:I:30:ILE:HG22	14:I:65:ILE:HB	1.94	0.49
15:J:10:LEU:O	15:J:71:LEU:HA	2.13	0.49
15:J:16:ARG:O	15:J:20:GLN:HG2	2.12	0.49
30:a:1589:U:H2'	30:a:1590:A:C8	2.47	0.49
30:a:2766:A:N7	64:a:6408:HOH:O	2.35	0.49
1:O:22:THR:HG21	30:a:2419:U:H4'	1.94	0.49
6:A:61:G:H2'	6:A:62:U:O4'	2.12	0.49
6:A:875:U:O2'	13:H:15:ARG:NH1	2.39	0.49
7:B:186:ILE:HD12	7:B:200:ILE:O	2.13	0.49
13:H:113:ASP:OD2	13:H:117:ARG:NH2	2.45	0.49
14:I:12:ARG:HG2	14:I:74:GLY:HA2	1.94	0.49
15:J:53:ILE:HD11	15:J:63:ASP:CB	2.42	0.49
30:a:152:A:H2'	30:a:153:U:C6	2.46	0.49
30:a:476:G:H4'	30:a:502:A:N1	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2020:A:H5'	55:z:9:THR:CG2	2.41	0.49
36:g:4:VAL:HG13	36:g:69:ARG:HD2	1.93	0.49
48:s:6:ARG:HH22	48:s:37:ASP:CG	2.21	0.49
6:A:39:G:H2'	6:A:40:C:H6	1.77	0.49
6:A:665:A:H1'	6:A:733:G:H5'	1.94	0.49
6:A:1306:A:H2'	6:A:1307:U:O4'	2.13	0.49
7:B:108:ARG:HA	7:B:111:ILE:HD12	1.94	0.49
12:G:36:LYS:O	12:G:40:GLU:HG3	2.13	0.49
29:Z:58:A:H1'	29:Z:60:U:OP2	2.13	0.49
30:a:813:U:H2'	30:a:814:C:H6	1.76	0.49
30:a:2687:U:H2'	30:a:2688:G:O4'	2.13	0.49
35:f:6:ASP:O	35:f:10:ASP:HB2	2.11	0.49
6:A:501:C:H2'	6:A:502:A:H8	1.78	0.49
6:A:537:G:H2'	6:A:538:G:H8	1.78	0.49
6:A:674:G:H2'	6:A:675:A:C8	2.44	0.49
6:A:855:U:OP2	6:A:871:U:N3	2.43	0.49
6:A:1464:U:H2'	6:A:1465:A:H8	1.77	0.49
14:I:58:VAL:HG13	14:I:59:GLU:H	1.78	0.49
24:S:36:ARG:HB3	24:S:72:GLY:HA3	1.92	0.49
35:f:52:ASN:HB3	35:f:150:ARG:NH2	2.27	0.49
6:A:92:U:H2'	6:A:93:U:C6	2.48	0.49
6:A:382:A:H2'	6:A:383:A:C8	2.47	0.49
6:A:696:A:N3	6:A:786:G:O2'	2.38	0.49
6:A:1013:G:N2	6:A:1016:A:OP2	2.40	0.49
6:A:1444:U:H2'	6:A:1445:U:C6	2.48	0.49
13:H:106:THR:OG1	13:H:109:GLY:O	2.27	0.49
30:a:729:G:C6	32:c:207:LYS:HB2	2.48	0.49
36:g:91:GLY:HA3	36:g:160:LYS:HG2	1.94	0.49
6:A:78:A:H2'	6:A:79:G:C8	2.47	0.49
6:A:149:A:H2'	6:A:150:U:H6	1.77	0.49
6:A:391:G:H5''	21:P:8:ARG:HD2	1.94	0.49
6:A:1055:A:O2'	8:C:161:GLU:O	2.27	0.49
7:B:10:LEU:HD12	7:B:15:HIS:ND1	2.27	0.49
14:I:96:SER:HA	14:I:99:ARG:HB3	1.94	0.49
30:a:479:A:N3	30:a:481:G:H5''	2.28	0.49
30:a:852:U:H2'	30:a:853:C:C6	2.48	0.49
30:a:893:C:H2'	30:a:894:U:O4'	2.12	0.49
6:A:119:A:H4'	6:A:120:A:C4	2.48	0.49
6:A:321:A:H2'	6:A:322:C:C6	2.48	0.49
6:A:881:G:H2'	6:A:882:C:O4'	2.12	0.49
6:A:1113:C:H4'	8:C:14:ILE:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:207:ILE:HA	7:B:210:VAL:HB	1.94	0.49
8:C:107:ARG:O	8:C:108:LYS:HG2	2.13	0.49
19:N:23:LYS:H	19:N:23:LYS:HD2	1.78	0.49
30:a:158:U:H2'	30:a:159:G:C8	2.48	0.49
30:a:2590:A:H2'	30:a:2591:C:H6	1.77	0.49
31:b:60:C:H2'	31:b:61:G:H8	1.77	0.49
7:B:56:GLU:HG2	7:B:198:PHE:CZ	2.48	0.49
15:J:42:LEU:HB2	15:J:71:LEU:O	2.13	0.49
30:a:1447:C:H2'	30:a:1448:G:H8	1.78	0.49
36:g:23:VAL:HG22	36:g:36:THR:HB	1.93	0.49
6:A:1123:U:O2'	6:A:1124:G:H5'	2.13	0.49
12:G:71:PRO:HG3	12:G:103:TRP:CZ3	2.48	0.49
20:O:47:LYS:HA	20:O:53:ARG:HH22	1.78	0.49
24:S:42:PRO:O	24:S:45:ILE:HD12	2.13	0.49
26:U:47:ARG:NE	26:U:47:ARG:HA	2.27	0.49
30:a:72:U:OP2	53:x:54:LYS:HE3	2.13	0.49
30:a:143:C:H2'	30:a:144:A:C8	2.48	0.49
34:e:194:LYS:O	34:e:198:GLU:HG2	2.13	0.49
52:w:68:LEU:O	52:w:72:ARG:HG3	2.13	0.49
6:A:491:G:H2'	6:A:492:C:H6	1.78	0.48
6:A:545:C:OP1	9:D:58:LYS:NZ	2.46	0.48
6:A:908:A:H2'	6:A:909:A:C8	2.48	0.48
6:A:1343:G:H1'	14:I:123:ARG:NH1	2.27	0.48
9:D:15:GLU:HG3	9:D:19:LEU:HD11	1.93	0.48
10:E:41:ASP:CG	10:E:45:ARG:HB2	2.37	0.48
10:E:83:HIS:CE1	10:E:85:VAL:HG12	2.48	0.48
14:I:63:LEU:HD23	14:I:65:ILE:HD11	1.95	0.48
28:Y:32:U:H2'	28:Y:33:U:C6	2.48	0.48
30:a:546:U:H5''	30:a:548:G:N2	2.27	0.48
30:a:1672:A:C2	30:a:2582:G:H5'	2.48	0.48
34:e:136:GLN:HA	34:e:139:LYS:HG2	1.95	0.48
36:g:101:ASN:OD1	36:g:101:ASN:N	2.46	0.48
6:A:227:G:H2'	6:A:228:A:C8	2.48	0.48
6:A:723:U:O4	26:U:53:VAL:HG23	2.13	0.48
15:J:76:ILE:HG22	15:J:79:PRO:HB3	1.94	0.48
30:a:64:A:H2'	30:a:65:U:H6	1.77	0.48
30:a:285:G:C6	30:a:356:G:C6	3.02	0.48
32:c:175:ARG:HH21	32:c:181:MET:HE1	1.78	0.48
35:f:60:ILE:HD13	35:f:138:PHE:HB2	1.95	0.48
36:g:86:LYS:HG3	36:g:165:ALA:HB2	1.95	0.48
6:A:175:C:H2'	6:A:176:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1366:C:H2'	6:A:1367:C:C6	2.49	0.48
8:C:177:THR:HG22	8:C:180:ALA:H	1.78	0.48
10:E:150:PRO:HB3	10:E:165:LEU:HD11	1.95	0.48
11:F:26:THR:O	11:F:30:THR:OG1	2.27	0.48
16:K:61:PHE:O	16:K:65:VAL:HG23	2.12	0.48
28:Y:19:G:C2	30:a:882:G:H1'	2.48	0.48
30:a:286:U:H2'	30:a:287:G:H8	1.77	0.48
30:a:947:A:H2'	30:a:948:C:C6	2.48	0.48
30:a:1378:A:O2'	30:a:1380:G:N7	2.46	0.48
34:e:145:ASP:HA	34:e:166:LYS:O	2.12	0.48
6:A:385:C:H2'	6:A:386:C:C6	2.48	0.48
6:A:459:A:C6	6:A:474:G:C6	3.02	0.48
6:A:562:U:H1'	17:L:12:ARG:HB3	1.96	0.48
6:A:652:U:O4	6:A:752:G:O2'	2.24	0.48
6:A:868:C:H2'	6:A:869:G:O4'	2.12	0.48
6:A:1358:U:OP2	6:A:1359:C:N4	2.45	0.48
6:A:1435:G:H2'	6:A:1436:U:C6	2.48	0.48
7:B:133:GLU:O	7:B:137:ARG:HD3	2.14	0.48
9:D:150:LYS:O	9:D:156:LYS:NZ	2.46	0.48
12:G:97:ASN:O	12:G:101:MET:HG3	2.13	0.48
18:M:15:ALA:O	18:M:19:LEU:HG	2.14	0.48
30:a:886:A:H2'	30:a:887:U:O4'	2.14	0.48
30:a:1447:C:H2'	30:a:1448:G:C8	2.48	0.48
33:d:135:GLY:CA	63:d:301:SPD:N10	2.77	0.48
36:g:159:GLY:HA2	36:g:169:VAL:HG11	1.96	0.48
6:A:828:U:OP1	13:H:22:LYS:NZ	2.44	0.48
6:A:1001:C:H2'	6:A:1002:G:C8	2.48	0.48
7:B:84:ALA:CB	7:B:91:PHE:HB3	2.43	0.48
18:M:88:GLY:O	18:M:92:ARG:HG3	2.13	0.48
30:a:1198:U:H2'	30:a:1199:U:C6	2.48	0.48
30:a:1902:C:H4'	32:c:242:LYS:O	2.14	0.48
32:c:5:LYS:HD3	32:c:17:VAL:HG22	1.96	0.48
5:4:28:VAL:HG13	35:f:140:GLU:HG3	1.95	0.48
6:A:1070:U:H2'	6:A:1071:C:C6	2.48	0.48
9:D:65:TYR:OH	9:D:95:GLU:OE2	2.16	0.48
31:b:9:G:OP1	43:n:15:ARG:HD3	2.14	0.48
36:g:17:VAL:O	36:g:17:VAL:HG23	2.13	0.48
5:4:24:ILE:HD12	35:f:102:ARG:HD2	1.96	0.48
18:M:40:ALA:HB3	18:M:43:VAL:HG23	1.95	0.48
24:S:36:ARG:HD2	24:S:52:HIS:O	2.13	0.48
30:a:576:U:H2'	30:a:577:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2032:G:N7	64:a:6411:HOH:O	2.35	0.48
30:a:2649:C:H2'	30:a:2650:U:H6	1.78	0.48
35:f:78:LYS:HD3	35:f:78:LYS:HA	1.65	0.48
38:i:11:VAL:HG21	38:i:50:THR:HG22	1.96	0.48
41:l:8:LYS:HG3	41:l:9:PHE:CD2	2.49	0.48
6:A:105:G:H2'	6:A:106:C:C6	2.49	0.48
6:A:409:U:H2'	6:A:410:G:C8	2.49	0.48
6:A:997:U:H2'	6:A:998:C:O4'	2.14	0.48
8:C:111:LEU:HD22	8:C:204:LYS:HE3	1.94	0.48
10:E:89:HIS:CD2	10:E:138:ARG:HB3	2.49	0.48
17:L:66:TYR:O	17:L:97:THR:HG23	2.14	0.48
25:T:9:LYS:O	25:T:13:GLN:HG2	2.14	0.48
29:Z:24:U:O2'	30:a:1923:U:OP1	2.32	0.48
29:Z:54:U:H2'	29:Z:55:U:O4'	2.14	0.48
30:a:150:U:H2'	30:a:151:C:C6	2.48	0.48
30:a:357:C:H2'	30:a:358:U:C6	2.49	0.48
30:a:810:U:C4	40:k:29:LYS:O	2.67	0.48
30:a:1114:C:O2'	30:a:1115:G:OP1	2.28	0.48
36:g:43:VAL:HG13	36:g:52:PHE:CE1	2.49	0.48
44:o:22:PRO:HD3	44:o:50:ILE:HD12	1.96	0.48
6:A:663:A:H5''	23:R:50:LYS:HD2	1.94	0.48
6:A:993:G:H22	6:A:996:A:N6	2.09	0.48
6:A:1014:A:H4'	24:S:14:HIS:ND1	2.29	0.48
6:A:1081:A:N7	10:E:52:LYS:HE2	2.29	0.48
6:A:1225:A:H3'	18:M:102:THR:OG1	2.13	0.48
14:I:41:ARG:NE	14:I:41:ARG:HA	2.29	0.48
29:Z:53:G:H2'	29:Z:54:U:C6	2.48	0.48
42:m:86:ARG:NE	42:m:117:ASP:OD2	2.38	0.48
6:A:1319:A:C8	6:A:1323:G:C5	3.01	0.48
6:A:1489:G:OP1	57:A:1601:PAR:N64	2.47	0.48
10:E:60:ILE:HG23	10:E:64:MET:HE2	1.95	0.48
30:a:608:A:H2'	30:a:609:A:C8	2.49	0.48
30:a:711:G:N2	30:a:720:U:O2	2.39	0.48
30:a:1726:C:H2'	30:a:1727:C:C6	2.49	0.48
30:a:2228:G:H2'	30:a:2229:U:C6	2.49	0.48
6:A:229:U:H2'	6:A:230:G:O4'	2.14	0.47
6:A:1317:C:H4'	19:N:48:LEU:HD21	1.95	0.47
6:A:1410:A:H2'	6:A:1411:C:C6	2.49	0.47
20:O:80:GLN:O	20:O:84:ARG:HG3	2.13	0.47
30:a:172:A:H2'	30:a:173:A:C8	2.49	0.47
30:a:634:C:H2'	30:a:635:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1183:U:H2'	30:a:1184:U:C6	2.49	0.47
30:a:2345:G:N3	30:a:2381:A:H2'	2.29	0.47
31:b:28:C:H2'	31:b:29:A:C8	2.48	0.47
31:b:39:A:H2'	31:b:40:U:C6	2.49	0.47
35:f:98:GLU:O	35:f:102:ARG:HG3	2.14	0.47
38:i:19:ASP:O	38:i:23:LYS:NZ	2.31	0.47
43:n:56:LYS:O	43:n:60:GLU:HG2	2.14	0.47
53:x:27:ASN:O	53:x:31:GLN:HG3	2.14	0.47
1:0:26:ASN:OD1	1:0:28:ARG:HB2	2.14	0.47
6:A:737:C:H2'	6:A:738:C:H6	1.79	0.47
6:A:986:U:H2'	6:A:987:G:C8	2.49	0.47
16:K:93:ARG:O	16:K:96:THR:HG22	2.14	0.47
19:N:64:CYS:HB2	19:N:80:SER:HB3	1.96	0.47
25:T:31:PHE:O	25:T:35:VAL:HG23	2.13	0.47
26:U:59:LYS:O	26:U:63:GLU:HG2	2.14	0.47
30:a:1306:C:H2'	30:a:1307:A:H8	1.78	0.47
30:a:1838:C:H4'	30:a:1839:G:C8	2.49	0.47
30:a:2030:6MZ:H8	64:a:6446:HOH:O	2.14	0.47
33:d:149:ASN:OD1	33:d:150:MEQ:N	2.45	0.47
5:4:36:VAL:HA	5:4:40:CYS:SG	2.54	0.47
6:A:144:G:H2'	6:A:145:G:C8	2.49	0.47
6:A:985:C:H2'	6:A:986:U:C6	2.49	0.47
10:E:80:THR:HA	10:E:120:VAL:HG13	1.95	0.47
30:a:281:C:H3'	30:a:282:A:H8	1.79	0.47
30:a:717:C:H2'	30:a:718:A:O4'	2.14	0.47
30:a:910:A:H2'	30:a:911:A:C8	2.49	0.47
30:a:1946:U:H2'	30:a:1947:C:C6	2.48	0.47
31:b:41:G:O6	35:f:69:LYS:HD2	2.14	0.47
6:A:232:G:H21	6:A:263:A:H2	1.61	0.47
6:A:373:A:O2'	6:A:451:A:N7	2.47	0.47
6:A:1358:U:H3'	6:A:1359:C:C6	2.49	0.47
6:A:1524:C:H2'	6:A:1525:G:C8	2.49	0.47
8:C:20:SER:HB3	8:C:22:TRP:NE1	2.29	0.47
10:E:153:VAL:HG21	13:H:99:LEU:HB3	1.95	0.47
14:I:31:ASN:C	14:I:32:GLN:HG3	2.39	0.47
15:J:9:ARG:HD3	15:J:99:GLN:OE1	2.14	0.47
28:Y:21:A:N6	28:Y:46:G:O2'	2.48	0.47
30:a:1716:U:H2'	30:a:1717:A:C8	2.49	0.47
30:a:2298:A:H2'	30:a:2299:U:O4'	2.14	0.47
30:a:2346:A:H3'	30:a:2347:C:H5''	1.96	0.47
30:a:2800:A:C2	30:a:2895:G:H1'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:107:LEU:O	36:g:152:ARG:NH2	2.44	0.47
6:A:363:A:H4'	17:L:81:LEU:HD11	1.97	0.47
6:A:687:A:C2	6:A:704:A:C5	3.03	0.47
6:A:860:A:H2'	6:A:861:G:O4'	2.15	0.47
6:A:865:A:H2'	6:A:866:C:C6	2.49	0.47
6:A:912:C:H2'	6:A:913:A:C8	2.49	0.47
6:A:983:A:H2	6:A:984:C:C6	2.33	0.47
6:A:1009:U:O2'	6:A:1010:U:H5'	2.14	0.47
6:A:1312:G:H2'	6:A:1313:U:H6	1.79	0.47
9:D:172:GLU:CG	9:D:183:LYS:HD2	2.38	0.47
21:P:45:GLU:O	21:P:46:LYS:HG3	2.15	0.47
28:Y:8:U:H3	28:Y:14:A:H62	1.63	0.47
30:a:2074:U:H2'	30:a:2075:U:C6	2.49	0.47
30:a:2292:U:H2'	30:a:2293:G:H8	1.78	0.47
35:f:74:VAL:HG12	35:f:77:PHE:H	1.79	0.47
40:k:77:ILE:CD1	40:k:108:ALA:HB1	2.44	0.47
6:A:637:C:H5''	22:Q:4:LYS:HG2	1.96	0.47
6:A:949:A:H2'	6:A:950:U:C6	2.49	0.47
6:A:980:C:H2'	6:A:981:U:O4'	2.14	0.47
6:A:1330:U:H2'	6:A:1331:G:O4'	2.15	0.47
15:J:41:PRO:HA	15:J:72:ARG:HD3	1.94	0.47
22:Q:31:HIS:N	22:Q:36:LYS:O	2.39	0.47
26:U:29:LEU:HA	26:U:32:VAL:HG22	1.95	0.47
30:a:1487:U:H2'	30:a:1488:C:H6	1.79	0.47
6:A:19:A:O2'	6:A:572:A:N1	2.47	0.47
6:A:113:G:H2'	6:A:114:U:C6	2.50	0.47
6:A:178:C:C2	6:A:179:A:C8	3.02	0.47
6:A:707:U:H4'	16:K:22:HIS:CG	2.50	0.47
6:A:857:C:H2'	6:A:858:G:O4'	2.14	0.47
6:A:982:U:H4'	6:A:983:A:O4'	2.15	0.47
6:A:1123:U:O2'	15:J:38:GLY:HA2	2.13	0.47
6:A:1446:A:O2'	6:A:1447:A:H5'	2.13	0.47
7:B:217:VAL:HA	7:B:220:THR:HG22	1.96	0.47
8:C:18:TRP:NE1	19:N:93:ILE:O	2.46	0.47
8:C:130:PHE:CE2	8:C:157:LEU:HD13	2.49	0.47
9:D:114:ALA:O	9:D:118:VAL:HG23	2.14	0.47
16:K:67:ALA:HB3	16:K:99:ALA:HB3	1.96	0.47
17:L:89:D2T:OD2	17:L:89:D2T:N	2.47	0.47
20:O:64:ARG:NH1	20:O:89:ARG:OXT	2.36	0.47
26:U:50:ALA:HA	26:U:53:VAL:HG12	1.96	0.47
33:d:137:SER:OG	63:d:301:SPD:C9	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:73:ASN:O	36:g:76:VAL:HG22	2.15	0.47
43:n:38:GLN:HB3	43:n:47:VAL:HG13	1.96	0.47
55:z:52:ARG:NH2	55:z:54:VAL:HG12	2.29	0.47
3:2:42:ARG:HG3	3:2:45:ARG:NH2	2.30	0.47
6:A:649:A:H2'	6:A:650:G:O4'	2.15	0.47
6:A:1060:U:C5'	15:J:53:ILE:HG22	2.45	0.47
6:A:1102:A:H2'	6:A:1103:C:C6	2.49	0.47
6:A:1343:G:H4'	14:I:124:ARG:HB2	1.97	0.47
14:I:19:VAL:HA	14:I:65:ILE:HG12	1.95	0.47
20:O:88:ARG:NH1	30:a:716:A:OP2	2.48	0.47
25:T:47:ALA:HB1	25:T:83:ILE:HG12	1.97	0.47
28:Y:25:C:C2	28:Y:26:A:C8	3.03	0.47
29:Z:56:C:H1'	35:f:80:ARG:HD3	1.97	0.47
30:a:278:A:N6	30:a:362:A:N7	2.63	0.47
30:a:360:U:H2'	30:a:361:G:C8	2.50	0.47
30:a:2333:A:H5'	30:a:2335:A:H1'	1.96	0.47
30:a:2783:U:H2'	30:a:2784:U:H6	1.80	0.47
36:g:20:ASN:N	36:g:20:ASN:OD1	2.47	0.47
6:A:252:U:O4	6:A:253:A:N6	2.46	0.47
6:A:637:C:H4'	22:Q:4:LYS:HE3	1.96	0.47
6:A:672:U:H2'	6:A:673:A:H8	1.79	0.47
6:A:1134:G:H2'	6:A:1135:U:O4'	2.15	0.47
8:C:111:LEU:HB3	8:C:204:LYS:HE3	1.96	0.47
8:C:123:GLN:HA	8:C:126:ARG:HE	1.78	0.47
15:J:92:LEU:HD23	15:J:93:ALA:N	2.29	0.47
18:M:10:PRO:HB2	18:M:13:LYS:HG3	1.96	0.47
19:N:82:ILE:O	19:N:86:GLU:HG2	2.15	0.47
6:A:2:A:H2'	6:A:3:A:C8	2.50	0.47
6:A:757:U:OP1	6:A:822:U:O2'	2.31	0.47
18:M:18:ALA:O	18:M:21:SER:OG	2.33	0.47
20:O:7:ALA:O	20:O:11:ILE:HG12	2.15	0.47
23:R:36:SER:O	23:R:72:ASP:N	2.48	0.47
25:T:10:ARG:HD3	25:T:13:GLN:NE2	2.29	0.47
30:a:586:A:N1	30:a:809:G:O2'	2.47	0.47
30:a:969:G:H2'	30:a:970:U:C6	2.50	0.47
30:a:1850:G:H2'	30:a:1851:U:C6	2.50	0.47
35:f:75:ALA:O	35:f:78:LYS:NZ	2.46	0.47
36:g:38:ASN:HD22	36:g:64:GLN:CD	2.21	0.47
47:r:20:VAL:HG11	47:r:44:ALA:HA	1.97	0.47
6:A:160:A:H2'	6:A:161:A:C8	2.49	0.46
6:A:191:G:H3'	6:A:192:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:476:U:H2'	6:A:477:C:C6	2.50	0.46
6:A:908:A:H2'	6:A:909:A:H8	1.79	0.46
6:A:966:2MG:HM23	6:A:967:5MC:H1'	1.96	0.46
6:A:1376:U:H2'	6:A:1377:A:C8	2.50	0.46
6:A:1412:C:H2'	6:A:1413:A:C8	2.51	0.46
9:D:88:GLU:HG3	9:D:188:ARG:HG2	1.97	0.46
14:I:22:LYS:HG2	14:I:23:PRO:HD2	1.97	0.46
15:J:48:ARG:HG2	15:J:66:GLU:HG3	1.97	0.46
16:K:85:MET:HB3	16:K:113:VAL:HG21	1.96	0.46
24:S:3:ARG:HE	24:S:7:LYS:HB2	1.80	0.46
30:a:1157:G:OP1	64:a:6315:HOH:O	2.20	0.46
31:b:104:A:H2'	31:b:105:G:O4'	2.14	0.46
53:x:18:LEU:O	53:x:22:LEU:HG	2.16	0.46
54:y:57:VAL:HG12	54:y:59:GLU:HG2	1.95	0.46
5:4:60:PHE:CE1	24:S:68:GLY:HA2	2.50	0.46
6:A:1151:A:O4'	15:J:41:PRO:HB2	2.15	0.46
15:J:7:ARG:HD2	15:J:73:LEU:HD11	1.97	0.46
24:S:50:ALA:HA	24:S:58:VAL:O	2.15	0.46
24:S:51:VAL:O	24:S:57:HIS:HA	2.15	0.46
30:a:1151:A:N3	64:a:6420:HOH:O	2.36	0.46
30:a:1680:U:H2'	30:a:1681:G:O4'	2.15	0.46
5:4:62:LYS:HE3	5:4:62:LYS:HB2	1.73	0.46
6:A:1206:G:C6	6:A:1207:2MG:C5	3.03	0.46
10:E:86:LYS:NZ	10:E:86:LYS:HB3	2.30	0.46
28:Y:18:G:N2	28:Y:58:A:OP1	2.48	0.46
28:Y:41:C:H2'	28:Y:42:C:H6	1.80	0.46
30:a:271:G:O2'	30:a:272:A:H8	1.99	0.46
30:a:1846:G:O2'	30:a:1847:A:H5'	2.15	0.46
40:k:78:ARG:HG2	40:k:113:ALA:HB3	1.96	0.46
55:z:54:VAL:HG23	55:z:55:ILE:HG12	1.97	0.46
6:A:20:U:H2'	6:A:21:G:O4'	2.16	0.46
6:A:73:C:O2'	6:A:74:A:H8	1.93	0.46
6:A:440:C:H2'	6:A:441:A:O4'	2.16	0.46
6:A:1124:G:N2	6:A:1125:U:O4	2.38	0.46
8:C:133:ALA:O	8:C:136:ARG:HG3	2.15	0.46
23:R:14:THR:HG23	23:R:51:TYR:HE2	1.80	0.46
28:Y:19:G:N2	30:a:896:A:N7	2.64	0.46
29:Z:6:G:H2'	29:Z:7:G:H8	1.80	0.46
30:a:2196:C:H2'	30:a:2197:U:C6	2.51	0.46
34:e:7:ASP:CG	34:e:122:GLU:H	2.22	0.46
39:j:107:LEU:HB2	39:j:116:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:l:53:MET:HE1	41:l:103:TYR:CD1	2.50	0.46
6:A:73:C:H42	6:A:97:G:H1	1.62	0.46
6:A:246:A:C2	6:A:282:A:C5	3.04	0.46
6:A:957:U:H5''	24:S:81:ARG:HH12	1.81	0.46
14:I:12:ARG:HH22	14:I:109:ARG:HH21	1.63	0.46
28:Y:53:G:H3'	28:Y:54:U:H6	1.80	0.46
30:a:27:G:N2	30:a:512:G:H1'	2.31	0.46
30:a:57:C:H2'	30:a:58:G:O4'	2.16	0.46
30:a:548:G:H2'	30:a:549:G:C1'	2.46	0.46
30:a:1182:G:H2'	30:a:1183:U:O4'	2.15	0.46
30:a:2627:G:O2'	30:a:2781:A:N1	2.42	0.46
31:b:22:U:H2'	31:b:23:G:C8	2.50	0.46
6:A:145:G:N2	6:A:178:C:C2	2.84	0.46
6:A:385:C:H2'	6:A:386:C:H6	1.81	0.46
6:A:442:G:H2'	6:A:443:C:C6	2.50	0.46
6:A:1053:G:H4'	6:A:1054:C:H3'	1.97	0.46
9:D:138:SER:O	9:D:141:ASP:HB2	2.15	0.46
15:J:30:LYS:HE2	15:J:35:GLN:HA	1.97	0.46
20:O:30:ALA:HA	20:O:85:LEU:HD21	1.97	0.46
30:a:2491[A]:U:H5''	30:a:2570:G:H5'	1.98	0.46
6:A:466:A:H2'	6:A:468:A:C8	2.51	0.46
6:A:1014:A:N3	6:A:1219:A:H1'	2.30	0.46
12:G:102:ARG:O	12:G:106:GLU:HG2	2.16	0.46
30:a:811:U:H2'	40:k:21:ARG:HA	1.98	0.46
30:a:2291:U:H2'	30:a:2292:U:H6	1.77	0.46
33:d:38:LYS:HD3	33:d:43:ASP:OD2	2.16	0.46
5:4:42:PRO:HB2	5:4:48:GLN:NE2	2.30	0.46
6:A:1070:U:H2'	6:A:1071:C:H6	1.80	0.46
6:A:1157:A:C2	6:A:1181:G:C5	3.04	0.46
6:A:1160:G:C2	6:A:1161:C:C6	3.04	0.46
30:a:1:G:H2'	30:a:2:G:C8	2.51	0.46
30:a:106:C:H2'	30:a:107:G:H8	1.81	0.46
30:a:280:U:H2'	30:a:281:C:O4'	2.16	0.46
34:e:12:LEU:HD12	34:e:12:LEU:HA	1.73	0.46
4:3:25:VAL:HB	4:3:35:GLN:HG2	1.96	0.46
6:A:74:A:H2	6:A:96:U:H3	1.64	0.46
6:A:156:C:H2'	6:A:157:U:O4'	2.15	0.46
6:A:201:G:O6	6:A:217:C:N4	2.49	0.46
6:A:613:C:H2'	6:A:614:C:H6	1.79	0.46
6:A:1228:C:H2'	6:A:1229:A:H8	1.81	0.46
6:A:1389:C:H2'	6:A:1390:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:32:PHE:HD2	7:B:42:ASN:ND2	2.14	0.46
8:C:105:GLU:OE1	8:C:107:ARG:NE	2.48	0.46
9:D:107:PHE:CE1	9:D:178:MET:HG2	2.50	0.46
15:J:19:ASP:HA	15:J:22:THR:HG22	1.98	0.46
16:K:23:ILE:HD13	16:K:96:THR:HG23	1.98	0.46
30:a:372:G:O2'	30:a:400:G:O6	2.32	0.46
36:g:2:SER:OG	36:g:3:ARG:N	2.37	0.46
47:r:92:ARG:NH1	64:r:205:HOH:O	2.48	0.46
49:t:54:GLN:H	49:t:54:GLN:NE2	2.13	0.46
6:A:945:G:C2	6:A:946:A:C8	3.04	0.46
6:A:1248:A:C5	6:A:1290:G:C2	3.04	0.46
17:L:42:PRO:HB2	17:L:89:D2T:H5	1.98	0.46
29:Z:49:G:C2	29:Z:50:U:C5	3.04	0.46
30:a:272:A:H2'	30:a:273:G:C8	2.51	0.46
30:a:886:A:H1'	30:a:891:G:N2	2.31	0.46
30:a:1338:G:O2'	30:a:1393:A:N1	2.39	0.46
30:a:1716:U:H2'	30:a:1717:A:H8	1.80	0.46
30:a:2469:A:H4'	41:l:55:ARG:NE	2.31	0.46
30:a:2649:C:H2'	30:a:2650:U:C6	2.51	0.46
30:a:2898:U:H2'	30:a:2899:A:C8	2.51	0.46
6:A:309:A:H2'	6:A:310:G:H8	1.80	0.45
6:A:332:G:OP1	25:T:4:ILE:HG12	2.16	0.45
6:A:608:A:H2'	6:A:609:A:O4'	2.16	0.45
6:A:1346:A:N1	6:A:1374:A:H5''	2.32	0.45
8:C:134:MET:HE1	8:C:167:TRP:HA	1.97	0.45
11:F:51:ILE:O	11:F:54:LEU:HB2	2.16	0.45
12:G:23:LEU:HD21	12:G:47:LEU:HD11	1.96	0.45
12:G:50:LEU:HD11	12:G:125:SER:HB2	1.97	0.45
20:O:25:THR:O	20:O:29:VAL:HG23	2.16	0.45
30:a:373:U:H2'	30:a:374:A:H8	1.81	0.45
30:a:1316:U:H2'	30:a:1317:G:H8	1.81	0.45
30:a:1487:U:H2'	30:a:1488:C:C6	2.50	0.45
30:a:1794:A:H2'	30:a:1795:C:H6	1.81	0.45
30:a:2590:A:H2'	30:a:2591:C:C6	2.50	0.45
6:A:1130:A:C8	6:A:1146:A:C2	3.04	0.45
11:F:46:GLN:HA	11:F:56:LYS:HG3	1.97	0.45
11:F:55:HIS:O	11:F:56:LYS:HD3	2.16	0.45
30:a:244:A:H2'	30:a:245:G:O4'	2.16	0.45
30:a:2646:C:O5'	30:a:2646:C:H6	1.99	0.45
35:f:5:HIS:HB2	35:f:97:TRP:CD1	2.52	0.45
35:f:103:LEU:HA	35:f:107:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:111:G:H5'	21:P:25:ARG:O	2.16	0.45
6:A:280:C:N3	22:Q:41:THR:HG22	2.31	0.45
6:A:482:A:H2'	6:A:483:C:O4'	2.15	0.45
6:A:737:C:H2'	6:A:738:C:C6	2.51	0.45
6:A:821:G:H2'	6:A:822:U:C6	2.52	0.45
6:A:1195:C:H2'	6:A:1197:A:O4'	2.16	0.45
7:B:109:GLN:HA	7:B:112:LYS:HZ3	1.82	0.45
12:G:66:LEU:O	12:G:70:ARG:N	2.44	0.45
17:L:23:ALA:HB2	17:L:63:VAL:HG11	1.98	0.45
28:Y:53:G:H3'	28:Y:54:U:C6	2.51	0.45
30:a:2895:G:H2'	30:a:2896:C:C6	2.51	0.45
39:j:58:LEU:HA	39:j:89:ASN:ND2	2.31	0.45
41:l:64:TRP:CZ3	41:l:106:ASP:HB2	2.51	0.45
44:o:31:TRP:HB3	44:o:38:LYS:HE2	1.98	0.45
6:A:321:A:H62	6:A:328:C:H1'	1.81	0.45
6:A:568:G:O6	17:L:2:ALA:N	2.50	0.45
7:B:55:ALA:O	7:B:59:LYS:HG2	2.16	0.45
8:C:152:GLU:OE1	8:C:154:SER:OG	2.33	0.45
11:F:47:LEU:HD21	11:F:57:ALA:HB3	1.99	0.45
14:I:87:LEU:HD23	14:I:98:LEU:HD11	1.97	0.45
19:N:27:LEU:O	19:N:30:ILE:HG22	2.17	0.45
26:U:41:PRO:O	26:U:45:ARG:HG3	2.15	0.45
29:Z:23:C:H2'	29:Z:24:U:C6	2.52	0.45
30:a:419:U:H2'	30:a:420:C:C6	2.52	0.45
30:a:580:U:O3'	45:p:31:VAL:HG13	2.16	0.45
30:a:1019:U:O2'	30:a:1021:A:N7	2.46	0.45
30:a:1386:C:H2'	30:a:1387:A:H8	1.81	0.45
30:a:1469:A:H2'	30:a:1470:A:C8	2.52	0.45
30:a:1790:C:H2'	30:a:1791:A:C5	2.52	0.45
36:g:60:ASP:O	36:g:62:TRP:N	2.45	0.45
6:A:472:U:H2'	6:A:473:U:C6	2.52	0.45
7:B:109:GLN:OE1	7:B:109:GLN:N	2.50	0.45
8:C:22:TRP:CZ2	8:C:32:ASN:HB3	2.51	0.45
8:C:107:ARG:HG3	8:C:108:LYS:H	1.82	0.45
10:E:29:ARG:O	10:E:30:ILE:HD13	2.16	0.45
16:K:16:VAL:HG21	16:K:42:LEU:HD11	1.97	0.45
20:O:35:GLN:HG2	20:O:59:MET:SD	2.56	0.45
28:Y:28:G:H2'	28:Y:29:G:O4'	2.16	0.45
30:a:322:A:OP2	34:e:163:ASN:HB2	2.16	0.45
30:a:1306:C:H2'	30:a:1307:A:C8	2.52	0.45
30:a:2095:A:H5'	37:h:11:ASN:OD1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:f:47:LYS:HZ3	35:f:84:PRO:HG2	1.80	0.45
39:j:76:VAL:HG12	44:o:73:VAL:HB	1.99	0.45
52:w:71:LEU:HD22	52:w:76:GLU:HG3	1.98	0.45
6:A:195:A:H2'	6:A:196:A:C8	2.52	0.45
6:A:695:A:H2'	6:A:696:A:C8	2.51	0.45
6:A:741:G:H2'	6:A:742:G:O4'	2.16	0.45
6:A:1048:G:O6	6:A:1210:C:N4	2.49	0.45
7:B:64:LYS:HE2	7:B:225:ARG:CZ	2.47	0.45
8:C:202:ILE:HG22	8:C:204:LYS:HD3	1.98	0.45
12:G:72:THR:HA	12:G:96:ARG:NE	2.32	0.45
19:N:49:GLN:NE2	24:S:11:ILE:O	2.50	0.45
21:P:52:LEU:HB3	21:P:54:LEU:HG	1.98	0.45
30:a:283:G:O6	30:a:357:C:N4	2.43	0.45
30:a:1786:A:H1'	30:a:1938:A:N6	2.31	0.45
30:a:2484:G:H1'	41:l:123:LYS:HD2	1.99	0.45
30:a:2520:C:C6	30:a:2567:G:H1'	2.52	0.45
63:a:6212:SPD:H101	63:a:6212:SPD:H72	1.44	0.45
33:d:149:ASN:CG	33:d:150:MEQ:H	2.24	0.45
34:e:5:LEU:HG	34:e:120:VAL:HG12	1.98	0.45
47:r:65:ASP:HB3	47:r:68:ASP:OD2	2.17	0.45
6:A:505:G:H5'	6:A:534:U:H2'	1.99	0.45
6:A:678:U:H2'	6:A:679:C:C6	2.52	0.45
6:A:736:C:H2'	6:A:737:C:C6	2.51	0.45
6:A:1456:A:H2'	6:A:1457:G:O4'	2.16	0.45
7:B:143:LYS:HD2	7:B:143:LYS:HA	1.72	0.45
10:E:85:VAL:HG11	10:E:147:MET:HB3	1.99	0.45
13:H:92:LEU:O	13:H:117:ARG:NH1	2.49	0.45
15:J:35:GLN:HB3	15:J:78:GLU:OE1	2.17	0.45
18:M:9:ILE:HB	18:M:18:ALA:HB1	1.97	0.45
29:Z:64:G:C2	29:Z:65:C:H1'	2.52	0.45
30:a:2066:C:OP2	64:a:6317:HOH:O	2.21	0.45
30:a:2480:C:H2'	30:a:2481:G:O4'	2.16	0.45
30:a:2658:C:OP1	36:g:158:LYS:NZ	2.49	0.45
43:n:35:ILE:HG21	43:n:71:ALA:HA	1.99	0.45
46:q:5:PHE:HB3	46:q:59:ILE:HD12	1.99	0.45
47:r:95:ARG:HH11	47:r:97:LEU:HD21	1.80	0.45
5:4:42:PRO:HB3	5:4:47:LYS:HB2	1.99	0.45
5:4:64:PHE:CE1	24:S:5:LEU:HD23	2.52	0.45
6:A:193:C:H2'	6:A:194:C:C6	2.51	0.45
6:A:233:C:H2'	6:A:234:C:H6	1.81	0.45
6:A:278:G:N2	6:A:279:A:N1	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1035:A:C2	6:A:1036:A:C2	3.05	0.45
6:A:1326:U:H2'	6:A:1327:C:H6	1.80	0.45
6:A:1373:G:H5''	12:G:36:LYS:HD2	1.98	0.45
9:D:170:TRP:CD2	9:D:186:PRO:HB3	2.52	0.45
10:E:91:GLY:O	10:E:130:SER:N	2.49	0.45
17:L:43:LYS:HD3	17:L:91:PRO:HG3	1.99	0.45
18:M:82:ASP:N	18:M:82:ASP:OD1	2.50	0.45
30:a:92:U:H2'	30:a:93:G:O4'	2.16	0.45
30:a:1197:G:H2'	30:a:1198:U:H6	1.82	0.45
30:a:1932:A:H2'	30:a:1933:G:O4'	2.17	0.45
30:a:2086:U:H2'	30:a:2087:G:C8	2.51	0.45
30:a:2788:C:O2'	30:a:2809:A:N3	2.46	0.45
31:b:28:C:H2'	31:b:29:A:H8	1.81	0.45
42:m:96:ARG:HD2	42:m:114:GLU:OE2	2.16	0.45
45:p:11:ARG:HE	45:p:15:LYS:HG3	1.81	0.45
6:A:1014:A:H4'	24:S:14:HIS:CE1	2.52	0.45
6:A:1142:G:C5	6:A:1143:G:H1'	2.52	0.45
6:A:1250:A:C8	6:A:1287:A:N7	2.85	0.45
6:A:1367:C:OP1	14:I:117:GLY:N	2.32	0.45
6:A:1465:A:H2'	6:A:1466:C:C6	2.52	0.45
7:B:143:LYS:HA	7:B:146:ASN:OD1	2.17	0.45
11:F:43:GLY:HA2	11:F:58:HIS:CE1	2.52	0.45
14:I:81:HIS:NE2	14:I:104:VAL:O	2.47	0.45
27:X:16:A:H2'	27:X:17:U:O4'	2.16	0.45
30:a:600:G:H2'	30:a:601:C:C6	2.52	0.45
30:a:829:A:N7	30:a:2248:C:H5'	2.31	0.45
47:r:95:ARG:NH1	47:r:97:LEU:HD21	2.32	0.45
53:x:24:GLU:OE1	53:x:46:VAL:HG21	2.17	0.45
5:4:11:GLU:HA	5:4:25:ARG:HA	1.98	0.45
6:A:8:A:C5	9:D:206:LYS:HD3	2.51	0.45
6:A:599:C:H2'	6:A:600:A:H8	1.82	0.45
6:A:672:U:H2'	6:A:673:A:C8	2.52	0.45
6:A:676:A:H2'	6:A:677:U:H6	1.81	0.45
6:A:1436:U:C2	6:A:1437:A:C8	3.05	0.45
8:C:111:LEU:HD21	8:C:146:ALA:HB2	1.98	0.45
9:D:47:ARG:H	9:D:47:ARG:HD3	1.82	0.45
14:I:57:MET:HB3	14:I:61:LEU:HD12	2.00	0.45
17:L:50:ARG:HB2	17:L:90:LEU:HD11	1.99	0.45
26:U:28:VAL:O	26:U:32:VAL:HG13	2.17	0.45
28:Y:22:G:H2'	28:Y:23:A:H8	1.82	0.45
30:a:146:A:H2'	30:a:147:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:607:U:N3	30:a:608:A:N7	2.65	0.45
30:a:866:A:C8	30:a:914:G:C6	3.05	0.45
30:a:1485:U:H2'	30:a:1486:U:C6	2.52	0.45
30:a:2786:U:O2'	33:d:63:PRO:O	2.34	0.45
31:b:48:U:H2'	31:b:49:C:H6	1.81	0.45
34:e:149:ILE:HB	34:e:188:MET:HG3	1.98	0.45
6:A:255:G:H2'	6:A:256:U:C6	2.51	0.44
6:A:507:C:OP2	6:A:508:U:O2'	2.28	0.44
6:A:587:G:N1	6:A:754:C:OP2	2.41	0.44
6:A:653:U:N3	13:H:56:LYS:HG2	2.32	0.44
6:A:917:G:H2'	6:A:918:A:C8	2.52	0.44
6:A:953:G:H2'	6:A:954:G:O4'	2.16	0.44
6:A:958:A:H1'	6:A:985:C:O2'	2.17	0.44
8:C:107:ARG:HD3	8:C:109:PRO:HD3	1.99	0.44
30:a:354:A:H2'	30:a:355:U:O4'	2.18	0.44
30:a:852:U:H2'	30:a:853:C:H6	1.81	0.44
30:a:2661:G:H8	30:a:2661:G:OP2	1.99	0.44
34:e:5:LEU:HD11	34:e:12:LEU:HB2	1.98	0.44
34:e:139:LYS:HE2	34:e:139:LYS:HB2	1.66	0.44
34:e:149:ILE:HB	34:e:188:MET:CG	2.47	0.44
6:A:269:C:C2	6:A:270:A:N7	2.85	0.44
6:A:996:A:H2'	6:A:997:U:C6	2.52	0.44
6:A:1366:C:O2'	15:J:62:ARG:NH2	2.50	0.44
8:C:11:ARG:NH2	8:C:177:THR:O	2.43	0.44
8:C:22:TRP:CH2	8:C:32:ASN:HB3	2.52	0.44
19:N:27:LEU:HD12	19:N:27:LEU:HA	1.68	0.44
30:a:17:G:H2'	30:a:18:U:C6	2.52	0.44
30:a:30:G:H2'	30:a:31:C:H6	1.82	0.44
30:a:90:U:H3'	30:a:91:A:H2'	1.99	0.44
30:a:1747:U:H2'	30:a:1748:C:H6	1.81	0.44
30:a:2494:G:O2'	41:l:79:ALA:HA	2.16	0.44
49:t:98:SER:O	49:t:98:SER:OG	2.31	0.44
50:u:86:LEU:HD13	50:u:89:ILE:HD11	1.99	0.44
5:4:63:ARG:HB2	24:S:5:LEU:CD2	2.47	0.44
6:A:177:G:C5	6:A:178:C:C5	3.05	0.44
6:A:375:U:OP1	21:P:70:ARG:HD3	2.17	0.44
6:A:404:G:O2'	6:A:498:A:N1	2.46	0.44
6:A:469:C:H2'	6:A:470:C:C6	2.51	0.44
6:A:483:C:H5''	6:A:484:G:OP2	2.17	0.44
6:A:524:G:H2'	6:A:525:C:C6	2.53	0.44
6:A:981:U:H5''	19:N:63:ARG:HH22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:2:ARG:HD3	11:F:91:ARG:CZ	2.47	0.44
12:G:142:HIS:O	12:G:146:GLU:HG2	2.18	0.44
29:Z:24:U:H2'	29:Z:25:C:C6	2.52	0.44
30:a:152:A:H2'	30:a:153:U:H6	1.83	0.44
30:a:306:U:H2'	30:a:307:G:O4'	2.17	0.44
30:a:365:U:H6	30:a:365:U:O5'	2.00	0.44
6:A:1314:C:H2'	6:A:1315:U:H6	1.81	0.44
6:A:1315:U:H2'	6:A:1316:G:C8	2.52	0.44
25:T:61:GLN:HB3	25:T:66:LEU:HB3	1.99	0.44
25:T:79:LEU:HD23	25:T:79:LEU:HA	1.86	0.44
29:Z:13:C:O2'	30:a:1924:C:H4'	2.17	0.44
29:Z:19:G:OP1	29:Z:60:U:N3	2.51	0.44
30:a:275:C:H2'	30:a:276:U:O4'	2.17	0.44
30:a:2514:U:H2'	30:a:2515:C:C6	2.53	0.44
30:a:2533:U:H2'	30:a:2534:A:O4'	2.18	0.44
36:g:155:GLU:HG2	36:g:160:LYS:HB2	2.00	0.44
41:l:77:PRO:HG2	41:l:80:VAL:HG21	2.00	0.44
46:q:44:GLY:O	46:q:45:GLU:HB2	2.17	0.44
5:4:15:SER:O	5:4:33:ASN:HA	2.17	0.44
6:A:411:A:N3	6:A:412:A:O2'	2.46	0.44
6:A:451:A:H2'	6:A:481:G:O6	2.17	0.44
6:A:662:U:H2'	6:A:663:A:C8	2.52	0.44
6:A:1041:G:C2	6:A:1042:A:C8	3.06	0.44
6:A:1124:G:H4'	15:J:40:ILE:HD11	1.99	0.44
6:A:1209:C:H2'	6:A:1210:C:H6	1.82	0.44
6:A:1236:A:H2'	6:A:1237:C:C6	2.52	0.44
6:A:1308:U:OP1	18:M:97:VAL:HG12	2.18	0.44
6:A:1391:U:H2'	6:A:1392:G:C8	2.52	0.44
8:C:20:SER:O	19:N:94:PRO:HB3	2.17	0.44
9:D:11:LEU:CD2	9:D:63:ARG:HE	2.21	0.44
13:H:74:SER:OG	13:H:76:GLN:NE2	2.36	0.44
23:R:14:THR:HG23	23:R:51:TYR:CE2	2.53	0.44
30:a:548:G:H2'	30:a:549:G:H1'	1.99	0.44
30:a:1047:G:N2	30:a:1111:A:H62	2.16	0.44
30:a:1253:A:H5''	64:a:8105:HOH:O	2.17	0.44
30:a:2680:U:O2'	30:a:2681:C:H5'	2.17	0.44
6:A:1057:G:O3'	8:C:197:GLY:HA3	2.18	0.44
16:K:94:GLU:O	16:K:98:ARG:HG3	2.17	0.44
19:N:19:LYS:HE3	19:N:19:LYS:HB3	1.85	0.44
21:P:19:VAL:HG12	21:P:36:VAL:HG23	1.98	0.44
21:P:21:VAL:HG13	21:P:33:ILE:HB	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:16:LYS:HB3	22:Q:16:LYS:HE2	1.79	0.44
23:R:26:ILE:HD12	23:R:68:LEU:HG	2.00	0.44
25:T:81:ALA:O	25:T:85:LYS:HG3	2.17	0.44
30:a:156:A:H2'	30:a:157:C:C6	2.53	0.44
30:a:580:U:H2'	30:a:581:C:H6	1.81	0.44
30:a:863:A:H2'	30:a:864:G:C8	2.53	0.44
30:a:1049:C:C2	30:a:1050:A:C8	3.06	0.44
30:a:1946:U:H2'	30:a:1947:C:H6	1.81	0.44
6:A:383:A:C5	6:A:384:G:H1'	2.52	0.44
6:A:501:C:O2	6:A:549:C:O2'	2.29	0.44
6:A:766:A:OP2	6:A:812:G:N2	2.49	0.44
6:A:1064:G:H1'	6:A:1190:G:N2	2.33	0.44
8:C:113:ALA:HB3	8:C:185:ASN:HD22	1.83	0.44
14:I:28:ILE:O	14:I:34:SER:HA	2.18	0.44
22:Q:27:ARG:HG3	22:Q:29:VAL:CG2	2.47	0.44
26:U:36:GLU:HG2	26:U:37:PHE:CE2	2.51	0.44
30:a:886:A:C2	30:a:891:G:C6	3.06	0.44
30:a:1432:G:H2'	30:a:1433:A:C8	2.53	0.44
34:e:137:LYS:O	34:e:141:MET:HG3	2.17	0.44
36:g:103:ILE:HD11	36:g:117:LEU:HD11	1.99	0.44
48:s:56:GLU:HG3	48:s:57:VAL:N	2.33	0.44
1:O:30:LYS:HA	1:O:30:LYS:HD3	1.88	0.44
6:A:425:G:H2'	6:A:426:U:C6	2.53	0.44
6:A:539:A:H2'	6:A:540:G:H8	1.81	0.44
6:A:1018:G:H2'	6:A:1019:A:H8	1.81	0.44
6:A:1123:U:O4	6:A:1151:A:N6	2.51	0.44
6:A:1146:A:H2'	6:A:1146:A:N3	2.32	0.44
12:G:76:LYS:HZ2	12:G:89:VAL:HG21	1.82	0.44
15:J:50:THR:HB	15:J:64:GLN:HG2	2.00	0.44
15:J:53:ILE:HD11	15:J:63:ASP:N	2.33	0.44
30:a:151:C:H2'	30:a:152:A:C8	2.51	0.44
30:a:308:G:H2'	30:a:309:A:C8	2.53	0.44
30:a:1316:U:H2'	30:a:1317:G:C8	2.53	0.44
30:a:2314:A:H1'	35:f:155:THR:HG21	1.99	0.44
30:a:2875:C:OP1	42:m:4:ARG:NH2	2.50	0.44
6:A:227:G:H2'	6:A:228:A:H8	1.82	0.44
6:A:404:G:N7	9:D:2:ALA:HB3	2.33	0.44
6:A:409:U:OP1	9:D:23:SER:HB2	2.18	0.44
6:A:537:G:H2'	6:A:538:G:C8	2.53	0.44
6:A:745:G:H1'	6:A:836:G:O2'	2.17	0.44
6:A:1063:C:H2'	6:A:1064:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:16:PRO:HD2	12:G:44:TYR:OH	2.18	0.44
13:H:29:SER:HB2	13:H:59:LEU:H	1.83	0.44
14:I:22:LYS:O	14:I:62:ASP:N	2.36	0.44
16:K:13:ARG:HD3	16:K:14:LYS:N	2.33	0.44
22:Q:8:LEU:HD13	22:Q:73:TRP:CH2	2.52	0.44
24:S:36:ARG:HB3	24:S:72:GLY:CA	2.48	0.44
24:S:70:LYS:HA	24:S:70:LYS:HD3	1.78	0.44
25:T:8:LYS:O	25:T:12:ILE:HG13	2.18	0.44
30:a:134:G:H2'	30:a:135:U:C6	2.53	0.44
30:a:307:G:N1	30:a:310:A:OP2	2.47	0.44
30:a:1563:U:H2'	30:a:1564:C:C6	2.52	0.44
44:o:44:GLU:O	44:o:63:LYS:HE2	2.17	0.44
3:2:55:LEU:HD23	3:2:55:LEU:HA	1.90	0.43
6:A:54:C:H2'	6:A:352:C:H41	1.83	0.43
6:A:193:C:H2'	6:A:194:C:H6	1.83	0.43
6:A:232:G:H1'	6:A:262:A:N1	2.33	0.43
6:A:392:C:OP1	21:P:8:ARG:NH2	2.50	0.43
6:A:708:C:H2'	6:A:709:U:C6	2.53	0.43
7:B:88:ASP:OD2	7:B:225:ARG:NH1	2.51	0.43
7:B:107:VAL:O	7:B:111:ILE:HD12	2.18	0.43
9:D:58:LYS:NZ	9:D:69:GLU:OE2	2.48	0.43
16:K:23:ILE:CG2	16:K:96:THR:HG21	2.47	0.43
16:K:83:GLU:HG2	16:K:109:ASN:HB2	2.00	0.43
30:a:235:U:H2'	30:a:236:C:H6	1.82	0.43
33:d:146:ILE:HA	33:d:159:LYS:HE3	2.00	0.43
6:A:62:U:H2'	6:A:63:C:C6	2.53	0.43
6:A:1005:A:H3'	6:A:1006:G:C8	2.52	0.43
6:A:1014:A:H5'	24:S:18:LYS:HZ1	1.83	0.43
6:A:1118:U:H5'	14:I:106:ARG:HG3	2.00	0.43
25:T:39:ILE:HD13	25:T:82:GLN:CB	2.48	0.43
30:a:1868:C:H3'	30:a:1869:G:H5''	2.00	0.43
36:g:56:ASP:OD1	36:g:57:GLY:N	2.52	0.43
2:1:37:LYS:NZ	30:a:468:G:OP2	2.44	0.43
6:A:321:A:H2'	6:A:322:C:H6	1.83	0.43
6:A:403:C:H2'	6:A:404:G:C8	2.54	0.43
6:A:678:U:H2'	6:A:679:C:H6	1.82	0.43
6:A:983:A:C2	6:A:984:C:C6	3.06	0.43
6:A:1169:A:H2'	6:A:1170:A:C8	2.53	0.43
6:A:1360:A:C4	6:A:1361:G:C8	3.07	0.43
6:A:1366:C:H2'	6:A:1367:C:H6	1.84	0.43
6:A:1402:4OC:H2'	6:A:1403:C:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:126:PHE:CZ	7:B:137:ARG:HB3	2.53	0.43
8:C:62:LYS:HA	8:C:62:LYS:HD2	1.72	0.43
9:D:62:ARG:HG2	9:D:72:PHE:CD1	2.54	0.43
11:F:53:LYS:HA	11:F:53:LYS:HD2	1.57	0.43
14:I:13:LYS:H	14:I:13:LYS:HG3	1.60	0.43
19:N:39:GLU:O	19:N:43:ASN:ND2	2.51	0.43
30:a:584:C:H3'	45:p:6:ARG:HH11	1.84	0.43
30:a:1586:A:H3'	30:a:1587:G:H8	1.83	0.43
6:A:360:G:H2'	6:A:361:G:C8	2.53	0.43
6:A:411:A:H61	6:A:430:A:H62	1.65	0.43
6:A:966:2MG:O2'	14:I:129:LYS:O	2.36	0.43
6:A:1088:G:H2'	6:A:1089:G:O4'	2.18	0.43
6:A:1465:A:H2'	6:A:1466:C:H6	1.84	0.43
8:C:50:ALA:O	8:C:72:ARG:HB2	2.19	0.43
13:H:10:MET:HE3	13:H:61:LEU:HD11	2.00	0.43
14:I:88:MET:HE3	14:I:98:LEU:HD12	2.01	0.43
22:Q:53:CYS:SG	22:Q:75:LEU:HD11	2.58	0.43
30:a:184:C:H2'	30:a:185:G:H8	1.83	0.43
30:a:657:U:H2'	30:a:658:U:C6	2.53	0.43
30:a:723:C:H2'	30:a:724:U:O4'	2.19	0.43
30:a:1170:C:H2'	30:a:1171:G:H5''	2.00	0.43
30:a:1224:U:H2'	30:a:1225:G:C8	2.53	0.43
31:b:42:C:C6	35:f:66:LEU:HB2	2.53	0.43
36:g:127:THR:OG1	36:g:128:GLN:N	2.51	0.43
40:k:1:MET:HE2	40:k:1:MET:HB3	1.89	0.43
46:q:33:VAL:HG23	46:q:61:ALA:HB3	2.00	0.43
6:A:45:G:H2'	6:A:46:G:H8	1.81	0.43
6:A:59:A:H3'	6:A:331:G:H22	1.84	0.43
6:A:263:A:H2'	6:A:264:C:H6	1.82	0.43
6:A:625:U:H2'	6:A:626:G:H8	1.83	0.43
6:A:673:A:H2'	6:A:674:G:H8	1.77	0.43
8:C:119:SER:O	8:C:123:GLN:HG3	2.18	0.43
10:E:54:ARG:NH1	10:E:54:ARG:O	2.46	0.43
13:H:80:ARG:HG3	13:H:83:LEU:H	1.83	0.43
14:I:96:SER:HB2	14:I:100:LYS:NZ	2.33	0.43
21:P:5:ARG:NH2	21:P:26:ASN:O	2.51	0.43
30:a:587:C:C2	40:k:19:LEU:HD12	2.54	0.43
30:a:645:C:H2'	30:a:647:G:N7	2.33	0.43
30:a:1429:G:H2'	30:a:1430:G:H8	1.82	0.43
30:a:2229:U:H2'	30:a:2230:G:H8	1.82	0.43
30:a:2804:U:H2'	30:a:2805:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:e:123:LYS:HA	34:e:123:LYS:HD3	1.71	0.43
36:g:2:SER:O	36:g:6:LYS:HG2	2.18	0.43
5:4:32:LEU:HD23	5:4:34:LEU:HD21	2.00	0.43
6:A:176:C:H2'	6:A:177:G:O4'	2.19	0.43
6:A:659:U:H2'	6:A:660:C:C6	2.53	0.43
6:A:1308:U:OP1	18:M:97:VAL:N	2.43	0.43
6:A:1510:C:H2'	6:A:1511:G:C8	2.54	0.43
7:B:132:LYS:HE2	7:B:132:LYS:HB2	1.75	0.43
9:D:150:LYS:HZ3	9:D:178:MET:HE3	1.83	0.43
17:L:110:ARG:HA	17:L:110:ARG:HD2	1.46	0.43
19:N:47:LYS:HD3	19:N:47:LYS:HA	1.92	0.43
30:a:302:C:H2'	30:a:303:G:H8	1.83	0.43
30:a:857:G:H2'	30:a:858:G:O4'	2.18	0.43
30:a:2273:A:H2'	30:a:2274:A:C8	2.54	0.43
37:h:34:GLY:C	37:h:36:ALA:H	2.26	0.43
6:A:825:A:H2'	6:A:826:C:H6	1.84	0.43
6:A:1228:C:H2'	6:A:1229:A:C8	2.54	0.43
6:A:1410:A:H2'	6:A:1411:C:H6	1.84	0.43
7:B:100:MET:HE2	7:B:100:MET:HB3	1.86	0.43
22:Q:9:GLN:OE1	22:Q:60:GLU:HB3	2.18	0.43
23:R:9:LYS:HA	23:R:9:LYS:HE2	2.00	0.43
24:S:15:LEU:O	24:S:19:VAL:HG13	2.19	0.43
27:X:22:U:H2'	27:X:23:A:H5'	2.01	0.43
30:a:1842:G:H2'	30:a:1843:C:H6	1.84	0.43
30:a:2262:U:H2'	30:a:2263:C:H6	1.83	0.43
35:f:36:LEU:HD11	35:f:99:PHE:CZ	2.53	0.43
6:A:402:G:H2'	6:A:403:C:C6	2.53	0.43
6:A:412:A:H3'	6:A:412:A:P	2.58	0.43
6:A:661:G:H2'	6:A:662:U:C6	2.54	0.43
6:A:750:C:H2'	6:A:751:U:H6	1.83	0.43
6:A:1077:G:C6	6:A:1081:A:C6	3.07	0.43
7:B:42:ASN:OD1	7:B:45:LYS:HD3	2.19	0.43
9:D:54:GLN:HB3	9:D:203:LEU:HB2	2.01	0.43
10:E:38:VAL:HG11	10:E:114:VAL:HG22	2.01	0.43
13:H:92:LEU:HD21	13:H:122:GLY:HA2	2.01	0.43
14:I:27:LYS:HE3	14:I:27:LYS:HB3	1.47	0.43
14:I:57:MET:HE2	14:I:60:LYS:HD3	2.00	0.43
14:I:88:MET:HE1	14:I:94:LEU:C	2.43	0.43
21:P:6:LEU:HD12	21:P:18:GLN:O	2.18	0.43
25:T:15:GLU:O	25:T:19:LYS:HG2	2.19	0.43
30:a:150:U:H2'	30:a:151:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:639:U:H2'	30:a:640:C:H6	1.79	0.43
49:t:54:GLN:HG2	49:t:55:PRO:HD3	2.00	0.43
6:A:1108:G:N3	6:A:1108:G:H2'	2.33	0.43
6:A:1147:C:C2	6:A:1148:U:C5	3.07	0.43
6:A:1342:C:H2'	6:A:1343:G:H8	1.84	0.43
6:A:1480:A:H2'	6:A:1481:U:O4'	2.19	0.43
23:R:69:PRO:HB2	23:R:71:THR:O	2.19	0.43
28:Y:1:G:H2'	28:Y:2:C:C6	2.54	0.43
30:a:538:A:H2'	30:a:539:G:O4'	2.19	0.43
30:a:589:U:H2'	30:a:590:A:C8	2.54	0.43
30:a:833:A:H2'	30:a:834:G:H8	1.84	0.43
30:a:1589:U:H2'	30:a:1590:A:H8	1.82	0.43
30:a:1918:A:O2'	30:a:1920:C:N4	2.52	0.43
30:a:2820:A:N3	30:a:2820:A:H2'	2.34	0.43
44:o:32:VAL:HG23	44:o:39:ARG:HG3	2.01	0.43
45:p:49:ASP:HA	45:p:52:GLN:HB2	2.01	0.43
6:A:948:C:H2'	6:A:949:A:C8	2.54	0.43
6:A:1298:U:H4'	6:A:1299:A:O4'	2.19	0.43
7:B:84:ALA:HB2	7:B:91:PHE:HB3	2.00	0.43
10:E:143:GLY:HA2	10:E:146:ASN:HD21	1.84	0.43
13:H:46:ILE:HD12	13:H:48:ASP:O	2.19	0.43
15:J:52:LEU:HD11	15:J:59:LYS:HD2	2.01	0.43
30:a:598:U:H2'	30:a:599:A:C8	2.53	0.43
30:a:1370:C:H2'	30:a:1371:G:O4'	2.17	0.43
30:a:1410:G:H2'	30:a:1411:U:C6	2.54	0.43
30:a:1880:U:H2'	30:a:1881:C:C6	2.54	0.43
30:a:1965:C:H5''	30:a:1966:A:H2'	2.00	0.43
30:a:2305:U:C2	35:f:151:GLY:HA3	2.54	0.43
30:a:2849:U:H4'	30:a:2868:A:C2	2.54	0.43
31:b:60:C:H2'	31:b:61:G:C8	2.52	0.43
43:n:88:LYS:O	43:n:116:GLN:HB2	2.19	0.43
46:q:14:VAL:HG12	46:q:20:VAL:HG21	2.01	0.43
49:t:74:ASN:HA	49:t:96:PHE:CZ	2.53	0.43
6:A:124:C:H4'	6:A:291:U:O2'	2.19	0.42
6:A:555:U:H2'	6:A:556:C:C6	2.54	0.42
6:A:1324:A:H2'	6:A:1325:C:C6	2.54	0.42
8:C:39:VAL:HG13	8:C:91:VAL:HG22	2.01	0.42
11:F:14:GLN:OE1	11:F:14:GLN:N	2.52	0.42
11:F:90:MET:HE2	11:F:90:MET:HB3	1.86	0.42
24:S:80:TYR:CZ	24:S:82:GLY:HA2	2.53	0.42
29:Z:69:C:H2'	29:Z:70:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:235:U:H2'	30:a:236:C:C6	2.54	0.42
30:a:933:A:H5'	30:a:934:U:OP2	2.19	0.42
30:a:1278:C:H2'	30:a:1279:G:H8	1.84	0.42
30:a:1709:U:H2'	30:a:1710:G:C8	2.54	0.42
30:a:2489:U:H2'	30:a:2490:G:O4'	2.19	0.42
49:t:17:LYS:HE3	49:t:17:LYS:HB3	1.58	0.42
6:A:328:C:H4'	6:A:329:A:C5'	2.49	0.42
6:A:525:C:H2'	6:A:526:C:C6	2.54	0.42
6:A:922:G:N3	6:A:1398:A:H2	2.17	0.42
6:A:1417:G:O2'	6:A:1483:A:N6	2.45	0.42
7:B:105:LYS:HE2	7:B:105:LYS:HB2	1.87	0.42
8:C:87:LEU:HD22	8:C:101:ILE:HG13	2.00	0.42
8:C:136:ARG:O	8:C:140:ASN:ND2	2.37	0.42
8:C:152:GLU:HB3	8:C:199:LYS:HB2	2.01	0.42
14:I:55:VAL:HG11	14:I:87:LEU:HD21	2.01	0.42
30:a:7:G:H2'	30:a:8:C:C6	2.54	0.42
30:a:144:A:H2'	30:a:145:C:C6	2.54	0.42
30:a:1599:U:H2'	30:a:1600:C:C6	2.54	0.42
30:a:2025:C:H2'	30:a:2026:U:C6	2.54	0.42
30:a:2396:G:N7	64:a:6421:HOH:O	2.36	0.42
32:c:141:VAL:HG12	32:c:192:LEU:HA	2.01	0.42
35:f:42:GLU:HG2	35:f:49:LEU:HD23	2.01	0.42
47:r:2:GLU:OE1	47:r:72:THR:HG21	2.19	0.42
47:r:28:LYS:HE2	47:r:28:LYS:HB3	1.92	0.42
6:A:315:A:O2'	6:A:330:C:O2'	2.36	0.42
6:A:621:A:H2'	6:A:622:A:C8	2.55	0.42
6:A:1048:G:H5''	19:N:3:LYS:HD2	2.01	0.42
6:A:1086:U:C2	6:A:1087:G:C8	3.08	0.42
17:L:28:PRO:HB2	17:L:29:GLN:OE1	2.18	0.42
30:a:5:A:H2'	30:a:6:A:H8	1.84	0.42
30:a:332:A:O2'	30:a:334:C:OP2	2.29	0.42
30:a:871:U:H2'	30:a:872:U:H6	1.83	0.42
30:a:1710:G:H4'	30:a:2858:C:O2	2.19	0.42
30:a:2295:C:OP2	43:n:9:ARG:NH2	2.50	0.42
34:e:194:LYS:O	34:e:197:GLU:HG3	2.20	0.42
35:f:100:PHE:HE1	35:f:175:PHE:HE1	1.67	0.42
35:f:118:SER:HB2	35:f:178:ARG:NH2	2.34	0.42
6:A:53:A:H2'	6:A:54:C:O4'	2.19	0.42
6:A:420:U:H2'	6:A:422:C:O2	2.19	0.42
6:A:515:G:H2'	6:A:516:PSU:C6	2.52	0.42
6:A:600:A:C2	6:A:601:G:C5	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:625:U:H2'	6:A:626:G:C8	2.55	0.42
9:D:91:LEU:HD23	9:D:91:LEU:HA	1.70	0.42
14:I:127:PHE:CG	14:I:128:SER:N	2.87	0.42
28:Y:38:A:H5'	30:a:1913:A:C6	2.54	0.42
30:a:365:U:H2'	30:a:366:C:O4'	2.19	0.42
30:a:526:A:O2'	30:a:2043:C:O2	2.37	0.42
30:a:2557:G:H2'	30:a:2558:C:C6	2.54	0.42
35:f:103:LEU:HD11	35:f:154:ILE:HD13	2.01	0.42
35:f:138:PHE:HA	35:f:139:PRO:HD3	1.87	0.42
40:k:112:LEU:HD12	40:k:130:GLY:HA3	2.01	0.42
45:p:83:LEU:HD22	45:p:88:VAL:HG11	2.02	0.42
47:r:86:MET:HE2	47:r:96:ILE:HG13	2.01	0.42
48:s:5:GLU:N	48:s:5:GLU:OE1	2.50	0.42
6:A:298:A:H2'	6:A:299:G:C8	2.53	0.42
6:A:1404:C:H2'	6:A:1405:G:C8	2.54	0.42
7:B:6:MET:HE2	7:B:7:ARG:HH12	1.84	0.42
8:C:108:LYS:NZ	8:C:111:LEU:HD13	2.35	0.42
14:I:28:ILE:HD13	14:I:35:LEU:CD2	2.50	0.42
15:J:39:PRO:HB3	15:J:74:VAL:HG22	2.00	0.42
30:a:361:G:H8	30:a:361:G:OP2	2.03	0.42
30:a:722:A:H2'	30:a:723:C:O4'	2.20	0.42
30:a:832:U:H2'	30:a:833:A:C8	2.54	0.42
30:a:1442:U:H2'	30:a:1443:U:C6	2.53	0.42
32:c:200:HIS:O	32:c:203:ARG:HG2	2.19	0.42
35:f:116:GLY:HA3	35:f:178:ARG:HB3	2.02	0.42
55:z:53:LYS:HE3	55:z:55:ILE:O	2.19	0.42
6:A:360:G:C6	6:A:361:G:C6	3.07	0.42
6:A:375:U:H2'	6:A:376:G:C8	2.54	0.42
6:A:987:G:H2'	6:A:988:G:H8	1.84	0.42
6:A:1144:G:H21	6:A:1146:A:H62	1.67	0.42
6:A:1147:C:H4'	14:I:7:TYR:CE2	2.54	0.42
7:B:54:LEU:HD22	7:B:220:THR:HG21	2.02	0.42
9:D:118:VAL:HG22	9:D:123:ILE:HG13	2.00	0.42
10:E:15:LEU:HD11	10:E:18:VAL:HG23	2.02	0.42
16:K:42:LEU:HD13	16:K:77:TYR:CG	2.55	0.42
17:L:102:LEU:H	17:L:102:LEU:HG	1.57	0.42
19:N:30:ILE:HD12	19:N:30:ILE:HA	1.81	0.42
23:R:42:SER:HB2	23:R:52:GLN:HG2	2.00	0.42
24:S:33:THR:HG22	24:S:35:SER:H	1.84	0.42
30:a:624:C:O2'	30:a:657:U:OP1	2.35	0.42
30:a:1009:A:H5'	45:p:59:GLN:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:92:LEU:HD21	40:k:106:GLU:HA	2.01	0.42
54:y:5:ILE:HG22	54:y:59:GLU:HA	2.00	0.42
3:2:54:ASP:OD2	30:a:2359:C:O2'	2.34	0.42
6:A:642:A:C5	13:H:107:SER:HA	2.53	0.42
6:A:827:U:H2'	6:A:870:U:O4	2.19	0.42
6:A:978:A:C8	6:A:979:C:C5	3.08	0.42
6:A:1072:G:H2'	6:A:1073:U:C6	2.54	0.42
6:A:1283:U:H2'	6:A:1284:C:O4'	2.19	0.42
6:A:1414:U:H2'	6:A:1415:G:H8	1.84	0.42
8:C:40:ARG:NH1	19:N:92:GLU:HG3	2.35	0.42
10:E:23:LYS:HG2	10:E:30:ILE:HB	2.01	0.42
13:H:3:MET:HE2	13:H:6:PRO:HA	2.01	0.42
14:I:84:THR:O	14:I:88:MET:HG2	2.19	0.42
19:N:3:LYS:O	19:N:6:MET:N	2.53	0.42
19:N:14:VAL:HA	19:N:60:GLN:NE2	2.35	0.42
26:U:4:ILE:HD13	26:U:4:ILE:HA	1.78	0.42
30:a:4:U:H2'	30:a:5:A:O4'	2.19	0.42
30:a:279:A:H62	30:a:361:G:H1'	1.83	0.42
30:a:894:U:H5''	30:a:895:U:OP2	2.20	0.42
30:a:1443:U:H2'	30:a:1444:G:C8	2.54	0.42
30:a:1725:U:H2'	30:a:1726:C:C6	2.55	0.42
30:a:2636:C:H2'	30:a:2637:U:C6	2.54	0.42
6:A:959:A:N1	6:A:1221:G:O2'	2.49	0.42
6:A:1166:G:H21	6:A:1170:A:H62	1.68	0.42
6:A:1342:C:H4'	14:I:127:PHE:O	2.20	0.42
6:A:1356:G:H2'	6:A:1357:A:H8	1.80	0.42
9:D:149:ALA:O	9:D:152:GLN:HG3	2.19	0.42
11:F:97:THR:O	11:F:97:THR:OG1	2.31	0.42
16:K:15:GLN:HG2	16:K:77:TYR:O	2.19	0.42
18:M:57:ARG:HE	18:M:57:ARG:HB3	1.62	0.42
21:P:6:LEU:HG	21:P:17:TYR:HB3	2.02	0.42
23:R:49:ALA:O	23:R:53:ARG:HG3	2.19	0.42
24:S:3:ARG:NH2	24:S:7:LYS:HD3	2.35	0.42
25:T:57:ILE:HG13	25:T:58:VAL:N	2.35	0.42
30:a:2661:G:H2'	30:a:2662:A:O4'	2.20	0.42
36:g:54:PRO:HG3	36:g:62:TRP:CE2	2.54	0.42
2:1:37:LYS:HG2	30:a:458:G:C8	2.55	0.42
4:3:19:ARG:NE	30:a:2756:U:OP2	2.39	0.42
6:A:184:G:H2'	6:A:185:U:C6	2.55	0.42
6:A:431:A:H2'	6:A:432:A:O4'	2.19	0.42
6:A:475:C:H2'	6:A:476:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:884:U:H4'	6:A:885:G:H5''	2.02	0.42
6:A:985:C:H2'	6:A:986:U:H6	1.85	0.42
6:A:1352:C:H2'	6:A:1353:G:C8	2.54	0.42
9:D:9:LEU:HD13	9:D:32:CYS:SG	2.60	0.42
12:G:2:PRO:HD2	12:G:7:ILE:HD11	2.01	0.42
18:M:22:ILE:H	18:M:22:ILE:HD12	1.84	0.42
30:a:184:C:H2'	30:a:185:G:C8	2.54	0.42
30:a:315:G:H2'	30:a:316:C:C6	2.55	0.42
30:a:558:U:OP1	38:i:113:PRO:HD2	2.20	0.42
30:a:713:G:H2'	30:a:714:U:C6	2.55	0.42
30:a:721:A:H2'	30:a:722:A:C8	2.54	0.42
30:a:2229:U:H2'	30:a:2230:G:C8	2.54	0.42
37:h:8:LYS:NZ	37:h:15:LEU:HB2	2.35	0.42
43:n:7:ARG:NH1	43:n:95:SER:O	2.44	0.42
43:n:111:ARG:HG3	43:n:117:PHE:CZ	2.55	0.42
6:A:5:U:H4'	6:A:6:G:O5'	2.20	0.42
6:A:147:G:H8	6:A:147:G:OP2	2.03	0.42
6:A:382:A:H2'	6:A:383:A:H8	1.85	0.42
6:A:837:U:H2'	6:A:838:G:H8	1.85	0.42
6:A:1188:A:H2'	6:A:1189:U:O4'	2.20	0.42
6:A:1486:G:H2'	6:A:1487:G:O4'	2.20	0.42
13:H:28:PRO:O	13:H:33:LYS:NZ	2.33	0.42
14:I:35:LEU:HD23	14:I:36:GLU:OE1	2.19	0.42
18:M:56:LEU:O	18:M:60:VAL:HG13	2.20	0.42
30:a:396:G:H1'	52:w:29:PHE:HB3	2.01	0.42
30:a:441:U:H2'	30:a:442:G:C8	2.55	0.42
30:a:930:G:H1'	54:y:25:LEU:HD11	2.02	0.42
30:a:1820:U:H4'	30:a:1821:A:OP2	2.20	0.42
30:a:2019:A:H4'	45:p:34:VAL:HG21	2.01	0.42
35:f:16:LEU:HD11	35:f:169:LEU:HA	2.02	0.42
35:f:58:ALA:O	35:f:62:GLY:N	2.44	0.42
37:h:8:LYS:HB2	37:h:8:LYS:HE2	1.84	0.42
38:i:34:ARG:HG3	38:i:39:LYS:HB2	2.01	0.42
6:A:28:A:O2'	6:A:296:U:OP1	2.15	0.41
6:A:73:C:C2	6:A:74:A:C8	3.08	0.41
6:A:77:A:H2'	6:A:78:A:C8	2.54	0.41
6:A:271:C:H2'	6:A:272:C:C6	2.55	0.41
6:A:376:G:H5''	21:P:5:ARG:HB2	2.02	0.41
6:A:1455:G:H2'	6:A:1456:A:H8	1.82	0.41
12:G:25:LYS:CB	12:G:101:MET:HE1	2.50	0.41
12:G:47:LEU:HB3	12:G:58:GLU:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:30:ILE:N	14:I:33:ARG:O	2.49	0.41
15:J:65:TYR:OH	19:N:85:ARG:HG3	2.20	0.41
17:L:36:ARG:HG2	17:L:38:TYR:CD1	2.55	0.41
20:O:78:TYR:OH	20:O:89:ARG:O	2.31	0.41
22:Q:10:GLY:HA3	22:Q:25:ILE:HD13	2.01	0.41
22:Q:61:ILE:HA	22:Q:76:VAL:HG23	2.02	0.41
24:S:23:VAL:HG21	24:S:43:ASN:HD22	1.84	0.41
27:X:23:A:H4'	27:X:24:A:O5'	2.20	0.41
30:a:83:A:OP1	49:t:2:ALA:HB2	2.19	0.41
30:a:358:U:H2'	30:a:359:G:C8	2.48	0.41
30:a:677:A:O2'	30:a:2071:A:H5'	2.19	0.41
30:a:754:U:H2'	30:a:755:U:C6	2.54	0.41
50:u:21:ARG:HA	50:u:25:LYS:O	2.20	0.41
6:A:9:G:H8	6:A:9:G:OP2	2.01	0.41
6:A:68:G:N2	6:A:152:A:H1'	2.33	0.41
6:A:154:U:H2'	6:A:155:A:C8	2.55	0.41
6:A:592:G:C6	6:A:648:A:C6	3.08	0.41
6:A:1151:A:HO2'	6:A:1152:A:H8	1.63	0.41
6:A:1175:G:H2'	6:A:1176:A:H8	1.85	0.41
8:C:42:TYR:O	8:C:46:GLU:HG2	2.20	0.41
10:E:80:THR:OG1	10:E:122:ASN:O	2.20	0.41
11:F:10:VAL:HB	11:F:58:HIS:HB3	2.02	0.41
16:K:52:PHE:O	16:K:53:ARG:HD2	2.20	0.41
24:S:14:HIS:HB2	24:S:18:LYS:NZ	2.35	0.41
30:a:277:G:H1'	30:a:278:A:C5	2.55	0.41
30:a:289:G:H2'	30:a:290:U:O4'	2.20	0.41
30:a:1441:G:H2'	30:a:1442:U:C6	2.55	0.41
30:a:1490:A:O2'	30:a:1491:G:H5'	2.19	0.41
30:a:1839:G:C2	30:a:1840:G:C8	3.08	0.41
30:a:1890:A:H2'	30:a:1891:G:O4'	2.20	0.41
30:a:2233:U:H2'	30:a:2234:G:H8	1.84	0.41
30:a:2522:U:O2'	30:a:2647:U:OP1	2.35	0.41
30:a:2528:U:H2'	30:a:2530:A:O5'	2.21	0.41
50:u:51:GLN:HG2	50:u:86:LEU:HD11	2.02	0.41
6:A:178:C:H2'	6:A:179:A:H8	1.85	0.41
6:A:298:A:H2'	6:A:299:G:O4'	2.20	0.41
6:A:546:A:H4'	6:A:548:G:O3'	2.20	0.41
6:A:923:A:H2'	6:A:924:C:H6	1.84	0.41
6:A:1530:G:H2'	6:A:1531:A:H8	1.85	0.41
7:B:9:MET:SD	7:B:47:VAL:HG22	2.60	0.41
19:N:36:ALA:HB3	19:N:41:ARG:CZ	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:1:MET:N	21:P:24:SER:OG	2.29	0.41
24:S:30:PRO:HA	24:S:48:THR:O	2.19	0.41
30:a:1440:U:H2'	30:a:1441:G:C8	2.55	0.41
30:a:1538:G:H2'	30:a:1539:U:H6	1.84	0.41
30:a:1802:A:H2'	30:a:1803:A:C8	2.55	0.41
30:a:2461:A:H2'	30:a:2462:C:C6	2.55	0.41
31:b:116:G:H2'	31:b:117:G:H8	1.85	0.41
34:e:195:GLN:HA	34:e:198:GLU:HG2	2.02	0.41
35:f:31:VAL:HG22	35:f:169:LEU:HD11	2.02	0.41
42:m:47:VAL:O	42:m:50:PRO:HD2	2.20	0.41
49:t:28:VAL:HG22	49:t:34:VAL:HG12	2.02	0.41
2:1:18:PHE:HA	2:1:43:THR:HG21	2.01	0.41
5:4:1:MET:HE1	35:f:95:ARG:HD2	2.01	0.41
6:A:407:U:C2	6:A:408:A:N7	2.88	0.41
6:A:620:C:H2'	6:A:621:A:O4'	2.19	0.41
6:A:955:U:O2	24:S:83:HIS:HE1	2.04	0.41
9:D:45:LYS:C	9:D:45:LYS:HD2	2.45	0.41
10:E:31:PHE:HE2	27:X:26:U:O4	2.03	0.41
15:J:42:LEU:HD13	15:J:71:LEU:HD12	2.03	0.41
20:O:36:ILE:O	20:O:40:GLN:HG2	2.20	0.41
23:R:13:PHE:HB2	23:R:51:TYR:CD2	2.56	0.41
25:T:24:ARG:HD2	25:T:27:MET:HE3	2.03	0.41
25:T:35:VAL:HG11	25:T:79:LEU:HD13	2.03	0.41
30:a:176:A:O2'	30:a:177:G:H5'	2.19	0.41
30:a:878:A:C2	30:a:900:A:H1'	2.54	0.41
30:a:1127:A:O5'	63:a:6212:SPD:N10	2.53	0.41
30:a:1399:C:H2'	30:a:1400:U:C6	2.56	0.41
30:a:2666:C:H42	36:g:109:PHE:HA	1.85	0.41
41:l:53:MET:HE2	41:l:117:PHE:CD1	2.55	0.41
6:A:128:G:O2'	6:A:129:A:H5'	2.21	0.41
6:A:392:C:H2'	6:A:393:A:O4'	2.19	0.41
6:A:691:G:O6	16:K:57:LYS:NZ	2.34	0.41
6:A:1121:U:H2'	6:A:1122:U:C6	2.55	0.41
6:A:1226:C:N4	18:M:103:LYS:HG3	2.35	0.41
6:A:1320:C:H2'	6:A:1321:U:C6	2.55	0.41
8:C:35:SER:HG	8:C:59:ARG:NH2	2.19	0.41
9:D:56:ARG:NH2	9:D:63:ARG:HH12	2.12	0.41
10:E:23:LYS:HB2	10:E:23:LYS:HE2	1.74	0.41
13:H:67:GLN:C	13:H:69:LYS:H	2.27	0.41
18:M:90:ARG:HD3	18:M:90:ARG:HA	1.23	0.41
30:a:277:G:O2'	30:a:278:A:O5'	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:814:C:H1'	30:a:1225:G:N2	2.35	0.41
30:a:1187:G:H5'	46:q:83:TYR:CE1	2.56	0.41
30:a:1413:A:H2'	30:a:1414:C:H6	1.84	0.41
31:b:114:C:H2'	31:b:115:A:H8	1.86	0.41
6:A:3:A:N3	6:A:613:C:H1'	2.36	0.41
6:A:359:G:H2'	6:A:360:G:H8	1.85	0.41
6:A:478:A:H5'	6:A:479:U:OP2	2.20	0.41
7:B:220:THR:O	7:B:223:GLU:HG3	2.21	0.41
12:G:72:THR:HG22	12:G:142:HIS:NE2	2.36	0.41
14:I:52:LEU:HD23	14:I:52:LEU:HA	1.75	0.41
26:U:4:ILE:HG13	26:U:19:PHE:HA	2.02	0.41
30:a:579:G:O2'	30:a:2019:A:OP1	2.38	0.41
30:a:1406:U:H2'	30:a:1407:G:C8	2.55	0.41
30:a:1769:U:O2'	30:a:1958:C:OP1	2.37	0.41
30:a:1778:U:H2'	30:a:1784:A:N6	2.35	0.41
30:a:1830:C:H2'	30:a:1831:G:H8	1.86	0.41
30:a:2038:G:H2'	30:a:2039:U:O4'	2.20	0.41
30:a:2650:U:H2'	30:a:2651:C:H6	1.86	0.41
30:a:2796:U:H3	30:a:2799:A:N6	2.18	0.41
30:a:2900:A:H2'	30:a:2901:C:O4'	2.21	0.41
45:p:17:ILE:HD13	45:p:17:ILE:HA	1.93	0.41
48:s:67:VAL:CG1	48:s:74:ILE:HD11	2.51	0.41
6:A:56:U:H2'	6:A:57:G:H8	1.83	0.41
6:A:513:C:H2'	6:A:514:C:C6	2.56	0.41
7:B:132:LYS:O	7:B:136:MET:HE2	2.20	0.41
8:C:140:ASN:HA	8:C:143:ARG:CZ	2.50	0.41
9:D:58:LYS:HE3	9:D:58:LYS:HB3	1.78	0.41
10:E:164:ILE:HD13	10:E:164:ILE:HA	1.91	0.41
11:F:88:MET:HG3	23:R:65:LEU:HD21	2.02	0.41
14:I:103:PHE:N	14:I:103:PHE:CD1	2.89	0.41
18:M:7:ILE:HD11	18:M:22:ILE:HG13	2.02	0.41
20:O:7:ALA:O	20:O:10:LYS:HB3	2.21	0.41
21:P:60:TRP:O	21:P:63:GLN:HB2	2.21	0.41
24:S:45:ILE:HG12	24:S:64:ASP:HA	2.02	0.41
30:a:328:U:O3'	49:t:66:GLN:HG3	2.20	0.41
30:a:820:A:H2'	30:a:821:A:O4'	2.21	0.41
30:a:858:G:N3	30:a:2268:A:H2'	2.35	0.41
30:a:1400:U:H2'	30:a:1401:G:C8	2.55	0.41
30:a:1470:A:H2'	30:a:1471:G:O4'	2.21	0.41
30:a:1709:U:H2'	30:a:1710:G:H8	1.85	0.41
30:a:2028:U:H2'	30:a:2029:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2262:U:OP1	30:a:2387:U:O2'	2.36	0.41
39:j:23:LYS:HD3	39:j:23:LYS:HA	1.94	0.41
43:n:92:PHE:HB2	43:n:117:PHE:CD2	2.55	0.41
6:A:411:A:H4'	6:A:412:A:O5'	2.20	0.41
6:A:530:G:H1'	28:Y:35:A:O2'	2.21	0.41
6:A:747:A:H2'	6:A:748:G:O4'	2.20	0.41
6:A:1000:A:N6	6:A:1041:G:O6	2.54	0.41
6:A:1106:G:H5''	8:C:172:ARG:HG2	2.03	0.41
6:A:1107:C:C4	6:A:1108:G:C8	3.09	0.41
6:A:1332:A:H2'	6:A:1333:A:C8	2.55	0.41
6:A:1365:G:H2'	6:A:1366:C:C6	2.55	0.41
6:A:1458:G:H2'	6:A:1459:G:C8	2.56	0.41
8:C:134:MET:HE3	8:C:151:VAL:HG12	2.02	0.41
9:D:198:HIS:HA	9:D:201:VAL:HG23	2.03	0.41
13:H:55:THR:O	13:H:57:PRO:HD3	2.20	0.41
24:S:19:VAL:HG11	24:S:44:MET:HE3	2.02	0.41
30:a:654:A:H5''	30:a:654:A:N3	2.36	0.41
30:a:2298:A:H61	30:a:2318:G:H1'	1.85	0.41
30:a:2700:A:H2'	30:a:2701:U:C6	2.55	0.41
36:g:123:ALA:HA	36:g:133:LEU:HA	2.02	0.41
6:A:74:A:H2'	6:A:75:G:O4'	2.21	0.41
6:A:167:A:N3	6:A:168:G:C8	2.89	0.41
6:A:618:C:N4	6:A:621:A:N7	2.69	0.41
6:A:833:G:H2'	6:A:834:U:C6	2.55	0.41
6:A:984:C:H2'	6:A:985:C:C6	2.56	0.41
6:A:1118:U:H1'	6:A:1179:A:C5	2.56	0.41
6:A:1181:G:H1'	6:A:1182:G:C8	2.56	0.41
6:A:1350:A:H2'	6:A:1351:U:C6	2.56	0.41
11:F:96:VAL:O	11:F:98:GLU:HG2	2.21	0.41
12:G:17:LYS:HE3	12:G:17:LYS:HB3	1.96	0.41
15:J:38:GLY:HA3	15:J:39:PRO:HA	1.83	0.41
15:J:46:LYS:HB3	15:J:66:GLU:OE1	2.21	0.41
15:J:53:ILE:HG23	19:N:85:ARG:CZ	2.50	0.41
15:J:65:TYR:CE1	19:N:89:MET:HE3	2.55	0.41
18:M:11:ASP:O	18:M:46:SER:HB2	2.20	0.41
18:M:73:ILE:O	18:M:77:ILE:HD12	2.21	0.41
19:N:53:ARG:HH21	24:S:37:ARG:HH22	1.66	0.41
20:O:74:ASP:HB3	20:O:77:ARG:HD3	2.02	0.41
22:Q:21:ILE:HG13	22:Q:46:VAL:HB	2.03	0.41
22:Q:38:ILE:HD13	22:Q:38:ILE:HA	1.87	0.41
30:a:2:G:H2'	30:a:3:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:84:A:N1	30:a:98:G:O2'	2.42	0.41
30:a:160:A:H2'	30:a:161:A:C8	2.56	0.41
30:a:221:A:N1	30:a:265:A:O2'	2.50	0.41
30:a:458:G:O2'	30:a:469:G:O6	2.33	0.41
30:a:463:G:N2	30:a:466:A:OP2	2.49	0.41
30:a:534:U:O2'	45:p:49:ASP:OD2	2.30	0.41
30:a:588:U:H2'	30:a:589:U:C6	2.56	0.41
30:a:690:G:H2'	30:a:691:C:O4'	2.20	0.41
30:a:756:A:H2'	30:a:757:G:O4'	2.20	0.41
30:a:1019:U:H2'	30:a:1020:A:C8	2.56	0.41
30:a:1394:U:H4'	30:a:1603:A:H4'	2.02	0.41
30:a:1736:U:H3'	30:a:1737:G:C8	2.55	0.41
30:a:1889:A:H2'	30:a:1890:A:C8	2.56	0.41
30:a:2303:G:O3'	35:f:121:SER:HA	2.21	0.41
30:a:2812:G:H2'	30:a:2813:A:C8	2.56	0.41
31:b:62:C:H2'	31:b:63:C:C6	2.56	0.41
35:f:12:VAL:HG13	35:f:172:ALA:HB3	2.02	0.41
35:f:118:SER:HB2	35:f:178:ARG:HH22	1.86	0.41
35:f:148:ARG:HB3	35:f:150:ARG:NE	2.36	0.41
39:j:110:GLU:HA	39:j:113:MET:HG2	2.02	0.41
53:x:36:GLN:CG	53:x:37:LEU:H	2.34	0.41
6:A:8:A:O2'	9:D:206:LYS:NZ	2.54	0.41
6:A:190:A:H2'	6:A:191:G:O4'	2.20	0.41
6:A:339:C:C2	6:A:340:U:C5	3.09	0.41
6:A:486:U:H2'	6:A:487:A:C8	2.56	0.41
6:A:751:U:H2'	6:A:752:G:O4'	2.20	0.41
6:A:956:U:H2'	6:A:957:U:O4'	2.21	0.41
6:A:1125:U:HO2'	6:A:1126:U:P	2.43	0.41
6:A:1241:G:H2'	6:A:1242:G:H8	1.86	0.41
6:A:1309:G:C6	6:A:1329:A:C6	3.09	0.41
6:A:1383:C:H2'	6:A:1384:C:C6	2.56	0.41
8:C:33:LEU:HD11	19:N:93:ILE:HG23	2.02	0.41
10:E:159:LYS:HB3	10:E:164:ILE:HG12	2.03	0.41
14:I:80:ARG:HH21	14:I:103:PHE:HA	1.86	0.41
17:L:31:ARG:O	17:L:58:THR:HG23	2.21	0.41
26:U:31:GLU:OE1	26:U:34:ARG:NH1	2.54	0.41
30:a:3:U:H2'	30:a:4:U:H6	1.86	0.41
30:a:1152:C:H4'	45:p:77:SER:HA	2.03	0.41
30:a:1539:U:C2	30:a:1540:G:C8	3.09	0.41
30:a:2591:C:H2'	30:a:2592:G:H8	1.86	0.41
35:f:164:GLU:O	35:f:167:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:18:LYS:HB3	36:g:25:THR:OG1	2.21	0.41
36:g:29:LYS:NZ	36:g:80:THR:HA	2.36	0.41
39:j:116:ILE:HD13	39:j:116:ILE:HA	1.92	0.41
42:m:20:MET:HE2	42:m:20:MET:HB3	1.98	0.41
52:w:6:GLN:O	52:w:71:LEU:HD21	2.21	0.41
6:A:201:G:H2'	6:A:202:G:H8	1.82	0.40
6:A:720:C:H5''	23:R:41:PRO:HA	2.03	0.40
6:A:1232:U:OP1	14:I:126:GLN:HG2	2.21	0.40
6:A:1290:G:P	12:G:35:LYS:HZ1	2.44	0.40
6:A:1342:C:H2'	6:A:1343:G:C8	2.56	0.40
6:A:1399:C:O2	6:A:1502:A:N6	2.54	0.40
6:A:1441:A:C2	44:o:114:LEU:HD11	2.56	0.40
8:C:142:MET:HE3	8:C:142:MET:HB3	1.89	0.40
8:C:148:GLY:HA3	8:C:172:ARG:O	2.21	0.40
13:H:87:LYS:HA	13:H:87:LYS:HD3	1.78	0.40
14:I:58:VAL:HG13	14:I:59:GLU:N	2.36	0.40
14:I:84:THR:HG21	14:I:103:PHE:CB	2.50	0.40
30:a:121:G:OP2	64:a:6319:HOH:O	2.22	0.40
30:a:794:A:H2'	30:a:795:C:C6	2.55	0.40
30:a:984:A:N3	30:a:984:A:H2'	2.36	0.40
30:a:1540:G:C6	30:a:1541:C:C4	3.08	0.40
30:a:1665:A:O2'	39:j:1:MET:HB3	2.21	0.40
30:a:1829:A:C8	30:a:1830:C:C5	3.09	0.40
31:b:115:A:H2'	31:b:116:G:H8	1.86	0.40
35:f:9:LYS:HB2	35:f:9:LYS:HE3	1.97	0.40
35:f:112:ARG:H	35:f:112:ARG:HG2	1.69	0.40
36:g:67:THR:O	36:g:71:LEU:HG	2.21	0.40
39:j:58:LEU:HA	39:j:89:ASN:HD21	1.84	0.40
5:4:14:ALA:HA	5:4:32:LEU:HB2	2.02	0.40
6:A:16:A:N1	6:A:919:A:H2	2.19	0.40
6:A:514:C:C2	6:A:515:G:C8	3.10	0.40
6:A:523:A:H61	17:L:89:D2T:CG	2.30	0.40
6:A:719:C:O2'	23:R:38:LYS:HB3	2.21	0.40
6:A:925:G:C2	6:A:927:G:C8	3.09	0.40
6:A:953:G:C6	6:A:1229:A:C6	3.09	0.40
6:A:1000:A:C6	6:A:1041:G:O6	2.74	0.40
6:A:1041:G:C2	6:A:1042:A:N7	2.90	0.40
6:A:1467:C:H2'	6:A:1468:A:C8	2.57	0.40
7:B:24:ASN:HA	7:B:25:PRO:HD3	1.99	0.40
14:I:92:GLU:OE1	14:I:92:GLU:HA	2.21	0.40
30:a:17:G:O6	64:a:6314:HOH:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:78:U:H2'	30:a:79:C:C6	2.57	0.40
30:a:265:A:N1	30:a:427:U:O2'	2.47	0.40
30:a:454:A:H4'	30:a:455:C:OP2	2.21	0.40
30:a:1180:U:H2'	30:a:1181:U:C6	2.56	0.40
30:a:1904:G:O2'	30:a:1928:A:N1	2.51	0.40
30:a:2250:G:O2'	30:a:2496:C:OP1	2.38	0.40
30:a:2373:G:H2'	30:a:2374:C:C6	2.57	0.40
64:a:8110:HOH:O	32:c:39:LYS:HB3	2.20	0.40
33:d:156:PHE:CE1	38:i:81:ILE:HD13	2.56	0.40
38:i:18:VAL:HG21	38:i:142:ILE:HD12	2.02	0.40
52:w:68:LEU:HD22	52:w:78:TYR:CE1	2.56	0.40
5:4:35:ASP:O	18:M:57:ARG:NH1	2.55	0.40
6:A:274:A:H4'	6:A:275:G:O5'	2.22	0.40
6:A:505:G:OP2	6:A:535:A:H5'	2.20	0.40
6:A:530:G:H3'	6:A:531:U:C5'	2.51	0.40
6:A:721:G:H4'	6:A:722:G:O4'	2.21	0.40
6:A:950:U:OP2	18:M:101:ARG:HD2	2.21	0.40
6:A:1170:A:H2'	6:A:1171:A:O4'	2.22	0.40
6:A:1310:G:H2'	6:A:1311:A:C8	2.55	0.40
7:B:26:LYS:HB2	7:B:26:LYS:HE2	1.69	0.40
9:D:15:GLU:OE1	9:D:60:LYS:HB2	2.22	0.40
10:E:48:PHE:HD1	10:E:141:ILE:HD12	1.86	0.40
16:K:13:ARG:C	16:K:13:ARG:HH11	2.29	0.40
22:Q:46:VAL:HG11	22:Q:61:ILE:HG21	2.03	0.40
23:R:73:ARG:HG2	23:R:73:ARG:O	2.21	0.40
25:T:80:THR:HA	25:T:83:ILE:HD12	2.03	0.40
30:a:221:A:C4	30:a:266:G:N7	2.89	0.40
30:a:1138:G:H2'	30:a:1139:G:O4'	2.21	0.40
30:a:1710:G:O2'	30:a:2858:C:N3	2.48	0.40
30:a:1792:G:H5'	32:c:204:VAL:HG13	2.04	0.40
30:a:2014:A:H2'	30:a:2015:A:C8	2.56	0.40
30:a:2305:U:H2'	30:a:2306:C:O4'	2.22	0.40
30:a:2312:U:O3'	35:f:68:THR:HG21	2.21	0.40
30:a:2460:U:C2	30:a:2461:A:C8	3.10	0.40
30:a:2797:U:H3'	30:a:2798:U:H5''	2.03	0.40
40:k:141:LYS:HB2	40:k:141:LYS:HE3	1.85	0.40
43:n:79:ALA:HB3	43:n:113:ALA:HB3	2.02	0.40
48:s:7:LEU:HD23	48:s:7:LEU:HA	1.88	0.40
49:t:49:VAL:HA	49:t:50:PRO:HD3	1.98	0.40
52:w:3:ARG:O	52:w:12:PRO:HD3	2.21	0.40
3:2:62:LEU:HB3	3:2:65:ALA:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:160:A:C6	6:A:161:A:C6	3.09	0.40
6:A:167:A:C2	6:A:168:G:C5	3.10	0.40
6:A:312:C:H2'	6:A:313:A:H8	1.86	0.40
6:A:499:A:H4'	6:A:500:G:H5'	2.02	0.40
6:A:992:U:O4	6:A:1043:G:O2'	2.36	0.40
6:A:1002:G:C6	6:A:1039:G:C6	3.10	0.40
6:A:1012:A:N6	6:A:1018:G:O6	2.55	0.40
6:A:1118:U:H2'	6:A:1119:C:H6	1.86	0.40
6:A:1233:G:H2'	6:A:1234:C:C6	2.56	0.40
6:A:1318:A:OP1	24:S:3:ARG:NH2	2.51	0.40
7:B:69:PHE:O	7:B:91:PHE:HA	2.20	0.40
7:B:99:GLY:O	7:B:103:ASN:HB3	2.22	0.40
7:B:176:ALA:O	7:B:180:GLY:N	2.54	0.40
10:E:12:GLN:HB3	10:E:14:LYS:NZ	2.37	0.40
14:I:12:ARG:O	14:I:13:LYS:C	2.64	0.40
16:K:81:ASN:HA	16:K:106:ARG:O	2.22	0.40
16:K:93:ARG:NH2	16:K:112:ASP:OD2	2.30	0.40
22:Q:57:ASP:OD2	22:Q:81:LYS:HG3	2.21	0.40
25:T:44:LYS:HD2	25:T:83:ILE:HG23	2.03	0.40
30:a:1113:U:H2'	30:a:1114:C:C6	2.56	0.40
30:a:1591:A:H2'	30:a:1592:C:C6	2.56	0.40
30:a:1703:G:H2'	30:a:1704:C:H6	1.86	0.40
30:a:2304:G:H22	30:a:2312:U:H3	1.70	0.40
30:a:2897:U:H2'	30:a:2898:U:C6	2.56	0.40
31:b:68:C:H2'	31:b:69:G:O4'	2.20	0.40
35:f:49:LEU:HD12	35:f:49:LEU:HA	1.78	0.40
36:g:63:ALA:O	36:g:67:THR:HG22	2.22	0.40
37:h:32:PRO:HA	52:w:39:TRP:CD1	2.57	0.40
49:t:99:ASN:C	49:t:99:ASN:OD1	2.64	0.40
6:A:320:A:H2'	6:A:321:A:O4'	2.21	0.40
6:A:651:C:H2'	6:A:652:U:C6	2.57	0.40
6:A:1045:C:H2'	6:A:1046:A:O4'	2.22	0.40
24:S:21:LYS:HA	24:S:24:GLU:CD	2.46	0.40
28:Y:40:C:H2'	28:Y:41:C:C6	2.57	0.40
30:a:320:A:N3	34:e:163:ASN:ND2	2.65	0.40
30:a:598:U:H2'	30:a:599:A:H8	1.87	0.40
30:a:600:G:OP1	34:e:24:ASN:ND2	2.53	0.40
30:a:1000:A:H2'	30:a:1001:A:C8	2.57	0.40
30:a:1278:C:H2'	30:a:1279:G:C8	2.56	0.40
30:a:1292:G:H2'	30:a:1293:C:C6	2.56	0.40
30:a:1405:U:H2'	30:a:1406:U:H6	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1881:C:H2'	30:a:1882:U:O4'	2.22	0.40
30:a:2343:U:O3'	30:a:2373:G:H4'	2.21	0.40
30:a:2619:C:H5'	33:d:155:VAL:O	2.22	0.40
36:g:49:THR:O	36:g:51:THR:N	2.52	0.40
46:q:14:VAL:CG1	46:q:20:VAL:HG21	2.51	0.40
46:q:38:VAL:O	46:q:54:VAL:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/55 (89%)	49 (100%)	0	0	100	100
2	1	44/46 (96%)	44 (100%)	0	0	100	100
3	2	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	7	2
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	53 (95%)	3 (5%)	0	100	100
7	B	222/241 (92%)	207 (93%)	15 (7%)	0	100	100
8	C	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	D	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
10	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
11	F	101/135 (75%)	95 (94%)	6 (6%)	0	100	100
12	G	151/179 (84%)	143 (95%)	8 (5%)	0	100	100
13	H	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
14	I	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
15	J	96/103 (93%)	91 (95%)	5 (5%)	0	100	100
16	K	113/129 (88%)	106 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
18	M	113/118 (96%)	101 (89%)	12 (11%)	0	100	100
19	N	98/101 (97%)	90 (92%)	8 (8%)	0	100	100
20	O	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
21	P	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
22	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
23	R	64/75 (85%)	59 (92%)	4 (6%)	1 (2%)	7	2
24	S	82/92 (89%)	78 (95%)	4 (5%)	0	100	100
25	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
26	U	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
32	c	269/273 (98%)	264 (98%)	5 (2%)	0	100	100
33	d	206/209 (99%)	199 (97%)	6 (3%)	1 (0%)	24	17
34	e	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
35	f	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
36	g	174/177 (98%)	156 (90%)	17 (10%)	1 (1%)	21	12
37	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
38	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
39	j	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
40	k	142/144 (99%)	138 (97%)	3 (2%)	1 (1%)	18	10
41	l	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
42	m	116/127 (91%)	108 (93%)	8 (7%)	0	100	100
43	n	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
44	o	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
45	p	115/118 (98%)	115 (100%)	0	0	100	100
46	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
47	r	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
48	s	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
49	t	100/104 (96%)	94 (94%)	5 (5%)	1 (1%)	12	5
50	u	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
51	v	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
52	w	75/78 (96%)	75 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	x	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
54	y	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
55	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
All	All	5480/5913 (93%)	5245 (96%)	229 (4%)	6 (0%)	49	45

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	32	ILE
23	R	23	TYR
36	g	47	ASP
40	k	36	LYS
33	d	149	ASN
49	t	99	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	
1	0	46/49 (94%)	45 (98%)	1 (2%)	45	45
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	50 (98%)	1 (2%)	48	48
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	48 (87%)	7 (13%)	4	1
7	B	186/199 (94%)	159 (86%)	27 (14%)	3	1
8	C	170/190 (90%)	155 (91%)	15 (9%)	9	4
9	D	172/173 (99%)	148 (86%)	24 (14%)	3	1
10	E	119/126 (94%)	110 (92%)	9 (8%)	12	6
11	F	90/116 (78%)	85 (94%)	5 (6%)	19	12
12	G	126/147 (86%)	113 (90%)	13 (10%)	7	2
13	H	104/105 (99%)	94 (90%)	10 (10%)	8	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	I	105/107 (98%)	95 (90%)	10 (10%)	8	3
15	J	86/90 (96%)	78 (91%)	8 (9%)	8	3
16	K	89/98 (91%)	80 (90%)	9 (10%)	7	2
17	L	102/103 (99%)	92 (90%)	10 (10%)	7	2
18	M	93/96 (97%)	76 (82%)	17 (18%)	2	0
19	N	83/84 (99%)	74 (89%)	9 (11%)	6	2
20	O	76/77 (99%)	68 (90%)	8 (10%)	6	2
21	P	65/65 (100%)	56 (86%)	9 (14%)	3	1
22	Q	73/78 (94%)	70 (96%)	3 (4%)	27	20
23	R	57/65 (88%)	53 (93%)	4 (7%)	14	7
24	S	72/79 (91%)	64 (89%)	8 (11%)	6	1
25	T	65/66 (98%)	58 (89%)	7 (11%)	6	2
26	U	60/61 (98%)	55 (92%)	5 (8%)	10	5
32	c	216/218 (99%)	209 (97%)	7 (3%)	34	30
33	d	163/163 (100%)	160 (98%)	3 (2%)	51	52
34	e	165/165 (100%)	163 (99%)	2 (1%)	63	65
35	f	148/150 (99%)	132 (89%)	16 (11%)	6	2
36	g	137/138 (99%)	124 (90%)	13 (10%)	8	3
37	h	32/114 (28%)	30 (94%)	2 (6%)	16	9
38	i	116/116 (100%)	114 (98%)	2 (2%)	53	53
39	j	104/104 (100%)	101 (97%)	3 (3%)	37	34
40	k	103/103 (100%)	99 (96%)	4 (4%)	28	22
41	l	107/107 (100%)	105 (98%)	2 (2%)	50	50
42	m	98/103 (95%)	96 (98%)	2 (2%)	48	48
43	n	86/87 (99%)	81 (94%)	5 (6%)	18	11
44	o	99/100 (99%)	97 (98%)	2 (2%)	48	48
45	p	89/90 (99%)	88 (99%)	1 (1%)	65	68
46	q	84/84 (100%)	80 (95%)	4 (5%)	23	15
47	r	93/93 (100%)	93 (100%)	0	100	100
48	s	80/84 (95%)	77 (96%)	3 (4%)	29	23
49	t	83/85 (98%)	78 (94%)	5 (6%)	17	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	u	78/78 (100%)	75 (96%)	3 (4%)	29	23
51	v	58/63 (92%)	57 (98%)	1 (2%)	53	53
52	w	67/68 (98%)	65 (97%)	2 (3%)	36	32
53	x	54/55 (98%)	50 (93%)	4 (7%)	13	7
54	y	48/49 (98%)	46 (96%)	2 (4%)	26	20
55	z	47/48 (98%)	47 (100%)	0	100	100
All	All	4572/4825 (95%)	4265 (93%)	307 (7%)	17	8

All (307) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	54	ILE
3	2	32	ILE
5	4	12	ILE
5	4	13	THR
5	4	22	MET
5	4	23	LYS
5	4	24	ILE
5	4	28	VAL
5	4	32	LEU
7	B	9	MET
7	B	11	LYS
7	B	18	HIS
7	B	38	VAL
7	B	44	GLU
7	B	45	LYS
7	B	54	LEU
7	B	58	ASN
7	B	63	ARG
7	B	77	SER
7	B	89	GLN
7	B	92	VAL
7	B	113	ARG
7	B	117	LEU
7	B	123	ASP
7	B	128	LYS
7	B	132	LYS
7	B	135	LEU
7	B	137	ARG
7	B	141	LEU

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Mol	Chain	Res	Type
7	B	152	LYS
7	B	164	ILE
7	B	173	ILE
7	B	175	GLU
7	B	186	ILE
7	B	189	THR
7	B	210	VAL
8	C	5	VAL
8	C	18	TRP
8	C	20	SER
8	C	21	THR
8	C	47	LEU
8	C	52	VAL
8	C	53	SER
8	C	125	GLU
8	C	132	ARG
8	C	135	LYS
8	C	139	GLN
8	C	149	ILE
8	C	162	ILE
8	C	170	GLU
8	C	207	ILE
9	D	8	LYS
9	D	17	THR
9	D	25	VAL
9	D	29	ASP
9	D	31	LYS
9	D	49	SER
9	D	77	LYS
9	D	82	LEU
9	D	90	LEU
9	D	98	LEU
9	D	101	VAL
9	D	102	VAL
9	D	119	SER
9	D	134	SER
9	D	136	GLN
9	D	137	VAL
9	D	138	SER
9	D	141	ASP
9	D	143	VAL
9	D	148	LYS

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Mol	Chain	Res	Type
9	D	151	LYS
9	D	163	GLU
9	D	177	LYS
9	D	191	LEU
10	E	11	LEU
10	E	16	ILE
10	E	22	SER
10	E	38	VAL
10	E	46	VAL
10	E	60	ILE
10	E	81	LEU
10	E	123	VAL
10	E	159	LYS
11	F	39	LEU
11	F	56	LYS
11	F	88	MET
11	F	96	VAL
11	F	102	MET
12	G	6	VAL
12	G	11	LYS
12	G	15	ASP
12	G	29	ILE
12	G	38	THR
12	G	56	LYS
12	G	57	SER
12	G	91	VAL
12	G	92	ARG
12	G	94	VAL
12	G	105	VAL
12	G	136	LYS
12	G	144	MET
13	H	3	MET
13	H	26	THR
13	H	31	LYS
13	H	50	LYS
13	H	63	LEU
13	H	71	VAL
13	H	87	LYS
13	H	101	ILE
13	H	111	MET
13	H	124	GLU
14	I	13	LYS

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Mol	Chain	Res	Type
14	I	27	LYS
14	I	29	VAL
14	I	55	VAL
14	I	59	GLU
14	I	67	VAL
14	I	100	LYS
14	I	112	GLU
14	I	123	ARG
14	I	128	SER
15	J	16	ARG
15	J	45	ARG
15	J	52	LEU
15	J	67	ILE
15	J	71	LEU
15	J	80	THR
15	J	82	LYS
15	J	83	THR
16	K	32	VAL
16	K	38	GLN
16	K	55	SER
16	K	56	ARG
16	K	79	ILE
16	K	86	VAL
16	K	98	ARG
16	K	113	VAL
16	K	129	VAL
17	L	10	LYS
17	L	33	VAL
17	L	63	VAL
17	L	67	ILE
17	L	75	GLN
17	L	88	LYS
17	L	97	THR
17	L	110	ARG
17	L	112	GLN
17	L	115	SER
18	M	20	THR
18	M	21	SER
18	M	30	SER
18	M	45	ILE
18	M	57	ARG
18	M	62	LYS

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Mol	Chain	Res	Type
18	M	64	VAL
18	M	65	VAL
18	M	69	LEU
18	M	71	ARG
18	M	73	ILE
18	M	77	ILE
18	M	82	ASP
18	M	83	LEU
18	M	90	ARG
18	M	104	THR
18	M	105	ASN
19	N	4	GLN
19	N	5	SER
19	N	19	LYS
19	N	27	LEU
19	N	30	ILE
19	N	32	SER
19	N	34	VAL
19	N	83	LYS
19	N	97	LYS
20	O	10	LYS
20	O	18	ASP
20	O	21	ASP
20	O	35	GLN
20	O	57	LEU
20	O	66	LEU
20	O	80	GLN
20	O	82	ILE
21	P	6	LEU
21	P	14	ARG
21	P	24	SER
21	P	57	ILE
21	P	66	THR
21	P	67	ILE
21	P	76	LYS
21	P	77	GLU
21	P	78	VAL
22	Q	7	THR
22	Q	67	LEU
22	Q	72	SER
23	R	14	THR
23	R	18	VAL

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Mol	Chain	Res	Type
23	R	30	LYS
23	R	71	THR
24	S	12	ASP
24	S	13	LEU
24	S	14	HIS
24	S	48	THR
24	S	51	VAL
24	S	55	ARG
24	S	56	GLN
24	S	64	ASP
25	T	4	ILE
25	T	54	MET
25	T	57	ILE
25	T	61	GLN
25	T	69	LYS
25	T	80	THR
25	T	86	LEU
26	U	4	ILE
26	U	5	LYS
26	U	43	THR
26	U	49	LYS
26	U	51	SER
32	c	77	VAL
32	c	94	VAL
32	c	104	ILE
32	c	162	VAL
32	c	192	LEU
32	c	259	SER
32	c	272	SER
33	d	1	MET
33	d	74	GLU
33	d	92	VAL
34	e	107	SER
34	e	139	LYS
35	f	4	LEU
35	f	14	LYS
35	f	25	VAL
35	f	40	VAL
35	f	48	LYS
35	f	60	ILE
35	f	67	ILE
35	f	78	LYS

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Mol	Chain	Res	Type
35	f	88	LYS
35	f	89	VAL
35	f	96	MET
35	f	108	VAL
35	f	121	SER
35	f	150	ARG
35	f	155	THR
35	f	175	PHE
36	g	9	VAL
36	g	25	THR
36	g	29	LYS
36	g	51	THR
36	g	60	ASP
36	g	74	SER
36	g	90	VAL
36	g	99	LYS
36	g	122	THR
36	g	133	LEU
36	g	144	VAL
36	g	155	GLU
36	g	168	VAL
37	h	6	LEU
37	h	19	VAL
38	i	12	LYS
38	i	96	ARG
39	j	41	ILE
39	j	88	ASN
39	j	93	GLN
40	k	112	LEU
40	k	115	GLU
40	k	116	VAL
40	k	120	VAL
41	l	58	LYS
41	l	135	VAL
42	m	6	SER
42	m	96	ARG
43	n	20	GLU
43	n	25	ARG
43	n	40	ILE
43	n	88	LYS
43	n	90	VAL
44	o	6	LYS

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Mol	Chain	Res	Type
44	o	80	VAL
45	p	87	SER
46	q	29	THR
46	q	45	GLU
46	q	46	GLU
46	q	102	SER
48	s	27	SER
48	s	53	VAL
48	s	93	LEU
49	t	26	LYS
49	t	54	GLN
49	t	79	LYS
49	t	98	SER
49	t	100	SER
50	u	7	GLU
50	u	35	GLU
50	u	69	GLU
51	v	10	THR
52	w	40	VAL
52	w	42	SER
53	x	10	SER
53	x	20	ASN
53	x	34	SER
53	x	45	GLN
54	y	58	GLU
54	y	59	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
5	4	48	GLN
7	B	18	HIS
7	B	42	ASN
7	B	58	ASN
7	B	89	GLN
7	B	227	GLN
8	C	185	ASN
9	D	136	GLN
10	E	70	ASN
11	F	3	HIS
11	F	63	ASN
13	H	4	GLN

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Mol	Chain	Res	Type
14	I	4	ASN
14	I	126	GLN
19	N	4	GLN
19	N	71	HIS
20	O	62	GLN
20	O	80	GLN
23	R	52	GLN
24	S	57	HIS
25	T	3	ASN
25	T	48	GLN
32	c	243	HIS
33	d	173	GLN
39	j	93	GLN
42	m	18	GLN
44	o	52	ASN
47	r	9	HIS
47	r	40	ASN
48	s	28	ASN
49	t	54	GLN
51	v	76	ASN
52	w	6	GLN
53	x	27	ASN
53	x	31	GLN
53	x	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	X	14/28 (50%)	5 (35%)	1 (7%)
28	Y	71/76 (93%)	25 (35%)	1 (1%)
29	Z	74/76 (97%)	20 (27%)	0
30	a	2747/2904 (94%)	316 (11%)	0
31	b	118/120 (98%)	19 (16%)	0
6	A	1516/1542 (98%)	278 (18%)	5 (0%)
All	All	4540/4746 (95%)	663 (14%)	7 (0%)

All (663) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	3	A
6	A	4	U

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Mol	Chain	Res	Type
6	A	5	U
6	A	6	G
6	A	7	A
6	A	9	G
6	A	13	U
6	A	22	G
6	A	39	G
6	A	42	G
6	A	44	A
6	A	47	C
6	A	48	C
6	A	49	U
6	A	51	A
6	A	53	A
6	A	56	U
6	A	59	A
6	A	65	A
6	A	69	G
6	A	70	U
6	A	74	A
6	A	75	G
6	A	84	U
6	A	86	G
6	A	87	C
6	A	88	U
6	A	91	U
6	A	94	G
6	A	95	C
6	A	96	U
6	A	98	A
6	A	99	C
6	A	110	C
6	A	121	U
6	A	122	G
6	A	130	A
6	A	131	A
6	A	137	U
6	A	141	G
6	A	143	A
6	A	144	G
6	A	146	G
6	A	147	G

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Mol	Chain	Res	Type
6	A	151	A
6	A	157	U
6	A	158	G
6	A	159	G
6	A	161	A
6	A	166	U
6	A	171	A
6	A	173	U
6	A	182	A
6	A	183	C
6	A	184	G
6	A	193	C
6	A	197	A
6	A	200	G
6	A	201	G
6	A	203	G
6	A	204	G
6	A	226	G
6	A	230	G
6	A	240	G
6	A	245	U
6	A	247	G
6	A	251	G
6	A	266	G
6	A	267	C
6	A	274	A
6	A	280	C
6	A	289	G
6	A	305	G
6	A	321	A
6	A	328	C
6	A	330	C
6	A	344	A
6	A	347	G
6	A	351	G
6	A	352	C
6	A	354	G
6	A	367	U
6	A	372	C
6	A	373	A
6	A	406	G
6	A	412	A

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Mol	Chain	Res	Type
6	A	414	A
6	A	415	A
6	A	418	C
6	A	421	U
6	A	422	C
6	A	424	G
6	A	428	G
6	A	429	U
6	A	435	A
6	A	439	U
6	A	455	G
6	A	456	A
6	A	457	G
6	A	458	U
6	A	459	A
6	A	463	U
6	A	465	A
6	A	468	A
6	A	469	C
6	A	474	G
6	A	478	A
6	A	479	U
6	A	481	G
6	A	484	G
6	A	485	U
6	A	486	U
6	A	490	C
6	A	494	G
6	A	495	A
6	A	496	A
6	A	497	G
6	A	499	A
6	A	511	C
6	A	512	U
6	A	518	C
6	A	519	C
6	A	521	G
6	A	522	C
6	A	531	U
6	A	533	A
6	A	547	A
6	A	559	A

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Mol	Chain	Res	Type
6	A	564	C
6	A	572	A
6	A	573	A
6	A	576	C
6	A	579	A
6	A	597	G
6	A	618	C
6	A	633	G
6	A	635	A
6	A	639	G
6	A	650	G
6	A	665	A
6	A	666	G
6	A	687	A
6	A	718	A
6	A	721	G
6	A	723	U
6	A	724	G
6	A	747	A
6	A	755	G
6	A	777	A
6	A	793	U
6	A	794	A
6	A	802	A
6	A	815	A
6	A	817	C
6	A	829	G
6	A	832	G
6	A	851	G
6	A	885	G
6	A	890	G
6	A	902	G
6	A	914	A
6	A	926	G
6	A	934	C
6	A	935	A
6	A	939	G
6	A	954	G
6	A	955	U
6	A	960	U
6	A	966	2MG
6	A	969	A

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Mol	Chain	Res	Type
6	A	971	G
6	A	975	A
6	A	976	G
6	A	977	A
6	A	978	A
6	A	987	G
6	A	989	U
6	A	1004	A
6	A	1005	A
6	A	1006	G
6	A	1008	U
6	A	1009	U
6	A	1010	U
6	A	1017	U
6	A	1024	G
6	A	1027	C
6	A	1028	C
6	A	1030	U
6	A	1031	C
6	A	1033	G
6	A	1034	G
6	A	1036	A
6	A	1037	C
6	A	1038	C
6	A	1039	G
6	A	1044	A
6	A	1046	A
6	A	1063	C
6	A	1065	U
6	A	1067	A
6	A	1070	U
6	A	1085	U
6	A	1089	G
6	A	1094	G
6	A	1095	U
6	A	1101	A
6	A	1108	G
6	A	1130	A
6	A	1137	C
6	A	1138	G
6	A	1139	G
6	A	1140	C

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Mol	Chain	Res	Type
6	A	1150	A
6	A	1157	A
6	A	1159	U
6	A	1160	G
6	A	1162	C
6	A	1169	A
6	A	1174	G
6	A	1175	G
6	A	1177	G
6	A	1178	G
6	A	1181	G
6	A	1187	G
6	A	1196	A
6	A	1197	A
6	A	1209	C
6	A	1211	U
6	A	1213	A
6	A	1219	A
6	A	1227	A
6	A	1238	A
6	A	1248	A
6	A	1249	C
6	A	1256	A
6	A	1258	G
6	A	1260	G
6	A	1276	G
6	A	1280	A
6	A	1282	C
6	A	1285	A
6	A	1287	A
6	A	1289	A
6	A	1300	G
6	A	1302	C
6	A	1305	G
6	A	1312	G
6	A	1317	C
6	A	1323	G
6	A	1325	C
6	A	1336	C
6	A	1340	A
6	A	1346	A
6	A	1353	G

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Mol	Chain	Res	Type
6	A	1363	A
6	A	1370	G
6	A	1378	C
6	A	1379	G
6	A	1397	C
6	A	1398	A
6	A	1406	U
6	A	1419	G
6	A	1432	G
6	A	1441	A
6	A	1445	U
6	A	1446	A
6	A	1451	U
6	A	1452	C
6	A	1487	G
6	A	1490	U
6	A	1492	A
6	A	1497	G
6	A	1503	A
6	A	1506	U
6	A	1517	G
6	A	1529	G
6	A	1530	G
6	A	1534	A
27	X	19	U
27	X	23	A
27	X	24	A
27	X	25	C
27	X	27	A
28	Y	4	C
28	Y	8	U
28	Y	9	A
28	Y	11	C
28	Y	12	U
28	Y	14	A
28	Y	20	U
28	Y	22	G
28	Y	34	G
28	Y	44	G
28	Y	45	U
28	Y	46	G
28	Y	47	U

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Mol	Chain	Res	Type
28	Y	48	C
28	Y	49	C
28	Y	50	U
28	Y	55	U
28	Y	56	C
28	Y	57	G
28	Y	58	A
28	Y	59	U
28	Y	61	C
28	Y	62	C
28	Y	63	G
28	Y	73	A
29	Z	3	C
29	Z	8	U
29	Z	9	G
29	Z	13	C
29	Z	16	C
29	Z	17(A)	U
29	Z	18	G
29	Z	20	U
29	Z	21	A
29	Z	45	G
29	Z	47	U
29	Z	48	C
29	Z	50	U
29	Z	53	G
29	Z	58	A
29	Z	61	C
29	Z	65	C
29	Z	69	C
29	Z	70	G
29	Z	71	C
30	a	10	A
30	a	15	G
30	a	34	U
30	a	51	G
30	a	58	G
30	a	63	A
30	a	71	A
30	a	74	A
30	a	75	G
30	a	101	A

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Mol	Chain	Res	Type
30	a	102	U
30	a	118	A
30	a	119	A
30	a	120	U
30	a	135	U
30	a	139	U
30	a	140	C
30	a	142	A
30	a	144	A
30	a	157	C
30	a	163	C
30	a	165	A
30	a	181	A
30	a	196	A
30	a	216	A
30	a	221	A
30	a	222	A
30	a	248	G
30	a	272	A
30	a	277	G
30	a	278	A
30	a	282	A
30	a	283	G
30	a	287	G
30	a	289	G
30	a	290	U
30	a	291	G
30	a	311	A
30	a	330	A
30	a	353	C
30	a	362	A
30	a	386	G
30	a	405	U
30	a	411	G
30	a	481	G
30	a	491	G
30	a	504	A
30	a	505	A
30	a	509	C
30	a	530	G
30	a	532	A
30	a	544	C

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Mol	Chain	Res	Type
30	a	545	U
30	a	546	U
30	a	547	A
30	a	548	G
30	a	549	G
30	a	563	A
30	a	573	U
30	a	575	A
30	a	603	A
30	a	613	A
30	a	615	U
30	a	627	A
30	a	637	A
30	a	645	C
30	a	646	U
30	a	647	G
30	a	653	U
30	a	654	A
30	a	655	A
30	a	686	U
30	a	711	G
30	a	715	A
30	a	719	C
30	a	730	A
30	a	747	5MU
30	a	764	A
30	a	775	G
30	a	776	G
30	a	782	A
30	a	784	G
30	a	785	G
30	a	789	A
30	a	805	G
30	a	812	C
30	a	827	U
30	a	828	U
30	a	845	A
30	a	846	U
30	a	847	U
30	a	859	G
30	a	868	U
30	a	877	A

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Mol	Chain	Res	Type
30	a	881	G
30	a	883	G
30	a	885	C
30	a	886	A
30	a	890	C
30	a	891	G
30	a	893	C
30	a	895	U
30	a	896	A
30	a	897	C
30	a	910	A
30	a	914	G
30	a	915	C
30	a	946	C
30	a	961	C
30	a	974	G
30	a	983	A
30	a	996	A
30	a	1012	U
30	a	1013	C
30	a	1017	G
30	a	1022	G
30	a	1026	G
30	a	1033	U
30	a	1042	G
30	a	1045	C
30	a	1046	A
30	a	1047	G
30	a	1048	A
30	a	1051	G
30	a	1108	U
30	a	1111	A
30	a	1112	G
30	a	1113	U
30	a	1115	G
30	a	1116	G
30	a	1117	C
30	a	1122	G
30	a	1132	U
30	a	1135	C
30	a	1142	A
30	a	1171	G

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Mol	Chain	Res	Type
30	a	1180	U
30	a	1250	G
30	a	1253	A
30	a	1256	G
30	a	1271	G
30	a	1272	A
30	a	1300	G
30	a	1301	A
30	a	1329	U
30	a	1352	U
30	a	1365	A
30	a	1379	U
30	a	1383	A
30	a	1409	U
30	a	1412	U
30	a	1416	G
30	a	1420	A
30	a	1421	G
30	a	1424	G
30	a	1427	A
30	a	1428	C
30	a	1452	G
30	a	1453	A
30	a	1460	U
30	a	1468	U
30	a	1482	G
30	a	1493	C
30	a	1494	A
30	a	1497	U
30	a	1509	A
30	a	1510	G
30	a	1515	A
30	a	1524	G
30	a	1535	A
30	a	1536	C
30	a	1566	A
30	a	1569	A
30	a	1578	U
30	a	1581	G
30	a	1584	U
30	a	1585	C
30	a	1586	A

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Mol	Chain	Res	Type
30	a	1591	A
30	a	1608	A
30	a	1647	U
30	a	1648	U
30	a	1649	G
30	a	1674	G
30	a	1715	G
30	a	1726	C
30	a	1729	U
30	a	1730	C
30	a	1733	G
30	a	1738	G
30	a	1744	A
30	a	1764	C
30	a	1773	A
30	a	1782	U
30	a	1791	A
30	a	1800	C
30	a	1801	A
30	a	1808	A
30	a	1816	C
30	a	1829	A
30	a	1847	A
30	a	1848	A
30	a	1858	A
30	a	1869	G
30	a	1871	A
30	a	1872	A
30	a	1873	G
30	a	1876	A
30	a	1906	G
30	a	1907	G
30	a	1929	G
30	a	1930	G
30	a	1937	A
30	a	1938	A
30	a	1955	U
30	a	1967	C
30	a	1970	A
30	a	1971	U
30	a	1972	G
30	a	1991	U

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Mol	Chain	Res	Type
30	a	1993	U
30	a	2023	C
30	a	2031	A
30	a	2033	A
30	a	2043	C
30	a	2055	C
30	a	2056	G
30	a	2059	A
30	a	2060	A
30	a	2061	G
30	a	2062	A
30	a	2069	G7M
30	a	2198	A
30	a	2204	G
30	a	2211	A
30	a	2223	G
30	a	2225	A
30	a	2238	G
30	a	2239	G
30	a	2268	A
30	a	2283	C
30	a	2287	A
30	a	2305	U
30	a	2307	G
30	a	2308	G
30	a	2309	A
30	a	2310	C
30	a	2322	A
30	a	2325	G
30	a	2333	A
30	a	2335	A
30	a	2347	C
30	a	2350	C
30	a	2361	G
30	a	2379	G
30	a	2383	G
30	a	2385	C
30	a	2402	U
30	a	2403	C
30	a	2406	A
30	a	2425	A
30	a	2429	G

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Mol	Chain	Res	Type
30	a	2434	A
30	a	2435	A
30	a	2441	U
30	a	2448	A
30	a	2475	C
30	a	2476	A
30	a	2478	A
30	a	2502	G
30	a	2505	G
30	a	2506	U
30	a	2518	A
30	a	2520	C
30	a	2529	G
30	a	2535	G
30	a	2547	A
30	a	2566	A
30	a	2567	G
30	a	2573	C
30	a	2585	U
30	a	2602	A
30	a	2609	U
30	a	2613	U
30	a	2629	U
30	a	2653	U
30	a	2656	U
30	a	2661	G
30	a	2663	G
30	a	2667	C
30	a	2689	U
30	a	2690	U
30	a	2714	G
30	a	2726	A
30	a	2733	A
30	a	2744	G
30	a	2748	A
30	a	2757	A
30	a	2765	A
30	a	2778	A
30	a	2792	A
30	a	2795	C
30	a	2797	U
30	a	2798	U

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Mol	Chain	Res	Type
30	a	2799	A
30	a	2800	A
30	a	2820	A
30	a	2821	A
30	a	2835	A
30	a	2861	U
30	a	2873	A
30	a	2883	A
30	a	2884	U
30	a	2891	U
30	a	2902	C
30	a	2903	U
31	b	2	G
31	b	17	C
31	b	24	G
31	b	34	A
31	b	35	C
31	b	36	C
31	b	37	C
31	b	44	G
31	b	45	A
31	b	53	A
31	b	56	G
31	b	66	A
31	b	67	G
31	b	89	U
31	b	90	C
31	b	99	A
31	b	108	A
31	b	109	A
31	b	110	C

All (7) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	5	U
6	A	83	C
6	A	1026	G
6	A	1035	A
6	A	1114	C
27	X	24	A
28	Y	56	C

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

39 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$
30	OMG	a	2251	62,29,30	23,26,27	1.22	3 (13%)	32,38,41	1.93	5 (15%)
30	PSU	a	1917	30	18,21,22	1.44	2 (11%)	21,30,33	2.01	3 (14%)
30	1MG	a	745	30	23,26,27	1.21	3 (13%)	33,39,42	1.70	6 (18%)
30	5MU	a	747	30	19,22,23	1.37	5 (26%)	27,32,35	1.99	6 (22%)
30	OMU	a	2552	30,58	19,22,23	1.33	3 (15%)	25,31,34	1.85	5 (20%)
6	G7M	A	527	6	23,26,27	1.54	3 (13%)	34,39,42	1.81	5 (14%)
30	6MZ	a	1618	30	22,25,26	1.51	4 (18%)	29,36,39	2.13	9 (31%)
6	2MG	A	1516	6	23,26,27	1.22	3 (13%)	33,38,41	2.18	7 (21%)
30	6MZ	a	2030	30	22,25,26	1.49	5 (22%)	29,36,39	2.41	11 (37%)
6	MA6	A	1518	6	23,26,27	1.51	4 (17%)	33,38,41	2.07	10 (30%)
30	G7M	a	2069	30	23,26,27	1.52	4 (17%)	34,39,42	1.75	5 (14%)
6	2MG	A	1207	6	23,26,27	1.25	4 (17%)	33,38,41	2.21	7 (21%)
30	PSU	a	2457	30	18,21,22	1.29	2 (11%)	21,30,33	2.07	4 (19%)
6	4OC	A	1402	6	20,23,24	0.72	0	25,32,35	0.99	2 (8%)
16	IAS	K	119	16	6,7,8	0.98	0	3,8,10	1.50	1 (33%)
17	D2T	L	89	17	8,9,10	2.52	3 (37%)	6,11,13	1.30	0
30	PSU	a	1911	30	18,21,22	1.36	2 (11%)	21,30,33	2.12	5 (23%)
41	MS6	l	82	41	5,7,8	0.16	0	2,7,9	0.38	0
33	MEQ	d	150	33	8,9,10	0.49	0	5,10,12	0.18	0
30	PSU	a	2605	30	18,21,22	1.27	3 (16%)	21,30,33	2.17	4 (19%)
30	PSU	a	2504	62,30	18,21,22	1.52	4 (22%)	21,30,33	2.02	4 (19%)
41	4D4	l	81	41	9,11,12	1.95	2 (22%)	7,13,15	0.81	0
30	5MU	a	1939	30	19,22,23	1.40	5 (26%)	27,32,35	2.12	6 (22%)
6	PSU	A	516	6	18,21,22	1.37	2 (11%)	21,30,33	2.02	4 (19%)
30	OMC	a	2498	30,58	19,22,23	0.84	1 (5%)	25,31,34	0.98	1 (4%)
30	PSU	a	2604	30	18,21,22	1.32	2 (11%)	21,30,33	2.12	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	2MA	a	2503	62,30,58	22,25,26	1.53	4 (18%)	32,37,40	2.71	11 (34%)
6	5MC	A	967	6	19,22,23	1.68	3 (15%)	26,32,35	1.16	2 (7%)
30	2MG	a	1835	30	23,26,27	1.22	3 (13%)	33,38,41	2.25	7 (21%)
30	3TD	a	1915	30	19,22,23	1.58	4 (21%)	23,32,35	2.03	3 (13%)
30	2MG	a	2445	30	23,26,27	1.31	4 (17%)	33,38,41	2.04	5 (15%)
6	2MG	A	966	6	23,26,27	1.29	4 (17%)	33,38,41	2.17	6 (18%)
30	PSU	a	746	30,58	18,21,22	1.47	4 (22%)	21,30,33	1.86	4 (19%)
6	UR3	A	1498	6	19,22,23	0.95	1 (5%)	26,32,35	1.73	3 (11%)
6	MA6	A	1519	6	23,26,27	1.55	5 (21%)	33,38,41	2.14	10 (30%)
6	5MC	A	1407	6	19,22,23	1.65	3 (15%)	26,32,35	1.27	4 (15%)
30	5MC	a	1962	30	19,22,23	1.64	3 (15%)	26,32,35	1.15	2 (7%)
30	PSU	a	2580	30	18,21,22	1.39	3 (16%)	21,30,33	2.08	4 (19%)
30	PSU	a	955	30	18,21,22	1.36	2 (11%)	21,30,33	2.01	3 (14%)

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
30	OMG	a	2251	62,29,30	-	1/9/27/28	0/3/3/3
30	PSU	a	1917	30	-	0/7/25/26	0/2/2/2
30	1MG	a	745	30	-	0/7/25/26	0/3/3/3
30	5MU	a	747	30	-	1/7/25/26	0/2/2/2
30	OMU	a	2552	30,58	-	1/9/27/28	0/2/2/2
6	G7M	A	527	6	-	1/7/25/26	0/3/3/3
30	6MZ	a	1618	30	-	0/9/27/28	0/3/3/3
6	2MG	A	1516	6	-	0/9/27/28	0/3/3/3
30	6MZ	a	2030	30	-	2/9/27/28	0/3/3/3
6	MA6	A	1518	6	-	0/11/29/30	0/3/3/3
30	G7M	a	2069	30	-	1/7/25/26	0/3/3/3
6	2MG	A	1207	6	-	2/9/27/28	0/3/3/3
30	PSU	a	2457	30	-	0/7/25/26	0/2/2/2
6	4OC	A	1402	6	-	2/9/29/30	0/2/2/2
16	IAS	K	119	16	-	1/7/7/8	-
17	D2T	L	89	17	-	1/7/12/14	-
30	PSU	a	1911	30	-	0/7/25/26	0/2/2/2
41	MS6	l	82	41	-	1/4/6/8	-
33	MEQ	d	150	33	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	PSU	a	2605	30	-	0/7/25/26	0/2/2/2
30	PSU	a	2504	62,30	-	1/7/25/26	0/2/2/2
41	4D4	l	81	41	-	1/11/12/14	-
30	5MU	a	1939	30	-	0/7/25/26	0/2/2/2
6	PSU	A	516	6	-	0/7/25/26	0/2/2/2
30	OMC	a	2498	30,58	-	0/9/27/28	0/2/2/2
30	PSU	a	2604	30	-	0/7/25/26	0/2/2/2
30	2MA	a	2503	62,30,58	-	2/7/25/26	0/3/3/3
6	5MC	A	967	6	-	0/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	0/9/27/28	0/3/3/3
30	3TD	a	1915	30	-	0/7/25/26	0/2/2/2
30	2MG	a	2445	30	-	0/9/27/28	0/3/3/3
6	2MG	A	966	6	-	0/9/27/28	0/3/3/3
30	PSU	a	746	30,58	-	2/7/25/26	0/2/2/2
6	UR3	A	1498	6	-	0/7/25/26	0/2/2/2
6	MA6	A	1519	6	-	2/11/29/30	0/3/3/3
6	5MC	A	1407	6	-	0/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	2/7/25/26	0/2/2/2
30	PSU	a	2580	30	-	0/7/25/26	0/2/2/2
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2

All (112) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	967	5MC	C5-C4	6.10	1.48	1.44
30	a	1962	5MC	C5-C4	6.05	1.48	1.44
6	A	1407	5MC	C5-C4	6.00	1.48	1.44
17	L	89	D2T	CB-CA	-5.29	1.53	1.54
6	A	527	G7M	C5-N7	-5.02	1.33	1.39
30	a	2069	G7M	C5-N7	-4.80	1.33	1.39
6	A	1518	MA6	C5-C4	4.75	1.47	1.39
30	a	2503	2MA	C5-C4	4.73	1.47	1.39
30	a	1618	6MZ	C5-C4	4.70	1.47	1.39
6	A	1519	MA6	C5-C4	4.66	1.47	1.39
30	a	2030	6MZ	C5-C4	4.17	1.46	1.39
41	l	81	4D4	CZ-NE	4.05	1.41	1.33
30	a	1917	PSU	C6-C5	3.53	1.39	1.35
30	a	746	PSU	C6-C5	3.51	1.39	1.35
30	a	2504	PSU	C6-C5	3.43	1.39	1.35
30	a	2580	PSU	C6-C5	3.40	1.39	1.35
30	a	1915	3TD	C6-C5	3.36	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	955	PSU	C6-C5	3.34	1.39	1.35
30	a	2552	OMU	C5-C4	-3.32	1.36	1.43
30	a	2457	PSU	C6-C5	3.29	1.38	1.35
6	A	1207	2MG	C5-C4	3.23	1.47	1.38
17	L	89	D2T	CB-CG	3.22	1.57	1.52
6	A	516	PSU	C6-C5	3.20	1.38	1.35
30	a	1915	3TD	C4-N3	-3.18	1.33	1.40
30	a	2445	2MG	C5-C4	3.18	1.47	1.38
6	A	966	2MG	C5-C4	3.15	1.47	1.38
6	A	527	G7M	C5-C4	3.15	1.46	1.38
30	a	745	1MG	C5-C4	3.14	1.47	1.38
30	a	2251	OMG	C5-C4	3.14	1.47	1.38
30	a	2069	G7M	C5-C4	3.09	1.46	1.38
6	A	1519	MA6	C5-C6	3.08	1.49	1.41
30	a	1915	3TD	C10-N3	3.03	1.52	1.47
30	a	1911	PSU	C6-C5	3.02	1.38	1.35
30	a	2552	OMU	C4-N3	-2.99	1.33	1.38
30	a	1835	2MG	C5-C4	2.99	1.47	1.38
30	a	2604	PSU	C6-C5	2.98	1.38	1.35
6	A	967	5MC	C6-C5	2.94	1.39	1.34
6	A	1518	MA6	C5-C6	2.92	1.48	1.41
6	A	1516	2MG	C5-C4	2.91	1.46	1.38
30	a	2251	OMG	C6-N1	-2.87	1.33	1.38
30	a	1939	5MU	C6-N1	-2.86	1.33	1.38
30	a	746	PSU	C4-N3	-2.85	1.33	1.38
30	a	955	PSU	C4-N3	-2.84	1.33	1.38
30	a	2030	6MZ	C5-N7	-2.80	1.34	1.39
30	a	1911	PSU	C4-N3	-2.80	1.33	1.38
30	a	2605	PSU	C4-N3	-2.79	1.33	1.38
30	a	2504	PSU	C2-N1	-2.78	1.33	1.36
30	a	1939	5MU	C4-N3	-2.77	1.33	1.38
30	a	1618	6MZ	C5-C6	2.76	1.48	1.41
30	a	2445	2MG	C6-N1	-2.74	1.33	1.38
6	A	966	2MG	C6-N1	-2.68	1.33	1.38
30	a	2504	PSU	C4-N3	-2.68	1.33	1.38
30	a	2604	PSU	C4-N3	-2.67	1.33	1.38
30	a	1917	PSU	C4-N3	-2.66	1.33	1.38
30	a	2605	PSU	C6-C5	2.66	1.38	1.35
30	a	747	5MU	C4-N3	-2.64	1.33	1.38
41	l	81	4D4	CZ-NH2	2.63	1.41	1.32
30	a	2030	6MZ	C5-C6	2.61	1.48	1.41
30	a	747	5MU	C6-C5	2.59	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2457	PSU	C4-N3	-2.58	1.34	1.38
17	L	89	D2T	CB-SB	2.57	1.84	1.82
30	a	745	1MG	C2-N1	2.57	1.41	1.37
6	A	516	PSU	C4-N3	-2.55	1.34	1.38
6	A	1407	5MC	C6-C5	2.54	1.38	1.34
30	a	1835	2MG	C6-N1	-2.54	1.34	1.38
6	A	1207	2MG	C6-N1	-2.53	1.34	1.38
30	a	1962	5MC	C6-C5	2.52	1.38	1.34
30	a	2503	2MA	C5-C6	2.50	1.47	1.41
30	a	2580	PSU	C4-N3	-2.47	1.34	1.38
30	a	1939	5MU	C2-N3	-2.44	1.33	1.38
6	A	1516	2MG	C6-N1	-2.44	1.34	1.38
30	a	2069	G7M	C6-N1	-2.43	1.34	1.38
30	a	2503	2MA	C5-N7	-2.43	1.34	1.39
6	A	1407	5MC	C6-N1	-2.40	1.33	1.38
6	A	1519	MA6	C8-N7	2.39	1.36	1.31
6	A	966	2MG	C2-N3	2.38	1.36	1.32
30	a	2030	6MZ	C4-N9	-2.36	1.32	1.37
30	a	1962	5MC	C6-N1	-2.35	1.34	1.38
30	a	747	5MU	C4-C5	2.35	1.48	1.44
30	a	745	1MG	C5-N7	-2.34	1.34	1.39
30	a	1939	5MU	C6-C5	2.33	1.38	1.34
30	a	746	PSU	C2-N3	-2.33	1.33	1.37
30	a	2552	OMU	C2-N3	-2.32	1.33	1.38
6	A	1207	2MG	C2-N3	2.32	1.36	1.32
30	a	1618	6MZ	C8-N7	2.29	1.36	1.31
6	A	527	G7M	C6-N1	-2.28	1.34	1.38
30	a	2580	PSU	O4'-C1'	-2.27	1.40	1.43
30	a	747	5MU	C6-N1	-2.23	1.34	1.38
6	A	1518	MA6	C5-N7	-2.23	1.35	1.39
30	a	747	5MU	C2-N3	-2.22	1.34	1.38
30	a	1618	6MZ	C5-N7	-2.21	1.35	1.39
30	a	1939	5MU	C4-C5	2.20	1.48	1.44
30	a	2445	2MG	C5-N7	-2.20	1.34	1.39
6	A	967	5MC	C6-N1	-2.20	1.34	1.38
30	a	2030	6MZ	C8-N7	2.19	1.35	1.31
30	a	1835	2MG	C5-N7	-2.19	1.34	1.39
6	A	1519	MA6	C4-N9	-2.18	1.33	1.37
30	a	1915	3TD	C2-N1	-2.17	1.34	1.37
6	A	1519	MA6	C5-N7	-2.16	1.35	1.39
30	a	2251	OMG	C5-N7	-2.15	1.34	1.39
30	a	2069	G7M	C4-N9	-2.13	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	966	2MG	C5-N7	-2.13	1.34	1.39
30	a	746	PSU	O4'-C1'	-2.12	1.40	1.43
6	A	1516	2MG	C4-N9	-2.12	1.32	1.38
30	a	2445	2MG	C4-N9	-2.08	1.32	1.38
6	A	1207	2MG	C5-N7	-2.07	1.34	1.39
30	a	2605	PSU	C2-N3	-2.06	1.34	1.37
30	a	2504	PSU	C2-N3	-2.06	1.34	1.37
6	A	1498	UR3	C2-N1	2.05	1.41	1.38
6	A	1518	MA6	C8-N7	2.05	1.35	1.31
30	a	2503	2MA	C8-N9	-2.03	1.34	1.37
30	a	2498	OMC	C6-C5	2.02	1.39	1.35

All (178) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2503	2MA	C5-C4-N3	-8.90	117.81	127.18
30	a	2503	2MA	N3-C4-N9	8.24	137.45	126.99
30	a	1915	3TD	N1-C2-N3	7.79	121.79	116.13
30	a	1835	2MG	C2-N3-C4	7.53	121.42	112.00
6	A	1207	2MG	C2-N3-C4	7.13	120.91	112.00
6	A	966	2MG	C2-N3-C4	7.09	120.87	112.00
6	A	1516	2MG	C2-N3-C4	7.05	120.81	112.00
6	A	1498	UR3	C4-N3-C2	-6.64	119.24	124.58
30	a	2445	2MG	C2-N3-C4	6.63	120.30	112.00
30	a	1911	PSU	N1-C2-N3	6.43	121.95	115.17
6	A	1207	2MG	C5-C4-N3	-6.42	118.18	128.39
30	a	2605	PSU	N1-C2-N3	6.39	121.91	115.17
30	a	2604	PSU	N1-C2-N3	6.34	121.86	115.17
30	a	2457	PSU	N1-C2-N3	6.32	121.83	115.17
30	a	955	PSU	N1-C2-N3	6.27	121.78	115.17
30	a	746	PSU	N1-C2-N3	6.26	121.77	115.17
6	A	966	2MG	C5-C4-N3	-6.24	118.45	128.39
6	A	516	PSU	N1-C2-N3	6.21	121.71	115.17
30	a	1917	PSU	N1-C2-N3	6.14	121.65	115.17
30	a	2030	6MZ	C5-C4-N3	-6.05	118.39	126.72
30	a	1835	2MG	C5-C4-N3	-5.96	118.91	128.39
30	a	2580	PSU	N1-C2-N3	5.96	121.45	115.17
30	a	2251	OMG	C5-C4-N3	-5.83	119.11	128.39
30	a	1618	6MZ	C5-C4-N3	-5.77	118.78	126.72
6	A	527	G7M	C5-C4-N3	-5.72	117.34	128.15
30	a	2445	2MG	C5-C4-N3	-5.72	119.29	128.39
6	A	527	G7M	N9-C4-N3	5.71	137.36	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1518	MA6	C5-C4-N3	-5.50	119.14	126.72
6	A	1516	2MG	C5-C4-N3	-5.46	119.70	128.39
30	a	2552	OMU	O4-C4-C5	-5.45	115.77	125.16
30	a	2504	PSU	N1-C2-N3	5.34	120.80	115.17
30	a	2069	G7M	N9-C4-N3	5.23	136.40	125.95
6	A	1519	MA6	C5-C4-N3	-5.15	119.62	126.72
30	a	1939	5MU	C4-N3-C2	-5.09	120.67	127.34
30	a	745	1MG	C5-C4-N3	-5.07	120.32	128.39
30	a	2069	G7M	C5-C4-N3	-5.06	118.58	128.15
6	A	966	2MG	N9-C4-N3	5.03	136.01	125.95
6	A	527	G7M	C2-N3-C4	4.98	120.88	112.30
30	a	2251	OMG	C2-N3-C4	4.96	120.84	112.30
6	A	1207	2MG	N9-C4-N3	4.95	135.86	125.95
30	a	2069	G7M	C2-N3-C4	4.80	120.57	112.30
30	a	2504	PSU	C6-C5-C4	-4.80	114.94	118.17
30	a	2030	6MZ	N3-C4-N9	4.79	135.32	127.17
30	a	1939	5MU	N3-C2-N1	4.72	121.04	114.89
30	a	2605	PSU	C4-N3-C2	-4.65	119.97	126.37
30	a	747	5MU	C4-N3-C2	-4.58	121.34	127.34
30	a	747	5MU	N3-C2-N1	4.55	120.82	114.89
30	a	745	1MG	C2-N3-C4	4.52	122.14	111.98
30	a	1911	PSU	C4-N3-C2	-4.47	120.21	126.37
6	A	1519	MA6	C2-N1-C6	4.47	122.74	111.83
30	a	1835	2MG	N9-C4-N3	4.46	134.88	125.95
30	a	2445	2MG	N9-C4-N3	4.44	134.82	125.95
30	a	1618	6MZ	N3-C4-N9	4.43	134.71	127.17
6	A	1519	MA6	C4-C5-N7	-4.42	105.53	110.58
30	a	2604	PSU	C4-N3-C2	-4.39	120.32	126.37
30	a	2457	PSU	C4-N3-C2	-4.38	120.34	126.37
6	A	1518	MA6	N3-C4-N9	4.31	134.50	127.17
6	A	1518	MA6	C2-N1-C6	4.24	122.19	111.83
30	a	747	5MU	O4-C4-C5	-4.20	120.11	124.92
30	a	2552	OMU	C5-C4-N3	4.16	120.62	114.80
30	a	955	PSU	C4-N3-C2	-4.15	120.65	126.37
30	a	1939	5MU	C5-C4-N3	4.13	118.91	115.32
30	a	1939	5MU	O4-C4-C5	-4.10	120.23	124.92
30	a	1939	5MU	C5-C6-N1	-4.06	118.90	123.31
30	a	1917	PSU	C4-N3-C2	-4.05	120.79	126.37
30	a	2503	2MA	C4-N9-C8	4.03	109.97	105.74
30	a	2251	OMG	N9-C4-N3	4.03	134.00	125.95
30	a	2604	PSU	O2-C2-N1	-4.01	118.65	122.79
6	A	967	5MC	C5-C6-N1	-4.00	118.97	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2030	6MZ	C2-N3-C4	3.96	121.51	111.83
30	a	2580	PSU	C4-N3-C2	-3.95	120.93	126.37
30	a	747	5MU	C5-C4-N3	3.92	118.73	115.32
30	a	2580	PSU	O2-C2-N1	-3.90	118.76	122.79
6	A	1516	2MG	C6-C5-N7	3.89	137.37	130.29
6	A	1518	MA6	C4-C5-N7	-3.88	106.14	110.58
30	a	2030	6MZ	C4-C5-N7	-3.85	106.18	110.58
6	A	1516	2MG	N9-C4-N3	3.80	133.55	125.95
30	a	1911	PSU	O2-C2-N1	-3.79	118.88	122.79
6	A	516	PSU	C4-N3-C2	-3.76	121.19	126.37
30	a	745	1MG	N9-C4-N3	3.75	133.44	125.95
30	a	2552	OMU	C4-N3-C2	-3.74	121.97	126.61
30	a	1618	6MZ	C2-N3-C4	3.71	120.89	111.83
30	a	2251	OMG	C6-C5-N7	3.71	137.03	130.29
30	a	2030	6MZ	N1-C2-N3	-3.68	123.01	128.58
30	a	1618	6MZ	C6-C5-N7	3.68	136.44	132.43
30	a	1915	3TD	C4-N3-C2	-3.65	120.75	124.61
30	a	2030	6MZ	C6-C5-N7	3.64	136.40	132.43
30	a	1618	6MZ	C4-C5-N7	-3.63	106.43	110.58
30	a	2605	PSU	O2-C2-N1	-3.63	119.05	122.79
6	A	1519	MA6	C2-N3-C4	3.63	120.69	111.83
6	A	1519	MA6	N3-C4-N9	3.62	133.32	127.17
30	a	1917	PSU	O2-C2-N1	-3.61	119.07	122.79
6	A	516	PSU	O2-C2-N1	-3.55	119.13	122.79
30	a	746	PSU	C4-N3-C2	-3.53	121.50	126.37
30	a	747	5MU	C5-C6-N1	-3.51	119.50	123.31
6	A	1518	MA6	C2-N3-C4	3.50	120.39	111.83
6	A	1519	MA6	N1-C2-N3	-3.49	123.30	128.58
30	a	1835	2MG	C6-C5-N7	3.45	136.56	130.29
30	a	2504	PSU	C4-N3-C2	-3.44	121.63	126.37
30	a	2503	2MA	C2-N1-C6	3.44	123.38	118.10
6	A	1498	UR3	C5-C4-N3	3.43	119.55	115.04
30	a	2030	6MZ	C4-N9-C8	3.40	109.31	105.74
30	a	2504	PSU	O2-C2-N1	-3.39	119.29	122.79
30	a	2030	6MZ	C9-N6-C6	-3.37	119.72	122.85
30	a	1618	6MZ	N1-C2-N3	-3.36	123.50	128.58
6	A	1407	5MC	C5-C6-N1	-3.35	119.67	123.31
30	a	2457	PSU	O2-C2-N1	-3.27	119.41	122.79
30	a	2445	2MG	C6-C5-N7	3.27	136.23	130.29
30	a	2503	2MA	C4-C5-N7	-3.15	106.98	110.58
6	A	1518	MA6	N1-C2-N3	-3.10	123.89	128.58
30	a	2030	6MZ	C5-N7-C8	3.08	108.29	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1962	5MC	C5-C6-N1	-3.08	119.97	123.31
6	A	1519	MA6	C5-N7-C8	3.07	108.28	103.45
30	a	2552	OMU	O4-C4-N3	2.99	123.61	119.27
30	a	955	PSU	O2-C2-N1	-2.99	119.71	122.79
30	a	1939	5MU	O2-C2-N1	-2.92	118.99	122.80
6	A	1519	MA6	C6-C5-N7	2.88	138.03	133.43
30	a	747	5MU	O2-C2-N1	-2.88	119.05	122.80
6	A	1207	2MG	C6-C5-N7	2.87	135.51	130.29
30	a	745	1MG	C6-C5-N7	2.86	135.71	129.36
30	a	2503	2MA	C5-N7-C8	2.85	107.93	103.45
30	a	1962	5MC	C5-C4-N3	-2.84	118.85	121.75
30	a	2030	6MZ	N9-C8-N7	-2.83	109.92	113.94
6	A	1518	MA6	C5-N7-C8	2.80	107.85	103.45
6	A	1519	MA6	C4-N9-C8	2.79	108.67	105.74
30	a	2251	OMG	C4-C5-N7	-2.79	106.25	110.67
6	A	1518	MA6	C4-N9-C8	2.77	108.65	105.74
6	A	967	5MC	C5-C4-N3	-2.76	118.93	121.75
6	A	1407	5MC	C5-C4-N3	-2.75	118.93	121.75
30	a	2503	2MA	CM2-C2-N1	2.75	121.24	117.13
30	a	2503	2MA	N3-C2-N1	-2.74	120.93	125.77
30	a	2069	G7M	O6-C6-C5	-2.73	121.92	128.01
6	A	966	2MG	C6-C5-N7	2.71	135.22	130.29
30	a	2503	2MA	C6-C5-N7	2.69	137.28	132.09
6	A	1516	2MG	C4-C5-N7	-2.67	106.44	110.67
6	A	1516	2MG	N1-C2-N2	2.66	119.28	116.56
30	a	2552	OMU	N3-C2-N1	2.65	118.35	114.89
30	a	2605	PSU	C5-C6-N1	-2.58	118.55	122.14
30	a	1835	2MG	C4-C5-N7	-2.56	106.61	110.67
30	a	745	1MG	C4-C5-N7	-2.56	106.62	110.67
6	A	1402	4OC	C6-C5-C4	2.55	120.07	117.00
30	a	2503	2MA	N9-C8-N7	-2.53	110.35	113.94
6	A	1407	5MC	O2-C2-N3	-2.53	118.34	122.33
30	a	2498	OMC	O2-C2-N3	-2.51	118.37	122.33
30	a	1835	2MG	N1-C2-N2	2.49	119.10	116.56
16	K	119	IAS	OD1-CG-CB	-2.47	118.19	125.38
30	a	2580	PSU	O4'-C1'-C2'	2.46	108.56	105.15
6	A	1519	MA6	N9-C8-N7	-2.45	110.46	113.94
30	a	1618	6MZ	C4-N9-C8	2.45	108.31	105.74
30	a	1618	6MZ	C5-N7-C8	2.43	107.26	103.45
6	A	1207	2MG	C4-C5-N7	-2.42	106.84	110.67
30	a	1911	PSU	C5-C6-N1	-2.41	118.79	122.14
6	A	516	PSU	O4'-C1'-C2'	2.38	108.44	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	527	G7M	O6-C6-C5	-2.37	122.73	128.01
30	a	2503	2MA	C2-N3-C4	2.36	123.12	115.02
30	a	746	PSU	O2-C2-N1	-2.34	120.37	122.79
6	A	1498	UR3	C1'-N1-C2	2.31	120.82	117.04
30	a	1835	2MG	O6-C6-C5	-2.29	120.49	126.53
30	a	2445	2MG	C4-C5-N7	-2.28	107.05	110.67
30	a	2069	G7M	C5-C6-N1	2.27	116.53	111.84
30	a	746	PSU	O2-C2-N3	-2.25	117.86	121.86
6	A	966	2MG	O6-C6-C5	-2.18	120.78	126.53
6	A	1518	MA6	N1-C6-N6	2.14	119.46	116.86
30	a	1915	3TD	C5-C6-N1	-2.14	119.17	122.14
6	A	1207	2MG	O6-C6-C5	-2.12	120.94	126.53
6	A	527	G7M	C5-C6-N1	2.12	116.22	111.84
6	A	966	2MG	C4-C5-N7	-2.09	107.36	110.67
30	a	1911	PSU	O4'-C1'-C2'	2.08	108.03	105.15
30	a	1618	6MZ	C2-N1-C6	2.08	122.14	115.24
6	A	1407	5MC	CM5-C5-C6	-2.07	120.05	122.85
6	A	1518	MA6	N9-C8-N7	-2.06	111.01	113.94
30	a	2457	PSU	O4'-C1'-C2'	2.04	107.97	105.15
6	A	1516	2MG	O6-C6-C5	-2.04	121.15	126.53
30	a	2030	6MZ	C2-N1-C6	2.04	121.99	115.24
30	a	2604	PSU	C5-C6-N1	-2.03	119.32	122.14
30	a	745	1MG	C6-C5-C4	-2.03	117.67	119.97
6	A	1207	2MG	C2-N1-C6	-2.02	122.11	124.55
6	A	1402	4OC	O2-C2-N3	-2.02	119.15	122.33

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1207	2MG	N1-C2-N2-CM2
6	A	1207	2MG	N3-C2-N2-CM2
30	a	2251	OMG	C1'-C2'-O2'-CM2
33	d	150	MEQ	NE2-CD-CG-CB
6	A	1519	MA6	O4'-C4'-C5'-O5'
33	d	150	MEQ	OE1-CD-CG-CB
30	a	2030	6MZ	O4'-C4'-C5'-O5'
6	A	1402	4OC	O4'-C4'-C5'-O5'
30	a	2030	6MZ	C3'-C4'-C5'-O5'
41	l	82	MS6	CB-CG-SD-CE
6	A	1519	MA6	C3'-C4'-C5'-O5'
17	L	89	D2T	CG-CB-SB-CB1

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Mol	Chain	Res	Type	Atoms
30	a	747	5MU	C3'-C4'-C5'-O5'
30	a	2503	2MA	C4'-C5'-O5'-P
30	a	746	PSU	O4'-C1'-C5-C6
30	a	2552	OMU	C3'-C2'-O2'-CM2
6	A	1402	4OC	C3'-C4'-C5'-O5'
30	a	2069	G7M	C4'-C5'-O5'-P
30	a	746	PSU	C2'-C1'-C5-C6
41	l	81	4D4	O-C-CA-CB
30	a	2504	PSU	O4'-C4'-C5'-O5'
30	a	1962	5MC	C2'-C1'-N1-C6
6	A	527	G7M	C4'-C5'-O5'-P
16	K	119	IAS	CA-CB-CG-OD1
30	a	1962	5MC	O4'-C1'-N1-C6
30	a	2503	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

14 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1516	2MG	1	0
30	a	2030	6MZ	2	0
6	A	1518	MA6	2	0
6	A	1207	2MG	1	0
6	A	1402	4OC	2	0
17	L	89	D2T	4	0
33	d	150	MEQ	2	0
30	a	1939	5MU	1	0
6	A	516	PSU	2	0
30	a	2604	PSU	1	0
6	A	967	5MC	1	0
6	A	966	2MG	2	0
6	A	1519	MA6	2	0
30	a	2580	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 348 ligands modelled in this entry, 336 are monoatomic - leaving 12 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
63	SPD	a	6217	-	9,9,9	0.16	0	8,8,8	0.20	0
63	SPD	a	6209	-	9,9,9	0.16	0	8,8,8	0.17	0
59	2AE	Y	101	28	10,10,10	2.36	1 (10%)	13,13,13	1.73	2 (15%)
60	8AN	Z	101	29,61,58	21,24,25	0.91	1 (4%)	26,35,38	1.02	2 (7%)
63	SPD	a	6208	-	9,9,9	0.15	0	8,8,8	0.17	0
57	PAR	A	1601	-	44,45,45	0.35	0	63,67,67	0.61	0
63	SPD	a	6213	-	9,9,9	0.15	0	8,8,8	0.21	0
63	SPD	a	6210	-	9,9,9	0.16	0	8,8,8	0.21	0
61	FME	Z	103	60	8,9,10	1.00	0	8,9,11	0.91	1 (12%)
63	SPD	d	301	-	9,9,9	0.16	0	8,8,8	0.19	0
63	SPD	a	6212	-	9,9,9	0.16	0	8,8,8	0.17	0
63	SPD	a	6211	-	9,9,9	0.16	0	8,8,8	0.18	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	SPD	a	6217	-	-	3/7/7/7	-
63	SPD	a	6209	-	-	4/7/7/7	-
59	2AE	Y	101	28	-	0/4/4/4	0/1/1/1
60	8AN	Z	101	29,61,58	-	1/7/25/26	0/3/3/3
63	SPD	a	6208	-	-	3/7/7/7	-
57	PAR	A	1601	-	-	2/18/94/94	0/4/4/4
63	SPD	a	6213	-	-	1/7/7/7	-
63	SPD	a	6210	-	-	1/7/7/7	-
61	FME	Z	103	60	-	2/7/9/11	-
63	SPD	d	301	-	-	2/7/7/7	-
63	SPD	a	6212	-	-	5/7/7/7	-
63	SPD	a	6211	-	-	4/7/7/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Y	101	2AE	C1-C	-6.85	1.40	1.50
60	Z	101	8AN	C3'-N3'	-2.96	1.42	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	Y	101	2AE	C1-C6-N2	-4.21	116.81	122.68
59	Y	101	2AE	C5-C6-C1	3.72	122.14	118.16
60	Z	101	8AN	C5-C4-N3	-2.20	123.69	126.72
60	Z	101	8AN	N3-C4-N9	2.14	130.81	127.17
61	Z	103	FME	C-CA-N	2.13	113.61	109.50

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	Z	103	FME	N-CA-CB-CG
63	a	6209	SPD	C8-C7-N6-C5
63	a	6212	SPD	C4-C5-N6-C7
63	a	6212	SPD	N6-C7-C8-C9
63	a	6217	SPD	C2-C3-C4-C5
60	Z	101	8AN	C4'-C5'-O5'-P
63	a	6209	SPD	C3-C4-C5-N6
63	a	6217	SPD	C3-C4-C5-N6
63	a	6208	SPD	N6-C7-C8-C9
63	a	6213	SPD	C2-C3-C4-C5
63	a	6209	SPD	N1-C2-C3-C4
63	a	6208	SPD	C8-C7-N6-C5
63	a	6209	SPD	C7-C8-C9-N10
63	a	6208	SPD	C3-C4-C5-N6
63	d	301	SPD	N6-C7-C8-C9
63	d	301	SPD	C2-C3-C4-C5
63	a	6211	SPD	C8-C7-N6-C5
63	a	6211	SPD	C2-C3-C4-C5
63	a	6210	SPD	C8-C7-N6-C5
63	a	6211	SPD	C4-C5-N6-C7
57	A	1601	PAR	C52-C42-O11-C11
63	a	6212	SPD	C2-C3-C4-C5
57	A	1601	PAR	O54-C54-C64-N64
63	a	6211	SPD	C7-C8-C9-N10
63	a	6212	SPD	C7-C8-C9-N10

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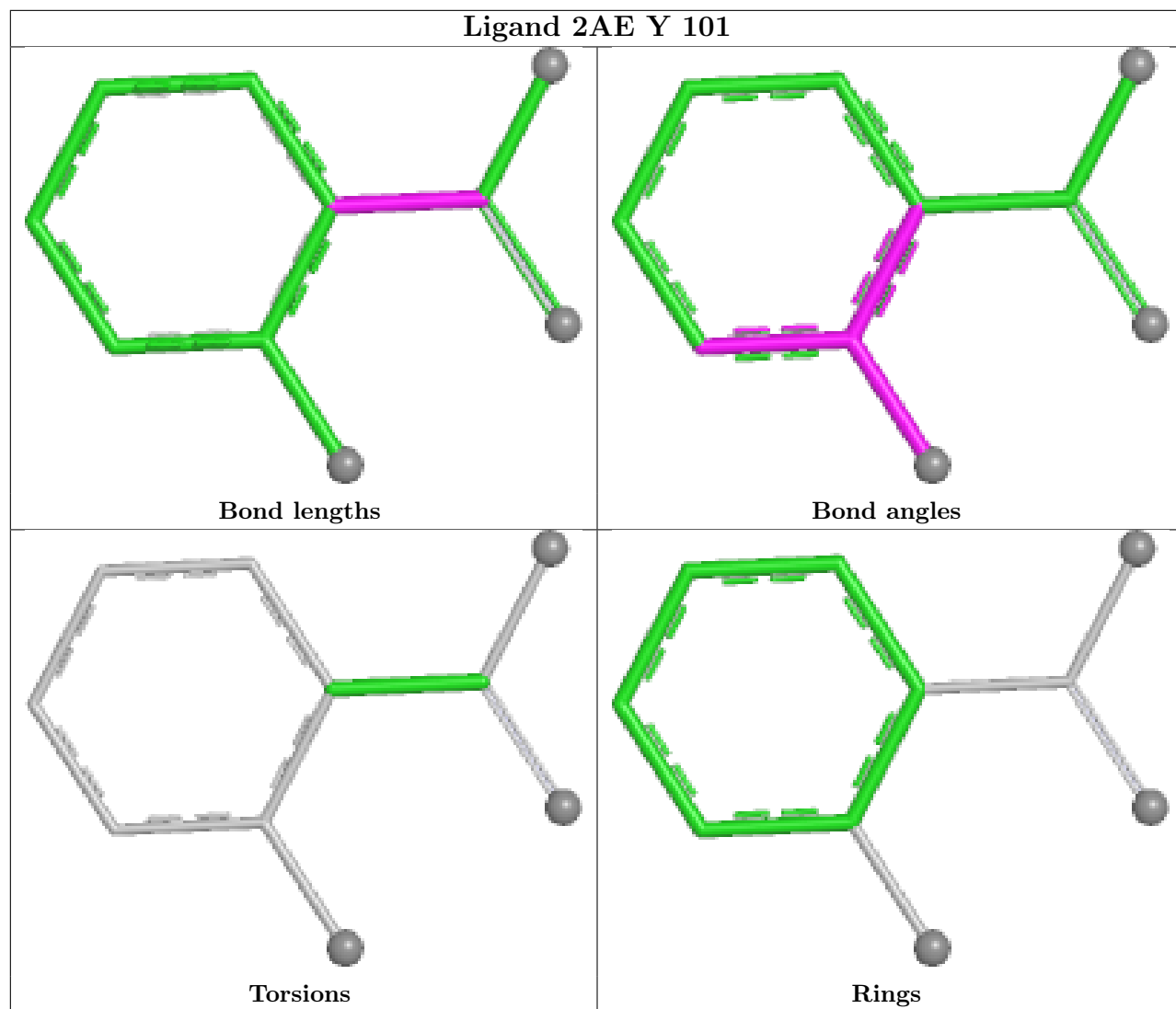
Mol	Chain	Res	Type	Atoms
61	Z	103	FME	C-CA-CB-CG
63	a	6212	SPD	N1-C2-C3-C4
63	a	6217	SPD	C4-C5-N6-C7

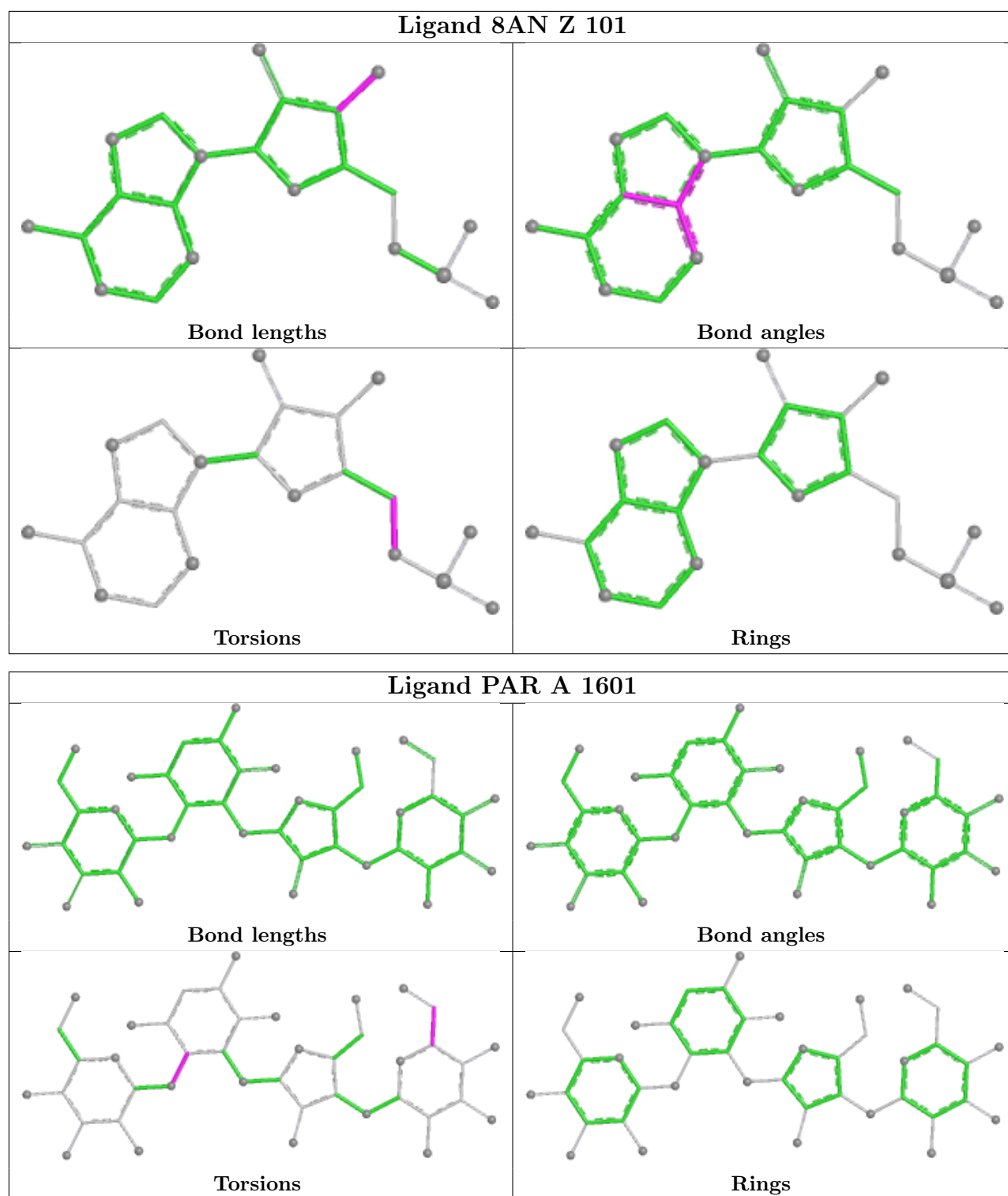
There are no ring outliers.

6 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Z	101	8AN	1	0
63	a	6208	SPD	1	0
57	A	1601	PAR	2	0
63	d	301	SPD	13	0
63	a	6212	SPD	4	0
63	a	6211	SPD	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

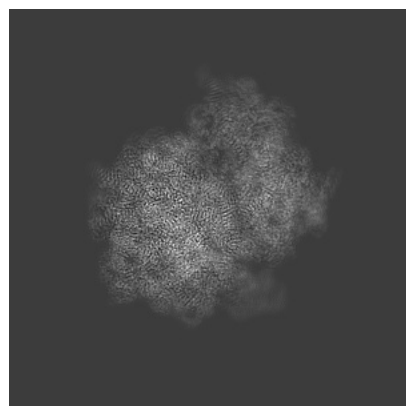
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29786. These allow visual inspection of the internal detail of the map and identification of artifacts.

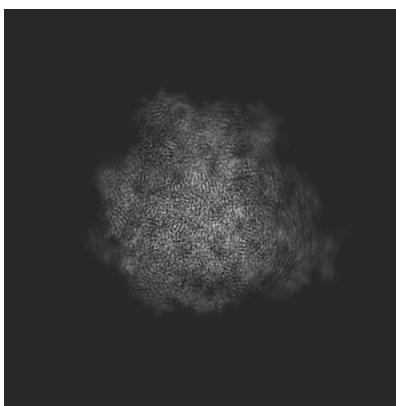
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

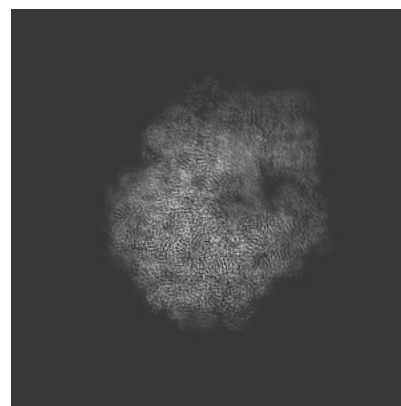
6.1.1 Primary map



X

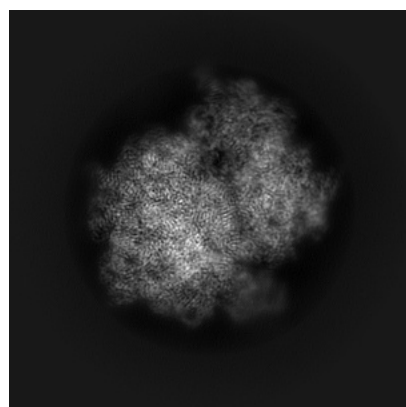


Y

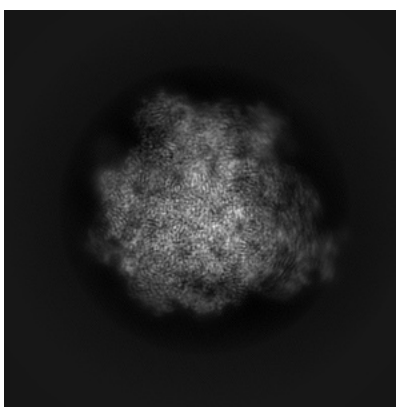


Z

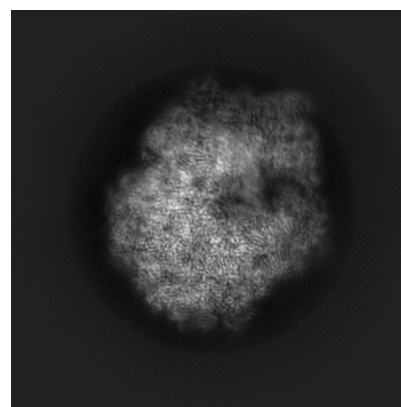
6.1.2 Raw map



X



Y

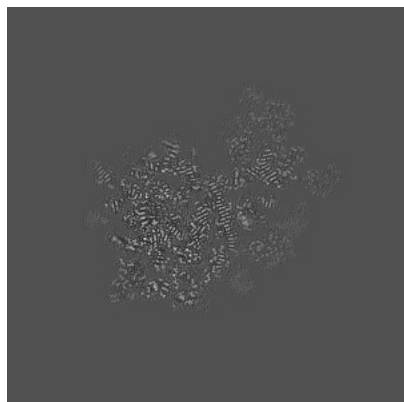


Z

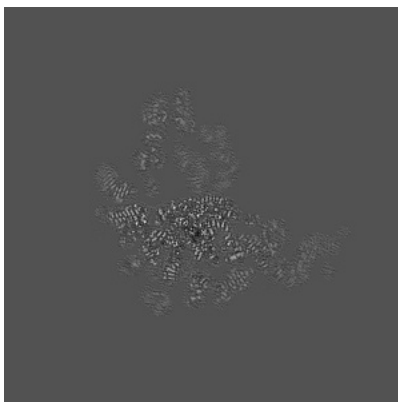
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

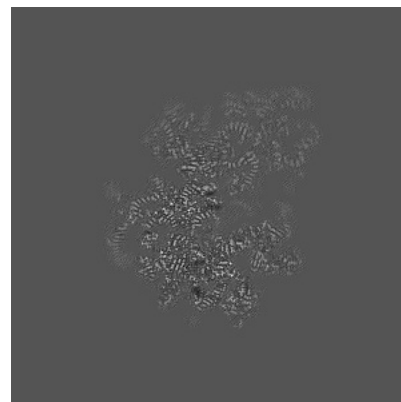
6.2.1 Primary map



X Index: 232

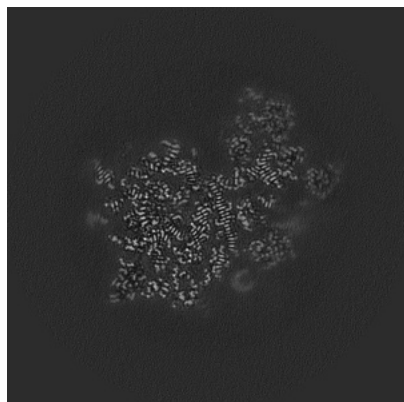


Y Index: 232

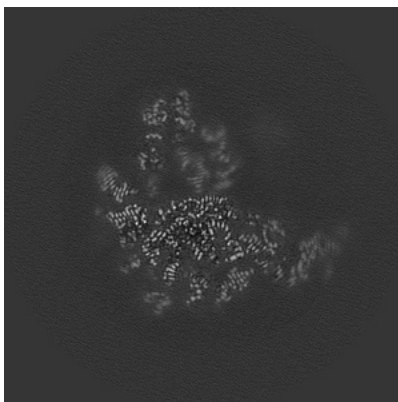


Z Index: 232

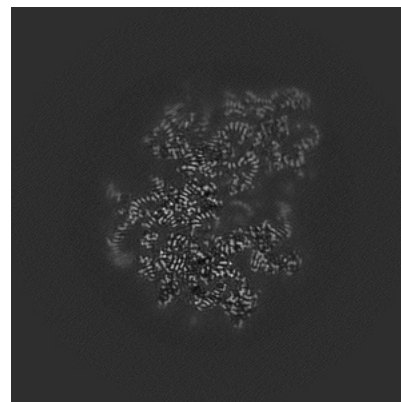
6.2.2 Raw map



X Index: 232



Y Index: 232



Z Index: 232

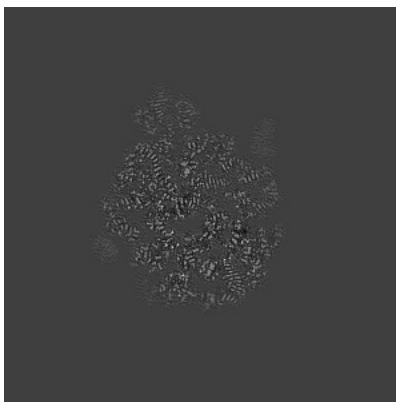
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

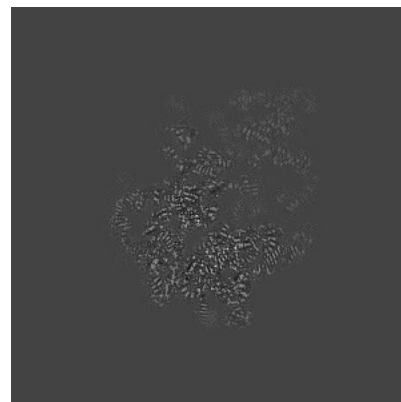
6.3.1 Primary map



X Index: 202

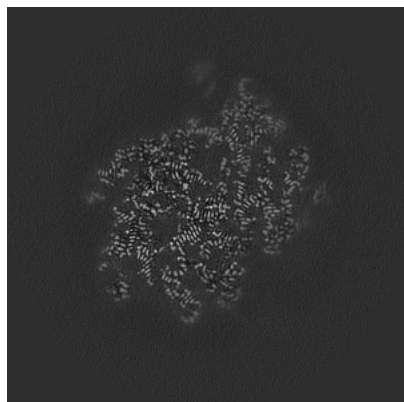


Y Index: 194

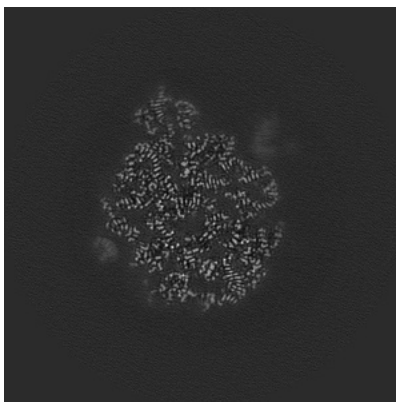


Z Index: 219

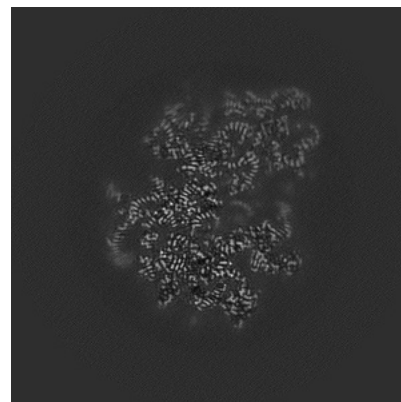
6.3.2 Raw map



X Index: 202



Y Index: 194

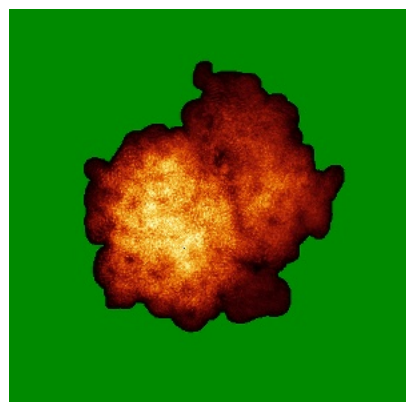


Z Index: 232

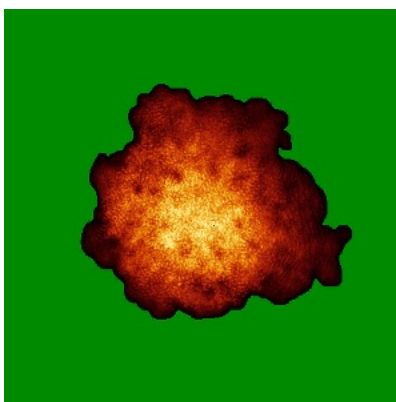
The images above show the largest variance slices of the map in three orthogonal directions.

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

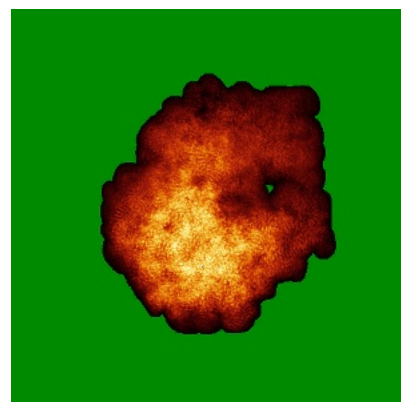
6.4.1 Primary map



X

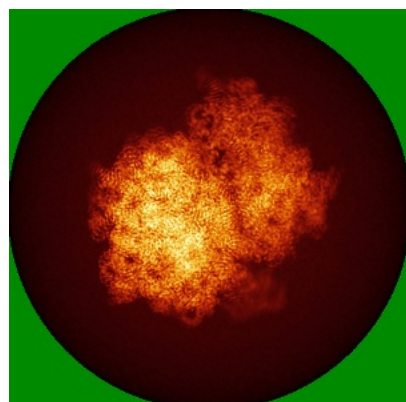


Y

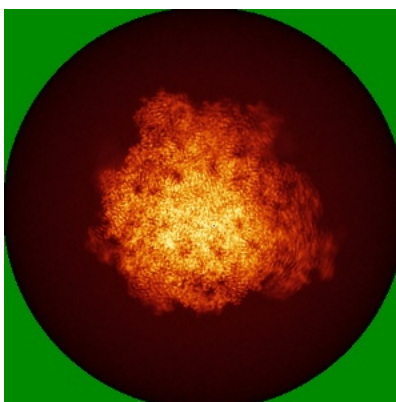


Z

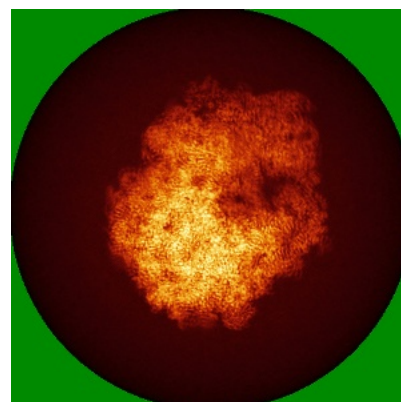
6.4.2 Raw map



X



Y

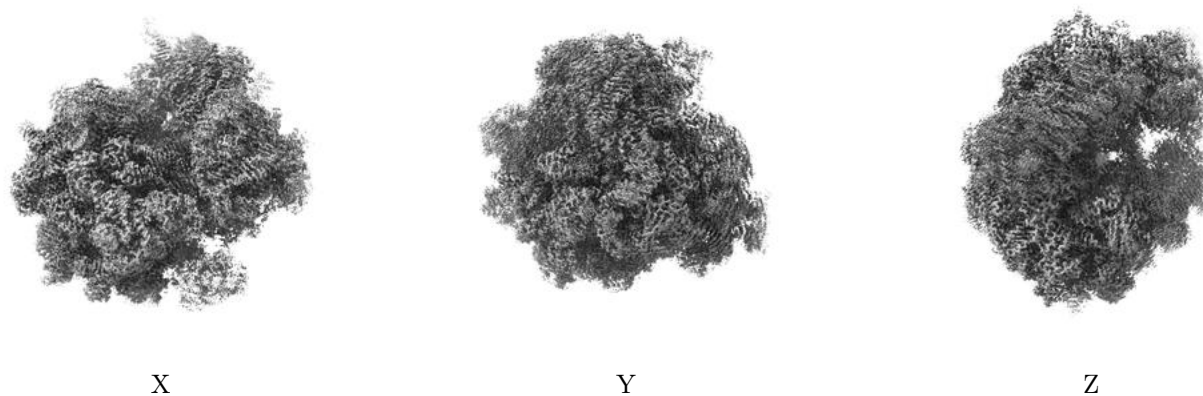


Z

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.

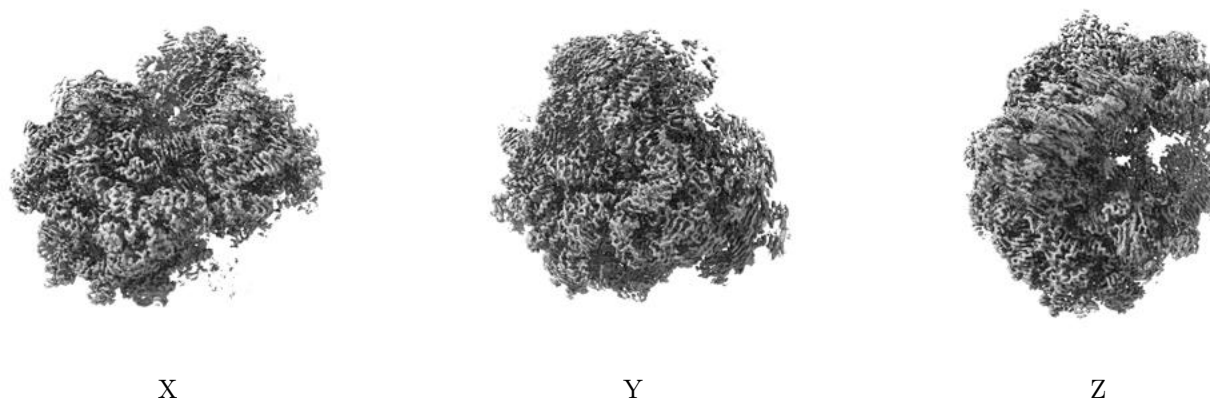
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0169. 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.

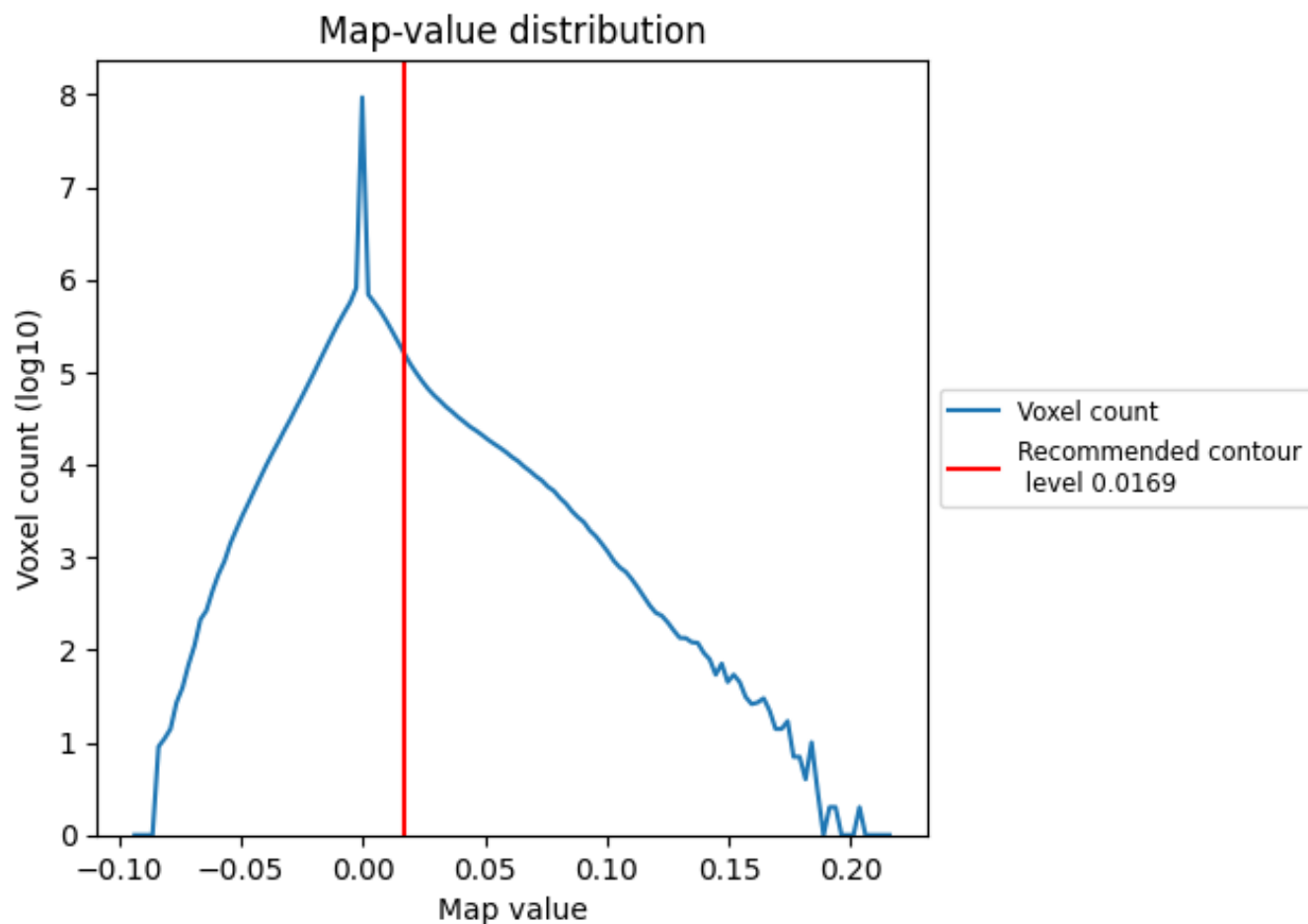
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

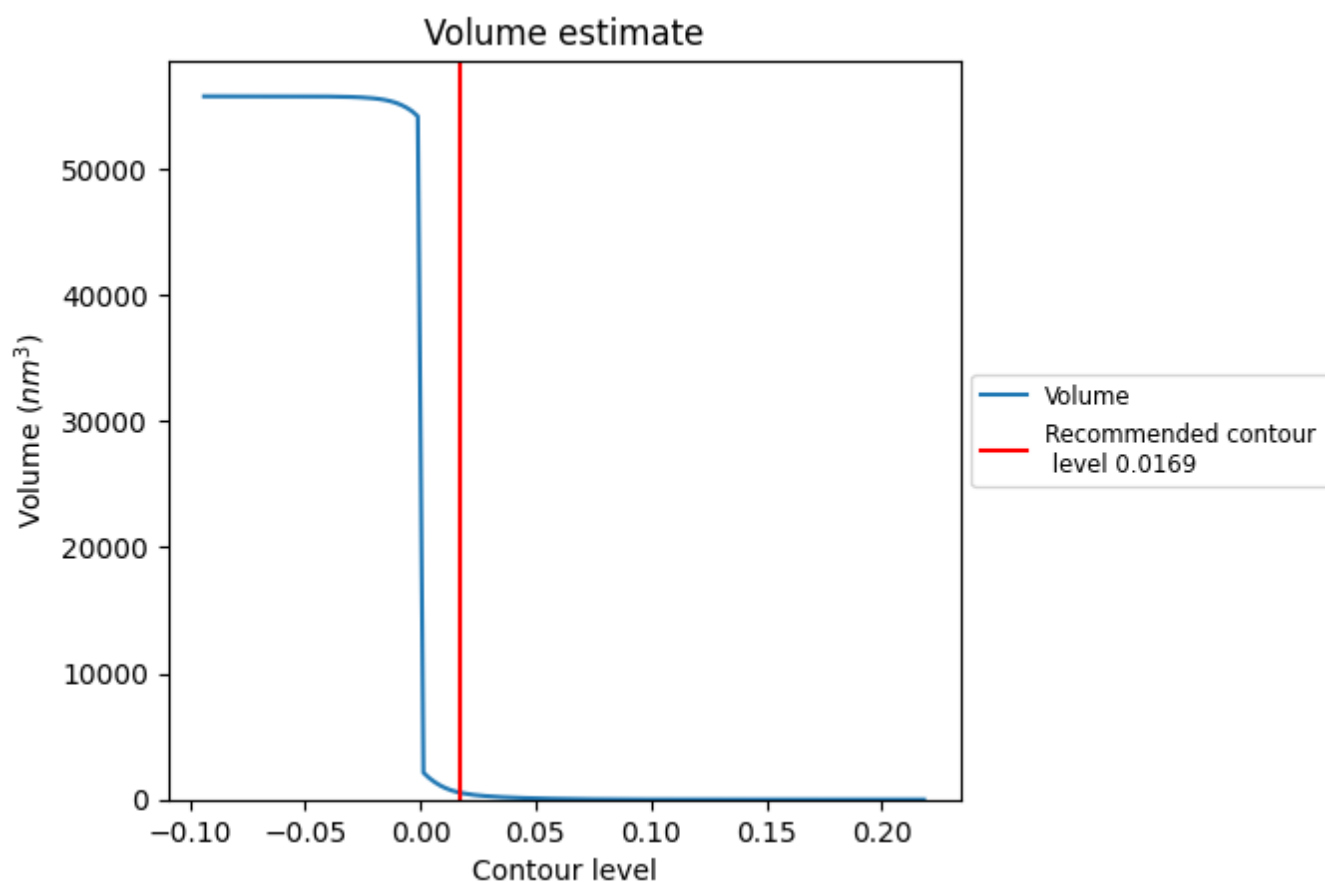
This section contains the results of statistical analysis of the map.

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.

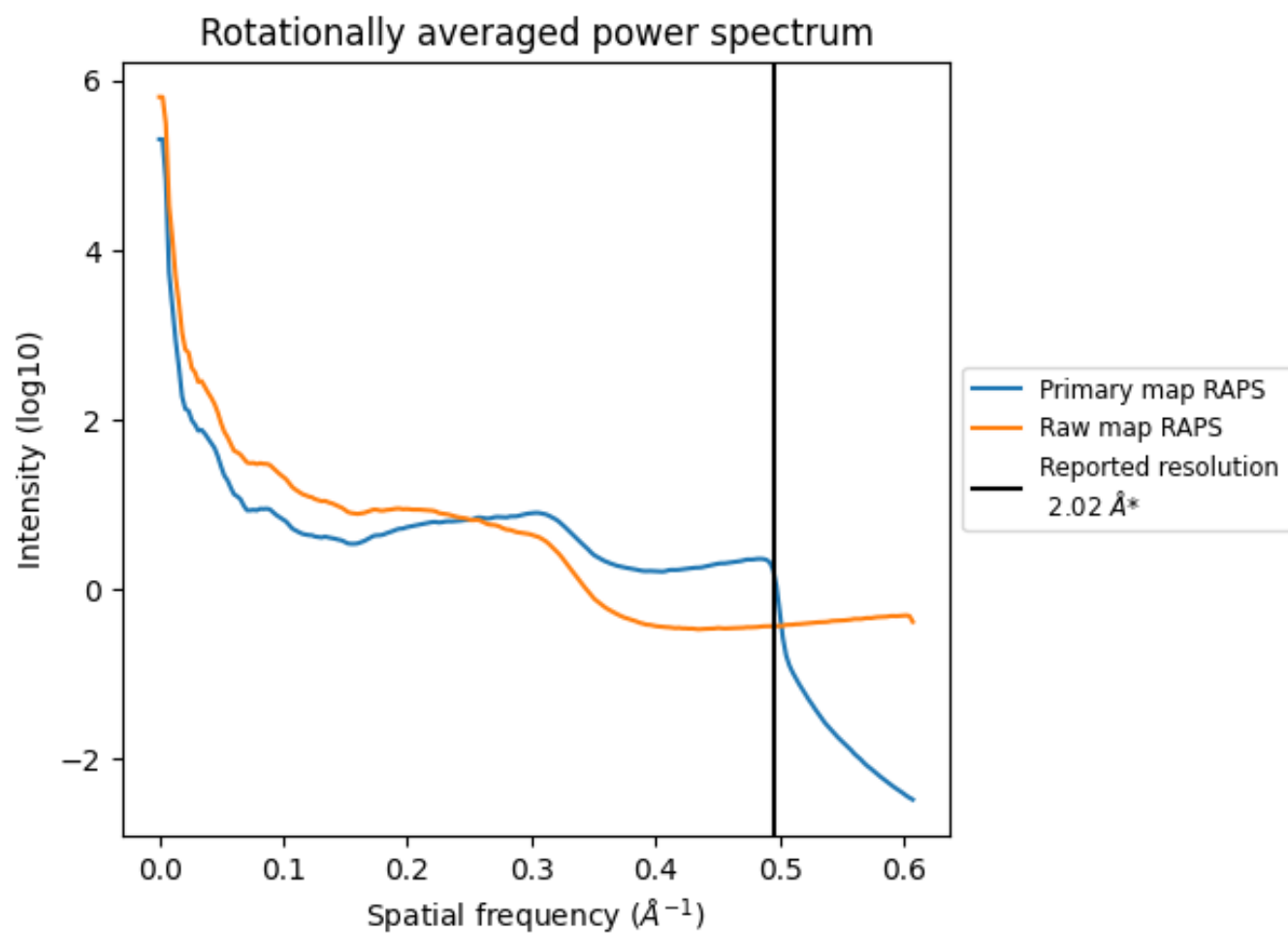
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 561 nm^3 ; this corresponds to an approximate mass of 507 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 ⓘ

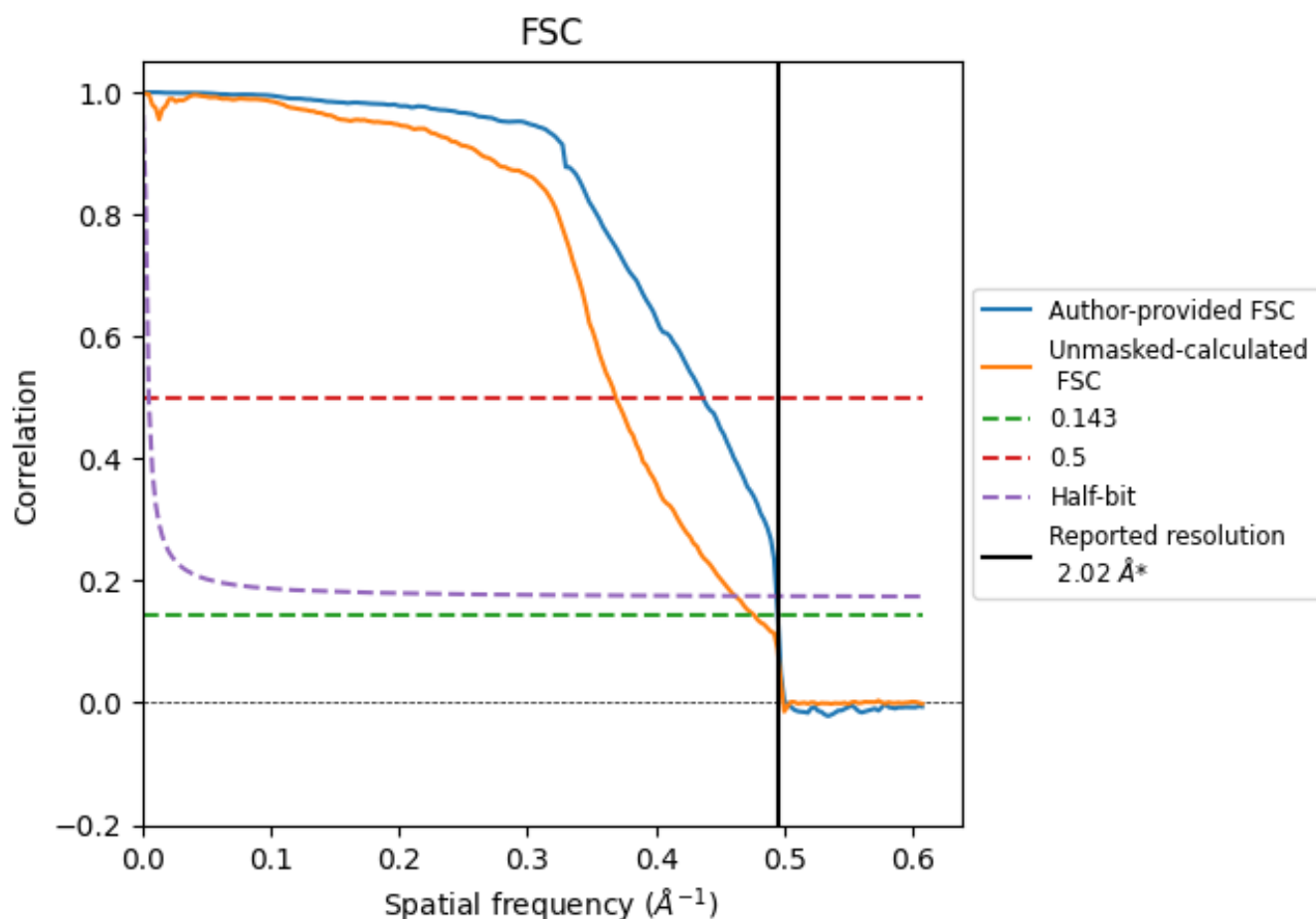


*Reported resolution corresponds to spatial frequency of $0.495 \text{ \AA}^{-1}$

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 0.495 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

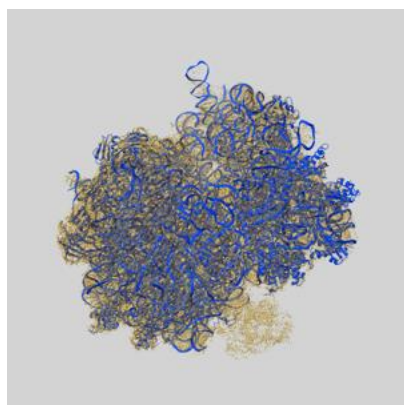
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.02	-	-
Author-provided FSC curve	2.02	2.29	2.02
Unmasked-calculated*	2.10	2.71	2.17

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

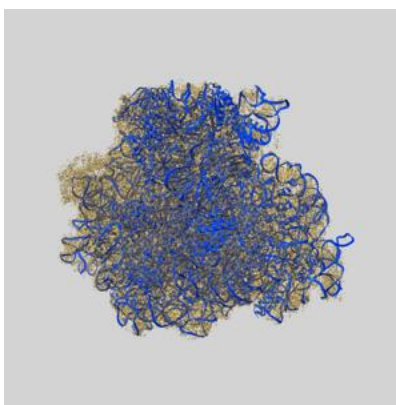
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29786 and PDB model 8G6W. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

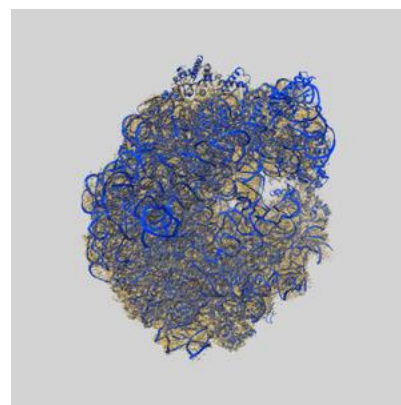
9.1 Map-model overlay [i](#)



X



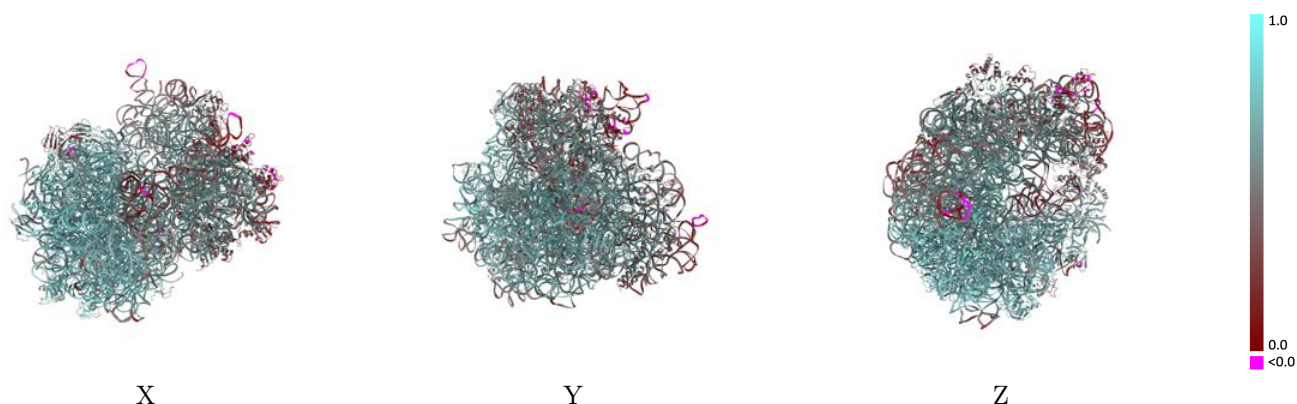
Y



Z

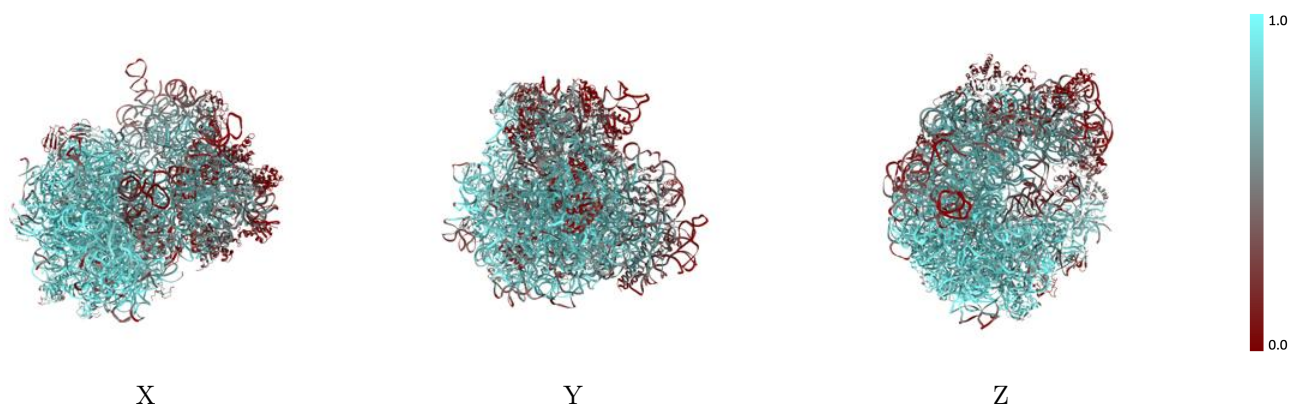
The images above show the 3D surface view of the map at the recommended contour level 0.0169 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



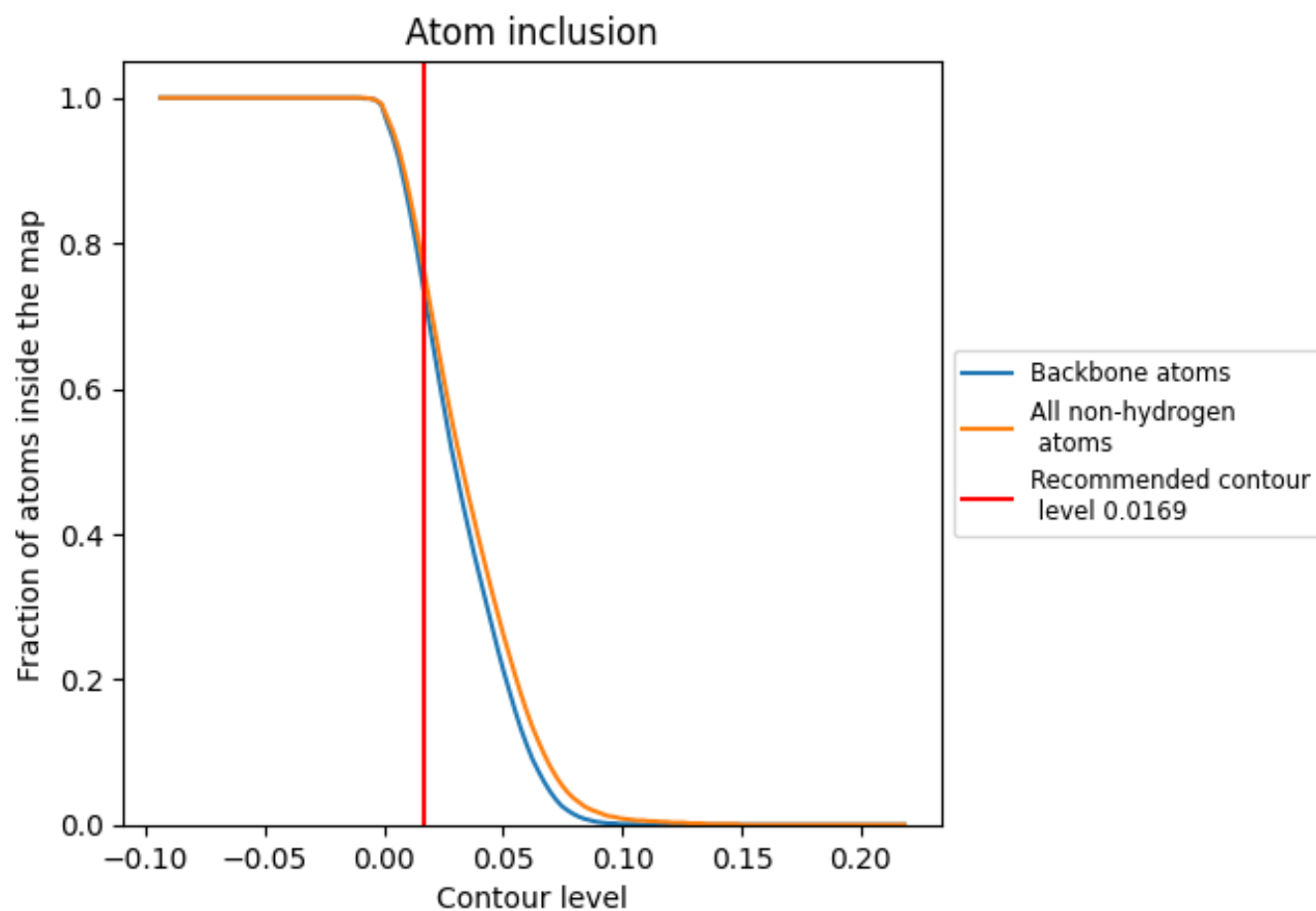
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0169).

9.4 Atom inclusion ⓘ



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 (0.0169) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.6280
0	 0.7730	 0.6740
1	 0.9410	 0.7730
2	 0.9430	 0.7650
3	 0.8460	 0.6920
4	 0.2010	 0.3590
A	 0.6870	 0.5610
B	 0.2350	 0.3930
C	 0.3070	 0.3850
D	 0.3020	 0.4210
E	 0.6860	 0.6000
F	 0.4510	 0.5200
G	 0.2760	 0.3900
H	 0.6590	 0.5790
I	 0.2750	 0.4120
J	 0.1950	 0.3030
K	 0.6250	 0.5790
L	 0.6370	 0.5920
M	 0.3780	 0.4600
N	 0.3150	 0.4430
O	 0.6220	 0.5710
P	 0.4510	 0.4920
Q	 0.4960	 0.5230
R	 0.5850	 0.5570
S	 0.2840	 0.3970
T	 0.4350	 0.4790
U	 0.3700	 0.4350
X	 0.4780	 0.4810
Y	 0.3430	 0.3620
Z	 0.5300	 0.4660
a	 0.9120	 0.7090
b	 0.8230	 0.6320
c	 0.9280	 0.7450
d	 0.9120	 0.7390
e	 0.8270	 0.7010



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Chain	Atom inclusion	Q-score
f	 0.4180	 0.4790
g	 0.4040	 0.4730
h	 0.4670	 0.5520
i	 0.9080	 0.7420
j	 0.8600	 0.7200
k	 0.8750	 0.7170
l	 0.8770	 0.7160
m	 0.9680	 0.7670
n	 0.7490	 0.6290
o	 0.8220	 0.6980
p	 0.9470	 0.7680
q	 0.8490	 0.7050
r	 0.9020	 0.7370
s	 0.8130	 0.6790
t	 0.7420	 0.6260
u	 0.7030	 0.6220
v	 0.9050	 0.7210
w	 0.8830	 0.7170
x	 0.6810	 0.6020
y	 0.8580	 0.7090
z	 0.8830	 0.7140