



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:38 PM UTC

PDB ID : 7QGU / pdb_00007qgu
EMDB ID : EMD-13959
Title : Structure of the B. subtilis disome - stalled 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-10
Resolution : 4.75 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

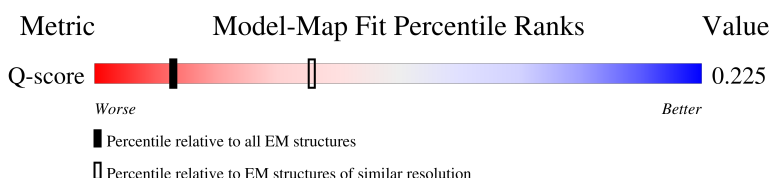
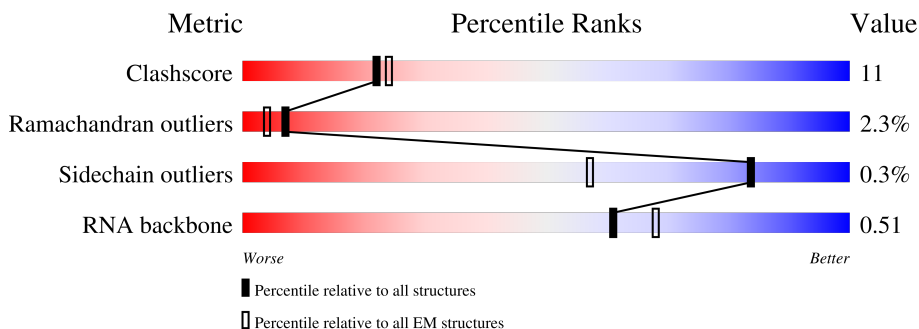
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.75 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	1613 (4.25 - 5.25)

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	2928	50% 36% 13%
2	B	119	51% 33% 9% 6%
3	C	277	40% 61% 37% ..

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Mol	Chain	Length	Quality of chain
4	D	208	
5	E	207	
6	F	179	
7	G	179	
8	H	166	
9	I	141	
10	J	145	
11	K	122	
12	L	146	
13	M	144	
14	N	120	
15	O	120	
16	P	115	
17	Q	119	
18	R	102	
19	S	113	
20	T	95	
21	U	103	
22	V	94	
23	X	149	
24	Y	62	
25	Z	66	
26	a	59	
27	b	59	
28	c	49	

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Mol	Chain	Length	Quality of chain
29	d	44	
30	e	66	
31	f	37	
32	W	1555	
33	g	246	
34	h	218	
35	i	200	
36	j	166	
37	k	95	
38	l	156	
39	m	132	
40	n	130	
41	o	102	
42	p	131	
43	q	138	
44	r	121	
45	s	61	
46	t	89	
47	u	90	
48	v	87	
49	w	79	
50	x	92	
51	y	88	
52	z	77	
53	2	95	

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Mol	Chain	Length	Quality of chain
54	3	66	9% 50% 17% • 32%

2 Entry composition [i](#)

There are 54 unique types of molecules in this entry. The entry contains 135606 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1558	C	G	conflict	GB 1864548803

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 7 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	154	THR	ALA	variant	UNP A0A063X7V1

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 23 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	149	Total	C	N	O		0	0
			733	435	149	149			

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	g	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	h	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	i	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	j	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	l	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	m	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	n	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	o	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	p	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	q	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	u	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	v	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	w	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	x	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	y	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 52 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 53 is a protein called YqzJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	24	Total	C	N	O	S	0	0
			107	64	28	14	1		

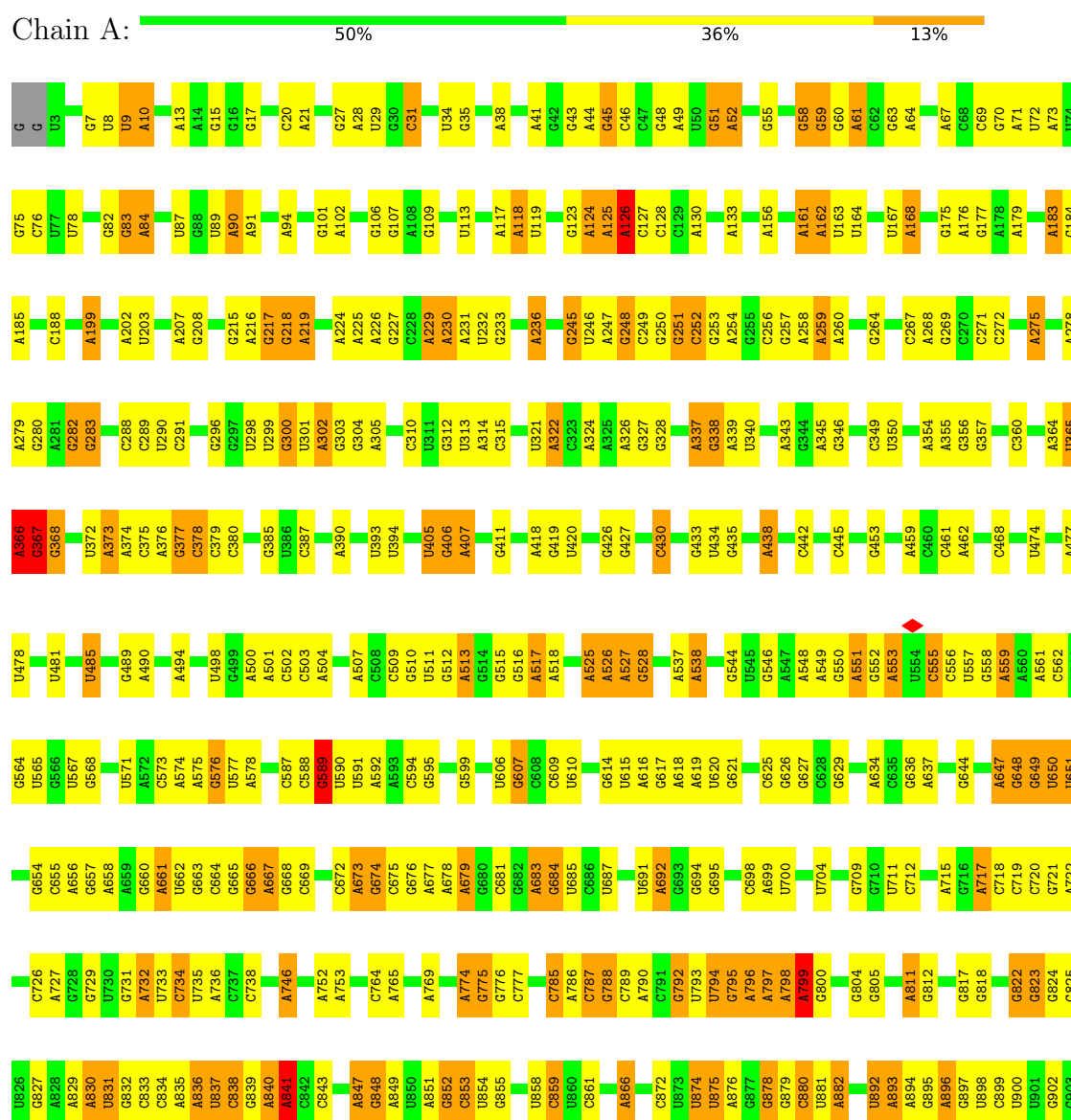
- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	45	Total	C	N	O	S	0	0
			366	227	66	71	2		

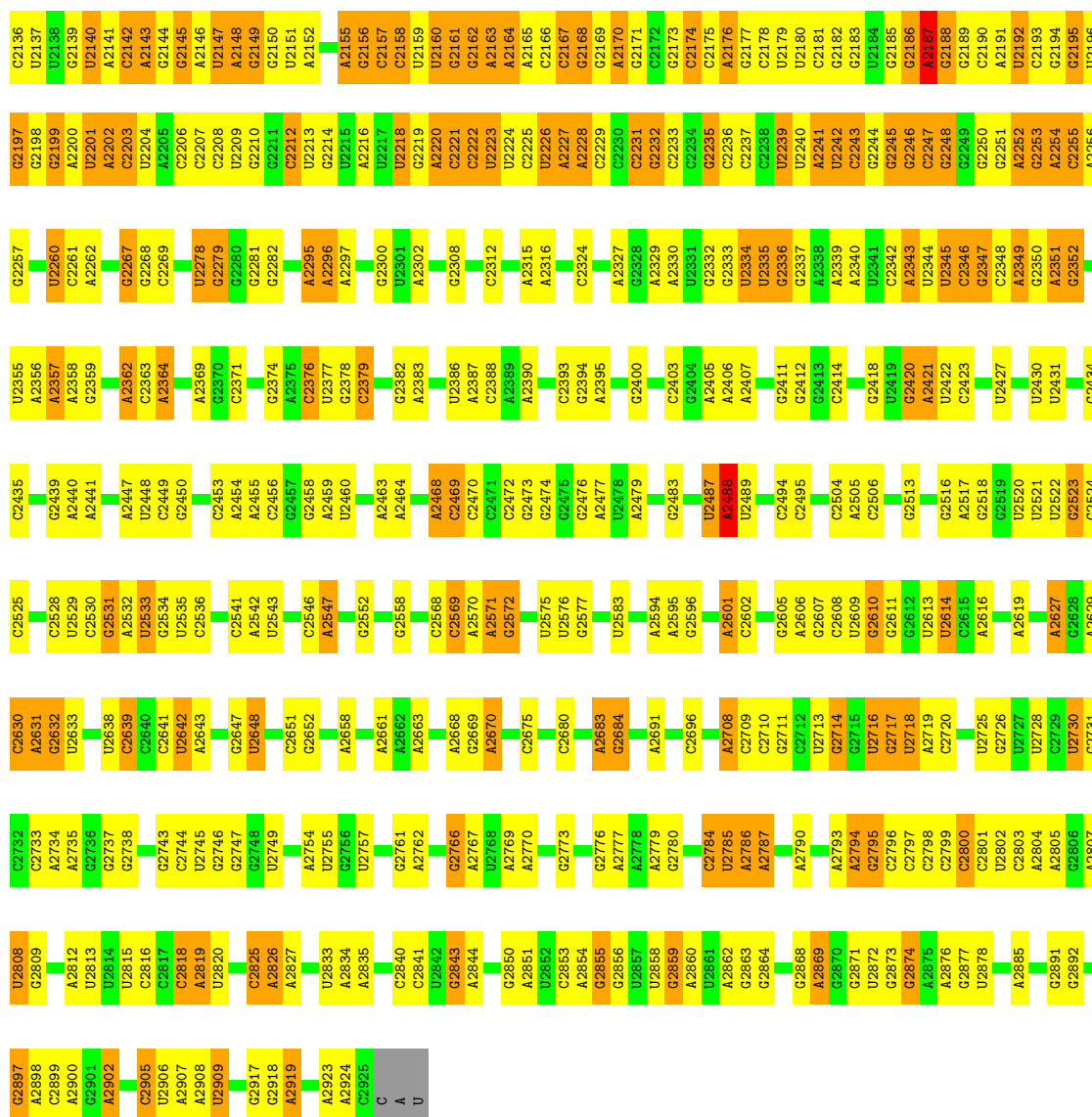
3 Residue-property plots

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: 23S rRNA

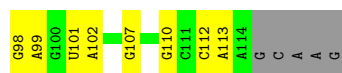






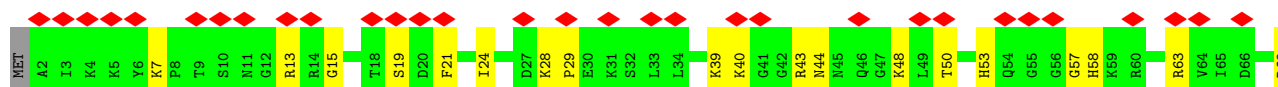
• Molecule 2: 5S rRNA

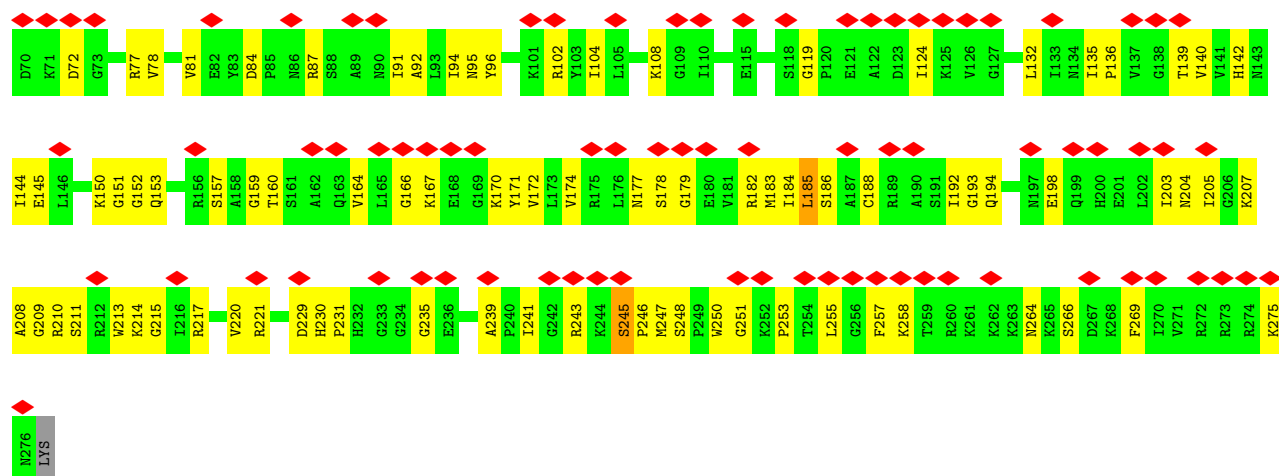
Chain B: 51% 33% 9% 6%



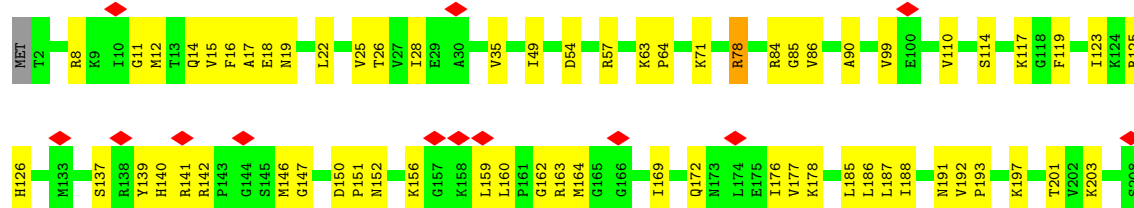
• Molecule 3: 50S ribosomal protein L2

Chain C: 40% 61% 37%

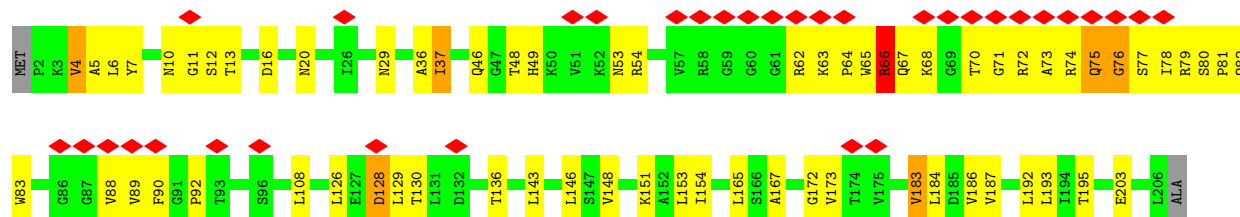




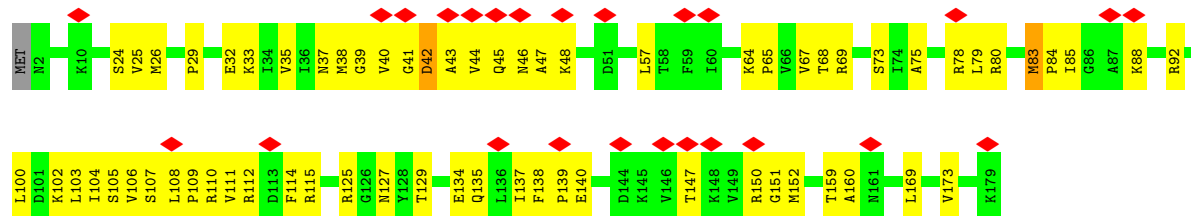
• Molecule 4: 50S ribosomal protein L3



• Molecule 5: 50S ribosomal protein L4

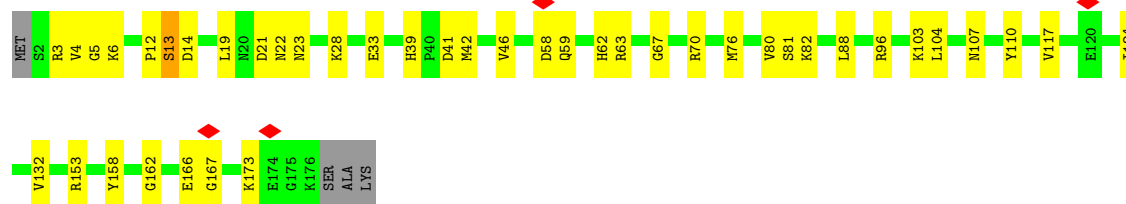


• Molecule 6: 50S ribosomal protein L5



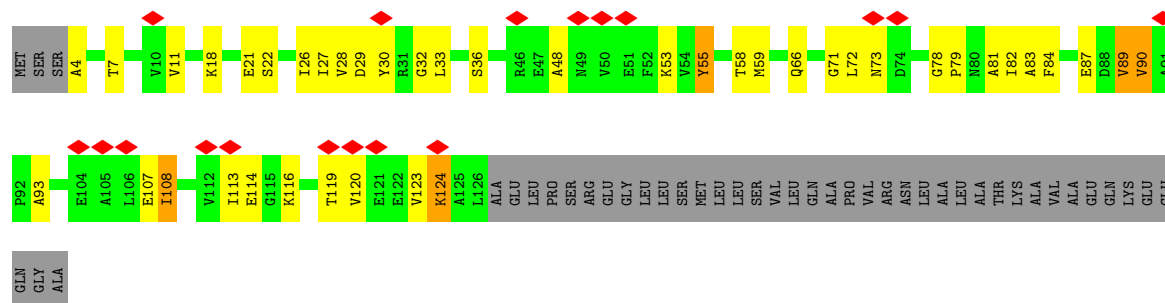
• Molecule 7: Ribosomal protein L6

Chain G:  74% 23% ..



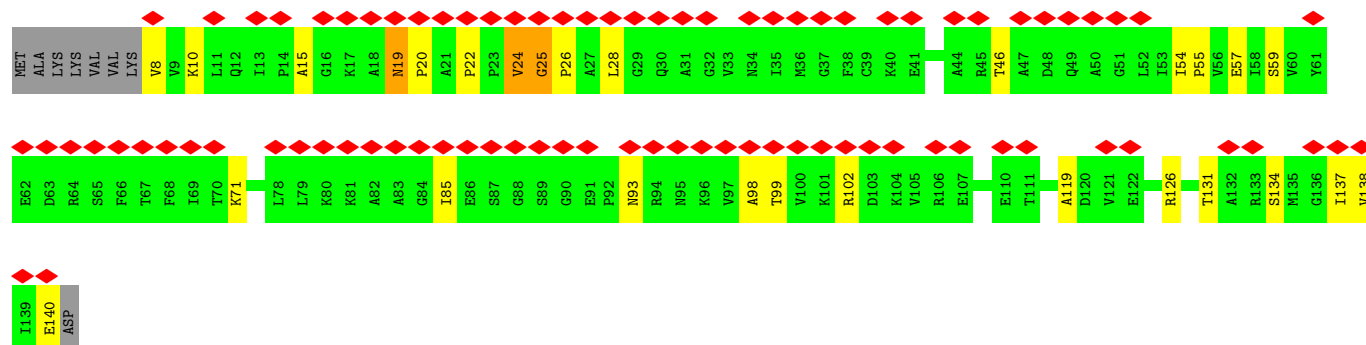
• Molecule 8: 50S ribosomal protein L10

Chain H:  11% 49% 22% 26%



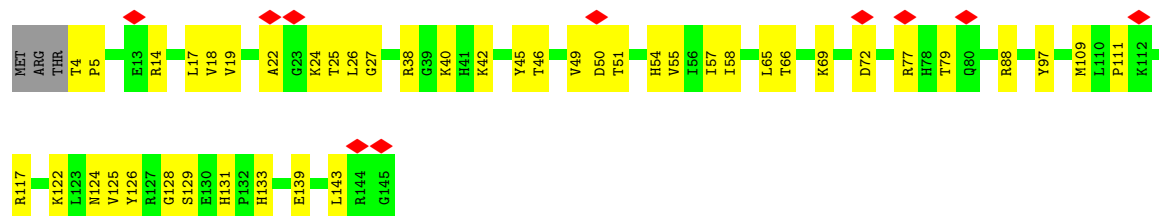
• Molecule 9: 50S ribosomal protein L11

Chain I:  60% 74% 18% 6%

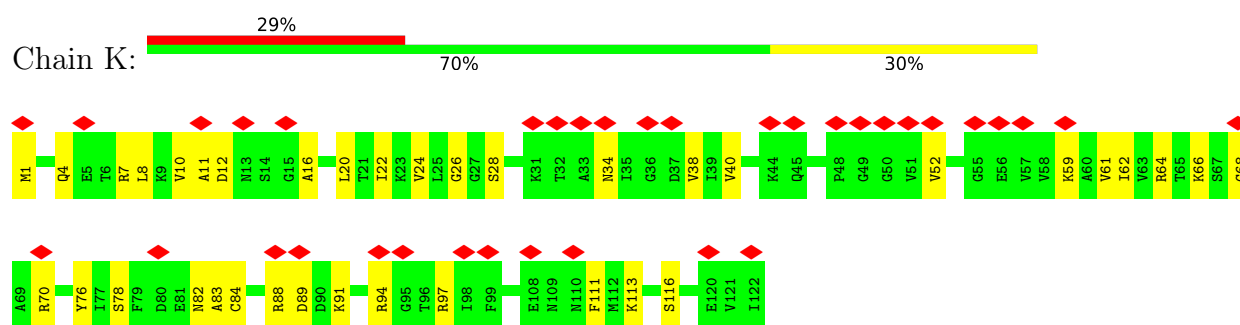


• Molecule 10: 50S ribosomal protein L13

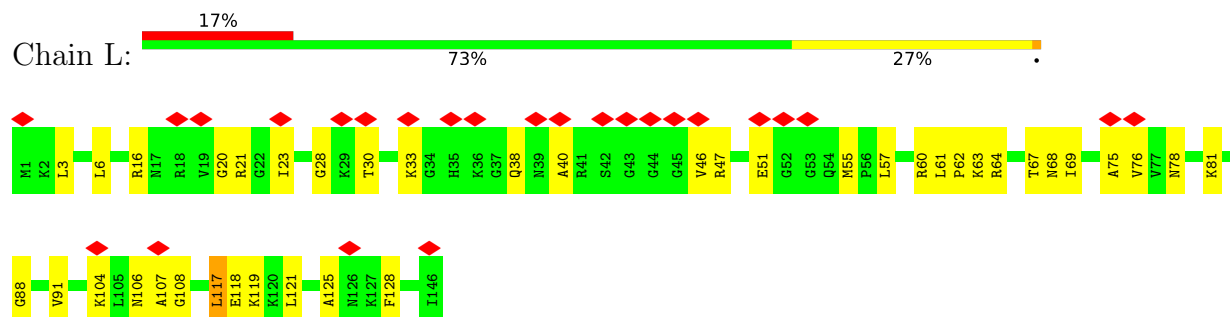
Chain J:  7% 68% 30%



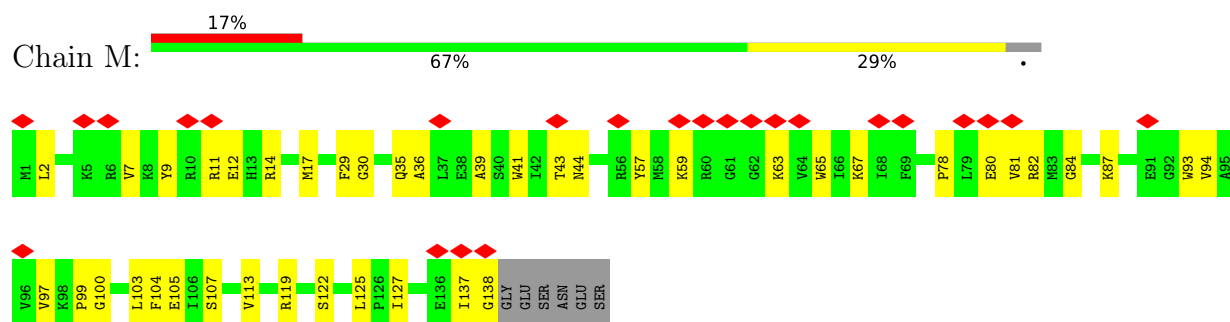
• Molecule 11: 50S ribosomal protein L14



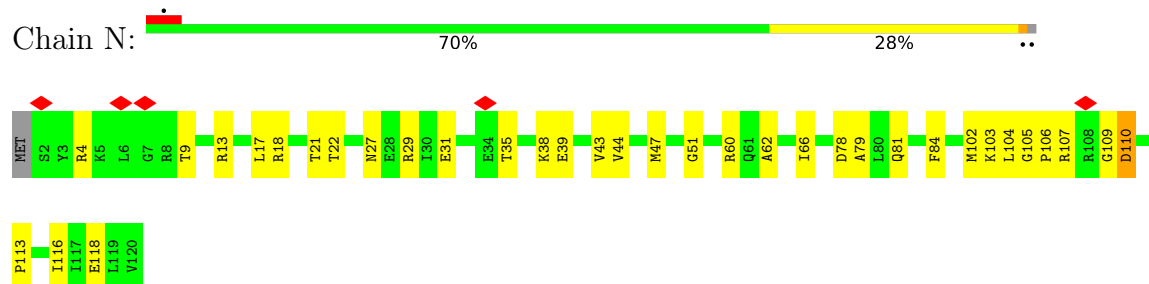
• Molecule 12: 50S ribosomal protein L15



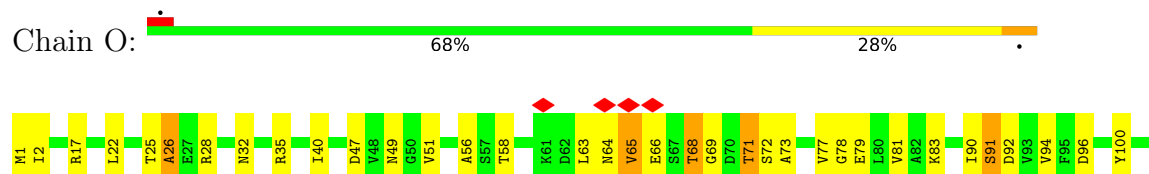
• Molecule 13: 50S ribosomal protein L16



• Molecule 14: 50S ribosomal protein L17

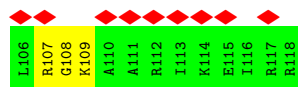


• Molecule 15: 50S ribosomal protein L18

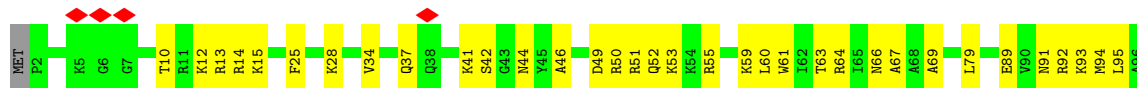




- Molecule 16: 50S ribosomal protein L19



- Molecule 17: 50S ribosomal protein L20



- Molecule 18: 50S ribosomal protein L21

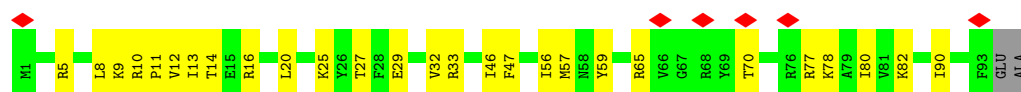


- Molecule 19: 50S ribosomal protein L22

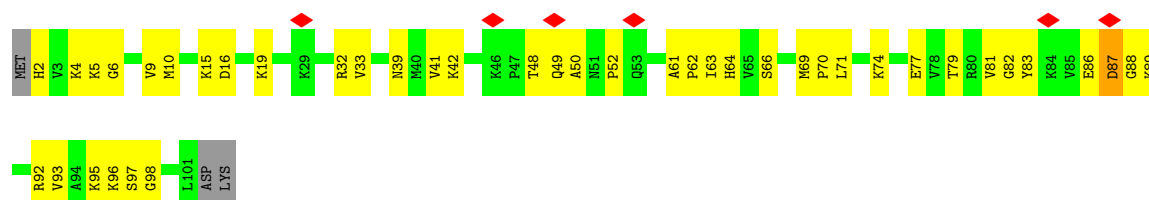


- Molecule 20: 50S ribosomal protein L23

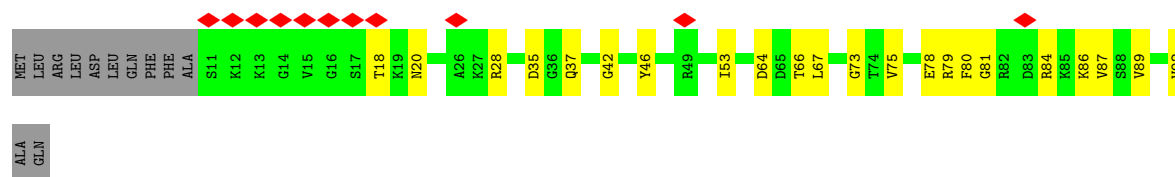




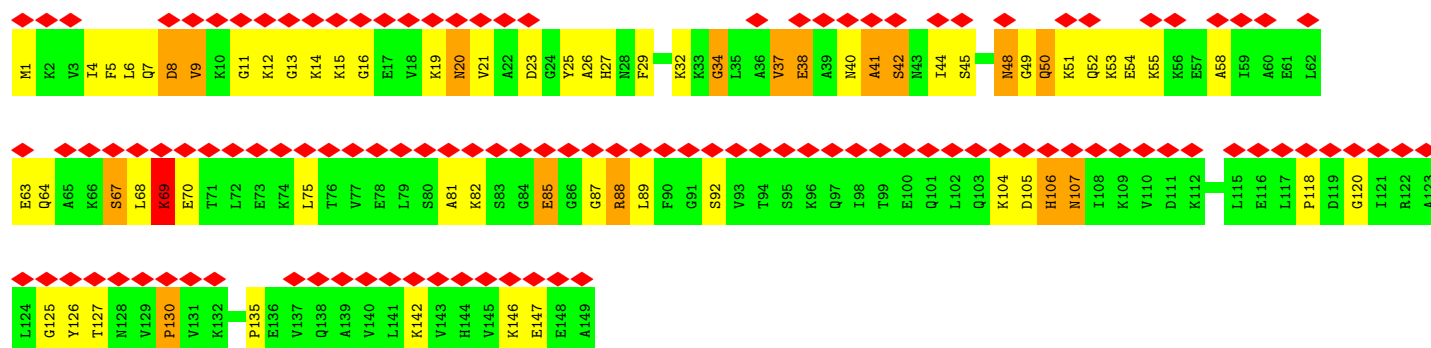
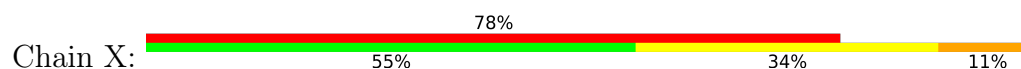
- Molecule 21: 50S ribosomal protein L24



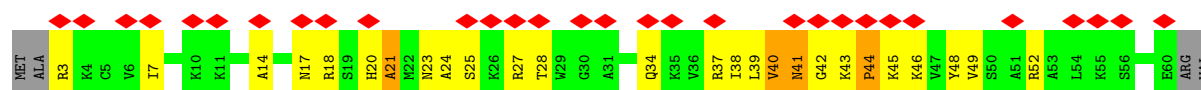
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L9



- Molecule 24: 50S ribosomal protein L28

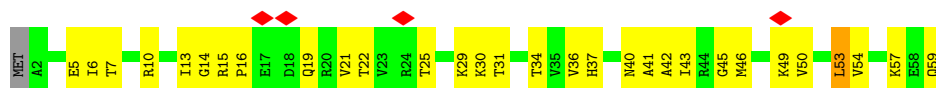


- Molecule 25: 50S ribosomal protein L29

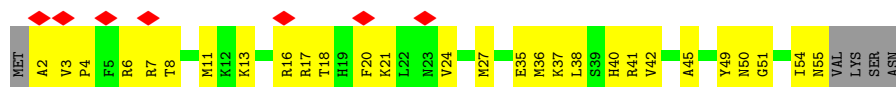
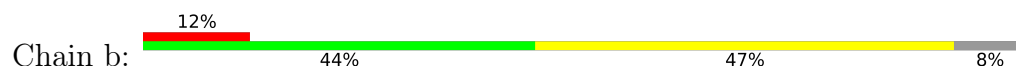




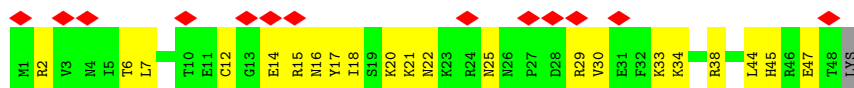
- Molecule 26: 50S ribosomal protein L30



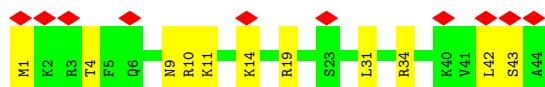
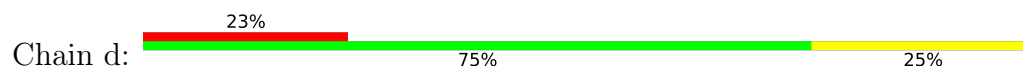
- Molecule 27: 50S ribosomal protein L32



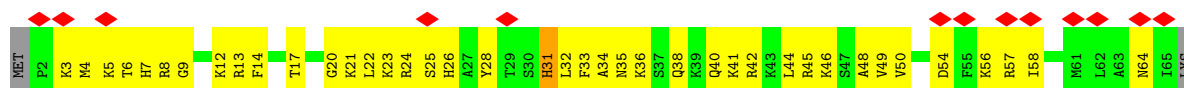
- Molecule 28: 50S ribosomal protein L33



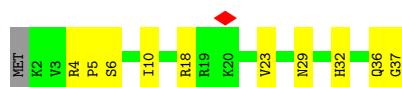
- Molecule 29: 50S ribosomal protein L34



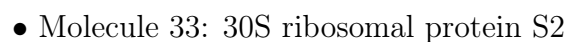
- Molecule 30: 50S ribosomal protein L35

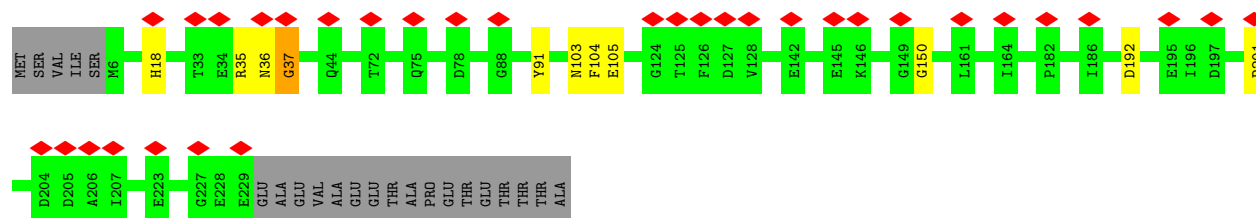
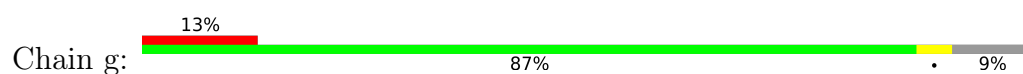


- Molecule 31: 50S ribosomal protein L36

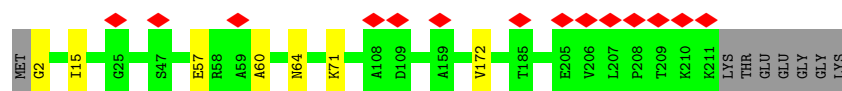
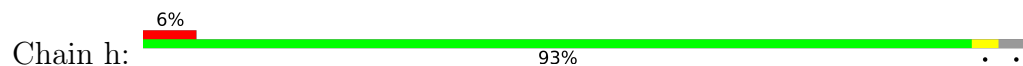


- Molecule 32: 16S rRNA

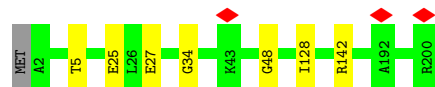




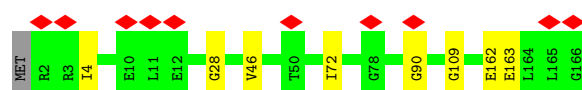
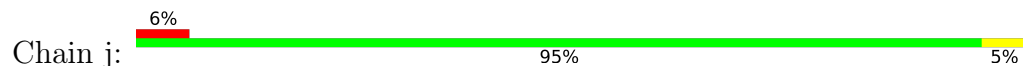
- Molecule 34: 30S ribosomal protein S3



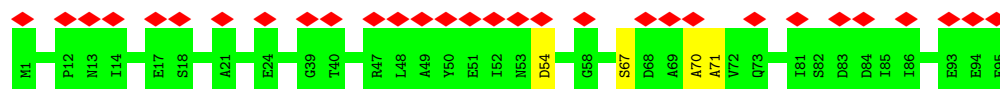
- Molecule 35: 30S ribosomal protein S4



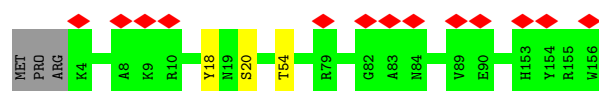
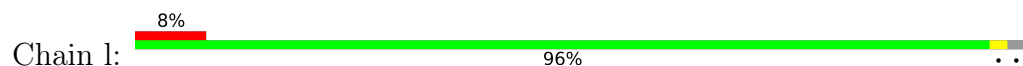
- Molecule 36: 30S ribosomal protein S5



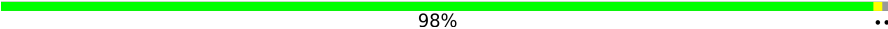
- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7

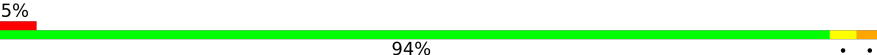


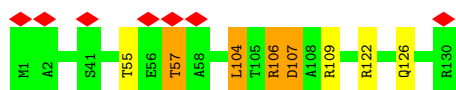
- Molecule 39: 30S ribosomal protein S8

Chain m:  98% ..

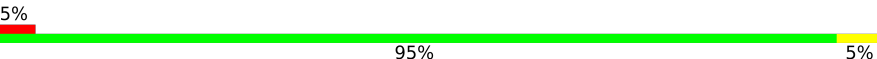


- Molecule 40: 30S ribosomal protein S9

Chain n:  5% 94% ..



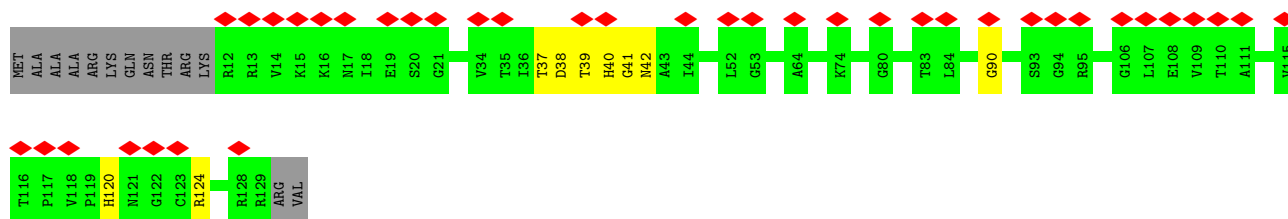
- Molecule 41: 30S ribosomal protein S10

Chain o:  5% 95% 5%

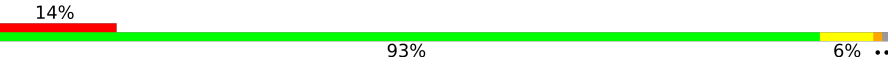


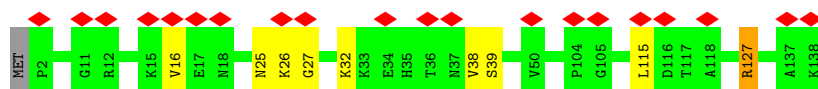
- Molecule 42: 30S ribosomal protein S11

Chain p:  30% 83% 7% 10%



- Molecule 43: 30S ribosomal protein S12

Chain q:  14% 93% 6% ..



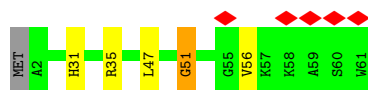
- Molecule 44: 30S ribosomal protein S13

Chain r:  7% 88% 8% ..

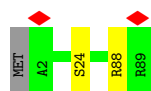


- Molecule 45: 30S ribosomal protein S14 type Z

Chain s:  8% 90% 7% ..



- Molecule 46: 30S ribosomal protein S15



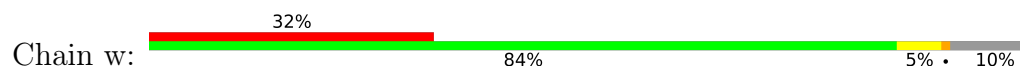
- Molecule 47: 30S ribosomal protein S16



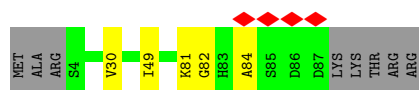
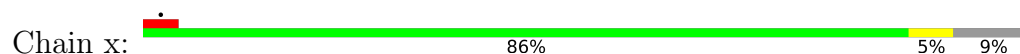
- Molecule 48: 30S ribosomal protein S17



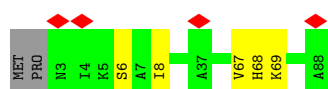
- Molecule 49: 30S ribosomal protein S18



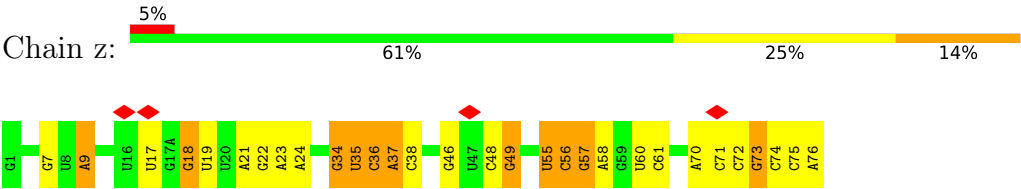
- Molecule 50: 30S ribosomal protein S19



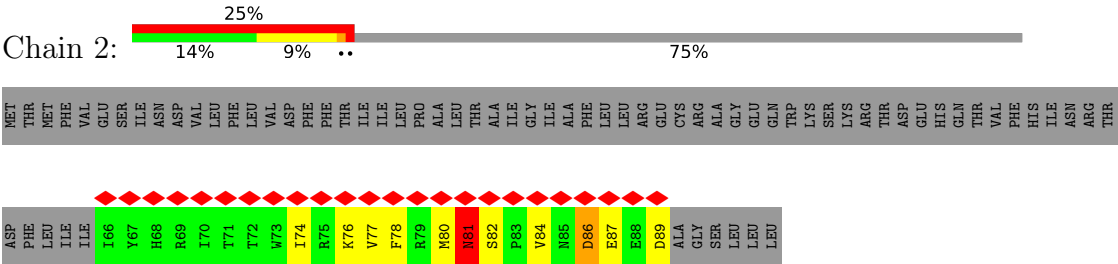
- Molecule 51: 30S ribosomal protein S20



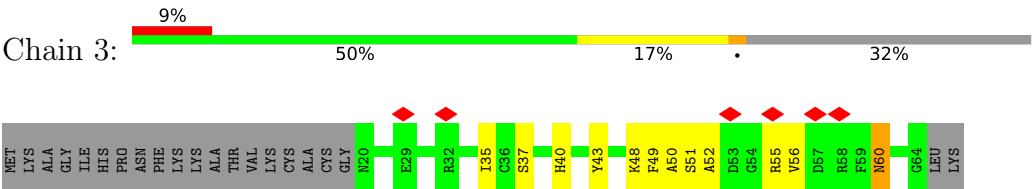
- Molecule 52: P-site tRNA



• Molecule 53: YqzJ



• Molecule 54: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12739	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.709	Depositor
Minimum map value	-0.823	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.090	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	650.4, 650.4, 650.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.53	0/70307	0.59	26/109687 (0.0%)
2	B	0.50	0/2678	0.52	0/4174
3	C	0.38	0/2148	0.85	2/2881 (0.1%)
4	D	0.39	0/1597	0.76	2/2140 (0.1%)
5	E	0.37	0/1580	0.80	3/2132 (0.1%)
6	F	0.40	0/1423	0.82	5/1910 (0.3%)
7	G	0.33	0/1360	0.76	0/1832
8	H	0.38	0/963	0.73	0/1298
9	I	0.42	0/995	0.90	5/1346 (0.4%)
10	J	0.36	0/1146	0.77	2/1542 (0.1%)
11	K	0.40	0/927	0.80	1/1245 (0.1%)
12	L	0.30	0/1093	0.78	2/1457 (0.1%)
13	M	0.29	0/1120	0.72	1/1496 (0.1%)
14	N	0.36	0/960	0.69	0/1284
15	O	0.44	0/921	0.84	1/1236 (0.1%)
16	P	0.33	0/949	0.73	0/1269
17	Q	0.34	0/952	0.66	0/1266
18	R	0.39	0/797	0.81	2/1070 (0.2%)
19	S	0.53	1/851 (0.1%)	0.88	2/1146 (0.2%)
20	T	0.40	0/759	0.74	0/1011
21	U	0.37	0/764	0.88	0/1022
22	V	0.40	0/638	0.77	0/847
23	X	1.03	5/732 (0.7%)	1.72	15/1016 (1.5%)
24	Y	0.38	0/448	0.89	2/596 (0.3%)
25	Z	0.30	0/531	0.65	0/707
26	a	0.33	0/457	0.68	0/613
27	b	0.30	0/433	0.75	0/574
28	c	0.34	0/406	0.69	0/540
29	d	0.26	0/370	0.76	1/483 (0.2%)
30	e	0.29	0/519	0.64	0/680
31	f	0.26	0/291	0.76	0/383
32	W	0.52	0/37074	0.53	0/57834
33	g	0.52	0/895	0.95	2/1117 (0.2%)
34	h	0.47	0/839	0.92	3/1047 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.44	0/796	1.03	4/992 (0.4%)
36	j	0.46	0/660	1.05	1/822 (0.1%)
37	k	0.51	0/380	1.00	2/472 (0.4%)
38	l	0.43	0/612	0.82	0/762
39	m	0.42	0/524	0.96	0/652
40	n	0.44	0/520	0.97	1/647 (0.2%)
41	o	0.50	0/408	1.00	2/507 (0.4%)
42	p	0.44	0/471	1.15	4/587 (0.7%)
43	q	0.42	0/548	1.12	0/682
44	r	0.49	0/475	1.00	1/592 (0.2%)
45	s	0.39	0/240	1.03	0/297
46	t	0.42	0/352	0.84	0/437
47	u	0.46	0/356	0.95	0/442
48	v	0.44	0/344	0.90	0/427
49	w	0.47	0/284	0.96	2/352 (0.6%)
50	x	0.53	0/335	0.98	1/417 (0.2%)
51	y	0.43	0/344	0.75	0/427
52	z	0.41	0/1834	0.47	0/2858
53	2	0.79	0/106	1.66	3/122 (2.5%)
54	3	0.40	0/373	0.76	0/497
All	All	0.50	6/147885 (0.0%)	0.64	98/221872 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	79
2	B	0	2
5	E	0	1
19	S	0	2
23	X	0	2
32	W	0	33
52	z	0	2
All	All	0	121

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	X	69	LYS	C-O	-11.68	1.09	1.24
23	X	63	GLU	C-O	-7.11	1.14	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	S	95	GLN	CA-C	-6.18	1.45	1.52
23	X	54	GLU	C-O	-5.90	1.15	1.23
23	X	48	ASN	CA-C	-5.52	1.45	1.52
23	X	69	LYS	CA-C	5.47	1.60	1.52

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	589	G	C4'-C3'-O3'	20.92	140.78	109.40
1	A	83	G	C4'-C3'-O3'	-17.73	82.81	109.40
23	X	69	LYS	CA-C-N	17.05	154.11	121.54
23	X	69	LYS	C-N-CA	17.05	154.11	121.54
23	X	51	LYS	N-CA-C	-16.80	93.10	111.07
1	A	82	G	C4'-C3'-O3'	-15.34	89.99	113.00
1	A	2487	U	C4'-C3'-O3'	14.72	131.48	109.40
23	X	55	LYS	N-CA-C	-12.92	95.64	111.40
1	A	366	A	C4'-C3'-O3'	12.40	128.00	109.40
23	X	67	SER	N-CA-C	-11.77	85.73	110.80
23	X	69	LYS	O-C-N	-10.03	109.25	122.59
23	X	64	GLN	N-CA-C	-9.22	101.18	111.14
1	A	589	G	C2'-C3'-O3'	-8.92	96.12	109.50
1	A	365	U	P-O3'-C3'	-8.64	107.23	120.20
1	A	2487	U	C2'-C3'-O3'	-8.30	97.05	109.50
23	X	58	ALA	N-CA-C	-8.27	101.96	110.97
53	2	81	ASN	N-CA-C	7.91	121.96	111.28
23	X	120	GLY	N-CA-C	-7.91	102.42	112.54
23	X	105	ASP	N-CA-C	-7.86	103.69	113.20
23	X	50	GLN	O-C-N	7.56	129.89	122.03
1	A	1294	A	C4'-C3'-O3'	-7.37	98.35	109.40
1	A	2227	A	C2'-C3'-O3'	-7.30	102.75	113.70
1	A	1294	A	C2'-C3'-O3'	7.29	120.44	109.50
42	p	124	ARG	CA-C-N	7.27	124.97	119.66
42	p	124	ARG	C-N-CA	7.27	124.97	119.66
3	C	28	LYS	CA-C-N	6.99	126.91	119.85
3	C	28	LYS	C-N-CA	6.99	126.91	119.85
1	A	83	G	C2'-C3'-O3'	6.92	119.87	109.50
1	A	590	U	P-O5'-C5'	6.81	131.11	120.90
34	h	15	ILE	N-CA-C	6.65	120.19	113.47
23	X	37	VAL	N-CA-C	6.62	123.12	109.34
53	2	76	LYS	N-CA-C	6.58	118.45	111.28
1	A	2488	A	C5'-C4'-C3'	-6.45	106.33	116.00
37	k	67	SER	N-CA-C	6.44	116.96	107.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	j	28	GLY	N-CA-C	6.43	118.80	110.45
1	A	1173	A	C5'-C4'-O4'	6.20	118.40	109.10
1	A	2187	A	C4'-C3'-O3'	6.19	118.68	109.40
15	O	65	VAL	N-CA-C	6.17	116.92	110.62
5	E	76	GLY	N-CA-C	6.07	119.53	112.50
1	A	792	G	C2'-C3'-O3'	-6.06	104.61	113.70
10	J	97	TYR	CA-C-N	6.00	125.88	119.28
10	J	97	TYR	C-N-CA	6.00	125.88	119.28
33	g	192	ASP	CA-C-N	5.98	125.86	119.28
33	g	192	ASP	C-N-CA	5.98	125.86	119.28
1	A	1173	A	C2'-C3'-O3'	-5.96	100.56	109.50
5	E	75	GLN	N-CA-C	5.93	119.36	111.30
5	E	183	VAL	N-CA-C	5.90	116.08	110.42
42	p	90	GLY	CA-C-N	5.87	125.82	119.78
42	p	90	GLY	C-N-CA	5.87	125.82	119.78
12	L	117	LEU	CA-C-N	5.86	132.25	121.70
12	L	117	LEU	C-N-CA	5.86	132.25	121.70
9	I	25	GLY	CA-C-N	5.85	125.72	119.28
9	I	25	GLY	C-N-CA	5.85	125.72	119.28
40	n	126	GLN	N-CA-C	5.84	117.73	108.79
35	i	34	GLY	CA-C-N	5.74	125.59	119.28
35	i	34	GLY	C-N-CA	5.74	125.59	119.28
1	A	1172	A	O3'-P-O5'	5.72	112.58	104.00
23	X	69	LYS	N-CA-C	5.69	122.91	110.80
53	2	82	SER	N-CA-C	5.61	121.31	113.57
9	I	22	PRO	N-CA-C	5.55	117.47	110.70
9	I	22	PRO	CA-C-N	-5.55	112.90	119.84
9	I	22	PRO	C-N-CA	-5.55	112.90	119.84
19	S	85	PHE	N-CA-C	-5.53	100.97	109.76
35	i	128	ILE	CA-C-N	5.50	125.33	119.28
35	i	128	ILE	C-N-CA	5.50	125.33	119.28
1	A	1293	A	C4'-C3'-O3'	5.49	117.64	109.40
34	h	71	LYS	CA-C-N	5.49	125.32	119.28
34	h	71	LYS	C-N-CA	5.49	125.32	119.28
1	A	2155	A	C4'-C3'-O3'	5.47	117.61	109.40
24	Y	21	ALA	N-CA-C	-5.46	103.87	111.52
4	D	147	GLY	CA-C-N	5.45	125.37	119.76
4	D	147	GLY	C-N-CA	5.45	125.37	119.76
19	S	93	ALA	N-CA-C	5.45	119.14	111.52
6	F	115	ARG	N-CA-C	-5.42	108.44	114.62
23	X	50	GLN	N-CA-C	5.40	116.86	110.97
41	o	40	ILE	CA-C-N	5.37	125.31	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	o	40	ILE	C-N-CA	5.37	125.31	119.78
44	r	94	GLY	N-CA-C	-5.33	107.97	115.32
13	M	59	LYS	CB-CA-C	-5.31	110.43	116.54
1	A	2260	U	C2'-C3'-O3'	-5.31	105.73	113.70
6	F	83	MET	CA-C-N	5.27	125.21	119.78
6	F	83	MET	C-N-CA	5.27	125.21	119.78
18	R	27	ALA	CB-CA-C	-5.25	110.09	117.23
37	k	71	ALA	N-CA-C	5.23	116.98	111.28
1	A	82	G	C2'-C3'-O3'	5.21	121.52	113.70
50	x	49	ILE	N-CA-C	5.20	115.45	108.17
6	F	138	PHE	CA-C-N	5.19	124.98	119.28
6	F	138	PHE	C-N-CA	5.19	124.98	119.28
23	X	106	HIS	N-CA-C	-5.17	108.73	114.62
1	A	2239	U	C4'-C3'-O3'	-5.12	101.72	109.40
29	d	43	SER	CB-CA-C	-5.09	109.73	115.79
24	Y	41	ASN	N-CA-C	-5.08	102.87	110.23
1	A	1173	A	O4'-C1'-C2'	5.07	110.87	105.80
11	K	28	SER	N-CA-C	5.07	116.80	111.28
49	w	45	LEU	CA-C-N	5.06	124.99	119.78
49	w	45	LEU	C-N-CA	5.06	124.99	119.78
1	A	367	G	C4'-C3'-O3'	-5.02	105.47	113.00
18	R	89	ARG	N-CA-C	-5.01	101.08	109.24

There are no chirality outliers.

All (121) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1006	A	Sidechain
1	A	1042	A	Sidechain
1	A	1075	A	Sidechain
1	A	1078	A	Sidechain
1	A	1094	A	Sidechain
1	A	1097	A	Sidechain
1	A	1172	A	Sidechain
1	A	1173	A	Sidechain
1	A	1253	A	Sidechain
1	A	126	A	Sidechain
1	A	1293	A	Sidechain
1	A	1294	A	Sidechain
1	A	1302	A	Sidechain
1	A	1393	A	Sidechain
1	A	1555	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1618	A	Sidechain
1	A	1619	A	Sidechain
1	A	1659	A	Sidechain
1	A	1661	A	Sidechain
1	A	168	A	Sidechain
1	A	1686	A	Sidechain
1	A	1724	A	Sidechain
1	A	183	A	Sidechain
1	A	1831	A	Sidechain
1	A	1839	A	Sidechain
1	A	1848	A	Sidechain
1	A	1883	A	Sidechain
1	A	1888	A	Sidechain
1	A	1957	A	Sidechain
1	A	1998	A	Sidechain
1	A	2006	A	Sidechain
1	A	2010	A	Sidechain
1	A	2062	A	Sidechain
1	A	2111	A	Sidechain
1	A	2316	A	Sidechain
1	A	2364	A	Sidechain
1	A	2383	A	Sidechain
1	A	2395	A	Sidechain
1	A	2407	A	Sidechain
1	A	2488	A	Sidechain
1	A	259	A	Sidechain
1	A	2601	A	Sidechain
1	A	2606	A	Sidechain
1	A	2616	A	Sidechain
1	A	2627	A	Sidechain
1	A	2631	A	Sidechain
1	A	2670	A	Sidechain
1	A	2691	A	Sidechain
1	A	2708	A	Sidechain
1	A	2805	A	Sidechain
1	A	2819	A	Sidechain
1	A	2827	A	Sidechain
1	A	2885	A	Sidechain
1	A	366	A	Sidechain
1	A	477	A	Sidechain
1	A	501	A	Sidechain
1	A	513	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	517	A	Sidechain
1	A	518	A	Sidechain
1	A	52	A	Sidechain
1	A	538	A	Sidechain
1	A	551	A	Sidechain
1	A	559	A	Sidechain
1	A	64	A	Sidechain
1	A	661	A	Sidechain
1	A	67	A	Sidechain
1	A	679	A	Sidechain
1	A	692	A	Sidechain
1	A	699	A	Sidechain
1	A	752	A	Sidechain
1	A	765	A	Sidechain
1	A	796	A	Sidechain
1	A	797	A	Sidechain
1	A	798	A	Sidechain
1	A	799	A	Sidechain
1	A	836	A	Sidechain
1	A	841	A	Sidechain
1	A	866	A	Sidechain
1	A	904	A	Sidechain
2	B	55	A	Sidechain
2	B	97	A	Sidechain
5	E	66	ARG	Sidechain
19	S	86	ARG	Sidechain
19	S	88	ARG	Sidechain
32	W	1026	A	Sidechain
32	W	1065	A	Sidechain
32	W	1261	A	Sidechain
32	W	1278	A	Sidechain
32	W	1297	A	Sidechain
32	W	1384	A	Sidechain
32	W	1407	A	Sidechain
32	W	1427	A	Sidechain
32	W	1442	A	Sidechain
32	W	1478	A	Sidechain
32	W	209	A	Sidechain
32	W	308	A	Sidechain
32	W	335	A	Sidechain
32	W	391	A	Sidechain
32	W	401	A	Sidechain

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Mol	Chain	Res	Type	Group
32	W	415	A	Sidechain
32	W	419	A	Sidechain
32	W	496	A	Sidechain
32	W	500	A	Sidechain
32	W	53	A	Sidechain
32	W	532	A	Sidechain
32	W	583	A	Sidechain
32	W	696	A	Sidechain
32	W	790	A	Sidechain
32	W	811	A	Sidechain
32	W	862	A	Sidechain
32	W	879	A	Sidechain
32	W	883	A	Sidechain
32	W	911	A	Sidechain
32	W	918	A	Sidechain
32	W	969	A	Sidechain
32	W	975	A	Sidechain
32	W	988	A	Sidechain
23	X	69	LYS	Mainchain,Peptide
52	z	37	A	Sidechain
52	z	9	A	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62767	0	31581	1262	0
2	B	2395	0	1212	21	0
3	C	2111	0	2200	90	0
4	D	1575	0	1642	47	0
5	E	1561	0	1647	88	0
6	F	1404	0	1467	67	0
7	G	1342	0	1388	29	0
8	H	955	0	990	26	0
9	I	981	0	1020	28	0
10	J	1123	0	1162	33	0
11	K	920	0	977	22	0
12	L	1081	0	1132	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1097	0	1165	27	0
14	N	953	0	983	39	0
15	O	912	0	947	35	0
16	P	936	0	1008	36	0
17	Q	940	0	1005	43	0
18	R	786	0	826	39	0
19	S	842	0	899	53	0
20	T	752	0	802	65	0
21	U	754	0	809	33	0
22	V	630	0	644	17	0
23	X	733	0	345	49	0
24	Y	444	0	486	86	0
25	Z	530	0	568	65	0
26	a	455	0	491	70	0
27	b	426	0	445	60	0
28	c	401	0	413	20	0
29	d	367	0	409	36	0
30	e	512	0	563	152	0
31	f	288	0	330	24	0
32	W	33115	0	16676	245	0
33	g	896	0	244	3	0
34	h	840	0	241	3	0
35	i	797	0	224	2	0
36	j	661	0	197	2	0
37	k	381	0	104	0	0
38	l	613	0	164	1	0
39	m	525	0	146	0	0
40	n	521	0	155	3	0
41	o	409	0	104	0	0
42	p	472	0	135	7	0
43	q	549	0	157	2	0
44	r	476	0	137	2	0
45	s	241	0	62	2	0
46	t	353	0	94	0	0
47	u	357	0	95	1	0
48	v	345	0	90	1	0
49	w	285	0	76	1	0
50	x	336	0	93	2	0
51	y	345	0	89	2	0
52	z	1643	0	830	36	0
53	2	107	0	58	20	0
54	3	366	0	343	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	135606	0	80070	2447	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 11.

All (2447) 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)
23:X:49:GLY:CA	23:X:52:GLN:CB	1.78	1.59
23:X:49:GLY:HA2	23:X:52:GLN:CB	1.31	1.56
1:A:2198:G:H3'	1:A:2198:G:N3	1.20	1.52
1:A:2157:C:C3'	1:A:2158:C:C6	1.92	1.50
1:A:2156:G:H21	1:A:2202:A:C1'	1.27	1.46
24:Y:37:ARG:NH1	24:Y:44:PRO:HG3	1.37	1.39
1:A:2224:U:H2'	1:A:2225:C:C6	1.59	1.37
1:A:2158:C:C6	1:A:2158:C:OP2	1.81	1.34
1:A:2174:C:H2'	1:A:2176:A:C2	1.63	1.33
1:A:2157:C:H3'	1:A:2158:C:C6	1.60	1.32
1:A:2158:C:H6	1:A:2158:C:P	1.53	1.31
1:A:2185:G:C2'	1:A:2186:G:C1'	2.09	1.30
1:A:427:G:OP1	24:Y:18:ARG:HB2	1.26	1.29
1:A:2185:G:C2'	1:A:2186:G:H1'	1.64	1.27
1:A:2378:G:OP2	30:e:42:ARG:NH2	1.64	1.27
1:A:974:A:C2	26:a:42:ALA:HB2	1.67	1.27
1:A:2192:U:C6	1:A:2192:U:OP2	1.88	1.27
9:I:15:ALA:HB1	9:I:46:THR:CG2	1.62	1.27
5:E:80:SER:OG	5:E:81:PRO:HD2	1.30	1.26
24:Y:37:ARG:HD2	24:Y:44:PRO:CB	1.65	1.26
1:A:2156:G:N2	1:A:2202:A:H1'	1.48	1.25
1:A:2378:G:OP2	30:e:42:ARG:CZ	1.84	1.25
1:A:2158:C:C6	1:A:2158:C:P	2.30	1.25
1:A:2157:C:O3'	1:A:2158:C:H6	1.20	1.23
1:A:2109:G:H4'	24:Y:23:ASN:ND2	1.53	1.23
1:A:2198:G:N3	1:A:2198:G:C3'	2.04	1.21
20:T:5:ARG:CZ	25:Z:23:GLU:HA	1.70	1.20
20:T:8:LEU:HD12	25:Z:26:PHE:CZ	1.76	1.20
1:A:2379:C:OP1	30:e:46:LYS:NZ	1.76	1.19
1:A:2450:G:OP2	30:e:32:LEU:HD23	1.43	1.19
1:A:2192:U:OP2	1:A:2193:C:C5	1.95	1.19
1:A:2185:G:H2'	1:A:2186:G:C1'	1.70	1.19
1:A:2421:A:H5'	30:e:28:TYR:CD2	1.78	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:A:C2	26:a:42:ALA:CB	2.26	1.18
1:A:2157:C:C2'	1:A:2158:C:C6	2.27	1.18
16:P:42:ARG:NH2	32:W:354:G:OP1	1.75	1.18
1:A:974:A:H2	26:a:42:ALA:CB	1.57	1.17
15:O:64:ASN:HB3	15:O:66:GLU:HG2	1.23	1.16
29:d:34:ARG:HG2	29:d:42:LEU:HD12	1.28	1.15
1:A:2185:G:H2'	1:A:2186:G:N9	1.61	1.15
20:T:5:ARG:NH2	25:Z:23:GLU:O	1.78	1.15
20:T:46:ILE:HG21	25:Z:26:PHE:CE2	1.81	1.15
23:X:49:GLY:N	23:X:52:GLN:CB	2.07	1.14
1:A:2181:C:H2'	1:A:2182:G:C8	1.83	1.14
1:A:2448:U:C6	30:e:33:PHE:HE2	1.65	1.14
1:A:2157:C:H3'	1:A:2158:C:C5	1.82	1.14
1:A:2207:C:O2'	1:A:2208:C:O4'	1.62	1.13
1:A:2157:C:H2'	1:A:2158:C:N1	1.63	1.13
1:A:2448:U:C5	30:e:33:PHE:HE2	1.65	1.13
9:I:15:ALA:CB	9:I:46:THR:HG21	1.79	1.13
9:I:15:ALA:CB	9:I:46:THR:CG2	2.26	1.13
12:L:57:LEU:CD1	30:e:54:ASP:OD2	1.96	1.13
20:T:5:ARG:NE	25:Z:23:GLU:HA	1.65	1.12
20:T:5:ARG:NE	25:Z:22:LYS:O	1.80	1.12
1:A:2181:C:H2'	1:A:2182:G:N9	1.63	1.12
21:U:87:ASP:HB3	21:U:88:GLY:HA3	1.31	1.12
1:A:374:A:C2	1:A:1250:G:H2'	1.85	1.11
1:A:2181:C:C3'	1:A:2182:G:H8	1.63	1.11
1:A:2185:G:O2'	1:A:2186:G:H1'	1.48	1.11
9:I:46:THR:HG23	9:I:54:ILE:HD12	1.31	1.11
9:I:15:ALA:HB1	9:I:46:THR:HG22	1.15	1.10
1:A:2170:A:C2	1:A:2180:U:C2	2.40	1.10
1:A:2427:U:O2'	28:c:15:ARG:NH1	1.85	1.09
1:A:2170:A:C2	1:A:2180:U:N3	2.20	1.09
1:A:2448:U:C6	30:e:33:PHE:CE2	2.40	1.09
1:A:2185:G:C2'	1:A:2186:G:N9	2.15	1.09
24:Y:37:ARG:HD3	24:Y:45:LYS:CG	1.83	1.08
1:A:72:U:N3	25:Z:55:THR:HB	1.68	1.08
1:A:2506:C:N4	31:f:10:ILE:HG12	1.69	1.08
23:X:48:ASN:C	23:X:52:GLN:CB	2.21	1.07
1:A:2182:G:C8	1:A:2182:G:OP2	2.07	1.07
1:A:2191:A:O2'	1:A:2192:U:O4'	1.71	1.07
1:A:2156:G:N2	1:A:2202:A:C1'	2.07	1.06
1:A:2181:C:C3'	1:A:2182:G:C8	2.38	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:38:ILE:HD11	24:Y:49:VAL:HB	1.30	1.06
24:Y:37:ARG:CD	24:Y:44:PRO:HB2	1.86	1.06
24:Y:37:ARG:HD2	24:Y:44:PRO:HB2	1.08	1.05
1:A:2181:C:C2'	1:A:2182:G:C8	2.40	1.05
1:A:2448:U:C5	30:e:33:PHE:CE2	2.43	1.05
12:L:57:LEU:HD13	30:e:54:ASP:CG	1.82	1.05
15:O:22:LEU:HD22	15:O:94:VAL:HG11	1.34	1.04
24:Y:45:LYS:HB3	24:Y:46:LYS:HB2	1.38	1.03
1:A:897:G:O2'	26:a:46:MET:HE3	1.58	1.03
1:A:377:G:H2'	1:A:378:C:H6	1.22	1.03
1:A:2046:U:O2	27:b:7:ARG:HB3	1.59	1.03
5:E:80:SER:HB3	5:E:83:TRP:HD1	1.23	1.03
1:A:899:C:H5'	26:a:45:GLY:CA	1.88	1.03
1:A:2109:G:H4'	24:Y:23:ASN:HD22	1.07	1.03
7:G:21:ASP:HB3	7:G:22:ASN:HB2	1.36	1.03
1:A:2157:C:C3'	1:A:2158:C:H6	1.49	1.02
1:A:2202:A:OP1	1:A:2202:A:N7	1.93	1.02
1:A:377:G:H2'	1:A:378:C:C6	1.95	1.01
1:A:899:C:C5'	26:a:45:GLY:HA3	1.89	1.01
20:T:46:ILE:HD13	25:Z:26:PHE:CZ	1.95	1.01
12:L:62:PRO:HG2	30:e:25:SER:HB2	1.42	1.01
1:A:254:A:OP2	30:e:7:HIS:NE2	1.92	1.01
1:A:2109:G:C4'	24:Y:23:ASN:ND2	2.23	1.01
1:A:1830:G:H5'	1:A:2232:G:H2'	1.41	1.00
1:A:2157:C:H2'	1:A:2158:C:C6	1.92	1.00
1:A:924:U:H3	1:A:946:G:H1	1.10	1.00
1:A:2110:C:H4'	24:Y:25:SER:HB3	1.42	1.00
12:L:64:ARG:HD3	30:e:25:SER:OG	1.60	1.00
29:d:34:ARG:HG2	29:d:42:LEU:CD1	1.91	1.00
1:A:2181:C:H2'	1:A:2182:G:C1'	1.92	1.00
1:A:1024:G:H1	1:A:1031:C:H42	1.04	0.99
23:X:49:GLY:C	23:X:52:GLN:CB	2.36	0.99
5:E:66:ARG:HH11	5:E:70:THR:CG2	1.76	0.99
1:A:2157:C:O3'	1:A:2158:C:O4'	1.81	0.99
5:E:77:SER:HB2	5:E:80:SER:HB2	1.40	0.99
1:A:899:C:H5'	26:a:45:GLY:HA3	1.01	0.99
6:F:109:PRO:HB3	54:3:43:TYR:HE2	1.27	0.98
1:A:248:G:N7	30:e:8:ARG:CZ	2.26	0.98
1:A:1264:G:H4'	18:R:87:GLY:O	1.63	0.98
1:A:2192:U:P	1:A:2193:C:H5	1.87	0.98
24:Y:37:ARG:CD	24:Y:45:LYS:HG2	1.94	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:C:H41	30:e:8:ARG:HG2	1.26	0.97
1:A:974:A:H2	26:a:42:ALA:HB2	0.83	0.97
1:A:2192:U:H5''	1:A:2201:U:C6	1.99	0.97
24:Y:37:ARG:HG3	24:Y:45:LYS:HG2	1.46	0.97
1:A:1171:G:H5'	31:f:37:GLY:HA2	1.45	0.97
24:Y:45:LYS:HB3	24:Y:46:LYS:CB	1.95	0.97
1:A:898:U:O4'	26:a:46:MET:HG2	1.64	0.97
1:A:2174:C:O5'	1:A:2174:C:C6	2.18	0.97
24:Y:37:ARG:HH11	24:Y:44:PRO:CG	1.78	0.97
5:E:65:TRP:CZ2	5:E:75:GLN:HB2	2.00	0.96
1:A:1303:U:H5''	27:b:13:LYS:HD3	1.46	0.96
1:A:2449:C:C5	30:e:31:HIS:O	2.18	0.96
24:Y:37:ARG:CG	24:Y:45:LYS:HG2	1.95	0.96
1:A:1024:G:H1	1:A:1031:C:N4	1.61	0.96
1:A:2206:C:C4	1:A:2207:C:N4	2.33	0.96
1:A:2192:U:OP2	1:A:2192:U:C5	2.17	0.96
24:Y:37:ARG:CD	24:Y:45:LYS:CG	2.44	0.96
1:A:2450:G:OP2	30:e:32:LEU:CD2	2.14	0.95
20:T:8:LEU:HD12	25:Z:26:PHE:HZ	1.25	0.95
1:A:2181:C:H3'	1:A:2182:G:C8	2.01	0.95
1:A:2206:C:N4	1:A:2207:C:N4	2.13	0.95
12:L:63:LYS:CG	30:e:13:ARG:NE	2.29	0.95
1:A:898:U:C1'	26:a:46:MET:HG3	1.96	0.95
20:T:8:LEU:HD12	25:Z:26:PHE:CE1	2.01	0.95
20:T:46:ILE:HG21	25:Z:26:PHE:HE2	1.26	0.95
1:A:528:G:H1	1:A:555:C:N4	1.63	0.95
1:A:2156:G:H21	1:A:2202:A:H1'	0.79	0.95
1:A:427:G:H5'	24:Y:18:ARG:HG3	1.46	0.95
1:A:2009:G:C6	1:A:2011:U:C4	2.55	0.94
1:A:123:G:C2	29:d:19:ARG:NH2	2.34	0.94
1:A:249:C:H41	30:e:8:ARG:CG	1.78	0.94
1:A:898:U:O4'	26:a:46:MET:CG	2.16	0.94
1:A:2421:A:H5'	30:e:28:TYR:CE2	2.02	0.94
1:A:2181:C:H3'	1:A:2182:G:H8	1.30	0.94
1:A:2185:G:H2'	1:A:2186:G:H1'	1.25	0.94
1:A:2224:U:H2'	1:A:2225:C:H6	1.13	0.93
1:A:1306:G:H2'	27:b:20:PHE:CZ	2.03	0.93
1:A:2192:U:C5'	1:A:2201:U:C5	2.52	0.93
5:E:73:ALA:HB3	5:E:75:GLN:HG2	1.49	0.93
12:L:61:LEU:CD1	30:e:24:ARG:HD2	1.97	0.93
1:A:2173:G:O2'	1:A:2174:C:C5	2.21	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:G:C4	29:d:19:ARG:NH1	2.37	0.93
1:A:2207:C:O2'	1:A:2208:C:C5'	2.16	0.93
1:A:248:G:N7	30:e:8:ARG:NE	2.16	0.92
1:A:898:U:O2	26:a:42:ALA:HB1	1.68	0.92
1:A:2046:U:O2'	27:b:7:ARG:HG2	1.69	0.92
1:A:254:A:P	30:e:7:HIS:HE2	1.92	0.92
12:L:63:LYS:HG2	30:e:13:ARG:NE	1.84	0.92
6:F:109:PRO:HD3	54:3:43:TYR:OH	1.69	0.92
1:A:2192:U:P	1:A:2193:C:C5	2.62	0.92
1:A:249:C:H41	30:e:8:ARG:CB	1.83	0.92
32:W:774:G:H1	32:W:821:G:HO2'	1.16	0.92
1:A:2799:C:C5	1:A:2800:C:C5	2.58	0.91
1:A:2450:G:N7	30:e:31:HIS:CD2	2.37	0.91
1:A:1295:U:C4	5:E:72:ARG:O	2.23	0.91
20:T:8:LEU:HB2	25:Z:26:PHE:HE1	1.32	0.91
1:A:1353:C:H42	1:A:1377:G:H1	0.97	0.91
1:A:2174:C:C2'	1:A:2176:A:C2	2.52	0.91
1:A:2185:G:O2'	1:A:2186:G:C1'	2.15	0.91
5:E:66:ARG:HH11	5:E:70:THR:HG22	1.33	0.91
1:A:796:A:H61	1:A:800:G:H21	1.20	0.90
18:R:67:ARG:HH11	18:R:89:ARG:NH1	1.69	0.90
1:A:898:U:H1'	26:a:46:MET:HG3	1.53	0.90
1:A:797:A:C2	1:A:799:A:H5'	2.07	0.90
24:Y:37:ARG:HB2	24:Y:45:LYS:HD3	1.51	0.90
5:E:65:TRP:CZ2	5:E:75:GLN:CB	2.55	0.90
24:Y:40:VAL:HG12	24:Y:41:ASN:H	1.36	0.90
5:E:75:GLN:HE22	5:E:82:GLN:NE2	1.68	0.90
42:p:40:HIS:N	42:p:41:GLY:HA2	1.87	0.90
3:C:243:ARG:HH22	3:C:247:MET:CB	1.85	0.90
1:A:2202:A:OP1	1:A:2202:A:C8	2.24	0.90
1:A:2449:C:OP2	30:e:33:PHE:HB2	1.71	0.90
24:Y:37:ARG:HD2	24:Y:44:PRO:CG	2.02	0.89
1:A:2182:G:H8	1:A:2182:G:P	1.95	0.89
42:p:38:ASP:O	42:p:41:GLY:CA	2.19	0.89
1:A:2192:U:H5''	1:A:2201:U:C5	2.08	0.89
1:A:72:U:H3	25:Z:55:THR:HB	1.30	0.89
1:A:2126:G:N2	1:A:2221:C:C2	2.40	0.89
1:A:2192:U:OP2	1:A:2193:C:C6	2.26	0.89
1:A:2198:G:H3'	1:A:2198:G:C4	2.09	0.88
1:A:609:C:OP2	18:R:79:LYS:HD3	1.73	0.88
1:A:2449:C:OP2	30:e:33:PHE:N	2.05	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2224:U:O2'	1:A:2225:C:O4'	1.88	0.88
1:A:2110:C:H4'	24:Y:25:SER:CB	2.03	0.88
1:A:2126:G:N2	1:A:2221:C:O2	2.06	0.88
5:E:75:GLN:NE2	5:E:82:GLN:NE2	2.21	0.88
1:A:1364:C:C2	19:S:86:ARG:CZ	2.56	0.88
1:A:2086:G:O2'	27:b:3:VAL:HG11	1.72	0.88
1:A:2157:C:C2'	1:A:2158:C:N1	2.36	0.88
1:A:1225:G:OP1	26:a:30:LYS:CE	2.22	0.88
1:A:1077:G:H21	31:f:36:GLN:HE22	1.16	0.88
12:L:63:LYS:CG	30:e:13:ARG:HE	1.86	0.87
12:L:57:LEU:HD13	30:e:54:ASP:CB	2.03	0.87
1:A:1353:C:N4	1:A:1377:G:H1	1.71	0.87
12:L:63:LYS:HG2	30:e:13:ARG:CD	2.03	0.87
1:A:2182:G:C8	1:A:2182:G:P	2.67	0.87
5:E:66:ARG:NH1	5:E:70:THR:HG22	1.88	0.87
1:A:72:U:H3	25:Z:55:THR:CB	1.87	0.87
12:L:57:LEU:HD13	30:e:54:ASP:OD2	1.70	0.87
1:A:2089:A:H3'	5:E:68:LYS:HE2	1.56	0.86
1:A:2170:A:N3	1:A:2180:U:O2	2.08	0.86
1:A:2447:A:OP1	30:e:45:ARG:CZ	2.23	0.86
1:A:2423:C:H5'	30:e:13:ARG:NH2	1.90	0.86
1:A:2224:U:C2'	1:A:2225:C:C6	2.55	0.86
1:A:2506:C:H41	31:f:10:ILE:HG23	1.40	0.86
15:O:64:ASN:CB	15:O:66:GLU:HG2	2.05	0.86
1:A:2614:U:O2	53:2:87:GLU:CD	2.19	0.86
1:A:2207:C:O2'	1:A:2208:C:C4'	2.22	0.86
29:d:34:ARG:CG	29:d:42:LEU:CD1	2.53	0.86
42:p:38:ASP:O	42:p:41:GLY:HA3	1.76	0.85
1:A:2157:C:O3'	1:A:2158:C:C6	2.06	0.85
1:A:2192:U:C5'	1:A:2201:U:C6	2.58	0.85
1:A:817:G:H5''	29:d:10:ARG:HD2	1.59	0.85
15:O:65:VAL:CG1	15:O:73:ALA:HB1	2.06	0.85
17:Q:103:LEU:HD12	17:Q:104:THR:HA	1.55	0.85
21:U:87:ASP:CB	21:U:88:GLY:HA3	2.04	0.85
1:A:2192:U:C6	1:A:2192:U:P	2.69	0.85
23:X:87:GLY:O	23:X:88:ARG:CB	2.24	0.85
1:A:2158:C:OP2	1:A:2159:U:H5	1.60	0.85
1:A:2355:U:H3	1:A:2418:G:H1	1.24	0.85
12:L:63:LYS:HA	30:e:13:ARG:HD3	1.57	0.85
1:A:2085:G:H21	27:b:3:VAL:H	1.21	0.85
5:E:80:SER:OG	5:E:81:PRO:CD	2.20	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:734:C:H1'	29:d:4:THR:HA	1.59	0.84
1:A:528:G:H1	1:A:555:C:H42	0.87	0.84
5:E:80:SER:HG	5:E:81:PRO:HD2	1.38	0.84
12:L:63:LYS:HG2	30:e:13:ARG:HD3	1.58	0.84
1:A:2173:G:O3'	1:A:2174:C:C5	2.31	0.84
1:A:2185:G:C3'	1:A:2186:G:N9	2.15	0.84
1:A:2185:G:H2'	1:A:2186:G:C4	2.13	0.84
1:A:734:C:C1'	29:d:4:THR:HA	2.08	0.84
6:F:105:SER:HA	54:3:37:SER:HB3	1.58	0.84
1:A:898:U:H4'	26:a:46:MET:HA	1.58	0.83
15:O:22:LEU:CD2	15:O:94:VAL:HG11	2.08	0.83
52:z:72:C:H6	52:z:72:C:H5''	1.43	0.83
5:E:62:ARG:O	5:E:78:ILE:HG13	1.78	0.83
6:F:109:PRO:HB3	54:3:43:TYR:CE2	2.12	0.83
15:O:22:LEU:HD22	15:O:94:VAL:CG1	2.09	0.82
1:A:2449:C:OP2	30:e:33:PHE:CB	2.27	0.82
24:Y:45:LYS:HB3	24:Y:46:LYS:CA	2.09	0.82
12:L:63:LYS:HG2	30:e:13:ARG:HE	1.40	0.82
12:L:61:LEU:HD11	30:e:24:ARG:HD2	1.61	0.82
1:A:2085:G:N2	27:b:3:VAL:H	1.78	0.82
1:A:2909:U:O2	27:b:50:ASN:ND2	2.12	0.82
1:A:2173:G:O3'	1:A:2174:C:H5	1.63	0.82
1:A:2207:C:HO2'	1:A:2208:C:C4'	1.92	0.82
19:S:88:ARG:HD2	19:S:94:SER:OG	1.80	0.82
1:A:1656:C:O2'	1:A:1657:C:H5'	1.80	0.82
12:L:117:LEU:HA	12:L:118:GLU:HB3	1.60	0.82
1:A:975:C:O2'	26:a:43:ILE:CD1	2.27	0.81
9:I:46:THR:HG23	9:I:54:ILE:CD1	2.10	0.81
23:X:82:LYS:C	23:X:92:SER:CB	2.53	0.81
1:A:1711:G:H1	1:A:2023:C:H42	1.24	0.81
1:A:2174:C:H2'	1:A:2176:A:N3	1.93	0.81
1:A:2191:A:C2'	1:A:2192:U:O4'	2.25	0.81
1:A:2506:C:H42	31:f:10:ILE:HG12	1.40	0.81
1:A:2799:C:H5	1:A:2800:C:C5	1.98	0.81
9:I:46:THR:CG2	9:I:54:ILE:HD12	2.10	0.81
19:S:85:PHE:HE2	53:2:74:ILE:CA	1.94	0.81
29:d:34:ARG:CG	29:d:42:LEU:HD13	2.11	0.81
1:A:72:U:C2	25:Z:55:THR:HB	2.14	0.81
12:L:64:ARG:HD3	30:e:25:SER:HG	1.46	0.81
20:T:5:ARG:NE	25:Z:23:GLU:CA	2.42	0.81
1:A:249:C:N4	30:e:8:ARG:CB	2.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1294:A:H3'	1:A:1295:U:H5''	1.60	0.81
1:A:1403:G:OP1	24:Y:3:ARG:NH1	2.14	0.81
1:A:15:G:H1	1:A:571:U:H3	1.29	0.81
19:S:85:PHE:CE2	53:2:74:ILE:CA	2.63	0.81
1:A:2089:A:H3'	5:E:68:LYS:CE	2.10	0.81
1:A:2202:A:C8	1:A:2202:A:P	2.74	0.81
12:L:63:LYS:HG3	30:e:13:ARG:NE	1.95	0.81
1:A:1834:C:H42	1:A:1841:G:H1	1.30	0.80
1:A:2181:C:C2'	1:A:2182:G:C1'	2.59	0.80
1:A:1297:C:H5'	5:E:75:GLN:OE1	1.81	0.80
19:S:82:LEU:HB2	19:S:98:LYS:HB2	1.62	0.80
20:T:11:PRO:HD2	25:Z:33:ALA:CB	2.10	0.80
20:T:46:ILE:CG2	25:Z:26:PHE:CE2	2.64	0.80
1:A:2614:U:H3	53:2:87:GLU:CD	1.89	0.80
1:A:2207:C:O2'	1:A:2208:C:H5'	1.81	0.79
1:A:2009:G:C5	1:A:2011:U:C5	2.69	0.79
1:A:2110:C:C5'	24:Y:25:SER:CB	2.60	0.79
24:Y:37:ARG:HH11	24:Y:44:PRO:HG3	0.98	0.79
5:E:62:ARG:O	5:E:78:ILE:CG1	2.30	0.79
1:A:897:G:H4'	26:a:22:THR:HG22	1.63	0.79
20:T:5:ARG:CD	25:Z:22:LYS:O	2.30	0.79
1:A:2173:G:O2'	1:A:2174:C:C6	2.34	0.78
12:L:64:ARG:NH1	30:e:25:SER:OG	2.13	0.78
24:Y:45:LYS:CB	24:Y:46:LYS:HB2	2.11	0.78
1:A:256:C:OP2	30:e:5:LYS:HG3	1.82	0.78
1:A:2182:G:H8	1:A:2182:G:OP2	1.66	0.78
15:O:65:VAL:CG1	15:O:73:ALA:CB	2.60	0.78
24:Y:37:ARG:HD3	24:Y:45:LYS:HG3	1.64	0.78
1:A:364:A:H4'	1:A:366:A:C8	2.18	0.78
1:A:427:G:OP1	24:Y:18:ARG:CB	2.21	0.78
1:A:2799:C:C5	1:A:2800:C:H5	1.99	0.78
20:T:5:ARG:CZ	25:Z:23:GLU:CA	2.60	0.78
1:A:2186:G:H3'	1:A:2186:G:OP2	1.84	0.78
32:W:268:G:N2	32:W:273:G:N7	2.29	0.78
1:A:2186:G:OP2	1:A:2186:G:C3'	2.30	0.78
1:A:2202:A:C8	1:A:2202:A:O5'	2.37	0.78
32:W:964:G:H21	32:W:1236:A:H62	1.30	0.78
24:Y:37:ARG:HD3	24:Y:45:LYS:CD	2.14	0.78
1:A:1103:A:N6	1:A:1133:G:OP2	2.16	0.78
1:A:1304:G:H5''	27:b:16:ARG:HH12	1.48	0.77
1:A:800:G:OP1	29:d:1:MET:HG3	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:37:ARG:CD	24:Y:44:PRO:CB	2.54	0.77
1:A:734:C:H1'	29:d:4:THR:HG22	1.65	0.77
5:E:80:SER:HB3	5:E:83:TRP:CD1	2.14	0.77
1:A:797:A:H2	1:A:799:A:H5'	1.48	0.77
1:A:2423:C:C5'	30:e:13:ARG:NH2	2.46	0.77
1:A:2450:G:C5	30:e:31:HIS:CD2	2.72	0.77
32:W:1546:C:H2'	32:W:1547:U:C6	2.19	0.77
1:A:817:G:OP2	29:d:11:LYS:HE3	1.82	0.77
1:A:2799:C:H5	1:A:2800:C:H5	1.29	0.77
19:S:89:ALA:O	19:S:90:MET:HB2	1.85	0.77
1:A:2799:C:H5'	1:A:2800:C:OP2	1.86	0.76
20:T:8:LEU:CD1	25:Z:26:PHE:HZ	1.97	0.76
1:A:1403:G:OP2	24:Y:3:ARG:HB2	1.84	0.76
20:T:11:PRO:HD3	25:Z:30:PHE:CD1	2.21	0.76
24:Y:37:ARG:NH1	24:Y:44:PRO:CG	2.33	0.76
1:A:1304:G:OP1	27:b:16:ARG:NH2	2.19	0.76
12:L:51:GLU:OE1	30:e:57:ARG:NH2	2.16	0.76
1:A:427:G:H5'	24:Y:18:ARG:CG	2.15	0.76
1:A:1263:G:C5	18:R:70:LYS:NZ	2.52	0.76
32:W:1323:C:H42	32:W:1332:G:H1	1.29	0.76
1:A:374:A:N1	1:A:1250:G:H2'	2.01	0.76
14:N:103:LYS:HD2	27:b:40:HIS:O	1.86	0.76
20:T:5:ARG:HH21	25:Z:23:GLU:C	1.93	0.76
24:Y:37:ARG:HB2	24:Y:45:LYS:CD	2.14	0.76
1:A:2158:C:OP2	1:A:2158:C:C5	2.38	0.75
5:E:65:TRP:HZ2	5:E:75:GLN:HB2	1.51	0.75
15:O:65:VAL:HG11	15:O:73:ALA:CB	2.17	0.75
1:A:2157:C:H2'	1:A:2158:C:C2	2.22	0.75
3:C:247:MET:HG2	3:C:248:SER:O	1.86	0.75
3:C:243:ARG:HH22	3:C:247:MET:HB3	1.51	0.75
18:R:67:ARG:HD3	18:R:89:ARG:CZ	2.17	0.75
1:A:1294:A:H3'	1:A:1295:U:C5'	2.16	0.75
23:X:67:SER:O	23:X:69:LYS:N	2.20	0.75
3:C:243:ARG:NH2	3:C:247:MET:HB3	2.01	0.75
1:A:1402:C:OP1	24:Y:48:TYR:OH	2.05	0.74
1:A:1829:C:H42	1:A:1846:G:H22	1.33	0.74
5:E:65:TRP:HZ2	5:E:75:GLN:CB	1.98	0.74
20:T:32:VAL:O	20:T:77:ARG:NH1	2.21	0.74
1:A:2110:C:C4'	24:Y:25:SER:CB	2.65	0.74
1:A:2174:C:O5'	1:A:2174:C:H6	1.66	0.74
1:A:2224:U:C2'	1:A:2225:C:H6	1.97	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2295:A:H62	1:A:2302:A:H62	1.35	0.74
1:A:875:U:H3	1:A:876:A:H62	1.36	0.74
1:A:975:C:O2'	26:a:43:ILE:HD11	1.86	0.74
1:A:1659:A:H2	19:S:93:ALA:HB2	1.52	0.74
1:A:2192:U:OP1	1:A:2193:C:H5	1.70	0.74
18:R:8:GLY:HA3	18:R:10:LYS:H	1.53	0.74
1:A:2420:G:O3'	30:e:28:TYR:HE2	1.71	0.74
2:B:76:A:H62	2:B:96:G:H21	1.35	0.74
19:S:38:LEU:HD22	27:b:27:MET:HE3	1.69	0.74
1:A:528:G:N2	1:A:555:C:N3	2.33	0.74
1:A:1364:C:C2	19:S:86:ARG:NH2	2.55	0.74
9:I:15:ALA:HB2	9:I:46:THR:HG21	1.67	0.74
18:R:68:ALA:N	18:R:90:GLN:O	2.20	0.74
1:A:426:G:H1	1:A:442:C:H42	1.35	0.73
12:L:57:LEU:HD12	30:e:54:ASP:OD2	1.88	0.73
1:A:245:G:C8	30:e:4:MET:O	2.41	0.73
1:A:1353:C:N3	1:A:1377:G:N2	2.35	0.73
1:A:2110:C:C5'	24:Y:25:SER:HB2	2.18	0.73
20:T:8:LEU:HB2	25:Z:26:PHE:CE1	2.21	0.73
1:A:245:G:N7	30:e:3:LYS:HB2	2.03	0.73
1:A:898:U:H1'	26:a:42:ALA:O	1.88	0.73
29:d:31:LEU:CD2	29:d:42:LEU:HD11	2.17	0.73
1:A:2450:G:N7	30:e:31:HIS:HD2	1.84	0.73
1:A:2614:U:C2	53:2:87:GLU:CD	2.66	0.73
1:A:607:G:H21	17:Q:37:GLN:HE22	1.37	0.73
12:L:63:LYS:CG	30:e:13:ARG:CD	2.67	0.73
1:A:785:C:N4	1:A:805:G:H1	1.86	0.73
1:A:977:U:O2'	26:a:25:THR:HA	1.87	0.73
1:A:2173:G:HO2'	1:A:2174:C:H5	1.23	0.73
20:T:5:ARG:NH2	25:Z:23:GLU:C	2.46	0.73
6:F:109:PRO:CB	54:3:43:TYR:HE2	1.98	0.73
24:Y:44:PRO:HB2	24:Y:45:LYS:HG2	1.71	0.73
1:A:2552:G:H1	1:A:2569:C:H42	1.36	0.73
32:W:850:U:H3	32:W:855:G:H22	1.34	0.73
5:E:67:GLN:HE22	5:E:74:ARG:CB	2.01	0.73
11:K:88:ARG:HD3	11:K:94:ARG:HH21	1.53	0.73
1:A:374:A:H2	1:A:1250:G:H2'	1.53	0.72
1:A:72:U:N3	25:Z:55:THR:CB	2.46	0.72
12:L:23:ILE:CG2	18:R:81:ASN:O	2.37	0.72
20:T:11:PRO:HD2	25:Z:33:ALA:HB2	1.71	0.72
18:R:25:LEU:HD12	18:R:27:ALA:H	1.52	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2447:A:OP1	30:e:45:ARG:NH2	2.22	0.72
18:R:67:ARG:HD3	18:R:89:ARG:NH1	2.04	0.72
11:K:24:VAL:HG12	11:K:26:GLY:H	1.53	0.72
20:T:8:LEU:CD1	25:Z:26:PHE:CZ	2.65	0.72
1:A:2448:U:H6	30:e:33:PHE:CE2	2.08	0.72
1:A:775:G:H5'	3:C:13:ARG:HH21	1.52	0.72
1:A:2031:G:OP1	14:N:13:ARG:NH2	2.23	0.72
1:A:2206:C:C4	1:A:2207:C:C4	2.77	0.72
1:A:1942:A:H62	32:W:1417:A:H2	1.37	0.72
10:J:19:VAL:HG13	10:J:143:LEU:HD11	1.72	0.72
15:O:65:VAL:HG13	15:O:73:ALA:HB1	1.70	0.72
54:3:51:SER:HA	54:3:52:ALA:HB3	1.72	0.72
1:A:734:C:O2	29:d:4:THR:HG22	1.89	0.72
1:A:898:U:H4'	26:a:46:MET:CA	2.20	0.72
12:L:57:LEU:HD13	30:e:54:ASP:HB3	1.70	0.72
32:W:965:U:N3	32:W:1234:A:C2	2.58	0.72
1:A:2494:C:O2'	31:f:5:PRO:HG3	1.90	0.72
12:L:64:ARG:HH11	30:e:25:SER:HG	1.36	0.72
4:D:123:ILE:HD13	4:D:141:ARG:HE	1.55	0.71
23:X:6:LEU:HA	23:X:15:LYS:C	2.14	0.71
1:A:1347:A:H62	1:A:1651:G:H8	1.38	0.71
1:A:1799:G:H1	1:A:2011:U:H3	1.38	0.71
1:A:2198:G:C3'	1:A:2198:G:C4	2.70	0.71
1:A:445:C:H5	24:Y:52:ARG:HH22	1.37	0.71
1:A:974:A:C2	26:a:42:ALA:HB1	2.23	0.71
21:U:86:GLU:O	21:U:87:ASP:CB	2.38	0.71
32:W:861:U:O4	32:W:862:A:N6	2.23	0.71
1:A:831:U:H5	1:A:840:A:C2	2.09	0.71
1:A:1303:U:H5''	27:b:13:LYS:CD	2.20	0.71
1:A:72:U:H1'	25:Z:51:ALA:HB1	1.71	0.71
1:A:1306:G:H2'	27:b:20:PHE:HZ	1.54	0.71
1:A:1016:U:OP1	26:a:13:ILE:HG23	1.90	0.71
1:A:1317:G:O2'	14:N:27:ASN:ND2	2.24	0.71
1:A:687:U:O2'	30:e:46:LYS:NZ	2.24	0.71
1:A:818:G:OP1	29:d:14:LYS:HD2	1.91	0.70
1:A:2181:C:O3'	1:A:2182:G:H8	1.73	0.70
1:A:2379:C:OP1	30:e:46:LYS:CE	2.38	0.70
12:L:61:LEU:CD1	30:e:24:ARG:CD	2.69	0.70
12:L:63:LYS:CG	30:e:13:ARG:HD3	2.21	0.70
52:z:71:C:H6	52:z:71:C:H5''	1.56	0.70
1:A:785:C:H42	1:A:805:G:H1	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1474:C:H42	1:A:1618:A:H62	1.38	0.70
5:E:154:ILE:HG12	5:E:193:LEU:HD12	1.73	0.70
1:A:738:C:OP1	3:C:217:ARG:NH2	2.23	0.70
1:A:2039:G:H5''	19:S:42:ALA:HB2	1.71	0.70
1:A:2182:G:OP2	1:A:2182:G:N7	2.23	0.70
15:O:65:VAL:HG13	15:O:73:ALA:CB	2.21	0.70
18:R:79:LYS:C	18:R:80:LYS:HG2	2.16	0.70
1:A:1035:G:OP1	26:a:31:THR:HG23	1.91	0.70
1:A:2374:G:H5'	1:A:2376:C:H5'	1.74	0.70
12:L:61:LEU:HD11	30:e:24:ARG:CD	2.21	0.70
1:A:2495:C:H5''	31:f:6:SER:OG	1.91	0.70
1:A:957:A:H62	13:M:12:GLU:HA	1.57	0.70
1:A:2495:C:OP1	31:f:4:ARG:HB2	1.92	0.70
1:A:2430:U:OP1	28:c:38:ARG:CZ	2.40	0.70
7:G:103:LYS:HG2	7:G:117:VAL:HG22	1.73	0.70
32:W:437:U:H3	32:W:439:A:H62	1.38	0.70
1:A:975:C:H1'	26:a:40:ASN:HD22	1.57	0.70
20:T:46:ILE:CG2	25:Z:26:PHE:HE2	2.02	0.70
21:U:39:ASN:HB3	21:U:61:ALA:HB3	1.74	0.70
28:c:2:ARG:HD2	28:c:20:LYS:HB3	1.74	0.70
1:A:1815:A:H5''	1:A:2009:G:N2	2.07	0.69
3:C:243:ARG:HH22	3:C:247:MET:HB2	1.56	0.69
27:b:38:LEU:HD11	27:b:41:ARG:HD2	1.74	0.69
12:L:61:LEU:HD13	30:e:24:ARG:HB2	1.73	0.69
19:S:23:LEU:HD13	27:b:24:VAL:HG12	1.73	0.69
1:A:1250:G:C5'	1:A:1251:U:H5''	2.21	0.69
1:A:1659:A:C2	19:S:93:ALA:HB2	2.27	0.69
1:A:1894:U:O2	1:A:1905:A:N7	2.25	0.69
1:A:2110:C:O5'	24:Y:25:SER:OG	2.10	0.69
32:W:970:U:H2'	32:W:1234:A:H62	1.57	0.69
1:A:2257:G:H22	24:Y:34:GLN:HE22	1.38	0.69
1:A:2009:G:C4	1:A:2011:U:C5	2.80	0.69
1:A:2198:G:N3	1:A:2198:G:C2'	2.56	0.69
1:A:2231:C:H42	1:A:2250:G:H1	1.41	0.69
20:T:5:ARG:NE	25:Z:22:LYS:C	2.50	0.69
52:z:72:C:H5''	52:z:72:C:C6	2.25	0.69
1:A:831:U:C5	1:A:840:A:C2	2.80	0.69
1:A:2206:C:N4	1:A:2207:C:H42	1.90	0.69
28:c:33:LYS:HB3	28:c:44:LEU:HD23	1.75	0.69
1:A:1225:G:OP1	26:a:30:LYS:HE2	1.92	0.69
1:A:1654:A:N6	1:A:1692:U:O4	2.17	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2614:U:N3	53:2:87:GLU:CD	2.51	0.69
6:F:135:GLN:HE22	6:F:150:ARG:H	1.41	0.69
16:P:63:THR:HG22	16:P:76:THR:HG22	1.73	0.69
19:S:88:ARG:HB2	19:S:92:ARG:HB2	1.73	0.69
20:T:5:ARG:HA	20:T:46:ILE:HD11	1.75	0.69
20:T:46:ILE:HD13	25:Z:26:PHE:CE2	2.27	0.69
24:Y:37:ARG:HD3	24:Y:45:LYS:HD3	1.75	0.69
42:p:38:ASP:O	42:p:41:GLY:HA2	1.91	0.69
14:N:102:MET:HE1	27:b:54:ILE:HB	1.75	0.69
1:A:245:G:HO2'	30:e:6:THR:CB	2.04	0.69
1:A:1371:G:N7	1:A:1654:A:O2'	2.26	0.69
23:X:81:ALA:HA	23:X:146:LYS:HA	1.74	0.69
3:C:29:PRO:HB3	3:C:63:ARG:HE	1.58	0.68
1:A:651:U:O2	1:A:667:A:N7	2.26	0.68
1:A:2506:C:N4	31:f:10:ILE:HG23	2.08	0.68
12:L:61:LEU:HD13	30:e:24:ARG:HD2	1.75	0.68
1:A:795:G:H5'	1:A:796:A:OP2	1.94	0.68
1:A:918:U:H3	1:A:953:G:H1	1.42	0.68
1:A:1042:A:H5'	17:Q:92:ARG:HE	1.59	0.68
1:A:2195:G:O6	1:A:2200:A:N6	2.26	0.68
19:S:72:SER:OG	19:S:106:VAL:CG1	2.41	0.68
29:d:31:LEU:HD23	29:d:42:LEU:HD11	1.73	0.68
16:P:67:ILE:HA	16:P:72:GLY:HA2	1.76	0.68
21:U:86:GLU:O	21:U:87:ASP:HB3	1.94	0.68
1:A:2207:C:H2'	1:A:2208:C:H6	1.58	0.68
1:A:1304:G:H5''	27:b:16:ARG:NH1	2.08	0.68
1:A:715:A:H2'	1:A:717:A:H62	1.57	0.68
5:E:66:ARG:NH1	5:E:70:THR:CG2	2.47	0.68
32:W:128:A:N6	32:W:193:G:O2'	2.27	0.68
1:A:2613:U:C3'	1:A:2614:U:H5'	2.24	0.68
3:C:142:HIS:ND1	3:C:193:GLY:O	2.27	0.68
1:A:2450:G:C6	30:e:31:HIS:CD2	2.81	0.68
9:I:15:ALA:HB2	9:I:46:THR:CG2	2.21	0.68
32:W:965:U:O4	32:W:1234:A:N1	2.27	0.68
1:A:2447:A:OP1	30:e:45:ARG:NE	2.26	0.67
18:R:8:GLY:HA3	18:R:10:LYS:N	2.08	0.67
32:W:1245:A:H4'	32:W:1313:G:H4'	1.76	0.67
1:A:2009:G:C5	1:A:2011:U:C4	2.82	0.67
1:A:1225:G:OP1	26:a:30:LYS:HD3	1.94	0.67
32:W:1367:U:O2	32:W:1372:A:N7	2.27	0.67
32:W:666:U:H3	32:W:758:A:H61	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1364:C:N3	19:S:86:ARG:NH2	2.41	0.67
6:F:57:LEU:HD23	6:F:65:PRO:HB3	1.75	0.67
11:K:22:ILE:HD12	11:K:40:VAL:HG12	1.76	0.67
1:A:1111:U:O2	1:A:1119:A:N7	2.28	0.67
1:A:2669:G:H1	1:A:2803:C:H42	1.42	0.67
1:A:1257:C:OP1	17:Q:15:LYS:NZ	2.27	0.67
1:A:2766:G:H1	1:A:2796:C:H42	1.41	0.67
4:D:28:ILE:HB	4:D:186:LEU:HB2	1.77	0.67
22:V:46:TYR:HB3	22:V:67:LEU:HD12	1.76	0.67
1:A:2709:C:H5'	4:D:193:PRO:HA	1.76	0.67
1:A:2105:U:OP2	1:A:2267:G:N2	2.28	0.67
1:A:2448:U:H3'	30:e:33:PHE:CD2	2.30	0.67
15:O:65:VAL:HG11	15:O:73:ALA:HB1	1.75	0.66
1:A:1711:G:H1	1:A:2023:C:N4	1.93	0.66
5:E:73:ALA:HB3	5:E:75:GLN:CG	2.24	0.66
6:F:64:LYS:HD2	6:F:65:PRO:HD2	1.77	0.66
26:a:5:GLU:HB2	26:a:57:LYS:HB3	1.77	0.66
1:A:1518:G:H3'	1:A:1519:C:H5''	1.77	0.66
12:L:57:LEU:CD1	30:e:54:ASP:CG	2.55	0.66
1:A:248:G:N7	30:e:8:ARG:NH2	2.43	0.66
1:A:797:A:N3	1:A:797:A:H2'	2.10	0.66
1:A:1379:U:H5''	20:T:57:MET:HE1	1.76	0.66
1:A:2449:C:P	30:e:33:PHE:HB2	2.34	0.66
12:L:64:ARG:CD	30:e:25:SER:OG	2.38	0.66
1:A:1035:G:N7	26:a:13:ILE:HD11	2.10	0.66
1:A:785:C:N3	1:A:805:G:N2	2.38	0.66
19:S:23:LEU:HD13	27:b:24:VAL:CG1	2.26	0.66
31:f:29:ASN:HB2	31:f:32:HIS:HD2	1.61	0.66
1:A:837:U:H4'	1:A:838:C:OP1	1.96	0.66
1:A:1931:C:H5''	3:C:241:ILE:HG21	1.77	0.66
4:D:178:LYS:HB2	4:D:187:LEU:HD12	1.77	0.66
1:A:2170:A:N3	1:A:2180:U:C2	2.62	0.66
11:K:11:ALA:HB2	11:K:83:ALA:HB1	1.77	0.66
18:R:67:ARG:HA	18:R:90:GLN:O	1.95	0.66
1:A:1096:A:H3'	1:A:1097:A:H8	1.62	0.65
1:A:2614:U:C2	53:2:87:GLU:OE2	2.49	0.65
15:O:56:ALA:HB3	15:O:81:VAL:HG22	1.78	0.65
24:Y:39:LEU:N	24:Y:39:LEU:HD12	2.11	0.65
1:A:734:C:O4'	29:d:4:THR:HA	1.96	0.65
1:A:2174:C:H6	1:A:2174:C:H3'	1.61	0.65
20:T:5:ARG:HD3	25:Z:22:LYS:C	2.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:898:U:H5''	26:a:49:LYS:HG3	1.79	0.65
1:A:1808:U:OP2	1:A:1813:A:N6	2.29	0.65
5:E:36:ALA:HB1	5:E:183:VAL:HG21	1.79	0.65
19:S:72:SER:OG	19:S:106:VAL:HG12	1.96	0.65
1:A:2203:C:H2'	1:A:2204:U:C6	2.32	0.65
6:F:78:ARG:HB3	6:F:79:LEU:HB2	1.78	0.65
1:A:1522:U:O2	1:A:1563:G:N2	2.30	0.65
1:A:2388:C:O2'	30:e:54:ASP:OD2	2.13	0.65
1:A:2818:C:O2'	1:A:2917:G:N2	2.29	0.65
1:A:1225:G:OP1	26:a:30:LYS:CD	2.44	0.65
1:A:898:U:O2'	26:a:42:ALA:O	2.12	0.65
1:A:2110:C:O5'	24:Y:25:SER:CB	2.44	0.65
1:A:2192:U:H5'	1:A:2201:U:C6	2.32	0.65
1:A:2571:A:H4'	1:A:2572:G:H5'	1.78	0.65
5:E:4:VAL:HG12	5:E:5:ALA:H	1.60	0.65
1:A:1897:C:H42	1:A:1902:G:H1	1.45	0.65
3:C:39:LYS:NZ	3:C:57:GLY:O	2.30	0.65
4:D:125:ARG:NH1	4:D:163:ARG:O	2.29	0.65
20:T:5:ARG:HE	25:Z:22:LYS:C	1.98	0.65
23:X:45:SER:O	23:X:48:ASN:CB	2.45	0.65
1:A:507:A:H62	1:A:516:G:H21	1.43	0.65
1:A:729:G:O6	1:A:841:A:N6	2.30	0.65
1:A:2157:C:C2'	1:A:2158:C:C1'	2.75	0.65
24:Y:40:VAL:HG12	24:Y:41:ASN:N	2.07	0.65
4:D:201:THR:CG2	4:D:203:LYS:HG3	2.27	0.65
1:A:1035:G:OP1	26:a:31:THR:CG2	2.44	0.64
1:A:2420:G:O3'	30:e:28:TYR:CE2	2.49	0.64
3:C:171:TYR:HB2	3:C:183:MET:HB3	1.77	0.64
32:W:446:G:N2	32:W:505:G:N7	2.45	0.64
24:Y:45:LYS:CE	24:Y:46:LYS:HE2	2.26	0.64
32:W:992:U:H4'	32:W:993:A:H5'	1.79	0.64
1:A:831:U:O4	1:A:840:A:N1	2.30	0.64
12:L:63:LYS:CA	30:e:13:ARG:HD3	2.27	0.64
1:A:1783:C:N3	1:A:2745:U:O2'	2.29	0.64
1:A:2192:U:H5'	1:A:2201:U:C5	2.32	0.64
1:A:2243:C:OP1	1:A:2244:G:OP2	2.15	0.64
1:A:2427:U:O2'	28:c:15:ARG:CZ	2.45	0.64
1:A:2908:A:OP1	27:b:49:TYR:OH	2.14	0.64
7:G:21:ASP:HB3	7:G:22:ASN:CB	2.21	0.64
1:A:1250:G:H4'	1:A:1251:U:OP2	1.96	0.64
1:A:1019:A:O2'	1:A:1227:G:N2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2109:G:OP1	24:Y:20:HIS:O	2.16	0.64
1:A:2449:C:H5	30:e:31:HIS:O	1.75	0.64
3:C:164:VAL:HG12	3:C:166:GLY:H	1.63	0.64
5:E:67:GLN:NE2	5:E:74:ARG:HG2	2.13	0.64
7:G:13:SER:HB3	7:G:14:ASP:HA	1.78	0.64
1:A:2614:U:N3	53:2:87:GLU:OE1	2.24	0.64
6:F:75:ALA:HB2	52:z:57:G:OP1	1.98	0.64
52:z:22:G:N7	52:z:46:G:N2	2.32	0.64
1:A:2199:G:H8	1:A:2200:A:C8	2.16	0.64
1:A:2206:C:N3	1:A:2207:C:C4	2.66	0.64
30:e:24:ARG:HD3	30:e:50:VAL:HG22	1.78	0.64
1:A:377:G:H4'	1:A:378:C:OP1	1.96	0.64
1:A:245:G:H3'	30:e:64:ASN:HB3	1.79	0.63
5:E:37:ILE:HG23	5:E:184:LEU:HD21	1.79	0.63
14:N:103:LYS:O	27:b:42:VAL:HG23	1.98	0.63
19:S:6:VAL:HG22	19:S:104:THR:HG22	1.80	0.63
1:A:2090:G:OP1	5:E:68:LYS:NZ	2.25	0.63
1:A:2185:G:HO2'	1:A:2186:G:C1'	2.09	0.63
6:F:100:LEU:HD23	6:F:103:LEU:HD12	1.80	0.63
52:z:35:U:H5'	52:z:35:U:H6	1.61	0.63
1:A:2009:G:C6	1:A:2011:U:O4	2.50	0.63
1:A:2151:U:H2'	1:A:2152:A:C8	2.32	0.63
5:E:66:ARG:HH11	5:E:70:THR:HG23	1.60	0.63
8:H:11:VAL:HA	8:H:66:GLN:HE21	1.64	0.63
15:O:65:VAL:N	15:O:66:GLU:HA	2.13	0.63
1:A:1123:A:O2'	9:I:93:ASN:ND2	2.32	0.63
1:A:1847:U:H5''	3:C:157:SER:HB3	1.79	0.63
1:A:1942:A:C2	32:W:1502:A:C5	2.86	0.63
24:Y:44:PRO:HB2	24:Y:45:LYS:CG	2.27	0.63
1:A:831:U:C5	1:A:840:A:N1	2.66	0.63
1:A:839:G:H4'	1:A:840:A:H5'	1.81	0.63
1:A:1263:G:C6	18:R:70:LYS:NZ	2.67	0.63
32:W:1313:G:H21	32:W:1342:A:H62	1.44	0.63
1:A:61:A:O2'	25:Z:40:THR:HG21	1.98	0.63
23:X:82:LYS:CA	23:X:92:SER:CB	2.76	0.63
32:W:591:C:OP2	32:W:767:G:N1	2.26	0.63
32:W:1544:A:H8	32:W:1544:A:O5'	1.81	0.63
1:A:2110:C:C4'	24:Y:25:SER:OG	2.47	0.63
1:A:2224:U:C2'	1:A:2225:C:O4'	2.46	0.63
32:W:268:G:N2	32:W:273:G:C5	2.64	0.63
32:W:965:U:H3	32:W:1234:A:H2	1.42	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:A:H2	1:A:485:U:H3	1.47	0.63
1:A:793:U:H5'	1:A:795:G:H1'	1.81	0.63
1:A:1056:A:OP1	17:Q:66:ASN:ND2	2.31	0.63
1:A:1250:G:H4'	1:A:1251:U:H5''	1.81	0.62
14:N:103:LYS:HB3	27:b:41:ARG:HG2	1.81	0.62
1:A:528:G:O2'	1:A:552:G:N2	2.31	0.62
1:A:2202:A:O5'	1:A:2202:A:H8	1.81	0.62
1:A:2421:A:C5'	30:e:28:TYR:CE2	2.81	0.62
1:A:72:U:O4'	25:Z:51:ALA:HA	1.99	0.62
1:A:798:A:H5''	1:A:799:A:OP1	1.98	0.62
1:A:2086:G:H1'	27:b:3:VAL:HB	1.82	0.62
16:P:109:LYS:HZ2	32:W:1473:C:H5''	1.65	0.62
16:P:109:LYS:NZ	32:W:1473:C:H5''	2.13	0.62
23:X:49:GLY:C	23:X:52:GLN:CA	2.68	0.62
1:A:2173:G:C3'	1:A:2174:C:H5	2.13	0.62
1:A:2282:G:C2	52:z:74:C:N3	2.68	0.62
19:S:89:ALA:O	19:S:92:ARG:HG2	1.99	0.62
1:A:2010:A:H3'	1:A:2011:U:H5'	1.82	0.62
5:E:73:ALA:CB	5:E:75:GLN:HG2	2.27	0.62
18:R:67:ARG:HD3	18:R:89:ARG:NE	2.13	0.62
1:A:835:A:H5''	1:A:837:U:H5	1.65	0.62
1:A:1268:G:OP2	17:Q:12:LYS:NZ	2.30	0.62
1:A:2479:A:N6	1:A:2530:C:O2	2.33	0.62
6:F:110:ARG:HH21	54:3:35:ILE:HB	1.64	0.62
11:K:16:ALA:HB2	11:K:52:VAL:HG11	1.82	0.62
12:L:75:ALA:HB1	12:L:76:VAL:HG22	1.82	0.62
13:M:2:LEU:O	13:M:44:ASN:ND2	2.33	0.62
28:c:29:ARG:HG3	28:c:47:GLU:HB3	1.80	0.62
30:e:32:LEU:O	30:e:36:LYS:NZ	2.33	0.62
1:A:1846:G:OP1	3:C:87:ARG:NH2	2.33	0.62
1:A:2181:C:H2'	1:A:2182:G:H1'	1.80	0.62
1:A:2777:A:H5''	7:G:4:VAL:HG21	1.80	0.62
15:O:113:ALA:HB1	15:O:118:LEU:HD12	1.81	0.62
23:X:82:LYS:O	23:X:92:SER:CB	2.47	0.62
1:A:350:U:O2'	1:A:1251:U:C5	2.52	0.62
1:A:1829:C:N4	1:A:1846:G:H22	1.98	0.62
1:A:2254:A:OP1	1:A:2255:C:C1'	2.48	0.62
10:J:57:ILE:HD12	10:J:125:VAL:HG22	1.82	0.62
1:A:2191:A:C8	1:A:2192:U:C5	2.88	0.62
1:A:2450:G:C5	30:e:31:HIS:NE2	2.67	0.62
16:P:109:LYS:HE2	32:W:1474:G:P	2.40	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:C:N3	30:e:12:LYS:NZ	2.47	0.62
1:A:2133:C:H2'	1:A:2134:A:C8	2.34	0.61
19:S:92:ARG:HA	19:S:92:ARG:HE	1.64	0.61
22:V:78:GLU:O	22:V:86:LYS:N	2.32	0.61
24:Y:45:LYS:HB3	24:Y:46:LYS:HA	1.80	0.61
10:J:18:VAL:HG13	10:J:58:ILE:HD13	1.82	0.61
1:A:245:G:N7	30:e:3:LYS:CB	2.63	0.61
1:A:245:G:H8	30:e:4:MET:O	1.82	0.61
1:A:1928:A:H4'	1:A:1930:A:H5''	1.82	0.61
1:A:2434:G:H4'	12:L:69:ILE:HD12	1.82	0.61
1:A:2518:G:N2	1:A:2520:U:O4	2.33	0.61
1:A:249:C:N4	30:e:8:ARG:HG2	2.07	0.61
1:A:2448:U:H3'	30:e:33:PHE:HD2	1.64	0.61
6:F:38:MET:HE1	6:F:152:MET:HG2	1.81	0.61
24:Y:43:LYS:O	24:Y:44:PRO:O	2.18	0.61
1:A:797:A:N3	1:A:799:A:H5'	2.16	0.61
1:A:2127:U:H3	1:A:2220:A:H61	1.48	0.61
1:A:1250:G:H5''	1:A:1251:U:H5''	1.82	0.61
1:A:2110:C:O5'	24:Y:25:SER:HB2	2.01	0.61
1:A:2192:U:H5''	1:A:2201:U:H6	1.58	0.61
1:A:2730:U:O4	1:A:2735:A:N1	2.33	0.61
3:C:132:LEU:HD23	3:C:135:ILE:HD12	1.81	0.61
32:W:965:U:N3	32:W:1234:A:H2	1.98	0.61
13:M:78:PRO:HG2	13:M:81:VAL:HG21	1.82	0.61
32:W:458:G:O6	32:W:493:G:O6	2.18	0.61
1:A:1065:U:N3	1:A:1188:A:N6	2.48	0.61
32:W:1096:U:H3	32:W:1109:G:H22	1.48	0.61
1:A:498:U:O2	1:A:500:A:N6	2.34	0.61
1:A:678:A:H2'	1:A:679:A:H8	1.65	0.61
1:A:1173:A:O2'	1:A:1174:A:H5''	2.01	0.61
1:A:1291:A:OP1	17:Q:13:ARG:NH2	2.32	0.61
1:A:2494:C:O3'	31:f:5:PRO:HD2	2.01	0.61
16:P:30:ARG:HD3	16:P:45:ILE:HD11	1.83	0.61
31:f:18:ARG:HA	31:f:23:VAL:HA	1.82	0.61
52:z:34:G:C2	52:z:35:U:C6	2.89	0.61
10:J:54:HIS:HB3	10:J:122:LYS:HB3	1.80	0.60
1:A:636:G:H1	1:A:712:C:H42	1.48	0.60
1:A:1815:A:H5''	1:A:2009:G:H22	1.66	0.60
1:A:1829:C:N3	1:A:1846:G:N1	2.43	0.60
1:A:2236:C:H2'	1:A:2237:C:C6	2.36	0.60
1:A:2909:U:H1'	27:b:50:ASN:HD22	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:126:LEU:HD13	5:E:193:LEU:HD22	1.82	0.60
7:G:59:GLN:HB2	7:G:62:HIS:HD2	1.65	0.60
8:H:26:ILE:HG13	8:H:114:GLU:HB2	1.81	0.60
10:J:42:LYS:NZ	10:J:51:THR:O	2.34	0.60
14:N:118:GLU:OE2	27:b:54:ILE:HD13	2.01	0.60
1:A:898:U:O4'	26:a:46:MET:HG3	1.89	0.60
1:A:839:G:C4'	1:A:840:A:H5'	2.31	0.60
1:A:2613:U:H2'	1:A:2614:U:H5'	1.84	0.60
6:F:80:ARG:NH1	52:z:56:C:H5	1.98	0.60
20:T:5:ARG:NH2	25:Z:23:GLU:HA	2.16	0.60
32:W:1323:C:N4	32:W:1332:G:H1	1.99	0.60
1:A:2157:C:O2'	1:A:2158:C:C1'	2.49	0.60
1:A:2191:A:C8	1:A:2192:U:C4	2.90	0.60
8:H:28:VAL:HG12	8:H:30:TYR:H	1.65	0.60
24:Y:43:LYS:HB3	24:Y:44:PRO:HD2	1.83	0.60
1:A:1015:G:OP1	26:a:16:PRO:HA	2.01	0.60
1:A:1706:G:N2	1:A:2717:G:OP1	2.33	0.60
6:F:73:SER:OG	52:z:56:C:H4'	2.02	0.60
19:S:6:VAL:HG12	19:S:8:ARG:HG3	1.82	0.60
23:X:40:ASN:O	23:X:41:ALA:C	2.45	0.60
5:E:66:ARG:HD3	5:E:70:THR:HG23	1.83	0.60
1:A:787:C:H42	1:A:804:G:H1	1.50	0.60
1:A:2048:U:OP2	27:b:6:ARG:NH2	2.35	0.60
1:A:2254:A:OP1	1:A:2255:C:O4'	2.20	0.60
9:I:15:ALA:CA	9:I:46:THR:HG21	2.30	0.60
32:W:69:C:H2'	32:W:70:G:C8	2.36	0.60
32:W:1546:C:H2'	32:W:1547:U:H6	1.64	0.60
1:A:721:G:H5''	5:E:76:GLY:H	1.67	0.60
1:A:1250:G:H4'	1:A:1251:U:C5'	2.32	0.60
1:A:2186:G:C1'	1:A:2186:G:OP2	2.23	0.60
3:C:241:ILE:O	3:C:241:ILE:HG23	2.01	0.60
8:H:29:ASP:HB2	8:H:81:ALA:HB1	1.82	0.60
12:L:117:LEU:HB2	12:L:119:LYS:N	2.17	0.60
1:A:2212:C:H2'	1:A:2213:U:C6	2.36	0.60
1:A:2254:A:OP1	1:A:2255:C:H1'	2.02	0.59
3:C:15:GLY:O	3:C:204:ASN:ND2	2.35	0.59
30:e:14:PHE:HB3	30:e:22:LEU:HD23	1.82	0.59
32:W:1295:C:H2'	32:W:1296:A:H4'	1.84	0.59
1:A:609:C:H5	18:R:79:LYS:HE2	1.67	0.59
32:W:385:G:O6	32:W:386:A:N6	2.35	0.59
1:A:576:G:N2	1:A:2052:A:OP2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2045:U:O2'	27:b:4:PRO:O	2.21	0.59
52:z:36:C:H6	52:z:36:C:H5''	1.68	0.59
1:A:106:G:H2'	1:A:107:G:H8	1.68	0.59
1:A:2247:C:H2'	1:A:2248:G:C8	2.37	0.59
1:A:2717:G:N1	1:A:2749:U:OP2	2.36	0.59
1:A:2785:U:O2'	1:A:2786:A:OP2	2.20	0.59
1:A:2833:U:H2'	1:A:2834:A:H8	1.66	0.59
1:A:123:G:N1	29:d:19:ARG:NH2	2.45	0.59
1:A:644:G:H1	1:A:704:U:H3	1.50	0.59
1:A:830:A:H2'	1:A:831:U:H4'	1.84	0.59
1:A:1537:G:H2'	1:A:1538:G:H8	1.67	0.59
5:E:67:GLN:HE22	5:E:74:ARG:CG	2.16	0.59
1:A:123:G:H2'	29:d:19:ARG:NH1	2.17	0.59
1:A:252:C:O2	30:e:12:LYS:NZ	2.30	0.59
1:A:515:G:O2'	5:E:62:ARG:NH2	2.36	0.59
1:A:1501:U:O4	1:A:2733:C:N3	2.35	0.59
1:A:1835:C:O2	3:C:44:ASN:ND2	2.35	0.59
1:A:217:G:N1	1:A:218:G:C6	2.71	0.59
1:A:811:A:H5''	3:C:209:GLY:HA2	1.83	0.59
1:A:902:G:O2'	22:V:35:ASP:OD2	2.20	0.59
1:A:1225:G:OP1	26:a:30:LYS:NZ	2.35	0.59
1:A:2181:C:O2'	1:A:2182:G:C1'	2.50	0.59
1:A:2241:A:H5'	1:A:2242:U:OP2	2.03	0.59
32:W:673:G:H22	32:W:750:G:H1	1.50	0.59
1:A:861:C:O2'	1:A:1264:G:N2	2.36	0.59
1:A:910:A:HO2'	2:B:98:G:HO2'	1.50	0.59
1:A:2909:U:O4	27:b:37:LYS:NZ	2.36	0.59
10:J:65:LEU:HD13	10:J:69:LYS:HB2	1.85	0.59
16:P:42:ARG:NH2	32:W:354:G:P	2.76	0.59
19:S:92:ARG:HA	19:S:92:ARG:NE	2.18	0.59
20:T:20:LEU:HD22	20:T:25:LYS:HD2	1.85	0.59
23:X:85:GLU:O	23:X:89:LEU:N	2.36	0.59
1:A:350:U:H4'	1:A:1251:U:H5	1.68	0.59
1:A:897:G:H4'	26:a:22:THR:CG2	2.31	0.59
1:A:898:U:C1'	26:a:46:MET:CG	2.70	0.59
1:A:2613:U:C2'	1:A:2614:U:H5'	2.33	0.59
21:U:16:ASP:HB3	21:U:19:LYS:HD2	1.85	0.59
32:W:412:G:N2	32:W:507:A:O2'	2.36	0.59
32:W:1549:C:C2	32:W:1550:U:C6	2.91	0.59
1:A:2450:G:O6	30:e:31:HIS:CD2	2.56	0.59
14:N:17:LEU:HD21	14:N:39:GLU:CD	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:G:O2'	1:A:654:G:O2'	2.20	0.58
1:A:822:G:H4'	1:A:823:G:H5'	1.84	0.58
1:A:41:A:N1	1:A:485:U:O4	2.35	0.58
1:A:898:U:O2'	26:a:45:GLY:CA	2.51	0.58
1:A:2427:U:HO2'	28:c:15:ARG:HH12	1.46	0.58
6:F:40:VAL:HG12	6:F:42:ASP:H	1.68	0.58
7:G:88:LEU:HB2	7:G:132:VAL:HB	1.84	0.58
12:L:63:LYS:HE3	30:e:13:ARG:HH21	1.69	0.58
1:A:1394:G:OP1	3:C:43:ARG:NH2	2.35	0.58
1:A:2220:A:H3'	1:A:2221:C:H6	1.67	0.58
1:A:2855:G:OP1	4:D:78:ARG:NH2	2.35	0.58
1:A:1834:C:N4	1:A:1841:G:H1	1.98	0.58
32:W:1154:C:H4'	32:W:1155:A:O5'	2.04	0.58
1:A:588:C:N4	1:A:589:G:O6	2.36	0.58
1:A:817:G:C5'	29:d:10:ARG:HD2	2.31	0.58
1:A:1024:G:N2	1:A:1031:C:N3	2.41	0.58
8:H:27:ILE:HB	8:H:83:ALA:HB3	1.86	0.58
12:L:78:ASN:HB2	12:L:81:LYS:HG2	1.85	0.58
21:U:86:GLU:HG3	21:U:87:ASP:H	1.68	0.58
1:A:898:U:O2'	26:a:46:MET:N	2.36	0.58
1:A:1101:G:H4'	8:H:33:LEU:HA	1.85	0.58
1:A:2122:G:N7	1:A:2254:A:H2'	2.18	0.58
12:L:117:LEU:HB2	12:L:119:LYS:H	1.69	0.58
18:R:10:LYS:HG3	18:R:12:ILE:HD11	1.85	0.58
26:a:7:THR:HG22	26:a:34:THR:HG22	1.85	0.58
1:A:2109:G:OP1	24:Y:21:ALA:HB3	2.04	0.58
1:A:2110:C:H5'	24:Y:25:SER:HB2	1.85	0.58
1:A:2487:U:H2'	1:A:2487:U:O2	2.02	0.58
52:z:36:C:N4	52:z:37:A:N6	2.52	0.58
1:A:1207:C:H1'	18:R:9:GLY:H	1.68	0.58
1:A:1855:C:O2'	1:A:2000:A:OP2	2.22	0.58
1:A:2164:A:H4'	1:A:2189:G:H4'	1.86	0.58
1:A:673:A:O2'	1:A:674:G:O4'	2.21	0.58
1:A:2156:G:N2	1:A:2202:A:O4'	2.36	0.58
1:A:2243:C:H2'	1:A:2244:G:O4'	2.04	0.58
23:X:106:HIS:O	23:X:107:ASN:CB	2.52	0.58
1:A:835:A:H5''	1:A:837:U:C5	2.39	0.57
1:A:934:U:H4'	1:A:935:A:H8	1.69	0.57
1:A:1600:G:O2'	1:A:1601:A:O4'	2.22	0.57
1:A:2186:G:OP2	1:A:2186:G:C2'	2.52	0.57
1:A:910:A:O2'	2:B:98:G:O2'	2.21	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1245:G:N2	1:A:1245:G:OP2	2.34	0.57
1:A:1261:C:N3	1:A:1268:G:O6	2.36	0.57
1:A:1306:G:OP2	27:b:17:ARG:NE	2.36	0.57
1:A:1578:G:N2	1:A:1587:U:OP2	2.36	0.57
1:A:2900:A:HO2'	16:P:5:GLN:N	2.02	0.57
5:E:136:THR:HG22	5:E:167:ALA:H	1.69	0.57
17:Q:95:LEU:HD12	17:Q:98:LEU:HD11	1.85	0.57
24:Y:45:LYS:NZ	24:Y:46:LYS:HE2	2.19	0.57
30:e:38:GLN:HA	30:e:41:LYS:HD3	1.86	0.57
32:W:113:G:H4'	32:W:114:A:O5'	2.03	0.57
1:A:377:G:C4	1:A:378:C:C5	2.92	0.57
1:A:426:G:H1	1:A:442:C:N4	2.02	0.57
1:A:683:A:O2'	1:A:684:G:OP2	2.22	0.57
1:A:1828:G:O2'	3:C:182:ARG:NH2	2.38	0.57
1:A:2174:C:C6	1:A:2174:C:C3'	2.87	0.57
1:A:2345:U:O2'	6:F:125:ARG:NH1	2.32	0.57
2:B:112:C:H2'	2:B:113:A:H8	1.69	0.57
29:d:31:LEU:HD22	29:d:42:LEU:HD11	1.87	0.57
1:A:792:G:H5'	1:A:793:U:OP2	2.04	0.57
1:A:1829:C:H42	1:A:1846:G:N2	2.02	0.57
1:A:2128:U:H2'	1:A:2129:G:C8	2.40	0.57
1:A:2714:G:OP2	16:P:52:LYS:NZ	2.37	0.57
18:R:14:VAL:HG11	18:R:97:ILE:HD12	1.86	0.57
20:T:5:ARG:CD	25:Z:22:LYS:C	2.78	0.57
20:T:5:ARG:HD3	25:Z:22:LYS:O	2.03	0.57
1:A:794:U:C4	1:A:2642:U:C5	2.93	0.57
1:A:2267:G:H1'	1:A:2269:C:H5	1.69	0.57
1:A:2472:C:H2'	1:A:2473:G:H8	1.69	0.57
1:A:2506:C:N4	31:f:10:ILE:CG1	2.56	0.57
4:D:119:PHE:HA	4:D:163:ARG:HA	1.87	0.57
4:D:185:LEU:HD21	16:P:7:LEU:HD21	1.86	0.57
32:W:64:U:O2'	32:W:387:C:O2	2.23	0.57
32:W:1293:C:H3'	32:W:1294:A:H8	1.69	0.57
1:A:831:U:C4	1:A:840:A:N1	2.72	0.57
1:A:2799:C:C5	1:A:2800:C:C6	2.92	0.57
3:C:150:LYS:HG2	3:C:153:GLN:HE22	1.68	0.57
19:S:38:LEU:CD2	27:b:27:MET:HE3	2.34	0.57
26:a:5:GLU:HG2	26:a:36:VAL:HG22	1.86	0.57
32:W:799:A:OP1	52:z:38:C:O2'	2.23	0.57
1:A:245:G:C8	30:e:3:LYS:HB3	2.40	0.57
1:A:249:C:N4	30:e:8:ARG:HB3	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:G:OP1	29:d:9:ASN:HB2	2.04	0.57
9:I:46:THR:HG22	9:I:46:THR:O	2.05	0.57
20:T:47:PHE:HD1	20:T:90:ILE:HD13	1.70	0.57
54:3:48:LYS:O	54:3:50:ALA:N	2.37	0.57
1:A:837:U:H3'	1:A:837:U:H6	1.70	0.57
1:A:2222:C:H2'	1:A:2223:U:C6	2.39	0.57
8:H:53:LYS:HB3	8:H:55:TYR:HD2	1.70	0.57
12:L:61:LEU:CD2	30:e:24:ARG:HH11	2.17	0.57
18:R:67:ARG:NH1	18:R:89:ARG:NH1	2.49	0.57
1:A:881:U:O4	1:A:882:A:N6	2.38	0.56
1:A:2157:C:H2'	1:A:2158:C:C1'	2.35	0.56
15:O:25:THR:HG21	15:O:47:ASP:HB2	1.87	0.56
1:A:673:A:H62	12:L:78:ASN:ND2	2.02	0.56
1:A:2071:A:N6	10:J:117:ARG:HH12	2.03	0.56
1:A:2246:G:OP2	24:Y:46:LYS:HE3	2.04	0.56
4:D:177:VAL:HG12	4:D:178:LYS:HG3	1.86	0.56
6:F:47:ALA:N	6:F:48:LYS:HA	2.19	0.56
7:G:39:HIS:CE1	7:G:42:MET:HG2	2.40	0.56
12:L:61:LEU:HD13	30:e:24:ARG:CB	2.35	0.56
13:M:137:ILE:N	13:M:138:GLY:HA3	2.19	0.56
21:U:48:THR:HB	21:U:49:GLN:C	2.30	0.56
1:A:881:U:H5'	30:e:56:LYS:NZ	2.20	0.56
1:A:2181:C:O2'	1:A:2182:G:H1'	2.05	0.56
1:A:2207:C:H2'	1:A:2208:C:C6	2.40	0.56
1:A:2221:C:O2	1:A:2221:C:H2'	2.03	0.56
6:F:78:ARG:HD2	6:F:79:LEU:HD13	1.88	0.56
6:F:80:ARG:HD3	52:z:56:C:C5	2.40	0.56
7:G:12:PRO:O	7:G:13:SER:HB2	2.06	0.56
10:J:38:ARG:HH12	10:J:111:PRO:HG3	1.71	0.56
15:O:22:LEU:CD2	15:O:94:VAL:CG1	2.78	0.56
19:S:84:ARG:HB2	19:S:96:ILE:HB	1.87	0.56
23:X:49:GLY:O	23:X:52:GLN:N	2.32	0.56
24:Y:45:LYS:HE3	24:Y:46:LYS:CE	2.35	0.56
32:W:106:G:H5'	32:W:107:A:H5''	1.87	0.56
32:W:1110:C:N4	32:W:1113:C:OP1	2.39	0.56
1:A:839:G:H4'	1:A:840:A:N3	2.20	0.56
5:E:65:TRP:HZ2	5:E:75:GLN:CG	2.19	0.56
7:G:13:SER:CB	7:G:14:ASP:HA	2.35	0.56
32:W:1087:G:N2	32:W:1090:A:OP2	2.38	0.56
32:W:1544:A:C5'	32:W:1544:A:C8	2.89	0.56
1:A:934:U:O2'	1:A:936:C:OP2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2046:U:HO2'	27:b:7:ARG:HG2	1.68	0.56
52:z:7:G:O2'	52:z:49:G:O5'	2.24	0.56
1:A:249:C:N4	30:e:8:ARG:HB2	2.20	0.56
1:A:252:C:C2	30:e:12:LYS:NZ	2.73	0.56
9:I:55:PRO:HG2	9:I:71:LYS:HB2	1.88	0.56
1:A:854:U:H2'	1:A:855:G:C8	2.40	0.56
1:A:1897:C:N4	1:A:1902:G:H1	2.03	0.56
1:A:2696:C:H1'	7:G:110:TYR:HD1	1.71	0.56
23:X:81:ALA:CB	23:X:147:GLU:H	2.18	0.56
24:Y:37:ARG:CB	24:Y:45:LYS:HD3	2.31	0.56
1:A:827:G:N1	3:C:229:ASP:OD2	2.35	0.56
16:P:95:VAL:HG13	16:P:100:LEU:HD21	1.88	0.56
32:W:986:G:O5'	32:W:1367:U:O2'	2.24	0.56
1:A:1365:U:HO2'	1:A:2039:G:HO2'	1.53	0.56
1:A:1528:U:H4'	1:A:1529:G:H5'	1.88	0.56
3:C:214:LYS:N	3:C:215:GLY:HA2	2.19	0.56
11:K:70:ARG:HG3	11:K:76:TYR:HE1	1.70	0.56
1:A:573:C:OP2	1:A:2808:U:N3	2.37	0.56
1:A:1108:G:H2'	1:A:1109:G:H8	1.70	0.56
1:A:2614:U:O2	53:2:87:GLU:OE2	2.23	0.56
6:F:24:SER:O	6:F:26:MET:N	2.33	0.56
16:P:95:VAL:HG12	16:P:97:ARG:H	1.70	0.56
20:T:11:PRO:CD	25:Z:33:ALA:CB	2.84	0.56
30:e:32:LEU:HD11	30:e:35:ASN:HD22	1.71	0.56
52:z:56:C:O2'	52:z:57:G:O4'	2.23	0.56
1:A:673:A:H62	12:L:78:ASN:HD22	1.54	0.55
1:A:734:C:H1'	29:d:4:THR:CA	2.34	0.55
1:A:1103:A:O2'	1:A:1104:U:OP1	2.23	0.55
1:A:2171:G:C2	1:A:2179:U:O2	2.58	0.55
1:A:2423:C:H5''	12:L:63:LYS:HE3	1.87	0.55
1:A:2909:U:O2	27:b:50:ASN:HB3	2.06	0.55
10:J:17:LEU:HB2	10:J:55:VAL:HG22	1.87	0.55
13:M:30:GLY:HA2	13:M:107:SER:HB3	1.88	0.55
15:O:65:VAL:CG1	15:O:73:ALA:HB2	2.35	0.55
32:W:1071:G:OP2	34:h:2:GLY:N	2.39	0.55
1:A:787:C:H2'	1:A:788:G:H5''	1.88	0.55
2:B:10:G:N1	22:V:79:ARG:O	2.39	0.55
11:K:38:VAL:HG22	11:K:61:VAL:HG22	1.89	0.55
1:A:72:U:OP2	25:Z:54:LYS:NZ	2.34	0.55
1:A:2430:U:OP1	28:c:38:ARG:NH2	2.39	0.55
12:L:55:MET:O	12:L:60:ARG:NH1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:102:MET:HE1	27:b:54:ILE:CB	2.37	0.55
19:S:21:MET:HA	19:S:24:ILE:HD12	1.87	0.55
32:W:105:G:OP1	32:W:333:A:N6	2.38	0.55
1:A:1067:A:H2'	1:A:1068:G:H4'	1.88	0.55
1:A:1314:A:N6	1:A:1335:A:H4'	2.22	0.55
9:I:85:ILE:HD12	9:I:98:ALA:HB2	1.88	0.55
24:Y:17:ASN:HD21	24:Y:27:ARG:HD2	1.71	0.55
1:A:1304:G:C5'	27:b:16:ARG:HH12	2.16	0.55
24:Y:43:LYS:C	24:Y:44:PRO:O	2.50	0.55
1:A:51:G:H21	1:A:117:A:H62	1.55	0.55
1:A:565:U:O3'	19:S:25:ARG:NH1	2.40	0.55
1:A:1111:U:O2	1:A:1119:A:C5	2.60	0.55
1:A:2142:C:H3'	1:A:2143:A:H8	1.71	0.55
1:A:2174:C:H6	1:A:2174:C:C3'	2.20	0.55
1:A:2344:U:OP1	6:F:33:LYS:NZ	2.39	0.55
6:F:109:PRO:HD3	54:3:43:TYR:CZ	2.41	0.55
12:L:61:LEU:HD13	30:e:24:ARG:CD	2.35	0.55
23:X:49:GLY:C	23:X:52:GLN:N	2.64	0.55
1:A:794:U:O5'	1:A:794:U:H6	1.89	0.55
1:A:921:G:OP1	13:M:63:LYS:NZ	2.40	0.55
1:A:2199:G:H3'	1:A:2200:A:H8	1.71	0.55
1:A:2614:U:H1'	53:2:89:ASP:HB2	1.89	0.55
3:C:248:SER:OG	3:C:250:TRP:O	2.25	0.55
5:E:63:LYS:HA	5:E:76:GLY:O	2.07	0.55
9:I:19:ASN:H	9:I:20:PRO:HD2	1.72	0.55
17:Q:103:LEU:HG	17:Q:104:THR:HG22	1.89	0.55
1:A:898:U:O2'	26:a:45:GLY:HA3	2.07	0.55
1:A:2351:A:O2'	1:A:2352:G:OP1	2.25	0.55
10:J:131:HIS:HD2	10:J:133:HIS:HB2	1.72	0.55
28:c:21:LYS:HE2	28:c:30:VAL:HB	1.88	0.55
32:W:1549:C:C4	32:W:1550:U:C5	2.95	0.55
1:A:1127:U:OP1	9:I:126:ARG:NH1	2.41	0.55
4:D:35:VAL:HG13	4:D:49:ILE:HG23	1.88	0.55
9:I:131:THR:O	9:I:134:SER:OG	2.24	0.55
21:U:82:GLY:N	21:U:93:VAL:O	2.37	0.55
26:a:10:ARG:HB3	26:a:53:LEU:HD13	1.88	0.55
32:W:1325:G:N1	32:W:1328:A:OP2	2.40	0.55
48:v:33:HIS:O	48:v:37:GLY:N	2.40	0.55
1:A:975:C:O2'	26:a:43:ILE:HD12	2.04	0.54
1:A:2170:A:H2	1:A:2180:U:C2	2.17	0.54
3:C:44:ASN:HB2	3:C:50:THR:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:67:GLN:NE2	5:E:74:ARG:CG	2.71	0.54
5:E:151:LYS:HG2	5:E:172:GLY:HA2	1.89	0.54
16:P:78:PRO:HG2	16:P:81:THR:HB	1.89	0.54
22:V:64:ASP:HB3	22:V:66:THR:HG23	1.90	0.54
1:A:78:U:H3	1:A:107:G:H1	1.56	0.54
1:A:1931:C:H5''	3:C:241:ILE:CG2	2.36	0.54
1:A:2489:U:H5	1:A:2521:U:H3	1.53	0.54
26:a:6:ILE:HG23	26:a:54:VAL:HG13	1.88	0.54
32:W:48:G:O2'	32:W:373:U:O2	2.24	0.54
32:W:692:G:H1	32:W:716:U:H3	1.55	0.54
32:W:970:U:H2'	32:W:1234:A:N6	2.21	0.54
1:A:2133:C:H2'	1:A:2134:A:H8	1.71	0.54
1:A:2449:C:OP2	30:e:33:PHE:CA	2.55	0.54
2:B:11:A:H8	2:B:67:G:H21	1.54	0.54
3:C:230:HIS:ND1	3:C:231:PRO:HD2	2.23	0.54
20:T:11:PRO:HG2	25:Z:33:ALA:CB	2.38	0.54
22:V:80:PHE:N	22:V:84:ARG:O	2.38	0.54
5:E:54:ARG:NH2	5:E:77:SER:OG	2.40	0.54
14:N:22:THR:HG22	14:N:66:ILE:HG23	1.89	0.54
24:Y:42:GLY:CA	24:Y:43:LYS:HD3	2.38	0.54
38:l:18:TYR:O	38:l:20:SER:N	2.34	0.54
52:z:34:G:H2'	52:z:35:U:H5''	1.88	0.54
1:A:245:G:N7	30:e:3:LYS:O	2.41	0.54
1:A:1094:A:H1'	1:A:1158:G:H21	1.73	0.54
1:A:1568:G:OP2	1:A:1568:G:N2	2.35	0.54
1:A:2195:G:C6	1:A:2200:A:N6	2.76	0.54
15:O:91:SER:OG	15:O:92:ASP:N	2.36	0.54
24:Y:37:ARG:CZ	24:Y:44:PRO:HG3	2.26	0.54
42:p:38:ASP:C	42:p:41:GLY:HA2	2.32	0.54
20:T:5:ARG:CZ	25:Z:26:PHE:HB3	2.38	0.54
1:A:245:G:C8	30:e:3:LYS:CB	2.91	0.54
1:A:245:G:N7	30:e:3:LYS:C	2.65	0.54
1:A:1066:A:O2'	1:A:1067:A:O5'	2.22	0.54
1:A:2167:C:H2'	1:A:2168:G:C8	2.43	0.54
1:A:257:G:N2	30:e:8:ARG:NH2	2.56	0.54
1:A:683:A:H4'	1:A:684:G:O5'	2.07	0.54
1:A:2220:A:H3'	1:A:2221:C:C6	2.43	0.54
3:C:140:VAL:HG11	3:C:194:GLN:HB3	1.89	0.54
10:J:26:LEU:N	10:J:27:GLY:HA3	2.23	0.54
1:A:1581:A:C6	1:A:1584:U:O2	2.60	0.53
1:A:2552:G:H1	1:A:2569:C:N4	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:99:THR:HG22	9:I:138:VAL:HB	1.90	0.53
19:S:89:ALA:O	19:S:90:MET:CB	2.55	0.53
23:X:6:LEU:HA	23:X:15:LYS:CA	2.37	0.53
23:X:9:VAL:C	23:X:11:GLY:H	2.15	0.53
1:A:1968:U:OP1	1:A:2633:U:O2'	2.26	0.53
22:V:73:GLY:HA2	22:V:92:VAL:HG23	1.90	0.53
26:a:5:GLU:OE2	26:a:59:GLN:NE2	2.41	0.53
1:A:1348:G:OP1	29:d:9:ASN:CB	2.56	0.53
1:A:1365:U:O4	1:A:1692:U:O2'	2.22	0.53
1:A:2117:A:H2'	1:A:2118:U:C6	2.43	0.53
1:A:2871:G:OP1	16:P:55:GLY:N	2.41	0.53
28:c:34:LYS:HB2	28:c:45:HIS:CE1	2.43	0.53
1:A:2162:G:H2'	1:A:2186:G:H22	1.72	0.53
1:A:2188:G:H2'	1:A:2189:G:C8	2.44	0.53
1:A:2535:U:O2	1:A:2535:U:H2'	2.07	0.53
1:A:2841:C:O4'	27:b:40:HIS:CD2	2.61	0.53
8:H:22:SER:OG	8:H:87:GLU:OE1	2.25	0.53
32:W:526:G:N2	32:W:539:G:OP1	2.39	0.53
1:A:510:G:N2	1:A:513:A:OP2	2.40	0.53
1:A:898:U:C4'	26:a:46:MET:HG2	2.38	0.53
1:A:1070:G:H3'	1:A:1071:G:H5''	1.90	0.53
1:A:1304:G:OP1	27:b:13:LYS:HG3	2.08	0.53
1:A:1322:G:N2	1:A:1325:A:OP2	2.42	0.53
1:A:1524:A:H2'	1:A:1525:G:C8	2.44	0.53
1:A:2784:C:O2'	1:A:2785:U:O5'	2.24	0.53
2:B:38:U:O2'	2:B:39:A:OP1	2.27	0.53
32:W:370:G:N2	32:W:373:U:OP2	2.32	0.53
42:p:37:THR:CA	42:p:42:ASN:O	2.57	0.53
1:A:2450:G:N7	30:e:31:HIS:NE2	2.57	0.53
1:A:2840:C:O2'	27:b:40:HIS:HD2	1.92	0.53
1:A:2900:A:O2'	16:P:5:GLN:N	2.41	0.53
12:L:62:PRO:CG	30:e:25:SER:HB2	2.28	0.53
32:W:518:A:H5'	35:i:48:GLY:HA3	1.89	0.53
1:A:199:A:H62	1:A:878:G:H21	1.56	0.53
1:A:648:G:O2'	1:A:649:G:O5'	2.27	0.53
1:A:805:G:HO2'	1:A:2010:A:H8	1.56	0.53
1:A:2144:G:H2'	1:A:2145:G:C5	2.44	0.53
1:A:848:G:O4'	5:E:54:ARG:NH1	2.41	0.53
1:A:2181:C:C2'	1:A:2182:G:H1'	2.37	0.53
5:E:65:TRP:CZ2	5:E:75:GLN:HB3	2.43	0.53
20:T:10:ARG:HB2	25:Z:33:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:616:A:OP1	32:W:640:G:N2	2.37	0.53
1:A:1500:U:OP1	14:N:81:GLN:NE2	2.40	0.53
1:A:1755:C:O2'	1:A:1756:U:OP1	2.24	0.53
1:A:2529:U:O2'	1:A:2533:U:OP1	2.24	0.53
1:A:2794:A:OP2	1:A:2795:G:N2	2.42	0.53
8:H:58:THR:HG22	8:H:84:PHE:CD2	2.44	0.53
1:A:1130:A:H4'	8:H:55:TYR:HA	1.91	0.53
1:A:2448:U:H5	30:e:33:PHE:CE2	2.15	0.53
1:A:2479:A:N6	1:A:2530:C:C2	2.77	0.53
5:E:29:ASN:HD22	5:E:108:LEU:HD21	1.73	0.53
7:G:4:VAL:O	7:G:70:ARG:NE	2.42	0.53
19:S:75:PHE:O	19:S:104:THR:OG1	2.24	0.53
32:W:1545:C:O2	32:W:1545:C:H2'	2.09	0.53
1:A:377:G:N3	1:A:378:C:C5	2.77	0.52
1:A:517:A:OP1	5:E:79:ARG:NH1	2.41	0.52
1:A:2191:A:O2'	1:A:2192:U:H5'	2.08	0.52
3:C:124:ILE:HG23	3:C:192:ILE:HD13	1.91	0.52
3:C:230:HIS:CG	3:C:231:PRO:HD2	2.43	0.52
9:I:10:LYS:HE2	9:I:57:GLU:HG2	1.91	0.52
1:A:732:A:H1'	1:A:735:U:H3	1.74	0.52
1:A:998:G:H21	1:A:2296:A:H2	1.57	0.52
10:J:77:ARG:HH12	10:J:88:ARG:HE	1.56	0.52
20:T:8:LEU:CD1	25:Z:26:PHE:CE1	2.85	0.52
21:U:33:VAL:N	21:U:63:ILE:O	2.32	0.52
32:W:66:G:N2	32:W:70:G:O6	2.30	0.52
32:W:842:U:O2'	32:W:843:U:OP1	2.26	0.52
1:A:797:A:H2	1:A:799:A:C5'	2.20	0.52
1:A:1055:A:OP1	10:J:40:LYS:NZ	2.42	0.52
3:C:21:PHE:HB3	3:C:24:ILE:HD12	1.90	0.52
5:E:153:LEU:HB2	5:E:192:LEU:HB2	1.92	0.52
13:M:39:ALA:HB2	13:M:99:PRO:HD3	1.91	0.52
17:Q:91:ASN:HD22	17:Q:109:LEU:HD21	1.75	0.52
22:V:18:THR:O	22:V:20:ASN:N	2.39	0.52
25:Z:8:ASP:HB3	25:Z:13:GLU:HG3	1.91	0.52
32:W:495:U:H2'	32:W:496:A:H8	1.74	0.52
1:A:796:A:H61	1:A:800:G:N2	1.99	0.52
1:A:1455:C:O2'	1:A:1456:A:OP1	2.27	0.52
1:A:1527:C:O2'	1:A:1528:U:OP1	2.27	0.52
1:A:2281:G:N2	52:z:75:C:C2	2.78	0.52
1:A:2713:U:OP2	16:P:54:ARG:NH1	2.42	0.52
1:A:2747:G:O2'	1:A:2872:U:OP1	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:8:ARG:NH1	4:D:197:LYS:O	2.42	0.52
4:D:201:THR:HG22	4:D:203:LYS:HG3	1.91	0.52
14:N:4:ARG:HH12	14:N:38:LYS:HD2	1.73	0.52
32:W:778:G:H4'	32:W:1523:A:H4'	1.92	0.52
32:W:1335:U:H2'	32:W:1336:G:H8	1.74	0.52
32:W:1549:C:N3	32:W:1550:U:C5	2.78	0.52
33:g:35:ARG:O	33:g:37:GLY:N	2.42	0.52
1:A:734:C:H1'	29:d:4:THR:CG2	2.37	0.52
6:F:109:PRO:HB2	54:3:40:HIS:CD2	2.45	0.52
11:K:40:VAL:HG22	11:K:59:LYS:HG2	1.91	0.52
32:W:596:G:N2	32:W:763:C:OP2	2.37	0.52
1:A:1377:G:H5''	20:T:14:THR:HG22	1.91	0.52
1:A:2143:A:H1'	1:A:2197:G:H1'	1.91	0.52
32:W:960:U:H3	32:W:1240:G:H1	1.57	0.52
32:W:1365:G:H2'	32:W:1366:A:C8	2.44	0.52
52:z:55:U:H3'	52:z:56:C:H5''	1.91	0.52
1:A:430:C:O2	1:A:438:A:N6	2.43	0.52
1:A:1303:U:O3'	27:b:8:THR:OG1	2.28	0.52
1:A:1901:A:O2'	1:A:1902:G:O5'	2.28	0.52
1:A:2164:A:H3'	1:A:2165:A:H8	1.74	0.52
1:A:2427:U:O2'	28:c:15:ARG:NH2	2.42	0.52
1:A:2495:C:OP1	31:f:4:ARG:HD3	2.09	0.52
1:A:2816:C:H1'	4:D:64:PRO:HB3	1.91	0.52
5:E:186:VAL:HG13	5:E:192:LEU:HD21	1.91	0.52
6:F:41:GLY:O	6:F:43:ALA:N	2.43	0.52
1:A:89:U:H3'	1:A:90:A:H8	1.75	0.52
1:A:934:U:H4'	1:A:935:A:C8	2.45	0.52
1:A:1014:A:O3'	26:a:16:PRO:HA	2.10	0.52
1:A:1093:G:H21	1:A:1157:A:H62	1.58	0.52
1:A:1474:C:N4	1:A:1618:A:H62	2.07	0.52
15:O:32:ASN:HA	15:O:96:ASP:HB2	1.92	0.52
26:a:50:VAL:HG12	26:a:53:LEU:HB3	1.92	0.52
32:W:1074:G:O2'	32:W:1199:G:N2	2.42	0.52
1:A:1024:G:N1	1:A:1031:C:N4	2.42	0.52
1:A:1077:G:N2	31:f:36:GLN:HE22	1.96	0.52
12:L:117:LEU:HA	12:L:118:GLU:CB	2.38	0.52
14:N:21:THR:HG22	14:N:44:VAL:HG22	1.91	0.52
17:Q:92:ARG:N	18:R:11:GLN:OE1	2.42	0.52
21:U:77:GLU:OE1	21:U:96:LYS:NZ	2.38	0.52
24:Y:43:LYS:O	24:Y:44:PRO:C	2.50	0.52
1:A:557:U:O2'	1:A:1255:G:N2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1715:C:O2	1:A:2022:U:O2'	2.23	0.52
1:A:2174:C:C2'	1:A:2176:A:N3	2.68	0.52
3:C:145:GLU:HB2	3:C:188:CYS:SG	2.50	0.52
18:R:90:GLN:OE1	18:R:91:PRO:HD2	2.09	0.52
1:A:898:U:C1'	26:a:42:ALA:O	2.57	0.51
12:L:61:LEU:HD21	30:e:24:ARG:NH1	2.25	0.51
17:Q:92:ARG:HG3	17:Q:94:MET:HG2	1.91	0.51
18:R:89:ARG:O	18:R:89:ARG:HG3	2.10	0.51
32:W:1274:C:H2'	32:W:1275:G:H8	1.75	0.51
6:F:29:PRO:HA	6:F:159:THR:HB	1.92	0.51
14:N:17:LEU:HD21	14:N:39:GLU:OE2	2.10	0.51
32:W:901:U:H2'	32:W:902:A:H8	1.74	0.51
32:W:1153:G:H21	32:W:1155:A:H62	1.57	0.51
1:A:527:A:O2'	21:U:42:LYS:O	2.29	0.51
1:A:644:G:N2	1:A:650:U:OP1	2.43	0.51
1:A:800:G:OP1	29:d:1:MET:CG	2.57	0.51
1:A:1581:A:C5	1:A:1584:U:O2	2.63	0.51
1:A:1887:G:N2	1:A:1912:G:O2'	2.40	0.51
1:A:2008:C:H2'	1:A:2009:G:H5''	1.91	0.51
1:A:2224:U:H2'	1:A:2225:C:O4'	2.10	0.51
1:A:2243:C:P	1:A:2244:G:OP2	2.68	0.51
1:A:2423:C:H5'	30:e:13:ARG:CZ	2.40	0.51
2:B:101:U:H2'	2:B:102:A:H8	1.75	0.51
3:C:182:ARG:HG3	3:C:269:PHE:HB3	1.91	0.51
17:Q:28:LYS:HA	17:Q:34:VAL:HG23	1.91	0.51
24:Y:37:ARG:CG	24:Y:45:LYS:CG	2.76	0.51
32:W:343:C:H2'	32:W:344:A:C8	2.45	0.51
1:A:1133:G:H1	1:A:1148:C:H42	1.58	0.51
1:A:1710:A:O2'	11:K:1:MET:O	2.25	0.51
1:A:2267:G:O2'	1:A:2269:C:OP2	2.27	0.51
1:A:2334:U:H3	6:F:151:GLY:HA3	1.75	0.51
1:A:2719:A:C2	14:N:17:LEU:CD1	2.93	0.51
1:A:2786:A:H3'	1:A:2787:A:H5''	1.93	0.51
1:A:1434:A:H4'	1:A:1435:U:OP1	2.10	0.51
1:A:2738:G:H5''	14:N:18:ARG:HH22	1.76	0.51
5:E:62:ARG:O	5:E:78:ILE:CD1	2.58	0.51
6:F:80:ARG:HD3	52:z:56:C:C6	2.46	0.51
7:G:153:ARG:HG2	7:G:162:GLY:HA3	1.93	0.51
9:I:8:VAL:HG22	9:I:59:SER:HA	1.92	0.51
23:X:6:LEU:H	23:X:16:GLY:N	2.09	0.51
32:W:988:A:O2'	32:W:1330:U:O4	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:1237:C:H2'	32:W:1238:A:H8	1.75	0.51
1:A:1202:A:O4'	17:Q:51:ARG:NH1	2.43	0.51
1:A:1251:U:O2	1:A:1251:U:O2'	2.26	0.51
1:A:2449:C:P	30:e:33:PHE:H	2.33	0.51
12:L:62:PRO:HG2	30:e:25:SER:CB	2.26	0.51
12:L:64:ARG:NH1	30:e:25:SER:HG	2.00	0.51
20:T:59:TYR:HE2	20:T:78:LYS:HE3	1.75	0.51
42:p:39:THR:C	42:p:41:GLY:HA2	2.35	0.51
1:A:257:G:H22	30:e:8:ARG:NH2	2.09	0.51
1:A:899:C:C5'	26:a:45:GLY:CA	2.68	0.51
1:A:2231:C:N4	1:A:2250:G:H1	2.07	0.51
4:D:110:VAL:HG11	4:D:192:VAL:HG13	1.91	0.51
25:Z:40:THR:HA	25:Z:43:ILE:HD12	1.93	0.51
1:A:683:A:O2'	1:A:684:G:O4'	2.24	0.51
1:A:1013:U:O4	1:A:1014:A:N6	2.43	0.51
1:A:1403:G:P	24:Y:3:ARG:HD2	2.50	0.51
1:A:2179:U:H2'	1:A:2180:U:C6	2.46	0.51
3:C:78:VAL:HG22	3:C:94:ILE:HG12	1.93	0.51
6:F:39:GLY:O	6:F:41:GLY:N	2.40	0.51
26:a:19:GLN:O	26:a:22:THR:OG1	2.22	0.51
32:W:1314:G:H21	32:W:1341:A:H2	1.59	0.51
1:A:2728:U:H3	1:A:2737:G:H1	1.59	0.51
16:P:55:GLY:HA2	16:P:60:GLU:HG2	1.93	0.51
21:U:2:HIS:HD2	21:U:81:VAL:HG21	1.76	0.51
32:W:404:A:O2'	32:W:406:C:OP1	2.24	0.51
32:W:683:G:H2'	32:W:684:A:C8	2.46	0.51
34:h:57:GLU:O	34:h:64:ASN:N	2.44	0.51
49:w:16:CYS:H	49:w:51:GLY:HA3	1.76	0.51
1:A:2324:C:H41	15:O:17:ARG:HH12	1.58	0.51
1:A:2785:U:C4	1:A:2787:A:N7	2.79	0.51
6:F:75:ALA:HB2	52:z:57:G:O5'	2.11	0.51
8:H:26:ILE:HD13	8:H:116:LYS:HE3	1.94	0.51
21:U:10:MET:HG2	21:U:71:LEU:HD11	1.93	0.51
22:V:79:ARG:HG2	22:V:81:GLY:H	1.76	0.51
1:A:792:G:N2	1:A:800:G:C6	2.79	0.50
1:A:2071:A:H62	10:J:117:ARG:HH12	1.59	0.50
4:D:114:SER:HB3	4:D:169:ILE:HD12	1.92	0.50
11:K:91:LYS:HE2	11:K:111:PHE:CE1	2.45	0.50
1:A:793:U:H5'	1:A:795:G:C1'	2.41	0.50
3:C:53:HIS:HA	3:C:217:ARG:HD2	1.93	0.50
6:F:75:ALA:HB2	52:z:57:G:P	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:58:ASP:O	7:G:63:ARG:NE	2.44	0.50
7:G:104:LEU:HD22	7:G:124:ILE:HG21	1.92	0.50
1:A:338:G:H2'	1:A:339:A:H8	1.76	0.50
1:A:1629:C:N4	1:A:1630:G:O6	2.45	0.50
1:A:2152:A:H61	1:A:2204:U:H3	1.59	0.50
19:S:86:ARG:HG2	19:S:87:PRO:HD2	1.93	0.50
20:T:5:ARG:NH2	25:Z:23:GLU:CA	2.71	0.50
1:A:343:A:C2	1:A:377:G:O2'	2.60	0.50
1:A:1250:G:C4'	1:A:1251:U:H5''	2.42	0.50
1:A:1306:G:H3'	27:b:20:PHE:CE1	2.46	0.50
1:A:2420:G:H4'	30:e:28:TYR:CE2	2.46	0.50
12:L:61:LEU:HD22	30:e:24:ARG:HH11	1.77	0.50
32:W:1246:C:O2'	32:W:1309:G:N2	2.40	0.50
1:A:83:G:H4'	1:A:84:A:OP1	2.10	0.50
1:A:256:C:OP2	30:e:5:LYS:HE3	2.11	0.50
1:A:854:U:H5'	1:A:2474:G:H4'	1.92	0.50
1:A:2524:G:OP1	13:M:82:ARG:NE	2.35	0.50
1:A:2605:G:O2'	1:A:2608:C:OP2	2.30	0.50
4:D:146:MET:HE1	4:D:160:LEU:HD21	1.93	0.50
8:H:27:ILE:O	8:H:83:ALA:N	2.45	0.50
19:S:41:ARG:HG3	19:S:43:ALA:H	1.77	0.50
52:z:72:C:H6	52:z:72:C:C5'	2.17	0.50
1:A:721:G:H1'	5:E:74:ARG:HD2	1.94	0.50
1:A:1873:U:H5''	3:C:258:LYS:HG2	1.93	0.50
1:A:2506:C:C4	31:f:10:ILE:HG12	2.42	0.50
1:A:2614:U:N3	53:2:87:GLU:OE2	2.45	0.50
5:E:62:ARG:O	5:E:78:ILE:HD11	2.11	0.50
9:I:24:VAL:HG13	9:I:28:LEU:HD12	1.93	0.50
13:M:103:LEU:HD13	13:M:125:LEU:HD13	1.94	0.50
32:W:154:C:H42	32:W:165:G:H1	1.58	0.50
32:W:437:U:O2	32:W:439:A:N7	2.45	0.50
1:A:350:U:H4'	1:A:1251:U:C5	2.45	0.50
1:A:365:U:C6	5:E:165:LEU:HD13	2.46	0.50
1:A:2250:G:H2'	1:A:2251:G:C8	2.47	0.50
1:A:2382:G:N2	22:V:42:GLY:O	2.43	0.50
1:A:2629:A:O2'	1:A:2630:C:H5'	2.12	0.50
4:D:11:GLY:HA3	16:P:8:ILE:HD11	1.92	0.50
4:D:126:HIS:CE1	4:D:159:LEU:HD22	2.46	0.50
15:O:71:THR:OG1	15:O:72:SER:N	2.45	0.50
19:S:88:ARG:CB	19:S:92:ARG:HB2	2.39	0.50
20:T:8:LEU:CB	25:Z:26:PHE:HE1	2.13	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:439:A:H2'	32:W:440:A:H8	1.76	0.50
1:A:897:G:C4'	26:a:22:THR:HG22	2.37	0.50
1:A:2448:U:C6	30:e:33:PHE:CD2	2.95	0.50
3:C:159:GLY:HA2	3:C:198:GLU:HG2	1.94	0.50
5:E:53:ASN:OD1	5:E:54:ARG:N	2.45	0.50
6:F:29:PRO:HB2	6:F:169:LEU:HD22	1.93	0.50
6:F:105:SER:CA	54:3:37:SER:HB3	2.35	0.50
14:N:31:GLU:HG2	14:N:116:ILE:HG12	1.94	0.50
24:Y:45:LYS:HE3	24:Y:46:LYS:HE2	1.92	0.50
32:W:1385:U:H2'	32:W:1386:A:H8	1.77	0.50
1:A:1339:A:H4'	1:A:1340:A:O5'	2.11	0.50
1:A:1438:C:O2'	1:A:1439:U:OP1	2.30	0.50
1:A:1893:U:OP1	1:A:2439:G:O2'	2.30	0.50
1:A:2187:A:H4'	1:A:2188:G:OP1	2.12	0.50
1:A:2785:U:O4	1:A:2787:A:N7	2.45	0.50
3:C:108:LYS:HE3	3:C:194:GLN:HE21	1.77	0.50
4:D:16:PHE:O	16:P:15:GLN:NE2	2.45	0.50
32:W:62:A:N6	32:W:108:C:N3	2.59	0.50
32:W:317:G:H2'	32:W:318:G:H8	1.76	0.50
50:x:81:LYS:H	50:x:82:GLY:HA2	1.77	0.50
1:A:1658:G:C2	1:A:1664:G:C6	3.00	0.49
1:A:2669:G:H1	1:A:2803:C:N4	2.09	0.49
3:C:243:ARG:HH12	3:C:247:MET:HE3	1.77	0.49
11:K:97:ARG:NH1	32:W:347:C:OP2	2.44	0.49
32:W:1227:C:H2'	32:W:1228:U:C6	2.47	0.49
53:2:81:ASN:N	53:2:81:ASN:ND2	2.60	0.49
1:A:364:A:H4'	1:A:366:A:H8	1.73	0.49
1:A:461:C:H2'	1:A:462:A:C8	2.47	0.49
18:R:73:VAL:HB	18:R:86:GLN:O	2.12	0.49
20:T:29:GLU:HA	20:T:78:LYS:HA	1.94	0.49
32:W:1265:C:O2'	32:W:1287:C:N4	2.45	0.49
1:A:69:C:O2	1:A:73:A:O2'	2.30	0.49
1:A:72:U:C1'	25:Z:51:ALA:HB1	2.39	0.49
1:A:1432:A:O2'	1:A:1433:U:H5'	2.12	0.49
1:A:2670:A:H5''	10:J:79:THR:HG22	1.95	0.49
10:J:45:TYR:O	17:Q:64:ARG:NE	2.38	0.49
13:M:36:ALA:HB2	13:M:103:LEU:HD11	1.94	0.49
15:O:79:GLU:HG2	15:O:83:LYS:HE3	1.93	0.49
28:c:7:LEU:HB2	28:c:17:TYR:HB2	1.93	0.49
54:3:56:VAL:HG11	54:3:60:ASN:HD22	1.77	0.49
1:A:84:A:H3'	21:U:4:LYS:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:G:H2'	1:A:107:G:C8	2.46	0.49
1:A:1929:A:H1'	1:A:1999:A:H2'	1.94	0.49
1:A:2009:G:H3'	1:A:2010:A:H5''	1.94	0.49
1:A:2109:G:C4'	24:Y:23:ASN:HD21	2.20	0.49
1:A:2156:G:H2'	1:A:2157:C:O4'	2.11	0.49
1:A:2766:G:H1	1:A:2796:C:N4	2.09	0.49
1:A:2815:U:OP1	4:D:71:LYS:NZ	2.45	0.49
21:U:49:GLN:N	21:U:50:ALA:HA	2.27	0.49
23:X:19:LYS:O	23:X:20:ASN:C	2.54	0.49
24:Y:39:LEU:N	24:Y:39:LEU:CD1	2.75	0.49
32:W:1058:G:H2'	32:W:1060:G:H8	1.77	0.49
1:A:852:G:O4'	12:L:38:GLN:NE2	2.46	0.49
1:A:934:U:O2'	1:A:935:A:O5'	2.23	0.49
1:A:1943:C:H41	32:W:1419:A:H5'	1.76	0.49
1:A:2219:G:H2'	1:A:2220:A:C8	2.47	0.49
1:A:2815:U:O2'	4:D:64:PRO:O	2.27	0.49
1:A:2876:A:O3'	14:N:60:ARG:NH1	2.45	0.49
3:C:145:GLU:HA	3:C:152:GLY:HA2	1.94	0.49
17:Q:44:ASN:HB2	18:R:76:TYR:CE1	2.47	0.49
19:S:40:PRO:O	19:S:44:SER:OG	2.27	0.49
32:W:630:A:N6	32:W:631:A:N6	2.60	0.49
1:A:113:U:O2'	20:T:33:ARG:NH1	2.46	0.49
1:A:275:A:H62	1:A:296:G:H21	1.59	0.49
1:A:568:G:O2'	1:A:587:C:O2'	2.28	0.49
1:A:2342:C:H1'	6:F:37:ASN:HD21	1.78	0.49
1:A:2799:C:C5'	1:A:2800:C:OP2	2.59	0.49
3:C:145:GLU:HG2	3:C:151:GLY:C	2.38	0.49
7:G:3:ARG:HB2	7:G:6:LYS:HE2	1.95	0.49
7:G:96:ARG:HG3	7:G:107:ASN:HD22	1.78	0.49
8:H:18:LYS:HA	8:H:21:GLU:HB2	1.94	0.49
14:N:17:LEU:HD13	14:N:43:VAL:HG21	1.94	0.49
14:N:27:ASN:C	14:N:29:ARG:H	2.20	0.49
20:T:8:LEU:HD13	25:Z:30:PHE:HZ	1.77	0.49
1:A:565:U:H4'	19:S:25:ARG:HH22	1.77	0.49
1:A:1586:G:O2'	1:A:1587:U:O4'	2.29	0.49
1:A:2488:A:OP2	1:A:2489:U:OP2	2.30	0.49
3:C:205:ILE:HG23	3:C:210:ARG:HB2	1.94	0.49
27:b:27:MET:HE2	27:b:36:MET:HE3	1.95	0.49
32:W:95:U:H2'	32:W:96:G:C8	2.48	0.49
32:W:1328:A:O2'	32:W:1332:G:N7	2.42	0.49
1:A:124:A:H2	29:d:9:ASN:ND2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:A:O2'	1:A:366:A:H2'	2.12	0.49
1:A:1015:G:P	26:a:16:PRO:HA	2.52	0.49
1:A:1295:U:C5	5:E:72:ARG:O	2.64	0.49
3:C:264:ASN:ND2	3:C:266:SER:OG	2.45	0.49
10:J:69:LYS:HA	10:J:72:ASP:HB3	1.94	0.49
15:O:58:THR:HG22	15:O:77:VAL:HG21	1.95	0.49
16:P:109:LYS:HE2	32:W:1474:G:OP2	2.12	0.49
52:z:23:A:H2'	52:z:24:A:C8	2.48	0.49
1:A:970:A:H2'	1:A:971:A:C8	2.48	0.49
1:A:997:C:H2'	1:A:998:G:H8	1.77	0.49
1:A:1080:G:O4'	31:f:18:ARG:NH1	2.45	0.49
1:A:1398:A:N7	1:A:1411:U:O4	2.46	0.49
1:A:1815:A:OP1	1:A:2009:G:N2	2.45	0.49
1:A:2128:U:H2'	1:A:2129:G:H8	1.76	0.49
1:A:2192:U:H4'	1:A:2201:U:H5''	1.94	0.49
1:A:2203:C:H2'	1:A:2204:U:H6	1.74	0.49
1:A:2228:A:H3'	1:A:2229:C:H6	1.78	0.49
1:A:2522:U:O2'	13:M:80:GLU:OE2	2.23	0.49
1:A:2793:A:N6	1:A:2795:G:N7	2.61	0.49
8:H:4:ALA:O	8:H:7:THR:OG1	2.25	0.49
29:d:34:ARG:CG	29:d:42:LEU:HD12	2.14	0.49
1:A:774:A:OP1	1:A:1477:A:O2'	2.28	0.49
1:A:1039:G:OP1	17:Q:50:ARG:NH2	2.43	0.49
1:A:1174:A:N6	1:A:2547:A:N6	2.60	0.49
1:A:2141:A:N6	1:A:2199:G:H22	2.11	0.49
1:A:2357:A:H2'	1:A:2358:A:C8	2.48	0.49
1:A:2609:U:H5'	4:D:137:SER:HA	1.94	0.49
28:c:30:VAL:HG12	28:c:47:GLU:HB2	1.94	0.49
32:W:1068:G:H1	32:W:1208:U:H3	1.61	0.49
1:A:837:U:H3'	1:A:837:U:C6	2.48	0.48
1:A:910:A:N6	1:A:911:G:O6	2.46	0.48
1:A:1452:C:H2'	1:A:1453:A:H8	1.78	0.48
1:A:2100:A:H2'	1:A:2101:G:C8	2.48	0.48
1:A:2160:U:H5'	1:A:2161:G:H5''	1.94	0.48
1:A:2421:A:C5'	30:e:28:TYR:CD2	2.72	0.48
1:A:2909:U:H1'	27:b:50:ASN:ND2	2.26	0.48
5:E:65:TRP:HZ2	5:E:75:GLN:HG3	1.77	0.48
18:R:73:VAL:N	18:R:86:GLN:O	2.46	0.48
23:X:37:VAL:O	23:X:38:GLU:C	2.56	0.48
24:Y:42:GLY:HA3	24:Y:43:LYS:HD3	1.95	0.48
32:W:956:A:H2'	32:W:957:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:1313:G:N2	32:W:1342:A:H62	2.10	0.48
1:A:52:A:H62	1:A:118:A:H62	1.61	0.48
1:A:257:G:N2	30:e:8:ARG:HH21	2.11	0.48
1:A:526:A:H1'	1:A:527:A:H5''	1.93	0.48
1:A:1292:G:H1	17:Q:37:GLN:HE21	1.61	0.48
1:A:1631:A:H4'	1:A:1632:G:H4'	1.93	0.48
2:B:52:G:H21	6:F:26:MET:HE1	1.76	0.48
6:F:109:PRO:HD3	54:3:43:TYR:HH	1.73	0.48
6:F:110:ARG:NE	54:3:35:ILE:HD12	2.27	0.48
30:e:21:LYS:HD2	30:e:49:VAL:HG11	1.94	0.48
32:W:666:U:H3	32:W:758:A:N6	2.10	0.48
43:q:26:LYS:N	43:q:27:GLY:HA2	2.28	0.48
1:A:1184:G:N3	10:J:109:MET:HE1	2.29	0.48
3:C:243:ARG:NH2	3:C:247:MET:CB	2.59	0.48
17:Q:60:LEU:O	17:Q:63:THR:OG1	2.30	0.48
22:V:53:ILE:HG21	22:V:87:VAL:HG23	1.95	0.48
29:d:34:ARG:HG3	29:d:42:LEU:HD13	1.91	0.48
32:W:965:U:C4	32:W:1234:A:N1	2.81	0.48
1:A:588:C:N4	1:A:589:G:C6	2.82	0.48
1:A:1347:A:N6	1:A:1651:G:H8	2.09	0.48
1:A:2191:A:H1'	1:A:2202:A:H5'	1.95	0.48
1:A:2201:U:H5'	1:A:2202:A:OP2	2.14	0.48
1:A:2761:G:H5''	1:A:2762:A:C8	2.47	0.48
12:L:91:VAL:HG21	12:L:121:LEU:HD22	1.94	0.48
32:W:23:G:H2'	32:W:24:G:C8	2.48	0.48
45:s:47:LEU:O	45:s:51:GLY:N	2.46	0.48
1:A:753:A:OP1	3:C:7:LYS:NZ	2.45	0.48
1:A:897:G:O2'	26:a:22:THR:HG22	2.14	0.48
14:N:106:PRO:HA	14:N:113:PRO:HA	1.95	0.48
18:R:79:LYS:O	18:R:80:LYS:HG2	2.12	0.48
23:X:32:LYS:C	23:X:34:GLY:H	2.21	0.48
23:X:41:ALA:O	23:X:42:SER:C	2.56	0.48
1:A:367:G:O2'	1:A:368:G:OP2	2.22	0.48
1:A:528:G:H2'	1:A:553:A:H62	1.78	0.48
1:A:898:U:C2'	26:a:42:ALA:O	2.61	0.48
1:A:2448:U:H5	30:e:33:PHE:HE2	1.42	0.48
4:D:139:TYR:HA	4:D:142:ARG:HH21	1.79	0.48
14:N:29:ARG:NH2	27:b:55:ASN:C	2.72	0.48
19:S:38:LEU:HD22	27:b:27:MET:CE	2.41	0.48
21:U:5:LYS:HA	21:U:6:GLY:HA2	1.55	0.48
32:W:954:G:N1	32:W:1347:G:OP2	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:1469:C:H2'	32:W:1470:A:H8	1.79	0.48
1:A:636:G:H1	1:A:712:C:N4	2.10	0.48
1:A:795:G:C5	1:A:797:A:C5	3.01	0.48
1:A:799:A:N6	53:2:80:MET:HE1	2.28	0.48
1:A:817:G:P	29:d:11:LYS:HE3	2.53	0.48
1:A:859:C:HO2'	1:A:1266:A:HO2'	1.59	0.48
1:A:2171:G:N1	1:A:2179:U:C2	2.81	0.48
1:A:2420:G:C3'	30:e:28:TYR:HE2	2.25	0.48
52:z:34:G:C6	52:z:35:U:C5	3.01	0.48
1:A:254:A:P	30:e:7:HIS:NE2	2.71	0.48
1:A:1364:C:C2	19:S:86:ARG:NH1	2.82	0.48
1:A:2157:C:O2'	1:A:2158:C:O4'	2.32	0.48
1:A:2173:G:H1'	1:A:2176:A:N6	2.29	0.48
3:C:53:HIS:HB2	3:C:217:ARG:HB3	1.96	0.48
16:P:29:LEU:HB3	16:P:89:VAL:HG22	1.95	0.48
27:b:13:LYS:O	27:b:17:ARG:HG2	2.14	0.48
32:W:843:U:H2'	32:W:844:A:C8	2.48	0.48
1:A:269:G:H1'	1:A:322:A:H2	1.79	0.48
1:A:377:G:N3	1:A:378:C:C6	2.82	0.48
1:A:1942:A:C2	32:W:1502:A:N7	2.81	0.48
1:A:2039:G:OP2	19:S:41:ARG:NH1	2.47	0.48
1:A:2082:G:H4'	4:D:152:ASN:HD22	1.78	0.48
1:A:2224:U:HO2'	1:A:2225:C:C4'	2.17	0.48
1:A:2719:A:N1	14:N:39:GLU:OE2	2.47	0.48
21:U:48:THR:HA	21:U:49:GLN:HB2	1.95	0.48
30:e:20:GLY:HA2	30:e:21:LYS:O	2.13	0.48
1:A:1290:G:OP2	12:L:21:ARG:NH1	2.47	0.48
1:A:1291:A:H5''	17:Q:13:ARG:NH2	2.29	0.48
1:A:2181:C:O3'	1:A:2182:G:O4'	2.32	0.48
3:C:243:ARG:HH12	3:C:247:MET:CE	2.26	0.48
21:U:48:THR:O	21:U:52:PRO:HA	2.14	0.48
24:Y:40:VAL:CG1	24:Y:41:ASN:H	2.13	0.48
25:Z:31:GLN:O	25:Z:35:GLY:N	2.44	0.48
30:e:9:GLY:O	30:e:13:ARG:HG2	2.12	0.48
1:A:898:U:H4'	26:a:46:MET:N	2.28	0.47
1:A:2572:G:H21	1:A:2675:C:H5''	1.79	0.47
5:E:20:ASN:ND2	5:E:203:GLU:OE1	2.47	0.47
40:n:107:ASP:O	40:n:109:ARG:N	2.47	0.47
1:A:2856:G:OP1	4:D:57:ARG:NH2	2.46	0.47
6:F:135:GLN:HE22	6:F:150:ARG:N	2.11	0.47
30:e:57:ARG:HG3	30:e:58:ILE:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:681:C:O2'	1:A:685:U:OP1	2.32	0.47
1:A:1294:A:C3'	1:A:1295:U:C5'	2.90	0.47
3:C:167:LYS:HB2	3:C:172:VAL:HG22	1.95	0.47
4:D:12:MET:SD	4:D:26:THR:HG22	2.53	0.47
5:E:67:GLN:HE22	5:E:74:ARG:HB3	1.78	0.47
14:N:47:MET:HE1	14:N:62:ALA:HA	1.96	0.47
18:R:22:ILE:O	18:R:93:THR:N	2.40	0.47
19:S:3:ALA:HB2	19:S:58:ALA:HB2	1.96	0.47
20:T:11:PRO:HG2	25:Z:33:ALA:HB1	1.97	0.47
23:X:11:GLY:C	23:X:13:GLY:H	2.21	0.47
32:W:547:U:H2'	32:W:548:A:C8	2.49	0.47
32:W:766:U:H2'	32:W:767:G:O4'	2.14	0.47
32:W:872:C:H1'	32:W:884:G:H5''	1.96	0.47
1:A:254:A:OP2	30:e:7:HIS:CD2	2.66	0.47
1:A:1656:C:O2'	1:A:1657:C:C5'	2.58	0.47
5:E:64:PRO:HB2	5:E:65:TRP:CE3	2.48	0.47
10:J:128:GLY:HA2	10:J:129:SER:HA	1.68	0.47
14:N:102:MET:HE1	27:b:54:ILE:CG2	2.45	0.47
3:C:253:PRO:HG2	3:C:257:PHE:CG	2.49	0.47
10:J:14:ARG:NH2	10:J:50:ASP:OD2	2.45	0.47
16:P:100:LEU:HB3	16:P:103:LEU:HD23	1.96	0.47
27:b:35:GLU:HA	27:b:36:MET:HA	1.72	0.47
32:W:510:C:O2	32:W:558:C:O2'	2.33	0.47
1:A:7:G:O6	1:A:2919:A:N6	2.47	0.47
1:A:229:A:O2'	1:A:230:A:OP1	2.33	0.47
1:A:839:G:C4'	1:A:840:A:C2	2.97	0.47
1:A:2181:C:C2'	1:A:2182:G:O4'	2.63	0.47
1:A:2449:C:OP1	30:e:34:ALA:N	2.48	0.47
1:A:2853:C:H2'	1:A:2854:A:H8	1.80	0.47
4:D:176:ILE:HA	4:D:188:ILE:HA	1.96	0.47
18:R:79:LYS:C	18:R:80:LYS:CG	2.84	0.47
20:T:20:LEU:HB3	20:T:25:LYS:HG3	1.97	0.47
25:Z:11:THR:HA	25:Z:14:ILE:HD12	1.95	0.47
32:W:848:G:H2'	32:W:849:G:C8	2.50	0.47
32:W:1117:C:OP1	34:h:172:VAL:N	2.46	0.47
1:A:2242:U:H3'	1:A:2243:C:H5'	1.95	0.47
1:A:2494:C:O2'	31:f:5:PRO:CG	2.61	0.47
1:A:2614:U:C1'	53:2:89:ASP:HB2	2.44	0.47
6:F:68:THR:OG1	6:F:85:ILE:O	2.32	0.47
20:T:11:PRO:CG	25:Z:33:ALA:HB3	2.44	0.47
20:T:13:ILE:HD13	25:Z:33:ALA:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:421:G:N2	32:W:436:G:H1'	2.30	0.47
32:W:987:A:N6	32:W:1233:U:O5'	2.48	0.47
32:W:1237:C:H2'	32:W:1238:A:C8	2.50	0.47
1:A:675:C:N4	1:A:676:G:O6	2.48	0.47
1:A:1433:U:H2'	1:A:1433:U:O2	2.14	0.47
1:A:2261:C:H2'	1:A:2262:A:H8	1.79	0.47
1:A:2629:A:C2'	1:A:2630:C:H5'	2.45	0.47
15:O:69:GLY:O	15:O:105:ARG:NH2	2.47	0.47
20:T:9:LYS:HB2	20:T:29:GLU:HB2	1.96	0.47
32:W:1525:C:H2'	32:W:1526:G:C8	2.50	0.47
1:A:669:C:OP2	12:L:104:LYS:NZ	2.40	0.47
1:A:2046:U:H1'	27:b:7:ARG:N	2.30	0.47
1:A:2335:U:H3'	1:A:2336:G:H5''	1.97	0.47
5:E:71:GLY:O	5:E:72:ARG:HD2	2.15	0.47
14:N:78:ASP:HB3	14:N:81:GLN:HG3	1.96	0.47
17:Q:52:GLN:HA	17:Q:55:ARG:HG2	1.96	0.47
32:W:413:U:H1'	32:W:507:A:H2'	1.97	0.47
1:A:822:G:H4'	1:A:823:G:C5'	2.45	0.47
1:A:831:U:C5	1:A:840:A:H2	2.27	0.47
1:A:852:G:H5'	1:A:853:C:H5	1.79	0.47
1:A:875:U:H3	1:A:876:A:N6	2.08	0.47
1:A:896:A:O2'	26:a:21:VAL:HG11	2.15	0.47
1:A:2158:C:OP2	1:A:2159:U:C5	2.52	0.47
1:A:2164:A:H3'	1:A:2165:A:C8	2.50	0.47
1:A:2386:U:OP1	22:V:28:ARG:NH1	2.48	0.47
1:A:2648:U:H4'	4:D:156:LYS:HA	1.97	0.47
20:T:11:PRO:CG	25:Z:33:ALA:CB	2.93	0.47
24:Y:37:ARG:CD	24:Y:45:LYS:HG3	2.33	0.47
27:b:18:THR:O	27:b:21:LYS:NZ	2.48	0.47
32:W:1074:G:H21	32:W:1199:G:H1'	1.80	0.47
32:W:1501:G:O2'	32:W:1502:A:OP1	2.29	0.47
1:A:248:G:OP2	12:L:67:THR:OG1	2.24	0.46
1:A:1524:A:H2'	1:A:1525:G:H8	1.78	0.46
1:A:1658:G:C6	1:A:1664:G:O6	2.68	0.46
1:A:2614:U:O2	53:2:87:GLU:CG	2.63	0.46
1:A:2835:A:H5''	4:D:63:LYS:HD2	1.97	0.46
5:E:6:LEU:HD13	5:E:7:TYR:N	2.30	0.46
5:E:65:TRP:CH2	5:E:72:ARG:NH2	2.83	0.46
8:H:84:PHE:HA	8:H:116:LYS:HZ3	1.80	0.46
32:W:960:U:H2'	32:W:961:G:C8	2.51	0.46
32:W:1066:U:H2'	32:W:1067:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:1317:C:OP1	44:r:97:VAL:N	2.48	0.46
1:A:45:G:N7	1:A:218:G:O2'	2.43	0.46
1:A:2472:C:H2'	1:A:2473:G:C8	2.50	0.46
1:A:2766:G:H2'	1:A:2767:A:C8	2.50	0.46
10:J:46:THR:O	10:J:49:VAL:HG12	2.15	0.46
13:M:41:TRP:HB3	13:M:94:VAL:HG11	1.97	0.46
23:X:1:MET:HA	23:X:21:VAL:O	2.15	0.46
29:d:34:ARG:CB	29:d:42:LEU:CD1	2.93	0.46
32:W:643:C:H2'	32:W:644:A:H8	1.80	0.46
32:W:1175:G:O2'	32:W:1178:A:N6	2.48	0.46
1:A:694:G:H2'	1:A:695:G:H8	1.79	0.46
1:A:1788:A:H5''	1:A:2744:C:H1'	1.98	0.46
3:C:132:LEU:HA	3:C:135:ILE:HD12	1.96	0.46
3:C:177:ASN:OD1	3:C:178:SER:N	2.48	0.46
3:C:241:ILE:HD11	3:C:246:PRO:HA	1.97	0.46
12:L:20:GLY:HA2	12:L:28:GLY:HA2	1.96	0.46
15:O:26:ALA:C	15:O:28:ARG:H	2.23	0.46
1:A:106:G:H4'	1:A:337:A:H5''	1.97	0.46
1:A:275:A:H62	1:A:296:G:N2	2.13	0.46
1:A:617:G:N1	1:A:2060:A:OP1	2.35	0.46
1:A:2126:G:H1	1:A:2221:C:H42	1.63	0.46
1:A:2834:A:N6	1:A:2835:A:N6	2.63	0.46
20:T:12:VAL:HG21	20:T:78:LYS:HE2	1.97	0.46
23:X:67:SER:C	23:X:69:LYS:H	2.24	0.46
24:Y:14:ALA:HA	24:Y:28:THR:HA	1.97	0.46
32:W:345:G:H2'	32:W:346:A:C8	2.51	0.46
32:W:1367:U:OP1	45:s:35:ARG:N	2.43	0.46
1:A:282:G:H1'	1:A:283:G:C8	2.51	0.46
1:A:304:G:H2'	1:A:305:A:H8	1.80	0.46
1:A:1015:G:N2	1:A:1031:C:OP1	2.44	0.46
1:A:1306:G:H3'	27:b:20:PHE:HE1	1.80	0.46
5:E:4:VAL:HG12	5:E:5:ALA:N	2.30	0.46
29:d:34:ARG:HB3	29:d:42:LEU:HD13	1.97	0.46
52:z:35:U:H5'	52:z:35:U:C6	2.45	0.46
1:A:647:A:H4'	1:A:648:G:O5'	2.15	0.46
1:A:1894:U:O2'	1:A:1904:G:N2	2.45	0.46
1:A:2173:G:O2'	1:A:2174:C:H5	1.80	0.46
1:A:2219:G:H2'	1:A:2220:A:H8	1.81	0.46
1:A:2332:G:O2'	6:F:129:THR:OG1	2.24	0.46
29:d:34:ARG:CB	29:d:42:LEU:HD13	2.45	0.46
1:A:365:U:O2	1:A:365:U:O2'	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:U:H2'	1:A:568:G:H8	1.80	0.46
1:A:626:G:H2'	1:A:627:G:C8	2.51	0.46
1:A:837:U:C6	1:A:837:U:C3'	2.98	0.46
1:A:1309:G:O2'	1:A:1364:C:N4	2.47	0.46
1:A:1848:A:OP1	3:C:157:SER:OG	2.28	0.46
1:A:2213:U:H2'	1:A:2214:G:C8	2.51	0.46
1:A:2245:G:H2'	1:A:2246:G:H8	1.80	0.46
1:A:2330:A:H61	1:A:2344:U:H3	1.64	0.46
7:G:166:GLU:HA	7:G:167:GLY:HA2	1.50	0.46
11:K:64:ARG:HH12	16:P:71:VAL:HG21	1.80	0.46
28:c:22:ASN:HD22	28:c:25:ASN:HD22	1.64	0.46
32:W:98:U:O2'	32:W:99:A:OP1	2.24	0.46
32:W:716:U:H2'	32:W:717:G:H8	1.81	0.46
32:W:1421:C:H2'	32:W:1422:A:C8	2.51	0.46
51:y:6:SER:O	51:y:8:ILE:N	2.44	0.46
1:A:337:A:O2'	1:A:338:G:O4'	2.34	0.46
1:A:507:A:H62	1:A:516:G:N2	2.12	0.46
1:A:721:G:C1'	5:E:74:ARG:HD2	2.46	0.46
1:A:1015:G:OP1	26:a:15:ARG:O	2.34	0.46
1:A:1155:C:H41	8:H:59:MET:HE1	1.80	0.46
1:A:2100:A:H2'	1:A:2101:G:H8	1.81	0.46
1:A:2777:A:H4'	7:G:67:GLY:HA3	1.97	0.46
10:J:77:ARG:NH2	10:J:88:ARG:HH21	2.14	0.46
21:U:79:THR:HB	21:U:95:LYS:H	1.80	0.46
21:U:86:GLU:HG3	21:U:87:ASP:N	2.31	0.46
32:W:54:U:H2'	32:W:55:A:C8	2.51	0.46
32:W:243:C:H2'	32:W:244:G:H8	1.81	0.46
32:W:1495:U:H2'	32:W:1496:G:H8	1.81	0.46
1:A:9:U:H2'	1:A:10:A:H8	1.81	0.46
1:A:72:U:H4'	25:Z:51:ALA:HB2	1.97	0.46
1:A:128:C:H5'	1:A:1644:C:O2'	2.15	0.46
1:A:789:C:H2'	1:A:790:A:C8	2.51	0.46
1:A:1128:U:OP1	9:I:119:ALA:N	2.43	0.46
1:A:1871:G:HO2'	3:C:245:SER:HG	1.51	0.46
1:A:2009:G:C4	1:A:2011:U:C6	3.04	0.46
1:A:2757:U:O2	4:D:191:ASN:ND2	2.49	0.46
1:A:2859:G:H21	1:A:2908:A:H62	1.64	0.46
2:B:98:G:H3'	2:B:99:A:C8	2.50	0.46
19:S:92:ARG:HE	19:S:92:ARG:CA	2.27	0.46
32:W:343:C:H2'	32:W:344:A:H8	1.81	0.46
32:W:415:A:H2'	32:W:416:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:960:U:H2'	32:W:961:G:H8	1.81	0.46
1:A:245:G:C5	30:e:3:LYS:HB2	2.49	0.46
1:A:678:A:O3'	12:L:68:ASN:ND2	2.32	0.46
1:A:898:U:C4'	26:a:46:MET:CG	2.92	0.46
1:A:1104:U:H2'	1:A:1105:G:C8	2.51	0.46
1:A:1108:G:H21	1:A:1123:A:H62	1.64	0.46
1:A:1501:U:O2'	1:A:2878:U:OP1	2.32	0.46
1:A:2009:G:O6	1:A:2011:U:O4	2.33	0.46
1:A:2228:A:H3'	1:A:2229:C:C6	2.51	0.46
3:C:247:MET:HE2	3:C:251:GLY:O	2.16	0.46
6:F:102:LYS:NZ	6:F:140:GLU:OE2	2.41	0.46
13:M:29:PHE:HB2	13:M:105:GLU:OE1	2.16	0.46
16:P:99:LYS:HB3	16:P:101:TYR:CE2	2.50	0.46
16:P:107:ARG:HA	16:P:108:GLY:HA2	1.59	0.46
17:Q:69:ALA:HB2	17:Q:79:LEU:HD22	1.98	0.46
24:Y:38:ILE:C	24:Y:39:LEU:HD12	2.41	0.46
1:A:776:G:OP2	3:C:207:LYS:NZ	2.48	0.45
1:A:896:A:C2	26:a:25:THR:HG22	2.51	0.45
2:B:11:A:H62	2:B:68:C:H5'	1.81	0.45
3:C:58:HIS:HB2	3:C:213:TRP:HE3	1.81	0.45
6:F:35:VAL:HG13	6:F:88:LYS:HG3	1.98	0.45
7:G:158:TYR:HA	7:G:173:LYS:HB2	1.97	0.45
10:J:40:LYS:O	17:Q:67:ALA:HB2	2.16	0.45
12:L:63:LYS:HA	30:e:13:ARG:CD	2.36	0.45
12:L:106:ASN:O	12:L:108:GLY:N	2.47	0.45
20:T:27:THR:HG22	20:T:80:ILE:HG13	1.98	0.45
28:c:14:GLU:O	28:c:16:ASN:ND2	2.49	0.45
32:W:833:U:H2'	32:W:834:G:H8	1.81	0.45
32:W:1335:U:H2'	32:W:1336:G:C8	2.51	0.45
1:A:1613:C:H2'	1:A:1614:A:H2'	1.97	0.45
1:A:1784:A:O2'	1:A:1785:G:OP1	2.27	0.45
3:C:40:LYS:O	3:C:43:ARG:HG2	2.16	0.45
16:P:50:VAL:HG22	16:P:64:VAL:HG22	1.98	0.45
18:R:77:LYS:HB2	18:R:82:VAL:HB	1.97	0.45
32:W:734:G:OP1	32:W:863:G:N2	2.40	0.45
1:A:1969:U:OP1	1:A:2632:G:N2	2.42	0.45
1:A:2117:A:H2'	1:A:2118:U:H6	1.80	0.45
1:A:2158:C:P	1:A:2158:C:O4'	2.74	0.45
1:A:2192:U:C5'	1:A:2201:U:H5	2.24	0.45
5:E:67:GLN:HE22	5:E:74:ARG:CA	2.28	0.45
16:P:38:GLY:HA2	16:P:39:ASN:HA	1.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:49:ASP:O	17:Q:53:LYS:N	2.47	0.45
23:X:14:LYS:C	23:X:16:GLY:N	2.74	0.45
32:W:224:U:H2'	32:W:225:A:C8	2.52	0.45
32:W:848:G:O2'	32:W:849:G:OP1	2.31	0.45
1:A:794:U:H2'	1:A:795:G:OP1	2.17	0.45
1:A:1171:G:C5'	31:f:37:GLY:HA2	2.32	0.45
1:A:1242:U:H2'	1:A:1243:A:C8	2.51	0.45
1:A:2422:U:OP1	30:e:28:TYR:N	2.49	0.45
5:E:71:GLY:O	5:E:72:ARG:HG2	2.16	0.45
11:K:52:VAL:HG22	11:K:94:ARG:HH11	1.81	0.45
23:X:130:PRO:O	23:X:142:LYS:N	2.45	0.45
32:W:307:G:N2	32:W:574:U:O2	2.50	0.45
52:z:72:C:N4	52:z:73:G:O6	2.49	0.45
1:A:338:G:H2'	1:A:339:A:C8	2.51	0.45
1:A:356:G:H2'	1:A:357:G:H8	1.81	0.45
1:A:1630:G:O2'	1:A:1631:A:O5'	2.31	0.45
1:A:2140:U:H1'	1:A:2148:A:H5''	1.98	0.45
1:A:2800:C:O2'	4:D:172:GLN:NE2	2.38	0.45
2:B:98:G:H3'	2:B:99:A:H8	1.82	0.45
4:D:15:VAL:HB	4:D:25:VAL:HG21	1.97	0.45
5:E:12:SER:HB2	5:E:13:THR:HB	1.97	0.45
7:G:5:GLY:HA2	7:G:70:ARG:HD3	1.98	0.45
15:O:65:VAL:HB	15:O:68:THR:H	1.82	0.45
23:X:82:LYS:HA	23:X:92:SER:CB	2.46	0.45
32:W:511:C:OP1	43:q:127:ARG:N	2.40	0.45
32:W:1210:A:H4'	32:W:1211:U:O5'	2.16	0.45
1:A:874:U:H4'	1:A:875:U:C6	2.50	0.45
1:A:1219:C:H3'	1:A:1220:G:H4'	1.98	0.45
1:A:1599:U:H2'	1:A:1600:G:H5'	1.98	0.45
1:A:1886:G:H21	1:A:1914:A:H62	1.65	0.45
1:A:2070:U:H2'	1:A:2071:A:H8	1.82	0.45
1:A:2516:G:H2'	1:A:2517:A:C8	2.52	0.45
6:F:107:SER:HB2	6:F:137:ILE:HG22	1.99	0.45
10:J:14:ARG:NH2	10:J:50:ASP:O	2.50	0.45
10:J:24:LYS:HE2	10:J:143:LEU:HD22	1.97	0.45
23:X:6:LEU:HA	23:X:15:LYS:HA	1.99	0.45
32:W:1066:U:H2'	32:W:1067:G:C8	2.52	0.45
1:A:224:A:H1'	1:A:236:A:H1'	1.99	0.45
1:A:1003:A:N1	1:A:2487:U:H4'	2.32	0.45
1:A:1619:A:H2'	1:A:1620:A:C8	2.52	0.45
1:A:2252:A:H2'	1:A:2253:G:O4'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:245:SER:HA	3:C:246:PRO:HD2	1.78	0.45
4:D:123:ILE:HD11	4:D:141:ARG:HA	1.98	0.45
10:J:77:ARG:NH1	10:J:88:ARG:HE	2.15	0.45
12:L:23:ILE:HG21	18:R:81:ASN:O	2.16	0.45
52:z:71:C:H5''	52:z:71:C:C6	2.44	0.45
1:A:675:C:O2	1:A:685:U:O2'	2.34	0.45
1:A:825:G:O6	1:A:833:C:N3	2.50	0.45
1:A:1068:G:N2	1:A:1069:U:O4	2.49	0.45
1:A:2182:G:H2'	1:A:2182:G:N3	2.32	0.45
1:A:2683:A:O2'	1:A:2684:G:O5'	2.26	0.45
6:F:109:PRO:CG	54:3:43:TYR:HE2	2.30	0.45
14:N:104:LEU:HD13	14:N:105:GLY:N	2.31	0.45
15:O:90:ILE:HA	15:O:91:SER:HB3	1.98	0.45
25:Z:17:LYS:HB3	25:Z:53:MET:HE1	1.98	0.45
30:e:40:GLN:O	30:e:44:LEU:HG	2.17	0.45
40:n:104:LEU:O	40:n:106:ARG:N	2.38	0.45
1:A:966:U:H4'	2:B:79:C:H4'	1.99	0.45
1:A:1298:C:H2'	1:A:1299:G:C8	2.52	0.45
1:A:1817:C:OP1	3:C:221:ARG:NH1	2.50	0.45
1:A:2157:C:O2'	1:A:2158:C:H1'	2.16	0.45
1:A:2279:G:O2'	1:A:2525:C:OP1	2.25	0.45
17:Q:42:SER:O	17:Q:46:ALA:N	2.50	0.45
32:W:1013:G:H2'	32:W:1014:A:H4'	1.99	0.45
1:A:839:G:O4'	1:A:840:A:C2	2.70	0.45
1:A:928:G:H2'	1:A:929:G:C8	2.52	0.45
1:A:1353:C:N4	1:A:1377:G:N1	2.43	0.45
1:A:1754:U:H2'	1:A:1755:C:C6	2.52	0.45
3:C:208:ALA:O	3:C:211:SER:OG	2.30	0.45
8:H:33:LEU:O	8:H:36:SER:OG	2.27	0.45
17:Q:114:LYS:HA	17:Q:117:LEU:HD12	1.99	0.45
23:X:9:VAL:C	23:X:11:GLY:N	2.75	0.45
32:W:328:G:H2'	32:W:329:A:C8	2.52	0.45
32:W:1400:U:H2'	32:W:1401:G:C8	2.52	0.45
32:W:1491:U:H2'	32:W:1492:G:C8	2.52	0.45
1:A:302:A:H2'	1:A:303:G:C8	2.52	0.44
1:A:719:C:H5'	1:A:848:G:H22	1.82	0.44
1:A:938:G:H2'	1:A:939:G:H8	1.82	0.44
1:A:2170:A:H2'	1:A:2171:G:C8	2.52	0.44
5:E:71:GLY:C	5:E:72:ARG:HG2	2.42	0.44
32:W:66:G:H4'	32:W:67:A:H5''	1.98	0.44
32:W:1469:C:H2'	32:W:1470:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:25:GLU:C	35:i:27:GLU:H	2.23	0.44
1:A:734:C:H42	1:A:834:C:H4'	1.80	0.44
1:A:823:G:H2'	1:A:824:G:OP1	2.18	0.44
1:A:1015:G:H4'	26:a:14:GLY:HA2	1.98	0.44
1:A:1187:U:OP2	10:J:66:THR:OG1	2.35	0.44
1:A:1478:G:H2'	1:A:1479:G:C8	2.52	0.44
1:A:2010:A:H3'	1:A:2011:U:C5'	2.47	0.44
1:A:2046:U:H1'	27:b:7:ARG:H	1.82	0.44
1:A:2349:A:O2'	1:A:2362:A:N6	2.50	0.44
1:A:2784:C:H4'	1:A:2785:U:OP1	2.17	0.44
2:B:36:C:H2'	2:B:37:A:O4'	2.17	0.44
2:B:39:A:H3'	2:B:40:C:H5'	1.98	0.44
15:O:35:ARG:HA	15:O:40:ILE:HG13	1.98	0.44
16:P:5:GLN:HB2	16:P:8:ILE:HB	1.99	0.44
17:Q:92:ARG:NH1	17:Q:93:LYS:HB2	2.32	0.44
17:Q:103:LEU:CD1	17:Q:104:THR:HA	2.38	0.44
20:T:46:ILE:HD13	25:Z:26:PHE:CE1	2.49	0.44
21:U:48:THR:HB	21:U:50:ALA:N	2.31	0.44
22:V:75:VAL:HG22	22:V:89:VAL:HG22	1.98	0.44
23:X:11:GLY:O	23:X:13:GLY:N	2.47	0.44
52:z:34:G:H2'	52:z:34:G:N3	2.32	0.44
1:A:677:A:OP1	12:L:64:ARG:NH2	2.49	0.44
1:A:1755:C:H2'	1:A:1756:U:C6	2.52	0.44
1:A:2202:A:OP1	1:A:2202:A:C5	2.69	0.44
3:C:94:ILE:HD12	3:C:104:ILE:HD12	1.99	0.44
4:D:185:LEU:HD13	16:P:11:ILE:HD11	1.99	0.44
6:F:67:VAL:HB	6:F:84:PRO:HB2	1.99	0.44
17:Q:25:PHE:HZ	27:b:11:MET:CE	2.30	0.44
17:Q:37:GLN:O	17:Q:41:LYS:HG2	2.17	0.44
18:R:4:ILE:O	18:R:38:VAL:HG13	2.17	0.44
23:X:23:ASP:C	23:X:25:TYR:H	2.23	0.44
24:Y:23:ASN:HB2	24:Y:24:ALA:HA	2.00	0.44
32:W:956:A:H2'	32:W:957:G:H8	1.81	0.44
32:W:1257:A:H2	32:W:1298:A:H62	1.65	0.44
1:A:279:A:H2'	1:A:280:G:C8	2.52	0.44
1:A:970:A:H4'	22:V:37:GLN:HE22	1.83	0.44
1:A:976:U:O3'	26:a:37:HIS:CE1	2.71	0.44
1:A:1829:C:P	3:C:182:ARG:HH22	2.40	0.44
5:E:10:ASN:H	5:E:12:SER:HB3	1.83	0.44
10:J:5:PRO:HB3	17:Q:61:TRP:HE1	1.82	0.44
13:M:67:LYS:HD2	13:M:105:GLU:OE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:z:17:U:OP1	52:z:60:U:O2'	2.22	0.44
1:A:377:G:C2	1:A:378:C:C4	3.05	0.44
1:A:1018:G:H3'	1:A:1019:A:H5''	2.00	0.44
1:A:1023:G:H5'	17:Q:55:ARG:HH12	1.83	0.44
1:A:2136:C:H2'	1:A:2137:U:C6	2.51	0.44
1:A:2923:A:H2'	1:A:2924:A:C8	2.52	0.44
2:B:76:A:H62	2:B:96:G:N2	2.07	0.44
3:C:81:VAL:HA	3:C:92:ALA:HA	1.99	0.44
4:D:49:ILE:HD12	4:D:86:VAL:HG21	2.00	0.44
5:E:46:GLN:HG2	5:E:48:THR:HG23	1.99	0.44
6:F:111:VAL:HG22	6:F:137:ILE:HG12	1.99	0.44
7:G:21:ASP:HA	7:G:22:ASN:HA	1.85	0.44
18:R:65:GLN:HG2	18:R:93:THR:HG23	2.00	0.44
32:W:523:C:H2'	32:W:524:G:H8	1.82	0.44
32:W:551:U:H2'	32:W:552:G:C8	2.53	0.44
32:W:739:G:C5	32:W:740:G:H1'	2.53	0.44
32:W:1074:G:N2	32:W:1199:G:H1'	2.32	0.44
52:z:18:G:O2'	52:z:57:G:N2	2.51	0.44
1:A:1046:A:H62	1:A:1200:G:H2'	1.82	0.44
1:A:2078:A:N6	1:A:2647:G:O6	2.51	0.44
1:A:2174:C:C6	1:A:2174:C:C5'	3.01	0.44
2:B:79:C:N4	2:B:80:G:O6	2.51	0.44
6:F:104:ILE:O	54:3:43:TYR:CZ	2.70	0.44
17:Q:10:THR:O	17:Q:14:ARG:HG2	2.18	0.44
17:Q:89:GLU:HG2	18:R:48:VAL:HG13	1.98	0.44
32:W:58:U:H2'	32:W:59:G:C8	2.53	0.44
32:W:500:A:H2'	32:W:501:A:H8	1.83	0.44
32:W:1111:A:H4'	32:W:1112:A:O5'	2.18	0.44
32:W:1544:A:H8	32:W:1544:A:C5'	2.29	0.44
36:j:46:VAL:O	36:j:72:ILE:N	2.50	0.44
50:x:81:LYS:N	50:x:82:GLY:HA2	2.33	0.44
51:y:67:VAL:H	51:y:68:HIS:CA	2.31	0.44
1:A:897:G:O6	1:A:974:A:N6	2.50	0.44
1:A:899:C:H4'	26:a:41:ALA:O	2.18	0.44
1:A:1231:G:OP1	12:L:30:THR:OG1	2.36	0.44
1:A:1364:C:N3	19:S:86:ARG:CZ	2.80	0.44
1:A:2163:A:H1'	1:A:2188:G:H1'	1.98	0.44
1:A:2476:G:N2	1:A:2479:A:OP2	2.51	0.44
1:A:2652:G:OP1	1:A:2851:A:O2'	2.27	0.44
1:A:2864:G:O6	1:A:2902:A:N6	2.50	0.44
2:B:30:C:H42	2:B:48:G:H1	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:179:GLY:HA3	3:C:275:LYS:HD3	1.99	0.44
6:F:69:ARG:HA	6:F:84:PRO:HA	2.00	0.44
8:H:58:THR:HG21	8:H:82:ILE:O	2.18	0.44
8:H:71:GLY:O	8:H:73:ASN:N	2.45	0.44
10:J:124:ASN:HB3	10:J:126:TYR:HE2	1.83	0.44
15:O:65:VAL:HG13	15:O:73:ALA:HB2	1.98	0.44
21:U:9:VAL:HG13	21:U:69:MET:H	1.82	0.44
32:W:119:C:H4'	32:W:120:A:O5'	2.17	0.44
32:W:974:A:H5''	32:W:1207:A:O3'	2.17	0.44
1:A:513:A:H8	1:A:513:A:O5'	2.01	0.44
1:A:615:U:O5'	1:A:2059:A:N6	2.49	0.44
1:A:678:A:H2'	1:A:679:A:C8	2.49	0.44
1:A:1171:G:O2'	31:f:5:PRO:HB3	2.18	0.44
1:A:1932:G:H2'	1:A:1933:G:H8	1.83	0.44
1:A:1944:U:O4	32:W:1418:C:H4'	2.17	0.44
1:A:2129:G:H1	1:A:2218:U:H3	1.65	0.44
1:A:2168:G:H2'	1:A:2169:G:C8	2.53	0.44
6:F:79:LEU:HD23	6:F:83:MET:HB2	1.99	0.44
6:F:108:LEU:N	6:F:109:PRO:HD2	2.32	0.44
8:H:32:GLY:HA2	8:H:108:ILE:HD11	1.99	0.44
8:H:84:PHE:HA	8:H:116:LYS:NZ	2.32	0.44
17:Q:25:PHE:HZ	27:b:11:MET:HE1	1.83	0.44
32:W:418:G:O6	32:W:437:U:O2'	2.31	0.44
32:W:992:U:O2	32:W:1231:G:N2	2.39	0.44
1:A:29:U:O2	1:A:1255:G:O2'	2.36	0.44
1:A:406:G:H2'	1:A:407:A:C8	2.53	0.44
1:A:938:G:H2'	1:A:939:G:C8	2.53	0.44
1:A:1537:G:H2'	1:A:1538:G:C8	2.49	0.44
1:A:1942:A:N1	32:W:1502:A:N7	2.65	0.44
1:A:2577:G:O2'	11:K:4:GLN:OE1	2.36	0.44
11:K:78:SER:OG	16:P:74:GLU:OE1	2.34	0.44
12:L:75:ALA:HA	12:L:76:VAL:HA	1.76	0.44
19:S:3:ALA:HB3	19:S:107:VAL:HB	1.99	0.44
32:W:73:C:H2'	32:W:74:A:C8	2.52	0.44
32:W:126:G:H1	32:W:241:C:N4	2.16	0.44
32:W:1525:C:H2'	32:W:1526:G:H8	1.83	0.44
32:W:1547:U:H6	32:W:1547:U:O5'	2.01	0.44
1:A:17:G:H4'	17:Q:25:PHE:HE1	1.82	0.43
1:A:719:C:H5'	1:A:848:G:N2	2.33	0.43
1:A:1848:A:H5''	3:C:160:THR:HG21	1.99	0.43
1:A:2468:A:H8	1:A:2468:A:H5'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:71:GLY:C	8:H:73:ASN:H	2.26	0.43
13:M:36:ALA:HB1	13:M:127:ILE:HG21	2.00	0.43
13:M:104:PHE:HE2	13:M:125:LEU:HD11	1.83	0.43
23:X:67:SER:C	23:X:69:LYS:N	2.75	0.43
30:e:26:HIS:ND1	30:e:46:LYS:O	2.50	0.43
32:W:398:C:H2'	32:W:399:G:H8	1.83	0.43
32:W:646:U:H2'	32:W:647:G:H8	1.83	0.43
32:W:1502:A:H5'	32:W:1503:A:OP2	2.18	0.43
1:A:365:U:H3	1:A:385:G:HO2'	1.59	0.43
1:A:377:G:C2	1:A:378:C:C5	3.06	0.43
1:A:1029:A:N6	1:A:1030:G:C6	2.86	0.43
1:A:1374:C:OP1	20:T:65:ARG:NH1	2.51	0.43
1:A:1438:C:OP1	20:T:82:LYS:NZ	2.40	0.43
1:A:1438:C:H2'	1:A:1439:U:C6	2.53	0.43
1:A:2151:U:H2'	1:A:2152:A:H8	1.80	0.43
4:D:150:ASP:N	4:D:151:PRO:HD2	2.33	0.43
8:H:78:GLY:N	8:H:79:PRO:HD2	2.34	0.43
8:H:89:VAL:HG12	8:H:90:VAL:H	1.81	0.43
12:L:61:LEU:CD2	30:e:24:ARG:NH1	2.81	0.43
17:Q:64:ARG:HD2	17:Q:97:ASP:OD2	2.18	0.43
32:W:104:C:H2'	32:W:105:G:C8	2.52	0.43
32:W:505:G:N2	32:W:507:A:OP2	2.51	0.43
32:W:1385:U:H2'	32:W:1386:A:C8	2.52	0.43
53:2:86:ASP:O	53:2:87:GLU:HB2	2.18	0.43
1:A:976:U:O3'	26:a:37:HIS:HE1	2.01	0.43
1:A:1023:G:H5'	17:Q:55:ARG:NH1	2.33	0.43
1:A:2127:U:H3	1:A:2220:A:N6	2.14	0.43
1:A:2192:U:OP2	1:A:2192:U:N1	2.45	0.43
1:A:2718:U:H5'	1:A:2897:G:H22	1.82	0.43
12:L:117:LEU:HD13	12:L:119:LYS:O	2.17	0.43
13:M:57:TYR:CE2	13:M:113:VAL:HG13	2.53	0.43
14:N:29:ARG:HH22	27:b:55:ASN:C	2.25	0.43
20:T:65:ARG:HB3	20:T:70:THR:HG22	2.00	0.43
23:X:5:PHE:C	23:X:7:GLN:H	2.26	0.43
1:A:300:G:N7	1:A:468:C:H2'	2.33	0.43
1:A:720:C:N4	1:A:721:G:O6	2.51	0.43
1:A:1242:U:H2'	1:A:1243:A:H8	1.83	0.43
1:A:1250:G:H5''	1:A:1252:G:O4'	2.18	0.43
1:A:1871:G:O2'	3:C:245:SER:OG	2.27	0.43
3:C:235:GLY:HA3	3:C:239:ALA:HB2	2.00	0.43
12:L:125:ALA:HB3	12:L:128:PHE:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:W:609:U:H2'	32:W:610:G:H8	1.83	0.43
1:A:245:G:H3'	30:e:64:ASN:CB	2.47	0.43
1:A:247:A:OP2	30:e:8:ARG:NH1	2.43	0.43
1:A:1248:C:O2	1:A:1248:C:H2'	2.17	0.43
1:A:1659:A:N7	1:A:1660:C:H5	2.15	0.43
1:A:1659:A:N6	19:S:88:ARG:O	2.44	0.43
1:A:2906:U:O4	1:A:2907:A:N6	2.52	0.43
4:D:117:LYS:HG3	4:D:164:MET:HE3	2.01	0.43
5:E:37:ILE:HD13	12:L:6:LEU:HD21	2.01	0.43
6:F:109:PRO:CG	54:3:43:TYR:CE2	3.01	0.43
15:O:65:VAL:HG21	15:O:68:THR:HA	2.00	0.43
21:U:32:ARG:HB3	21:U:62:PRO:HB2	1.99	0.43
22:V:80:PHE:HB2	22:V:84:ARG:HB3	2.01	0.43
23:X:40:ASN:O	23:X:42:SER:N	2.51	0.43
1:A:879:G:H2'	1:A:880:C:C6	2.53	0.43
1:A:1105:G:H2'	1:A:1106:U:C5	2.54	0.43
1:A:1813:A:H4'	1:A:1814:A:O5'	2.18	0.43
1:A:2776:G:N1	1:A:2785:U:OP1	2.52	0.43
17:Q:46:ALA:O	17:Q:50:ARG:HG3	2.18	0.43
19:S:79:GLY:H	19:S:101:SER:HA	1.84	0.43
24:Y:37:ARG:HH11	24:Y:44:PRO:CB	2.29	0.43
47:u:67:SER:O	47:u:71:ARG:N	2.42	0.43
1:A:746:A:H4'	1:A:1679:A:C6	2.54	0.43
1:A:1108:G:H1	1:A:1122:C:H42	1.66	0.43
1:A:1133:G:H1	1:A:1148:C:N4	2.17	0.43
1:A:1348:G:H21	1:A:1656:C:H5'	1.83	0.43
1:A:1783:C:H5'	16:P:102:TYR:CZ	2.54	0.43
1:A:2089:A:H1'	1:A:2531:G:H1'	2.01	0.43
1:A:2430:U:OP1	28:c:38:ARG:NH1	2.51	0.43
3:C:171:TYR:HB3	3:C:184:ILE:O	2.18	0.43
11:K:8:LEU:HD22	11:K:82:ASN:HB3	2.00	0.43
15:O:35:ARG:HB3	15:O:100:TYR:CE2	2.54	0.43
20:T:11:PRO:HD3	25:Z:30:PHE:HD1	1.78	0.43
28:c:14:GLU:HG2	28:c:16:ASN:H	1.84	0.43
32:W:345:G:H2'	32:W:346:A:H8	1.84	0.43
32:W:643:C:H2'	32:W:644:A:C8	2.54	0.43
1:A:275:A:N6	1:A:296:G:H21	2.16	0.43
1:A:365:U:H4'	5:E:165:LEU:O	2.18	0.43
1:A:2122:G:H1'	1:A:2254:A:C6	2.53	0.43
1:A:2193:C:H2'	1:A:2194:G:H8	1.83	0.43
1:A:2708:A:H2	4:D:191:ASN:HD22	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:187:VAL:HG12	12:L:3:LEU:HB2	2.01	0.43
9:I:98:ALA:HB3	9:I:137:ILE:HG12	2.00	0.43
23:X:81:ALA:HA	23:X:147:GLU:H	1.84	0.43
23:X:125:GLY:HA2	23:X:146:LYS:CB	2.49	0.43
32:W:754:U:H2'	32:W:755:G:C8	2.54	0.43
44:r:41:GLU:CA	44:r:42:ASP:O	2.66	0.43
1:A:1407:G:H2'	1:A:1408:G:H8	1.84	0.43
1:A:2165:A:C2	1:A:2185:G:H1'	2.53	0.43
1:A:2346:C:N4	1:A:2347:G:N7	2.66	0.43
1:A:2862:A:H2'	1:A:2863:G:C8	2.54	0.43
6:F:38:MET:HE3	6:F:57:LEU:HD13	2.01	0.43
21:U:97:SER:HA	21:U:98:GLY:HA2	1.64	0.43
32:W:266:A:H2'	32:W:267:G:C8	2.54	0.43
32:W:398:C:H2'	32:W:399:G:C8	2.54	0.43
32:W:930:U:H2'	32:W:931:U:C6	2.54	0.43
32:W:1473:C:H2'	32:W:1474:G:H8	1.84	0.43
52:z:36:C:N4	52:z:37:A:H62	2.16	0.43
1:A:1759:U:O4	1:A:1774:A:N7	2.52	0.43
1:A:2140:U:H2'	1:A:2147:U:H4'	2.00	0.43
1:A:2801:C:C2	1:A:2802:U:C5	3.07	0.43
3:C:84:ASP:HB2	3:C:91:ILE:HG13	2.00	0.43
4:D:201:THR:HG21	4:D:203:LYS:HG3	1.99	0.43
6:F:32:GLU:HG3	15:O:2:ILE:HD12	2.01	0.43
13:M:43:THR:HA	13:M:94:VAL:HG22	2.01	0.43
30:e:17:THR:HG21	30:e:23:LYS:HG3	2.01	0.43
32:W:126:G:O2'	32:W:127:U:OP1	2.23	0.43
32:W:609:U:H2'	32:W:610:G:C8	2.53	0.43
1:A:199:A:H62	1:A:878:G:N2	2.17	0.42
1:A:278:A:H2'	1:A:279:A:C8	2.54	0.42
1:A:898:U:O2	26:a:42:ALA:CB	2.54	0.42
1:A:1362:G:H3'	1:A:1363:G:H5''	2.01	0.42
1:A:1694:G:H2'	1:A:1695:A:C8	2.54	0.42
1:A:2173:G:H1'	1:A:2176:A:H61	1.82	0.42
1:A:2206:C:H2'	1:A:2207:C:C6	2.54	0.42
1:A:2334:U:N3	6:F:151:GLY:HA3	2.34	0.42
1:A:2614:U:O2	53:2:87:GLU:HG2	2.18	0.42
5:E:66:ARG:CD	5:E:70:THR:HG23	2.49	0.42
12:L:61:LEU:CD2	30:e:24:ARG:HD2	2.49	0.42
13:M:7:VAL:HG12	13:M:9:TYR:H	1.84	0.42
13:M:14:ARG:HD3	13:M:41:TRP:HH2	1.85	0.42
21:U:4:LYS:N	21:U:92:ARG:HH22	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:40:VAL:CG1	24:Y:41:ASN:N	2.75	0.42
1:A:58:G:H2'	1:A:59:G:C8	2.55	0.42
1:A:527:A:H1'	21:U:41:VAL:HG11	2.01	0.42
1:A:673:A:N7	12:L:76:VAL:HG11	2.34	0.42
1:A:970:A:O2'	22:V:37:GLN:NE2	2.52	0.42
1:A:1029:A:N6	1:A:1030:G:O6	2.51	0.42
1:A:1108:G:H2'	1:A:1109:G:C8	2.53	0.42
1:A:1199:C:H2'	1:A:1200:G:O4'	2.19	0.42
1:A:1345:U:O2'	1:A:1346:A:H5''	2.19	0.42
1:A:2186:G:C3'	1:A:2186:G:P	3.07	0.42
1:A:2207:C:C2'	1:A:2208:C:O4'	2.62	0.42
5:E:129:LEU:HD12	5:E:195:THR:HG22	2.00	0.42
6:F:42:ASP:HB3	6:F:45:GLN:H	1.84	0.42
10:J:45:TYR:H	17:Q:64:ARG:NE	2.17	0.42
17:Q:59:LYS:O	17:Q:63:THR:HG23	2.19	0.42
19:S:8:ARG:C	19:S:10:VAL:H	2.27	0.42
30:e:26:HIS:CE1	30:e:48:ALA:HB2	2.53	0.42
32:W:641:G:O2'	32:W:642:U:OP1	2.34	0.42
1:A:125:A:N6	1:A:126:A:N1	2.67	0.42
1:A:426:G:N2	1:A:442:C:N3	2.58	0.42
1:A:1364:C:C4	19:S:86:ARG:NH1	2.86	0.42
1:A:2029:G:H2'	1:A:2030:A:H8	1.84	0.42
1:A:2192:U:P	1:A:2192:U:C5	3.04	0.42
1:A:2825:C:H3'	1:A:2826:A:H8	1.85	0.42
3:C:185:LEU:HD12	3:C:186:SER:N	2.34	0.42
3:C:207:LYS:HE2	3:C:209:GLY:HA3	2.01	0.42
4:D:139:TYR:OH	4:D:142:ARG:O	2.37	0.42
5:E:6:LEU:H	5:E:16:ASP:HA	1.84	0.42
5:E:167:ALA:HB1	5:E:173:VAL:HG11	2.01	0.42
7:G:19:LEU:HD21	7:G:46:VAL:HG23	2.00	0.42
12:L:33:LYS:HB3	12:L:40:ALA:HA	2.01	0.42
24:Y:7:ILE:HD12	24:Y:49:VAL:HG23	2.00	0.42
25:Z:34:THR:HG22	25:Z:36:GLN:HG3	2.01	0.42
28:c:6:THR:HG22	28:c:18:ILE:HG12	2.00	0.42
32:W:473:G:N2	32:W:478:G:O6	2.52	0.42
1:A:525:A:N6	1:A:546:G:O2'	2.52	0.42
1:A:647:A:C2	1:A:672:C:H4'	2.54	0.42
1:A:666:G:H4'	1:A:667:A:C5'	2.48	0.42
1:A:839:G:H4'	1:A:840:A:C2	2.54	0.42
1:A:1305:A:HO2'	19:S:15:ARG:HH22	1.63	0.42
1:A:2342:C:H2'	1:A:2343:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2769:A:N6	1:A:2770:A:N6	2.67	0.42
2:B:41:C:O2'	2:B:42:G:H5'	2.19	0.42
14:N:17:LEU:CD2	14:N:39:GLU:OE2	2.67	0.42
14:N:103:LYS:HB2	27:b:40:HIS:O	2.18	0.42
20:T:12:VAL:HG11	20:T:78:LYS:NZ	2.34	0.42
23:X:5:PHE:O	23:X:6:LEU:CB	2.67	0.42
32:W:149:U:H2'	32:W:150:A:H8	1.84	0.42
32:W:1081:C:H2'	32:W:1082:G:H8	1.85	0.42
1:A:20:C:H2'	1:A:21:A:C8	2.55	0.42
1:A:217:G:O2'	1:A:219:A:O2'	2.32	0.42
1:A:259:A:H2'	1:A:260:A:C8	2.54	0.42
1:A:625:C:H2'	1:A:626:G:C8	2.54	0.42
1:A:933:C:H2'	1:A:934:U:H5'	2.02	0.42
1:A:1474:C:H42	1:A:1618:A:N6	2.11	0.42
1:A:1808:U:O2	1:A:1812:A:N6	2.53	0.42
1:A:2282:G:N2	52:z:74:C:C4	2.87	0.42
1:A:2405:A:N6	1:A:2406:A:C6	2.87	0.42
1:A:2506:C:N4	31:f:10:ILE:CG2	2.79	0.42
1:A:2868:G:H2'	1:A:2869:A:H8	1.84	0.42
3:C:185:LEU:HD12	3:C:186:SER:H	1.85	0.42
5:E:67:GLN:HE22	5:E:74:ARG:HA	1.84	0.42
25:Z:52:ARG:O	25:Z:56:VAL:HG23	2.19	0.42
1:A:2038:G:H1'	14:N:110:ASP:O	2.19	0.42
1:A:2110:C:C5'	24:Y:25:SER:HG	2.26	0.42
1:A:2468:A:H4'	1:A:2469:C:O5'	2.19	0.42
1:A:2610:G:H22	1:A:2639:C:H2'	1.84	0.42
4:D:84:ARG:HA	4:D:85:GLY:HA2	1.61	0.42
5:E:11:GLY:N	5:E:12:SER:HB3	2.34	0.42
7:G:22:ASN:HA	7:G:23:ASN:HA	1.74	0.42
13:M:119:ARG:O	13:M:122:SER:OG	2.22	0.42
18:R:67:ARG:HD2	18:R:89:ARG:HB2	2.02	0.42
25:Z:5:GLU:O	25:Z:60:ARG:NH2	2.53	0.42
32:W:73:C:H2'	32:W:74:A:H8	1.85	0.42
32:W:326:G:H2'	32:W:327:G:H8	1.84	0.42
32:W:502:C:H2'	32:W:503:C:C6	2.55	0.42
32:W:875:A:H5'	32:W:1088:U:C5	2.55	0.42
32:W:950:C:H2'	32:W:951:G:C8	2.54	0.42
32:W:1063:G:N7	32:W:1209:C:H5''	2.34	0.42
1:A:892:U:O2'	1:A:893:A:H5'	2.20	0.42
1:A:1340:A:N6	1:A:1686:A:C2	2.86	0.42
1:A:1433:U:H4'	1:A:1648:A:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2110:C:C5'	24:Y:25:SER:OG	2.66	0.42
1:A:2149:G:C6	1:A:2150:G:C6	3.07	0.42
1:A:2448:U:O5'	30:e:33:PHE:HD2	2.02	0.42
1:A:2746:G:O2'	16:P:97:ARG:NH1	2.52	0.42
6:F:106:VAL:HG11	6:F:139:PRO:HG3	2.01	0.42
6:F:169:LEU:O	6:F:173:VAL:HG23	2.19	0.42
8:H:123:VAL:O	8:H:124:LYS:HB2	2.20	0.42
11:K:10:VAL:HG12	11:K:12:ASP:H	1.85	0.42
15:O:49:ASN:HB3	15:O:51:VAL:HG23	2.01	0.42
19:S:8:ARG:O	19:S:10:VAL:N	2.50	0.42
19:S:77:ASP:O	19:S:102:HIS:N	2.41	0.42
24:Y:38:ILE:HG22	24:Y:39:LEU:N	2.34	0.42
29:d:34:ARG:HB3	29:d:42:LEU:CD1	2.50	0.42
32:W:245:C:H2'	32:W:246:G:C8	2.55	0.42
32:W:1403:A:N6	32:W:1511:C:H5'	2.33	0.42
1:A:124:A:O2'	1:A:125:A:O5'	2.29	0.42
1:A:908:A:H2'	1:A:909:G:O4'	2.20	0.42
1:A:1103:A:HO2'	1:A:1104:U:P	2.42	0.42
1:A:1818:A:H5''	3:C:220:VAL:HA	2.01	0.42
1:A:1847:U:H4'	1:A:1850:A:H1'	2.02	0.42
6:F:44:VAL:O	6:F:46:ASN:N	2.45	0.42
7:G:28:LYS:HA	7:G:33:GLU:HG2	2.02	0.42
20:T:56:ILE:CG2	20:T:77:ARG:HE	2.33	0.42
23:X:7:GLN:O	23:X:8:ASP:C	2.63	0.42
32:W:280:C:H2'	32:W:281:A:H8	1.84	0.42
32:W:510:C:H2'	32:W:511:C:C6	2.55	0.42
32:W:1129:U:H3	32:W:1163:G:H1	1.68	0.42
32:W:1434:A:O2'	32:W:1435:A:H5''	2.20	0.42
33:g:103:ASN:O	33:g:105:GLU:N	2.53	0.42
1:A:899:C:C4'	26:a:41:ALA:O	2.67	0.42
1:A:1626:U:H2'	1:A:1627:A:H8	1.84	0.42
1:A:1694:G:H2'	1:A:1695:A:H8	1.85	0.42
1:A:2158:C:P	1:A:2158:C:C5	3.04	0.42
1:A:2173:G:H4'	1:A:2174:C:H41	1.85	0.42
1:A:2209:U:H2'	1:A:2210:G:C8	2.55	0.42
1:A:2245:G:H2'	1:A:2246:G:C8	2.55	0.42
1:A:2358:A:N6	1:A:2359:G:C6	2.88	0.42
1:A:2495:C:H5'	31:f:5:PRO:HG2	2.02	0.42
3:C:174:VAL:HG21	3:C:184:ILE:HD12	2.02	0.42
14:N:107:ARG:HG2	14:N:109:GLY:H	1.84	0.42
23:X:4:ILE:H	23:X:37:VAL:CB	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:13:LYS:HA	27:b:16:ARG:HE	1.85	0.42
32:W:995:C:H2'	32:W:996:A:C8	2.54	0.42
52:z:34:G:C2'	52:z:35:U:H5''	2.50	0.42
1:A:340:U:H5''	21:U:83:TYR:HB2	2.02	0.42
1:A:377:G:O2'	1:A:378:C:P	2.78	0.42
1:A:509:C:N4	1:A:510:G:O6	2.52	0.42
1:A:709:G:H5''	12:L:16:ARG:HA	2.01	0.42
1:A:1080:G:C1'	31:f:18:ARG:HH12	2.33	0.42
1:A:2011:U:O2'	1:A:2012:C:H5'	2.20	0.42
1:A:2178:C:H2'	1:A:2179:U:O4'	2.20	0.42
1:A:2191:A:C4	1:A:2192:U:C2	3.08	0.42
13:M:11:ARG:HE	13:M:87:LYS:HD3	1.85	0.42
14:N:78:ASP:OD1	14:N:79:ALA:N	2.53	0.42
17:Q:92:ARG:CG	17:Q:94:MET:HG2	2.49	0.42
17:Q:103:LEU:HA	17:Q:104:THR:HA	1.76	0.42
32:W:95:U:H2'	32:W:96:G:H8	1.84	0.42
32:W:126:G:H1	32:W:241:C:H42	1.68	0.42
32:W:874:A:H5'	36:j:90:GLY:C	2.45	0.42
32:W:989:C:OP1	32:W:1232:C:N4	2.52	0.42
52:z:58:A:N6	52:z:61:C:O2	2.53	0.42
1:A:614:G:H2'	1:A:2059:A:N7	2.35	0.41
1:A:620:U:O2'	1:A:2531:G:O6	2.37	0.41
1:A:629:G:H21	1:A:1294:A:H62	1.68	0.41
1:A:1003:A:C2	1:A:2487:U:H4'	2.54	0.41
1:A:1093:G:N2	1:A:1157:A:H62	2.17	0.41
1:A:1562:A:H3'	1:A:1563:G:C8	2.55	0.41
1:A:2278:U:O2'	1:A:2279:G:OP1	2.37	0.41
1:A:2488:A:N6	1:A:2523:G:C2	2.88	0.41
1:A:2863:G:H1	1:A:2905:C:H42	1.68	0.41
1:A:2874:G:N2	1:A:2891:G:H1'	2.35	0.41
8:H:119:THR:OG1	8:H:120:VAL:N	2.52	0.41
10:J:17:LEU:HD23	10:J:139:GLU:HB2	2.01	0.41
28:c:12:CYS:SG	28:c:38:ARG:HD3	2.60	0.41
32:W:74:A:H2'	32:W:75:G:O4'	2.20	0.41
32:W:974:A:N6	32:W:975:A:N6	2.67	0.41
32:W:1012:U:H2'	32:W:1013:G:O4'	2.20	0.41
32:W:1495:U:H2'	32:W:1496:G:C8	2.55	0.41
1:A:649:G:HO2'	1:A:650:U:P	2.42	0.41
1:A:825:G:H5''	3:C:48:LYS:HE3	2.02	0.41
1:A:984:G:H2'	1:A:985:G:H8	1.85	0.41
1:A:1905:A:N6	1:A:1906:A:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2327:A:H62	1:A:2347:G:H8	1.67	0.41
1:A:2440:A:H2'	1:A:2441:A:C8	2.55	0.41
1:A:2447:A:H5''	30:e:45:ARG:NH2	2.35	0.41
1:A:2488:A:N6	1:A:2523:G:N3	2.68	0.41
6:F:127:ASN:N	15:O:1:MET:SD	2.86	0.41
11:K:7:ARG:HA	11:K:20:LEU:HA	2.01	0.41
18:R:67:ARG:HH11	18:R:89:ARG:HH12	1.61	0.41
23:X:6:LEU:H	23:X:16:GLY:CA	2.34	0.41
32:W:1513:A:H5'	32:W:1541:A:O4'	2.20	0.41
1:A:574:A:H62	1:A:2072:C:C5'	2.33	0.41
1:A:1060:U:H2'	1:A:1061:A:H8	1.85	0.41
1:A:1107:U:C6	1:A:1116:A:H4'	2.55	0.41
1:A:2144:G:H5''	1:A:2195:G:H2'	2.01	0.41
1:A:2225:C:O2'	1:A:2226:U:H5'	2.20	0.41
1:A:2719:A:C2	14:N:17:LEU:HD11	2.55	0.41
1:A:2843:G:H2'	1:A:2844:A:C8	2.56	0.41
6:F:109:PRO:CB	54:3:43:TYR:CE2	2.88	0.41
6:F:134:GLU:HB2	6:F:137:ILE:HG13	2.02	0.41
9:I:15:ALA:HA	9:I:46:THR:HG21	2.00	0.41
23:X:26:ALA:O	23:X:27:HIS:C	2.63	0.41
32:W:35:A:N6	32:W:559:G:O6	2.53	0.41
32:W:363:C:H1'	32:W:396:G:H1'	2.02	0.41
1:A:251:G:O5'	1:A:252:C:H5''	2.20	0.41
1:A:511:U:H2'	1:A:512:G:O4'	2.20	0.41
1:A:818:G:OP2	29:d:11:LYS:HG2	2.20	0.41
1:A:1065:U:C2	1:A:1188:A:N6	2.88	0.41
1:A:1304:G:H2'	1:A:2043:A:N6	2.36	0.41
1:A:2042:A:O2'	19:S:94:SER:HB3	2.20	0.41
1:A:2109:G:P	24:Y:21:ALA:HB3	2.60	0.41
1:A:2164:A:H2'	1:A:2165:A:O4'	2.20	0.41
1:A:2279:G:N2	13:M:84:GLY:HA3	2.36	0.41
1:A:2296:A:H5''	1:A:2297:A:H5'	2.01	0.41
1:A:2725:U:H2'	1:A:2726:G:C8	2.56	0.41
3:C:144:ILE:HG21	3:C:184:ILE:HD13	2.01	0.41
5:E:154:ILE:HA	5:E:193:LEU:HB2	2.03	0.41
21:U:64:HIS:HD2	21:U:66:SER:OG	2.03	0.41
27:b:27:MET:HE2	27:b:36:MET:HB2	2.02	0.41
32:W:36:C:H2'	32:W:37:G:C8	2.56	0.41
32:W:266:A:H2'	32:W:267:G:H8	1.86	0.41
32:W:335:A:O2'	32:W:336:C:O4'	2.37	0.41
32:W:988:A:N6	32:W:1327:A:H62	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:C:O2'	1:A:1278:G:OP1	2.35	0.41
1:A:275:A:N6	1:A:296:G:N2	2.69	0.41
1:A:373:A:N6	21:U:15:LYS:H	2.17	0.41
1:A:975:C:C2'	26:a:43:ILE:HD11	2.50	0.41
1:A:983:U:H2'	1:A:984:G:C8	2.56	0.41
1:A:1056:A:H1'	1:A:1199:C:H1'	2.02	0.41
1:A:1378:G:H5'	20:T:16:ARG:HG3	2.02	0.41
1:A:2171:G:C2	1:A:2179:U:C2	3.08	0.41
1:A:2191:A:N9	1:A:2192:U:C5	2.87	0.41
1:A:2235:G:H2'	1:A:2235:G:N3	2.35	0.41
3:C:29:PRO:HB3	3:C:63:ARG:NE	2.31	0.41
10:J:4:THR:N	10:J:5:PRO:HD2	2.35	0.41
11:K:113:LYS:O	11:K:116:SER:OG	2.38	0.41
12:L:46:VAL:HG22	12:L:47:ARG:H	1.86	0.41
12:L:57:LEU:HD11	30:e:54:ASP:OD2	2.05	0.41
13:M:17:MET:HE2	13:M:97:VAL:H	1.86	0.41
16:P:61:THR:HG22	16:P:78:PRO:HA	2.02	0.41
20:T:5:ARG:HG2	25:Z:26:PHE:HB2	2.02	0.41
24:Y:37:ARG:CB	24:Y:45:LYS:CD	2.94	0.41
32:W:104:C:H2'	32:W:105:G:H8	1.85	0.41
1:A:847:A:H1'	1:A:849:A:OP2	2.21	0.41
1:A:1065:U:OP1	1:A:1081:U:O2'	2.37	0.41
1:A:1305:A:O2'	1:A:1306:G:O5'	2.29	0.41
1:A:1823:U:H2'	1:A:1824:C:C6	2.55	0.41
1:A:1938:C:H2'	1:A:1939:G:C8	2.55	0.41
1:A:2449:C:N4	30:e:31:HIS:HA	2.36	0.41
1:A:2568:C:H2'	1:A:2569:C:H5''	2.03	0.41
3:C:72:ASP:HB2	3:C:119:GLY:HA2	2.02	0.41
3:C:136:PRO:HG2	3:C:139:THR:HG21	2.01	0.41
5:E:88:VAL:O	5:E:90:PHE:N	2.54	0.41
5:E:128:ASP:OD1	5:E:130:THR:HG23	2.20	0.41
13:M:7:VAL:HG21	13:M:93:TRP:CH2	2.56	0.41
16:P:51:ILE:HG23	16:P:100:LEU:N	2.36	0.41
23:X:104:LYS:C	23:X:106:HIS:H	2.27	0.41
28:c:22:ASN:HD22	28:c:25:ASN:ND2	2.18	0.41
32:W:146:G:H2'	32:W:147:G:C8	2.55	0.41
32:W:1483:G:H2'	32:W:1484:G:C8	2.55	0.41
1:A:161:A:H2'	1:A:162:A:C8	2.55	0.41
1:A:621:G:H5'	1:A:2531:G:C6	2.56	0.41
1:A:2066:A:H2'	1:A:2067:G:C8	2.56	0.41
1:A:2126:G:N1	1:A:2221:C:N3	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2191:A:O2'	1:A:2192:U:C4'	2.65	0.41
1:A:2607:G:OP1	1:A:2643:A:N6	2.53	0.41
1:A:2641:C:H2'	27:b:2:ALA:N	2.35	0.41
1:A:2868:G:H2'	1:A:2869:A:C8	2.56	0.41
3:C:231:PRO:HB2	3:C:243:ARG:NH2	2.35	0.41
4:D:17:ALA:O	4:D:19:ASN:N	2.54	0.41
6:F:29:PRO:HB3	6:F:160:ALA:HB2	2.03	0.41
13:M:65:TRP:HB2	13:M:105:GLU:HB2	2.03	0.41
14:N:103:LYS:HB2	27:b:41:ARG:HA	2.02	0.41
32:W:478:G:H2'	32:W:479:G:C8	2.55	0.41
32:W:792:C:H2'	32:W:793:A:H8	1.86	0.41
32:W:1414:G:H2'	32:W:1415:U:C6	2.55	0.41
1:A:970:A:H2'	1:A:971:A:H8	1.85	0.41
1:A:1659:A:N6	19:S:91:GLY:HA2	2.35	0.41
1:A:2329:A:N6	1:A:2330:A:N6	2.68	0.41
1:A:2371:C:O2'	1:A:2403:C:H5''	2.21	0.41
1:A:2614:U:C6	53:2:89:ASP:O	2.74	0.41
1:A:2648:U:H5'	4:D:156:LYS:HG3	2.01	0.41
3:C:69:ARG:NH1	3:C:104:ILE:HD13	2.35	0.41
3:C:96:TYR:HE2	3:C:102:ARG:HB2	1.85	0.41
3:C:170:LYS:HA	3:C:171:TYR:HA	1.73	0.41
6:F:80:ARG:HH11	52:z:56:C:H5	1.68	0.41
10:J:25:THR:OG1	10:J:26:LEU:N	2.53	0.41
32:W:1516:U:N3	32:W:1532:U:OP1	2.44	0.41
32:W:1522:U:H2'	32:W:1523:A:C8	2.56	0.41
53:2:80:MET:HG3	53:2:81:ASN:N	2.35	0.41
1:A:124:A:C2	29:d:9:ASN:ND2	2.88	0.41
1:A:377:G:O2'	1:A:378:C:OP1	2.38	0.41
1:A:661:A:H2'	1:A:662:U:O4'	2.20	0.41
1:A:694:G:H2'	1:A:695:G:C8	2.55	0.41
1:A:726:C:H2'	1:A:727:A:C8	2.56	0.41
1:A:837:U:O2'	1:A:838:C:P	2.78	0.41
1:A:1005:A:H2'	1:A:1006:A:C8	2.55	0.41
1:A:1006:A:H8	1:A:1006:A:O5'	2.04	0.41
1:A:1111:U:C2	1:A:1119:A:N7	2.89	0.41
1:A:1119:A:N6	1:A:1120:G:C2	2.88	0.41
1:A:1251:U:O2	1:A:1251:U:C2'	2.69	0.41
1:A:1345:U:O2'	1:A:1651:G:O6	2.28	0.41
1:A:1867:C:H4'	1:A:1868:G:C8	2.56	0.41
1:A:2131:U:H2'	1:A:2132:A:C8	2.56	0.41
1:A:2149:G:H2'	1:A:2150:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2191:A:H1'	1:A:2202:A:C5'	2.51	0.41
3:C:246:PRO:HG3	3:C:255:LEU:HD12	2.03	0.41
4:D:119:PHE:CE1	4:D:162:GLY:HA2	2.55	0.41
5:E:62:ARG:HG3	5:E:78:ILE:HD11	2.03	0.41
5:E:65:TRP:CH2	5:E:83:TRP:CZ2	3.09	0.41
5:E:126:LEU:HD21	5:E:146:LEU:HD11	2.03	0.41
5:E:143:LEU:O	5:E:148:VAL:HG22	2.21	0.41
9:I:25:GLY:HA3	9:I:26:PRO:HD2	1.83	0.41
9:I:102:ARG:HG3	9:I:140:GLU:C	2.46	0.41
11:K:66:LYS:N	11:K:82:ASN:OD1	2.48	0.41
12:L:61:LEU:HD21	30:e:24:ARG:HH11	1.83	0.41
12:L:63:LYS:CE	30:e:13:ARG:HE	2.34	0.41
13:M:35:GLN:HE21	13:M:100:GLY:HA2	1.85	0.41
14:N:9:THR:O	14:N:13:ARG:HG3	2.20	0.41
14:N:51:GLY:HA2	14:N:84:PHE:CE1	2.54	0.41
18:R:67:ARG:HD3	18:R:89:ARG:HH11	1.82	0.41
18:R:78:PRO:O	18:R:79:LYS:HB2	2.21	0.41
24:Y:37:ARG:CG	24:Y:44:PRO:HB2	2.47	0.41
32:W:738:A:N6	32:W:739:G:C6	2.89	0.41
32:W:815:C:N4	32:W:816:A:H62	2.18	0.41
32:W:1430:U:H2'	32:W:1431:U:C6	2.56	0.41
40:n:55:THR:O	40:n:57:THR:N	2.49	0.41
1:A:167:U:H2'	1:A:168:A:C8	2.56	0.41
1:A:372:U:H4'	21:U:64:HIS:CG	2.56	0.41
1:A:1126:A:O2'	9:I:126:ARG:HB3	2.21	0.41
1:A:1820:A:H4'	3:C:205:ILE:HB	2.03	0.41
1:A:2300:G:H5'	22:V:28:ARG:NE	2.36	0.41
1:A:2405:A:H2'	1:A:2406:A:O4'	2.21	0.41
1:A:2420:G:O2'	30:e:28:TYR:OH	2.18	0.41
1:A:2449:C:OP2	30:e:33:PHE:CG	2.74	0.41
1:A:2468:A:H5'	1:A:2468:A:C8	2.56	0.41
1:A:2716:U:O2'	1:A:2717:G:OP1	2.35	0.41
3:C:19:SER:HB3	3:C:203:ILE:HD11	2.02	0.41
5:E:49:HIS:CD2	5:E:92:PRO:HB2	2.56	0.41
6:F:33:LYS:HD3	6:F:92:ARG:NH1	2.35	0.41
7:G:39:HIS:CE1	7:G:41:ASP:HB2	2.57	0.41
11:K:62:ILE:HA	11:K:84:CYS:SG	2.61	0.41
11:K:68:GLY:HA2	11:K:78:SER:HB3	2.02	0.41
19:S:36:LEU:HB3	19:S:44:SER:HB2	2.02	0.41
32:W:833:U:H2'	32:W:834:G:C8	2.55	0.41
32:W:988:A:C6	32:W:1327:A:N6	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:3:55:ARG:HA	54:3:56:VAL:HA	1.55	0.41
1:A:1224:A:H2'	1:A:1225:G:H8	1.85	0.40
1:A:1596:U:H2'	1:A:1597:C:C6	2.56	0.40
1:A:1657:C:C5'	1:A:1657:C:H6	2.34	0.40
1:A:2144:G:O6	1:A:2146:A:H3'	2.21	0.40
1:A:2181:C:O2'	1:A:2182:G:O4'	2.35	0.40
1:A:2448:U:O5'	30:e:33:PHE:CD2	2.74	0.40
1:A:2734:A:O2'	1:A:2877:G:OP1	2.30	0.40
2:B:3:U:H2'	2:B:4:G:H8	1.87	0.40
19:S:92:ARG:NE	19:S:92:ARG:CA	2.84	0.40
21:U:70:PRO:HG3	21:U:81:VAL:HG22	2.03	0.40
32:W:246:G:H2'	32:W:247:G:C8	2.57	0.40
32:W:1423:C:H2'	32:W:1424:G:H8	1.85	0.40
1:A:246:U:OP2	30:e:6:THR:CB	2.70	0.40
1:A:278:A:H2'	1:A:279:A:H8	1.87	0.40
1:A:405:U:H2'	1:A:406:G:C8	2.57	0.40
1:A:731:G:N2	1:A:835:A:OP2	2.47	0.40
1:A:1013:U:H2'	1:A:1014:A:C8	2.56	0.40
1:A:1019:A:O2'	1:A:1020:A:OP1	2.37	0.40
1:A:1148:C:H2'	1:A:1149:A:C8	2.57	0.40
1:A:2181:C:O3'	1:A:2182:G:C8	2.61	0.40
4:D:14:GLN:HB3	4:D:22:LEU:HD11	2.03	0.40
7:G:76:MET:O	7:G:80:VAL:HG23	2.21	0.40
32:W:390:A:H2'	32:W:391:A:H8	1.86	0.40
32:W:861:U:C4	32:W:862:A:N6	2.87	0.40
32:W:912:G:H2'	32:W:913:A:C8	2.56	0.40
1:A:610:U:OP1	18:R:81:ASN:ND2	2.55	0.40
1:A:799:A:H62	53:2:80:MET:HE1	1.85	0.40
1:A:1087:U:H2'	1:A:1088:G:H8	1.86	0.40
1:A:1298:C:H2'	1:A:1299:G:H8	1.85	0.40
1:A:1355:U:H5'	1:A:1431:G:H1'	2.02	0.40
1:A:1941:A:N1	32:W:1417:A:O4'	2.55	0.40
1:A:2195:G:O6	1:A:2200:A:C6	2.74	0.40
1:A:2393:C:H2'	1:A:2394:G:O4'	2.21	0.40
1:A:2627:A:H8	1:A:2627:A:O5'	2.04	0.40
6:F:111:VAL:HB	6:F:114:PHE:HB3	2.02	0.40
9:I:46:THR:CG2	9:I:46:THR:O	2.69	0.40
14:N:17:LEU:HD21	14:N:39:GLU:OE1	2.21	0.40
15:O:78:GLY:HA3	15:O:109:LEU:HG	2.03	0.40
21:U:87:ASP:CB	21:U:88:GLY:CA	2.84	0.40
23:X:50:GLN:HA	23:X:53:LYS:CB	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:29:ASN:HB2	31:f:32:HIS:CD2	2.49	0.40
32:W:268:G:N2	32:W:273:G:C6	2.89	0.40
1:A:1015:G:H21	1:A:1031:C:P	2.45	0.40
1:A:1600:G:OP2	1:A:1600:G:N2	2.30	0.40
1:A:2010:A:N3	1:A:2010:A:C2'	2.84	0.40
1:A:2221:C:O2	1:A:2221:C:C2'	2.67	0.40
1:A:2295:A:N6	1:A:2302:A:H62	2.10	0.40
1:A:2651:C:O2'	1:A:2850:G:N7	2.54	0.40
3:C:77:ARG:O	3:C:95:ASN:N	2.51	0.40
4:D:140:HIS:C	4:D:142:ARG:H	2.28	0.40
6:F:109:PRO:HD3	54:3:43:TYR:CE2	2.56	0.40
16:P:109:LYS:NZ	32:W:1473:C:OP1	2.53	0.40
27:b:50:ASN:N	27:b:51:GLY:HA2	2.36	0.40
32:W:554:C:O2'	32:W:558:C:H5''	2.22	0.40
32:W:792:C:H2'	32:W:793:A:C8	2.56	0.40
32:W:1515:G:H5'	32:W:1516:U:H3'	2.04	0.40
33:g:91:TYR:O	33:g:150:GLY:HA3	2.21	0.40
1:A:250:G:O6	30:e:8:ARG:HB3	2.22	0.40
1:A:377:G:C2'	1:A:378:C:H6	2.11	0.40
1:A:896:A:H2	26:a:25:THR:HG22	1.87	0.40
1:A:1019:A:H8	1:A:1019:A:OP1	2.05	0.40
1:A:1222:A:N6	1:A:1223:C:N4	2.70	0.40
1:A:1262:C:H2'	1:A:1263:G:H8	1.86	0.40
1:A:1285:G:O6	1:A:1286:A:N6	2.54	0.40
1:A:1379:U:H4'	1:A:1433:U:H1'	2.04	0.40
1:A:1696:G:O5'	14:N:35:THR:OG1	2.30	0.40
1:A:1825:U:H2'	1:A:1826:C:C6	2.55	0.40
1:A:2535:U:O2	1:A:2535:U:C2'	2.70	0.40
1:A:2909:U:C1'	27:b:50:ASN:HD22	2.34	0.40
2:B:55:A:H5'	6:F:24:SER:HB3	2.03	0.40
7:G:4:VAL:HG13	7:G:70:ARG:HH21	1.86	0.40
7:G:81:SER:OG	7:G:82:LYS:N	2.52	0.40
19:S:66:ALA:HA	19:S:69:LEU:HD12	2.03	0.40
19:S:79:GLY:N	19:S:101:SER:HA	2.37	0.40
32:W:383:U:H2'	32:W:384:G:C8	2.57	0.40
32:W:1332:G:H2'	32:W:1333:A:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/277 (99%)	264 (97%)	8 (3%)	1 (0%)	30	67
4	D	205/208 (99%)	189 (92%)	11 (5%)	5 (2%)	4	27
5	E	203/207 (98%)	185 (91%)	15 (7%)	3 (2%)	8	38
6	F	176/179 (98%)	154 (88%)	18 (10%)	4 (2%)	5	28
7	G	173/179 (97%)	164 (95%)	8 (5%)	1 (1%)	21	58
8	H	121/166 (73%)	97 (80%)	14 (12%)	10 (8%)	0	9
9	I	131/141 (93%)	122 (93%)	7 (5%)	2 (2%)	8	38
10	J	140/145 (97%)	130 (93%)	9 (6%)	1 (1%)	18	55
11	K	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7	35
12	L	144/146 (99%)	132 (92%)	10 (7%)	2 (1%)	9	39
13	M	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	N	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	49
15	O	118/120 (98%)	106 (90%)	7 (6%)	5 (4%)	2	17
16	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
17	Q	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
18	R	99/102 (97%)	82 (83%)	15 (15%)	2 (2%)	6	31
19	S	107/113 (95%)	96 (90%)	8 (8%)	3 (3%)	4	24
20	T	91/95 (96%)	86 (94%)	5 (6%)	0	100	100
21	U	98/103 (95%)	87 (89%)	8 (8%)	3 (3%)	3	21
22	V	80/94 (85%)	77 (96%)	3 (4%)	0	100	100
23	X	147/149 (99%)	83 (56%)	42 (29%)	22 (15%)	0	3
24	Y	56/62 (90%)	53 (95%)	1 (2%)	2 (4%)	2	20
25	Z	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
26	a	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	33
27	b	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	c	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
29	d	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
30	e	62/66 (94%)	56 (90%)	5 (8%)	1 (2%)	7	37
31	f	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
33	g	222/246 (90%)	204 (92%)	13 (6%)	5 (2%)	5	28
34	h	208/218 (95%)	193 (93%)	14 (7%)	1 (0%)	24	63
35	i	197/200 (98%)	191 (97%)	4 (2%)	2 (1%)	12	47
36	j	163/166 (98%)	150 (92%)	9 (6%)	4 (2%)	4	26
37	k	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	28
38	l	151/156 (97%)	144 (95%)	6 (4%)	1 (1%)	18	55
39	m	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	52
40	n	128/130 (98%)	113 (88%)	10 (8%)	5 (4%)	2	18
41	o	100/102 (98%)	88 (88%)	8 (8%)	4 (4%)	2	18
42	p	116/131 (88%)	106 (91%)	9 (8%)	1 (1%)	14	49
43	q	135/138 (98%)	119 (88%)	9 (7%)	7 (5%)	1	15
44	r	117/121 (97%)	94 (80%)	13 (11%)	10 (8%)	0	9
45	s	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	1	15
46	t	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	28
47	u	87/90 (97%)	82 (94%)	3 (3%)	2 (2%)	5	28
48	v	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
49	w	69/79 (87%)	64 (93%)	2 (3%)	3 (4%)	2	17
50	x	82/92 (89%)	75 (92%)	5 (6%)	2 (2%)	4	27
51	y	84/88 (96%)	77 (92%)	6 (7%)	1 (1%)	10	43
53	2	22/95 (23%)	17 (77%)	2 (9%)	3 (14%)	0	3
54	3	43/66 (65%)	37 (86%)	4 (9%)	2 (5%)	2	16
All	All	5691/6068 (94%)	5180 (91%)	378 (7%)	133 (2%)	7	28

All (133) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	93	ALA
9	I	19	ASN
15	O	26	ALA

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Mol	Chain	Res	Type
21	U	87	ASP
23	X	29	PHE
23	X	41	ALA
23	X	68	LEU
23	X	70	GLU
23	X	88	ARG
23	X	107	ASN
23	X	130	PRO
23	X	135	PRO
36	j	4	ILE
37	k	70	ALA
43	q	127	ARG
44	r	101	ASN
53	2	78	PHE
53	2	84	VAL
4	D	18	GLU
4	D	78	ARG
4	D	90	ALA
4	D	99	VAL
6	F	42	ASP
8	H	48	ALA
8	H	72	LEU
8	H	89	VAL
8	H	108	ILE
8	H	124	LYS
15	O	68	THR
15	O	91	SER
19	S	8	ARG
23	X	8	ASP
23	X	38	GLU
33	g	18	HIS
33	g	36	ASN
33	g	104	PHE
36	j	163	GLU
37	k	54	ASP
38	l	54	THR
39	m	71	GLU
40	n	106	ARG
40	n	122	ARG
43	q	38	VAL
44	r	41	GLU
44	r	46	ARG

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Mol	Chain	Res	Type
44	r	65	VAL
44	r	102	SER
44	r	112	PRO
54	3	49	PHE
5	E	4	VAL
8	H	55	TYR
8	H	90	VAL
8	H	113	ILE
11	K	89	ASP
15	O	63	LEU
18	R	28	GLU
19	S	41	ARG
19	S	65	ASP
21	U	74	LYS
21	U	89	LYS
23	X	20	ASN
23	X	44	ILE
23	X	69	LYS
23	X	85	GLU
23	X	126	TYR
23	X	127	THR
30	e	31	HIS
34	h	60	ALA
35	i	5	THR
40	n	57	THR
41	o	35	SER
43	q	32	LYS
43	q	39	SER
43	q	115	LEU
44	r	42	ASP
44	r	66	GLU
46	t	88	ARG
50	x	84	ALA
53	2	77	VAL
3	C	245	SER
4	D	54	ASP
5	E	128	ASP
6	F	112	ARG
6	F	147	THR
7	G	13	SER
11	K	34	ASN
15	O	71	THR

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Mol	Chain	Res	Type
23	X	12	LYS
23	X	42	SER
23	X	118	PRO
26	a	29	LYS
27	b	45	ALA
33	g	37	GLY
35	i	142	ARG
41	o	44	THR
43	q	25	ASN
44	r	10	PRO
47	u	44	ALA
47	u	47	ALA
49	w	28	TYR
5	E	89	VAL
8	H	107	GLU
10	J	22	ALA
12	L	107	ALA
14	N	110	ASP
18	R	52	THR
23	X	75	LEU
24	Y	44	PRO
41	o	36	VAL
43	q	16	VAL
45	s	31	HIS
45	s	56	VAL
50	x	30	VAL
51	y	69	LYS
54	3	60	ASN
24	Y	40	VAL
36	j	162	GLU
40	n	104	LEU
40	n	107	ASP
42	p	120	HIS
49	w	16	CYS
36	j	109	GLY
12	L	88	GLY
44	r	84	GLY
45	s	51	GLY
23	X	34	GLY
41	o	80	THR
46	t	24	SER
49	w	23	ILE

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Mol	Chain	Res	Type
23	X	9	VAL
33	g	201	PRO
6	F	25	VAL
9	I	24	VAL

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	
3	C	223/225 (99%)	222 (100%)	1 (0%)	84	83
4	D	168/169 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	167 (99%)	2 (1%)	63	73
6	F	153/154 (99%)	153 (100%)	0	100	100
7	G	148/151 (98%)	148 (100%)	0	100	100
8	H	105/139 (76%)	105 (100%)	0	100	100
9	I	103/110 (94%)	103 (100%)	0	100	100
10	J	120/123 (98%)	120 (100%)	0	100	100
11	K	101/101 (100%)	101 (100%)	0	100	100
12	L	110/110 (100%)	110 (100%)	0	100	100
13	M	111/116 (96%)	111 (100%)	0	100	100
14	N	99/100 (99%)	99 (100%)	0	100	100
15	O	93/93 (100%)	93 (100%)	0	100	100
16	P	99/100 (99%)	99 (100%)	0	100	100
17	Q	96/98 (98%)	96 (100%)	0	100	100
18	R	83/84 (99%)	83 (100%)	0	100	100
19	S	90/93 (97%)	89 (99%)	1 (1%)	65	74
20	T	84/85 (99%)	84 (100%)	0	100	100
21	U	84/87 (97%)	84 (100%)	0	100	100
22	V	64/74 (86%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	Y	47/50 (94%)	47 (100%)	0	100	100
25	Z	56/57 (98%)	56 (100%)	0	100	100
26	a	52/53 (98%)	51 (98%)	1 (2%)	50	66
27	b	48/53 (91%)	48 (100%)	0	100	100
28	c	46/47 (98%)	46 (100%)	0	100	100
29	d	39/39 (100%)	39 (100%)	0	100	100
30	e	54/56 (96%)	54 (100%)	0	100	100
31	f	34/35 (97%)	34 (100%)	0	100	100
53	2	6/87 (7%)	4 (67%)	2 (33%)	0	2
54	3	39/55 (71%)	39 (100%)	0	100	100
All	All	2724/2914 (94%)	2717 (100%)	7 (0%)	84	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	185	LEU
5	E	37	ILE
5	E	66	ARG
19	S	90	MET
26	a	53	LEU
53	2	81	ASN
53	2	86	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	38	HIS
3	C	54	GLN
3	C	194	GLN
3	C	199	GLN
3	C	264	ASN
4	D	152	ASN
4	D	172	GLN
4	D	191	ASN
5	E	29	ASN
5	E	67	GLN
5	E	82	GLN

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Mol	Chain	Res	Type
6	F	37	ASN
6	F	135	GLN
7	G	62	HIS
7	G	107	ASN
9	I	93	ASN
10	J	59	ASN
10	J	81	HIS
12	L	38	GLN
12	L	78	ASN
12	L	106	ASN
14	N	27	ASN
14	N	76	ASN
16	P	80	HIS
17	Q	37	GLN
17	Q	91	ASN
18	R	45	ASN
19	S	60	HIS
19	S	102	HIS
21	U	2	HIS
21	U	39	ASN
21	U	64	HIS
22	V	37	GLN
24	Y	23	ASN
24	Y	34	GLN
26	a	37	HIS
26	a	40	ASN
27	b	40	HIS
28	c	25	ASN
29	d	9	ASN
29	d	16	HIS
30	e	31	HIS
30	e	35	ASN
30	e	60	GLN
31	f	36	GLN
53	2	81	ASN
54	3	60	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2922/2928 (99%)	829 (28%)	85 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	111/119 (93%)	32 (28%)	4 (3%)
32	W	1543/1555 (99%)	235 (15%)	17 (1%)
52	z	76/77 (98%)	15 (19%)	0
All	All	4652/4679 (99%)	1111 (23%)	106 (2%)

All (1111) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	10	A
1	A	13	A
1	A	27	G
1	A	28	A
1	A	31	C
1	A	34	U
1	A	35	G
1	A	38	A
1	A	44	A
1	A	45	G
1	A	46	C
1	A	48	G
1	A	49	A
1	A	51	G
1	A	55	G
1	A	59	G
1	A	60	G
1	A	61	A
1	A	63	G
1	A	70	G
1	A	71	A
1	A	75	G
1	A	76	C
1	A	84	A
1	A	87	U
1	A	90	A
1	A	91	A
1	A	94	A
1	A	101	G
1	A	102	A
1	A	109	G
1	A	118	A

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Mol	Chain	Res	Type
1	A	119	U
1	A	124	A
1	A	125	A
1	A	126	A
1	A	127	C
1	A	130	A
1	A	133	A
1	A	156	A
1	A	161	A
1	A	162	A
1	A	163	U
1	A	164	U
1	A	176	A
1	A	177	G
1	A	179	A
1	A	183	A
1	A	184	G
1	A	185	A
1	A	188	C
1	A	199	A
1	A	202	A
1	A	203	U
1	A	207	A
1	A	208	G
1	A	215	G
1	A	216	A
1	A	217	G
1	A	218	G
1	A	219	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	230	A
1	A	231	A
1	A	232	U
1	A	233	G
1	A	236	A
1	A	245	G
1	A	248	G
1	A	251	G
1	A	252	C
1	A	253	G

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Mol	Chain	Res	Type
1	A	258	A
1	A	267	C
1	A	268	A
1	A	272	C
1	A	275	A
1	A	282	G
1	A	283	G
1	A	289	C
1	A	290	U
1	A	291	C
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	310	C
1	A	312	G
1	A	313	U
1	A	314	A
1	A	315	C
1	A	321	U
1	A	322	A
1	A	324	A
1	A	326	A
1	A	327	G
1	A	328	G
1	A	337	A
1	A	338	G
1	A	345	A
1	A	346	G
1	A	349	C
1	A	354	A
1	A	355	A
1	A	360	C
1	A	367	G
1	A	368	G
1	A	373	A
1	A	375	C
1	A	376	A
1	A	378	C
1	A	379	C
1	A	380	C
1	A	387	C

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Mol	Chain	Res	Type
1	A	390	A
1	A	393	U
1	A	394	U
1	A	405	U
1	A	406	G
1	A	407	A
1	A	411	G
1	A	418	A
1	A	419	G
1	A	420	U
1	A	430	C
1	A	433	G
1	A	434	U
1	A	435	G
1	A	438	A
1	A	453	G
1	A	459	A
1	A	474	U
1	A	478	U
1	A	481	U
1	A	485	U
1	A	489	G
1	A	490	A
1	A	494	A
1	A	502	C
1	A	503	C
1	A	504	A
1	A	525	A
1	A	526	A
1	A	527	A
1	A	528	G
1	A	537	A
1	A	538	A
1	A	544	G
1	A	548	A
1	A	550	G
1	A	551	A
1	A	553	A
1	A	555	C
1	A	556	C
1	A	558	G
1	A	559	A

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Mol	Chain	Res	Type
1	A	561	A
1	A	562	C
1	A	564	G
1	A	575	A
1	A	576	G
1	A	577	U
1	A	578	A
1	A	589	G
1	A	591	U
1	A	592	A
1	A	594	C
1	A	595	G
1	A	599	G
1	A	606	U
1	A	607	G
1	A	616	A
1	A	618	A
1	A	619	A
1	A	634	A
1	A	637	A
1	A	647	A
1	A	648	G
1	A	649	G
1	A	650	U
1	A	651	U
1	A	655	C
1	A	656	A
1	A	657	G
1	A	658	A
1	A	660	G
1	A	663	G
1	A	664	C
1	A	665	G
1	A	666	G
1	A	667	A
1	A	668	G
1	A	673	A
1	A	674	G
1	A	684	G
1	A	691	U
1	A	692	A
1	A	698	C

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Mol	Chain	Res	Type
1	A	700	U
1	A	711	U
1	A	718	C
1	A	722	A
1	A	732	A
1	A	733	U
1	A	734	C
1	A	736	A
1	A	746	A
1	A	764	C
1	A	769	A
1	A	774	A
1	A	775	G
1	A	777	C
1	A	785	C
1	A	786	A
1	A	787	C
1	A	788	G
1	A	794	U
1	A	795	G
1	A	799	A
1	A	811	A
1	A	812	G
1	A	822	G
1	A	823	G
1	A	829	A
1	A	830	A
1	A	831	U
1	A	832	G
1	A	836	A
1	A	837	U
1	A	838	C
1	A	840	A
1	A	841	A
1	A	843	C
1	A	847	A
1	A	848	G
1	A	851	A
1	A	852	G
1	A	853	C
1	A	858	U
1	A	859	C

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Mol	Chain	Res	Type
1	A	866	A
1	A	872	C
1	A	874	U
1	A	875	U
1	A	878	G
1	A	880	C
1	A	882	A
1	A	892	U
1	A	893	A
1	A	894	A
1	A	895	G
1	A	896	A
1	A	900	U
1	A	908	A
1	A	910	A
1	A	912	C
1	A	913	A
1	A	914	C
1	A	915	U
1	A	916	G
1	A	918	U
1	A	924	U
1	A	925	A
1	A	928	G
1	A	931	C
1	A	932	C
1	A	933	C
1	A	934	U
1	A	935	A
1	A	937	C
1	A	942	U
1	A	943	A
1	A	944	C
1	A	948	A
1	A	952	A
1	A	956	A
1	A	957	A
1	A	959	C
1	A	964	A
1	A	970	A
1	A	972	U
1	A	974	A

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Mol	Chain	Res	Type
1	A	976	U
1	A	977	U
1	A	978	A
1	A	981	C
1	A	987	A
1	A	992	G
1	A	998	G
1	A	1005	A
1	A	1007	G
1	A	1019	A
1	A	1020	A
1	A	1025	A
1	A	1027	A
1	A	1030	G
1	A	1031	C
1	A	1034	A
1	A	1035	G
1	A	1037	C
1	A	1042	A
1	A	1055	A
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1071	G
1	A	1072	A
1	A	1073	A
1	A	1079	U
1	A	1093	G
1	A	1096	A
1	A	1097	A
1	A	1100	A
1	A	1102	G
1	A	1103	A
1	A	1104	U
1	A	1107	U
1	A	1108	G
1	A	1111	U
1	A	1113	A
1	A	1115	A
1	A	1116	A

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Mol	Chain	Res	Type
1	A	1117	G
1	A	1118	C
1	A	1121	C
1	A	1122	C
1	A	1123	A
1	A	1124	C
1	A	1126	A
1	A	1128	U
1	A	1129	U
1	A	1130	A
1	A	1131	A
1	A	1134	A
1	A	1135	G
1	A	1136	U
1	A	1138	C
1	A	1139	G
1	A	1141	A
1	A	1145	G
1	A	1148	C
1	A	1150	C
1	A	1152	G
1	A	1158	G
1	A	1177	G
1	A	1178	U
1	A	1179	A
1	A	1181	C
1	A	1182	G
1	A	1188	A
1	A	1189	A
1	A	1194	A
1	A	1197	A
1	A	1201	A
1	A	1202	A
1	A	1209	G
1	A	1218	U
1	A	1219	C
1	A	1220	G
1	A	1222	A
1	A	1236	G
1	A	1244	A
1	A	1246	G
1	A	1247	G

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Mol	Chain	Res	Type
1	A	1248	C
1	A	1249	U
1	A	1250	G
1	A	1251	U
1	A	1268	G
1	A	1269	A
1	A	1278	G
1	A	1286	A
1	A	1289	U
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1305	A
1	A	1306	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1319	G
1	A	1327	U
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1352	U
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1375	A
1	A	1376	G
1	A	1380	U
1	A	1381	A
1	A	1382	G
1	A	1384	C
1	A	1388	A
1	A	1404	A
1	A	1417	A
1	A	1418	U
1	A	1423	A
1	A	1424	A

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Mol	Chain	Res	Type
1	A	1426	A
1	A	1432	A
1	A	1433	U
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1439	U
1	A	1441	U
1	A	1442	A
1	A	1450	C
1	A	1456	A
1	A	1459	U
1	A	1460	G
1	A	1464	A
1	A	1473	A
1	A	1474	C
1	A	1495	C
1	A	1496	G
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1504	A
1	A	1507	U
1	A	1513	U
1	A	1516	A
1	A	1517	A
1	A	1519	C
1	A	1520	A
1	A	1521	G
1	A	1523	U
1	A	1524	A
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1536	A
1	A	1539	C
1	A	1543	U
1	A	1553	A
1	A	1555	A
1	A	1558	C
1	A	1561	G
1	A	1562	A

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Mol	Chain	Res	Type
1	A	1572	G
1	A	1573	C
1	A	1578	G
1	A	1581	A
1	A	1582	U
1	A	1583	A
1	A	1584	U
1	A	1585	A
1	A	1596	U
1	A	1600	G
1	A	1601	A
1	A	1607	C
1	A	1608	A
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1631	A
1	A	1632	G
1	A	1638	A
1	A	1640	G
1	A	1647	U
1	A	1648	A
1	A	1651	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1657	C
1	A	1658	G
1	A	1660	C
1	A	1667	A
1	A	1674	G
1	A	1679	A
1	A	1680	A
1	A	1688	G
1	A	1691	A
1	A	1693	C
1	A	1695	A
1	A	1696	G
1	A	1697	A
1	A	1707	U
1	A	1708	U
1	A	1712	G

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Mol	Chain	Res	Type
1	A	1713	A
1	A	1719	G
1	A	1727	A
1	A	1728	C
1	A	1739	C
1	A	1744	G
1	A	1745	A
1	A	1752	G
1	A	1756	U
1	A	1757	G
1	A	1758	U
1	A	1759	U
1	A	1767	A
1	A	1769	G
1	A	1771	C
1	A	1774	A
1	A	1776	A
1	A	1777	G
1	A	1778	A
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1785	G
1	A	1787	G
1	A	1788	A
1	A	1790	U
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1796	C
1	A	1802	A
1	A	1810	G
1	A	1811	C
1	A	1814	A
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1832	A
1	A	1834	C
1	A	1839	A
1	A	1858	A
1	A	1862	C

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Mol	Chain	Res	Type
1	A	1876	A
1	A	1877	A
1	A	1882	A
1	A	1897	C
1	A	1900	A
1	A	1901	A
1	A	1902	G
1	A	1910	G
1	A	1912	G
1	A	1913	A
1	A	1916	U
1	A	1918	A
1	A	1919	A
1	A	1925	A
1	A	1930	A
1	A	1935	G
1	A	1942	A
1	A	1943	C
1	A	1944	U
1	A	1948	A
1	A	1954	C
1	A	1959	G
1	A	1960	U
1	A	1966	A
1	A	1967	A
1	A	1968	U
1	A	1969	U
1	A	1972	U
1	A	1981	A
1	A	1984	U
1	A	1992	C
1	A	1995	A
1	A	1996	C
1	A	1999	A
1	A	2000	A
1	A	2001	G
1	A	2010	A
1	A	2011	U
1	A	2012	C
1	A	2020	U
1	A	2024	U
1	A	2026	A

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Mol	Chain	Res	Type
1	A	2027	A
1	A	2033	G
1	A	2042	A
1	A	2047	A
1	A	2052	A
1	A	2059	A
1	A	2060	A
1	A	2062	A
1	A	2072	C
1	A	2084	C
1	A	2085	G
1	A	2088	A
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2092	C
1	A	2098	G
1	A	2111	A
1	A	2116	G
1	A	2117	A
1	A	2119	A
1	A	2121	U
1	A	2123	A
1	A	2124	A
1	A	2125	U
1	A	2126	G
1	A	2130	G
1	A	2131	U
1	A	2132	A
1	A	2139	G
1	A	2140	U
1	A	2142	C
1	A	2143	A
1	A	2145	G
1	A	2147	U
1	A	2148	A
1	A	2149	G
1	A	2155	A
1	A	2156	G
1	A	2157	C
1	A	2158	C
1	A	2160	U

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Mol	Chain	Res	Type
1	A	2161	G
1	A	2162	G
1	A	2163	A
1	A	2164	A
1	A	2166	C
1	A	2167	C
1	A	2168	G
1	A	2170	A
1	A	2174	C
1	A	2175	C
1	A	2176	A
1	A	2177	G
1	A	2183	G
1	A	2186	G
1	A	2187	A
1	A	2188	G
1	A	2190	C
1	A	2192	U
1	A	2195	G
1	A	2196	U
1	A	2197	G
1	A	2199	G
1	A	2201	U
1	A	2202	A
1	A	2203	C
1	A	2212	C
1	A	2216	A
1	A	2218	U
1	A	2220	A
1	A	2221	C
1	A	2222	C
1	A	2223	U
1	A	2226	U
1	A	2227	A
1	A	2228	A
1	A	2231	C
1	A	2232	G
1	A	2233	C
1	A	2235	G
1	A	2239	U
1	A	2240	U
1	A	2241	A

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Mol	Chain	Res	Type
1	A	2242	U
1	A	2243	C
1	A	2245	G
1	A	2246	G
1	A	2247	C
1	A	2248	G
1	A	2252	A
1	A	2253	G
1	A	2254	A
1	A	2255	C
1	A	2256	A
1	A	2260	U
1	A	2267	G
1	A	2268	G
1	A	2279	G
1	A	2295	A
1	A	2296	A
1	A	2308	G
1	A	2312	C
1	A	2315	A
1	A	2333	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2339	A
1	A	2340	A
1	A	2343	A
1	A	2345	U
1	A	2346	C
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2350	G
1	A	2351	A
1	A	2352	G
1	A	2356	A
1	A	2357	A
1	A	2362	A
1	A	2363	C
1	A	2364	A
1	A	2369	A

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Mol	Chain	Res	Type
1	A	2376	C
1	A	2377	U
1	A	2379	C
1	A	2387	A
1	A	2390	A
1	A	2400	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2420	G
1	A	2421	A
1	A	2431	U
1	A	2435	C
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2463	A
1	A	2464	A
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2477	A
1	A	2483	G
1	A	2505	A
1	A	2513	G
1	A	2523	G
1	A	2528	C
1	A	2531	G
1	A	2532	A
1	A	2533	U
1	A	2534	G
1	A	2536	C
1	A	2541	C
1	A	2542	A
1	A	2543	U
1	A	2546	C
1	A	2547	A
1	A	2558	G

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Mol	Chain	Res	Type
1	A	2569	C
1	A	2570	A
1	A	2571	A
1	A	2572	G
1	A	2575	U
1	A	2576	U
1	A	2583	U
1	A	2594	A
1	A	2595	A
1	A	2596	G
1	A	2601	A
1	A	2602	C
1	A	2610	G
1	A	2611	G
1	A	2614	U
1	A	2619	A
1	A	2630	C
1	A	2631	A
1	A	2632	G
1	A	2638	U
1	A	2639	C
1	A	2642	U
1	A	2648	U
1	A	2658	A
1	A	2661	A
1	A	2663	A
1	A	2668	A
1	A	2680	C
1	A	2683	A
1	A	2684	G
1	A	2711	G
1	A	2714	G
1	A	2717	G
1	A	2718	U
1	A	2720	C
1	A	2730	U
1	A	2731	G
1	A	2743	G
1	A	2754	A
1	A	2755	U
1	A	2766	G
1	A	2773	G

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Mol	Chain	Res	Type
1	A	2779	A
1	A	2780	G
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2790	A
1	A	2794	A
1	A	2795	G
1	A	2797	C
1	A	2798	C
1	A	2800	C
1	A	2804	A
1	A	2807	A
1	A	2808	U
1	A	2809	G
1	A	2813	U
1	A	2818	C
1	A	2819	A
1	A	2820	U
1	A	2825	C
1	A	2826	A
1	A	2843	G
1	A	2855	G
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2869	A
1	A	2873	G
1	A	2874	G
1	A	2892	G
1	A	2897	G
1	A	2898	A
1	A	2899	C
1	A	2902	A
1	A	2905	C
1	A	2909	U
1	A	2918	G
1	A	2919	A
2	B	10	G
2	B	11	A
2	B	12	U

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Mol	Chain	Res	Type
2	B	13	A
2	B	20	A
2	B	23	U
2	B	28	C
2	B	37	A
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	46	A
2	B	48	G
2	B	49	G
2	B	50	A
2	B	51	A
2	B	55	A
2	B	59	U
2	B	60	C
2	B	61	U
2	B	63	C
2	B	64	A
2	B	81	G
2	B	85	U
2	B	86	U
2	B	87	U
2	B	88	C
2	B	96	G
2	B	97	A
2	B	107	G
2	B	110	G
32	W	10	A
32	W	11	G
32	W	34	A
32	W	41	G
32	W	49	C
32	W	50	C
32	W	52	A
32	W	53	A
32	W	83	C
32	W	85	U
32	W	87	C
32	W	88	U
32	W	99	A

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Mol	Chain	Res	Type
32	W	114	A
32	W	118	A
32	W	119	C
32	W	120	A
32	W	127	U
32	W	129	A
32	W	130	C
32	W	140	A
32	W	142	A
32	W	143	C
32	W	151	A
32	W	158	G
32	W	162	C
32	W	163	C
32	W	182	U
32	W	183	U
32	W	194	C
32	W	195	A
32	W	197	G
32	W	210	A
32	W	222	G
32	W	249	G
32	W	255	G
32	W	258	A
32	W	259	G
32	W	274	G
32	W	275	C
32	W	287	A
32	W	288	C
32	W	297	G
32	W	336	C
32	W	337	A
32	W	338	C
32	W	340	G
32	W	355	G
32	W	360	C
32	W	362	G
32	W	375	U
32	W	380	C
32	W	405	A
32	W	414	G
32	W	419	A

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Mol	Chain	Res	Type
32	W	420	U
32	W	421	G
32	W	422	A
32	W	429	U
32	W	430	C
32	W	432	G
32	W	437	U
32	W	456	A
32	W	457	A
32	W	460	A
32	W	472	C
32	W	474	A
32	W	475	A
32	W	476	U
32	W	477	A
32	W	488	U
32	W	490	G
32	W	491	A
32	W	494	G
32	W	506	A
32	W	507	A
32	W	518	A
32	W	520	C
32	W	527	C
32	W	528	C
32	W	533	G
32	W	536	G
32	W	541	A
32	W	556	A
32	W	568	A
32	W	572	A
32	W	581	A
32	W	582	A
32	W	585	G
32	W	586	G
32	W	605	A
32	W	642	U
32	W	643	C
32	W	651	A
32	W	662	U
32	W	674	A
32	W	696	A

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Mol	Chain	Res	Type
32	W	704	A
32	W	711	A
32	W	727	A
32	W	728	C
32	W	729	C
32	W	730	A
32	W	732	U
32	W	740	G
32	W	741	C
32	W	756	U
32	W	757	A
32	W	764	G
32	W	786	A
32	W	793	A
32	W	802	U
32	W	803	A
32	W	823	A
32	W	824	A
32	W	826	C
32	W	830	G
32	W	837	A
32	W	838	A
32	W	843	U
32	W	849	G
32	W	856	C
32	W	865	G
32	W	874	A
32	W	880	U
32	W	881	U
32	W	882	A
32	W	883	A
32	W	924	A
32	W	936	G
32	W	944	C
32	W	945	A
32	W	948	A
32	W	970	U
32	W	974	A
32	W	979	A
32	W	981	G
32	W	984	A
32	W	985	A

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Mol	Chain	Res	Type
32	W	986	G
32	W	987	A
32	W	992	U
32	W	993	A
32	W	1003	G
32	W	1004	A
32	W	1012	U
32	W	1014	A
32	W	1018	U
32	W	1027	U
32	W	1028	A
32	W	1033	G
32	W	1036	C
32	W	1040	U
32	W	1042	G
32	W	1044	G
32	W	1046	G
32	W	1053	G
32	W	1054	A
32	W	1060	G
32	W	1064	C
32	W	1075	U
32	W	1104	G
32	W	1105	U
32	W	1111	A
32	W	1112	A
32	W	1143	A
32	W	1148	G
32	W	1149	U
32	W	1150	U
32	W	1151	G
32	W	1155	A
32	W	1161	A
32	W	1168	U
32	W	1169	G
32	W	1170	C
32	W	1177	C
32	W	1191	G
32	W	1192	U
32	W	1193	G
32	W	1200	A
32	W	1205	A

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Mol	Chain	Res	Type
32	W	1206	A
32	W	1210	A
32	W	1211	U
32	W	1221	U
32	W	1222	A
32	W	1223	U
32	W	1230	G
32	W	1237	C
32	W	1247	A
32	W	1250	G
32	W	1266	A
32	W	1269	G
32	W	1289	A
32	W	1295	C
32	W	1296	A
32	W	1308	A
32	W	1313	G
32	W	1314	G
32	W	1326	C
32	W	1329	C
32	W	1331	C
32	W	1332	G
32	W	1341	A
32	W	1343	G
32	W	1345	U
32	W	1346	G
32	W	1355	A
32	W	1373	U
32	W	1377	G
32	W	1407	A
32	W	1435	A
32	W	1451	A
32	W	1452	G
32	W	1455	A
32	W	1461	U
32	W	1462	U
32	W	1463	A
32	W	1464	G
32	W	1490	A
32	W	1502	A
32	W	1503	A
32	W	1504	G

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Mol	Chain	Res	Type
32	W	1509	A
32	W	1513	A
32	W	1515	G
32	W	1516	U
32	W	1527	G
32	W	1539	G
32	W	1540	G
32	W	1541	A
32	W	1544	A
32	W	1545	C
32	W	1547	U
32	W	1548	C
52	z	9	A
52	z	18	G
52	z	19	U
52	z	21	A
52	z	34	G
52	z	35	U
52	z	36	C
52	z	48	C
52	z	49	G
52	z	55	U
52	z	56	C
52	z	57	G
52	z	70	A
52	z	73	G
52	z	76	A

All (106) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	43	G
1	A	58	G
1	A	90	A
1	A	118	A
1	A	124	A
1	A	163	U
1	A	175	G
1	A	183	A
1	A	207	A
1	A	229	A
1	A	252	C

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Mol	Chain	Res	Type
1	A	271	C
1	A	288	C
1	A	298	U
1	A	366	A
1	A	377	G
1	A	405	U
1	A	419	G
1	A	526	A
1	A	549	A
1	A	647	A
1	A	649	G
1	A	666	G
1	A	683	A
1	A	717	A
1	A	785	C
1	A	837	U
1	A	847	A
1	A	934	U
1	A	936	C
1	A	1019	A
1	A	1066	A
1	A	1092	A
1	A	1103	A
1	A	1107	U
1	A	1117	G
1	A	1173	A
1	A	1245	G
1	A	1250	G
1	A	1305	A
1	A	1339	A
1	A	1351	U
1	A	1434	A
1	A	1438	C
1	A	1455	C
1	A	1527	C
1	A	1535	U
1	A	1581	A
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1679	A
1	A	1755	C

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Mol	Chain	Res	Type
1	A	1779	G
1	A	1784	A
1	A	1813	A
1	A	1876	A
1	A	1965	A
1	A	2122	G
1	A	2139	G
1	A	2155	A
1	A	2174	C
1	A	2187	A
1	A	2226	U
1	A	2241	A
1	A	2254	A
1	A	2267	G
1	A	2278	U
1	A	2295	A
1	A	2334	U
1	A	2348	C
1	A	2351	A
1	A	2454	A
1	A	2468	A
1	A	2504	C
1	A	2595	A
1	A	2631	A
1	A	2683	A
1	A	2710	C
1	A	2716	U
1	A	2779	A
1	A	2784	C
1	A	2785	U
1	A	2807	A
1	A	2812	A
2	B	38	U
2	B	47	C
2	B	54	U
2	B	59	U
32	W	98	U
32	W	113	G
32	W	119	C
32	W	126	G
32	W	436	G
32	W	641	G

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Mol	Chain	Res	Type
32	W	842	U
32	W	848	G
32	W	855	G
32	W	864	U
32	W	873	U
32	W	1111	A
32	W	1154	C
32	W	1210	A
32	W	1461	U
32	W	1501	G
32	W	1544	A

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.

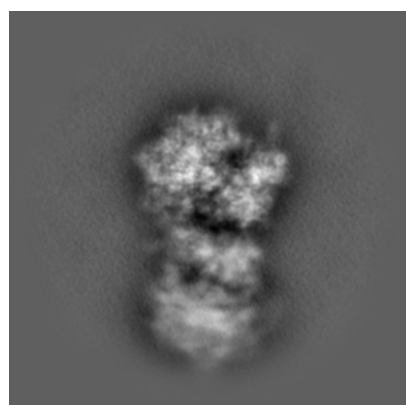
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13959. These allow visual inspection of the internal detail of the map and identification of artifacts.

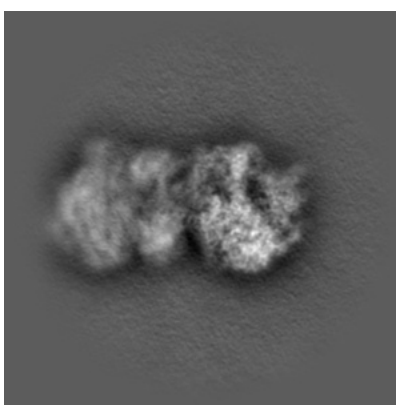
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

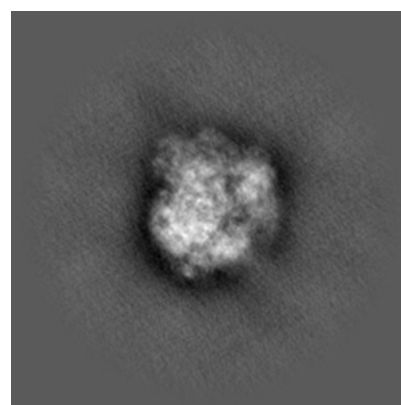
6.1.1 Primary map



X



Y

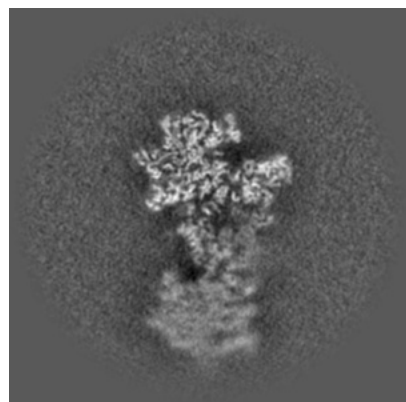


Z

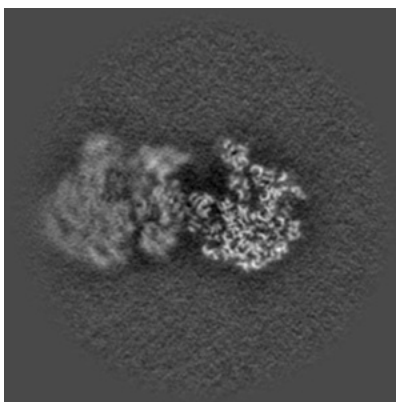
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

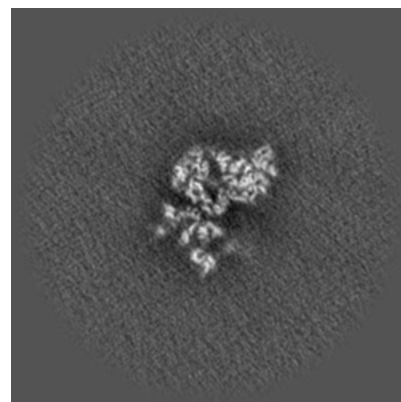
6.2.1 Primary map



X Index: 300



Y Index: 300

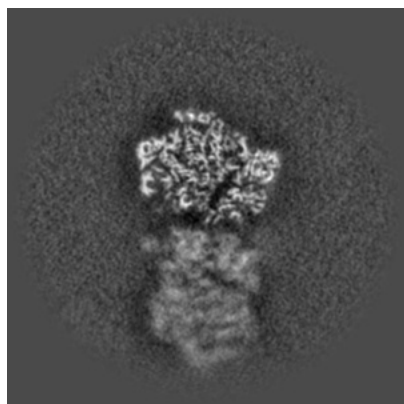


Z Index: 300

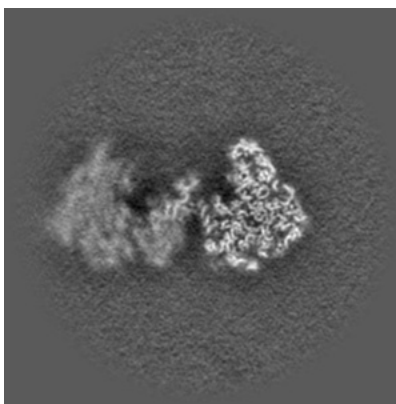
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

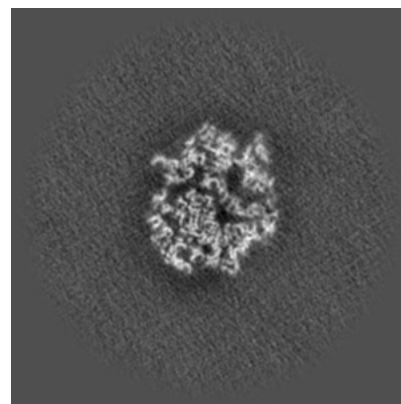
6.3.1 Primary map



X Index: 267



Y Index: 275

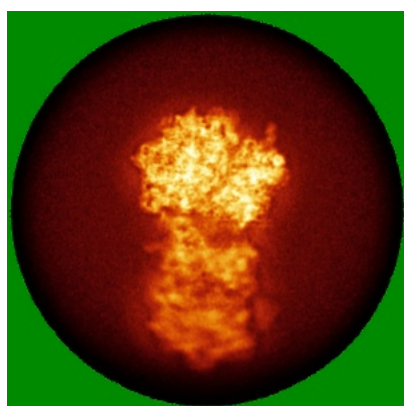


Z Index: 349

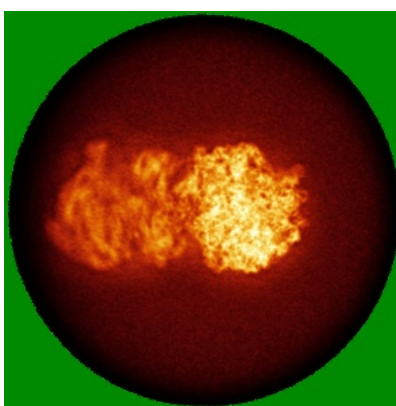
The images above show the largest variance slices of the map in three orthogonal directions.

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

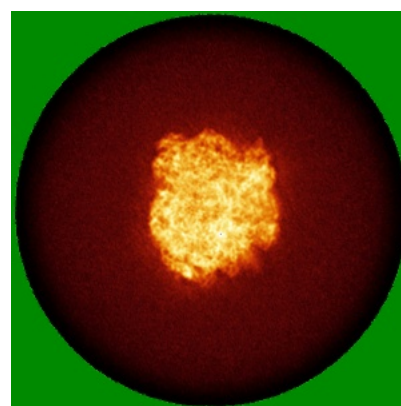
6.4.1 Primary map



X



Y

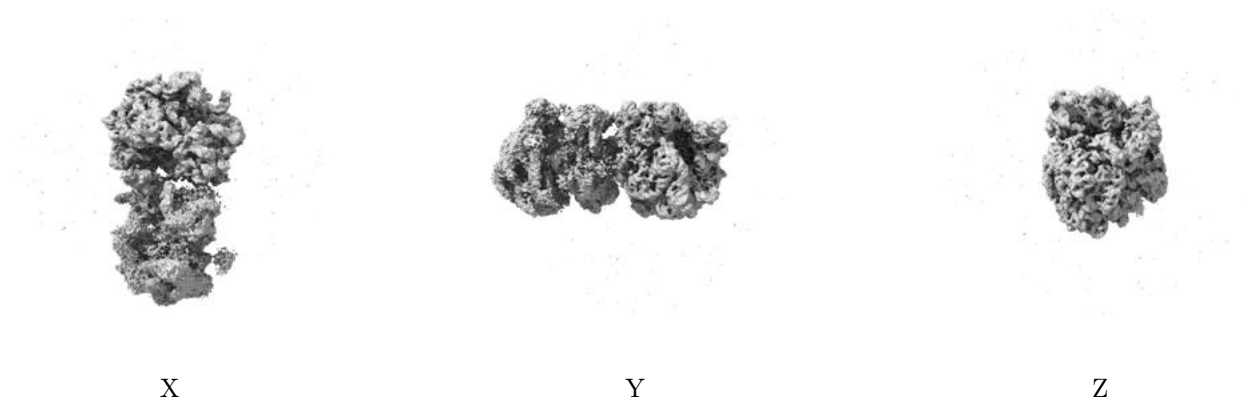


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

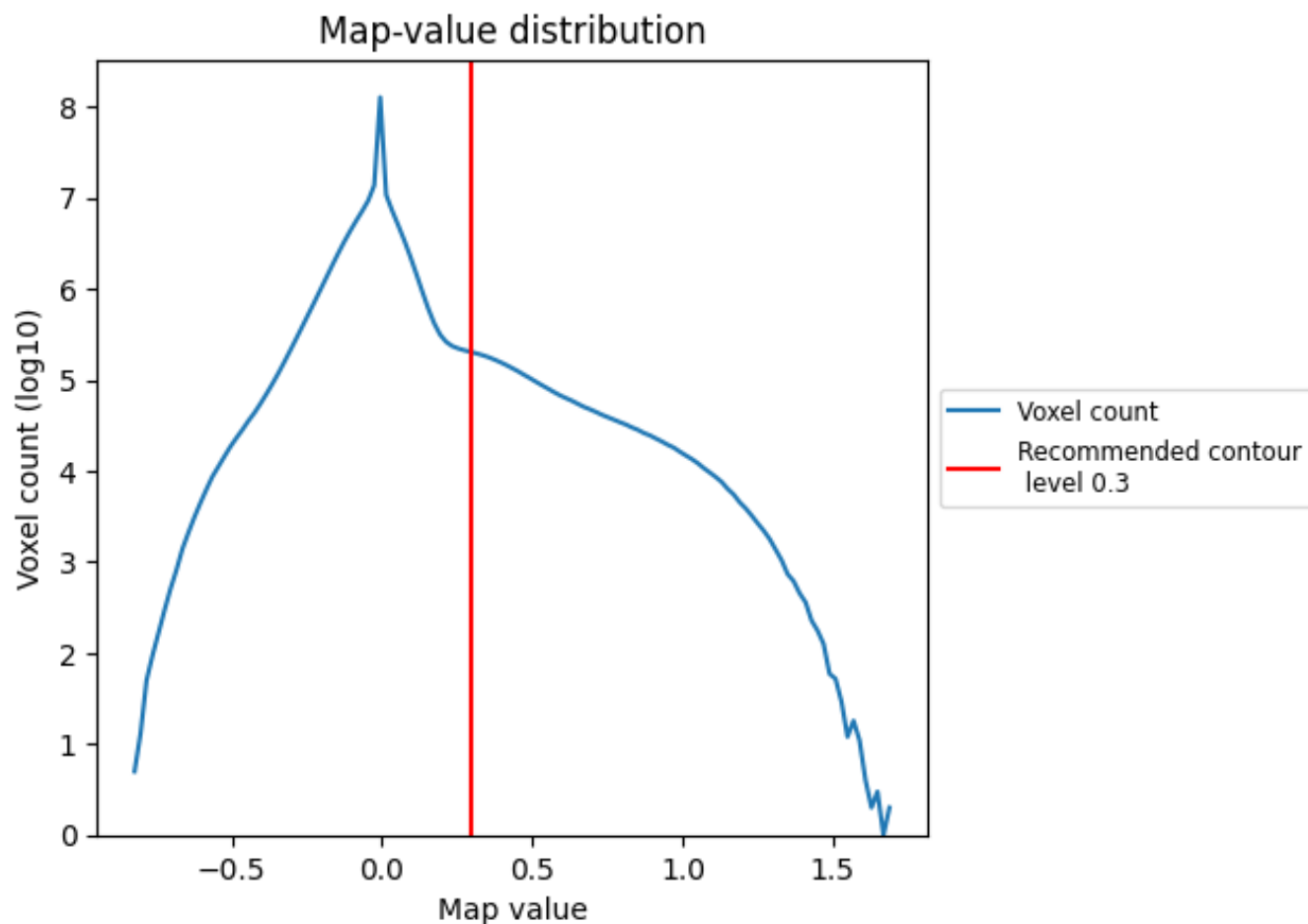
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

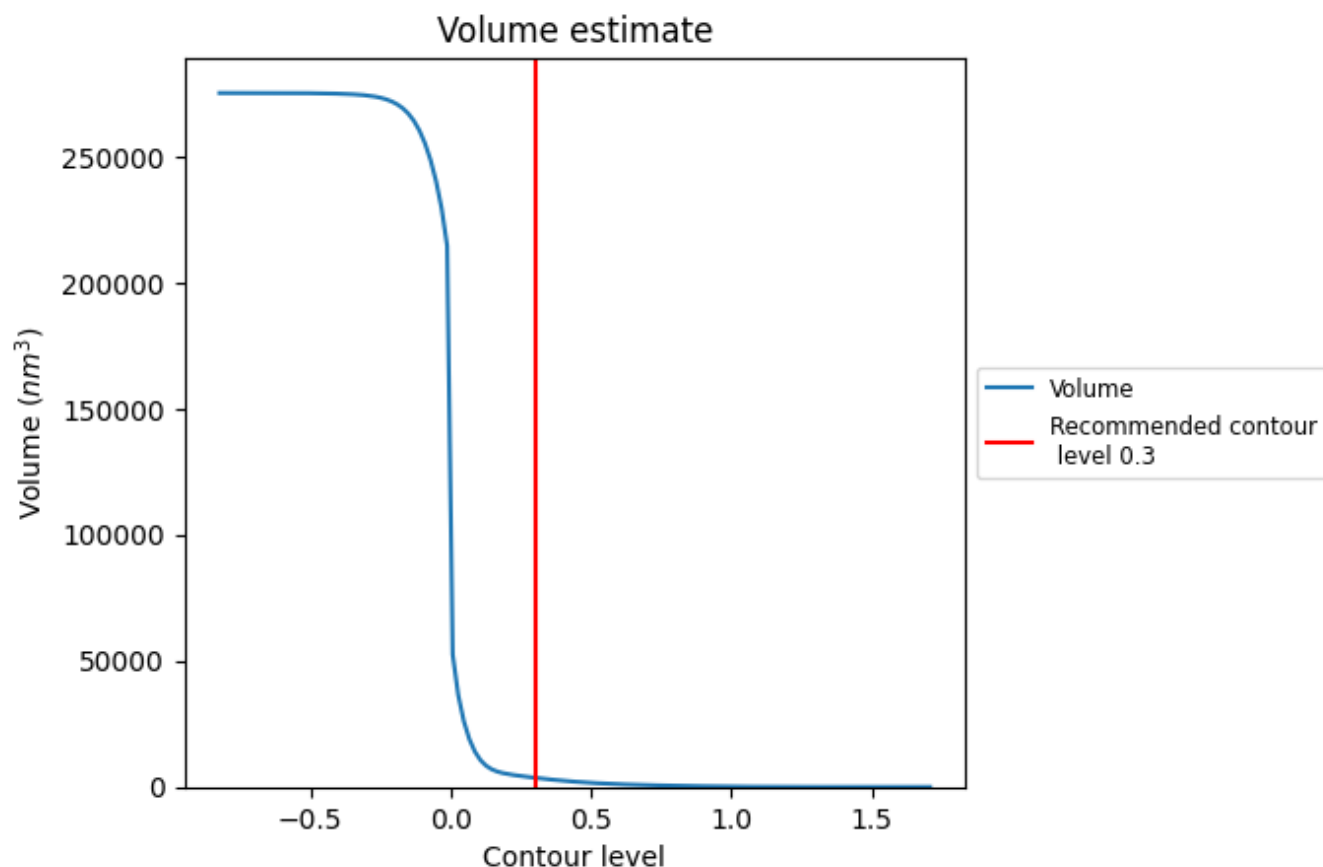
This section contains the results of statistical analysis of the map.

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.

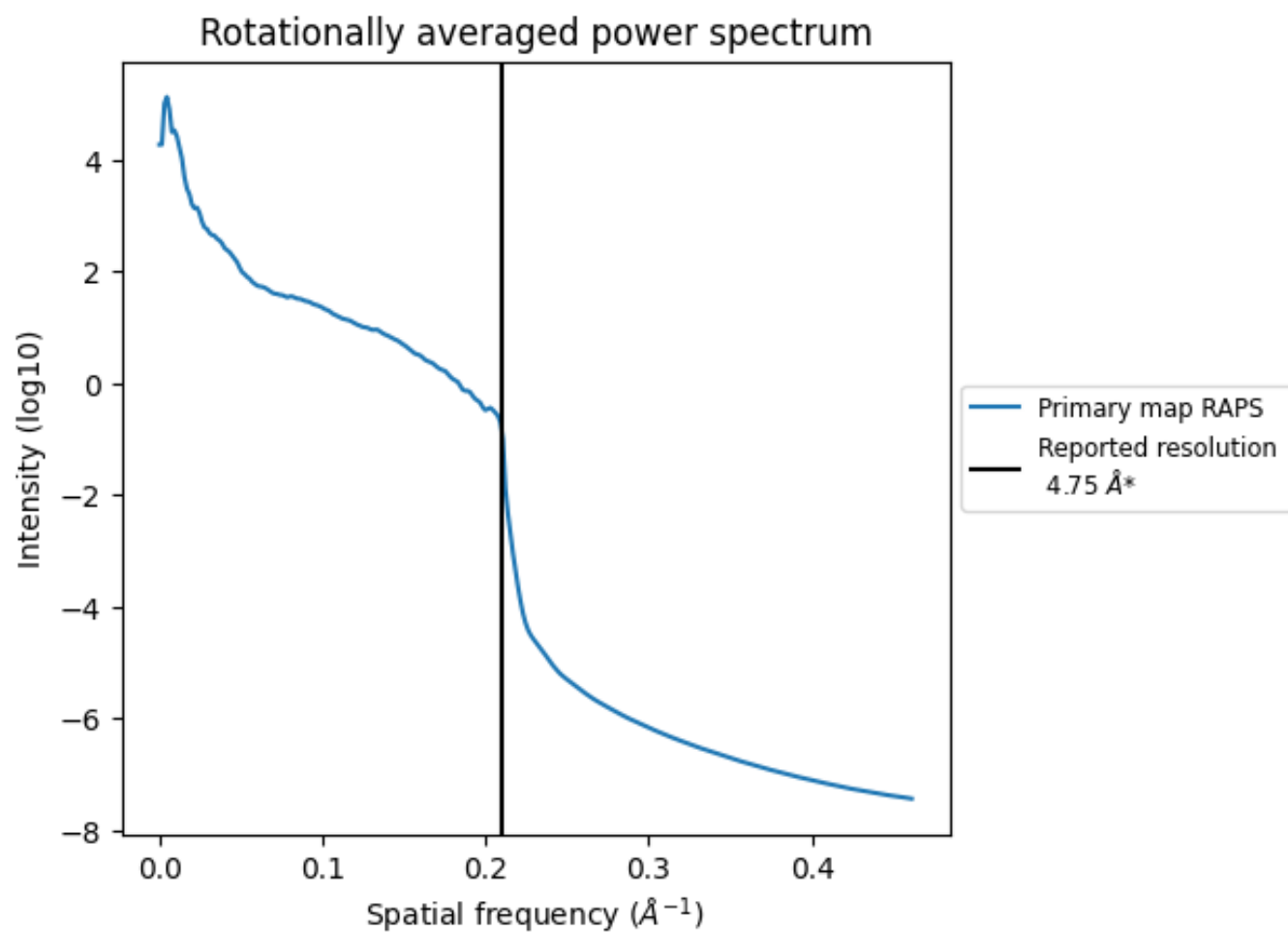
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3652 nm³; this corresponds to an approximate mass of 3299 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 0.211 Å⁻¹

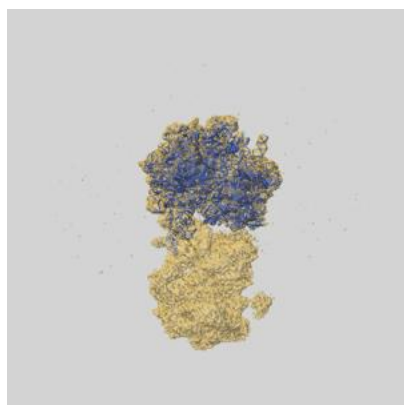
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

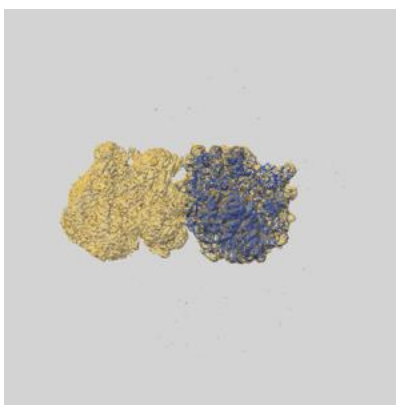
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13959 and PDB model 7QGU. Per-residue inclusion information can be found in section [3](#) on page [15](#).

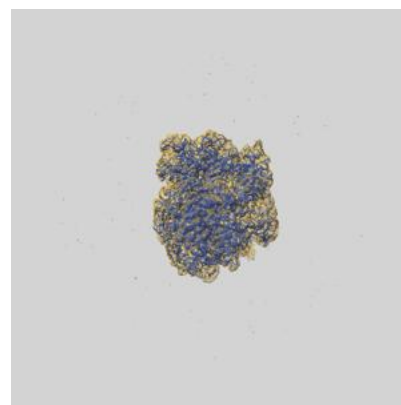
9.1 Map-model overlay [i](#)



X



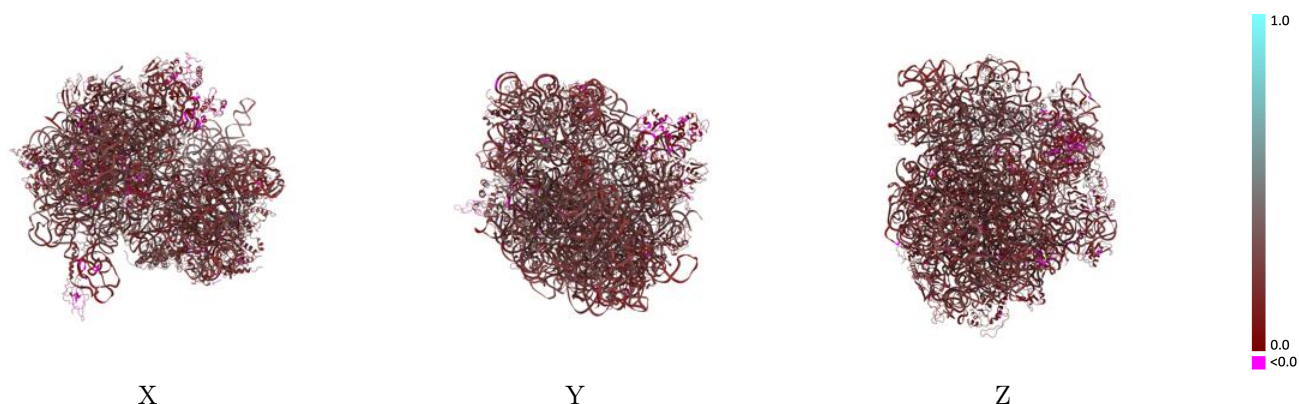
Y



Z

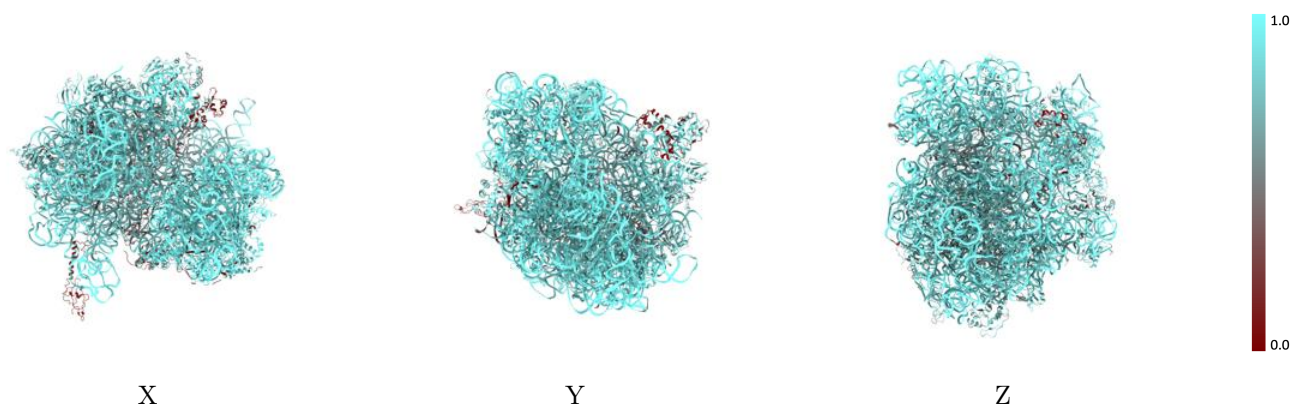
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



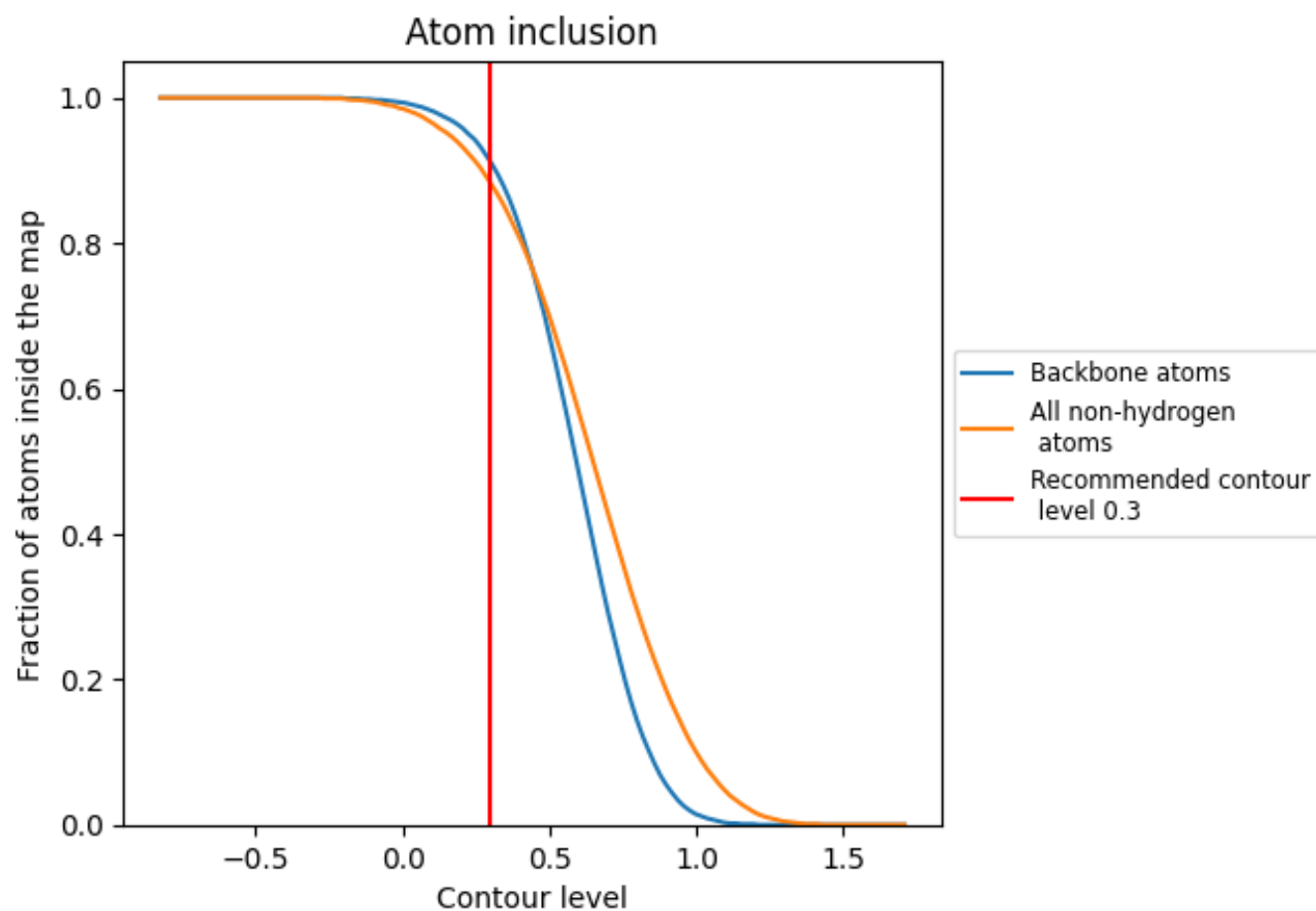
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8830	 0.2250
2	 0.0380	 0.1920
3	 0.7720	 0.1350
A	 0.9460	 0.2410
B	 0.9770	 0.2340
C	 0.4580	 0.1710
D	 0.7070	 0.1810
E	 0.6430	 0.1760
F	 0.6920	 0.1480
G	 0.8030	 0.1800
H	 0.7230	 0.0760
I	 0.3210	 0.0580
J	 0.7190	 0.1850
K	 0.5130	 0.1810
L	 0.6860	 0.1560
M	 0.6150	 0.1930
N	 0.7360	 0.1580
O	 0.8300	 0.1530
P	 0.6890	 0.1770
Q	 0.7420	 0.1400
R	 0.7680	 0.1870
S	 0.6120	 0.1770
T	 0.7160	 0.1760
U	 0.7340	 0.1640
V	 0.7110	 0.1570
W	 0.9520	 0.2320
X	 0.2320	 0.0990
Y	 0.4280	 0.1200
Z	 0.7020	 0.1510
a	 0.7660	 0.1420
b	 0.6800	 0.1730
c	 0.6180	 0.1400
d	 0.5590	 0.1310
e	 0.6110	 0.1430
f	 0.7380	 0.1730



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Chain	Atom inclusion	Q-score
g	 0.8040	 0.2740
h	 0.9000	 0.2780
i	 0.9650	 0.2740
j	 0.9210	 0.2940
k	 0.6270	 0.2930
l	 0.8790	 0.2850
m	 0.9790	 0.2960
n	 0.9170	 0.2620
o	 0.9270	 0.2700
p	 0.5930	 0.2830
q	 0.8110	 0.2800
r	 0.9120	 0.2550
s	 0.9090	 0.2540
t	 0.9520	 0.2970
u	 0.9610	 0.2840
v	 0.8440	 0.2900
w	 0.5510	 0.2780
x	 0.9520	 0.2850
y	 0.9270	 0.2630
z	 0.8210	 0.2190