



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:56 PM UTC

PDB ID : 8BH6 / pdb_00008bh6
EMDB ID : EMD-16048
Title : Mature 30S ribosomal subunit from Staphylococcus aureus
Authors : Garaeva, N.; Fatkhullin, B.; Jenner, L.; Soufari, H.; Yusupov, M.; Usachev, K.
Deposited on : 2022-10-30
Resolution : 3.70 Å (reported)

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

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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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

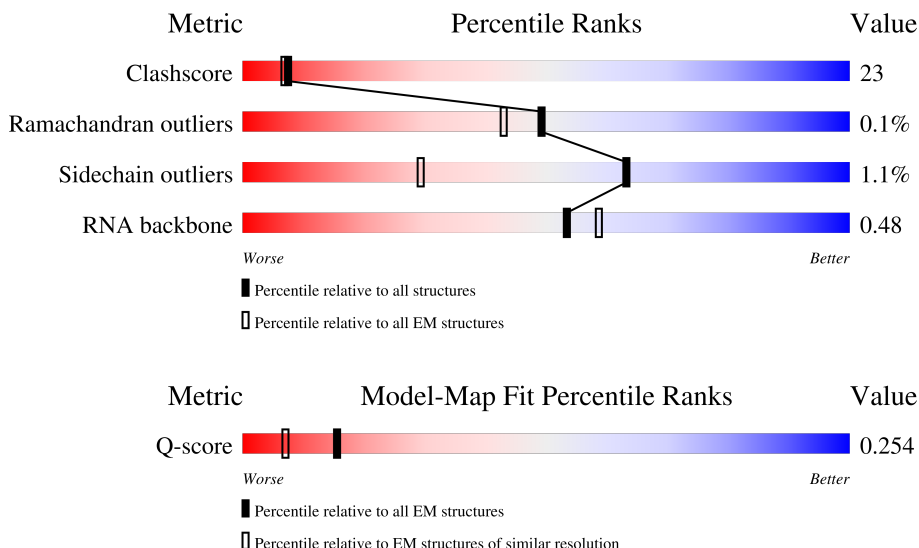
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



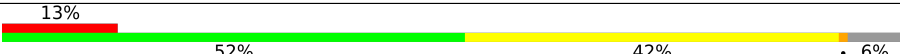
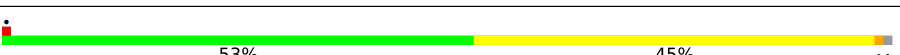
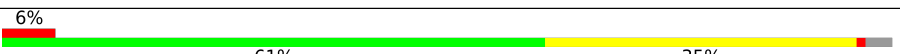
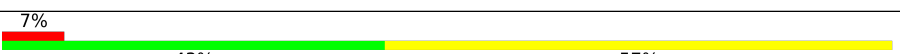
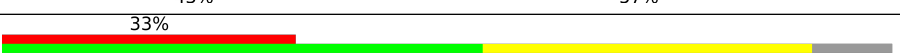
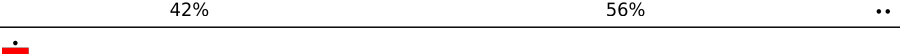
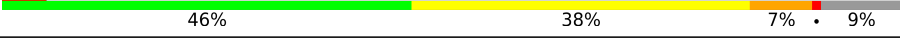
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	a	1547	27% 63% 10%
2	b	255	51% 54% 33% 12%
3	c	217	11% 69% 27% 5%

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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	166	
6	f	98	
7	g	156	
8	h	132	
9	i	132	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	91	
17	q	87	
18	r	80	
19	s	92	
20	t	83	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 51548 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1547	Total	C	N	O	P	0	0
			33126	14790	6036	10753	1547		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1802	1147	315	333	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	207	Total	C	N	O	S	0	0
			1634	1030	305	297	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	192	Total	C	N	O	S	0	0
			1570	992	294	282	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	164	Total	C	N	O	S	0	0
			1234	772	228	232	2		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			798	503	139	153	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	147	Total	C	N	O	S	0	0
			1189	744	227	214	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	102	Total	C	N	O	S	0	0
			813	512	148	150	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	118	Total	C	N	O	S	0	0
			880	543	169	165	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			1062	658	218	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	109	Total	C	N	O	S	0	0
			873	535	174	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			493	309	99	80	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	86	Total	C	N	O	S	0	0
			707	447	126	133	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	70	Total	C	N	O	S	0	0
			585	370	114	98	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	84	Total	C	N	O	S	0	0
			677	434	120	121	2		

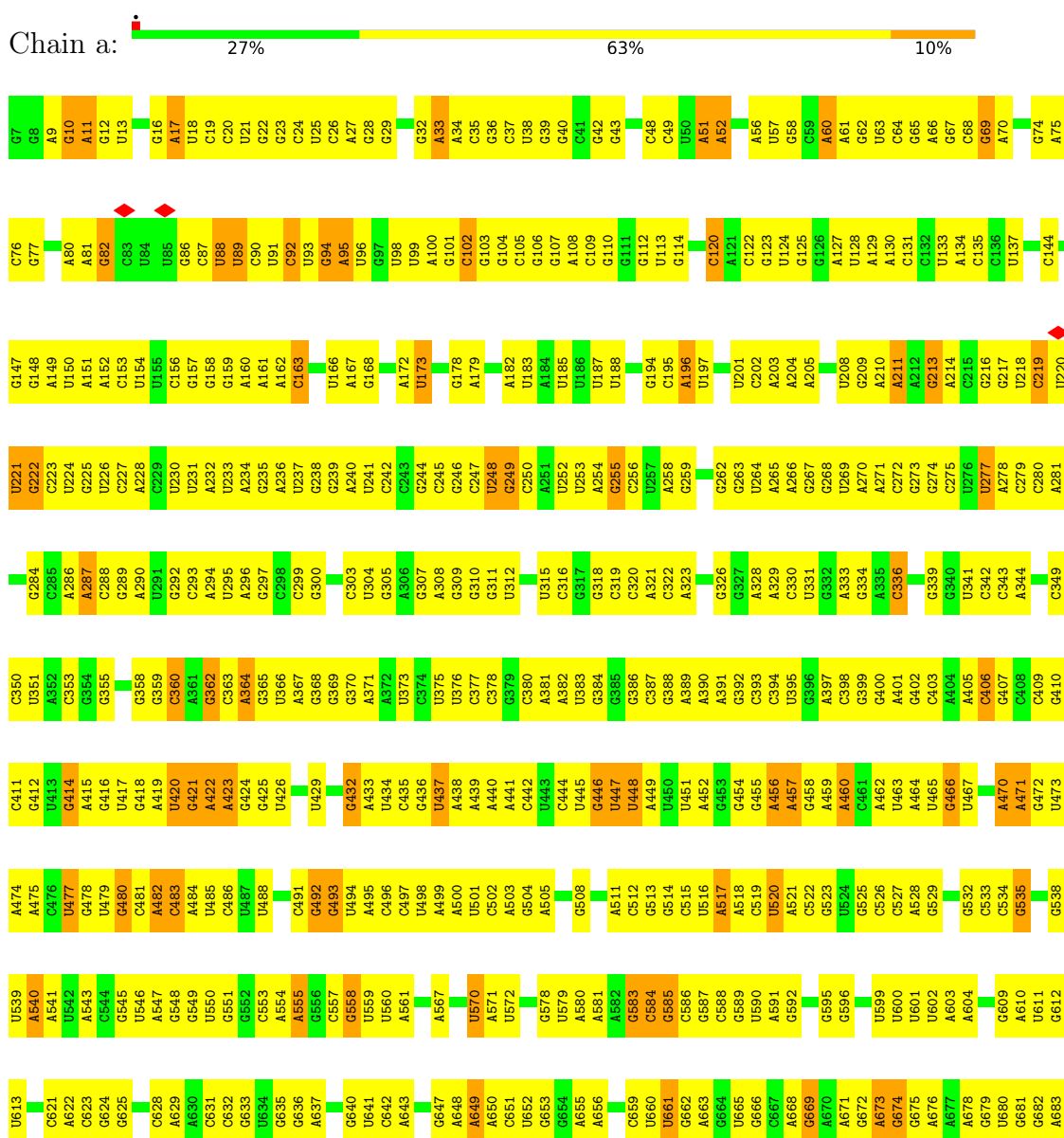
- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

3 Residue-property plots

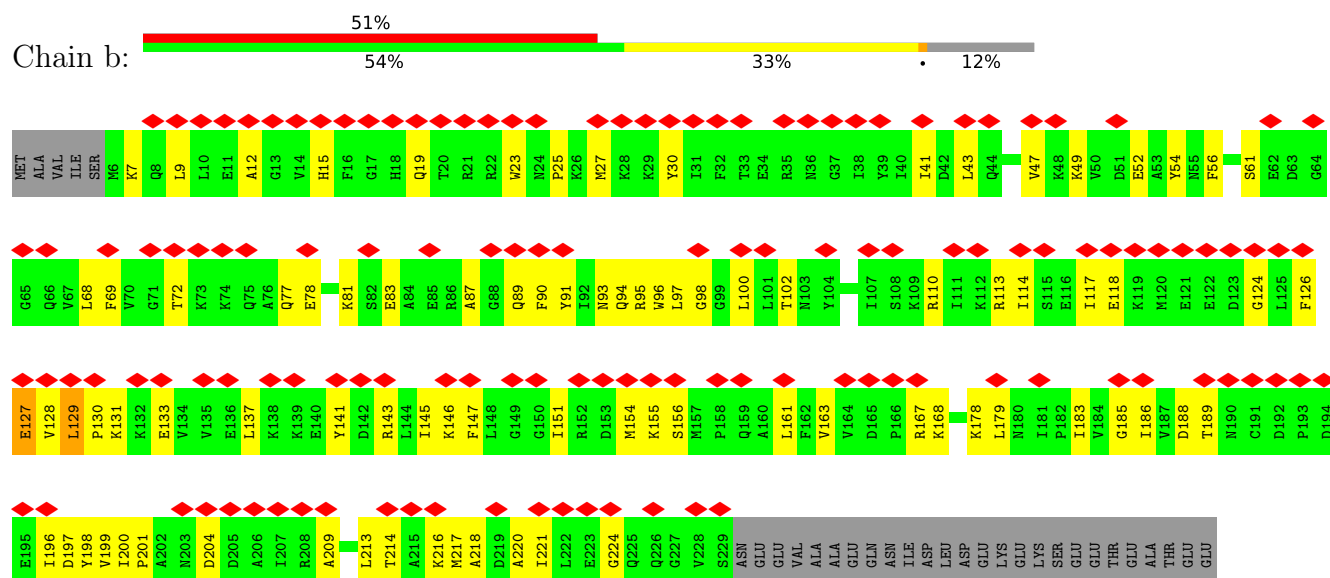
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

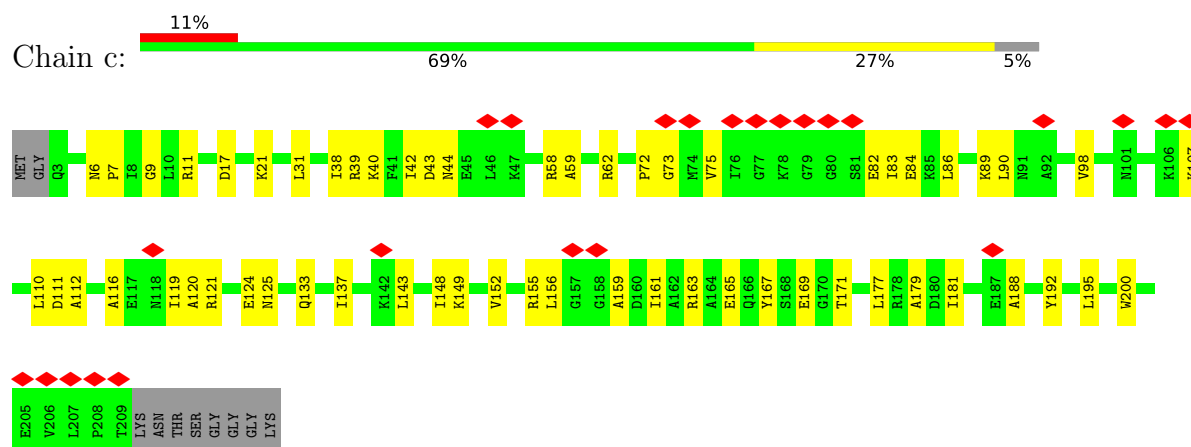




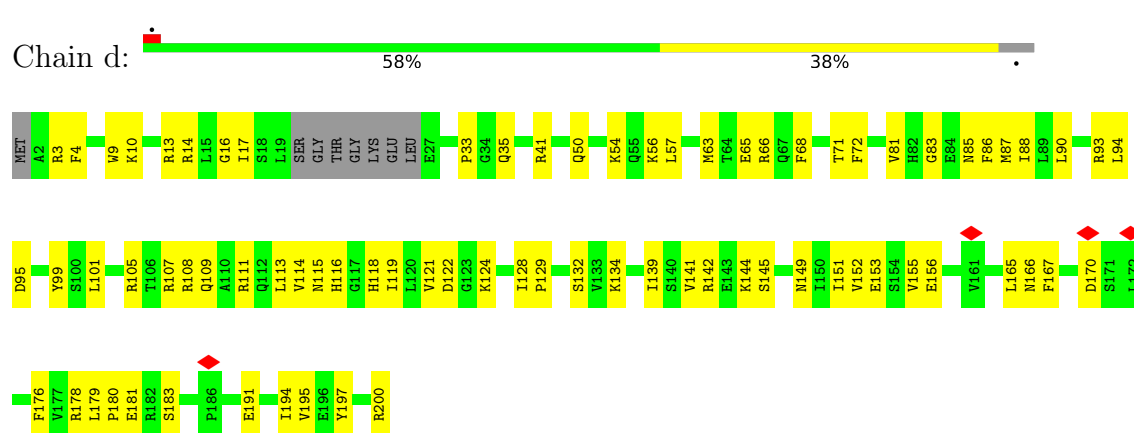
- Molecule 2: 30S ribosomal protein S2



- Molecule 3: 30S ribosomal protein S3

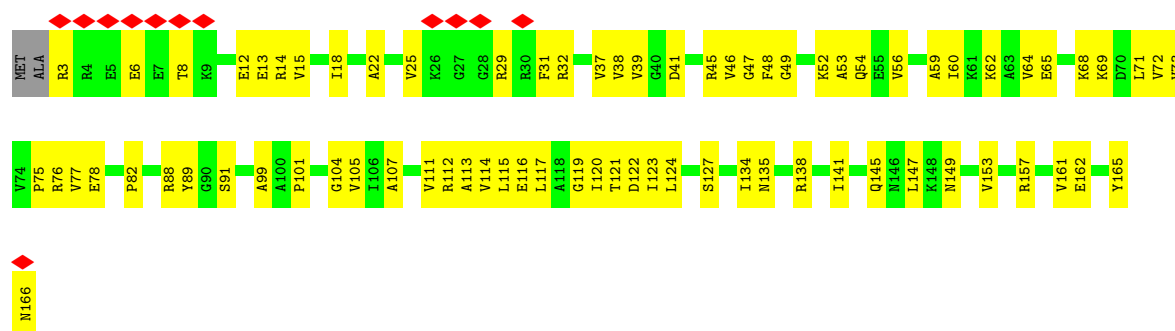


- Molecule 4: 30S ribosomal protein S4



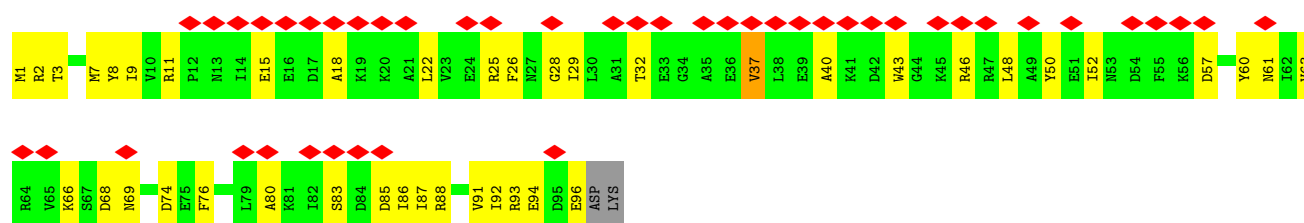
- Molecule 5: 30S ribosomal protein S5

Chain e: 



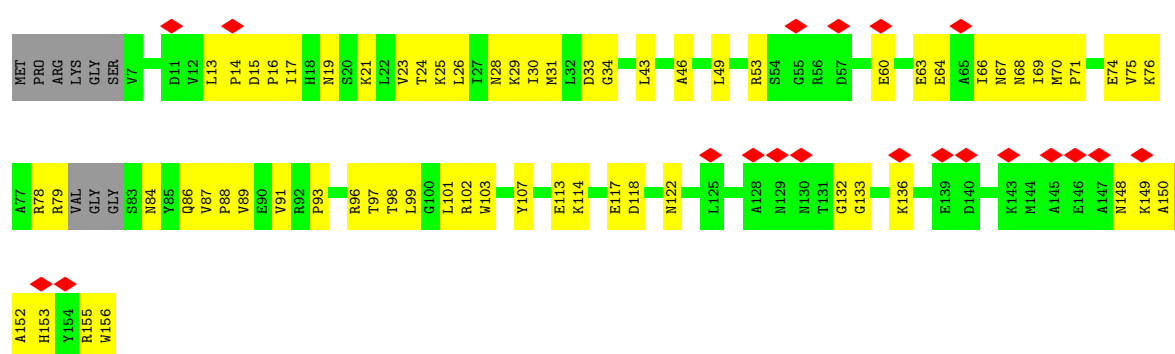
• Molecule 6: 30S ribosomal protein S6

Chain f: 



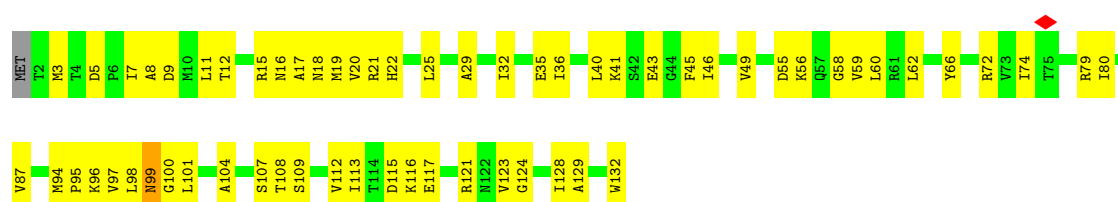
• Molecule 7: 30S ribosomal protein S7

Chain g: 

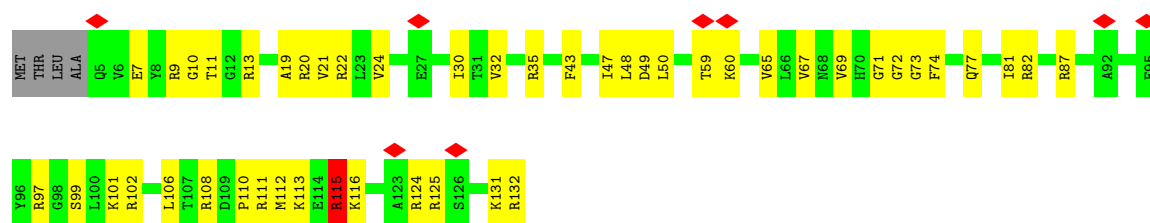


• Molecule 8: 30S ribosomal protein S8

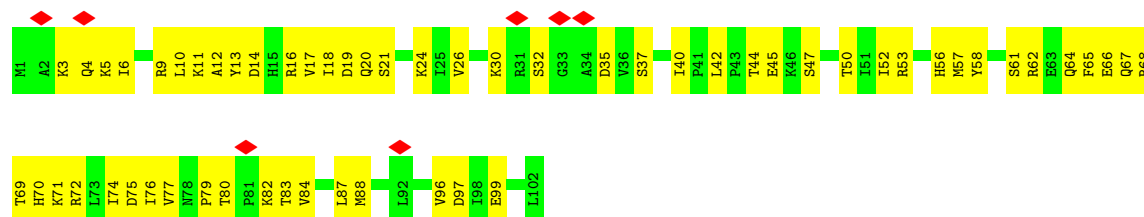
Chain h: 



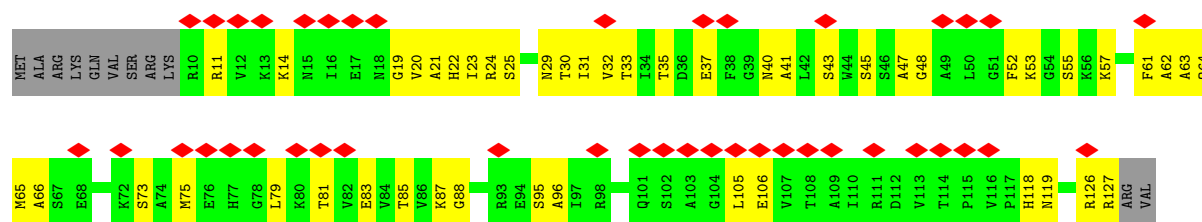
• Molecule 9: 30S ribosomal protein S9



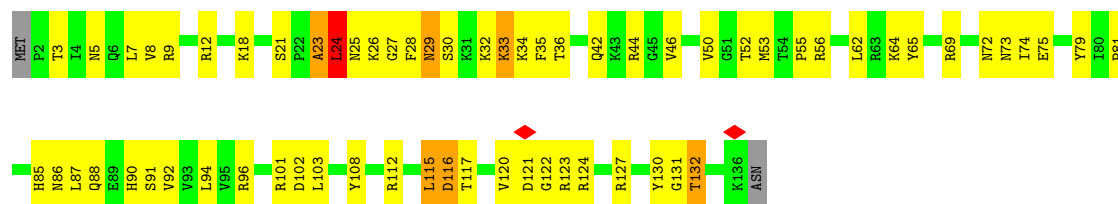
- Molecule 10: 30S ribosomal protein S10



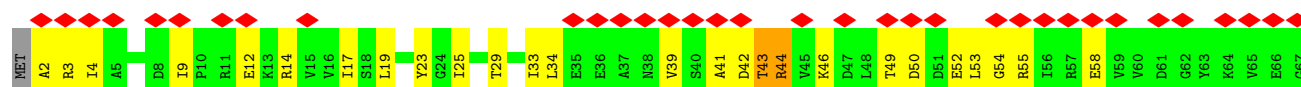
- Molecule 11: 30S ribosomal protein S11

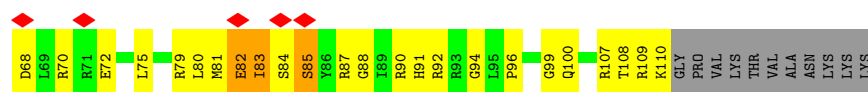


- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

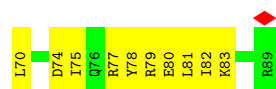
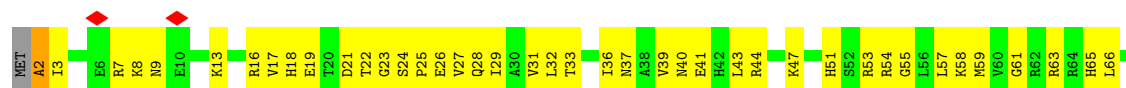




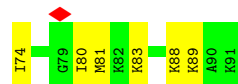
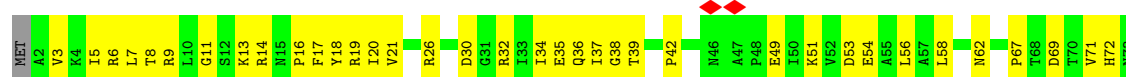
- Molecule 14: 30S ribosomal protein S14 type Z



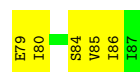
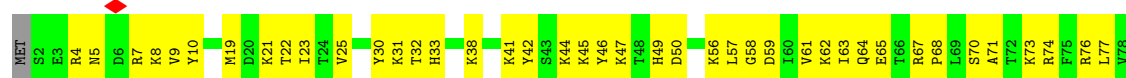
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16

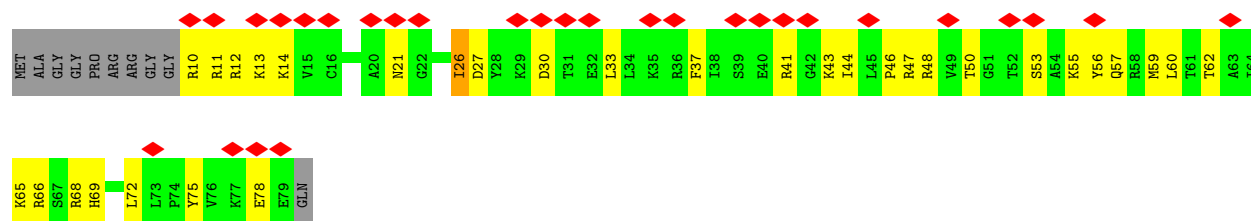


- Molecule 17: 30S ribosomal protein S17

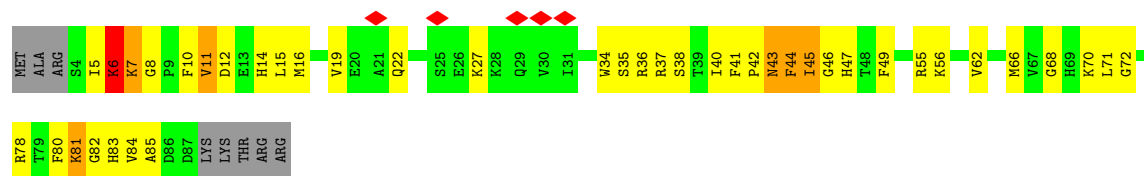


- Molecule 18: 30S ribosomal protein S18

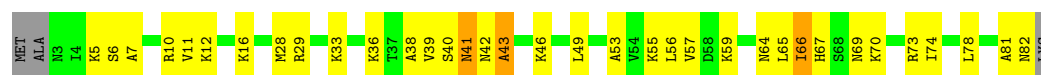




• Molecule 19: 30S ribosomal protein S19



• Molecule 20: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	326920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.7	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	3.439	Depositor
Minimum map value	-1.008	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.423	Depositor
Map size ($\text{\AA}$)	460.80002, 460.80002, 460.80002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2, 1.2, 1.2	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	a	0.19	0/37086	0.32	0/57833
2	b	0.21	0/1829	0.54	0/2454
3	c	0.19	0/1657	0.48	0/2228
4	d	0.22	0/1599	0.49	0/2146
5	e	0.23	0/1248	0.47	0/1680
6	f	0.19	0/809	0.51	1/1085 (0.1%)
7	g	0.20	0/1207	0.56	1/1625 (0.1%)
8	h	0.24	0/1044	0.57	1/1401 (0.1%)
9	i	0.31	1/1033 (0.1%)	0.58	2/1386 (0.1%)
10	j	0.30	0/825	0.60	0/1110
11	k	0.22	0/895	0.50	0/1207
12	l	0.34	1/1079 (0.1%)	0.66	2/1445 (0.1%)
13	m	0.24	0/879	0.82	2/1177 (0.2%)
14	n	0.25	0/501	0.85	3/662 (0.5%)
15	o	0.19	0/747	0.59	2/996 (0.2%)
16	p	0.22	0/723	0.58	0/971
17	q	0.21	0/715	0.50	0/955
18	r	0.17	0/594	0.56	2/792 (0.3%)
19	s	0.22	0/695	0.67	3/934 (0.3%)
20	t	0.27	0/606	0.71	4/810 (0.5%)
All	All	0.21	2/55771 (0.0%)	0.42	23/82897 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	i	115	ARG	CA-C	-5.40	1.45	1.53
12	l	131	GLY	C-N	-5.29	1.26	1.33

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	m	43	THR	N-CA-C	-15.06	83.62	108.48
12	l	24	LEU	N-CA-C	-11.98	97.93	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	n	19	ARG	N-CA-C	-10.69	98.52	112.41
13	m	43	THR	CB-CA-C	9.62	131.93	114.52
20	t	43	ALA	CB-CA-C	-8.99	93.62	111.60
14	n	18	VAL	N-CA-C	8.78	118.91	106.53
12	l	23	ALA	N-CA-C	-7.69	101.41	111.71
19	s	6	LYS	N-CA-C	-6.62	105.23	113.38
9	i	43	PHE	CA-C-N	6.42	133.25	121.70
9	i	43	PHE	C-N-CA	6.42	133.25	121.70
18	r	26	ILE	CA-C-N	5.75	132.05	121.70
18	r	26	ILE	C-N-CA	5.75	132.05	121.70
20	t	66	ILE	CA-C-N	5.58	131.74	121.70
20	t	66	ILE	C-N-CA	5.58	131.74	121.70
19	s	81	LYS	CA-C-N	5.51	131.62	121.70
19	s	81	LYS	C-N-CA	5.51	131.62	121.70
15	o	2	ALA	CA-C-N	5.44	131.49	121.70
15	o	2	ALA	C-N-CA	5.44	131.49	121.70
14	n	56	VAL	N-CA-C	5.40	116.47	108.65
8	h	99	ASN	CB-CA-C	-5.39	110.34	116.54
6	f	37	VAL	N-CA-C	-5.38	101.67	108.93
20	t	43	ALA	N-CA-C	-5.30	102.17	110.17
7	g	151	PHE	N-CA-C	5.28	117.84	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	33126	0	16679	1200	0
2	b	1802	0	1861	70	0
3	c	1634	0	1699	45	0
4	d	1570	0	1597	66	0
5	e	1234	0	1293	61	0
6	f	798	0	794	40	0
7	g	1189	0	1218	54	0
8	h	1032	0	1082	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	i	1017	0	1039	43	0
10	j	813	0	859	60	0
11	k	880	0	899	58	0
12	l	1062	0	1130	67	0
13	m	873	0	916	53	0
14	n	493	0	519	40	0
15	o	738	0	769	45	0
16	p	712	0	744	41	0
17	q	707	0	749	47	0
18	r	585	0	625	31	0
19	s	677	0	672	53	0
20	t	606	0	650	44	0
All	All	51548	0	35794	1955	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 23.

All (1955) 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)
20:t:43:ALA:O	20:t:46:LYS:HG2	1.38	1.23
1:a:673:A:H62	1:a:732:G:H1	1.08	0.98
1:a:602:U:H3	1:a:653:G:H1	1.13	0.96
1:a:901:U:H2'	1:a:902:A:H8	1.32	0.95
19:s:12:ASP:H	19:s:38:SER:HB3	1.29	0.95
20:t:46:LYS:HB2	20:t:82:ASN:HD22	1.31	0.93
18:r:26:ILE:HD11	18:r:33:LEU:HB3	1.52	0.92
1:a:935:G:H1	1:a:1402:U:H3	1.10	0.91
6:f:52:ILE:HD12	6:f:87:ILE:HG21	1.54	0.90
1:a:1093:G:N7	5:e:52:LYS:NZ	2.21	0.88
1:a:1316:G:H1	1:a:1342:G:HO2'	1.21	0.88
12:l:127:ARG:HB2	12:l:132:THR:HG22	1.54	0.87
2:b:72:THR:HB	2:b:168:LYS:HZ3	1.40	0.86
8:h:96:LYS:HG2	8:h:99:ASN:HA	1.54	0.86
1:a:553:C:H2'	1:a:554:A:C8	2.11	0.85
20:t:38:ALA:HB2	20:t:49:LEU:HD12	1.59	0.84
4:d:17:ILE:CD1	4:d:56:LYS:HD2	2.06	0.84
11:k:63:ALA:HB1	11:k:96:ALA:HB2	1.56	0.84
1:a:970:U:H2'	1:a:1236:A:H62	1.42	0.84
4:d:119:ILE:HB	4:d:139:ILE:HD11	1.58	0.84
18:r:21:ASN:HD22	18:r:33:LEU:HD21	1.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:553:C:H2'	1:a:554:A:H8	1.45	0.81
1:a:369:G:H4'	12:l:29:ASN:ND2	1.96	0.81
1:a:836:A:H62	1:a:868:G:H21	1.28	0.81
5:e:45:ARG:HH12	5:e:71:LEU:HD13	1.45	0.81
2:b:81:LYS:HG2	2:b:93:ASN:ND2	1.95	0.81
1:a:1360:A:H61	1:a:1384:G:H1'	1.45	0.80
19:s:45:ILE:HA	19:s:62:VAL:HG11	1.64	0.79
3:c:86:LEU:HA	3:c:89:LYS:HE3	1.63	0.79
12:l:90:HIS:ND1	12:l:90:HIS:O	2.15	0.79
1:a:958:C:H5	13:m:107:ARG:HH22	1.31	0.78
16:p:67:PRO:HG2	16:p:72:HIS:HE1	1.49	0.78
1:a:814:C:H2'	1:a:815:A:H8	1.48	0.78
16:p:34:ILE:HG22	16:p:35:GLU:HG2	1.65	0.77
7:g:15:ASP:HB2	7:g:24:THR:HG23	1.64	0.77
1:a:223:C:H2'	1:a:224:U:H6	1.48	0.77
12:l:65:TYR:HA	12:l:79:TYR:HA	1.67	0.77
1:a:937:G:H1	1:a:1401:U:H3	1.33	0.77
8:h:18:ASN:HB3	8:h:72:ARG:HH11	1.49	0.76
11:k:61:PHE:HA	11:k:64:GLN:HG2	1.67	0.76
1:a:819:C:H2'	1:a:820:G:C8	2.20	0.76
13:m:34:LEU:HG	13:m:39:VAL:HG23	1.67	0.76
4:d:17:ILE:HD11	4:d:56:LYS:HD2	1.65	0.76
19:s:81:LYS:H	19:s:82:GLY:HA2	1.51	0.76
1:a:63:U:H3	1:a:104:G:H1	1.32	0.75
1:a:1426:G:H2'	1:a:1427:A:H8	1.50	0.75
19:s:14:HIS:HB3	19:s:34:TRP:HH2	1.51	0.75
2:b:183:ILE:HG12	2:b:196:ILE:HG13	1.69	0.75
19:s:70:LYS:HG3	19:s:72:GLY:H	1.51	0.75
1:a:105:C:H2'	1:a:106:G:H8	1.52	0.75
1:a:592:G:H1	1:a:765:U:H3	1.33	0.75
13:m:87:ARG:NH1	19:s:68:GLY:O	2.20	0.75
17:q:70:SER:HB2	17:q:73:LYS:HG2	1.69	0.75
6:f:43:TRP:HD1	6:f:60:TYR:HD2	1.35	0.75
1:a:1526:U:H2'	1:a:1527:C:H6	1.51	0.75
1:a:1276:C:H2'	1:a:1277:G:C8	2.21	0.74
8:h:45:PHE:CE2	8:h:74:ILE:HG23	2.21	0.74
1:a:1526:U:H2'	1:a:1527:C:C6	2.21	0.74
1:a:583:G:H4'	1:a:584:C:H5''	1.66	0.74
1:a:957:G:P	13:m:107:ARG:HE	2.10	0.74
1:a:699:G:H1'	1:a:704:A:N6	2.02	0.74
2:b:83:GLU:HG2	2:b:214:THR:HB	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:305:G:N2	1:a:308:A:OP2	2.20	0.74
1:a:459:A:H61	1:a:491:C:H41	1.32	0.74
12:l:23:ALA:HB3	12:l:108:TYR:OH	1.88	0.74
19:s:6:LYS:HA	19:s:6:LYS:HE3	1.69	0.74
7:g:13:LEU:HB2	7:g:14:PRO:HD3	1.69	0.74
7:g:150:ALA:HB1	11:k:61:PHE:H	1.53	0.74
1:a:445:U:H2'	1:a:446:G:H8	1.50	0.74
15:o:55:GLY:HA2	15:o:58:LYS:HE2	1.69	0.74
20:t:46:LYS:HD3	20:t:82:ASN:HB2	1.69	0.74
9:i:30:ILE:HG22	9:i:65:VAL:HB	1.70	0.73
20:t:43:ALA:O	20:t:46:LYS:CG	2.28	0.73
1:a:319:C:OP1	16:p:32:ARG:NH1	2.22	0.73
4:d:101:LEU:HG	4:d:167:PHE:HE1	1.53	0.73
1:a:424:G:H2'	1:a:425:G:H8	1.52	0.73
1:a:907:C:H2'	1:a:908:G:C8	2.24	0.73
4:d:57:LEU:HD22	4:d:194:ILE:HD13	1.70	0.73
1:a:546:U:H2'	1:a:547:A:H8	1.54	0.72
11:k:22:HIS:HA	11:k:85:THR:HB	1.70	0.72
13:m:14:ARG:HB3	13:m:44:ARG:HA	1.71	0.72
1:a:956:A:H2'	1:a:957:G:C8	2.25	0.72
1:a:1360:A:N6	1:a:1384:G:H1'	2.04	0.72
1:a:1362:U:OP2	9:i:125:ARG:NH2	2.22	0.72
1:a:1377:C:O3'	10:j:62:ARG:NH1	2.23	0.72
7:g:150:ALA:HB2	11:k:61:PHE:HB2	1.70	0.72
5:e:76:ARG:NH1	5:e:119:GLY:O	2.23	0.71
10:j:10:LEU:HB2	10:j:72:ARG:HB3	1.71	0.71
1:a:526:C:H5''	1:a:527:C:C6	2.25	0.71
1:a:1291:A:OP2	10:j:9:ARG:NH2	2.22	0.71
14:n:6:MET:HA	14:n:9:LYS:HB2	1.72	0.71
1:a:74:G:N2	1:a:96:U:O4	2.24	0.71
11:k:23:ILE:HG12	11:k:32:VAL:HG23	1.72	0.71
1:a:445:U:O2'	1:a:446:G:H5'	1.90	0.71
1:a:499:A:H2'	1:a:500:A:H8	1.56	0.71
1:a:685:U:H3	1:a:721:G:H1	1.39	0.71
1:a:901:U:H2'	1:a:902:A:C8	2.19	0.70
1:a:681:G:H2'	1:a:682:G:C8	2.25	0.70
1:a:223:C:H2'	1:a:224:U:C6	2.27	0.70
1:a:412:G:H4'	1:a:447:U:H1'	1.73	0.70
2:b:81:LYS:HG2	2:b:93:ASN:HD21	1.56	0.70
2:b:196:ILE:HG23	2:b:199:VAL:HG12	1.74	0.70
1:a:471:A:H2'	1:a:472:G:C8	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:682:G:H2'	1:a:683:A:H8	1.53	0.70
15:o:55:GLY:O	15:o:59:MET:HG2	1.91	0.70
1:a:956:A:H2'	1:a:957:G:H8	1.57	0.70
8:h:32:ILE:HD11	8:h:112:VAL:HG21	1.74	0.70
1:a:1052:A:H2'	1:a:1053:G:H8	1.55	0.69
8:h:29:ALA:HB2	8:h:60:LEU:HB2	1.74	0.69
17:q:19:MET:HG3	17:q:22:THR:HB	1.73	0.69
1:a:329:A:N7	1:a:336:C:O2'	2.25	0.69
1:a:771:G:H2'	1:a:772:C:C6	2.26	0.69
8:h:11:LEU:HD22	8:h:79:ARG:HG3	1.74	0.69
3:c:155:ARG:HB2	3:c:192:TYR:HE2	1.56	0.69
5:e:3:ARG:N	5:e:69:LYS:O	2.25	0.69
1:a:732:G:H2'	1:a:733:G:C8	2.28	0.69
1:a:522:C:H2'	1:a:523:G:H8	1.57	0.69
1:a:673:A:N6	1:a:732:G:H1	1.89	0.69
12:l:7:LEU:HD21	12:l:12:ARG:HD3	1.75	0.69
15:o:80:GLU:HA	15:o:83:LYS:HE3	1.75	0.69
20:t:28:MET:HE1	20:t:57:VAL:HA	1.74	0.69
1:a:1083:C:H2'	1:a:1084:G:H8	1.57	0.69
1:a:1366:A:H2'	1:a:1367:G:C8	2.28	0.69
9:i:74:PHE:HA	9:i:77:GLN:HE21	1.58	0.69
19:s:45:ILE:HA	19:s:62:VAL:CG1	2.23	0.69
1:a:700:U:H2'	1:a:702:A:OP2	1.93	0.69
7:g:64:GLU:OE2	7:g:68:ASN:ND2	2.25	0.69
1:a:749:G:H1'	15:o:51:HIS:HB2	1.76	0.68
1:a:1052:A:H2'	1:a:1053:G:C8	2.28	0.68
10:j:67:GLN:HG3	14:n:55:GLY:HA3	1.75	0.68
1:a:343:C:H2'	1:a:344:A:H8	1.57	0.68
1:a:1049:C:H2'	1:a:1050:A:C8	2.29	0.68
1:a:366:U:H2'	1:a:367:A:H8	1.59	0.68
1:a:22:G:H2'	1:a:23:G:C8	2.28	0.68
8:h:108:THR:HG22	8:h:109:SER:N	2.09	0.68
7:g:88:PRO:HG2	7:g:149:LYS:HD3	1.75	0.68
1:a:1138:U:O4	10:j:9:ARG:NH1	2.27	0.68
9:i:19:ALA:HA	9:i:69:VAL:HG22	1.76	0.68
10:j:11:LYS:HB2	10:j:97:ASP:HB2	1.75	0.68
16:p:39:THR:HG22	16:p:51:LYS:HG2	1.76	0.68
1:a:56:A:N1	1:a:376:U:H5	1.92	0.68
13:m:41:ALA:N	13:m:42:ASP:HA	2.08	0.68
19:s:5:ILE:HD11	19:s:7:LYS:HD3	1.75	0.68
1:a:818:C:H2'	1:a:819:C:H6	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:89:TYR:HE2	5:e:138:ARG:HE	1.40	0.68
1:a:479:U:H2'	1:a:480:G:H8	1.59	0.67
1:a:919:A:OP1	12:l:18:LYS:NZ	2.27	0.67
1:a:1327:G:N1	1:a:1330:A:OP2	2.28	0.67
2:b:72:THR:HB	2:b:168:LYS:NZ	2.09	0.67
8:h:98:LEU:HB3	8:h:101:LEU:HB2	1.75	0.67
16:p:38:GLY:HA2	16:p:51:LYS:HG3	1.77	0.67
1:a:400:G:H2'	1:a:401:A:H8	1.59	0.67
1:a:1021:U:H2'	1:a:1022:A:H8	1.60	0.67
1:a:1248:C:O3'	1:a:1311:G:N2	2.26	0.67
1:a:1131:G:OP2	9:i:13:ARG:NH1	2.26	0.67
3:c:90:LEU:HD23	3:c:98:VAL:HG11	1.75	0.67
8:h:45:PHE:HE2	8:h:74:ILE:HG23	1.58	0.67
1:a:20:C:OP1	5:e:135:ASN:ND2	2.26	0.67
1:a:997:A:H2'	1:a:998:A:H8	1.59	0.67
19:s:81:LYS:HB3	19:s:83:HIS:N	2.10	0.67
1:a:720:A:H2'	1:a:721:G:C8	2.30	0.67
13:m:34:LEU:HG	13:m:39:VAL:CG2	2.24	0.67
11:k:20:VAL:HG22	11:k:83:GLU:HB3	1.76	0.67
1:a:1186:G:H2'	1:a:1187:A:H8	1.58	0.67
1:a:526:C:H5''	1:a:527:C:H6	1.59	0.67
8:h:104:ALA:HB3	8:h:115:ASP:HB2	1.76	0.67
1:a:1525:A:H2'	1:a:1526:U:C6	2.30	0.66
1:a:1107:U:OP1	1:a:1120:G:N2	2.27	0.66
5:e:54:GLN:OE1	5:e:54:GLN:N	2.21	0.66
19:s:14:HIS:HB3	19:s:34:TRP:CH2	2.30	0.66
1:a:451:U:H2'	1:a:452:A:C8	2.30	0.66
1:a:836:A:H62	1:a:868:G:N2	1.93	0.66
1:a:1367:G:H2'	1:a:1368:A:C8	2.30	0.66
1:a:483:C:H2'	1:a:484:A:C8	2.31	0.66
1:a:546:U:H2'	1:a:547:A:C8	2.31	0.66
1:a:1426:G:H2'	1:a:1427:A:C8	2.29	0.66
1:a:1051:A:H2'	1:a:1052:A:C8	2.31	0.66
1:a:1238:A:H5'	13:m:110:LYS:NZ	2.09	0.66
1:a:826:G:N2	1:a:828:U:O2	2.29	0.66
1:a:1450:G:OP1	20:t:33:LYS:NZ	2.28	0.66
1:a:370:G:N2	1:a:373:U:OP2	2.28	0.66
1:a:997:A:H2'	1:a:998:A:C8	2.30	0.66
2:b:94:GLN:NE2	2:b:146:LYS:O	2.28	0.66
20:t:39:VAL:HG11	20:t:81:ALA:HB1	1.78	0.66
1:a:196:A:O2'	17:q:76:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:893:C:H2'	1:a:894:U:C6	2.31	0.66
1:a:590:U:OP2	1:a:766:G:N1	2.28	0.65
17:q:56:LYS:HE2	17:q:84:SER:H	1.61	0.65
1:a:1261:A:H2	1:a:1381:G:H1'	1.60	0.65
1:a:393:C:H2'	1:a:394:C:C6	2.31	0.65
1:a:451:U:H2'	1:a:452:A:H8	1.61	0.65
1:a:673:A:N7	1:a:732:G:N2	2.30	0.65
1:a:777:G:H4'	1:a:1525:A:H4'	1.77	0.65
1:a:1015:C:N4	1:a:1035:U:OP1	2.29	0.65
1:a:1489:C:H2'	1:a:1490:A:H8	1.61	0.65
3:c:9:GLY:HA3	14:n:49:TYR:HD1	1.61	0.65
1:a:422:A:H3'	1:a:423:A:H8	1.62	0.65
7:g:113:GLU:HG2	7:g:114:LYS:H	1.62	0.65
1:a:719:G:H2'	1:a:720:A:H8	1.61	0.65
1:a:720:A:H2'	1:a:721:G:H8	1.60	0.65
1:a:1229:U:H2'	1:a:1230:U:C6	2.32	0.65
1:a:1276:C:H2'	1:a:1277:G:H8	1.62	0.65
15:o:16:ARG:NH2	15:o:19:GLU:OE1	2.30	0.65
1:a:686:U:H2'	1:a:687:C:C6	2.31	0.65
8:h:49:VAL:HG12	8:h:62:LEU:HD11	1.78	0.65
1:a:358:G:H2'	1:a:359:G:C8	2.32	0.65
1:a:1051:A:H2'	1:a:1052:A:H8	1.60	0.65
16:p:11:GLY:HA3	16:p:16:PRO:HA	1.77	0.65
1:a:928:A:H2'	1:a:929:A:C8	2.32	0.65
1:a:1527:C:H2'	1:a:1528:G:C8	2.31	0.65
1:a:1268:A:H2	1:a:1289:A:H62	1.42	0.65
10:j:6:ILE:HD11	10:j:79:PRO:HB3	1.77	0.65
12:l:24:LEU:HD13	12:l:25:ASN:N	2.12	0.65
1:a:412:G:OP2	4:d:3:ARG:HG3	1.97	0.64
7:g:150:ALA:HB2	11:k:61:PHE:CB	2.26	0.64
8:h:108:THR:CG2	8:h:123:VAL:HG22	2.28	0.64
1:a:225:G:H2'	1:a:226:U:C6	2.33	0.64
1:a:269:U:O4	20:t:73:ARG:NH1	2.31	0.64
1:a:781:G:O6	1:a:815:A:N6	2.30	0.64
1:a:987:A:HO2'	1:a:991:U:H3	1.43	0.64
13:m:14:ARG:HB2	13:m:41:ALA:HB1	1.78	0.64
1:a:960:U:H2'	1:a:961:G:C8	2.32	0.64
1:a:745:U:H2'	1:a:746:U:H6	1.62	0.64
1:a:1409:A:H5''	1:a:1412:G:H4'	1.78	0.64
1:a:693:G:N1	1:a:712:A:OP2	2.31	0.64
11:k:22:HIS:O	11:k:24:ARG:NH2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:112:ARG:HB2	12:l:130:TYR:HA	1.80	0.64
13:m:41:ALA:CB	13:m:43:THR:O	2.45	0.64
15:o:43:LEU:HD11	15:o:53:ARG:HE	1.63	0.64
1:a:1153:G:H2'	1:a:1154:G:O4'	1.97	0.64
4:d:71:THR:OG1	4:d:93:ARG:NH2	2.31	0.64
11:k:64:GLN:HE22	11:k:95:SER:HB3	1.61	0.64
1:a:88:U:H2'	1:a:89:U:C5	2.33	0.64
13:m:94:GLY:O	13:m:100:GLN:NE2	2.30	0.64
1:a:682:G:H2'	1:a:683:A:C8	2.32	0.64
10:j:10:LEU:HB3	10:j:18:ILE:HD11	1.79	0.63
11:k:47:ALA:HB2	11:k:62:ALA:HB1	1.80	0.63
12:l:28:PHE:N	12:l:36:THR:H	1.95	0.63
19:s:40:ILE:HG12	19:s:71:LEU:HB2	1.80	0.63
1:a:839:U:O2	1:a:865:G:N2	2.31	0.63
1:a:1132:C:H2'	1:a:1133:U:C6	2.33	0.63
1:a:678:A:H2'	1:a:679:G:C8	2.33	0.63
1:a:1331:C:N4	19:s:36:ARG:O	2.32	0.63
4:d:101:LEU:HD13	4:d:165:LEU:HB3	1.79	0.63
18:r:53:SER:HB2	18:r:56:TYR:HD2	1.63	0.63
1:a:550:U:OP1	4:d:10:LYS:NZ	2.29	0.63
11:k:81:THR:HG22	11:k:106:GLU:HB2	1.80	0.63
10:j:11:LYS:O	10:j:97:ASP:N	2.32	0.63
1:a:458:G:H22	16:p:14:ARG:HG3	1.63	0.63
1:a:1366:A:H2'	1:a:1367:G:H8	1.62	0.63
1:a:1534:U:H2'	1:a:1535:G:H8	1.63	0.63
15:o:79:ARG:O	15:o:83:LYS:HG3	1.99	0.63
1:a:230:U:H2'	1:a:231:U:H6	1.64	0.63
1:a:900:G:N2	1:a:916:G:H2'	2.13	0.63
1:a:1329:A:H4'	19:s:10:PHE:CD1	2.34	0.63
1:a:1163:A:OP1	10:j:70:HIS:ND1	2.32	0.63
6:f:1:MET:HA	6:f:68:ASP:HA	1.80	0.63
1:a:1435:U:H2'	1:a:1436:A:C8	2.34	0.62
1:a:1498:G:H2'	1:a:1499:G:C8	2.34	0.62
2:b:77:GLN:HG2	2:b:93:ASN:HB3	1.81	0.62
15:o:33:THR:O	15:o:37:ASN:ND2	2.32	0.62
1:a:63:U:H2'	1:a:64:C:C6	2.33	0.62
1:a:454:G:H2'	1:a:455:G:C8	2.33	0.62
1:a:1239:C:H2'	1:a:1240:A:H8	1.64	0.62
1:a:1406:C:H2'	1:a:1407:A:C8	2.34	0.62
7:g:53:ARG:NH1	7:g:122:ASN:OD1	2.25	0.62
8:h:108:THR:HG21	8:h:123:VAL:HG22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:41:ALA:HB1	13:m:43:THR:O	1.99	0.62
16:p:67:PRO:HG2	16:p:72:HIS:CE1	2.32	0.62
1:a:57:U:H2'	1:a:58:G:C8	2.34	0.62
1:a:266:A:H2'	1:a:267:G:H8	1.64	0.62
1:a:745:U:H2'	1:a:746:U:C6	2.34	0.62
1:a:105:C:H2'	1:a:106:G:C8	2.34	0.62
20:t:66:ILE:H	20:t:67:HIS:HA	1.63	0.62
1:a:513:G:H2'	1:a:514:G:C8	2.35	0.62
1:a:932:G:H4'	5:e:25:VAL:HA	1.82	0.62
1:a:1143:U:OP1	9:i:22:ARG:NH2	2.31	0.62
1:a:221:U:H4'	1:a:222:G:H8	1.65	0.62
1:a:446:G:H4'	1:a:447:U:H5'	1.82	0.62
1:a:532:G:H2'	1:a:533:C:C6	2.35	0.62
1:a:746:U:OP1	6:f:69:ASN:ND2	2.32	0.62
1:a:1100:G:H21	1:a:1178:A:H61	1.47	0.62
1:a:1211:C:H5''	1:a:1212:A:H3'	1.80	0.62
1:a:328:A:H2'	1:a:329:A:C8	2.35	0.62
1:a:1186:G:H2'	1:a:1187:A:C8	2.35	0.62
12:l:120:VAL:HG22	12:l:122:GLY:H	1.64	0.62
6:f:91:VAL:C	6:f:92:ILE:HD13	2.24	0.61
15:o:25:PRO:O	15:o:29:ILE:HG12	2.00	0.61
1:a:204:A:H2'	1:a:205:A:H8	1.66	0.61
1:a:360:C:O2	1:a:363:C:N4	2.31	0.61
1:a:804:C:H5''	11:k:127:ARG:HE	1.65	0.61
1:a:829:G:H2'	1:a:830:A:H8	1.65	0.61
1:a:366:U:H2'	1:a:367:A:C8	2.35	0.61
1:a:731:U:H4'	1:a:732:G:H5''	1.82	0.61
1:a:1311:G:O2'	1:a:1314:C:N4	2.34	0.61
4:d:101:LEU:HG	4:d:167:PHE:CE1	2.35	0.61
1:a:209:G:H2'	1:a:210:A:C8	2.35	0.61
2:b:143:ARG:HA	2:b:146:LYS:HE2	1.81	0.61
6:f:9:ILE:HG22	6:f:87:ILE:HD13	1.81	0.61
18:r:66:ARG:O	18:r:69:HIS:HB2	1.99	0.61
1:a:995:C:H2'	1:a:996:A:H8	1.64	0.61
1:a:1048:A:H2'	1:a:1049:C:H6	1.65	0.61
1:a:1367:G:H2'	1:a:1368:A:H8	1.65	0.61
1:a:1503:G:H4'	12:l:56:ARG:HH11	1.65	0.61
5:e:6:GLU:OE2	5:e:45:ARG:NH2	2.33	0.61
1:a:237:U:H4'	16:p:3:VAL:HG11	1.82	0.61
1:a:415:A:H5'	4:d:4:PHE:CE2	2.35	0.61
1:a:970:U:H2'	1:a:1236:A:N6	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:81:VAL:O	4:d:85:ASN:ND2	2.34	0.61
12:l:102:ASP:OD1	12:l:103:LEU:N	2.33	0.61
1:a:384:G:H5''	16:p:6:ARG:HB2	1.83	0.61
12:l:28:PHE:H	12:l:35:PHE:HA	1.65	0.61
1:a:415:A:OP1	4:d:108:ARG:NH2	2.34	0.61
1:a:1061:U:HO2'	14:n:2:ALA:N	1.99	0.61
9:i:112:MET:N	9:i:112:MET:SD	2.74	0.61
1:a:679:G:H2'	1:a:680:U:C6	2.35	0.60
1:a:717:U:H2'	1:a:718:G:C8	2.35	0.60
1:a:1329:A:H5''	19:s:10:PHE:HB2	1.83	0.60
9:i:115:ARG:CZ	9:i:115:ARG:HB2	2.29	0.60
12:l:124:ARG:O	12:l:127:ARG:NH2	2.33	0.60
2:b:41:ILE:HD11	2:b:201:PRO:HB3	1.83	0.60
1:a:89:U:H2'	1:a:90:C:C6	2.36	0.60
1:a:587:G:O3'	15:o:54:ARG:NH1	2.33	0.60
1:a:960:U:H3	1:a:1242:G:H1	1.47	0.60
1:a:1021:U:H2'	1:a:1022:A:C8	2.37	0.60
1:a:1267:C:H5'	1:a:1269:G:H1'	1.82	0.60
10:j:64:GLN:O	14:n:59:ALA:HB2	2.02	0.60
1:a:416:G:H4'	4:d:105:ARG:HD2	1.83	0.60
1:a:501:U:H2'	1:a:502:C:C6	2.37	0.60
1:a:286:A:OP2	17:q:45:LYS:NZ	2.34	0.60
14:n:3:LYS:HA	14:n:6:MET:SD	2.42	0.60
1:a:57:U:H2'	1:a:58:G:H8	1.67	0.60
1:a:364:A:H3'	1:a:365:G:H8	1.65	0.60
1:a:1507:U:H2'	1:a:1508:C:C6	2.36	0.60
1:a:703:A:H61	1:a:805:C:H1'	1.66	0.60
1:a:719:G:H2'	1:a:720:A:C8	2.36	0.60
1:a:1177:G:N1	1:a:1180:A:OP2	2.30	0.60
16:p:9:ARG:HH21	16:p:16:PRO:HB3	1.65	0.60
1:a:167:A:H2'	1:a:168:G:H8	1.66	0.60
1:a:244:G:O3'	17:q:44:LYS:NZ	2.33	0.60
1:a:570:U:O2'	12:l:12:ARG:HG3	2.02	0.60
1:a:1415:C:H2'	1:a:1416:G:C8	2.37	0.60
7:g:60:GLU:N	7:g:60:GLU:OE2	2.34	0.60
7:g:74:GLU:O	7:g:89:VAL:N	2.22	0.60
1:a:623:C:H2'	1:a:624:G:H8	1.67	0.59
1:a:307:G:H2'	1:a:308:A:C8	2.36	0.59
1:a:950:C:H2'	1:a:951:G:C8	2.36	0.59
1:a:1451:U:H3	1:a:1473:G:H1	1.50	0.59
6:f:11:ARG:HD2	6:f:87:ILE:HD11	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:j:21:SER:HA	10:j:24:LYS:HD3	1.84	0.59
1:a:419:A:N3	1:a:420:U:N3	2.51	0.59
1:a:458:G:H1	16:p:14:ARG:HD2	1.65	0.59
1:a:685:U:H2'	1:a:686:U:H6	1.67	0.59
11:k:64:GLN:NE2	11:k:95:SER:HB3	2.16	0.59
12:l:52:THR:HG23	12:l:64:LYS:HA	1.82	0.59
1:a:147:G:H2'	1:a:148:G:C8	2.37	0.59
1:a:349:C:H2'	1:a:350:C:C6	2.37	0.59
1:a:675:G:H1'	15:o:51:HIS:CE1	2.37	0.59
1:a:685:U:H2'	1:a:686:U:C6	2.37	0.59
1:a:445:U:H2'	1:a:446:G:C8	2.35	0.59
1:a:572:U:OP1	12:l:12:ARG:NH2	2.35	0.59
1:a:790:A:H62	1:a:808:G:H21	1.49	0.59
1:a:842:U:H2'	1:a:843:A:C8	2.38	0.59
1:a:926:G:H2'	1:a:927:G:H8	1.68	0.59
1:a:1043:G:N2	1:a:1043:G:OP2	2.35	0.59
1:a:1475:C:H2'	1:a:1476:G:H8	1.66	0.59
3:c:111:ASP:OD1	3:c:112:ALA:N	2.35	0.59
6:f:15:GLU:HG3	6:f:18:ALA:H	1.67	0.59
7:g:79:ARG:NH2	7:g:84:ASN:OD1	2.36	0.59
9:i:101:LYS:HD3	9:i:106:LEU:HD23	1.83	0.59
13:m:90:ARG:NH1	13:m:96:PRO:O	2.35	0.59
1:a:589:G:N2	1:a:767:A:OP2	2.32	0.59
1:a:744:U:H4'	6:f:92:ILE:HD12	1.83	0.59
2:b:19:GLN:OE1	2:b:167:ARG:NH2	2.32	0.59
1:a:699:G:H1	11:k:53:LYS:NZ	2.00	0.59
1:a:745:U:H5''	6:f:93:ARG:HG3	1.83	0.59
1:a:770:U:H2'	1:a:771:G:C8	2.38	0.59
1:a:1047:G:OP2	1:a:1048:A:N6	2.36	0.59
3:c:39:ARG:HD3	3:c:42:ILE:HD11	1.85	0.59
19:s:47:HIS:H	19:s:62:VAL:HB	1.68	0.59
1:a:127:A:O2'	17:q:7:ARG:NH1	2.28	0.59
1:a:699:G:H1'	1:a:704:A:H62	1.65	0.59
1:a:1380:C:H2'	1:a:1381:G:C8	2.37	0.59
18:r:62:THR:HA	18:r:65:LYS:HD2	1.83	0.59
1:a:938:G:H2'	1:a:939:A:H8	1.68	0.59
11:k:21:ALA:N	11:k:83:GLU:O	2.25	0.59
15:o:25:PRO:HB3	15:o:66:LEU:HD12	1.85	0.59
16:p:49:GLU:OE1	16:p:49:GLU:N	2.32	0.59
1:a:424:G:H2'	1:a:425:G:C8	2.36	0.59
1:a:722:G:H2'	1:a:723:A:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:63:MET:HE1	4:d:68:PHE:HA	1.83	0.59
1:a:692:U:OP1	11:k:11:ARG:NH1	2.35	0.58
1:a:1116:G:OP1	2:b:110:ARG:NH2	2.35	0.58
1:a:1387:U:H5'	7:g:98:THR:HG21	1.84	0.58
17:q:30:TYR:HA	17:q:41:LYS:HA	1.85	0.58
1:a:42:G:H2'	1:a:43:G:H8	1.68	0.58
1:a:743:C:H5'	18:r:65:LYS:HD3	1.85	0.58
1:a:995:C:H2'	1:a:996:A:C8	2.38	0.58
1:a:1013:G:H2'	1:a:1014:A:H4'	1.85	0.58
2:b:163:VAL:HG22	2:b:185:GLY:HA3	1.85	0.58
6:f:46:ARG:HD3	6:f:60:TYR:HE2	1.68	0.58
9:i:11:THR:O	9:i:108:ARG:NH2	2.36	0.58
1:a:459:A:H4'	16:p:42:PRO:HB2	1.84	0.58
1:a:866:C:H2'	1:a:867:U:H6	1.68	0.58
10:j:32:SER:HB2	10:j:82:LYS:HB3	1.85	0.58
10:j:37:SER:HB2	10:j:75:ASP:H	1.69	0.58
1:a:1024:A:C2	1:a:1230:U:H1'	2.38	0.58
1:a:1261:A:C2	1:a:1381:G:H1'	2.37	0.58
20:t:39:VAL:HA	20:t:46:LYS:HE2	1.86	0.58
1:a:122:C:OP1	1:a:319:C:O2'	2.20	0.58
1:a:671:A:H2'	1:a:672:G:C8	2.38	0.58
1:a:839:U:H3	1:a:865:G:H1	1.52	0.58
1:a:446:G:H5''	4:d:116:HIS:CD2	2.38	0.58
1:a:1130:A:H2'	1:a:1131:G:H8	1.68	0.58
1:a:1173:C:H2'	1:a:1174:G:H8	1.68	0.58
5:e:12:GLU:HB3	5:e:117:LEU:CD1	2.33	0.58
1:a:74:G:HO2'	1:a:75:A:H8	1.50	0.58
1:a:482:A:OP2	16:p:81:MET:HE1	2.03	0.58
8:h:17:ALA:HA	8:h:22:HIS:CE1	2.38	0.58
1:a:227:C:H2'	1:a:228:A:H8	1.69	0.58
3:c:179:ALA:HB1	3:c:181:ILE:HG23	1.86	0.58
10:j:47:SER:HB2	10:j:67:GLN:H	1.68	0.58
15:o:47:LYS:O	15:o:53:ARG:NH2	2.37	0.58
16:p:20:ILE:HG22	16:p:37:ILE:HG13	1.85	0.58
1:a:68:C:H4'	1:a:172:A:O4'	2.03	0.58
1:a:446:G:H4'	1:a:447:U:C5'	2.34	0.58
1:a:1423:C:H2'	1:a:1424:A:C8	2.38	0.58
1:a:1534:U:H2'	1:a:1535:G:C8	2.39	0.58
9:i:99:SER:HA	9:i:102:ARG:HH12	1.69	0.58
15:o:25:PRO:O	15:o:29:ILE:N	2.26	0.58
1:a:204:A:H2'	1:a:205:A:C8	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:29:ARG:HH12	5:e:31:PHE:HB3	1.69	0.57
10:j:80:THR:HG23	10:j:83:THR:H	1.68	0.57
1:a:272:C:O2'	17:q:68:PRO:O	2.20	0.57
1:a:1536:C:H2'	1:a:1537:G:H8	1.68	0.57
7:g:21:LYS:O	7:g:25:LYS:NZ	2.35	0.57
11:k:24:ARG:HB2	11:k:31:ILE:HB	1.85	0.57
1:a:759:U:H5'	15:o:21:ASP:OD1	2.04	0.57
1:a:886:A:OP1	8:h:15:ARG:NH1	2.30	0.57
1:a:1333:C:OP1	19:s:78:ARG:NH2	2.37	0.57
15:o:61:GLY:O	15:o:65:HIS:ND1	2.34	0.57
1:a:783:G:H2'	1:a:784:G:C8	2.40	0.57
10:j:84:VAL:O	10:j:88:MET:HG2	2.04	0.57
1:a:99:U:O2'	1:a:100:A:H8	1.88	0.57
1:a:1049:C:H2'	1:a:1050:A:H8	1.68	0.57
1:a:1137:U:O2'	1:a:1138:U:O5'	2.18	0.57
3:c:83:ILE:HA	3:c:86:LEU:HD12	1.86	0.57
1:a:213:G:H2'	1:a:214:A:C8	2.38	0.57
1:a:266:A:H2'	1:a:267:G:C8	2.39	0.57
1:a:409:C:H2'	1:a:410:G:C8	2.40	0.57
1:a:927:G:H2'	1:a:928:A:H8	1.70	0.57
1:a:1230:U:H2'	1:a:1231:G:C8	2.40	0.57
1:a:1489:C:H2'	1:a:1490:A:C8	2.39	0.57
8:h:11:LEU:HD22	8:h:79:ARG:CG	2.33	0.57
10:j:12:ALA:HB2	10:j:96:VAL:HG22	1.87	0.57
1:a:162:A:N6	1:a:163:C:O2	2.38	0.57
1:a:1002:U:O2'	1:a:1054:U:N3	2.37	0.57
7:g:88:PRO:CG	7:g:149:LYS:HD3	2.34	0.57
1:a:479:U:H2'	1:a:480:G:C8	2.40	0.57
1:a:194:G:H21	1:a:196:A:H2	1.52	0.57
1:a:369:G:H4'	12:l:29:ASN:HD21	1.69	0.57
1:a:1047:G:O2'	1:a:1048:A:O4'	2.23	0.57
1:a:1136:G:N2	1:a:1137:U:O4	2.35	0.57
1:a:25:U:H2'	1:a:26:C:C6	2.39	0.57
1:a:415:A:H5'	4:d:4:PHE:HE2	1.70	0.57
1:a:420:U:O4	1:a:439:A:N6	2.38	0.57
1:a:433:A:H2'	1:a:434:U:C6	2.40	0.57
1:a:1098:U:H3	1:a:1111:G:H22	1.52	0.57
1:a:1365:U:H2'	1:a:1366:A:C8	2.40	0.57
1:a:1536:C:H2'	1:a:1537:G:C8	2.39	0.57
2:b:77:GLN:CG	2:b:93:ASN:HB3	2.35	0.56
2:b:114:ILE:O	2:b:118:GLU:HG2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:88:ARG:HH21	5:e:91:SER:H	1.50	0.56
1:a:441:A:H2'	1:a:442:C:C6	2.40	0.56
1:a:1069:G:H2'	1:a:1070:G:O4'	2.05	0.56
1:a:390:A:H2'	1:a:391:A:C8	2.41	0.56
1:a:1100:G:H21	1:a:1178:A:N6	2.04	0.56
1:a:1377:C:H2'	1:a:1378:U:C6	2.40	0.56
1:a:1416:G:H2'	1:a:1417:U:H6	1.70	0.56
1:a:547:A:H2'	1:a:548:G:C8	2.41	0.56
19:s:45:ILE:HD13	19:s:46:GLY:H	1.70	0.56
20:t:29:ARG:O	20:t:33:LYS:HG2	2.04	0.56
1:a:18:U:H2'	1:a:19:C:C6	2.41	0.56
1:a:23:G:H2'	1:a:24:C:H6	1.71	0.56
1:a:213:G:H2'	1:a:214:A:H8	1.71	0.56
1:a:932:G:H2'	1:a:933:A:C8	2.41	0.56
1:a:1014:A:H2'	1:a:1015:C:C6	2.41	0.56
13:m:4:ILE:HG12	13:m:9:ILE:HG21	1.87	0.56
1:a:320:C:H2'	1:a:321:A:H8	1.70	0.56
1:a:814:C:H2'	1:a:815:A:C8	2.36	0.56
1:a:381:A:H61	1:a:399:G:H1'	1.71	0.56
1:a:635:G:H2'	1:a:636:G:H8	1.70	0.56
1:a:681:G:H2'	1:a:682:G:H8	1.68	0.56
1:a:765:U:O2'	1:a:889:C:O2	2.21	0.56
1:a:60:A:H3'	1:a:339:G:H22	1.71	0.56
1:a:293:C:H2'	1:a:294:A:C8	2.39	0.56
1:a:698:G:H2'	1:a:699:G:C8	2.40	0.56
1:a:829:G:H2'	1:a:830:A:C8	2.40	0.56
1:a:866:C:H2'	1:a:867:U:C6	2.40	0.56
13:m:41:ALA:HB3	13:m:42:ASP:C	2.29	0.56
1:a:755:U:H3'	1:a:756:A:C8	2.41	0.56
1:a:1408:C:H5''	1:a:1409:A:N7	2.21	0.56
2:b:141:TYR:O	2:b:145:ILE:HG12	2.06	0.56
17:q:10:TYR:HD2	17:q:46:TYR:HE2	1.54	0.56
1:a:1030:A:H2'	1:a:1031:G:H8	1.70	0.56
4:d:50:GLN:HB3	4:d:197:TYR:HB2	1.87	0.56
7:g:29:LYS:NZ	7:g:102:ARG:HE	2.04	0.56
13:m:81:MET:O	13:m:81:MET:HG3	2.06	0.56
1:a:279:C:H2'	1:a:280:C:H6	1.70	0.55
1:a:908:G:N2	1:a:911:A:OP2	2.39	0.55
3:c:163:ARG:NH2	3:c:165:GLU:OE1	2.40	0.55
8:h:25:LEU:HD21	8:h:62:LEU:HB3	1.87	0.55
1:a:310:G:H2'	1:a:311:G:H8	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:343:C:H2'	1:a:344:A:C8	2.38	0.55
1:a:1237:C:H5'	19:s:81:LYS:HG3	1.88	0.55
4:d:118:HIS:NE2	4:d:145:SER:O	2.40	0.55
11:k:75:MET:SD	11:k:105:LEU:HD21	2.47	0.55
1:a:287:A:H5''	1:a:288:C:H3'	1.89	0.55
7:g:67:ASN:HA	7:g:70:MET:SD	2.46	0.55
10:j:64:GLN:HB2	14:n:59:ALA:HB1	1.88	0.55
1:a:370:G:OP2	12:l:44:ARG:NH2	2.40	0.55
1:a:623:C:H2'	1:a:624:G:C8	2.42	0.55
1:a:732:G:H2'	1:a:733:G:H8	1.70	0.55
1:a:844:G:H1	1:a:860:U:H3	1.54	0.55
1:a:1334:G:H1'	1:a:1372:G:H21	1.72	0.55
11:k:37:GLU:CD	11:k:37:GLU:H	2.15	0.55
14:n:57:ARG:HG2	14:n:57:ARG:O	2.06	0.55
1:a:74:G:H1'	1:a:95:A:H61	1.72	0.55
1:a:305:G:N2	1:a:309:G:N7	2.54	0.55
1:a:322:C:H2'	1:a:323:A:C8	2.41	0.55
1:a:559:U:H2'	1:a:560:U:C6	2.42	0.55
11:k:61:PHE:O	11:k:64:GLN:HB2	2.06	0.55
12:l:27:GLY:HA3	12:l:35:PHE:HD2	1.71	0.55
1:a:470:A:N3	16:p:89:LYS:NZ	2.53	0.55
1:a:765:U:H2'	1:a:766:G:O4'	2.07	0.55
1:a:839:U:O2'	1:a:1551:C:H5''	2.07	0.55
1:a:927:G:H2'	1:a:928:A:C8	2.41	0.55
1:a:1053:G:H2'	1:a:1054:U:O4'	2.07	0.55
1:a:1163:A:O2'	10:j:16:ARG:NH2	2.40	0.55
1:a:1485:G:H2'	1:a:1486:G:C8	2.41	0.55
2:b:213:LEU:HA	2:b:216:LYS:HZ1	1.72	0.55
20:t:56:LEU:HA	20:t:59:LYS:HB2	1.88	0.55
1:a:25:U:H2'	1:a:26:C:H6	1.72	0.55
1:a:954:G:N1	1:a:1349:G:OP2	2.34	0.55
1:a:1014:A:C6	1:a:1037:C:H1'	2.40	0.55
1:a:1224:A:O2'	1:a:1226:G:N7	2.36	0.55
7:g:71:PRO:HG2	7:g:103:TRP:HZ3	1.72	0.55
7:g:75:VAL:HA	7:g:88:PRO:HA	1.88	0.55
11:k:24:ARG:HE	11:k:31:ILE:HB	1.72	0.55
1:a:219:C:H4'	1:a:220:U:H5	1.71	0.55
1:a:230:U:H2'	1:a:231:U:C6	2.41	0.55
1:a:534:C:OP2	12:l:101:ARG:NH1	2.39	0.55
1:a:1114:A:O2'	2:b:98:GLY:HA3	2.06	0.55
19:s:62:VAL:HG13	19:s:66:MET:HE2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:106:G:O6	20:t:10:ARG:HD3	2.07	0.55
1:a:134:A:H1'	1:a:333:A:C5	2.40	0.55
1:a:315:U:H5''	1:a:316:C:H5	1.71	0.55
1:a:642:C:H2'	1:a:643:A:C8	2.40	0.55
1:a:714:A:H2'	1:a:715:U:C6	2.42	0.55
1:a:794:G:H2'	1:a:795:A:H8	1.72	0.55
1:a:1054:U:H2'	1:a:1055:G:N7	2.22	0.55
1:a:1112:C:OP2	2:b:95:ARG:NH1	2.29	0.55
1:a:1229:U:H2'	1:a:1230:U:H6	1.72	0.55
8:h:108:THR:HG23	8:h:124:GLY:O	2.07	0.55
1:a:466:G:O6	1:a:484:A:N6	2.39	0.55
1:a:759:U:O2	15:o:23:GLY:HA3	2.07	0.55
1:a:1017:A:H2'	1:a:1018:C:C6	2.42	0.55
1:a:1233:G:OP1	19:s:78:ARG:NH1	2.40	0.55
1:a:1482:G:H2'	1:a:1483:G:H8	1.72	0.55
2:b:81:LYS:HE2	2:b:91:TYR:CD1	2.42	0.55
1:a:432:G:H2'	1:a:433:A:H8	1.71	0.54
1:a:873:U:H2'	1:a:875:A:OP2	2.06	0.54
1:a:912:G:H2'	1:a:913:G:H8	1.72	0.54
1:a:1497:U:H2'	1:a:1498:G:C8	2.42	0.54
1:a:1528:G:N2	1:a:1531:A:OP2	2.40	0.54
15:o:25:PRO:HG2	15:o:70:LEU:HD11	1.88	0.54
16:p:21:VAL:HG23	16:p:36:GLN:HA	1.88	0.54
17:q:56:LYS:HG2	17:q:59:ASP:HB2	1.89	0.54
1:a:23:G:H2'	1:a:24:C:C6	2.42	0.54
1:a:558:G:H2'	1:a:559:U:C6	2.43	0.54
1:a:1016:A:H2'	1:a:1017:A:C8	2.42	0.54
12:l:32:LYS:CG	12:l:34:LYS:HG2	2.38	0.54
12:l:85:HIS:HB2	12:l:87:LEU:HD22	1.89	0.54
1:a:310:G:H2'	1:a:311:G:C8	2.43	0.54
1:a:388:G:H22	1:a:390:A:H3'	1.72	0.54
1:a:1247:A:H4'	1:a:1315:G:H4'	1.88	0.54
5:e:54:GLN:H	5:e:54:GLN:CD	2.14	0.54
11:k:14:LYS:HZ1	11:k:40:ASN:HB3	1.72	0.54
17:q:23:ILE:HG23	17:q:50:ASP:OD2	2.08	0.54
1:a:419:A:O3'	1:a:420:U:H2'	2.07	0.54
1:a:560:U:H2'	1:a:561:A:C8	2.42	0.54
1:a:585:G:H2'	1:a:586:C:C6	2.41	0.54
1:a:955:G:C2	1:a:956:A:C8	2.96	0.54
1:a:1083:C:H2'	1:a:1084:G:C8	2.40	0.54
1:a:1398:G:H2'	1:a:1399:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1498:G:H2'	1:a:1499:G:H8	1.72	0.54
17:q:62:LYS:NZ	17:q:79:GLU:OE2	2.40	0.54
1:a:655:A:H2'	1:a:656:A:H8	1.72	0.54
1:a:765:U:H1'	1:a:889:C:H1'	1.89	0.54
1:a:791:C:H2'	1:a:792:A:H8	1.72	0.54
1:a:1320:G:OP1	13:m:91:HIS:NE2	2.29	0.54
3:c:155:ARG:NE	3:c:159:ALA:O	2.35	0.54
9:i:47:ILE:HA	9:i:50:LEU:HD13	1.89	0.54
1:a:240:A:H2'	1:a:241:U:C6	2.42	0.54
2:b:151:ILE:HD11	2:b:154:MET:HB2	1.90	0.54
3:c:155:ARG:HB2	3:c:192:TYR:CE2	2.40	0.54
8:h:41:LYS:HD3	8:h:49:VAL:HG13	1.89	0.54
1:a:271:A:H2'	1:a:272:C:C6	2.43	0.54
1:a:722:G:H1'	1:a:785:A:C8	2.43	0.54
1:a:1132:C:H2'	1:a:1133:U:H6	1.73	0.54
7:g:150:ALA:CB	11:k:61:PHE:H	2.19	0.54
8:h:32:ILE:O	8:h:36:ILE:HG12	2.08	0.54
16:p:58:LEU:HD11	16:p:83:LYS:HD3	1.88	0.54
18:r:41:ARG:NH2	18:r:78:GLU:OE1	2.41	0.54
1:a:10:G:OP1	5:e:127:SER:OG	2.23	0.54
1:a:401:A:OP2	16:p:13:LYS:NZ	2.39	0.54
1:a:1261:A:H4'	9:i:71:GLY:HA2	1.89	0.54
15:o:3:ILE:HB	15:o:7:ARG:NH2	2.22	0.54
19:s:35:SER:HB2	19:s:71:LEU:HD21	1.89	0.54
1:a:63:U:H5''	1:a:393:C:O2	2.08	0.54
1:a:398:C:H2'	1:a:399:G:H8	1.73	0.54
1:a:465:U:H3	1:a:486:C:H42	1.54	0.54
1:a:838:G:H2'	1:a:839:U:C6	2.43	0.54
1:a:1358:G:H5''	9:i:111:ARG:HD2	1.89	0.54
3:c:40:LYS:HE3	14:n:26:ARG:HH11	1.73	0.54
6:f:11:ARG:NH2	6:f:57:ASP:O	2.35	0.54
12:l:8:VAL:HG21	17:q:38:LYS:HD3	1.90	0.54
1:a:1230:U:H2'	1:a:1231:G:H8	1.71	0.54
1:a:1241:C:H2'	1:a:1242:G:C8	2.43	0.54
1:a:1380:C:H2'	1:a:1381:G:H8	1.72	0.54
1:a:81:A:H61	1:a:87:C:H42	1.56	0.53
1:a:459:A:N6	1:a:491:C:H41	2.03	0.53
1:a:1024:A:H2	1:a:1230:U:H1'	1.72	0.53
1:a:1138:U:N3	1:a:1291:A:OP1	2.28	0.53
1:a:1436:A:O2'	1:a:1437:A:O5'	2.26	0.53
3:c:120:ALA:O	3:c:124:GLU:HG2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:74:G:H1'	1:a:95:A:N6	2.23	0.53
1:a:687:C:H2'	1:a:688:C:C6	2.44	0.53
1:a:1261:A:OP1	9:i:71:GLY:N	2.37	0.53
1:a:1290:A:OP2	10:j:11:LYS:NZ	2.41	0.53
4:d:142:ARG:HG2	4:d:144:LYS:HG2	1.90	0.53
15:o:9:ASN:O	15:o:13:LYS:NZ	2.37	0.53
19:s:15:LEU:HD23	19:s:44:PHE:CZ	2.44	0.53
20:t:38:ALA:HB1	20:t:46:LYS:HA	1.90	0.53
1:a:150:U:HO2'	1:a:151:A:H8	1.57	0.53
1:a:584:C:H3'	1:a:585:G:H5''	1.90	0.53
1:a:1238:A:H5'	13:m:110:LYS:HZ3	1.72	0.53
1:a:1488:A:H2'	1:a:1489:C:C6	2.43	0.53
1:a:963:G:H2'	1:a:964:G:O4'	2.09	0.53
1:a:1237:C:H4'	1:a:1238:A:OP1	2.09	0.53
2:b:69:PHE:HE2	2:b:89:GLN:HB2	1.72	0.53
4:d:95:ASP:OD2	4:d:111:ARG:HG2	2.08	0.53
6:f:28:GLY:O	6:f:32:THR:N	2.39	0.53
1:a:293:C:H2'	1:a:294:A:H8	1.72	0.53
1:a:578:G:H2'	1:a:579:U:C6	2.43	0.53
1:a:865:G:H2'	1:a:866:C:C6	2.43	0.53
1:a:1530:A:H2'	1:a:1531:A:C8	2.43	0.53
1:a:1533:G:H2'	1:a:1534:U:C6	2.43	0.53
7:g:113:GLU:HG2	7:g:114:LYS:N	2.23	0.53
1:a:318:G:H5''	16:p:32:ARG:HB3	1.90	0.53
1:a:603:A:O2'	1:a:649:A:N6	2.41	0.53
1:a:724:A:H1'	11:k:119:ASN:O	2.08	0.53
2:b:110:ARG:HA	2:b:113:ARG:HE	1.74	0.53
6:f:83:SER:HB2	6:f:86:ILE:HG22	1.90	0.53
13:m:80:LEU:O	13:m:85:SER:HB3	2.07	0.53
1:a:9:A:C5	4:d:200:ARG:HB3	2.43	0.53
1:a:65:G:N2	1:a:70:A:H61	2.07	0.53
1:a:950:C:H2'	1:a:951:G:H8	1.71	0.53
1:a:1416:G:O2'	1:a:1530:A:O2'	2.27	0.53
17:q:21:LYS:HE3	17:q:49:HIS:CD2	2.44	0.53
1:a:349:C:H2'	1:a:350:C:H6	1.74	0.53
4:d:17:ILE:HG13	4:d:56:LYS:HG3	1.91	0.53
8:h:108:THR:CG2	8:h:109:SER:N	2.72	0.53
15:o:18:HIS:CE1	15:o:21:ASP:HB2	2.44	0.53
1:a:377:C:H2'	1:a:378:C:C6	2.44	0.53
1:a:498:U:O4	1:a:499:A:N6	2.42	0.53
1:a:579:U:H5''	1:a:827:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:804:C:O3'	11:k:127:ARG:NH2	2.42	0.53
2:b:68:LEU:HD13	2:b:161:LEU:HB3	1.91	0.53
2:b:178:LYS:O	5:e:3:ARG:HG2	2.09	0.53
4:d:115:ASN:OD1	4:d:129:PRO:HD3	2.07	0.53
10:j:16:ARG:NH2	10:j:19:ASP:OD2	2.42	0.53
13:m:19:LEU:HD23	13:m:19:LEU:O	2.09	0.53
1:a:680:U:H2'	1:a:681:G:C8	2.45	0.53
2:b:146:LYS:HE3	2:b:147:PHE:CG	2.44	0.53
3:c:137:ILE:HG22	3:c:148:ILE:HD11	1.91	0.53
6:f:1:MET:O	6:f:2:ARG:NE	2.42	0.53
13:m:94:GLY:HA3	13:m:109:ARG:HD2	1.91	0.53
1:a:11:A:H2'	1:a:12:G:C8	2.44	0.52
1:a:18:U:H2'	1:a:19:C:H6	1.74	0.52
1:a:390:A:H2'	1:a:391:A:H8	1.74	0.52
1:a:609:G:H2'	1:a:610:A:H8	1.73	0.52
1:a:771:G:H2'	1:a:772:C:H6	1.74	0.52
10:j:52:ILE:HG22	10:j:62:ARG:HG3	1.89	0.52
10:j:68:ARG:HH22	10:j:70:HIS:HB2	1.73	0.52
15:o:40:ASN:O	15:o:44:ARG:HG2	2.09	0.52
20:t:42:ASN:HA	20:t:46:LYS:HE3	1.91	0.52
1:a:651:C:H2'	1:a:652:U:H6	1.74	0.52
1:a:1023:G:N2	1:a:1025:G:H5''	2.24	0.52
1:a:1339:C:H2'	1:a:1340:A:H8	1.73	0.52
1:a:1354:G:H2'	1:a:1355:C:C6	2.44	0.52
1:a:1357:A:H61	1:a:1385:A:H3'	1.74	0.52
3:c:107:LYS:HG2	3:c:110:LEU:HB2	1.91	0.52
7:g:91:VAL:HG13	7:g:96:ARG:HE	1.74	0.52
14:n:27:CYS:SG	14:n:43:CYS:HB2	2.49	0.52
1:a:278:A:H2'	1:a:279:C:C6	2.45	0.52
1:a:387:C:H2'	1:a:388:G:C8	2.45	0.52
1:a:770:U:H2'	1:a:771:G:H8	1.73	0.52
4:d:151:ILE:O	4:d:155:VAL:HG13	2.09	0.52
14:n:49:TYR:HE1	14:n:57:ARG:HD2	1.73	0.52
16:p:9:ARG:HA	16:p:18:TYR:HA	1.91	0.52
1:a:209:G:H2'	1:a:210:A:H8	1.74	0.52
1:a:249:G:H2'	1:a:250:C:C6	2.44	0.52
1:a:398:C:H2'	1:a:399:G:C8	2.44	0.52
1:a:790:A:H4'	1:a:1526:U:O2'	2.10	0.52
5:e:115:LEU:HD13	5:e:120:ILE:HD13	1.91	0.52
11:k:24:ARG:HH22	11:k:33:THR:HG22	1.75	0.52
13:m:80:LEU:HD11	13:m:87:ARG:HD2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:s:44:PHE:O	19:s:62:VAL:HG11	2.09	0.52
1:a:872:C:H2'	1:a:873:U:C6	2.43	0.52
1:a:1072:U:OP1	14:n:45:ARG:NH2	2.43	0.52
1:a:1173:C:H2'	1:a:1174:G:C8	2.45	0.52
1:a:1537:G:H2'	1:a:1538:G:H8	1.74	0.52
3:c:156:LEU:HD13	3:c:163:ARG:HG3	1.91	0.52
7:g:15:ASP:HB2	7:g:24:THR:CG2	2.37	0.52
1:a:24:C:H2'	1:a:25:U:C6	2.45	0.52
1:a:98:U:H2'	1:a:99:U:N1	2.25	0.52
1:a:516:U:H1'	1:a:517:A:N7	2.25	0.52
1:a:659:C:H2'	1:a:660:U:C6	2.45	0.52
1:a:675:G:H2'	1:a:676:A:H8	1.75	0.52
1:a:1261:A:N3	1:a:1381:G:O2'	2.32	0.52
4:d:14:ARG:HH22	4:d:41:ARG:NH2	2.07	0.52
8:h:98:LEU:HG	8:h:132:TRP:HB2	1.92	0.52
12:l:127:ARG:CB	12:l:132:THR:HG22	2.34	0.52
20:t:38:ALA:CB	20:t:49:LEU:HD12	2.36	0.52
1:a:246:G:H2'	1:a:247:C:O4'	2.10	0.52
1:a:263:G:H2'	1:a:264:U:H6	1.73	0.52
1:a:636:G:H2'	1:a:637:A:C8	2.44	0.52
4:d:72:PHE:HZ	4:d:195:VAL:HG23	1.75	0.52
13:m:79:ARG:HA	13:m:82:GLU:HB2	1.90	0.52
1:a:33:A:N6	1:a:561:A:N6	2.57	0.52
1:a:891:G:P	12:l:9:ARG:HH22	2.31	0.52
1:a:1244:G:H2'	1:a:1245:C:C6	2.45	0.52
6:f:3:THR:OG1	6:f:94:GLU:HB2	2.09	0.52
6:f:26:PHE:HA	6:f:29:ILE:HG12	1.92	0.52
17:q:57:LEU:HD12	17:q:58:GLY:N	2.24	0.52
1:a:712:A:H3'	1:a:713:G:H8	1.74	0.52
1:a:909:C:H3'	1:a:910:A:C8	2.45	0.52
1:a:988:A:N6	1:a:1327:G:O2'	2.42	0.52
4:d:114:VAL:HG23	4:d:119:ILE:HD11	1.92	0.52
10:j:66:GLU:HG2	14:n:56:VAL:HG23	1.90	0.52
1:a:112:G:H2'	1:a:113:U:C6	2.45	0.52
1:a:363:C:H2'	1:a:364:A:O4'	2.10	0.52
1:a:775:A:H2'	1:a:776:A:O4'	2.10	0.52
1:a:790:A:O3'	1:a:1527:C:H4'	2.10	0.52
1:a:1420:C:H2'	1:a:1421:A:H8	1.75	0.52
8:h:108:THR:HG21	8:h:123:VAL:CG2	2.40	0.52
11:k:25:SER:OG	11:k:88:GLY:O	2.24	0.52
1:a:21:U:H2'	1:a:22:G:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:446:G:O3'	1:a:448:U:H5	1.93	0.51
1:a:731:U:H5''	1:a:732:G:H8	1.75	0.51
1:a:901:U:O2'	1:a:902:A:H5'	2.10	0.51
1:a:1136:G:H4'	10:j:40:ILE:HD11	1.92	0.51
1:a:1261:A:H2'	1:a:1262:A:C8	2.44	0.51
8:h:80:ILE:HG22	8:h:87:VAL:HG11	1.92	0.51
8:h:97:VAL:HG22	8:h:98:LEU:HD23	1.92	0.51
10:j:52:ILE:HD11	14:n:41:ARG:CZ	2.40	0.51
11:k:25:SER:H	11:k:87:LYS:NZ	2.09	0.51
1:a:264:U:H2'	1:a:265:A:C8	2.45	0.51
1:a:471:A:H2'	1:a:472:G:H8	1.72	0.51
1:a:987:A:O2'	1:a:991:U:N3	2.31	0.51
3:c:188:ALA:O	3:c:195:LEU:N	2.42	0.51
4:d:13:ARG:HD2	4:d:33:PRO:HG3	1.93	0.51
8:h:8:ALA:HB2	8:h:79:ARG:HH11	1.75	0.51
12:l:88:GLN:N	12:l:88:GLN:OE1	2.43	0.51
1:a:935:G:H1'	1:a:1514:A:C4	2.46	0.51
10:j:19:ASP:OD1	10:j:20:GLN:N	2.43	0.51
14:n:16:TYR:CE1	14:n:19:ARG:HD2	2.44	0.51
1:a:388:G:N2	1:a:390:A:H3'	2.25	0.51
1:a:694:U:O4	1:a:711:G:H1'	2.11	0.51
1:a:856:C:H2'	1:a:857:C:C6	2.45	0.51
1:a:1468:A:H2'	1:a:1469:G:O4'	2.10	0.51
2:b:129:LEU:HB2	2:b:130:PRO:HD2	1.92	0.51
6:f:8:TYR:HB2	6:f:86:ILE:HD13	1.91	0.51
1:a:668:A:H2'	1:a:669:G:O4'	2.11	0.51
1:a:796:U:H2'	1:a:797:U:O4'	2.11	0.51
1:a:1241:C:H2'	1:a:1242:G:H8	1.75	0.51
1:a:1272:A:H5'	1:a:1294:C:H4'	1.92	0.51
1:a:1331:C:H2'	1:a:1332:U:C6	2.46	0.51
10:j:67:GLN:OE1	14:n:55:GLY:HA3	2.11	0.51
1:a:195:C:O2'	17:q:64:GLN:NE2	2.44	0.51
1:a:758:C:H1'	15:o:22:THR:HG22	1.92	0.51
1:a:921:U:H2'	1:a:922:C:C6	2.45	0.51
1:a:1361:A:O2'	7:g:33:ASP:OD1	2.25	0.51
1:a:1412:G:H2'	1:a:1413:C:O4'	2.11	0.51
2:b:61:SER:OG	2:b:221:ILE:HD12	2.10	0.51
3:c:149:LYS:HB3	3:c:200:TRP:HB2	1.92	0.51
5:e:75:PRO:HG2	5:e:147:LEU:HD23	1.92	0.51
8:h:108:THR:CG2	8:h:123:VAL:CG2	2.88	0.51
1:a:612:G:H2'	1:a:613:U:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:715:U:H2'	1:a:716:A:C8	2.46	0.51
1:a:1050:A:H2'	1:a:1051:A:C8	2.45	0.51
1:a:1128:U:H2'	1:a:1129:A:H8	1.75	0.51
1:a:1151:U:O2'	1:a:1152:U:H6	1.94	0.51
5:e:82:PRO:HD2	5:e:147:LEU:HD21	1.93	0.51
8:h:21:ARG:HA	8:h:66:TYR:OH	2.11	0.51
10:j:42:LEU:HB3	10:j:71:LYS:HE3	1.92	0.51
1:a:65:G:H4'	1:a:66:A:H5''	1.93	0.51
1:a:127:A:H5''	17:q:5:ASN:HB2	1.93	0.51
1:a:515:C:OP2	1:a:516:U:O2'	2.26	0.51
1:a:642:C:H2'	1:a:643:A:H8	1.76	0.51
1:a:1006:A:H2'	1:a:1007:U:C6	2.46	0.51
1:a:1198:G:H2'	1:a:1199:A:C8	2.46	0.51
6:f:7:MET:SD	6:f:9:ILE:HG13	2.50	0.51
10:j:44:THR:H	10:j:71:LYS:HE2	1.74	0.51
13:m:92:ARG:O	13:m:92:ARG:NH1	2.44	0.51
1:a:406:C:H2'	1:a:407:G:H8	1.76	0.51
1:a:782:G:H2'	1:a:783:G:C8	2.45	0.51
1:a:1434:G:H2'	1:a:1435:U:C6	2.46	0.51
8:h:21:ARG:HH21	8:h:72:ARG:HG3	1.76	0.51
1:a:22:G:H2'	1:a:23:G:H8	1.74	0.51
1:a:67:G:H2'	1:a:68:C:C6	2.46	0.51
1:a:414:G:H2'	1:a:415:A:C8	2.47	0.51
1:a:441:A:H2'	1:a:442:C:H6	1.76	0.51
1:a:466:G:H1	1:a:486:C:N4	2.08	0.51
1:a:502:C:H2'	1:a:504:G:H8	1.75	0.51
1:a:585:G:C6	1:a:773:G:C2	2.99	0.51
8:h:98:LEU:O	8:h:101:LEU:HB2	2.10	0.51
1:a:98:U:H2'	1:a:99:U:C2	2.46	0.50
1:a:284:G:H5'	17:q:19:MET:HE1	1.92	0.50
1:a:545:G:H5''	12:l:123:ARG:NH1	2.27	0.50
1:a:668:A:C6	1:a:754:G:C6	2.99	0.50
1:a:763:G:H2'	1:a:764:C:H6	1.76	0.50
1:a:1400:C:H2'	1:a:1401:U:H6	1.76	0.50
2:b:127:GLU:C	2:b:129:LEU:H	2.19	0.50
4:d:54:LYS:HD3	4:d:197:TYR:CE2	2.47	0.50
9:i:21:VAL:HA	9:i:67:VAL:HG12	1.93	0.50
10:j:68:ARG:HH12	10:j:70:HIS:HB2	1.75	0.50
15:o:28:GLN:OE1	15:o:32:LEU:HG	2.11	0.50
17:q:21:LYS:O	17:q:50:ASP:N	2.40	0.50
19:s:11:VAL:HG21	19:s:16:MET:SD	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:364:A:H2'	1:a:365:G:O4'	2.11	0.50
1:a:1102:U:H2'	1:a:1103:U:C6	2.46	0.50
1:a:1174:G:H2'	1:a:1175:G:H8	1.76	0.50
1:a:1488:A:H2'	1:a:1489:C:H6	1.76	0.50
5:e:76:ARG:HD2	5:e:77:VAL:N	2.25	0.50
8:h:7:ILE:HG22	8:h:79:ARG:HD2	1.93	0.50
1:a:102:C:H2'	1:a:103:G:C8	2.46	0.50
1:a:624:G:H2'	1:a:625:G:C8	2.45	0.50
1:a:631:C:H2'	1:a:632:C:C6	2.47	0.50
1:a:763:G:H2'	1:a:764:C:C6	2.46	0.50
1:a:773:G:H3'	1:a:820:G:H22	1.77	0.50
1:a:1266:G:N1	1:a:1294:C:N3	2.59	0.50
3:c:43:ASP:OD1	3:c:44:ASN:N	2.44	0.50
16:p:16:PRO:HB2	16:p:18:TYR:CE1	2.46	0.50
19:s:12:ASP:H	19:s:38:SER:CB	2.14	0.50
1:a:466:G:H2'	1:a:467:U:H6	1.75	0.50
1:a:700:U:H1'	1:a:702:A:N7	2.26	0.50
2:b:72:THR:HA	2:b:93:ASN:O	2.11	0.50
11:k:43:SER:HB3	11:k:73:SER:HB3	1.92	0.50
13:m:83:ILE:O	13:m:84:SER:C	2.51	0.50
15:o:54:ARG:O	15:o:58:LYS:HG3	2.12	0.50
1:a:13:U:H3	1:a:23:G:H1	1.57	0.50
1:a:432:G:H2'	1:a:433:A:C8	2.45	0.50
1:a:926:G:H2'	1:a:927:G:C8	2.47	0.50
1:a:996:A:H2'	1:a:997:A:C8	2.46	0.50
1:a:1082:U:H2'	1:a:1083:C:C6	2.46	0.50
1:a:1172:C:H2'	1:a:1173:C:C6	2.47	0.50
1:a:1508:C:H2'	1:a:1509:G:C8	2.46	0.50
2:b:7:LYS:HB3	2:b:47:VAL:HG13	1.93	0.50
1:a:632:C:H2'	1:a:633:G:C8	2.47	0.50
1:a:702:A:OP1	11:k:55:SER:OG	2.29	0.50
1:a:1073:G:H5'	10:j:61:SER:OG	2.11	0.50
1:a:1158:C:H1'	9:i:9:ARG:NH2	2.27	0.50
11:k:22:HIS:HB3	11:k:24:ARG:HH12	1.76	0.50
1:a:11:A:H2'	1:a:12:G:H8	1.77	0.50
1:a:254:A:N6	1:a:289:G:C2	2.79	0.50
1:a:270:A:O3'	20:t:69:ASN:ND2	2.36	0.50
1:a:986:G:OP2	1:a:1369:U:O2'	2.28	0.50
1:a:1434:G:H2'	1:a:1435:U:H6	1.77	0.50
2:b:68:LEU:HG	2:b:90:PHE:HE1	1.76	0.50
4:d:121:VAL:HG22	4:d:122:ASP:OD1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:74:ILE:HG22	8:h:132:TRP:C	2.36	0.50
18:r:26:ILE:H	18:r:27:ASP:HA	1.76	0.50
1:a:547:A:H2'	1:a:548:G:H8	1.77	0.50
1:a:635:G:H2'	1:a:636:G:C8	2.47	0.50
1:a:960:U:O2	1:a:1242:G:N2	2.42	0.50
1:a:1019:U:C2	1:a:1020:C:C5	3.00	0.50
3:c:72:PRO:HA	3:c:75:VAL:HG12	1.93	0.50
4:d:81:VAL:HG12	5:e:101:PRO:HB2	1.93	0.50
4:d:170:ASP:OD1	4:d:170:ASP:N	2.43	0.50
5:e:105:VAL:HG11	5:e:116:GLU:HG2	1.92	0.50
8:h:79:ARG:HA	8:h:129:ALA:HA	1.94	0.50
1:a:167:A:H2'	1:a:168:G:C8	2.47	0.50
2:b:217:MET:HA	2:b:217:MET:HE3	1.94	0.50
3:c:121:ARG:NE	3:c:121:ARG:HA	2.27	0.50
7:g:93:PRO:O	7:g:97:THR:HG23	2.12	0.50
8:h:21:ARG:HG2	8:h:66:TYR:CE1	2.47	0.50
12:l:24:LEU:O	12:l:24:LEU:HD22	2.11	0.50
1:a:466:G:H2'	1:a:467:U:C6	2.47	0.49
1:a:1270:C:H3'	1:a:1271:G:H5''	1.94	0.49
3:c:11:ARG:HE	3:c:179:ALA:HB3	1.77	0.49
20:t:28:MET:CE	20:t:57:VAL:HA	2.41	0.49
20:t:38:ALA:CB	20:t:46:LYS:HA	2.42	0.49
1:a:76:C:N4	1:a:77:G:O6	2.44	0.49
1:a:88:U:H2'	1:a:89:U:H5	1.76	0.49
1:a:292:G:H2'	1:a:293:C:C6	2.47	0.49
1:a:588:C:H2'	1:a:589:G:O4'	2.12	0.49
1:a:814:C:N4	1:a:815:A:H62	2.10	0.49
1:a:1024:A:H5''	19:s:14:HIS:CE1	2.47	0.49
1:a:1293:C:H2'	1:a:1294:C:C6	2.47	0.49
1:a:1398:G:H2'	1:a:1399:U:H6	1.75	0.49
1:a:1482:G:H2'	1:a:1483:G:C8	2.47	0.49
2:b:12:ALA:HB1	2:b:43:LEU:HD22	1.94	0.49
4:d:17:ILE:CG1	4:d:56:LYS:HD2	2.42	0.49
10:j:83:THR:O	10:j:87:LEU:HG	2.12	0.49
11:k:47:ALA:HB3	11:k:57:LYS:HG2	1.94	0.49
18:r:53:SER:HB2	18:r:56:TYR:CD2	2.44	0.49
1:a:56:A:N1	1:a:376:U:C5	2.78	0.49
1:a:383:U:H2'	1:a:384:G:O4'	2.12	0.49
1:a:456:A:H2'	1:a:456:A:N3	2.27	0.49
1:a:728:C:H5''	18:r:46:PRO:HB3	1.94	0.49
1:a:790:A:H62	1:a:808:G:N2	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1245:C:H2'	1:a:1246:U:C6	2.45	0.49
1:a:1337:U:H2'	1:a:1338:A:C8	2.47	0.49
1:a:1382:G:H2'	1:a:1383:U:C6	2.47	0.49
1:a:1402:U:H2'	1:a:1403:G:H8	1.77	0.49
2:b:52:GLU:O	2:b:56:PHE:HD1	1.95	0.49
5:e:104:GLY:N	5:e:122:ASP:OD1	2.45	0.49
16:p:7:LEU:HA	16:p:19:ARG:O	2.13	0.49
1:a:123:G:C6	1:a:246:G:N1	2.80	0.49
1:a:303:C:N3	1:a:311:G:N1	2.60	0.49
1:a:387:C:H2'	1:a:388:G:H8	1.76	0.49
1:a:410:G:H2'	1:a:411:C:C6	2.47	0.49
1:a:660:U:O4	1:a:760:G:O2'	2.28	0.49
1:a:686:U:H2'	1:a:687:C:H6	1.74	0.49
1:a:702:A:N6	1:a:795:A:O2'	2.45	0.49
1:a:1108:C:H2'	1:a:1109:C:H6	1.77	0.49
1:a:1133:U:H2'	1:a:1134:U:C6	2.47	0.49
20:t:41:ASN:HD22	20:t:41:ASN:N	2.10	0.49
1:a:42:G:H2'	1:a:43:G:C8	2.46	0.49
1:a:456:A:H4'	1:a:457:A:C5'	2.42	0.49
1:a:499:A:H2'	1:a:500:A:C8	2.42	0.49
1:a:609:G:H2'	1:a:610:A:C8	2.48	0.49
1:a:819:C:H5''	1:a:908:G:H4'	1.94	0.49
1:a:900:G:H1'	1:a:901:U:H5	1.76	0.49
5:e:38:VAL:HG11	5:e:114:VAL:HG22	1.94	0.49
1:a:341:U:H2'	1:a:342:C:C6	2.48	0.49
1:a:587:G:H1	1:a:770:U:H3	1.60	0.49
1:a:621:C:H2'	1:a:622:A:C8	2.48	0.49
1:a:1006:A:H2'	1:a:1007:U:H6	1.78	0.49
1:a:1013:G:OP2	1:a:1036:C:N4	2.34	0.49
1:a:1436:A:O2'	1:a:1437:A:H8	1.95	0.49
5:e:37:VAL:O	5:e:49:GLY:N	2.45	0.49
9:i:113:LYS:HD3	9:i:124:ARG:HH22	1.77	0.49
18:r:10:ARG:HH12	18:r:47:ARG:HD2	1.77	0.49
1:a:166:U:O4	1:a:167:A:N6	2.45	0.49
1:a:420:U:O2'	1:a:421:G:O4'	2.28	0.49
1:a:513:G:H2'	1:a:514:G:H8	1.76	0.49
1:a:683:A:H1'	11:k:118:HIS:HE2	1.78	0.49
1:a:890:C:OP1	12:l:5:ASN:ND2	2.46	0.49
1:a:1328:C:O2'	1:a:1329:A:H5'	2.13	0.49
1:a:1500:G:H2'	1:a:1501:G:H8	1.77	0.49
13:m:14:ARG:CB	13:m:41:ALA:HB1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:381:A:C2	1:a:382:A:C8	3.00	0.49
1:a:957:G:O3'	13:m:108:THR:HB	2.13	0.49
1:a:1277:G:N2	1:a:1280:A:OP2	2.46	0.49
1:a:1383:U:H2'	1:a:1384:G:C8	2.48	0.49
8:h:5:ASP:CG	8:h:79:ARG:HH12	2.20	0.49
8:h:19:MET:SD	8:h:20:VAL:HB	2.52	0.49
18:r:55:LYS:O	18:r:59:MET:HG3	2.13	0.49
1:a:81:A:O2'	1:a:82:G:N7	2.43	0.49
1:a:417:U:H2'	1:a:418:G:O4'	2.12	0.49
1:a:721:G:N2	1:a:785:A:O2'	2.45	0.49
1:a:774:A:H3'	1:a:775:A:H8	1.77	0.49
1:a:1303:U:C2	1:a:1304:G:C8	3.01	0.49
1:a:1438:C:H2'	1:a:1439:A:H8	1.78	0.49
15:o:33:THR:HA	15:o:36:ILE:HG12	1.95	0.49
19:s:19:VAL:HA	19:s:22:GLN:HB2	1.94	0.49
1:a:455:G:N1	1:a:494:U:OP2	2.45	0.49
1:a:772:C:H2'	1:a:773:G:O4'	2.13	0.49
1:a:775:A:H1'	1:a:1537:G:H1'	1.94	0.49
1:a:1129:A:O2'	9:i:110:PRO:HB3	2.13	0.49
2:b:96:TRP:CZ2	2:b:100:LEU:HB2	2.47	0.49
5:e:123:ILE:HD12	5:e:124:LEU:H	1.77	0.49
1:a:326:G:C6	1:a:344:A:C6	3.01	0.48
1:a:622:A:H2'	1:a:623:C:C6	2.48	0.48
1:a:703:A:H2'	1:a:704:A:O4'	2.13	0.48
1:a:833:G:O6	1:a:886:A:N6	2.46	0.48
1:a:1147:U:O2'	1:a:1149:A:N7	2.40	0.48
1:a:1233:G:H5''	19:s:78:ARG:NH1	2.28	0.48
1:a:470:A:H2	1:a:481:C:C2	2.31	0.48
1:a:857:C:H2'	1:a:858:C:C6	2.47	0.48
1:a:1185:G:H2'	1:a:1186:G:H8	1.78	0.48
1:a:1378:U:H4'	10:j:50:THR:HG21	1.95	0.48
7:g:151:PHE:O	7:g:155:ARG:NH1	2.46	0.48
10:j:13:TYR:HE1	10:j:69:THR:HG23	1.77	0.48
11:k:20:VAL:O	11:k:35:THR:N	2.28	0.48
13:m:19:LEU:HD21	13:m:33:ILE:HD11	1.95	0.48
1:a:26:C:H2'	1:a:27:A:C8	2.48	0.48
1:a:34:A:O2'	12:l:42:GLN:NE2	2.46	0.48
1:a:751:U:H2'	1:a:752:C:C6	2.48	0.48
1:a:1338:A:H2'	1:a:1339:C:C6	2.48	0.48
19:s:45:ILE:HD13	19:s:46:GLY:N	2.28	0.48
1:a:255:G:H2'	1:a:256:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:263:G:H5''	17:q:21:LYS:HE2	1.95	0.48
1:a:1030:A:H2'	1:a:1031:G:C8	2.48	0.48
1:a:1471:U:H2'	1:a:1472:A:H8	1.79	0.48
2:b:126:PHE:O	2:b:127:GLU:HB2	2.13	0.48
2:b:154:MET:HE3	2:b:155:LYS:N	2.28	0.48
5:e:12:GLU:HB3	5:e:117:LEU:HD11	1.94	0.48
19:s:43:ASN:OD1	19:s:43:ASN:N	2.45	0.48
1:a:263:G:OP1	17:q:73:LYS:NZ	2.43	0.48
1:a:371:A:H5''	12:l:44:ARG:HD3	1.94	0.48
1:a:419:A:N6	1:a:437:U:O5'	2.46	0.48
1:a:1016:A:H2'	1:a:1017:A:H8	1.79	0.48
1:a:1238:A:C5	19:s:83:HIS:HE1	2.31	0.48
1:a:1261:A:H4'	9:i:72:GLY:H	1.78	0.48
2:b:124:GLY:O	2:b:128:VAL:HG11	2.13	0.48
3:c:38:ILE:HD12	3:c:90:LEU:HD11	1.95	0.48
3:c:59:ALA:HB3	3:c:62:ARG:HG3	1.95	0.48
3:c:84:GLU:OE1	3:c:84:GLU:N	2.47	0.48
10:j:26:VAL:O	10:j:30:LYS:HG2	2.13	0.48
12:l:33:LYS:HD2	12:l:34:LYS:N	2.29	0.48
1:a:588:C:O2'	15:o:57:LEU:HD22	2.14	0.48
1:a:733:G:H2'	1:a:734:C:C6	2.49	0.48
1:a:887:C:H2'	1:a:888:U:C6	2.48	0.48
5:e:38:VAL:HA	5:e:48:PHE:HA	1.95	0.48
9:i:81:ILE:HG23	9:i:82:ARG:HD3	1.96	0.48
1:a:217:G:H2'	1:a:218:U:C6	2.49	0.48
1:a:245:C:P	17:q:44:LYS:HZ3	2.36	0.48
1:a:491:C:O2	1:a:492:G:H2'	2.14	0.48
4:d:176:PHE:HZ	4:d:180:PRO:HD3	1.78	0.48
5:e:41:ASP:OD1	5:e:45:ARG:HB2	2.12	0.48
5:e:77:VAL:HB	5:e:149:ASN:HD21	1.78	0.48
7:g:14:PRO:HB2	9:i:49:ASP:OD1	2.14	0.48
15:o:32:LEU:HD13	15:o:63:ARG:HB2	1.96	0.48
17:q:85:VAL:HG22	17:q:86:ILE:H	1.78	0.48
1:a:51:A:H4'	1:a:52:A:H5'	1.96	0.48
1:a:393:C:H2'	1:a:394:C:H6	1.77	0.48
1:a:787:C:H2'	1:a:788:A:H8	1.79	0.48
1:a:1102:U:H2'	1:a:1103:U:H6	1.78	0.48
9:i:24:VAL:O	9:i:24:VAL:HG23	2.14	0.48
12:l:81:PRO:HB2	12:l:130:TYR:HE1	1.78	0.48
15:o:36:ILE:HA	15:o:39:VAL:HG22	1.95	0.48
16:p:53:ASP:O	16:p:54:GLU:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:525:G:H1	1:a:540:A:H5''	1.78	0.48
1:a:535:G:O2'	1:a:543:A:N1	2.41	0.48
1:a:585:G:H2'	1:a:586:C:H6	1.78	0.48
1:a:938:G:H2'	1:a:939:A:C8	2.47	0.48
1:a:955:G:H2'	1:a:955:G:N3	2.28	0.48
1:a:984:A:OP2	14:n:41:ARG:NH2	2.47	0.48
1:a:1148:A:C6	1:a:1149:A:C6	3.01	0.48
5:e:39:VAL:HG11	5:e:68:LYS:HZ2	1.77	0.48
8:h:108:THR:HG22	8:h:109:SER:H	1.77	0.48
10:j:99:GLU:OE1	10:j:99:GLU:N	2.47	0.48
15:o:37:ASN:O	15:o:41:GLU:HG2	2.13	0.48
1:a:35:C:H2'	1:a:36:G:C8	2.48	0.48
1:a:666:G:H1'	15:o:22:THR:HG21	1.96	0.48
1:a:781:G:H2'	1:a:782:G:H8	1.78	0.48
1:a:818:C:H1'	1:a:909:C:H41	1.79	0.48
1:a:1404:U:H2'	1:a:1406:C:H5	1.79	0.48
11:k:62:ALA:HA	11:k:65:MET:SD	2.53	0.48
13:m:41:ALA:HB3	13:m:43:THR:O	2.12	0.48
19:s:55:ARG:C	19:s:56:LYS:HD2	2.39	0.48
1:a:35:C:H2'	1:a:36:G:H8	1.79	0.47
1:a:109:C:O2'	16:p:26:ARG:O	2.32	0.47
1:a:270:A:O2'	20:t:69:ASN:ND2	2.47	0.47
1:a:412:G:C4'	1:a:447:U:H1'	2.43	0.47
1:a:446:G:N2	1:a:504:G:N7	2.62	0.47
1:a:558:G:H2'	1:a:559:U:H6	1.78	0.47
1:a:889:C:C5	12:l:3:THR:HG21	2.49	0.47
1:a:1003:G:H5''	1:a:1005:C:H41	1.78	0.47
1:a:1060:G:H5''	14:n:2:ALA:HB1	1.96	0.47
1:a:1402:U:C2	1:a:1403:G:C8	3.02	0.47
3:c:31:LEU:HD22	3:c:58:ARG:HD3	1.95	0.47
4:d:94:LEU:HD23	4:d:114:VAL:HG21	1.96	0.47
6:f:3:THR:HB	6:f:66:LYS:NZ	2.29	0.47
7:g:148:ASN:C	7:g:150:ALA:H	2.22	0.47
8:h:121:ARG:HB2	8:h:123:VAL:HG12	1.95	0.47
1:a:16:G:H2'	1:a:17:A:C8	2.49	0.47
1:a:279:C:H2'	1:a:280:C:C6	2.49	0.47
1:a:446:G:C5'	4:d:116:HIS:CD2	2.96	0.47
1:a:989:C:OP1	1:a:1234:C:N4	2.47	0.47
1:a:1114:A:H2'	1:a:1115:C:C6	2.49	0.47
1:a:1256:A:C6	1:a:1304:G:C6	3.02	0.47
1:a:1367:G:C2	1:a:1368:A:C5	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1443:G:N2	1:a:1480:A:OP2	2.46	0.47
13:m:23:TYR:OH	13:m:70:ARG:NE	2.46	0.47
15:o:77:ARG:O	15:o:81:LEU:HG	2.14	0.47
16:p:16:PRO:HB2	16:p:18:TYR:HE1	1.79	0.47
19:s:15:LEU:HD23	19:s:44:PHE:HZ	1.79	0.47
1:a:225:G:H2'	1:a:226:U:H6	1.77	0.47
1:a:678:A:H2'	1:a:679:G:H8	1.79	0.47
1:a:992:U:H5'	14:n:6:MET:HE1	1.96	0.47
1:a:1315:G:H1'	1:a:1345:G:N2	2.29	0.47
4:d:105:ARG:HG2	4:d:109:GLN:OE1	2.14	0.47
6:f:74:ASP:OD1	6:f:74:ASP:N	2.48	0.47
17:q:76:ARG:HG3	17:q:77:LEU:N	2.29	0.47
19:s:27:LYS:NZ	19:s:46:GLY:HA3	2.29	0.47
1:a:51:A:O2'	1:a:368:G:N2	2.47	0.47
1:a:65:G:O6	1:a:100:A:N6	2.48	0.47
1:a:135:C:H42	1:a:236:A:H2	1.61	0.47
1:a:265:A:H2'	1:a:266:A:C8	2.50	0.47
1:a:631:C:H2'	1:a:632:C:H6	1.79	0.47
1:a:650:A:N7	8:h:109:SER:HA	2.29	0.47
1:a:1073:G:H2'	1:a:1074:U:C6	2.50	0.47
1:a:1159:U:H2'	1:a:1160:C:O4'	2.15	0.47
1:a:1377:C:H2'	1:a:1378:U:H6	1.79	0.47
1:a:1549:U:OP2	18:r:11:ARG:NH2	2.47	0.47
10:j:4:GLN:O	10:j:77:VAL:HG13	2.14	0.47
1:a:271:A:H5'	20:t:69:ASN:ND2	2.29	0.47
1:a:363:C:C4	1:a:364:A:N7	2.82	0.47
1:a:632:C:H2'	1:a:633:G:H8	1.77	0.47
1:a:721:G:H2'	1:a:722:G:C8	2.49	0.47
1:a:787:C:C2	1:a:788:A:C8	3.02	0.47
1:a:1209:A:O2'	10:j:57:MET:HE1	2.15	0.47
1:a:1337:U:H2'	1:a:1338:A:H8	1.80	0.47
6:f:48:LEU:H	6:f:57:ASP:HA	1.79	0.47
12:l:86:ASN:OD1	12:l:86:ASN:O	2.31	0.47
16:p:62:ASN:OD1	16:p:88:LYS:NZ	2.44	0.47
1:a:101:G:O2'	1:a:102:C:H5'	2.15	0.47
1:a:550:U:H2'	1:a:551:G:C8	2.50	0.47
1:a:655:A:H2'	1:a:656:A:C8	2.49	0.47
1:a:731:U:H5''	1:a:732:G:C8	2.49	0.47
1:a:1180:A:H2'	1:a:1181:A:C8	2.49	0.47
7:g:76:LYS:O	7:g:87:VAL:N	2.46	0.47
17:q:65:GLU:OE2	17:q:74:ARG:NH1	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:127:A:O2'	1:a:128:U:H5'	2.15	0.47
1:a:485:U:H2'	1:a:486:C:C6	2.50	0.47
1:a:508:G:H1'	1:a:555:A:N1	2.30	0.47
1:a:610:A:H2'	1:a:611:U:C6	2.49	0.47
1:a:621:C:H2'	1:a:622:A:H8	1.79	0.47
1:a:692:U:H2'	1:a:693:G:O4'	2.14	0.47
1:a:872:C:H2'	1:a:873:U:H6	1.78	0.47
1:a:877:G:H2'	1:a:878:C:C6	2.49	0.47
1:a:1037:C:OP2	1:a:1039:C:N4	2.44	0.47
1:a:1171:G:H1	1:a:1187:A:N6	2.13	0.47
1:a:1209:A:H2'	1:a:1210:U:C6	2.50	0.47
1:a:1343:A:H2'	1:a:1344:A:C8	2.50	0.47
1:a:1358:G:H4'	1:a:1359:U:H6	1.78	0.47
1:a:1500:G:H2'	1:a:1501:G:C8	2.49	0.47
4:d:85:ASN:HA	4:d:88:ILE:HG12	1.96	0.47
12:l:33:LYS:HD2	12:l:33:LYS:C	2.39	0.47
13:m:43:THR:HG23	13:m:44:ARG:H	1.80	0.47
16:p:5:ILE:HB	16:p:67:PRO:HB3	1.97	0.47
16:p:5:ILE:HG22	16:p:71:VAL:HG21	1.96	0.47
17:q:9:VAL:HA	17:q:63:ILE:O	2.15	0.47
17:q:67:ARG:O	17:q:74:ARG:HG3	2.13	0.47
1:a:553:C:H5''	4:d:65:GLU:OE1	2.14	0.47
1:a:988:A:O2'	1:a:1333:C:N3	2.45	0.47
1:a:1100:G:N2	1:a:1178:A:H61	2.11	0.47
1:a:1187:A:H2'	1:a:1188:G:C8	2.50	0.47
1:a:1197:G:H2'	1:a:1198:G:H8	1.79	0.47
1:a:1267:C:H1'	1:a:1268:A:N3	2.29	0.47
1:a:1314:C:H2'	1:a:1315:G:C8	2.49	0.47
1:a:1438:C:H2'	1:a:1439:A:C8	2.50	0.47
11:k:19:GLY:N	11:k:79:LEU:HD11	2.30	0.47
1:a:294:A:H2'	1:a:295:U:C6	2.50	0.47
1:a:459:A:H5''	1:a:460:A:H5''	1.97	0.47
1:a:550:U:H2'	1:a:551:G:H8	1.79	0.47
1:a:584:C:H3'	1:a:585:G:C5'	2.44	0.47
1:a:856:C:H2'	1:a:857:C:H6	1.80	0.47
1:a:966:U:H5'	19:s:84:VAL:HG13	1.97	0.47
1:a:1416:G:H2'	1:a:1417:U:C6	2.49	0.47
3:c:125:ASN:OD1	3:c:125:ASN:N	2.47	0.47
7:g:26:LEU:HD13	7:g:101:LEU:HD22	1.95	0.47
1:a:235:G:H2'	1:a:236:A:C8	2.50	0.47
1:a:262:G:OP2	17:q:71:ALA:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:463:U:H2'	1:a:464:A:C8	2.50	0.47
1:a:875:A:H2'	1:a:876:C:C6	2.49	0.47
1:a:1094:A:H2'	1:a:1095:U:O4'	2.15	0.47
1:a:1125:C:H2'	1:a:1126:C:H6	1.80	0.47
2:b:102:THR:HB	2:b:179:LEU:HD21	1.97	0.47
7:g:15:ASP:C	7:g:17:ILE:H	2.22	0.47
13:m:81:MET:HA	13:m:88:GLY:HA3	1.96	0.47
19:s:41:PHE:HB2	19:s:42:PRO:HD2	1.97	0.47
1:a:255:G:H2'	1:a:256:C:H6	1.79	0.46
1:a:522:C:H2'	1:a:523:G:C8	2.43	0.46
1:a:1065:G:H4'	1:a:1066:C:H5''	1.97	0.46
1:a:1307:C:H4'	13:m:14:ARG:CZ	2.45	0.46
9:i:32:VAL:N	9:i:35:ARG:O	2.48	0.46
1:a:239:G:H2'	1:a:240:A:H8	1.79	0.46
1:a:511:A:H2'	1:a:512:C:C6	2.50	0.46
1:a:628:C:C2	1:a:629:A:C8	3.03	0.46
1:a:659:C:N4	1:a:761:A:OP2	2.48	0.46
1:a:1349:G:H2'	1:a:1350:A:C8	2.50	0.46
1:a:1399:U:H2'	1:a:1400:C:H6	1.79	0.46
4:d:87:MET:HA	4:d:90:LEU:HG	1.97	0.46
6:f:46:ARG:HH12	18:r:72:LEU:HA	1.80	0.46
8:h:58:GLY:HA3	8:h:59:VAL:HA	1.55	0.46
12:l:55:PRO:HB3	12:l:102:ASP:HB2	1.96	0.46
15:o:32:LEU:HD22	15:o:59:MET:HB3	1.97	0.46
1:a:80:A:H2'	1:a:81:A:H5'	1.98	0.46
1:a:211:A:N1	1:a:228:A:O2'	2.41	0.46
1:a:216:G:H1	1:a:224:U:H3	1.63	0.46
1:a:976:G:H2'	1:a:977:C:C6	2.51	0.46
1:a:1076:G:H1'	1:a:1201:G:H21	1.80	0.46
1:a:1086:G:OP1	5:e:69:LYS:NZ	2.47	0.46
1:a:1123:A:O2'	1:a:1124:C:O5'	2.33	0.46
1:a:1245:C:OP1	9:i:125:ARG:NH1	2.48	0.46
1:a:1248:C:O5'	1:a:1249:A:H5'	2.15	0.46
1:a:1542:G:O2'	1:a:1543:A:O4'	2.27	0.46
2:b:54:TYR:CE1	2:b:220:ALA:HB2	2.50	0.46
4:d:121:VAL:O	4:d:124:LYS:HG2	2.15	0.46
5:e:22:ALA:HA	5:e:31:PHE:HA	1.97	0.46
16:p:53:ASP:OD2	16:p:56:LEU:HB3	2.14	0.46
1:a:659:C:H1'	8:h:56:LYS:NZ	2.30	0.46
1:a:900:G:H22	1:a:916:G:H2'	1.79	0.46
1:a:1238:A:H5'	13:m:110:LYS:HZ1	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1282:G:H2'	1:a:1283:U:C6	2.51	0.46
2:b:113:ARG:O	2:b:117:ILE:HG12	2.16	0.46
2:b:186:ILE:HA	2:b:200:ILE:HG23	1.98	0.46
3:c:6:ASN:OD1	3:c:7:PRO:HD2	2.16	0.46
10:j:44:THR:HG23	10:j:44:THR:O	2.16	0.46
11:k:24:ARG:N	11:k:31:ILE:O	2.25	0.46
11:k:48:GLY:HA2	11:k:52:PHE:O	2.16	0.46
1:a:160:A:H2'	1:a:161:A:O4'	2.15	0.46
1:a:420:U:O2	1:a:422:A:H5''	2.15	0.46
1:a:603:A:N6	1:a:649:A:O2'	2.46	0.46
1:a:1324:U:OP2	19:s:6:LYS:HB2	2.15	0.46
1:a:1382:G:O3'	9:i:73:GLY:HA3	2.15	0.46
2:b:81:LYS:HA	2:b:81:LYS:HD3	1.57	0.46
4:d:181:GLU:HG3	4:d:183:SER:H	1.81	0.46
5:e:99:ALA:HB2	5:e:124:LEU:HG	1.96	0.46
6:f:25:ARG:O	6:f:29:ILE:HG23	2.16	0.46
7:g:113:GLU:OE2	7:g:118:ASP:HB3	2.15	0.46
10:j:37:SER:O	10:j:74:ILE:HG23	2.15	0.46
1:a:157:G:H2'	1:a:158:G:H8	1.80	0.46
1:a:807:G:H3'	1:a:808:G:H8	1.81	0.46
1:a:1014:A:N6	1:a:1037:C:H1'	2.31	0.46
1:a:1341:U:C4	1:a:1342:G:C6	3.03	0.46
19:s:16:MET:HE1	19:s:41:PHE:CZ	2.51	0.46
20:t:39:VAL:HG11	20:t:81:ALA:CB	2.44	0.46
1:a:475:A:H2'	1:a:477:U:N3	2.30	0.46
1:a:700:U:O2	1:a:702:A:H3'	2.15	0.46
1:a:702:A:N1	1:a:796:U:H5'	2.31	0.46
1:a:815:A:H2'	1:a:816:C:C6	2.51	0.46
1:a:830:A:N6	1:a:889:C:H42	2.14	0.46
1:a:1379:A:OP2	9:i:116:LYS:HG2	2.15	0.46
5:e:45:ARG:HH22	5:e:71:LEU:HD11	1.81	0.46
6:f:96:GLU:HB3	18:r:26:ILE:C	2.41	0.46
7:g:78:ARG:HG2	7:g:156:TRP:HZ2	1.80	0.46
8:h:55:ASP:HA	8:h:56:LYS:HA	1.68	0.46
12:l:115:LEU:O	12:l:116:ASP:C	2.58	0.46
14:n:49:TYR:CE1	14:n:57:ARG:HD2	2.50	0.46
20:t:74:ILE:O	20:t:78:LEU:CB	2.64	0.46
1:a:1326:U:H2'	1:a:1327:G:C8	2.50	0.46
4:d:149:ASN:O	4:d:153:GLU:HB2	2.16	0.46
15:o:74:ASP:OD1	15:o:75:ILE:N	2.45	0.46
1:a:421:G:H4'	1:a:422:A:H5''	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:435:C:H2'	1:a:436:G:C8	2.51	0.46
1:a:682:G:H4'	18:r:75:TYR:CE2	2.51	0.46
1:a:749:G:O4'	15:o:51:HIS:HD2	1.99	0.46
1:a:751:U:H2'	1:a:752:C:H6	1.80	0.46
1:a:830:A:N1	1:a:889:C:N3	2.64	0.46
1:a:869:C:H2'	1:a:870:A:C8	2.51	0.46
1:a:1402:U:H2'	1:a:1403:G:C8	2.51	0.46
5:e:77:VAL:HG22	5:e:78:GLU:CD	2.41	0.46
13:m:54:GLY:O	13:m:58:GLU:HG2	2.16	0.46
16:p:71:VAL:O	16:p:74:ILE:HG13	2.16	0.46
1:a:86:G:H1'	1:a:87:C:C6	2.51	0.46
1:a:150:U:O2'	1:a:151:A:O4'	2.34	0.46
1:a:713:G:H2'	1:a:714:A:O4'	2.16	0.46
1:a:1458:A:O2'	1:a:1459:C:H5'	2.16	0.46
2:b:204:ASP:OD1	2:b:204:ASP:N	2.47	0.46
3:c:137:ILE:HB	3:c:169:GLU:OE1	2.16	0.46
16:p:11:GLY:H	16:p:17:PHE:H	1.64	0.46
16:p:80:ILE:HG13	16:p:81:MET:N	2.30	0.46
1:a:241:U:H2'	1:a:242:C:C6	2.51	0.45
1:a:560:U:H2'	1:a:561:A:H8	1.80	0.45
1:a:1124:C:H2'	3:c:177:LEU:HB2	1.99	0.45
2:b:27:MET:HB2	2:b:30:TYR:HD2	1.80	0.45
7:g:78:ARG:HG2	7:g:156:TRP:CZ2	2.51	0.45
10:j:64:GLN:HB2	14:n:59:ALA:CB	2.46	0.45
13:m:50:ASP:N	13:m:50:ASP:OD1	2.48	0.45
18:r:13:LYS:HG2	18:r:14:LYS:H	1.81	0.45
1:a:74:G:O2'	1:a:75:A:H8	1.98	0.45
1:a:295:U:C2	1:a:296:A:C8	3.05	0.45
1:a:1119:C:C4	1:a:1120:G:C8	3.04	0.45
6:f:40:ALA:HA	6:f:63:VAL:HG12	1.97	0.45
12:l:121:ASP:HA	12:l:132:THR:OG1	2.15	0.45
20:t:36:LYS:O	20:t:40:SER:N	2.46	0.45
20:t:41:ASN:ND2	20:t:41:ASN:H	2.13	0.45
1:a:152:A:H2'	1:a:153:C:H5'	1.98	0.45
1:a:248:U:C2	1:a:249:G:N7	2.85	0.45
1:a:624:G:H2'	1:a:625:G:H8	1.81	0.45
1:a:1174:G:H2'	1:a:1175:G:C8	2.50	0.45
1:a:1317:A:N6	1:a:1341:U:O2	2.49	0.45
2:b:129:LEU:HD13	2:b:133:GLU:HB2	1.97	0.45
3:c:17:ASP:OD2	3:c:21:LYS:NZ	2.29	0.45
7:g:107:TYR:CZ	7:g:133:GLY:HA3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:27:GLY:HA3	12:l:35:PHE:CD2	2.51	0.45
12:l:32:LYS:HG3	12:l:34:LYS:HG2	1.98	0.45
13:m:12:GLU:HA	13:m:46:LYS:H	1.81	0.45
19:s:12:ASP:OD1	19:s:37:ARG:HB2	2.16	0.45
19:s:12:ASP:N	19:s:38:SER:HB3	2.13	0.45
1:a:99:U:C2'	1:a:100:A:H8	2.30	0.45
1:a:203:A:H2'	1:a:204:A:C8	2.52	0.45
1:a:263:G:H5''	17:q:21:LYS:CE	2.46	0.45
1:a:333:A:H2'	1:a:334:G:O4'	2.15	0.45
1:a:680:U:H4'	6:f:88:ARG:NH2	2.30	0.45
1:a:886:A:H1'	8:h:12:THR:HG21	1.99	0.45
1:a:1024:A:H3'	1:a:1025:G:C8	2.52	0.45
1:a:1436:A:OP2	1:a:1436:A:H8	1.99	0.45
2:b:49:LYS:NZ	2:b:52:GLU:OE1	2.31	0.45
9:i:115:ARG:CZ	9:i:115:ARG:CB	2.93	0.45
18:r:12:ARG:HE	18:r:48:ARG:HG3	1.81	0.45
20:t:5:LYS:HG3	20:t:6:SER:H	1.82	0.45
1:a:1381:G:C2	1:a:1382:G:C8	3.04	0.45
1:a:1428:G:H2'	1:a:1494:G:N2	2.31	0.45
1:a:1503:G:H4'	12:l:56:ARG:HD2	1.99	0.45
6:f:37:VAL:HG13	6:f:37:VAL:O	2.16	0.45
14:n:18:VAL:HG13	14:n:20:GLU:HG3	1.99	0.45
17:q:56:LYS:HE2	17:q:84:SER:O	2.16	0.45
1:a:320:C:H2'	1:a:321:A:C8	2.51	0.45
1:a:700:U:H1'	1:a:702:A:C8	2.52	0.45
1:a:716:A:H2'	1:a:717:U:C6	2.51	0.45
1:a:1089:G:N2	1:a:1091:G:H3'	2.32	0.45
1:a:1091:G:H5'	5:e:134:ILE:CD1	2.47	0.45
1:a:1324:U:H2'	1:a:1325:C:C6	2.51	0.45
2:b:78:GLU:OE1	2:b:78:GLU:N	2.42	0.45
5:e:29:ARG:NH1	5:e:31:PHE:HB3	2.31	0.45
6:f:1:MET:N	6:f:68:ASP:OD1	2.47	0.45
7:g:99:LEU:HB3	7:g:103:TRP:CZ3	2.52	0.45
1:a:690:U:H2'	1:a:691:G:H8	1.82	0.45
1:a:712:A:H3'	1:a:713:G:C8	2.51	0.45
1:a:1404:U:H2'	1:a:1406:C:C5	2.51	0.45
1:a:1538:G:H2'	1:a:1539:C:C6	2.52	0.45
2:b:96:TRP:CD2	2:b:100:LEU:HD12	2.52	0.45
7:g:29:LYS:HE2	7:g:102:ARG:HA	1.98	0.45
7:g:31:MET:HE2	7:g:34:GLY:HA2	1.99	0.45
11:k:24:ARG:O	11:k:31:ILE:N	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:14:ARG:HG3	13:m:17:ILE:HG12	1.97	0.45
13:m:25:ILE:HG23	13:m:29:THR:OG1	2.16	0.45
13:m:87:ARG:NH2	19:s:70:LYS:HG2	2.32	0.45
16:p:69:ASP:OD1	16:p:69:ASP:N	2.49	0.45
20:t:12:LYS:O	20:t:16:LYS:HG3	2.17	0.45
1:a:112:G:H2'	1:a:113:U:H6	1.81	0.45
1:a:222:G:H3'	1:a:223:C:H6	1.82	0.45
1:a:341:U:H2'	1:a:342:C:H6	1.82	0.45
1:a:612:G:C6	1:a:643:A:C6	3.05	0.45
1:a:1108:C:H2'	1:a:1109:C:C6	2.51	0.45
1:a:1165:U:H2'	1:a:1166:U:C6	2.52	0.45
3:c:72:PRO:O	3:c:73:GLY:C	2.59	0.45
4:d:83:GLY:O	4:d:86:PHE:N	2.50	0.45
1:a:263:G:H2'	1:a:264:U:C6	2.50	0.45
1:a:729:A:H8	1:a:729:A:OP1	1.99	0.45
1:a:765:U:H4'	1:a:830:A:N3	2.32	0.45
1:a:871:G:C6	1:a:872:C:C4	3.04	0.45
1:a:1074:U:H2'	1:a:1075:C:C6	2.52	0.45
1:a:1128:U:H2'	1:a:1129:A:C8	2.50	0.45
10:j:42:LEU:O	10:j:44:THR:N	2.50	0.45
11:k:47:ALA:HB1	11:k:52:PHE:HD2	1.81	0.45
12:l:28:PHE:CG	12:l:32:LYS:HB3	2.52	0.45
18:r:43:LYS:HA	18:r:43:LYS:HD3	1.63	0.45
1:a:106:G:C2	1:a:107:G:H1'	2.52	0.45
1:a:124:U:H2'	1:a:125:G:C8	2.52	0.45
1:a:173:U:OP1	1:a:213:G:H4'	2.18	0.45
1:a:270:A:H2'	1:a:271:A:O4'	2.17	0.45
1:a:474:A:H2'	1:a:475:A:C8	2.53	0.45
1:a:647:G:C2	1:a:648:A:C5	3.05	0.45
1:a:672:G:OP1	18:r:55:LYS:HE2	2.17	0.45
1:a:830:A:H61	1:a:889:C:H42	1.65	0.45
1:a:833:G:H2'	1:a:834:C:C6	2.52	0.45
1:a:842:U:H2'	1:a:843:A:H8	1.80	0.45
1:a:1024:A:H8	1:a:1024:A:OP1	2.00	0.45
1:a:1137:U:C2	1:a:1139:G:C8	3.05	0.45
1:a:1209:A:H2'	1:a:1210:U:H6	1.81	0.45
1:a:1381:G:C8	9:i:113:LYS:NZ	2.85	0.45
5:e:71:LEU:HA	5:e:71:LEU:HD23	1.75	0.45
6:f:7:MET:HA	6:f:61:ASN:O	2.18	0.45
9:i:47:ILE:H	9:i:47:ILE:HD12	1.82	0.45
10:j:67:GLN:HG3	14:n:55:GLY:CA	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:633:G:H4'	16:p:17:PHE:CD2	2.52	0.44
1:a:758:C:H2'	1:a:759:U:C2	2.53	0.44
1:a:789:A:H2	1:a:1526:U:H4'	1.81	0.44
1:a:1381:G:H3'	9:i:113:LYS:NZ	2.33	0.44
8:h:3:MET:SD	8:h:5:ASP:N	2.79	0.44
8:h:107:SER:HB3	8:h:128:ILE:HD11	1.99	0.44
9:i:87:ARG:HE	9:i:108:ARG:NH2	2.14	0.44
13:m:49:THR:O	13:m:53:LEU:HD23	2.16	0.44
14:n:58:LYS:HE3	14:n:58:LYS:HB3	1.53	0.44
17:q:32:THR:OG1	17:q:33:HIS:N	2.49	0.44
1:a:194:G:N2	1:a:197:U:OP2	2.47	0.44
1:a:201:U:H2'	1:a:202:C:C6	2.52	0.44
1:a:216:G:C6	1:a:225:G:C6	3.05	0.44
1:a:254:A:C2	1:a:290:A:C5	3.05	0.44
1:a:904:G:C6	1:a:905:A:C5	3.06	0.44
8:h:12:THR:O	8:h:16:ASN:ND2	2.51	0.44
11:k:65:MET:HE2	11:k:65:MET:C	2.42	0.44
13:m:2:ALA:HA	13:m:3:ARG:HA	1.52	0.44
19:s:27:LYS:HZ2	19:s:46:GLY:HA3	1.80	0.44
1:a:9:A:N7	4:d:200:ARG:HB3	2.32	0.44
1:a:151:A:C2	1:a:152:A:H1'	2.52	0.44
1:a:227:C:H2'	1:a:228:A:C8	2.51	0.44
1:a:446:G:H1'	1:a:447:U:H5	1.83	0.44
1:a:698:G:OP2	11:k:29:ASN:ND2	2.49	0.44
1:a:988:A:H61	1:a:1327:G:H1'	1.83	0.44
1:a:1152:U:O2'	1:a:1153:G:H8	2.00	0.44
1:a:1165:U:H2'	1:a:1166:U:H6	1.82	0.44
1:a:1298:A:H2'	1:a:1299:A:C8	2.52	0.44
1:a:1302:U:C2	1:a:1303:U:C5	3.05	0.44
1:a:1519:A:H2'	1:a:1520:G:C8	2.53	0.44
13:m:4:ILE:HG22	13:m:53:LEU:HD11	1.99	0.44
20:t:64:ASN:OD1	20:t:65:LEU:N	2.51	0.44
1:a:51:A:H62	12:l:30:SER:HB2	1.82	0.44
1:a:239:G:C4	1:a:240:A:C8	3.05	0.44
1:a:268:G:H2'	1:a:269:U:C6	2.52	0.44
1:a:272:C:H2'	1:a:273:G:O4'	2.18	0.44
1:a:277:U:H2'	1:a:278:A:C8	2.53	0.44
1:a:330:C:H2'	1:a:331:U:C6	2.52	0.44
1:a:555:A:OP1	4:d:66:ARG:NH2	2.47	0.44
1:a:712:A:H2'	1:a:713:G:O4'	2.18	0.44
1:a:723:A:H1'	1:a:785:A:C2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:946:C:C4	1:a:947:A:N7	2.85	0.44
1:a:1100:G:H2'	1:a:1101:G:H8	1.82	0.44
1:a:1141:C:H5'	9:i:20:ARG:HH12	1.82	0.44
1:a:1327:G:H5'	1:a:1371:A:O2'	2.17	0.44
1:a:1550:C:H2'	1:a:1551:C:C6	2.52	0.44
4:d:17:ILE:HG13	4:d:56:LYS:HD2	1.99	0.44
4:d:101:LEU:HD11	4:d:166:ASN:O	2.17	0.44
7:g:49:LEU:HD22	7:g:117:GLU:HG3	1.99	0.44
8:h:108:THR:CG2	8:h:109:SER:H	2.29	0.44
13:m:68:ASP:O	13:m:72:GLU:HG2	2.17	0.44
1:a:36:G:H2'	1:a:37:C:H6	1.82	0.44
1:a:149:A:H1'	1:a:1457:A:C2	2.53	0.44
1:a:268:G:N7	20:t:73:ARG:NH2	2.65	0.44
1:a:426:U:O2	4:d:35:GLN:NE2	2.51	0.44
1:a:665:U:H4'	15:o:28:GLN:NE2	2.33	0.44
1:a:683:A:H1'	11:k:118:HIS:NE2	2.33	0.44
1:a:838:G:H2'	1:a:839:U:H6	1.82	0.44
1:a:869:C:H2'	1:a:870:A:H8	1.83	0.44
1:a:1244:G:H2'	1:a:1245:C:H6	1.83	0.44
1:a:1315:G:N1	1:a:1343:A:OP2	2.22	0.44
5:e:107:ALA:HB1	5:e:111:VAL:HG13	1.98	0.44
6:f:9:ILE:HG12	6:f:60:TYR:HD1	1.81	0.44
11:k:126:ARG:HA	11:k:127:ARG:HA	1.50	0.44
12:l:24:LEU:HD22	12:l:24:LEU:C	2.43	0.44
14:n:10:GLN:HG3	14:n:23:ARG:NE	2.33	0.44
1:a:36:G:H2'	1:a:37:C:C6	2.53	0.44
1:a:69:G:N2	1:a:70:A:H1'	2.33	0.44
1:a:134:A:H1'	1:a:333:A:N7	2.32	0.44
1:a:252:U:H4'	1:a:253:U:H5''	1.99	0.44
1:a:446:G:C2	1:a:504:G:N7	2.86	0.44
1:a:449:A:N1	1:a:502:C:N4	2.65	0.44
1:a:466:G:C6	1:a:484:A:N1	2.85	0.44
6:f:26:PHE:HE1	6:f:76:PHE:CD1	2.35	0.44
12:l:26:LYS:CG	12:l:72:ASN:HB3	2.48	0.44
15:o:24:SER:O	15:o:26:GLU:N	2.51	0.44
1:a:329:A:H2'	1:a:330:C:C6	2.52	0.44
1:a:391:A:C6	1:a:392:G:H1'	2.52	0.44
1:a:1031:G:H2'	1:a:1032:C:O4'	2.18	0.44
1:a:1169:C:C4	1:a:1171:G:O4'	2.71	0.44
1:a:1353:C:H2'	1:a:1354:G:C8	2.52	0.44
4:d:99:TYR:CD2	4:d:107:ARG:HD3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:66:ILE:HA	7:g:69:ILE:HG12	2.00	0.44
7:g:87:VAL:HG11	7:g:156:TRP:HE1	1.82	0.44
8:h:113:ILE:HD12	8:h:117:GLU:HB2	2.00	0.44
9:i:7:GLU:HG2	9:i:24:VAL:CG1	2.47	0.44
11:k:14:LYS:NZ	11:k:40:ASN:HB3	2.32	0.44
18:r:46:PRO:HA	18:r:57:GLN:NE2	2.33	0.44
1:a:91:U:C4	1:a:92:C:H1'	2.53	0.44
1:a:109:C:H2'	1:a:110:G:O4'	2.17	0.44
1:a:366:U:C2	1:a:367:A:C8	3.05	0.44
1:a:470:A:C2	1:a:481:C:C2	3.06	0.44
1:a:557:C:N4	1:a:558:G:O6	2.51	0.44
1:a:590:U:C2	1:a:591:A:C8	3.05	0.44
1:a:843:A:N6	1:a:862:A:N1	2.65	0.44
1:a:931:U:H2'	1:a:932:G:C8	2.53	0.44
1:a:1130:A:H1'	1:a:1190:A:C5	2.52	0.44
1:a:1131:G:H2'	1:a:1132:C:H6	1.81	0.44
1:a:1131:G:H2'	1:a:1132:C:C6	2.53	0.44
7:g:46:ALA:HA	7:g:117:GLU:HB2	1.99	0.44
12:l:69:ARG:HG2	12:l:75:GLU:OE2	2.17	0.44
1:a:38:U:H2'	1:a:39:G:H8	1.82	0.44
1:a:232:A:H2'	1:a:233:U:C6	2.53	0.44
1:a:724:A:H2'	1:a:725:C:O4'	2.18	0.44
1:a:726:A:H5'	11:k:118:HIS:HB3	1.99	0.44
1:a:959:A:H2'	1:a:960:U:C6	2.52	0.44
1:a:1234:C:H5''	1:a:1235:U:H5''	2.00	0.44
3:c:121:ARG:HE	3:c:124:GLU:HG3	1.82	0.44
4:d:176:PHE:CZ	4:d:180:PRO:HD3	2.53	0.44
6:f:46:ARG:NH1	18:r:72:LEU:HD23	2.33	0.44
12:l:50:VAL:HG21	12:l:87:LEU:HD21	2.00	0.44
13:m:96:PRO:HG2	13:m:99:GLY:H	1.83	0.44
1:a:401:A:C4	1:a:402:G:C8	3.07	0.43
1:a:974:A:O2'	10:j:57:MET:HE3	2.18	0.43
1:a:1072:U:H5''	14:n:45:ARG:HH22	1.82	0.43
1:a:1365:U:H2'	1:a:1366:A:H8	1.79	0.43
1:a:1426:G:H1	1:a:1497:U:H3	1.66	0.43
5:e:14:ARG:HB3	5:e:117:LEU:HD22	2.00	0.43
7:g:26:LEU:O	7:g:30:ILE:HD12	2.18	0.43
7:g:87:VAL:HG11	7:g:156:TRP:NE1	2.33	0.43
9:i:59:THR:HA	9:i:60:LYS:HA	1.71	0.43
10:j:45:GLU:H	10:j:71:LYS:HZ3	1.66	0.43
10:j:53:ARG:HA	14:n:45:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:32:LYS:HG2	12:l:34:LYS:HG2	1.99	0.43
18:r:37:PHE:CE2	18:r:44:ILE:HD11	2.53	0.43
1:a:157:G:H2'	1:a:158:G:C8	2.52	0.43
1:a:241:U:H2'	1:a:242:C:H6	1.83	0.43
1:a:525:G:H4'	1:a:527:C:C5	2.53	0.43
1:a:612:G:O6	1:a:643:A:N6	2.52	0.43
1:a:1172:C:H2'	1:a:1173:C:H6	1.83	0.43
1:a:1341:U:H2'	1:a:1342:G:O4'	2.17	0.43
1:a:1341:U:H4'	13:m:23:TYR:CE1	2.53	0.43
1:a:1419:A:N6	1:a:1506:G:C6	2.86	0.43
1:a:1436:A:O2'	1:a:1437:A:O4'	2.31	0.43
4:d:191:GLU:O	4:d:195:VAL:HG12	2.18	0.43
5:e:15:VAL:HG21	5:e:18:ILE:HD11	2.00	0.43
10:j:64:GLN:O	10:j:65:PHE:HD1	2.01	0.43
11:k:75:MET:N	11:k:75:MET:HE2	2.32	0.43
12:l:25:ASN:OD1	12:l:26:LYS:N	2.51	0.43
12:l:74:ILE:HG13	12:l:75:GLU:H	1.83	0.43
16:p:30:ASP:OD1	16:p:30:ASP:N	2.38	0.43
19:s:83:HIS:CD2	19:s:85:ALA:H	2.36	0.43
1:a:472:G:H2'	1:a:473:U:C6	2.54	0.43
1:a:837:A:N6	1:a:838:G:O6	2.52	0.43
1:a:1119:C:N3	1:a:1120:G:C8	2.87	0.43
1:a:1385:A:O2'	7:g:28:ASN:HB3	2.19	0.43
1:a:1485:G:H2'	1:a:1486:G:H8	1.83	0.43
5:e:14:ARG:HG2	5:e:113:ALA:HB1	2.00	0.43
8:h:108:THR:HG23	8:h:123:VAL:HG22	2.01	0.43
10:j:56:HIS:HB3	10:j:57:MET:SD	2.58	0.43
12:l:26:LYS:HG2	12:l:72:ASN:HB3	2.01	0.43
1:a:351:U:N3	1:a:353:C:N3	2.65	0.43
1:a:962:U:H5'	1:a:982:C:H41	1.83	0.43
1:a:1008:C:H2'	1:a:1009:C:H6	1.83	0.43
1:a:1283:U:H2'	1:a:1284:C:O4'	2.19	0.43
1:a:1465:A:H2'	1:a:1466:G:H8	1.83	0.43
1:a:1547:C:H2'	1:a:1548:C:H5	1.82	0.43
1:a:63:U:H2'	1:a:64:C:H6	1.80	0.43
1:a:410:G:C6	1:a:411:C:C4	3.06	0.43
1:a:419:A:C6	1:a:421:G:C2	3.06	0.43
1:a:460:A:N1	1:a:488:U:H2'	2.34	0.43
1:a:787:C:H2'	1:a:788:A:C8	2.53	0.43
1:a:986:G:N1	1:a:1374:A:OP2	2.44	0.43
1:a:1067:A:H8	1:a:1067:A:O5'	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1490:A:H2'	1:a:1491:A:C8	2.53	0.43
1:a:1549:U:H2'	1:a:1550:C:C6	2.54	0.43
2:b:154:MET:HE1	2:b:156:SER:O	2.19	0.43
3:c:9:GLY:O	14:n:57:ARG:HD3	2.19	0.43
3:c:137:ILE:HA	3:c:148:ILE:HD11	1.99	0.43
7:g:149:LYS:O	7:g:153:HIS:HB3	2.18	0.43
9:i:48:LEU:H	9:i:48:LEU:HD12	1.83	0.43
10:j:6:ILE:N	10:j:76:ILE:O	2.36	0.43
11:k:24:ARG:NH2	11:k:33:THR:HG22	2.32	0.43
17:q:49:HIS:O	17:q:76:ARG:HD2	2.19	0.43
17:q:57:LEU:HD12	17:q:58:GLY:H	1.83	0.43
17:q:59:ASP:OD2	17:q:80:ILE:HG23	2.19	0.43
1:a:37:C:H2'	1:a:38:U:H6	1.82	0.43
1:a:123:G:H2'	1:a:124:U:O4'	2.18	0.43
1:a:125:G:OP1	1:a:640:G:N2	2.51	0.43
1:a:482:A:P	16:p:81:MET:HE1	2.58	0.43
1:a:525:G:N1	1:a:541:A:OP2	2.52	0.43
1:a:1103:U:C2	1:a:1107:U:C4	3.07	0.43
1:a:1302:U:H2'	1:a:1303:U:H6	1.84	0.43
1:a:1315:G:H1'	1:a:1345:G:H22	1.84	0.43
2:b:137:LEU:HD23	2:b:137:LEU:HA	1.83	0.43
3:c:152:VAL:HG12	3:c:165:GLU:HG2	2.00	0.43
4:d:4:PHE:O	4:d:4:PHE:CG	2.70	0.43
7:g:16:PRO:HA	7:g:19:ASN:HA	2.01	0.43
20:t:39:VAL:HG13	20:t:46:LYS:HZ1	1.84	0.43
1:a:284:G:O3'	17:q:47:LYS:NZ	2.42	0.43
1:a:299:C:H2'	1:a:300:G:C8	2.53	0.43
1:a:315:U:H5''	1:a:316:C:C5	2.53	0.43
1:a:397:A:C5	1:a:398:C:H1'	2.54	0.43
1:a:420:U:O4	1:a:438:A:N6	2.51	0.43
1:a:522:C:C2	1:a:523:G:C8	3.07	0.43
1:a:773:G:N2	1:a:821:U:H5	2.16	0.43
1:a:836:A:N6	1:a:868:G:H21	2.05	0.43
1:a:1012:U:C2	1:a:1050:A:C2	3.07	0.43
5:e:39:VAL:O	5:e:47:GLY:N	2.50	0.43
5:e:149:ASN:O	5:e:153:VAL:HG22	2.19	0.43
5:e:165:TYR:N	8:h:100:GLY:HA3	2.33	0.43
7:g:132:GLY:O	7:g:136:LYS:HG3	2.19	0.43
10:j:3:LYS:HE3	10:j:5:LYS:HB3	2.01	0.43
12:l:21:SER:C	12:l:23:ALA:H	2.27	0.43
17:q:31:LYS:HB2	17:q:42:TYR:HE1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:q:61:VAL:HG21	17:q:77:LEU:HD23	2.01	0.43
1:a:24:C:H2'	1:a:25:U:H6	1.81	0.43
1:a:905:A:C6	1:a:906:C:C4	3.07	0.43
1:a:1272:A:H2'	1:a:1273:A:C8	2.54	0.43
1:a:1280:A:H2	1:a:1323:G:N3	2.17	0.43
1:a:1305:U:H2'	1:a:1306:U:C6	2.54	0.43
1:a:1461:U:H2'	1:a:1462:U:O4'	2.19	0.43
15:o:2:ALA:N	15:o:3:ILE:HA	2.34	0.43
15:o:13:LYS:HD3	15:o:16:ARG:CZ	2.49	0.43
20:t:41:ASN:O	20:t:42:ASN:C	2.61	0.43
20:t:70:LYS:HA	20:t:70:LYS:HD2	1.86	0.43
1:a:93:U:H2'	1:a:94:G:O4'	2.19	0.43
1:a:240:A:H2'	1:a:241:U:H6	1.82	0.43
1:a:402:G:H2'	1:a:403:C:C6	2.53	0.43
1:a:411:C:H2'	1:a:412:G:C8	2.53	0.43
1:a:559:U:O2'	12:l:96:ARG:NH1	2.52	0.43
1:a:636:G:H2'	1:a:637:A:H8	1.84	0.43
1:a:696:G:C6	1:a:708:G:C2	3.06	0.43
1:a:733:G:H2'	1:a:734:C:H6	1.83	0.43
1:a:938:G:C4'	1:a:1544:U:H4'	2.49	0.43
1:a:983:G:OP2	1:a:984:A:O2'	2.37	0.43
1:a:1130:A:H2'	1:a:1131:G:C8	2.49	0.43
1:a:1154:G:H2'	1:a:1155:G:C8	2.54	0.43
1:a:1266:G:O2'	1:a:1269:G:N3	2.51	0.43
1:a:1415:C:H1'	1:a:1511:A:C6	2.54	0.43
1:a:1427:A:H3'	1:a:1428:G:H8	1.83	0.43
3:c:40:LYS:HE2	14:n:26:ARG:HD3	2.01	0.43
14:n:22:THR:O	14:n:33:VAL:HG11	2.18	0.43
14:n:25:GLU:H	14:n:25:GLU:CD	2.27	0.43
1:a:459:A:H61	1:a:491:C:N4	2.07	0.43
1:a:1147:U:O2	1:a:1149:A:H8	2.01	0.43
1:a:1291:A:H5'	10:j:42:LEU:HD22	2.00	0.43
4:d:128:ILE:O	4:d:128:ILE:HG13	2.19	0.43
13:m:83:ILE:O	13:m:83:ILE:HG13	2.19	0.43
19:s:80:PHE:CD1	19:s:80:PHE:C	2.95	0.43
20:t:74:ILE:O	20:t:78:LEU:HB3	2.19	0.43
1:a:231:U:H2'	1:a:232:A:H8	1.84	0.42
1:a:456:A:O2'	1:a:492:G:N2	2.46	0.42
1:a:459:A:N1	1:a:491:C:H5	2.17	0.42
1:a:599:U:H2'	1:a:600:U:C6	2.54	0.42
1:a:847:G:H2'	1:a:848:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1320:G:H2'	1:a:1321:U:C6	2.54	0.42
1:a:1328:C:H5	14:n:16:TYR:CG	2.37	0.42
1:a:1415:C:H2'	1:a:1416:G:H8	1.83	0.42
1:a:1428:G:H1'	1:a:1495:A:H61	1.83	0.42
4:d:153:GLU:HA	4:d:156:GLU:OE1	2.18	0.42
5:e:13:GLU:CD	5:e:64:VAL:HG21	2.43	0.42
15:o:27:VAL:O	15:o:31:VAL:HG22	2.19	0.42
1:a:272:C:O2'	17:q:67:ARG:NH1	2.52	0.42
1:a:400:G:H2'	1:a:401:A:C8	2.48	0.42
1:a:528:A:OP1	12:l:62:LEU:HB3	2.18	0.42
1:a:601:U:H2'	1:a:602:U:H6	1.83	0.42
1:a:622:A:H2'	1:a:623:C:H6	1.84	0.42
1:a:628:C:H2'	1:a:629:A:H8	1.83	0.42
1:a:794:G:H2'	1:a:795:A:C8	2.51	0.42
1:a:957:G:OP1	13:m:107:ARG:HB3	2.19	0.42
1:a:1344:A:H2'	1:a:1345:G:O4'	2.18	0.42
1:a:1480:A:C4	1:a:1481:A:C8	3.06	0.42
5:e:12:GLU:OE1	5:e:117:LEU:HD13	2.19	0.42
13:m:72:GLU:HA	13:m:75:LEU:HG	2.00	0.42
14:n:7:VAL:O	14:n:11:GLN:HB2	2.19	0.42
17:q:50:ASP:OD1	17:q:77:LEU:HD11	2.18	0.42
18:r:37:PHE:CD2	18:r:60:LEU:HD13	2.54	0.42
1:a:231:U:H2'	1:a:232:A:C8	2.55	0.42
1:a:267:G:H2'	1:a:268:G:C8	2.53	0.42
1:a:362:G:H2'	1:a:363:C:C6	2.53	0.42
1:a:391:A:C5	1:a:392:G:H1'	2.55	0.42
1:a:440:A:H2'	1:a:441:A:O4'	2.19	0.42
1:a:715:U:H2'	1:a:716:A:H8	1.84	0.42
1:a:1125:C:H2'	1:a:1126:C:C6	2.54	0.42
1:a:1137:U:HO2'	1:a:1138:U:P	2.40	0.42
1:a:1249:A:N3	1:a:1252:G:O2'	2.52	0.42
1:a:1262:A:H2'	1:a:1263:A:C8	2.55	0.42
1:a:1282:G:H2'	1:a:1283:U:H6	1.83	0.42
1:a:1427:A:C4	1:a:1428:G:C8	3.07	0.42
1:a:1478:C:H2'	1:a:1479:G:O4'	2.19	0.42
5:e:6:GLU:HB2	5:e:8:THR:HG22	2.01	0.42
7:g:23:VAL:HG13	7:g:43:LEU:HD21	2.01	0.42
7:g:29:LYS:HZ3	7:g:102:ARG:HE	1.67	0.42
12:l:53:MET:HE3	12:l:103:LEU:HD23	2.02	0.42
12:l:72:ASN:O	12:l:73:ASN:ND2	2.52	0.42
1:a:106:G:N2	1:a:107:G:H1'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:113:U:H2'	1:a:114:G:C8	2.54	0.42
1:a:438:A:OP1	4:d:9:TRP:HB2	2.18	0.42
1:a:520:U:H2'	1:a:521:A:C8	2.54	0.42
1:a:602:U:H3'	1:a:603:A:H8	1.84	0.42
1:a:1109:C:H1'	1:a:1181:A:H1'	2.01	0.42
1:a:1112:C:N4	1:a:1115:C:OP1	2.53	0.42
1:a:1401:U:H2'	1:a:1402:U:H6	1.84	0.42
1:a:1474:C:H2'	1:a:1475:C:C6	2.54	0.42
4:d:178:ARG:HG2	4:d:179:LEU:N	2.35	0.42
8:h:62:LEU:HD12	8:h:62:LEU:HA	1.93	0.42
15:o:7:ARG:HH22	15:o:8:LYS:HB2	1.84	0.42
1:a:120:C:N4	1:a:244:G:OP2	2.40	0.42
1:a:303:C:H2'	1:a:304:U:O4'	2.20	0.42
1:a:311:G:H2'	1:a:312:U:C6	2.55	0.42
1:a:833:G:H1'	8:h:9:ASP:OD1	2.20	0.42
1:a:887:C:H2'	1:a:888:U:H6	1.83	0.42
1:a:943:G:N2	1:a:945:A:O4'	2.53	0.42
1:a:1363:C:C2	1:a:1382:G:C2	3.07	0.42
2:b:7:LYS:NZ	2:b:15:HIS:HE1	2.18	0.42
10:j:35:ASP:OD2	10:j:77:VAL:HB	2.19	0.42
1:a:67:G:H2'	1:a:68:C:H6	1.85	0.42
1:a:124:U:H2'	1:a:125:G:H8	1.85	0.42
1:a:237:U:H2'	1:a:238:G:C8	2.55	0.42
1:a:392:G:O2'	1:a:393:C:H5'	2.20	0.42
1:a:458:G:H3'	1:a:459:A:C8	2.53	0.42
1:a:496:C:H2'	1:a:497:C:C6	2.55	0.42
1:a:687:C:H2'	1:a:688:C:H6	1.83	0.42
1:a:712:A:C4	1:a:713:G:C8	3.08	0.42
1:a:1524:U:H2'	1:a:1525:A:C8	2.54	0.42
2:b:197:ASP:OD1	2:b:198:TYR:N	2.52	0.42
4:d:16:GLY:O	4:d:17:ILE:HD13	2.19	0.42
5:e:161:VAL:HG22	5:e:162:GLU:H	1.84	0.42
6:f:11:ARG:NH1	6:f:52:ILE:HD11	2.35	0.42
11:k:47:ALA:HB2	11:k:62:ALA:CB	2.49	0.42
16:p:8:THR:HG23	16:p:30:ASP:HA	2.01	0.42
1:a:294:A:H2'	1:a:295:U:H6	1.84	0.42
1:a:494:U:C2	1:a:495:A:C8	3.08	0.42
1:a:984:A:H5'	14:n:31:HIS:HB3	2.00	0.42
5:e:157:ARG:NH1	8:h:43:GLU:OE2	2.47	0.42
8:h:35:GLU:CD	8:h:112:VAL:HB	2.44	0.42
10:j:68:ARG:NH2	10:j:70:HIS:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:22:HIS:CB	11:k:24:ARG:HH12	2.32	0.42
12:l:7:LEU:HA	12:l:7:LEU:HD23	1.75	0.42
13:m:80:LEU:HD23	13:m:91:HIS:CE1	2.54	0.42
1:a:106:G:H4'	1:a:386:G:O3'	2.20	0.42
1:a:178:G:C2	1:a:179:A:C8	3.08	0.42
1:a:389:A:H2'	1:a:390:A:C8	2.55	0.42
1:a:409:C:H2'	1:a:410:G:H8	1.84	0.42
1:a:707:C:H2'	1:a:708:G:C8	2.55	0.42
1:a:1446:G:H2'	1:a:1447:C:C6	2.55	0.42
1:a:1451:U:H2'	1:a:1452:G:O4'	2.20	0.42
3:c:110:LEU:HD13	3:c:143:LEU:HB2	2.02	0.42
5:e:46:VAL:HG12	5:e:72:VAL:HB	2.02	0.42
11:k:25:SER:H	11:k:87:LYS:HZ3	1.67	0.42
18:r:12:ARG:HE	18:r:48:ARG:CD	2.32	0.42
18:r:26:ILE:HD13	18:r:30:ASP:O	2.19	0.42
19:s:40:ILE:HG13	19:s:66:MET:HE3	2.01	0.42
1:a:62:G:C6	1:a:106:G:C4	3.07	0.42
1:a:92:C:H2'	1:a:93:U:C5	2.55	0.42
1:a:661:U:O2'	1:a:662:G:H8	2.02	0.42
1:a:945:A:H2'	1:a:946:C:O4'	2.20	0.42
1:a:1037:C:N4	1:a:1046:G:H1	2.17	0.42
1:a:1053:G:H3'	1:a:1054:U:H6	1.84	0.42
1:a:1254:A:H2'	1:a:1255:C:C6	2.55	0.42
1:a:1397:G:H2'	1:a:1398:G:H8	1.84	0.42
1:a:1453:G:O2'	1:a:1454:A:H8	2.03	0.42
2:b:188:ASP:OD1	2:b:189:THR:N	2.53	0.42
5:e:56:VAL:O	5:e:60:ILE:HG22	2.20	0.42
13:m:41:ALA:N	13:m:42:ASP:CA	2.82	0.42
17:q:8:LYS:HB3	17:q:10:TYR:CE1	2.55	0.42
19:s:15:LEU:HD11	19:s:49:PHE:CE1	2.55	0.42
19:s:80:PHE:C	19:s:80:PHE:HD1	2.28	0.42
1:a:102:C:H2'	1:a:103:G:H8	1.84	0.42
1:a:103:G:OP1	20:t:16:LYS:NZ	2.51	0.42
1:a:322:C:H2'	1:a:323:A:H8	1.82	0.42
1:a:456:A:N7	1:a:493:G:O2'	2.50	0.42
1:a:511:A:H2'	1:a:512:C:H6	1.85	0.42
1:a:518:A:H1'	1:a:551:G:H1'	2.00	0.42
1:a:786:U:C4	1:a:787:C:C4	3.08	0.42
1:a:1048:A:H2'	1:a:1049:C:C6	2.51	0.42
1:a:1080:G:N7	1:a:1106:G:O2'	2.44	0.42
1:a:1110:C:H1'	1:a:1178:A:C2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1181:A:H3'	1:a:1182:A:H8	1.84	0.42
1:a:1357:A:N6	1:a:1385:A:H3'	2.35	0.42
3:c:188:ALA:HB3	3:c:195:LEU:HB2	2.01	0.42
7:g:15:ASP:HB3	7:g:24:THR:OG1	2.20	0.42
8:h:3:MET:HE2	8:h:3:MET:HA	2.01	0.42
17:q:25:VAL:O	17:q:46:TYR:N	2.49	0.42
17:q:46:TYR:HD2	17:q:63:ILE:HD11	1.85	0.42
20:t:16:LYS:HB2	20:t:16:LYS:HE2	1.76	0.42
1:a:419:A:N3	1:a:420:U:C2	2.89	0.41
1:a:439:A:C5	1:a:440:A:C8	3.08	0.41
1:a:599:U:H2'	1:a:600:U:H6	1.84	0.41
1:a:1018:C:H2'	1:a:1019:U:C6	2.55	0.41
3:c:133:GLN:OE1	3:c:167:TYR:HD1	2.02	0.41
10:j:66:GLU:HG2	14:n:56:VAL:CG2	2.50	0.41
18:r:37:PHE:CE1	18:r:50:THR:HG21	2.55	0.41
20:t:53:ALA:O	20:t:57:VAL:HG23	2.20	0.41
1:a:392:G:H2'	1:a:393:C:H6	1.84	0.41
1:a:422:A:N6	1:a:439:A:H1'	2.36	0.41
1:a:533:C:H2'	1:a:534:C:C6	2.55	0.41
1:a:650:A:C5	8:h:109:SER:HA	2.55	0.41
1:a:938:G:H4'	1:a:1544:U:H4'	2.01	0.41
1:a:989:C:N3	14:n:16:TYR:OH	2.52	0.41
1:a:1012:U:C2	1:a:1013:G:C8	3.07	0.41
1:a:1233:G:H2'	1:a:1234:C:C6	2.55	0.41
5:e:105:VAL:O	5:e:112:ARG:NH1	2.52	0.41
5:e:141:ILE:O	5:e:145:GLN:HG2	2.20	0.41
6:f:76:PHE:CE1	6:f:80:ALA:HB2	2.55	0.41
9:i:97:ARG:CZ	9:i:101:LYS:HG3	2.50	0.41
12:l:88:GLN:OE1	12:l:91:SER:HB3	2.20	0.41
15:o:17:VAL:HG13	15:o:24:SER:HB3	2.02	0.41
17:q:65:GLU:CD	17:q:74:ARG:HH12	2.27	0.41
19:s:5:ILE:HD11	19:s:7:LYS:CD	2.44	0.41
1:a:394:C:H2'	1:a:395:U:C6	2.55	0.41
1:a:457:A:H2'	1:a:458:G:C8	2.56	0.41
1:a:588:C:HO2'	15:o:57:LEU:HD22	1.86	0.41
1:a:682:G:H21	11:k:118:HIS:CD2	2.39	0.41
1:a:730:G:H4'	1:a:1548:C:O2	2.19	0.41
1:a:1086:G:H2'	1:a:1087:U:H6	1.86	0.41
1:a:1118:G:H5''	3:c:171:THR:HB	2.01	0.41
1:a:1169:C:H1'	2:b:131:LYS:HG3	2.02	0.41
1:a:1171:G:O2'	1:a:1172:C:O5'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1379:A:OP2	9:i:116:LYS:NZ	2.45	0.41
5:e:29:ARG:HH22	5:e:31:PHE:HB3	1.84	0.41
7:g:152:ALA:HA	7:g:155:ARG:HD2	2.02	0.41
12:l:26:LYS:NZ	12:l:29:ASN:HB2	2.36	0.41
16:p:5:ILE:HG21	16:p:71:VAL:HG11	2.01	0.41
19:s:40:ILE:HD13	19:s:44:PHE:CD2	2.54	0.41
20:t:7:ALA:O	20:t:11:VAL:HG23	2.20	0.41
20:t:41:ASN:HD22	20:t:41:ASN:H	1.66	0.41
1:a:262:G:C6	1:a:281:A:C6	3.08	0.41
1:a:532:G:H2'	1:a:533:C:H6	1.82	0.41
1:a:586:C:H2'	1:a:587:G:H8	1.83	0.41
1:a:628:C:H2'	1:a:629:A:C8	2.56	0.41
1:a:691:G:H2'	1:a:692:U:H6	1.84	0.41
1:a:975:A:O2'	1:a:979:A:N7	2.53	0.41
1:a:1260:C:O2'	9:i:77:GLN:NE2	2.50	0.41
1:a:1360:A:C4	1:a:1361:A:C8	3.09	0.41
1:a:1399:U:H2'	1:a:1400:C:C6	2.55	0.41
1:a:1417:U:H4'	1:a:1530:A:H4'	2.02	0.41
1:a:1547:C:H2'	1:a:1548:C:C5	2.55	0.41
6:f:22:LEU:HD22	6:f:85:ASP:OD2	2.20	0.41
10:j:66:GLU:N	10:j:66:GLU:OE2	2.54	0.41
13:m:83:ILE:C	13:m:85:SER:N	2.77	0.41
1:a:33:A:OP1	1:a:406:C:H1'	2.20	0.41
1:a:38:U:C2	1:a:39:G:C8	3.09	0.41
1:a:187:U:H2'	1:a:188:U:C6	2.55	0.41
1:a:548:G:H2'	1:a:549:G:C8	2.56	0.41
1:a:610:A:H2'	1:a:611:U:H6	1.85	0.41
1:a:834:C:H2'	1:a:835:U:C6	2.55	0.41
1:a:1415:C:H1'	1:a:1511:A:N1	2.35	0.41
1:a:1514:A:O2'	1:a:1515:A:H3'	2.21	0.41
1:a:1525:A:C5	1:a:1526:U:C4	3.08	0.41
3:c:82:GLU:O	3:c:86:LEU:HG	2.21	0.41
4:d:152:VAL:HA	4:d:155:VAL:HG22	2.01	0.41
8:h:107:SER:HA	8:h:112:VAL:HG22	2.01	0.41
10:j:57:MET:HB2	10:j:58:TYR:CD1	2.55	0.41
11:k:75:MET:HE1	11:k:79:LEU:HD23	2.03	0.41
20:t:38:ALA:O	20:t:41:ASN:ND2	2.53	0.41
1:a:134:A:H1'	1:a:333:A:C8	2.55	0.41
1:a:371:A:OP2	12:l:44:ARG:HG2	2.21	0.41
1:a:857:C:H2'	1:a:858:C:H6	1.85	0.41
1:a:973:G:H2'	1:a:974:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1003:G:H2'	1:a:1005:C:N4	2.35	0.41
1:a:1380:C:C2	1:a:1381:G:C8	3.08	0.41
1:a:1432:U:H2'	1:a:1433:U:C6	2.56	0.41
4:d:113:LEU:HD23	4:d:113:LEU:HA	1.93	0.41
17:q:7:ARG:HB2	17:q:64:GLN:HB2	2.03	0.41
1:a:61:A:O2'	20:t:5:LYS:HD2	2.21	0.41
1:a:455:G:H8	1:a:455:G:O5'	2.04	0.41
1:a:526:C:H4'	1:a:527:C:H5''	2.02	0.41
1:a:628:C:C2	4:d:128:ILE:HD13	2.55	0.41
1:a:648:A:H2'	1:a:649:A:C8	2.55	0.41
1:a:674:G:C2	1:a:675:G:C8	3.09	0.41
1:a:722:G:H2'	1:a:723:A:H8	1.80	0.41
1:a:1267:C:C2	1:a:1269:G:C6	3.09	0.41
1:a:1322:A:C6	1:a:1323:G:C5	3.09	0.41
1:a:1417:U:H2'	1:a:1418:C:O4'	2.21	0.41
2:b:9:LEU:HD22	2:b:47:VAL:HG21	2.03	0.41
2:b:130:PRO:HG2	2:b:133:GLU:OE1	2.20	0.41
3:c:86:LEU:HD23	3:c:89:LYS:HE3	2.02	0.41
4:d:142:ARG:O	4:d:144:LYS:N	2.54	0.41
8:h:19:MET:SD	8:h:19:MET:C	3.04	0.41
9:i:87:ARG:HH21	9:i:108:ARG:CZ	2.34	0.41
11:k:45:SER:HB2	11:k:66:ALA:O	2.20	0.41
15:o:78:TYR:O	15:o:82:ILE:HG12	2.21	0.41
1:a:28:G:H2'	1:a:29:G:H8	1.85	0.41
1:a:557:C:H2'	1:a:558:G:C8	2.56	0.41
1:a:587:G:O2'	15:o:54:ARG:NH1	2.53	0.41
1:a:764:C:H2'	1:a:765:U:H6	1.85	0.41
1:a:963:G:C6	1:a:1240:A:N6	2.88	0.41
1:a:1115:C:H5''	2:b:97:LEU:HG	2.03	0.41
1:a:1441:C:C2	1:a:1483:G:C2	3.09	0.41
2:b:110:ARG:N	2:b:113:ARG:HH21	2.19	0.41
4:d:132:SER:OG	4:d:134:LYS:NZ	2.53	0.41
12:l:79:TYR:CD1	12:l:79:TYR:C	2.98	0.41
14:n:50:LYS:HE2	14:n:50:LYS:HB2	1.94	0.41
1:a:9:A:O2'	4:d:200:ARG:NE	2.54	0.41
1:a:263:G:P	17:q:73:LYS:HZ3	2.44	0.41
1:a:368:G:H2'	1:a:369:G:C8	2.56	0.41
1:a:400:G:C4	1:a:401:A:C8	3.09	0.41
1:a:662:G:C6	1:a:663:A:C5	3.08	0.41
1:a:681:G:C6	1:a:742:A:C2	3.08	0.41
1:a:707:C:H2'	1:a:708:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:755:U:O2'	1:a:757:A:H2	2.04	0.41
1:a:920:C:H2'	1:a:921:U:C6	2.55	0.41
1:a:1086:G:H2'	1:a:1087:U:C6	2.56	0.41
1:a:1279:G:O2'	1:a:1337:U:O2'	2.32	0.41
1:a:1330:A:C4	1:a:1334:G:C8	3.08	0.41
1:a:1420:C:H2'	1:a:1421:A:C8	2.53	0.41
1:a:1539:C:H2'	1:a:1540:U:C6	2.56	0.41
2:b:23:TRP:CZ3	2:b:25:PRO:HA	2.56	0.41
2:b:87:ALA:HB1	2:b:221:ILE:HG21	2.03	0.41
5:e:73:VAL:HG23	5:e:75:PRO:HD3	2.03	0.41
6:f:50:TYR:OH	18:r:68:ARG:O	2.35	0.41
7:g:63:GLU:O	7:g:66:ILE:HG13	2.21	0.41
7:g:86:GLN:H	7:g:151:PHE:HE1	1.68	0.41
9:i:10:GLY:O	9:i:21:VAL:HB	2.21	0.41
9:i:99:SER:HA	9:i:102:ARG:NH1	2.34	0.41
12:l:94:LEU:N	12:l:115:LEU:HD23	2.36	0.41
16:p:38:GLY:HA2	16:p:51:LYS:NZ	2.36	0.41
19:s:5:ILE:HD13	19:s:8:GLY:O	2.20	0.41
1:a:208:U:H5'	20:t:55:LYS:HG2	2.02	0.41
1:a:457:A:C5	1:a:495:A:C2	3.09	0.41
1:a:1169:C:H6	2:b:131:LYS:HG3	1.85	0.41
1:a:1272:A:C8	1:a:1286:A:C6	3.08	0.41
1:a:1320:G:H2'	1:a:1321:U:H6	1.86	0.41
2:b:61:SER:HB2	2:b:224:GLY:HA3	2.03	0.41
5:e:53:ALA:HB3	5:e:59:ALA:HB2	2.02	0.41
5:e:166:ASN:OD1	8:h:99:ASN:HB2	2.21	0.41
6:f:46:ARG:NH1	18:r:72:LEU:HA	2.36	0.41
10:j:80:THR:O	10:j:83:THR:HG22	2.21	0.41
13:m:52:GLU:HG2	13:m:55:ARG:HH21	1.86	0.41
20:t:41:ASN:N	20:t:41:ASN:ND2	2.69	0.41
1:a:127:A:OP1	17:q:4:ARG:NE	2.54	0.40
1:a:264:U:H2'	1:a:265:A:H8	1.85	0.40
1:a:342:C:H2'	1:a:343:C:C6	2.56	0.40
1:a:871:G:C5	1:a:872:C:C4	3.09	0.40
1:a:1082:U:H2'	1:a:1083:C:H6	1.86	0.40
1:a:1166:U:H2'	1:a:1167:G:O4'	2.21	0.40
1:a:1207:A:N1	3:c:161:ILE:HG21	2.36	0.40
1:a:1279:G:HO2'	1:a:1337:U:HO2'	1.61	0.40
1:a:1324:U:H2'	1:a:1325:C:H6	1.87	0.40
5:e:121:THR:OG1	5:e:122:ASP:N	2.54	0.40
6:f:11:ARG:HD2	6:f:87:ILE:CD1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:16:ASN:HA	8:h:19:MET:HG3	2.03	0.40
8:h:49:VAL:HA	8:h:62:LEU:HD12	2.02	0.40
11:k:25:SER:HA	11:k:30:THR:HA	2.02	0.40
1:a:477:U:H2'	1:a:478:G:O4'	2.22	0.40
1:a:583:G:C6	1:a:891:G:C6	3.10	0.40
1:a:746:U:H2'	1:a:747:C:C6	2.56	0.40
1:a:764:C:H2'	1:a:765:U:C6	2.56	0.40
1:a:781:G:H2'	1:a:782:G:C8	2.55	0.40
1:a:1059:G:O3'	14:n:4:THR:HG21	2.22	0.40
1:a:1149:A:C5	1:a:1151:U:O4'	2.73	0.40
2:b:72:THR:HG23	2:b:94:GLN:HA	2.03	0.40
3:c:116:ALA:HA	3:c:119:ILE:HG12	2.03	0.40
6:f:86:ILE:HD11	6:f:88:ARG:O	2.21	0.40
8:h:40:LEU:HB3	8:h:46:ILE:HG12	2.03	0.40
14:n:57:ARG:HH21	14:n:58:LYS:HA	1.86	0.40
18:r:56:TYR:HA	18:r:59:MET:SD	2.61	0.40
1:a:87:C:C4	1:a:88:U:H1'	2.57	0.40
1:a:133:U:C2	1:a:238:G:N1	2.90	0.40
1:a:682:G:C1'	18:r:68:ARG:HH22	2.35	0.40
1:a:1220:C:O2'	1:a:1225:U:O4	2.27	0.40
1:a:1277:G:C2	1:a:1281:G:C6	3.09	0.40
1:a:1510:U:H1'	1:a:1511:A:N7	2.36	0.40
4:d:118:HIS:CE1	4:d:141:VAL:HB	2.56	0.40
5:e:62:LYS:HA	5:e:65:GLU:HG2	2.02	0.40
8:h:94:MET:HG3	8:h:95:PRO:HD2	2.03	0.40
9:i:131:LYS:HG3	9:i:132:ARG:HG3	2.04	0.40
10:j:14:ASP:HB2	10:j:17:VAL:HG12	2.03	0.40
11:k:35:THR:HG22	11:k:41:ALA:HA	2.02	0.40
11:k:35:THR:HA	11:k:40:ASN:O	2.21	0.40
1:a:699:G:H2'	1:a:700:U:C5	2.57	0.40
1:a:918:A:H2'	1:a:919:A:H8	1.86	0.40
1:a:1116:G:P	2:b:110:ARG:HH21	2.45	0.40
1:a:1132:C:C2	1:a:1133:U:C5	3.09	0.40
1:a:1133:U:C2	1:a:1164:G:N2	2.90	0.40
1:a:1227:A:OP1	14:n:2:ALA:HB3	2.21	0.40
2:b:96:TRP:CH2	2:b:100:LEU:HB2	2.57	0.40
2:b:209:ALA:O	2:b:213:LEU:HG	2.21	0.40
2:b:218:ALA:O	2:b:221:ILE:HG22	2.22	0.40
19:s:40:ILE:HA	19:s:44:PHE:HD2	1.87	0.40
19:s:41:PHE:HB2	19:s:42:PRO:CD	2.51	0.40
1:a:80:A:N6	1:a:81:A:C6	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:125:G:C6	1:a:244:G:O6	2.75	0.40
1:a:754:G:C6	1:a:755:U:N3	2.90	0.40
1:a:949:G:H2'	1:a:950:C:C6	2.56	0.40
1:a:1176:U:H2'	1:a:1177:G:O4'	2.21	0.40
5:e:32:ARG:HE	5:e:52:LYS:HD3	1.86	0.40
12:l:46:VAL:HA	12:l:92:VAL:HA	2.03	0.40
12:l:115:LEU:HD12	12:l:116:ASP:H	1.85	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	
2	b	222/255 (87%)	207 (93%)	15 (7%)	0	100	100
3	c	205/217 (94%)	195 (95%)	10 (5%)	0	100	100
4	d	188/200 (94%)	179 (95%)	9 (5%)	0	100	100
5	e	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
6	f	94/98 (96%)	88 (94%)	6 (6%)	0	100	100
7	g	143/156 (92%)	132 (92%)	11 (8%)	0	100	100
8	h	129/132 (98%)	125 (97%)	3 (2%)	1 (1%)	16	48
9	i	126/132 (96%)	118 (94%)	8 (6%)	0	100	100
10	j	100/102 (98%)	91 (91%)	9 (9%)	0	100	100
11	k	116/129 (90%)	112 (97%)	4 (3%)	0	100	100
12	l	133/137 (97%)	118 (89%)	14 (10%)	1 (1%)	16	48
13	m	107/121 (88%)	100 (94%)	6 (6%)	1 (1%)	14	45
14	n	58/61 (95%)	50 (86%)	8 (14%)	0	100	100
15	o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	p	88/91 (97%)	82 (93%)	6 (7%)	0	100	100
17	q	84/87 (97%)	70 (83%)	14 (17%)	0	100	100
18	r	68/80 (85%)	64 (94%)	4 (6%)	0	100	100
19	s	82/92 (89%)	74 (90%)	8 (10%)	0	100	100
20	t	78/83 (94%)	76 (97%)	2 (3%)	0	100	100
All	All	2269/2428 (94%)	2118 (93%)	148 (6%)	3 (0%)	49	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	h	116	LYS
12	l	29	ASN
13	m	83	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	194/221 (88%)	192 (99%)	2 (1%)	68	74
3	c	169/175 (97%)	169 (100%)	0	100	100
4	d	169/175 (97%)	169 (100%)	0	100	100
5	e	130/131 (99%)	130 (100%)	0	100	100
6	f	84/86 (98%)	84 (100%)	0	100	100
7	g	126/132 (96%)	126 (100%)	0	100	100
8	h	112/113 (99%)	112 (100%)	0	100	100
9	i	106/109 (97%)	105 (99%)	1 (1%)	70	75
10	j	91/91 (100%)	91 (100%)	0	100	100
11	k	94/104 (90%)	94 (100%)	0	100	100
12	l	117/119 (98%)	111 (95%)	6 (5%)	21	47
13	m	94/104 (90%)	91 (97%)	3 (3%)	34	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	n	51/53 (96%)	49 (96%)	2 (4%)	28	53
15	o	80/81 (99%)	80 (100%)	0	100	100
16	p	76/77 (99%)	76 (100%)	0	100	100
17	q	81/82 (99%)	81 (100%)	0	100	100
18	r	63/68 (93%)	63 (100%)	0	100	100
19	s	73/80 (91%)	67 (92%)	6 (8%)	10	36
20	t	67/69 (97%)	66 (98%)	1 (2%)	57	68
All	All	1977/2070 (96%)	1956 (99%)	21 (1%)	63	73

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	127	GLU
2	b	129	LEU
9	i	115	ARG
12	l	24	LEU
12	l	33	LYS
12	l	115	LEU
12	l	116	ASP
12	l	117	THR
12	l	132	THR
13	m	44	ARG
13	m	82	GLU
13	m	85	SER
14	n	57	ARG
14	n	58	LYS
19	s	6	LYS
19	s	7	LYS
19	s	11	VAL
19	s	43	ASN
19	s	44	PHE
19	s	45	ILE
20	t	41	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	15	HIS

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Mol	Chain	Res	Type
2	b	24	ASN
2	b	94	GLN
3	c	61	ASN
4	d	70	ASN
4	d	116	HIS
4	d	192	GLN
7	g	67	ASN
7	g	106	ASN
7	g	142	HIS
9	i	29	ASN
9	i	77	GLN
11	k	40	ASN
12	l	29	ASN
12	l	77	ASN
12	l	85	HIS
13	m	76	ASN
15	o	9	ASN
15	o	37	ASN
15	o	51	HIS
16	p	72	HIS
17	q	5	ASN
19	s	83	HIS
20	t	21	ASN
20	t	41	ASN
20	t	42	ASN
20	t	69	ASN
20	t	82	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1546/1547 (99%)	258 (16%)	0

All (258) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	10	G
1	a	11	A
1	a	17	A
1	a	32	G
1	a	33	A

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Mol	Chain	Res	Type
1	a	40	G
1	a	48	C
1	a	49	C
1	a	51	A
1	a	52	A
1	a	60	A
1	a	69	G
1	a	82	G
1	a	88	U
1	a	89	U
1	a	92	C
1	a	94	G
1	a	95	A
1	a	102	C
1	a	108	A
1	a	120	C
1	a	129	A
1	a	130	A
1	a	131	C
1	a	137	U
1	a	144	C
1	a	154	U
1	a	156	C
1	a	159	G
1	a	163	C
1	a	173	U
1	a	182	A
1	a	183	U
1	a	185	U
1	a	196	A
1	a	211	A
1	a	213	G
1	a	219	C
1	a	221	U
1	a	222	G
1	a	234	A
1	a	248	U
1	a	249	G
1	a	255	G
1	a	258	A
1	a	259	G
1	a	274	G

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Mol	Chain	Res	Type
1	a	275	C
1	a	277	U
1	a	287	A
1	a	297	G
1	a	336	C
1	a	355	G
1	a	360	C
1	a	362	G
1	a	364	A
1	a	375	U
1	a	380	C
1	a	405	A
1	a	406	C
1	a	414	G
1	a	420	U
1	a	421	G
1	a	422	A
1	a	423	A
1	a	429	U
1	a	432	G
1	a	437	U
1	a	444	C
1	a	446	G
1	a	447	U
1	a	448	U
1	a	456	A
1	a	457	A
1	a	460	A
1	a	462	A
1	a	466	G
1	a	470	A
1	a	471	A
1	a	477	U
1	a	480	G
1	a	482	A
1	a	483	C
1	a	492	G
1	a	493	G
1	a	503	A
1	a	505	A
1	a	517	A
1	a	519	C

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Mol	Chain	Res	Type
1	a	520	U
1	a	529	G
1	a	535	G
1	a	538	G
1	a	539	U
1	a	540	A
1	a	555	A
1	a	558	G
1	a	567	A
1	a	570	U
1	a	571	A
1	a	580	A
1	a	581	A
1	a	583	G
1	a	584	C
1	a	585	G
1	a	595	G
1	a	596	G
1	a	604	A
1	a	641	U
1	a	649	A
1	a	661	U
1	a	669	G
1	a	673	A
1	a	674	G
1	a	695	A
1	a	700	U
1	a	703	A
1	a	710	A
1	a	716	A
1	a	724	A
1	a	739	G
1	a	741	G
1	a	742	A
1	a	757	A
1	a	762	C
1	a	763	G
1	a	785	A
1	a	800	A
1	a	807	G
1	a	821	U
1	a	825	C

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Mol	Chain	Res	Type
1	a	836	A
1	a	840	G
1	a	854	C
1	a	855	G
1	a	856	C
1	a	861	U
1	a	863	G
1	a	865	G
1	a	882	A
1	a	886	A
1	a	899	A
1	a	901	U
1	a	912	G
1	a	944	C
1	a	970	U
1	a	975	A
1	a	979	A
1	a	981	G
1	a	985	A
1	a	986	G
1	a	988	A
1	a	992	U
1	a	993	A
1	a	999	U
1	a	1001	U
1	a	1002	U
1	a	1003	G
1	a	1014	A
1	a	1016	A
1	a	1025	G
1	a	1027	U
1	a	1028	A
1	a	1034	U
1	a	1035	U
1	a	1036	C
1	a	1038	C
1	a	1039	C
1	a	1041	U
1	a	1042	C
1	a	1044	G
1	a	1047	G
1	a	1057	C

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Mol	Chain	Res	Type
1	a	1073	G
1	a	1076	G
1	a	1077	U
1	a	1090	U
1	a	1096	G
1	a	1106	G
1	a	1107	U
1	a	1113	A
1	a	1124	C
1	a	1142	A
1	a	1144	C
1	a	1150	G
1	a	1151	U
1	a	1152	U
1	a	1153	G
1	a	1166	U
1	a	1169	C
1	a	1170	U
1	a	1171	G
1	a	1172	C
1	a	1179	C
1	a	1192	G
1	a	1195	G
1	a	1204	G
1	a	1207	A
1	a	1208	A
1	a	1223	U
1	a	1225	U
1	a	1235	U
1	a	1238	A
1	a	1249	A
1	a	1251	U
1	a	1252	G
1	a	1268	A
1	a	1271	G
1	a	1272	A
1	a	1281	G
1	a	1291	A
1	a	1297	U
1	a	1298	A
1	a	1304	G
1	a	1310	A

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Mol	Chain	Res	Type
1	a	1313	U
1	a	1314	C
1	a	1315	G
1	a	1316	G
1	a	1328	C
1	a	1329	A
1	a	1330	A
1	a	1331	C
1	a	1332	U
1	a	1333	C
1	a	1334	G
1	a	1346	C
1	a	1347	U
1	a	1357	A
1	a	1358	G
1	a	1359	U
1	a	1371	A
1	a	1375	U
1	a	1381	G
1	a	1385	A
1	a	1405	A
1	a	1409	A
1	a	1410	C
1	a	1412	G
1	a	1430	G
1	a	1436	A
1	a	1437	A
1	a	1453	G
1	a	1457	A
1	a	1459	C
1	a	1463	U
1	a	1465	A
1	a	1492	A
1	a	1496	U
1	a	1511	A
1	a	1515	A
1	a	1518	U
1	a	1519	A
1	a	1535	G
1	a	1541	G
1	a	1542	G
1	a	1547	C

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Mol	Chain	Res	Type
1	a	1549	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

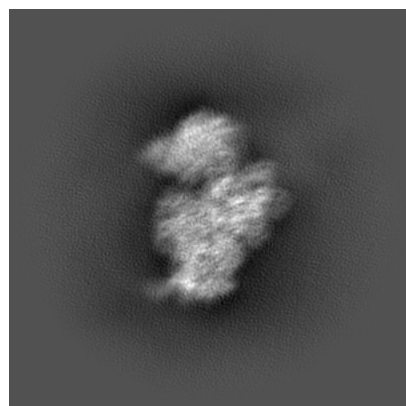
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16048. These allow visual inspection of the internal detail of the map and identification of artifacts.

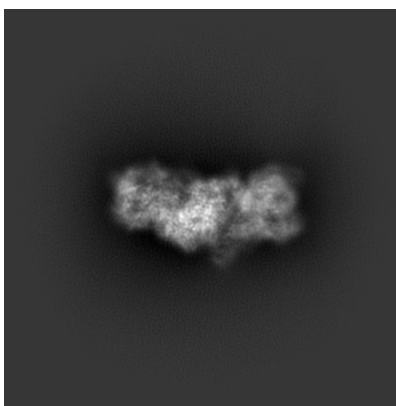
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

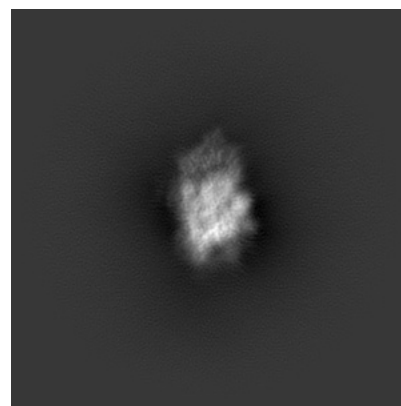
6.1.1 Primary map



X

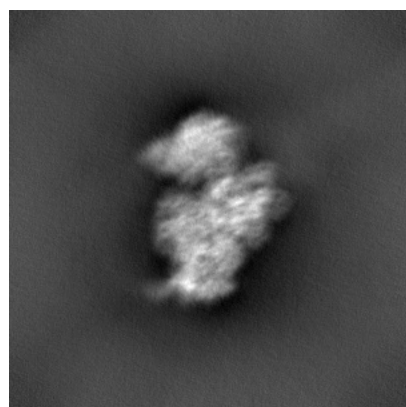


Y

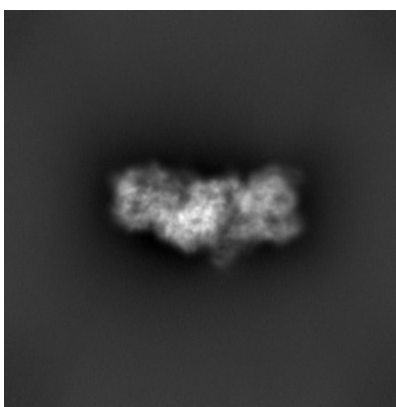


Z

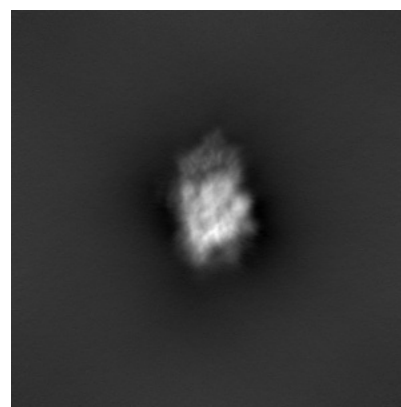
6.1.2 Raw map



X



Y

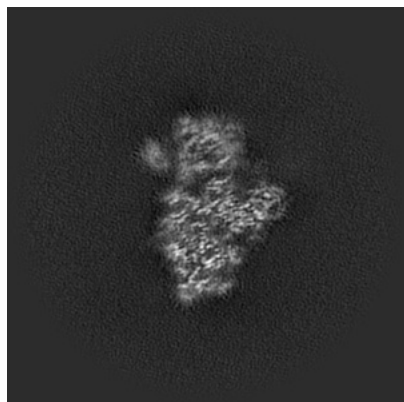


Z

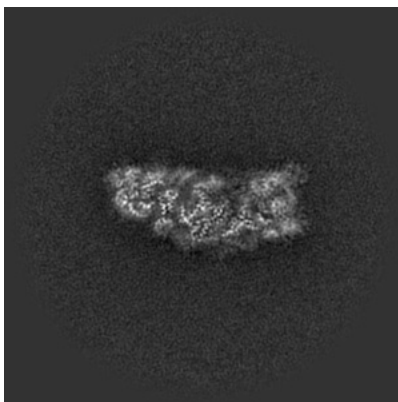
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

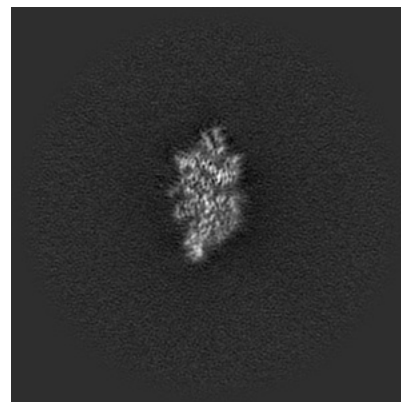
6.2.1 Primary map



X Index: 192

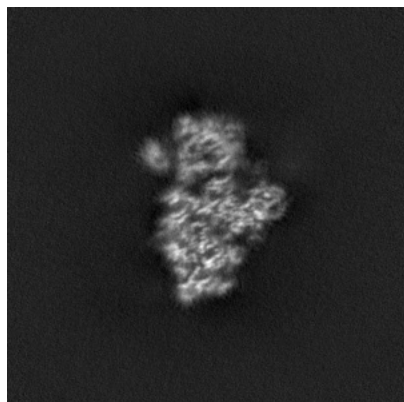


Y Index: 192

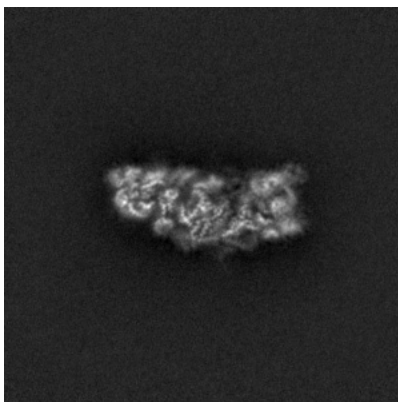


Z Index: 192

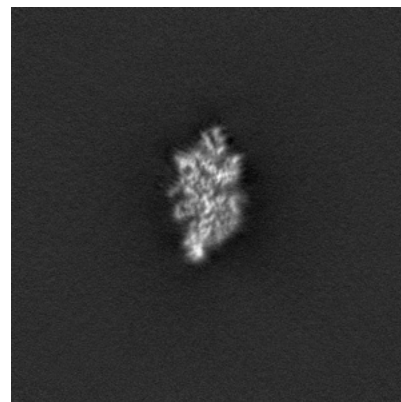
6.2.2 Raw map



X Index: 192



Y Index: 192

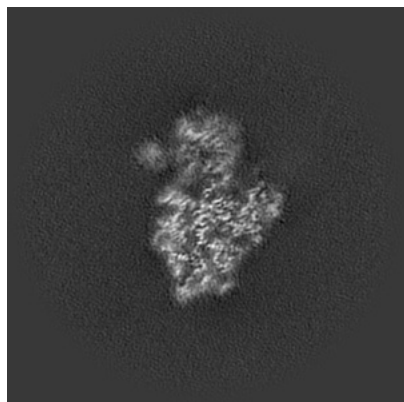


Z Index: 192

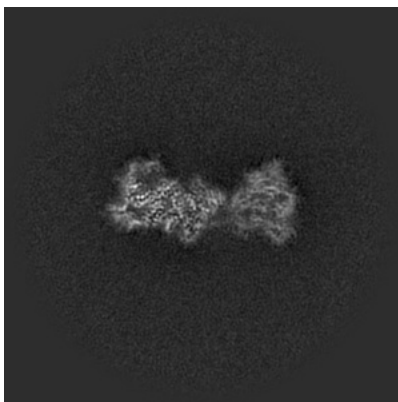
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

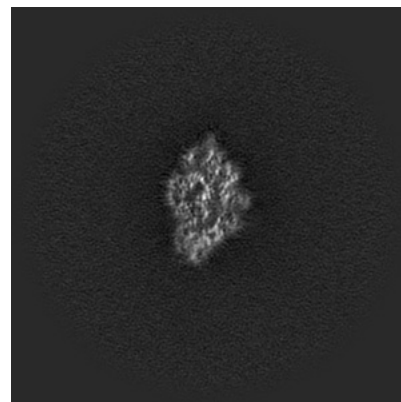
6.3.1 Primary map



X Index: 188

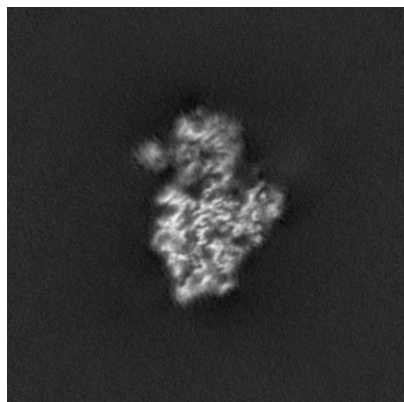


Y Index: 170

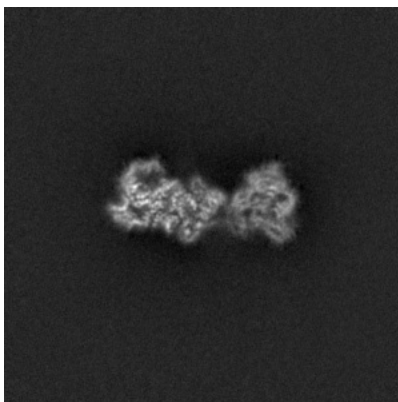


Z Index: 181

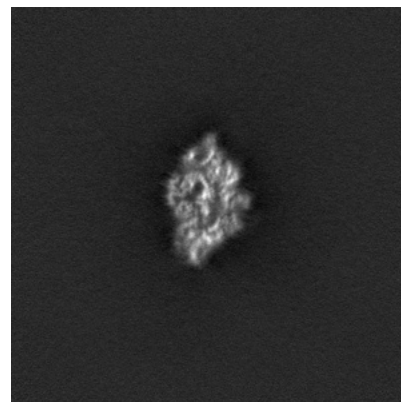
6.3.2 Raw map



X Index: 188



Y Index: 171

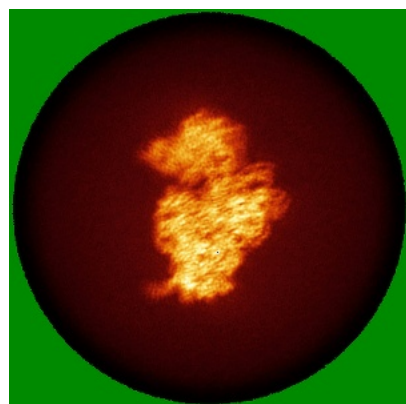


Z Index: 182

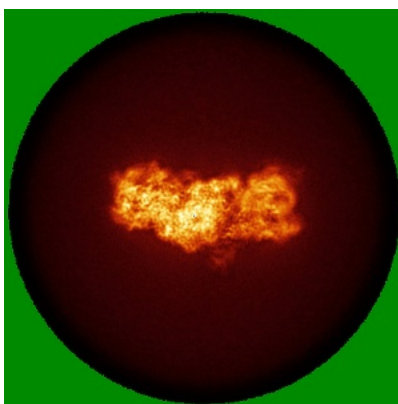
The images above show the largest variance slices of the map in three orthogonal directions.

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

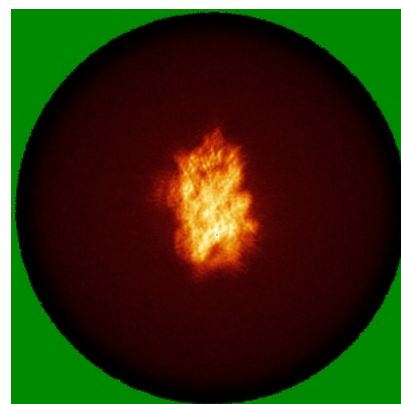
6.4.1 Primary map



X



Y

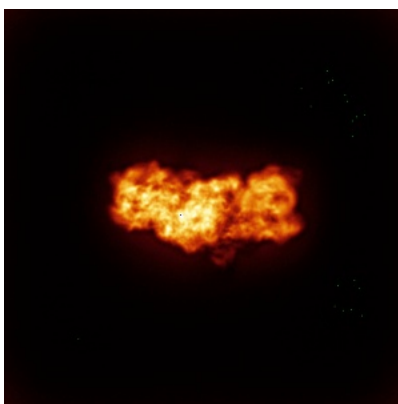


Z

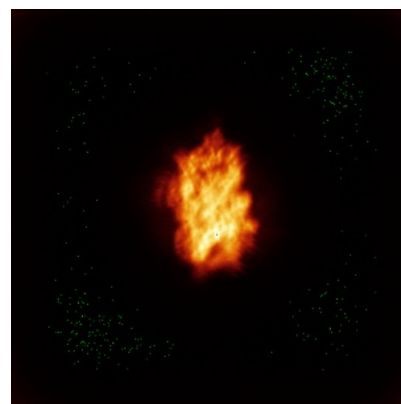
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.423. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

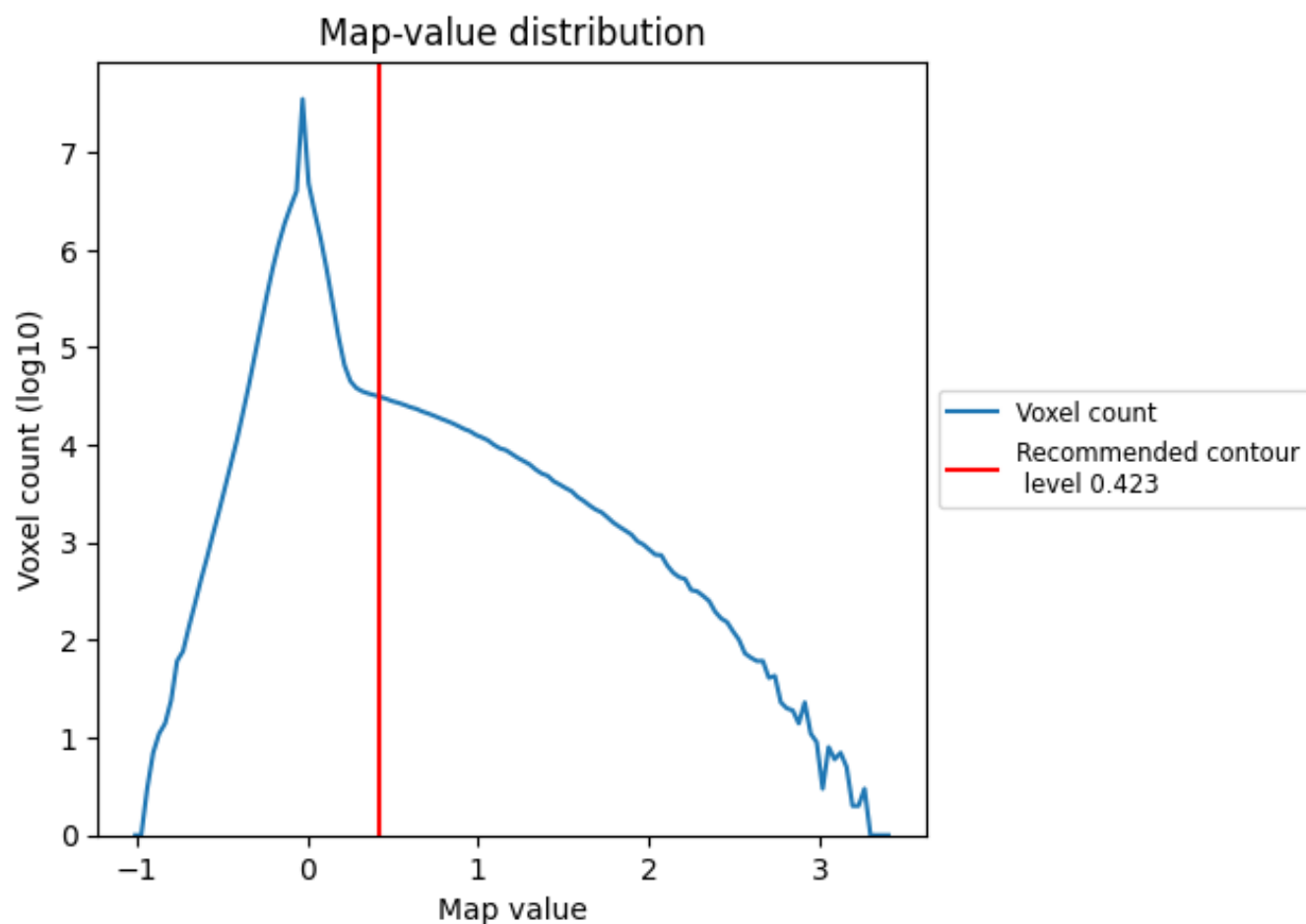
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

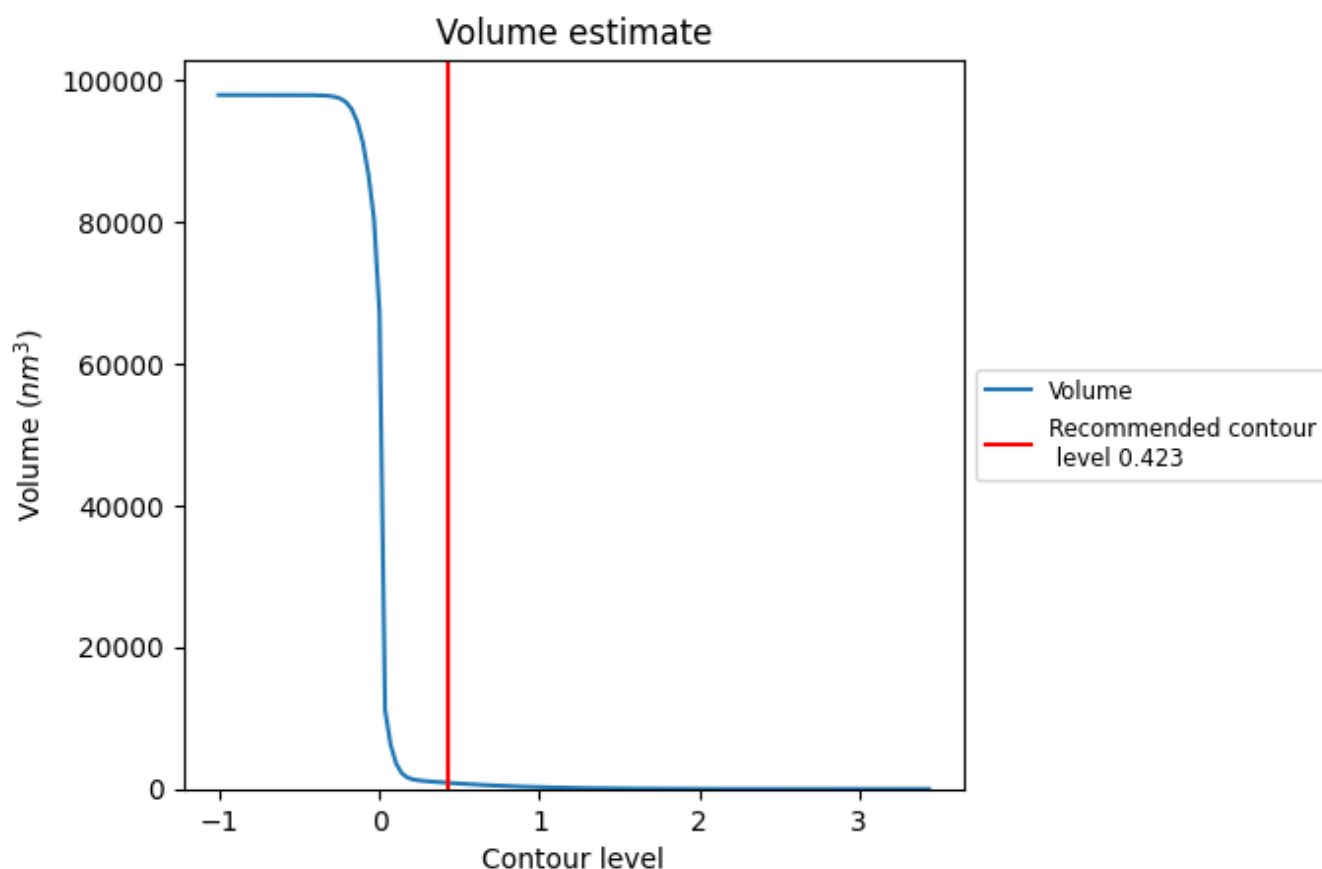
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

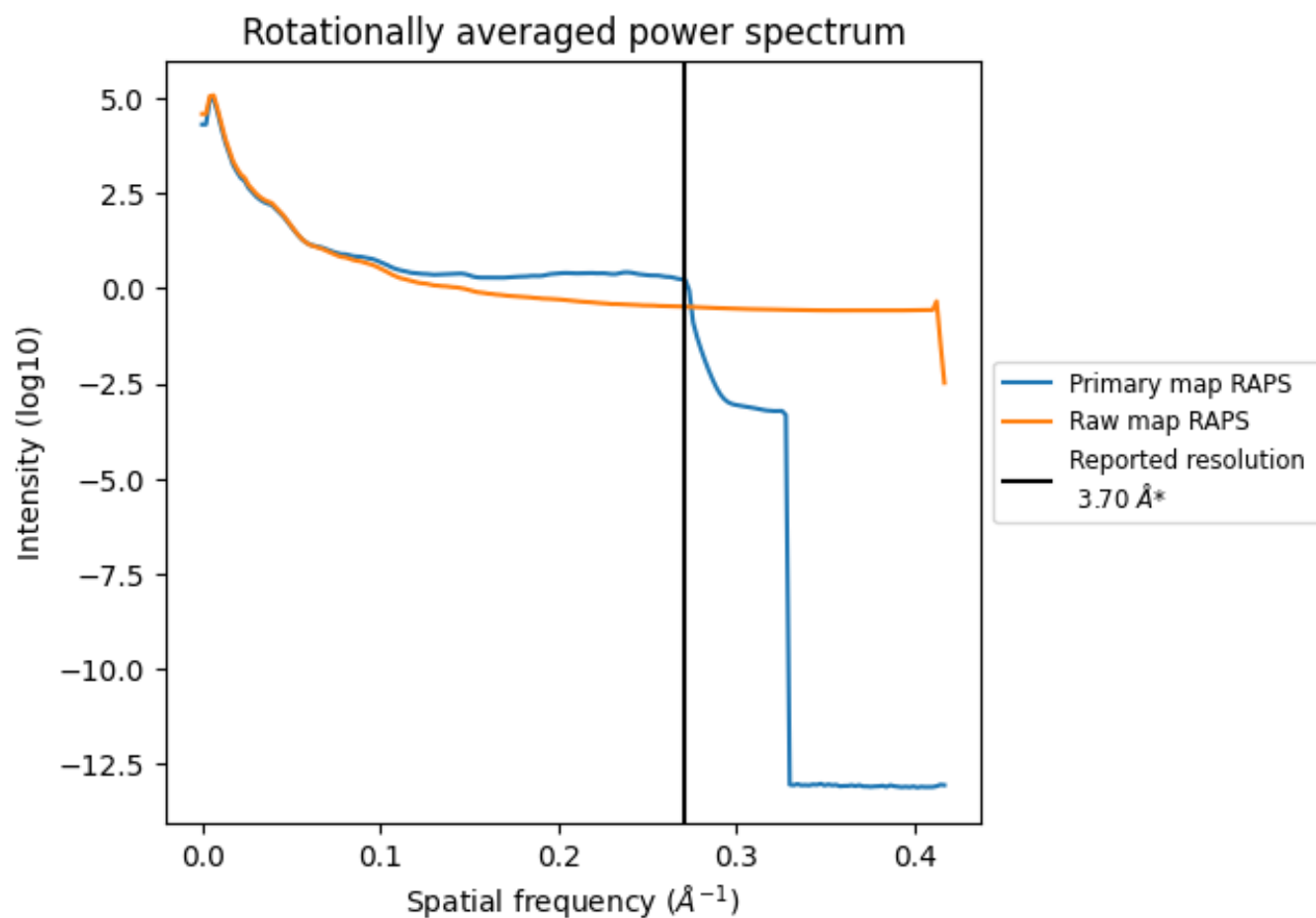
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 874 nm^3 ; this corresponds to an approximate mass of 789 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

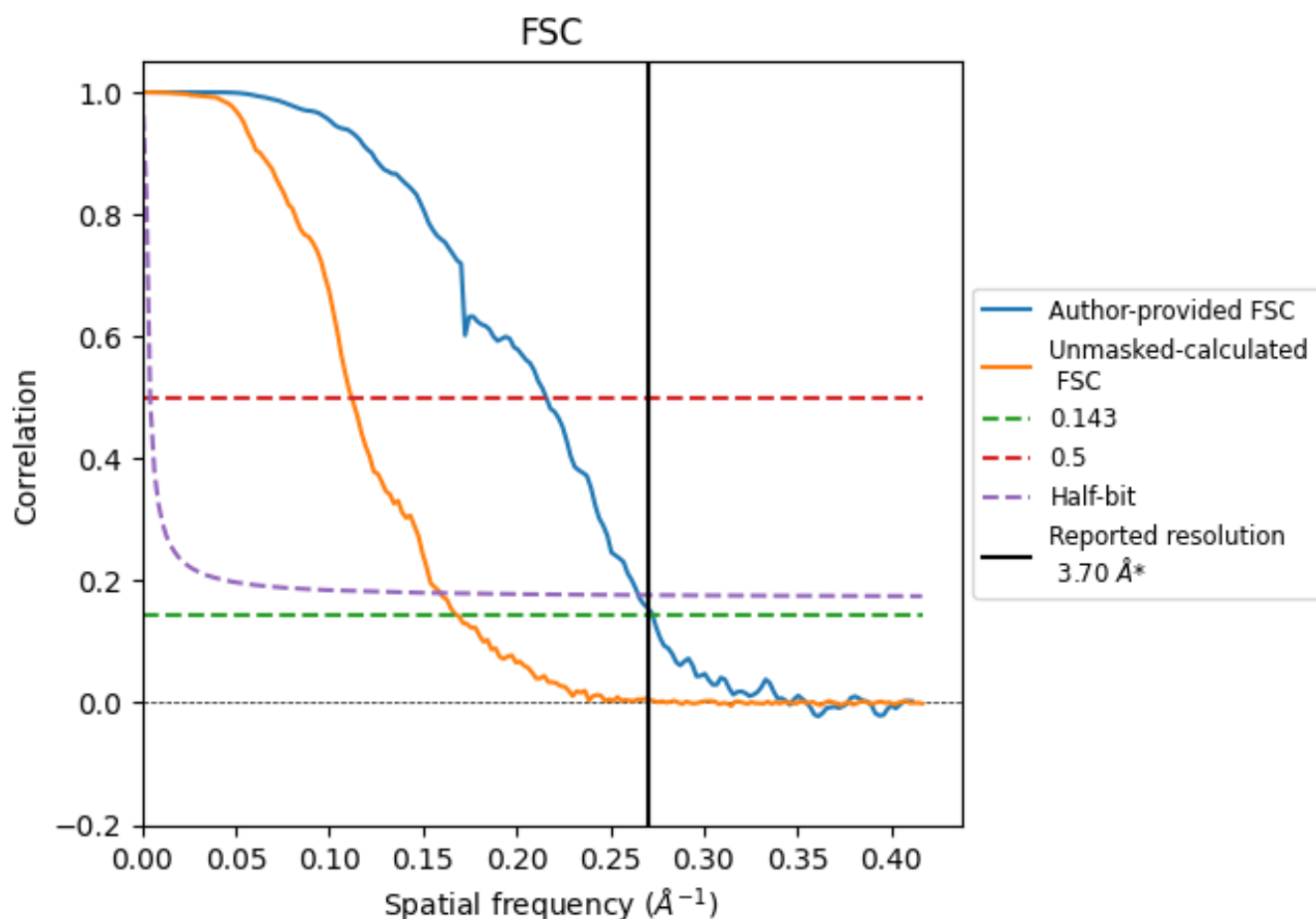


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

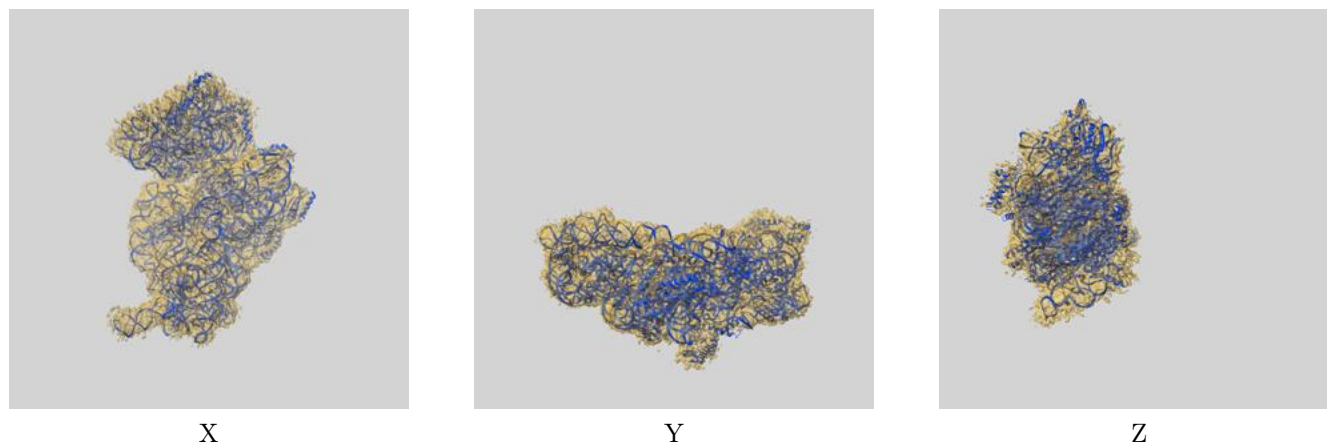
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.67	4.63	3.77
Unmasked-calculated*	5.94	8.94	6.28

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.94 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

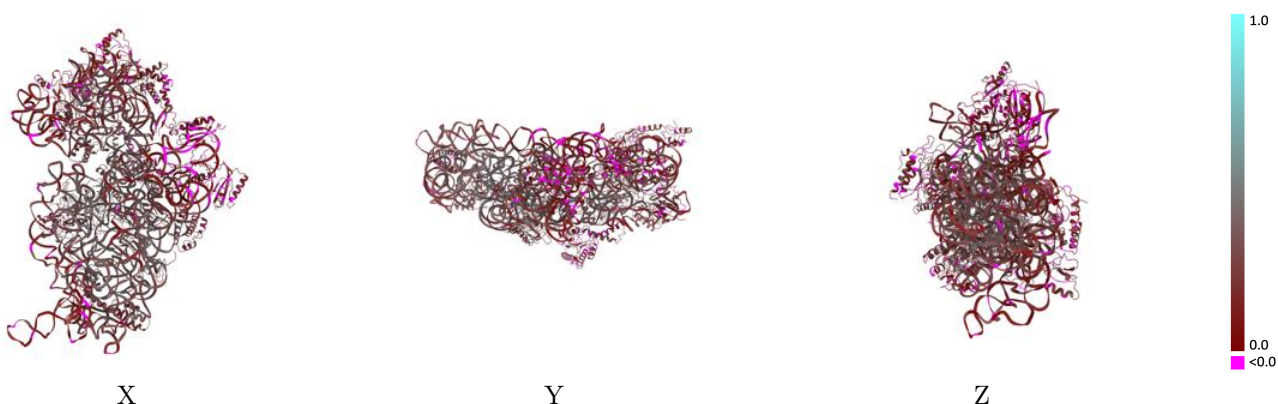
This section contains information regarding the fit between EMDB map EMD-16048 and PDB model 8BH6. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



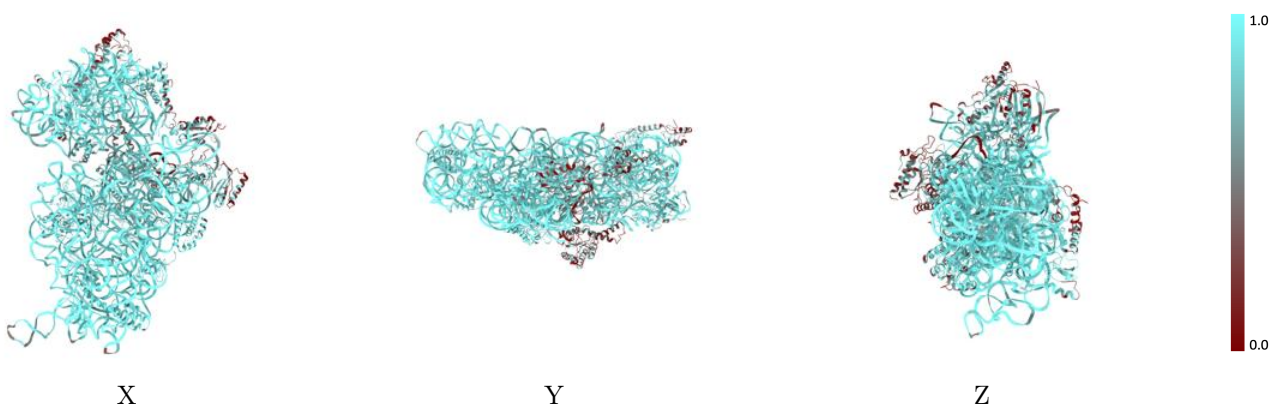
The images above show the 3D surface view of the map at the recommended contour level 0.423 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



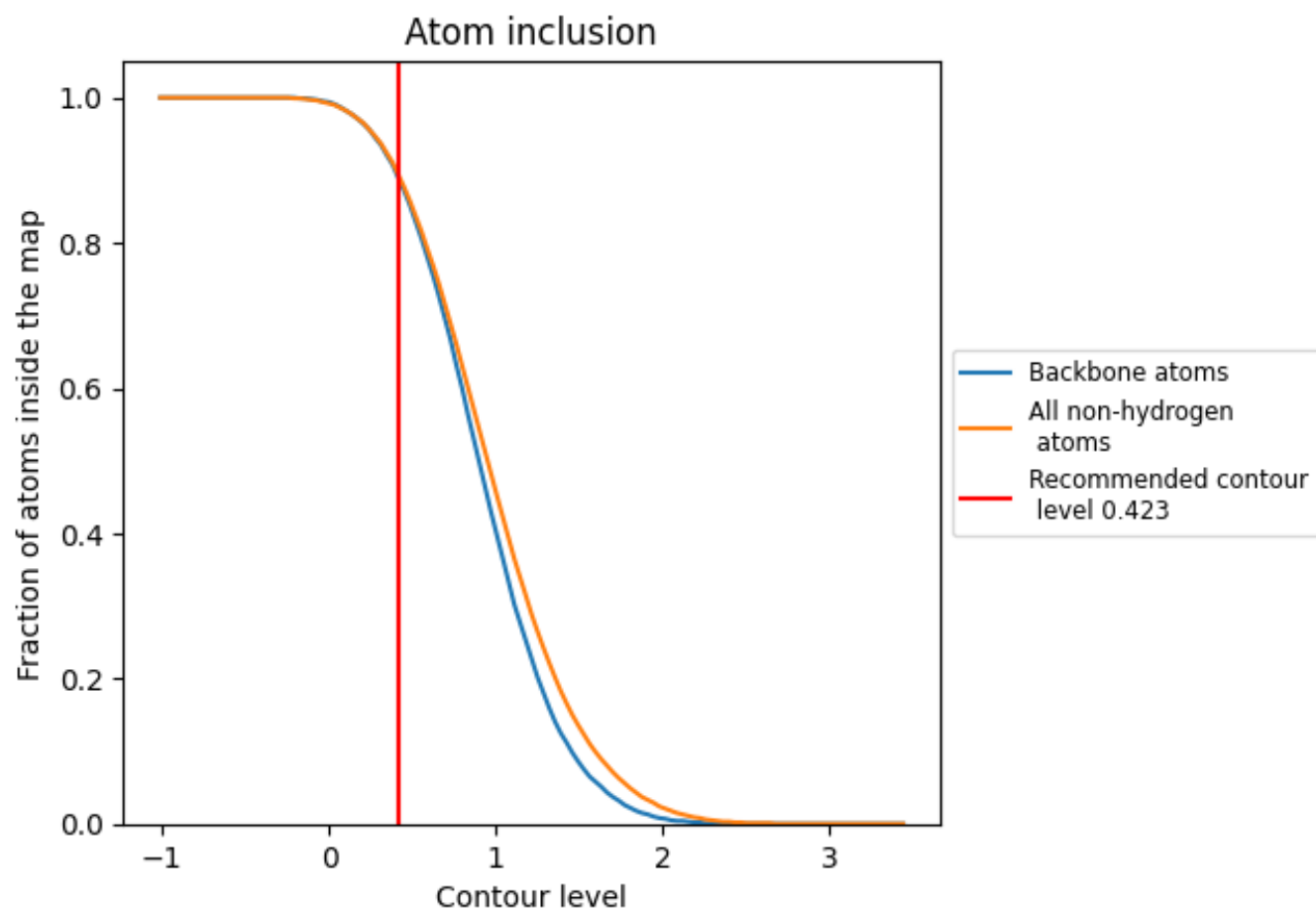
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.423).

9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.423) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.2540
a	 0.9540	 0.2660
b	 0.3760	 0.1820
c	 0.7810	 0.2580
d	 0.9250	 0.2630
e	 0.8510	 0.3470
f	 0.4860	 0.1080
g	 0.7930	 0.1780
h	 0.9370	 0.3300
i	 0.8470	 0.2060
j	 0.8790	 0.2450
k	 0.5530	 0.0970
l	 0.9390	 0.3400
m	 0.5780	 0.1400
n	 0.9790	 0.2830
o	 0.9180	 0.2380
p	 0.9440	 0.3100
q	 0.9390	 0.3380
r	 0.5120	 0.0660
s	 0.8680	 0.1810
t	 0.9600	 0.2890

