



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:51 AM UTC

PDB ID : 8EUG / pdb_00008eug
EMDB ID : EMD-24412
Title : Ytm1 associated nascent 60S ribosome State 3
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-18
Resolution : 2.80 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:

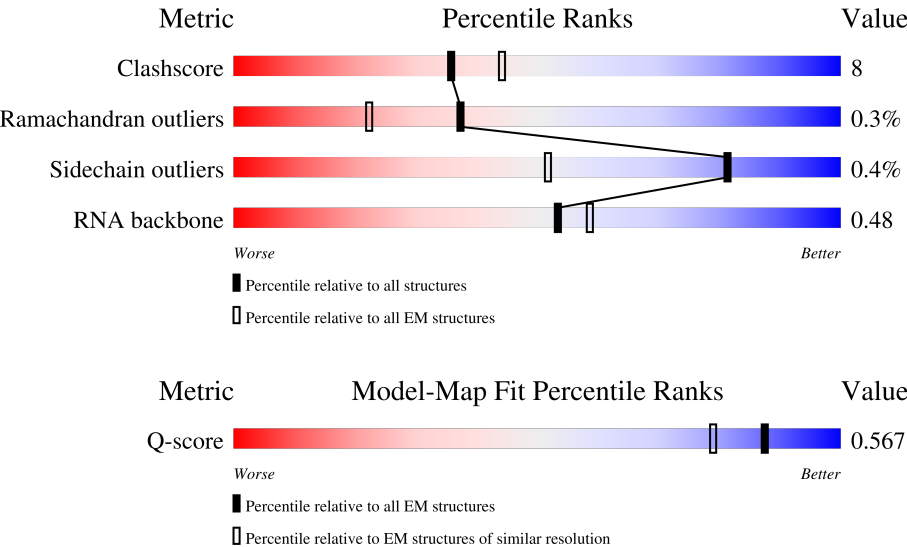
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	1	3498	
2	2	165	
3	3	302	

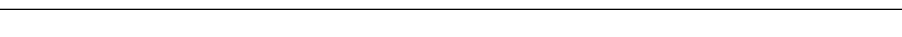
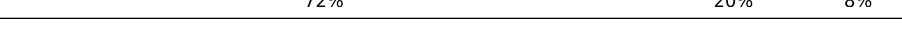
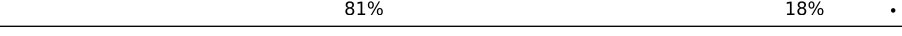
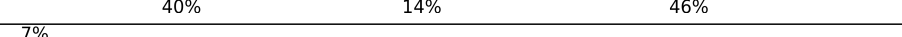
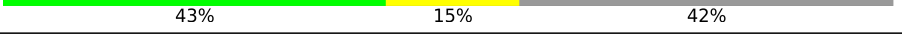
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Mol	Chain	Length	Quality of chain
4	8	51	
5	9	229	
6	A	253	
7	B	388	
8	C	363	
9	D	294	
10	E	195	
11	F	250	
12	G	259	
13	H	190	
14	I	221	
15	J	174	
16	K	94	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	R	193	
24	S	176	
25	T	160	
26	U	117	
27	V	139	
28	X	141	

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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	136	
31	a	148	
32	b	61	
33	c	117	
34	d	113	
35	e	127	
36	f	108	
37	g	112	
38	h	122	
39	i	99	
40	j	91	
41	k	74	
42	m	740	
43	n	607	
44	o	106	
45	p	440	
46	u	192	

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 123162 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 RNA (2863-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2869	Total	C	N	O	P	0	0
			61386	27430	11112	19975	2869		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483
1	2185	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	151	Total	C	N	O	P	0	0
			3211	1437	569	1054	151		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	119	Total	C	N	O	S	0	0
			1006	637	188	175	6		

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	50	Total	C	N	O	S	0	0
			437	273	98	65	1		

- Molecule 5 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	118	Total	C	N	O	P	0	0
			2519	1124	452	825	118		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	244	Total	C	N	O	S	0	0
			1847	1152	370	320	5		

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	377	Total	C	N	O	S	0	0
			3003	1901	567	525	10		

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 9 is a protein called 60S ribosomal protein L5-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	287	Total	C	N	O	S	0	0
			2305	1457	409	435	4		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	172	Total	C	N	O	S	0	0
			1338	860	245	230	3		

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	214	Total	C	N	O	S	0	0
			1745	1124	320	298	3		

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	1	0
			1817	1161	334	319	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	178	Total	C	N	O	S	0	0
			1415	892	260	257	6		

- Molecule 14 is a protein called 60S ribosomal protein L10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	170	Total	C	N	O	S	0	0
			1372	869	256	242	5		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	157	Total	C	N	O	S	0	0
			1276	806	242	223	5		

- Molecule 16 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	90	Total	C	N	O	S	0	0
			695	428	144	117	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	202	Total	C	N	O	S	0	0
			1612	1008	321	282	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	171	Total	C	N	O	S	0	0
			1357	857	262	235	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	186	Total	C	N	O	S	0	0
			1486	933	300	252	1		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	148	Total	C	N	O	S	0	0
			1220	759	259	197	5		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	167	Total	C	N	O	S	0	0
			1388	896	259	228	5		

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	158	Total	C	N	O	S	0	0
			1282	807	247	225	3		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	98	Total	C	N	O	0	0
			791	513	137	141		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	137	Total	C	N	O	S	0	0
			1026	644	193	181	8		

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	120	Total	C	N	O	S	0	0
			962	614	178	169	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	134	Total	C	N	O	S	0	0
			1072	693	199	178	2		

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	147	Total	C	N	O	S	0	0
			1169	740	235	192	2		

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	54	Total	C	N	O	0	0
			463	281	106	76		

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	95	Total	C	N	O	S	0	0
			714	454	124	132	4		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	102	Total	C	N	O	S	0	0
			849	534	165	147	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	117	Total	C	N	O	S	0	0
			939	588	190	156	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	121	Total	C	N	O		0	0
			999	629	194	176			

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	96	Total	C	N	O	S	0	0
			767	478	160	128	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	83	Total	C	N	O	S	0	0
			657	402	141	107	7		

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	398	Total	C	N	O	S	0	0
			3127	2001	557	558	11		

- Molecule 43 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	354	Total	C	N	O	S	0	0
			2903	1892	496	503	12		

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	97	Total	C	N	O	S	0	0
			789	498	158	128	5		

- Molecule 45 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	p	290	Total	C	N	O	0	0
			1431	851	290	290		

- Molecule 46 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	59	Total	C	N	O	S	0	0
			493	315	100	72	6		

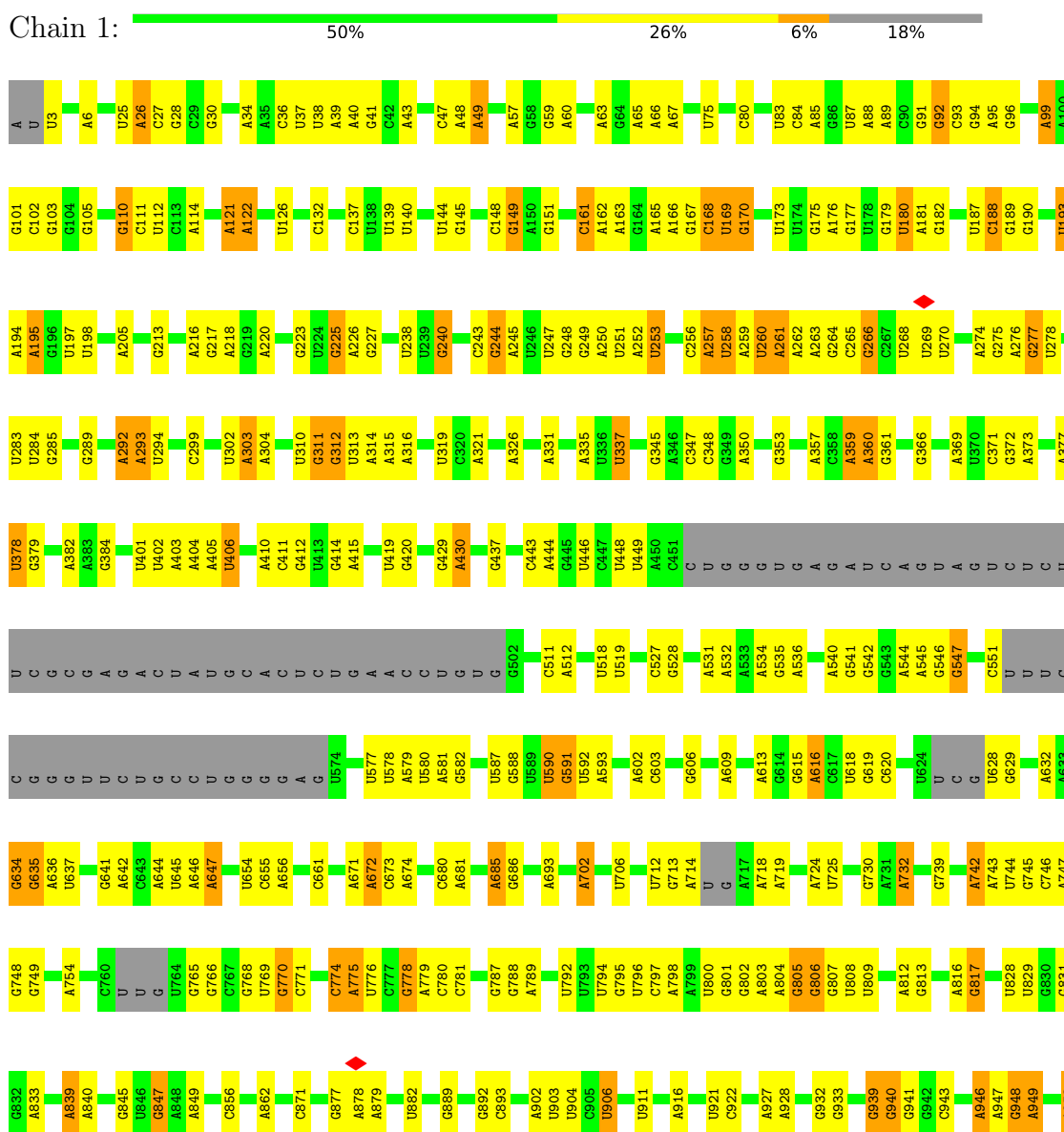
- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

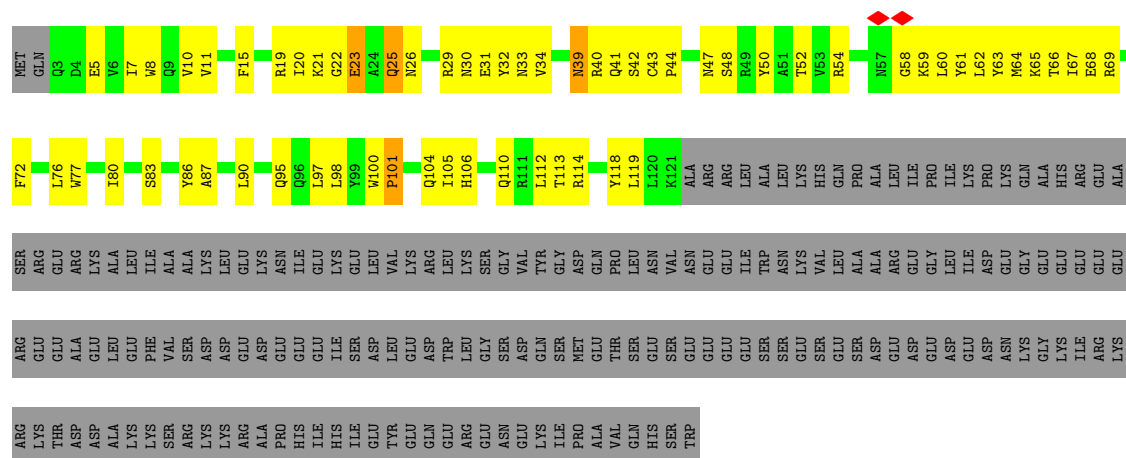
• Molecule 1: RNA (2863-MER)







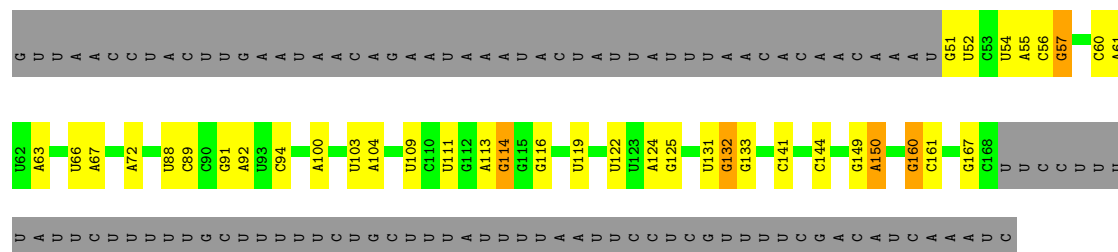
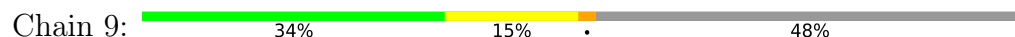
- Molecule 3: Protein mak16



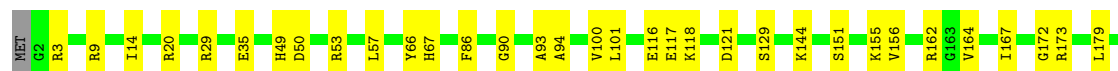
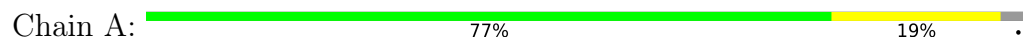
- Molecule 4: 60S ribosomal protein L39



- Molecule 5: RNA (118-MER)



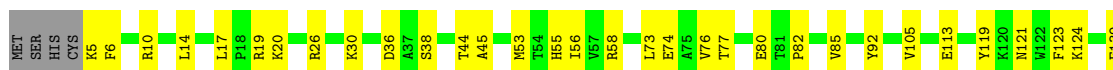
- Molecule 6: 60S ribosomal protein L2-A





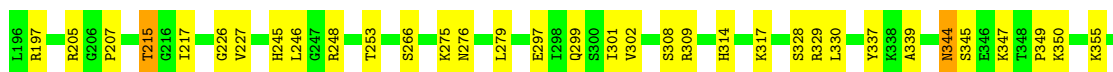
• Molecule 7: 60S ribosomal protein L3-A

Chain B: 73% 24%



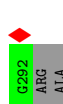
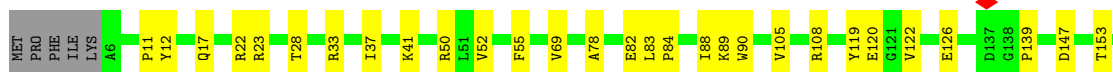
• Molecule 8: 60S ribosomal protein L4-B

Chain C: 81% 17%



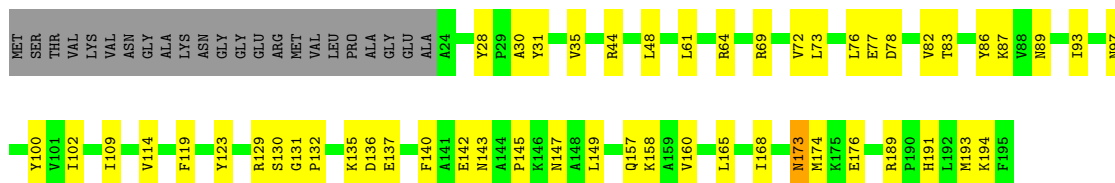
• Molecule 9: 60S ribosomal protein L5-A

Chain D: 78% 20%



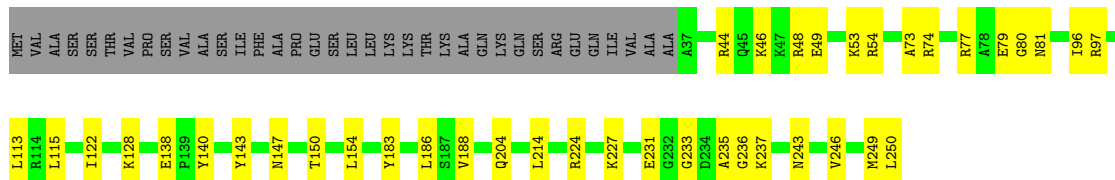
• Molecule 10: 60S ribosomal protein L6

Chain E: 62% 26% 12%



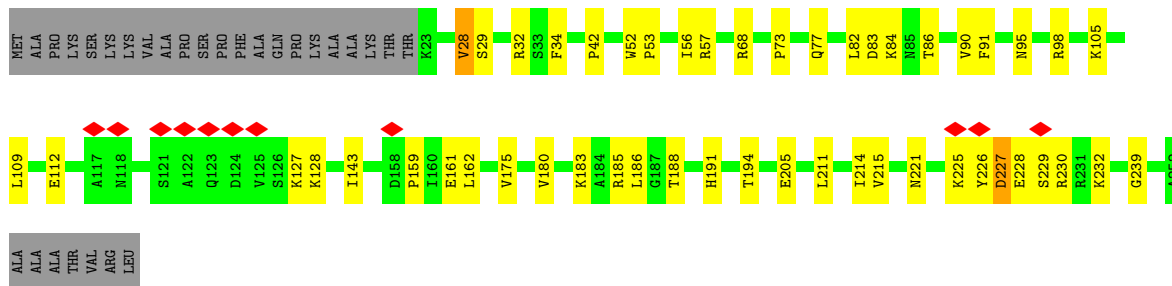
- Molecule 11: 60S ribosomal protein L7-B

Chain F: 70% 16% 14%



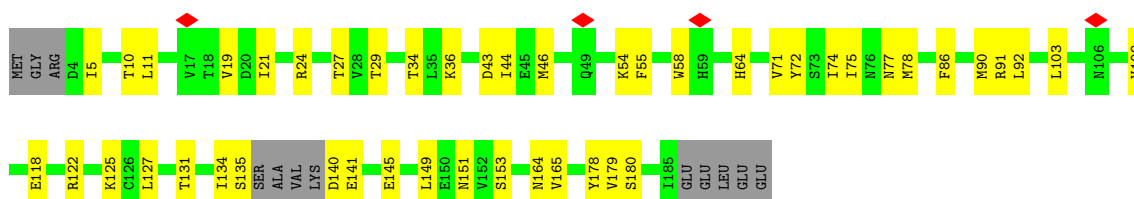
- Molecule 12: 60S ribosomal protein L8

Chain G: 69% 19% 11%



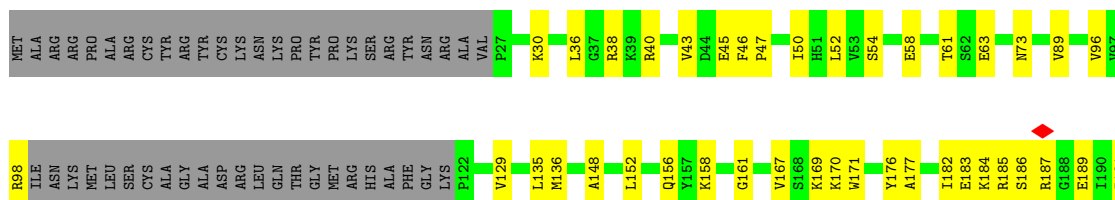
- Molecule 13: 60S ribosomal protein L9-A

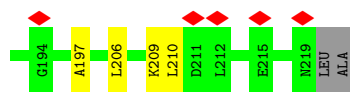
Chain H: 69% 25% 6%



- Molecule 14: 60S ribosomal protein L10-A

Chain I: 57% 20% 23%





- Molecule 15: 60S ribosomal protein L11-A

Chain J: 67% 22% 10%



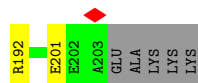
- Molecule 16: 60S ribosomal protein L43-A

Chain K: 80% 16%



- Molecule 17: 60S ribosomal protein L13

Chain L: 81% 15%



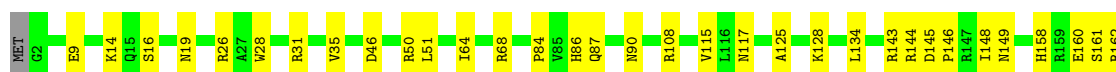
- Molecule 18: 60S ribosomal protein L14

Chain M: 70% 22% 7%



- Molecule 19: 60S ribosomal protein L15-A

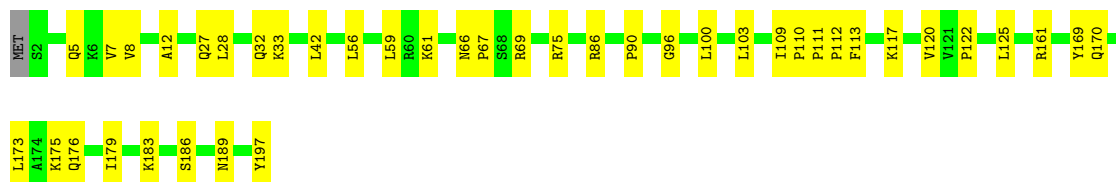
Chain N: 76% 23%





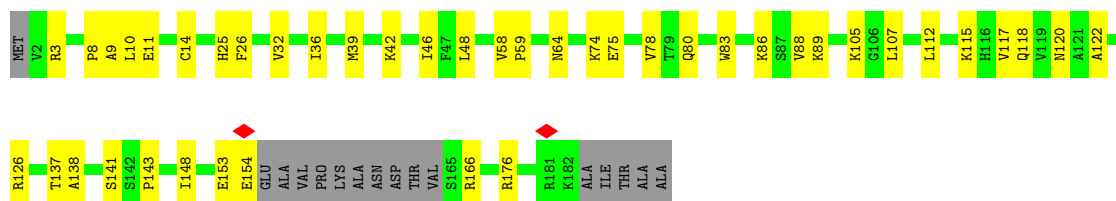
- Molecule 20: 60S ribosomal protein L16-B

Chain O: 79% 21%



- Molecule 21: 60S ribosomal protein L17-A

Chain P: 68% 23% 9%



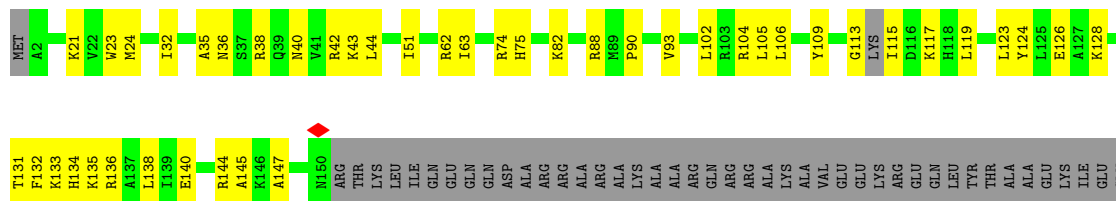
- Molecule 22: 60S ribosomal protein L18-A

Chain Q: 83% 15%



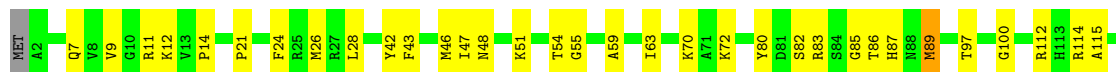
- Molecule 23: 60S ribosomal protein L19-A

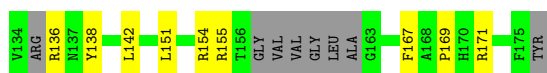
Chain R: 54% 23% 23%



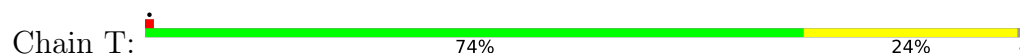
- Molecule 24: 60S ribosomal protein L20-A

Chain S: 71% 23% 5%

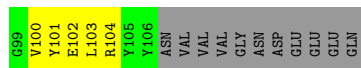
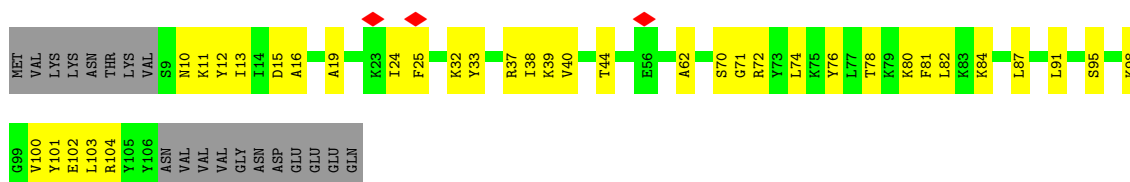




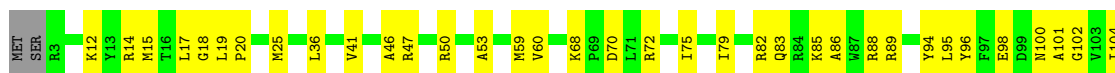
- Molecule 25: 60S ribosomal protein L21-A



- Molecule 26: 60S ribosomal protein L22



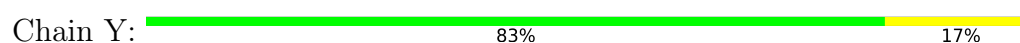
- Molecule 27: 60S ribosomal protein L23-A

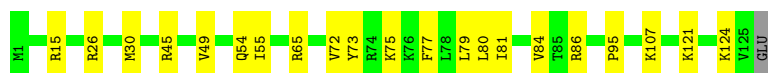


- Molecule 28: 60S ribosomal protein L25-A

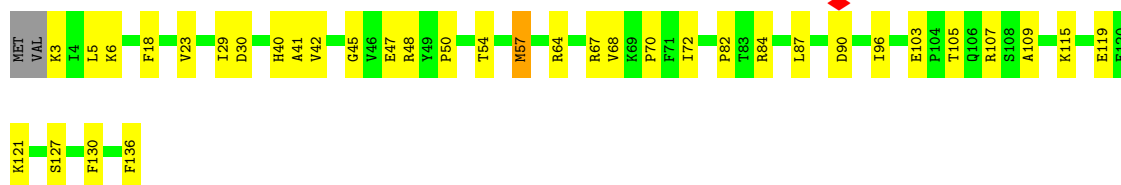


- Molecule 29: 60S ribosomal protein L26

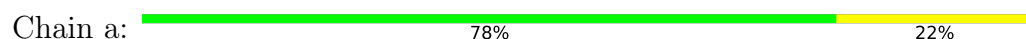




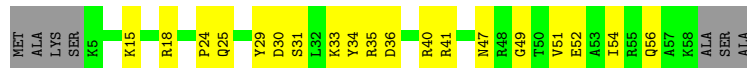
- Molecule 30: 60S ribosomal protein L27-A



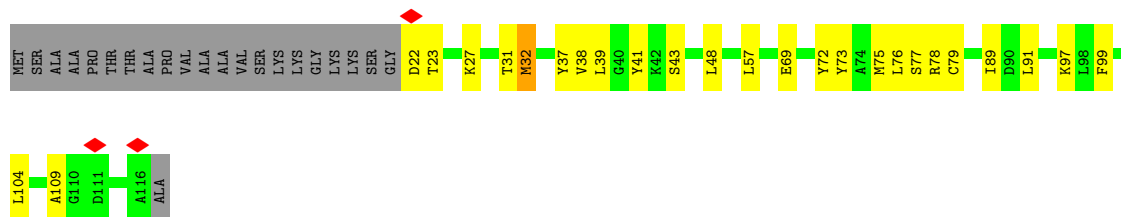
- Molecule 31: 60S ribosomal protein L28-A



- Molecule 32: 60S ribosomal protein L29



- Molecule 33: 60S ribosomal protein L30-2



- Molecule 34: 60S ribosomal protein L31

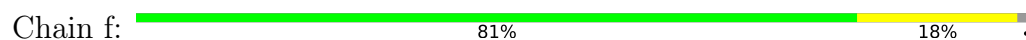


- Molecule 35: 60S ribosomal protein L32-A





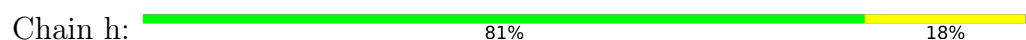
- Molecule 36: 60S ribosomal protein L33-B



- Molecule 37: 60S ribosomal protein L34-A



- Molecule 38: 60S ribosomal protein L35



- Molecule 39: 60S ribosomal protein L36-B



- Molecule 40: 60S ribosomal protein L37-B



- Molecule 41: 60S ribosomal protein L38-1



- Molecule 42: Ribosome biogenesis protein erb1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.870	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	1	0.11	0/68700	0.25	2/107035 (0.0%)
2	2	0.13	0/3589	0.25	0/5586
3	3	0.25	0/1028	0.57	0/1384
4	8	0.13	0/448	0.32	0/597
5	9	0.09	0/2816	0.18	0/4388
6	A	0.13	0/1885	0.32	0/2542
7	B	0.12	0/3069	0.30	0/4130
8	C	0.14	0/2848	0.32	0/3842
9	D	0.10	0/2354	0.26	0/3166
10	E	0.12	0/1366	0.34	0/1843
11	F	0.11	0/1781	0.29	0/2389
12	G	0.13	0/1846	0.35	0/2485
13	H	0.11	0/1433	0.33	0/1931
14	I	0.11	0/1398	0.33	0/1873
15	J	0.14	0/1296	0.38	0/1732
16	K	0.11	0/704	0.30	0/941
17	L	0.14	0/1644	0.32	0/2215
18	M	0.10	0/1024	0.28	0/1375
19	N	0.14	0/1717	0.33	0/2304
20	O	0.13	0/1588	0.32	0/2128
21	P	0.13	0/1381	0.32	0/1849
22	Q	0.12	0/1510	0.34	0/2017
23	R	0.13	0/1238	0.33	0/1647
24	S	0.12	0/1422	0.31	0/1909
25	T	0.12	0/1309	0.29	0/1761
26	U	0.14	0/805	0.40	0/1080
27	V	0.13	0/1042	0.32	0/1402
28	X	0.14	0/978	0.32	0/1314
29	Y	0.12	0/1008	0.33	0/1341
30	Z	0.14	0/1095	0.32	0/1467
31	a	0.13	0/1198	0.35	0/1608
32	b	0.15	0/471	0.37	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.13	0/723	0.32	0/973
34	d	0.11	0/864	0.27	0/1161
35	e	0.10	0/953	0.26	0/1271
36	f	0.11	0/859	0.27	0/1152
37	g	0.13	0/873	0.32	0/1170
38	h	0.11	0/1008	0.30	0/1340
39	i	0.11	0/774	0.29	0/1028
40	j	0.13	0/671	0.35	0/888
41	k	0.17	0/566	0.43	0/757
42	m	0.13	0/3209	0.38	1/4357 (0.0%)
43	n	0.11	0/2971	0.30	0/3997
44	o	0.10	0/803	0.34	0/1064
45	p	0.07	0/1426	0.21	0/1977
46	u	0.17	0/509	0.38	0/678
All	All	0.12	0/132200	0.28	3/193717 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	m	370	PRO	N-CA-C	-12.72	101.45	114.68
1	1	1388	G	C2'-C3'-O3'	-5.68	105.17	113.70
1	1	2657	A	C4'-C3'-O3'	5.55	117.73	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	61386	0	30879	602	0
2	2	3211	0	1623	26	0
3	3	1006	0	1007	66	0
4	8	437	0	463	5	0
5	9	2519	0	1273	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1847	0	1891	50	0
7	B	3003	0	3086	73	0
8	C	2795	0	2918	53	0
9	D	2305	0	2266	53	0
10	E	1338	0	1418	41	0
11	F	1745	0	1818	27	0
12	G	1817	0	1937	29	0
13	H	1415	0	1472	33	0
14	I	1372	0	1397	35	0
15	J	1276	0	1316	28	0
16	K	695	0	733	14	0
17	L	1612	0	1655	27	0
18	M	1007	0	1072	26	0
19	N	1676	0	1712	38	0
20	O	1557	0	1652	30	0
21	P	1357	0	1400	32	0
22	Q	1486	0	1588	22	0
23	R	1220	0	1300	36	0
24	S	1388	0	1442	37	0
25	T	1282	0	1308	33	0
26	U	791	0	825	29	0
27	V	1026	0	1076	31	0
28	X	962	0	1030	20	0
29	Y	998	0	1090	18	0
30	Z	1072	0	1145	26	0
31	a	1169	0	1215	28	0
32	b	463	0	471	17	0
33	c	714	0	753	17	0
34	d	849	0	885	16	0
35	e	939	0	1000	23	0
36	f	839	0	866	13	0
37	g	861	0	930	22	0
38	h	999	0	1092	18	0
39	i	767	0	851	19	0
40	j	657	0	668	14	0
41	k	560	0	608	15	0
42	m	3127	0	3104	81	0
43	n	2903	0	2972	64	0
44	o	789	0	853	17	0
45	p	1431	0	633	16	0
46	u	493	0	497	19	0
47	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	123162	0	91190	1577	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 8.

All (1577) 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)
14:I:183:GLU:HG3	14:I:187:ARG:HH21	1.25	0.99
17:L:47:ALA:HB1	17:L:48:PRO:HD2	1.46	0.97
1:1:188:C:H41	1:1:244:G:H21	1.16	0.93
3:3:90:LEU:HD21	10:E:28:TYR:HE1	1.32	0.93
1:1:3369:A:H5''	1:1:3370:U:H3'	1.56	0.88
7:B:331:PRO:HD2	7:B:334:ARG:HE	1.41	0.86
39:i:95:SER:OG	39:i:96:ARG:NH1	2.09	0.84
1:1:1747:A:H61	1:1:1777:U:H3	1.24	0.84
3:3:95:GLN:HA	3:3:98:LEU:HD23	1.62	0.81
43:n:564:MET:HB3	43:n:567:ASN:HB3	1.62	0.80
26:U:91:LEU:HG	26:U:103:LEU:HD12	1.64	0.78
14:I:189:GLU:OE1	14:I:189:GLU:N	2.18	0.77
1:1:1338:G:H5''	20:O:61:LYS:HE3	1.68	0.76
3:3:32:TYR:HA	3:3:52:THR:HG21	1.67	0.76
5:9:91:G:H1'	5:9:94:C:H42	1.49	0.76
22:Q:92:GLU:OE2	22:Q:92:GLU:N	2.19	0.75
1:1:3064:A:N7	6:A:214:ASN:ND2	2.34	0.74
15:J:17:LEU:HD23	15:J:129:VAL:HG22	1.68	0.74
43:n:374:ARG:NE	43:n:374:ARG:O	2.19	0.74
5:9:111:U:H5''	9:D:283:ARG:HH22	1.52	0.74
14:I:170:LYS:HA	14:I:177:ALA:HA	1.67	0.74
1:1:2452:G:H22	1:1:2484:G:H1'	1.53	0.74
18:M:56:VAL:O	24:S:154:ARG:NH1	2.21	0.74
1:1:724:A:OP1	8:C:275:LYS:HE2	1.88	0.74
33:c:77:SER:OG	33:c:79:CYS:SG	2.44	0.74
14:I:43:VAL:HG11	14:I:197:ALA:HB2	1.70	0.73
37:g:14:ASN:O	37:g:14:ASN:ND2	2.21	0.73
42:m:597:ARG:HG2	42:m:609:THR:HG22	1.71	0.73
6:A:179:LEU:HD11	16:K:26:VAL:HG21	1.70	0.73
1:1:1011:G:H1'	1:1:1012:A:C8	2.23	0.72
26:U:15:ASP:HB3	26:U:102:GLU:HB3	1.69	0.72
26:U:32:LYS:HE2	26:U:32:LYS:HA	1.71	0.72
42:m:297:GLU:HB2	43:n:453:VAL:HG21	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:9:113:A:N7	14:I:209:LYS:NZ	2.37	0.72
18:M:65:LEU:HD11	18:M:74:VAL:HG22	1.71	0.72
24:S:12:LYS:HA	24:S:55:GLY:HA2	1.69	0.72
29:Y:55:ILE:HD11	29:Y:81:ILE:HG12	1.71	0.72
1:1:774:C:OP1	22:Q:146:HIS:ND1	2.20	0.72
28:X:67:ASN:HD22	38:h:35:ILE:HD12	1.54	0.72
1:1:2769:A:H4'	15:J:105:GLY:HA3	1.71	0.71
1:1:1655:G:H1	1:1:1880:A:H61	1.37	0.71
1:1:251:U:H2'	1:1:252:A:H8	1.54	0.71
1:1:1158:G:N2	1:1:1161:A:OP2	2.22	0.71
7:B:10:ARG:NH1	7:B:263:THR:O	2.24	0.71
8:C:328:SER:O	11:F:48:ARG:NH2	2.24	0.71
1:1:3083:C:OP1	20:O:66:ASN:ND2	2.24	0.71
1:1:1901:C:OP1	1:1:1904:C:N4	2.24	0.70
15:J:32:ARG:HA	15:J:35:LYS:HE3	1.73	0.70
3:3:58:GLY:HA2	3:3:119:LEU:HD22	1.74	0.70
1:1:361:G:O6	40:j:55:ARG:NH2	2.25	0.70
24:S:51:LYS:HB2	24:S:54:THR:HG22	1.72	0.70
8:C:60:HIS:HA	8:C:92:PHE:HE1	1.57	0.70
10:E:114:VAL:HG21	10:E:160:VAL:HG23	1.74	0.69
3:3:19:ARG:HE	3:3:21:LYS:HZ3	1.39	0.69
13:H:5:ILE:HG12	18:M:34:HIS:HE1	1.58	0.69
26:U:24:ILE:HG23	26:U:87:LEU:HD11	1.75	0.69
12:G:52:TRP:O	12:G:57:ARG:NH1	2.25	0.69
20:O:27:GLN:NE2	20:O:32:GLN:OE1	2.25	0.69
12:G:53:PRO:HD2	12:G:56:ILE:HD12	1.73	0.69
1:1:845:G:O2'	40:j:45:ARG:NH2	2.25	0.69
29:Y:72:VAL:HG12	29:Y:79:LEU:HD22	1.75	0.69
3:3:19:ARG:HH21	3:3:21:LYS:HE2	1.57	0.69
24:S:11:ARG:HD2	24:S:21:PRO:HG2	1.73	0.69
12:G:191:HIS:ND1	43:n:99:GLU:OE2	2.26	0.69
3:3:68:GLU:HG3	3:3:69:ARG:HG3	1.75	0.68
1:1:2840:G:N2	1:1:2843:A:OP2	2.24	0.68
12:G:226:TYR:O	12:G:228:GLU:N	2.26	0.68
1:1:1244:G:H4'	24:S:89:MET:HG2	1.74	0.68
6:A:100:VAL:HG22	6:A:164:VAL:HG22	1.74	0.68
19:N:183:SER:HB3	19:N:184:PRO:HD2	1.75	0.68
26:U:11:LYS:HE3	26:U:13:ILE:HD11	1.73	0.68
36:f:57:SER:O	36:f:64:LYS:NZ	2.26	0.68
3:3:5:GLU:N	3:3:5:GLU:OE2	2.26	0.68
1:1:2512:A:OP1	19:N:90:ASN:ND2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:100:TRP:HD1	3:3:101:PRO:HG3	1.59	0.67
26:U:71:GLY:HA2	26:U:74:LEU:HD13	1.76	0.67
44:o:64:VAL:HG13	44:o:65:THR:HG23	1.76	0.67
1:1:2822:A:OP2	1:1:2823:G:N2	2.27	0.67
15:J:49:LYS:HB3	15:J:62:ASN:HA	1.77	0.67
1:1:619:G:N1	1:1:634:G:OP1	2.23	0.67
7:B:26:ARG:NH1	7:B:178:LEU:O	2.27	0.67
12:G:205:GLU:OE2	12:G:205:GLU:N	2.26	0.67
42:m:708:LYS:HD2	42:m:733:GLY:HA3	1.77	0.67
1:1:1594:G:H5'	28:X:32:ARG:HH21	1.59	0.67
38:h:98:GLU:HA	38:h:101:ARG:HG2	1.76	0.67
24:S:97:THR:HG23	24:S:100:GLY:H	1.58	0.67
9:D:204:VAL:HG12	9:D:208:MET:HE2	1.76	0.66
17:L:201:GLU:OE1	17:L:201:GLU:N	2.29	0.66
11:F:154:LEU:HD23	11:F:250:LEU:HD21	1.78	0.66
20:O:183:LYS:O	20:O:189:ASN:ND2	2.29	0.66
1:1:1755:A:H4'	1:1:1756:U:H5'	1.77	0.66
35:e:78:ASP:HA	35:e:81:LEU:HD12	1.78	0.66
1:1:1628:A:N6	43:n:2:ALA:O	2.27	0.66
27:V:17:LEU:HD13	27:V:53:ALA:HB3	1.78	0.66
28:X:89:ALA:O	28:X:119:LYS:NZ	2.27	0.66
42:m:612:THR:HA	42:m:641:PHE:HZ	1.59	0.66
1:1:1042:G:H4'	14:I:40:ARG:HG2	1.77	0.66
1:1:781:C:H5''	31:a:132:ARG:NH1	2.11	0.66
1:1:1488:A:H5''	1:1:3174:A:H2	1.61	0.66
7:B:85:VAL:HG22	7:B:202:THR:HG22	1.78	0.66
1:1:1666:C:OP2	30:Z:48:ARG:NH1	2.25	0.65
15:J:47:PHE:HD2	15:J:64:LYS:HD3	1.59	0.65
1:1:2235:A:OP2	6:A:199:ARG:NH1	2.30	0.65
16:K:36:ARG:HB3	16:K:45:ASN:ND2	2.12	0.65
18:M:121:ARG:NH1	18:M:122:GLU:OE2	2.29	0.65
1:1:620:C:OP1	11:F:44:ARG:NH1	2.30	0.65
27:V:15:MET:HE1	27:V:123:GLU:HG2	1.79	0.65
3:3:61:TYR:HB3	3:3:63:TYR:HE1	1.61	0.65
18:M:53:TYR:HB3	24:S:151:LEU:HD11	1.78	0.65
1:1:1665:A:P	30:Z:67:ARG:HH21	2.19	0.65
1:1:2480:C:O2'	7:B:266:ARG:NH1	2.29	0.65
1:1:2783:U:N3	9:D:17:GLN:O	2.25	0.65
1:1:1870:U:O2'	43:n:575:LYS:NZ	2.29	0.65
1:1:3085:G:H5'	7:B:20:LYS:HB3	1.78	0.65
1:1:1670:G:N2	1:1:1673:A:OP2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3432:U:OP1	46:u:33:ARG:NH2	2.30	0.65
7:B:304:ARG:HG3	7:B:304:ARG:HH11	1.62	0.65
1:1:1674:C:OP2	37:g:74:ARG:NH2	2.30	0.64
7:B:232:ARG:HG3	7:B:270:ALA:HB2	1.78	0.64
1:1:1234:A:H61	1:1:1331:G:H2'	1.63	0.64
1:1:2947:C:O2	14:I:158:LYS:NZ	2.30	0.64
25:T:47:ALA:O	25:T:49:GLN:NE2	2.30	0.64
1:1:2264:U:OP1	6:A:53:ARG:NH2	2.29	0.64
31:a:7:LYS:O	31:a:8:THR:HG22	1.96	0.64
1:1:2225:U:OP2	1:1:2230:A:N6	2.29	0.64
2:2:137:A:OP2	43:n:14:ARG:NH2	2.30	0.64
1:1:1551:A:OP1	4:8:41:ARG:NH1	2.29	0.64
17:L:47:ALA:HB1	17:L:48:PRO:CD	2.25	0.64
14:I:169:LYS:NZ	25:T:158:THR:O	2.30	0.64
7:B:119:TYR:O	7:B:175:LYS:NZ	2.30	0.63
21:P:153:GLU:HG2	21:P:154:GLU:H	1.62	0.63
27:V:12:LYS:HE2	27:V:15:MET:HE3	1.80	0.63
8:C:355:LYS:HD3	11:F:80:GLY:HA3	1.80	0.63
25:T:36:VAL:HG11	32:b:35:ARG:HH12	1.63	0.63
1:1:3138:U:H5''	27:V:47:ARG:HD2	1.80	0.63
15:J:21:ILE:HG12	15:J:125:MET:HB2	1.78	0.63
28:X:58:GLU:HG3	28:X:101:LEU:HG	1.79	0.63
1:1:3491:A:O2'	1:1:3492:G:O5'	2.17	0.63
10:E:76:LEU:HG	10:E:77:GLU:H	1.64	0.63
33:c:57:LEU:HB2	33:c:104:LEU:HG	1.80	0.63
17:L:78:GLU:OE2	39:i:18:ARG:NH2	2.24	0.63
1:1:1628:A:N3	1:1:1650:C:O2'	2.31	0.62
10:E:109:ILE:HD11	10:E:174:MET:HE3	1.81	0.62
13:H:5:ILE:HG12	18:M:34:HIS:CE1	2.34	0.62
23:R:105:LEU:HD22	23:R:135:LYS:HG3	1.80	0.62
1:1:1438:G:N2	1:1:1441:A:OP2	2.23	0.62
1:1:2265:G:N2	6:A:117:GLU:OE2	2.30	0.62
20:O:186:SER:OG	20:O:189:ASN:ND2	2.30	0.62
21:P:115:LYS:NZ	21:P:153:GLU:O	2.31	0.62
1:1:3104:G:OP2	20:O:75:ARG:NH1	2.32	0.62
9:D:122:VAL:O	9:D:248:ARG:NH2	2.32	0.62
42:m:413:MET:HE3	42:m:413:MET:H	1.63	0.62
1:1:3:U:O4	2:2:163:A:N6	2.33	0.62
19:N:180:PHE:C	19:N:182:ASN:H	2.07	0.62
1:1:63:A:OP1	19:N:172:ARG:NH2	2.33	0.62
1:1:285:G:H5'	44:o:49:GLY:HA2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1871:U:H5'	43:n:571:LYS:HB3	1.81	0.62
1:1:2655:U:OP2	12:G:32:ARG:NH2	2.31	0.62
10:E:140:PHE:O	21:P:176:ARG:NH1	2.31	0.62
35:e:116:VAL:HB	35:e:119:ALA:HB2	1.82	0.62
1:1:1647:A:OP1	41:k:24:ARG:NH2	2.31	0.62
12:G:98:ARG:NH2	12:G:188:THR:O	2.33	0.62
30:Z:42:VAL:HG21	30:Z:96:ILE:HG12	1.81	0.62
1:1:1588:A:N6	1:1:1617:U:OP2	2.31	0.62
1:1:3235:A:OP2	7:B:30:LYS:NZ	2.26	0.62
8:C:330:LEU:HD23	11:F:188:VAL:HG21	1.81	0.61
1:1:712:U:OP2	17:L:36:ARG:NH2	2.33	0.61
11:F:54:ARG:HH22	11:F:186:LEU:HB2	1.65	0.61
12:G:211:LEU:O	12:G:215:VAL:HG23	2.00	0.61
13:H:10:THR:HG22	13:H:54:LYS:HG3	1.81	0.61
46:u:50:ALA:HA	46:u:55:TYR:CD1	2.34	0.61
10:E:83:THR:HB	10:E:93:ILE:HA	1.82	0.61
1:1:997:A:H5''	17:L:4:HIS:HB3	1.82	0.61
1:1:3015:U:H3	1:1:3021:A:H61	1.47	0.61
16:K:36:ARG:HB3	16:K:45:ASN:HD21	1.65	0.61
20:O:86:ARG:HG3	20:O:100:LEU:HD11	1.83	0.61
33:c:91:LEU:HD21	33:c:104:LEU:HD23	1.82	0.61
1:1:311:G:H5'	1:1:312:G:H5'	1.82	0.61
3:3:19:ARG:NH1	3:3:19:ARG:HB3	2.15	0.61
13:H:118:GLU:OE1	13:H:122:ARG:NH2	2.34	0.61
1:1:1326:G:H4'	24:S:114:ARG:HG2	1.82	0.61
8:C:347:LYS:HE2	8:C:347:LYS:HA	1.83	0.61
11:F:128:LYS:HB2	25:T:133:ALA:HB3	1.83	0.61
1:1:2477:C:O2'	1:1:3408:A:N1	2.34	0.61
1:1:2521:U:H1'	19:N:125:ALA:HB2	1.82	0.61
1:1:359:A:H61	4:8:38:ASN:HA	1.65	0.60
32:b:35:ARG:HG2	32:b:36:ASP:H	1.65	0.60
18:M:78:TRP:NE1	18:M:84:CYS:SG	2.72	0.60
1:1:1704:C:OP1	37:g:24:LYS:NZ	2.32	0.60
7:B:92:TYR:HB2	7:B:157:VAL:HB	1.83	0.60
1:1:805:G:O2'	1:1:806:G:OP1	2.17	0.60
1:1:1326:G:OP1	24:S:83:ARG:HD3	2.01	0.60
9:D:41:LYS:NZ	25:T:30:TYR:O	2.28	0.60
43:n:358:PHE:HD1	43:n:403:ILE:HD11	1.67	0.60
1:1:260:U:C4	42:m:236:LEU:HD21	2.36	0.60
15:J:21:ILE:HG12	15:J:125:MET:CB	2.32	0.60
29:Y:80:LEU:HD22	29:Y:95:PRO:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1581:G:OP1	19:N:108:ARG:NH2	2.32	0.60
8:C:55:SER:HB2	8:C:58:ALA:HB2	1.84	0.60
20:O:122:PRO:HA	20:O:125:LEU:HD12	1.83	0.60
21:P:122:ALA:HB3	21:P:143:PRO:HB2	1.83	0.60
37:g:23:ILE:HG21	37:g:33:LEU:HD12	1.82	0.60
42:m:705:ARG:HB3	42:m:705:ARG:NH1	2.16	0.60
1:1:2198:G:H1	1:1:2202:C:H42	1.47	0.60
18:M:12:ARG:NH1	18:M:59:THR:O	2.34	0.60
45:p:313:LEU:HA	45:p:329:SER:HA	1.84	0.60
1:1:3182:G:H4'	7:B:366:GLY:HA2	1.82	0.60
13:H:91:ARG:HH12	13:H:178:TYR:HD2	1.50	0.60
40:j:39:TYR:CD1	40:j:40:PRO:HA	2.37	0.60
1:1:969:G:H5''	31:a:29:PRO:HA	1.84	0.59
1:1:1219:U:OP1	1:1:1241:U:O2'	2.20	0.59
19:N:68:ARG:HG2	19:N:128:LYS:HG3	1.83	0.59
19:N:143:ARG:O	19:N:149:ASN:ND2	2.33	0.59
26:U:11:LYS:HZ1	26:U:62:ALA:HB1	1.67	0.59
1:1:1608:C:H5'	43:n:29:THR:HG21	1.84	0.59
1:1:3345:G:H5'	1:1:3346:U:H5''	1.84	0.59
9:D:208:MET:HG2	9:D:219:TYR:HE1	1.66	0.59
17:L:55:ARG:NH1	17:L:73:ARG:O	2.32	0.59
1:1:1348:A:OP1	24:S:155:ARG:NH2	2.35	0.59
9:D:83:LEU:HB3	9:D:88:ILE:HB	1.83	0.59
12:G:180:VAL:HG21	12:G:186:LEU:HD21	1.83	0.59
13:H:43:ASP:HB2	13:H:64:HIS:HE2	1.67	0.59
36:f:48:LYS:HB2	36:f:72:ILE:HD13	1.83	0.59
1:1:188:C:H41	1:1:244:G:N2	1.95	0.59
3:3:32:TYR:OH	3:3:65:LYS:HG2	2.02	0.59
12:G:68:ARG:NH2	12:G:239:GLY:O	2.35	0.59
14:I:183:GLU:HG3	14:I:187:ARG:NH2	2.07	0.59
10:E:147:ASN:O	10:E:149:LEU:N	2.35	0.59
13:H:92:LEU:HD12	13:H:140:ASP:HB2	1.85	0.59
3:3:40:ARG:O	3:3:47:ASN:ND2	2.36	0.59
27:V:20:PRO:HA	27:V:53:ALA:HA	1.83	0.59
1:1:75:U:H1'	17:L:61:PRO:HG3	1.85	0.59
1:1:187:U:H3	1:1:245:A:H61	1.51	0.59
1:1:1638:A:OP1	23:R:38:ARG:NH2	2.34	0.59
34:d:30:PHE:HB3	34:d:70:ARG:HG2	1.85	0.59
35:e:31:LYS:HD2	35:e:32:PRO:HD2	1.85	0.59
1:1:3136:A:H5'	27:V:14:ARG:HB2	1.84	0.58
3:3:110:GLN:HG2	10:E:30:ALA:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:19:ARG:HD2	7:B:273:MET:HE1	1.84	0.58
1:1:121:A:OP2	42:m:230:HIS:NE2	2.34	0.58
1:1:277:G:H5''	19:N:14:LYS:NZ	2.17	0.58
1:1:1012:A:O2'	1:1:1013:U:O5'	2.14	0.58
6:A:118:LYS:NZ	6:A:121:ASP:OD2	2.36	0.58
9:D:277:ALA:HA	9:D:280:ARG:HG2	1.84	0.58
26:U:76:TYR:O	26:U:80:LYS:HG2	2.02	0.58
45:p:372:ALA:HA	45:p:382:VAL:HA	1.85	0.58
3:3:113:THR:HG21	10:E:28:TYR:O	2.03	0.58
13:H:109:VAL:HG22	13:H:125:LYS:HG3	1.86	0.58
15:J:15:SER:HB3	15:J:132:ASP:CG	2.29	0.58
46:u:53:LYS:HE3	46:u:57:LYS:HD2	1.85	0.58
1:1:1764:U:OP2	23:R:128:LYS:NZ	2.33	0.58
3:3:66:THR:OG1	3:3:69:ARG:NH1	2.37	0.58
5:9:57:G:OP1	9:D:33:ARG:NH1	2.34	0.58
14:I:89:VAL:HG12	14:I:136:MET:HG2	1.85	0.58
1:1:984:A:OP1	32:b:18:ARG:NH2	2.33	0.58
13:H:135:SER:HB3	13:H:141:GLU:HB2	1.85	0.58
15:J:141:ARG:O	15:J:145:ARG:NE	2.36	0.58
2:2:114:C:H4'	2:2:115:G:H5''	1.85	0.58
11:F:97:ARG:HD2	11:F:140:TYR:HD1	1.69	0.58
1:1:2985:A:O2'	1:1:3028:A:N3	2.36	0.58
3:3:39:ASN:O	3:3:43:CYS:N	2.37	0.58
12:G:221:ASN:HA	12:G:225:LYS:HD3	1.84	0.58
1:1:1094:A:H5''	1:1:1095:G:H5'	1.86	0.58
1:1:3484:G:N2	34:d:107:GLU:OE2	2.27	0.58
7:B:273:MET:HE2	7:B:275:ARG:HH22	1.69	0.58
1:1:1035:A:H5'	9:D:11:PRO:HB3	1.85	0.57
1:1:1871:U:H5'	43:n:571:LYS:HE3	1.85	0.57
1:1:3195:C:H42	1:1:3231:U:H3	1.52	0.57
7:B:214:MET:HE2	7:B:281:LYS:HB2	1.85	0.57
1:1:719:A:OP1	19:N:199:ARG:NH2	2.35	0.57
1:1:2779:C:O2'	1:1:2780:G:O5'	2.18	0.57
9:D:184:ASP:HB3	9:D:187:THR:HG22	1.86	0.57
30:Z:5:LEU:HD21	30:Z:82:PRO:HB3	1.86	0.57
36:f:53:VAL:HG22	36:f:67:VAL:HG22	1.86	0.57
29:Y:124:LYS:HD2	29:Y:124:LYS:C	2.30	0.57
35:e:32:PRO:HG3	35:e:39:VAL:HG23	1.86	0.57
39:i:60:ARG:HE	39:i:96:ARG:NH2	2.02	0.57
1:1:968:A:O2'	1:1:970:C:N4	2.36	0.57
2:2:111:G:OP2	2:2:113:A:O2'	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:211:LEU:HB3	9:D:219:TYR:HB2	1.87	0.57
20:O:117:LYS:NZ	24:S:169:PRO:O	2.35	0.57
1:1:1617:U:H3'	1:1:1618:A:H5'	1.85	0.57
1:1:1819:G:O2'	1:1:1821:G:OP2	2.23	0.57
9:D:120:GLU:O	9:D:248:ARG:NH1	2.36	0.57
25:T:147:GLU:OE2	25:T:147:GLU:N	2.24	0.57
27:V:36:LEU:HD21	27:V:104:ILE:HD11	1.85	0.57
45:p:222:GLY:HA2	45:p:264:LEU:HA	1.86	0.57
1:1:173:U:H5''	17:L:134:LYS:HB3	1.87	0.57
1:1:527:C:H5''	8:C:344:ASN:HD21	1.70	0.57
1:1:1490:A:C8	34:d:31:LYS:HD2	2.40	0.57
1:1:1907:G:H4'	40:j:6:GLN:HG2	1.86	0.57
1:1:6:A:H5''	43:n:93:LYS:HG3	1.86	0.57
1:1:1379:U:OP1	22:Q:38:ARG:NH1	2.38	0.57
18:M:64:LYS:HB2	18:M:81:GLN:HE22	1.70	0.57
26:U:102:GLU:OE1	26:U:104:ARG:NE	2.38	0.57
43:n:438:LEU:HD21	43:n:446:PRO:HG2	1.85	0.57
3:3:32:TYR:HD1	3:3:44:PRO:HB3	1.70	0.57
7:B:331:PRO:HD2	7:B:334:ARG:NE	2.18	0.57
42:m:379:PHE:HB2	42:m:736:ILE:HB	1.87	0.57
1:1:1661:A:OP1	42:m:637:ARG:NH2	2.38	0.56
45:p:201:GLU:H	45:p:216:SER:HA	1.69	0.56
1:1:114:A:N1	1:1:274:A:O2'	2.35	0.56
1:1:2215:U:O2'	1:1:2389:U:OP1	2.23	0.56
1:1:3164:U:OP2	23:R:62:ARG:NH2	2.36	0.56
14:I:45:GLU:HG2	14:I:46:PHE:CE1	2.41	0.56
39:i:81:ALA:O	39:i:85:ILE:HG12	2.06	0.56
41:k:26:LYS:HA	41:k:70:VAL:HG12	1.88	0.56
1:1:1631:C:O2'	1:1:1731:A:N3	2.36	0.56
1:1:1798:G:OP1	26:U:104:ARG:NH1	2.39	0.56
17:L:104:ARG:HG2	39:i:20:LEU:HD11	1.88	0.56
39:i:63:GLN:HB3	39:i:66:ARG:HB2	1.88	0.56
42:m:386:VAL:HB	42:m:730:ALA:HB1	1.87	0.56
1:1:984:A:H5''	32:b:15:LYS:HD3	1.86	0.56
1:1:251:U:H2'	1:1:252:A:C8	2.38	0.56
1:1:2245:G:N7	6:A:151:SER:OG	2.36	0.56
1:1:2272:U:OP2	6:A:197:ARG:NH2	2.39	0.56
3:3:52:THR:HG22	3:3:63:TYR:HB2	1.86	0.56
10:E:72:VAL:HA	10:E:82:VAL:HG23	1.88	0.56
26:U:33:TYR:HE2	26:U:84:LYS:HD3	1.71	0.56
1:1:223:G:OP1	29:Y:15:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:620:C:P	11:F:44:ARG:HH22	2.29	0.56
11:F:143:TYR:CZ	11:F:237:LYS:HB3	2.41	0.56
1:1:278:U:H3	1:1:303:A:H2	1.54	0.56
1:1:1127:U:H4'	1:1:1128:C:H3'	1.88	0.56
25:T:24:GLN:HE22	25:T:27:LEU:HD11	1.71	0.56
1:1:3040:G:H5'	1:1:3042:G:N7	2.20	0.56
5:9:144:C:OP1	24:S:42:TYR:OH	2.20	0.56
1:1:49:A:OP1	17:L:16:LYS:NZ	2.37	0.55
1:1:781:C:H5''	31:a:132:ARG:HH12	1.71	0.55
28:X:67:ASN:ND2	38:h:35:ILE:HD12	2.20	0.55
1:1:2004:G:OP1	23:R:104:ARG:NH1	2.39	0.55
8:C:301:ILE:HD12	22:Q:134:THR:HG23	1.87	0.55
42:m:684:PHE:HD1	42:m:700:PRO:HA	1.71	0.55
1:1:41:G:N2	1:1:2898:A:N7	2.54	0.55
41:k:9:LYS:HB2	42:m:645:PHE:HA	1.88	0.55
43:n:175:ASN:O	43:n:178:ARG:NH1	2.29	0.55
1:1:644:A:OP1	21:P:166:ARG:HD3	2.05	0.55
1:1:1764:U:H1'	1:1:1765:C:C6	2.41	0.55
30:Z:50:PRO:HD3	30:Z:68:VAL:HG22	1.89	0.55
38:h:7:GLU:HA	38:h:10:LYS:HG2	1.86	0.55
45:p:192:LEU:O	45:p:258:ALA:N	2.39	0.55
45:p:383:TRP:HA	45:p:392:ILE:H	1.70	0.55
1:1:3431:A:H4'	7:B:366:GLY:HA3	1.89	0.55
27:V:106:ASN:OD1	27:V:110:GLU:N	2.37	0.55
46:u:8:PHE:HB3	46:u:36:CYS:HB3	1.87	0.55
1:1:831:G:O2'	17:L:18:TRP:NE1	2.39	0.55
1:1:2916:C:H42	1:1:2964:U:H3	1.54	0.55
16:K:45:ASN:C	16:K:45:ASN:HD22	2.14	0.55
43:n:175:ASN:HD22	43:n:350:THR:HG22	1.71	0.55
1:1:166:A:H61	1:1:268:U:H3	1.55	0.55
1:1:238:U:H5'	1:1:240:G:H5'	1.88	0.55
13:H:91:ARG:HD2	13:H:180:SER:HB3	1.89	0.55
25:T:80:VAL:O	25:T:83:ARG:NH1	2.40	0.55
44:o:28:TYR:HB3	44:o:69:VAL:HB	1.87	0.55
46:u:22:VAL:HG22	46:u:28:VAL:HG22	1.88	0.55
1:1:137:C:O2	1:1:139:U:O2'	2.23	0.55
1:1:2383:A:H1'	27:V:75:ILE:HD11	1.88	0.55
1:1:3359:U:H4'	1:1:3360:G:H5'	1.88	0.55
7:B:5:LYS:HG3	7:B:6:PHE:H	1.72	0.55
24:S:11:ARG:HH12	24:S:14:PRO:HD3	1.72	0.55
26:U:78:THR:O	26:U:82:LEU:HD13	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2726:U:OP1	1:1:2852:U:O2'	2.25	0.55
3:3:42:SER:HA	3:3:50:TYR:HE1	1.72	0.55
40:j:21:ARG:NH1	40:j:41:ALA:O	2.32	0.55
1:1:277:G:H5''	19:N:14:LYS:HZ2	1.72	0.54
1:1:1952:G:O2'	27:V:18:GLY:O	2.25	0.54
42:m:387:ARG:H	42:m:402:GLY:HA2	1.72	0.54
42:m:660:LEU:HD11	42:m:674:SER:HB2	1.90	0.54
1:1:3444:G:O2'	1:1:3463:A:N6	2.40	0.54
10:E:109:ILE:HD12	10:E:168:ILE:HG22	1.89	0.54
38:h:56:ILE:O	38:h:60:ILE:HG12	2.07	0.54
1:1:2002:G:H1	1:1:2189:C:H42	1.54	0.54
3:3:29:ARG:HB3	35:e:81:LEU:HD21	1.88	0.54
3:3:54:ARG:NH1	3:3:54:ARG:HB3	2.22	0.54
3:3:90:LEU:HD21	10:E:28:TYR:CE1	2.25	0.54
14:I:50:ILE:HG12	14:I:167:VAL:HG22	1.89	0.54
21:P:118:GLN:OE1	21:P:120:ASN:ND2	2.40	0.54
25:T:53:PRO:HD3	25:T:91:VAL:HG23	1.89	0.54
27:V:25:MET:HE3	27:V:102:GLY:HA3	1.87	0.54
27:V:82:ARG:HD3	27:V:119:PRO:HG2	1.89	0.54
1:1:2459:G:H2'	1:1:2461:A:OP1	2.07	0.54
26:U:33:TYR:CE1	26:U:37:ARG:HD2	2.42	0.54
33:c:41:TYR:OH	33:c:69:GLU:OE1	2.26	0.54
1:1:2651:G:O2'	30:Z:136:PHE:O	2.23	0.54
3:3:19:ARG:HE	3:3:21:LYS:NZ	2.05	0.54
3:3:52:THR:O	3:3:62:LEU:HD12	2.08	0.54
1:1:545:A:N6	1:1:547:G:N3	2.55	0.54
1:1:1207:C:H2'	1:1:1208:G:N2	2.23	0.54
45:p:408:LEU:HA	45:p:423:GLY:HA3	1.89	0.54
3:3:10:VAL:HG22	8:C:34:PRO:HG3	1.89	0.54
8:C:299:GLN:HA	8:C:302:VAL:HG22	1.89	0.54
17:L:137:ASP:OD1	38:h:116:ARG:NH2	2.41	0.54
29:Y:54:GLN:HB3	29:Y:107:LYS:HB3	1.90	0.54
33:c:31:THR:HG23	33:c:109:ALA:HA	1.89	0.54
43:n:34:ARG:O	43:n:38:ILE:HG12	2.07	0.54
46:u:10:SER:HB2	46:u:53:LYS:HE2	1.90	0.54
1:1:38:U:H4'	31:a:32:ARG:HD2	1.89	0.54
1:1:193:U:OP1	29:Y:121:LYS:HG2	2.07	0.54
1:1:743:A:OP1	31:a:136:LYS:NZ	2.40	0.54
1:1:2658:A:H61	1:1:2673:U:H3	1.56	0.54
1:1:3396:A:H5'	7:B:119:TYR:HE1	1.71	0.54
2:2:156:G:OP2	43:n:89:ARG:NH2	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:20:ILE:HD13	35:e:81:LEU:HD21	1.90	0.54
6:A:35:GLU:HG2	6:A:90:GLY:HA2	1.90	0.54
11:F:115:LEU:HD21	11:F:122:ILE:HG12	1.89	0.54
13:H:21:ILE:HG12	13:H:46:MET:HE1	1.89	0.54
11:F:150:THR:HG23	11:F:246:VAL:HG11	1.89	0.54
12:G:91:PHE:O	12:G:95:ASN:ND2	2.41	0.54
21:P:107:LEU:HD23	21:P:112:LEU:HD21	1.90	0.54
1:1:34:A:H5'	19:N:86:HIS:CE1	2.42	0.54
24:S:82:SER:H	24:S:85:GLY:HA2	1.73	0.54
44:o:22:VAL:O	44:o:75:VAL:HG22	2.08	0.54
1:1:194:A:N1	1:1:218:A:O2'	2.37	0.53
1:1:1025:G:N3	1:1:2732:A:H2'	2.22	0.53
2:2:132:G:H1	2:2:137:A:H61	1.54	0.53
3:3:32:TYR:CD1	3:3:44:PRO:HB3	2.42	0.53
32:b:33:LYS:HA	32:b:40:ARG:HD3	1.89	0.53
3:3:21:LYS:HG3	3:3:26:ASN:ND2	2.22	0.53
9:D:23:ARG:O	9:D:23:ARG:NH1	2.41	0.53
9:D:205:ALA:HA	9:D:208:MET:HE3	1.89	0.53
14:I:50:ILE:HD12	14:I:148:ALA:HB3	1.91	0.53
17:L:76:THR:HG22	17:L:101:ARG:HB3	1.90	0.53
19:N:46:ASP:OD2	19:N:50:ARG:NH2	2.40	0.53
42:m:652:ASN:N	43:n:563:MET:SD	2.81	0.53
1:1:1231:A:N3	1:1:1231:A:H2'	2.23	0.53
43:n:116:ASP:OD1	43:n:117:HIS:N	2.41	0.53
1:1:265:C:H2'	1:1:266:G:H8	1.73	0.53
1:1:2846:G:OP1	25:T:50:LYS:NZ	2.37	0.53
42:m:340:LEU:O	42:m:345:ARG:NH2	2.33	0.53
45:p:231:GLU:HA	45:p:259:ARG:HA	1.89	0.53
41:k:20:ALA:HB1	41:k:37:LEU:HD11	1.90	0.53
43:n:46:GLU:HB2	43:n:50:LYS:HE2	1.90	0.53
1:1:2274:U:O2'	1:1:2401:A:N3	2.30	0.53
6:A:117:GLU:HG2	6:A:155:LYS:HZ3	1.72	0.53
15:J:53:THR:HG22	15:J:61:ARG:H	1.74	0.53
19:N:190:LEU:O	19:N:194:THR:OG1	2.22	0.53
21:P:117:VAL:HG23	21:P:148:ILE:HG12	1.90	0.53
40:j:48:ASN:OD1	40:j:54:LYS:NZ	2.40	0.53
2:2:20:A:OP1	21:P:3:ARG:NE	2.42	0.53
6:A:241:ARG:HG2	6:A:242:THR:N	2.24	0.53
39:i:64:ASP:OD1	39:i:65:LYS:N	2.42	0.53
42:m:681:VAL:HG11	42:m:727:LEU:HD21	1.90	0.53
43:n:148:VAL:HG22	43:n:157:VAL:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:370:GLU:HG2	43:n:380:VAL:HG11	1.91	0.53
1:1:2281:U:H5''	1:1:2282:G:H5'	1.91	0.53
1:1:3030:U:H5	27:V:46:ALA:HB2	1.73	0.53
13:H:46:MET:HA	13:H:54:LYS:O	2.09	0.53
28:X:64:ASN:O	28:X:84:HIS:N	2.42	0.53
1:1:615:G:N2	1:1:637:U:OP1	2.37	0.53
1:1:1453:A:OP1	2:2:28:U:O2'	2.24	0.53
1:1:1982:G:C8	16:K:16:VAL:HG12	2.44	0.53
10:E:129:ARG:HG3	10:E:130:SER:N	2.24	0.53
22:Q:74:SER:O	22:Q:76:SER:N	2.42	0.53
29:Y:65:ARG:HG2	29:Y:84:VAL:HG22	1.91	0.53
1:1:2949:U:OP1	14:I:61:THR:OG1	2.26	0.53
8:C:344:ASN:H	8:C:344:ASN:ND2	2.06	0.53
18:M:120:ARG:NH1	20:O:189:ASN:OD1	2.42	0.53
19:N:51:LEU:HD22	19:N:117:ASN:ND2	2.23	0.53
25:T:8:ARG:O	25:T:11:THR:OG1	2.25	0.53
34:d:21:MET:HE3	34:d:37:ALA:HB1	1.91	0.53
42:m:662:ASP:OD1	42:m:663:VAL:N	2.41	0.53
1:1:1388:G:OP2	3:3:39:ASN:ND2	2.42	0.52
14:I:129:VAL:HG11	14:I:135:LEU:HD21	1.90	0.52
17:L:12:ALA:HB1	17:L:14:PHE:HD2	1.72	0.52
22:Q:177:ARG:N	31:a:51:GLY:HA2	2.24	0.52
26:U:38:ILE:HG22	26:U:40:VAL:HG23	1.91	0.52
42:m:289:PRO:O	42:m:290:LYS:HG2	2.09	0.52
42:m:413:MET:HG2	42:m:414:THR:HG23	1.89	0.52
42:m:631:ILE:HB	42:m:639:CYS:HB2	1.91	0.52
3:3:7:ILE:O	3:3:11:VAL:HG22	2.09	0.52
10:E:189:ARG:HB3	10:E:191:HIS:CE1	2.44	0.52
14:I:30:LYS:HG3	14:I:63:GLU:HG3	1.91	0.52
18:M:85:ASN:HA	18:M:88:ALA:HB3	1.91	0.52
23:R:32:ILE:HA	23:R:44:LEU:HD21	1.91	0.52
42:m:393:VAL:O	42:m:723:LYS:NZ	2.41	0.52
1:1:975:U:H3'	31:a:13:GLY:HA2	1.91	0.52
1:1:3398:U:O4	7:B:124:LYS:NZ	2.42	0.52
15:J:32:ARG:NE	15:J:123:TYR:OH	2.42	0.52
20:O:28:LEU:HD11	20:O:103:LEU:HB2	1.91	0.52
1:1:943:C:H5''	6:A:14:ILE:HD13	1.89	0.52
1:1:3059:G:N2	1:1:3062:A:OP2	2.37	0.52
1:1:3315:A:OP2	18:M:118:LYS:NZ	2.43	0.52
3:3:22:GLY:C	3:3:23:GLU:HG3	2.35	0.52
25:T:17:ARG:HG2	25:T:22:HIS:HA	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:7:LYS:C	31:a:9:ARG:H	2.16	0.52
31:a:72:THR:HG22	31:a:110:LYS:HB3	1.91	0.52
1:1:1524:A:O2'	40:j:12:HIS:O	2.25	0.52
19:N:115:VAL:HA	19:N:134:LEU:HD23	1.90	0.52
20:O:110:PRO:HG2	20:O:113:PHE:HD2	1.73	0.52
30:Z:115:LYS:O	30:Z:119:GLU:HG2	2.09	0.52
34:d:56:VAL:HG13	34:d:60:LEU:HD23	1.90	0.52
1:1:360:A:H61	1:1:373:A:H5''	1.75	0.52
1:1:401:U:O3'	29:Y:86:ARG:NH2	2.43	0.52
1:1:419:U:H2'	1:1:420:G:C8	2.45	0.52
5:9:57:G:H5''	9:D:22:ARG:HD3	1.91	0.52
7:B:55:HIS:CD2	7:B:73:LEU:HD11	2.45	0.52
1:1:3470:G:H22	7:B:381:GLY:H	1.58	0.52
3:3:39:ASN:OD1	3:3:41:GLN:HB3	2.09	0.52
5:9:133:G:O3'	11:F:224:ARG:NH2	2.42	0.52
19:N:180:PHE:O	19:N:182:ASN:N	2.42	0.52
46:u:21:PHE:HB3	46:u:31:PHE:HE1	1.74	0.52
1:1:680:C:H2'	1:1:681:A:C8	2.45	0.52
1:1:2427:C:OP1	27:V:50:ARG:NH1	2.43	0.52
1:1:3099:G:HO2'	7:B:92:TYR:HH	1.57	0.52
10:E:165:LEU:HD13	10:E:168:ILE:HD11	1.92	0.52
26:U:78:THR:HA	26:U:81:PHE:CE1	2.45	0.52
1:1:932:G:H1'	1:1:1624:A:N6	2.25	0.52
1:1:1488:A:H5''	1:1:3174:A:C2	2.43	0.52
3:3:62:LEU:HD23	3:3:80:ILE:HD11	1.91	0.52
7:B:379:PHE:CE1	46:u:12:PRO:HD3	2.45	0.52
8:C:159:GLN:HA	8:C:217:ILE:HB	1.90	0.52
33:c:38:VAL:HB	33:c:43:SER:HB3	1.91	0.52
42:m:413:MET:H	42:m:413:MET:CE	2.22	0.52
1:1:632:A:OP1	10:E:44:ARG:NH2	2.43	0.51
1:1:182:G:H1	1:1:250:A:H61	1.58	0.51
1:1:807:G:OP1	32:b:41:ARG:NH2	2.43	0.51
3:3:101:PRO:CB	3:3:104:GLN:HB2	2.40	0.51
6:A:226:ARG:HG3	6:A:226:ARG:HH11	1.75	0.51
14:I:52:LEU:HB2	14:I:152:LEU:HD13	1.92	0.51
30:Z:54:THR:H	30:Z:57:MET:HE2	1.74	0.51
30:Z:87:LEU:HD11	30:Z:121:LYS:HD3	1.92	0.51
7:B:80:GLU:HG2	7:B:82:PRO:HD3	1.91	0.51
7:B:214:MET:HE2	7:B:281:LYS:HE2	1.93	0.51
28:X:76:GLU:HG2	28:X:132:LEU:HD21	1.93	0.51
1:1:1165:G:O2'	1:1:2737:A:N3	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2445:A:H2'	1:1:2446:A:C8	2.45	0.51
1:1:3006:A:H4'	1:1:3007:G:C8	2.46	0.51
1:1:3368:A:C8	10:E:145:PRO:HB3	2.46	0.51
19:N:16:SER:OG	19:N:19:ASN:ND2	2.42	0.51
23:R:106:LEU:HD21	23:R:123:LEU:O	2.10	0.51
1:1:1371:G:OP2	35:e:58:LYS:NZ	2.37	0.51
1:1:2651:G:H4'	37:g:88:ARG:HD3	1.92	0.51
8:C:10:ILE:HD12	8:C:20:GLU:HG3	1.92	0.51
1:1:216:A:OP2	8:C:165:LYS:NZ	2.37	0.51
1:1:258:U:C4	42:m:236:LEU:HB3	2.46	0.51
1:1:366:G:N2	1:1:369:A:OP2	2.41	0.51
1:1:2203:G:H22	1:1:2208:A:H1'	1.75	0.51
8:C:275:LYS:HG2	8:C:276:ASN:OD1	2.10	0.51
15:J:16:LYS:HE3	15:J:130:VAL:HG21	1.92	0.51
26:U:24:ILE:HG22	26:U:25:PHE:CD1	2.46	0.51
1:1:1147:G:N2	1:1:2912:A:O4'	2.44	0.51
1:1:1242:U:O2'	24:S:112:ARG:NH1	2.43	0.51
7:B:375:GLU:HA	7:B:378:GLN:HG2	1.93	0.51
18:M:41:SER:HB3	18:M:46:PHE:HB3	1.91	0.51
29:Y:73:TYR:HE2	29:Y:75:LYS:HG2	1.76	0.51
44:o:6:LYS:HZ2	44:o:24:ARG:HG2	1.76	0.51
1:1:718:A:N1	2:2:36:C:O2'	2.43	0.51
1:1:1531:C:H2'	1:1:1532:A:C8	2.46	0.51
1:1:2729:U:O4	25:T:3:HIS:NE2	2.42	0.51
1:1:3207:U:H4'	13:H:149:LEU:CD2	2.41	0.51
3:3:97:LEU:HD13	3:3:101:PRO:HG2	1.92	0.51
1:1:2783:U:OP1	9:D:12:TYR:OH	2.27	0.51
5:9:113:A:OP1	14:I:206:LEU:N	2.44	0.51
27:V:59:MET:HE3	27:V:79:ILE:HD11	1.92	0.51
34:d:101:VAL:HG11	34:d:106:MET:HE1	1.92	0.51
43:n:18:THR:HG23	43:n:21:GLN:H	1.76	0.51
1:1:1424:A:N6	1:1:1452:A:O2'	2.44	0.51
1:1:1655:G:H1	1:1:1880:A:N6	2.06	0.51
1:1:2905:C:OP2	1:1:3050:U:O2'	2.29	0.51
1:1:3083:C:OP1	20:O:69:ARG:HD2	2.11	0.51
1:1:3186:U:H2'	1:1:3187:A:C8	2.45	0.51
3:3:106:HIS:NE2	3:3:110:GLN:OE1	2.43	0.51
6:A:226:ARG:HG3	6:A:226:ARG:NH1	2.26	0.51
20:O:120:VAL:HG11	24:S:171:ARG:HE	1.76	0.51
24:S:46:MET:HG3	24:S:47:ILE:HG23	1.93	0.51
24:S:80:TYR:CE2	24:S:82:SER:HB2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:5:LEU:O	39:i:7:VAL:N	2.39	0.51
41:k:69:GLU:HG2	41:k:70:VAL:N	2.26	0.51
1:1:635:G:N1	1:1:1368:A:OP1	2.37	0.50
1:1:1628:A:O2'	1:1:1629:A:OP1	2.26	0.50
1:1:1995:G:H21	1:1:3463:A:H8	1.59	0.50
5:9:56:C:OP2	9:D:22:ARG:NH2	2.41	0.50
8:C:13:LYS:HE3	8:C:161:PHE:HE1	1.76	0.50
23:R:133:LYS:HG3	23:R:134:HIS:HD2	1.76	0.50
42:m:333:LYS:HG3	43:n:142:LEU:HD22	1.93	0.50
43:n:179:LYS:HB2	43:n:190:GLN:HB3	1.93	0.50
1:1:87:U:H2'	1:1:88:A:C8	2.46	0.50
1:1:446:U:OP1	35:e:115:LYS:HE2	2.12	0.50
1:1:1636:U:OP2	23:R:42:ARG:NH2	2.44	0.50
6:A:205:PRO:HG3	6:A:212:GLY:HA3	1.94	0.50
7:B:113:GLU:HB3	7:B:176:ALA:HB2	1.93	0.50
15:J:160:ILE:HG23	15:J:171:VAL:HG21	1.94	0.50
27:V:89:ARG:HG3	27:V:95:LEU:HD23	1.94	0.50
1:1:39:A:H5''	31:a:35:ALA:HB2	1.94	0.50
1:1:680:C:H5'	35:e:23:LYS:HE2	1.94	0.50
1:1:2650:A:OP1	37:g:91:ARG:NH1	2.44	0.50
2:2:83:G:OP2	29:Y:73:TYR:OH	2.30	0.50
3:3:65:LYS:HD2	3:3:76:LEU:HD21	1.93	0.50
12:G:229:SER:O	12:G:232:LYS:HG2	2.10	0.50
27:V:83:GLN:HE21	27:V:85:LYS:HB3	1.76	0.50
30:Z:23:VAL:HG12	30:Z:45:GLY:HA3	1.92	0.50
30:Z:68:VAL:O	30:Z:115:LYS:NZ	2.44	0.50
3:3:101:PRO:HB2	3:3:104:GLN:HB2	1.93	0.50
7:B:159:ARG:HG2	7:B:182:GLN:HA	1.94	0.50
9:D:163:MET:HG3	9:D:173:ILE:HG21	1.93	0.50
15:J:47:PHE:CD2	15:J:64:LYS:HD3	2.44	0.50
21:P:11:GLU:O	21:P:105:LYS:HD3	2.12	0.50
23:R:74:ARG:HB3	23:R:75:HIS:HD2	1.76	0.50
45:p:109:GLY:HA3	45:p:148:SER:HA	1.93	0.50
1:1:2647:U:O4	6:A:94:ALA:N	2.39	0.50
1:1:2842:A:H5'	9:D:175:HIS:HA	1.93	0.50
1:1:2867:C:OP2	44:o:15:LYS:NZ	2.39	0.50
37:g:41:ILE:HG13	37:g:56:ALA:HB2	1.92	0.50
43:n:437:ASP:OD1	43:n:437:ASP:N	2.45	0.50
1:1:195:A:H5''	29:Y:45:ARG:HH21	1.76	0.50
2:2:55:C:H1'	2:2:69:A:H2'	1.94	0.50
1:1:378:U:H4'	1:1:412:G:H5'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1094:A:O2'	1:1:1130:A:OP1	2.27	0.50
1:1:1660:A:OP1	42:m:654:ARG:NH2	2.44	0.50
3:3:19:ARG:HB3	3:3:19:ARG:HH11	1.77	0.50
10:E:129:ARG:NH1	10:E:131:GLY:O	2.45	0.50
20:O:186:SER:HG	20:O:189:ASN:ND2	2.09	0.50
36:f:43:GLN:HA	36:f:46:LEU:HG	1.94	0.50
39:i:56:MET:HG3	39:i:88:LEU:HD13	1.93	0.50
42:m:608:LYS:NZ	42:m:643:LEU:O	2.45	0.50
1:1:2695:C:H2'	1:1:2696:A:H8	1.77	0.50
5:9:61:A:N1	5:9:116:G:O2'	2.44	0.50
7:B:217:VAL:HG11	7:B:328:THR:HG22	1.94	0.50
10:E:194:LYS:O	18:M:110:ARG:NH2	2.45	0.50
1:1:80:C:OP1	19:N:191:ARG:HD3	2.12	0.50
1:1:775:A:H2'	1:1:776:U:O4'	2.12	0.50
1:1:1160:A:N3	1:1:2921:U:O2'	2.43	0.50
1:1:2730:A:N6	1:1:2737:A:OP2	2.37	0.50
27:V:19:LEU:HD11	27:V:100:ASN:HB3	1.94	0.50
1:1:1017:U:H2'	1:1:1018:U:C6	2.47	0.49
1:1:1655:G:N2	1:1:1880:A:N1	2.43	0.49
1:1:1918:G:N1	1:1:1921:C:OP2	2.43	0.49
1:1:3111:C:H2'	1:1:3112:A:C8	2.47	0.49
3:3:8:TRP:CG	3:3:40:ARG:HG3	2.47	0.49
8:C:60:HIS:NE2	8:C:100:ARG:HD3	2.27	0.49
27:V:82:ARG:HB2	27:V:101:ALA:HB3	1.93	0.49
33:c:77:SER:C	33:c:78:ARG:HD3	2.37	0.49
34:d:84:ARG:HG3	34:d:84:ARG:HH11	1.77	0.49
44:o:70:LEU:HD11	44:o:85:LEU:HD11	1.93	0.49
10:E:31:TYR:HH	35:e:87:LYS:H	1.60	0.49
14:I:176:TYR:HE2	14:I:184:LYS:HE3	1.76	0.49
38:h:84:GLN:OE1	38:h:86:LYS:NZ	2.42	0.49
42:m:369:ARG:C	42:m:371:PHE:H	2.20	0.49
1:1:126:U:OP1	19:N:144:ARG:NH1	2.43	0.49
12:G:143:ILE:HG23	12:G:175:VAL:HG21	1.93	0.49
31:a:126:THR:O	31:a:147:ILE:N	2.43	0.49
45:p:296:TRP:HA	45:p:303:ASN:HA	1.93	0.49
1:1:2320:A:N3	1:1:2516:U:O2'	2.42	0.49
1:1:2695:C:H2'	1:1:2696:A:C8	2.47	0.49
1:1:2768:A:P	15:J:95:ASN:HA	2.52	0.49
3:3:40:ARG:O	3:3:41:GLN:C	2.55	0.49
24:S:80:TYR:CZ	24:S:82:SER:HB2	2.48	0.49
39:i:53:ARG:O	39:i:57:GLU:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:721:HIS:HB2	42:m:726:TRP:HB2	1.93	0.49
1:1:414:G:H1'	2:2:24:G:N2	2.28	0.49
22:Q:88:VAL:HG21	22:Q:102:ILE:HG21	1.93	0.49
26:U:81:PHE:HA	26:U:84:LYS:HB2	1.95	0.49
42:m:642:ASP:HB3	42:m:645:PHE:HB3	1.94	0.49
43:n:140:LEU:HD11	43:n:230:MET:HG3	1.94	0.49
8:C:9:SER:HA	8:C:21:THR:HG22	1.95	0.49
19:N:9:GLU:HB2	39:i:42:VAL:HG21	1.94	0.49
25:T:75:LEU:HD21	25:T:86:GLU:HG2	1.94	0.49
43:n:376:PHE:HE2	43:n:428:ILE:HB	1.77	0.49
1:1:303:A:H2'	1:1:304:A:O4'	2.13	0.49
1:1:3180:C:H2'	1:1:3181:G:O4'	2.13	0.49
8:C:37:VAL:HG21	8:C:246:LEU:HD21	1.95	0.49
23:R:102:LEU:O	23:R:106:LEU:HB2	2.12	0.49
23:R:133:LYS:HD2	23:R:133:LYS:O	2.11	0.49
28:X:108:LYS:HB3	28:X:124:LYS:HB3	1.94	0.49
30:Z:90:ASP:OD1	30:Z:90:ASP:N	2.43	0.49
13:H:131:THR:OG1	13:H:145:GLU:OE2	2.30	0.49
15:J:77:GLU:O	15:J:81:GLU:HG2	2.12	0.49
31:a:131:ARG:NH2	31:a:132:ARG:HH21	2.10	0.49
45:p:97:TYR:HA	45:p:431:ASN:HA	1.93	0.49
1:1:1338:G:H1'	1:1:1339:A:C5	2.47	0.49
11:F:224:ARG:HB2	11:F:227:LYS:HE2	1.95	0.49
24:S:7:GLN:HB2	24:S:63:ILE:HD11	1.94	0.49
38:h:23:LEU:HD22	38:h:49:THR:HG23	1.95	0.49
1:1:994:A:N1	1:1:2909:G:O2'	2.41	0.49
1:1:2792:A:H2'	1:1:2793:G:C8	2.48	0.48
1:1:3415:U:H5''	7:B:174:LYS:HE2	1.95	0.48
16:K:41:PHE:HE2	16:K:66:LEU:HD11	1.77	0.48
28:X:45:TYR:CD1	38:h:77:TYR:HB3	2.48	0.48
1:1:1397:A:H2'	1:1:1398:C:O4'	2.14	0.48
1:1:1453:A:H5''	8:C:195:LYS:HE3	1.94	0.48
1:1:1999:U:O2	1:1:2193:G:N2	2.46	0.48
1:1:2332:A:O2'	6:A:222:THR:HG22	2.14	0.48
17:L:48:PRO:HB2	38:h:119:ALA:HB2	1.95	0.48
21:P:64:ASN:O	21:P:80:GLN:NE2	2.45	0.48
1:1:1010:A:H1'	1:1:1011:G:H21	1.79	0.48
1:1:1034:A:H2'	1:1:1035:A:H8	1.79	0.48
24:S:24:PHE:HB3	25:T:151:LEU:HD12	1.95	0.48
32:b:47:ASN:O	32:b:51:VAL:HG13	2.13	0.48
41:k:61:LEU:HD22	41:k:65:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:371:PHE:CA	42:m:701:LEU:HD21	2.42	0.48
1:1:613:A:H1'	1:1:1368:A:H5''	1.95	0.48
1:1:645:U:H2'	1:1:647:A:C8	2.48	0.48
1:1:2823:G:C8	25:T:85:MET:HE1	2.49	0.48
13:H:86:PHE:CE1	13:H:149:LEU:HD12	2.49	0.48
24:S:138:TYR:O	24:S:142:LEU:HG	2.14	0.48
1:1:348:C:OP2	8:C:197:ARG:NH1	2.42	0.48
1:1:587:U:H2'	1:1:588:G:H8	1.78	0.48
7:B:74:GLU:HG2	7:B:283:TYR:HE2	1.79	0.48
9:D:202:GLY:O	9:D:205:ALA:N	2.47	0.48
11:F:113:LEU:O	11:F:122:ILE:HD13	2.13	0.48
20:O:176:GLN:HA	20:O:179:ILE:HG22	1.94	0.48
24:S:80:TYR:HE1	24:S:115:ALA:HB2	1.78	0.48
42:m:582:HIS:NE2	42:m:626:GLY:O	2.42	0.48
9:D:50:ARG:HG2	9:D:147:ASP:HB2	1.96	0.48
32:b:30:ASP:OD1	32:b:31:SER:N	2.46	0.48
43:n:150:ASP:OD1	43:n:150:ASP:N	2.45	0.48
1:1:1400:A:O2'	35:e:42:ARG:NH2	2.46	0.48
1:1:1954:G:O2'	1:1:2422:U:O4	2.23	0.48
1:1:3112:A:H2'	1:1:3113:A:C8	2.49	0.48
5:9:88:U:N3	5:9:91:G:OP2	2.41	0.48
6:A:172:GLY:O	16:K:71:TRP:NE1	2.45	0.48
14:I:54:SER:HB2	14:I:135:LEU:HD11	1.94	0.48
20:O:56:LEU:HD23	20:O:59:LEU:HD12	1.95	0.48
20:O:170:GLN:HA	20:O:170:GLN:OE1	2.13	0.48
31:a:37:GLY:H	31:a:41:LEU:HB2	1.77	0.48
40:j:5:THR:O	40:j:6:GLN:HB3	2.13	0.48
42:m:603:LYS:HG3	42:m:605:GLU:HG3	1.96	0.48
1:1:87:U:H2'	1:1:88:A:H8	1.79	0.48
1:1:645:U:O2'	36:f:61:ARG:NH2	2.47	0.48
1:1:1207:C:H4'	20:O:90:PRO:HD3	1.95	0.48
1:1:2662:U:H3	1:1:2669:G:H1	1.59	0.48
10:E:129:ARG:HG3	10:E:130:SER:H	1.77	0.48
23:R:126:GLU:O	23:R:131:THR:OG1	2.27	0.48
26:U:33:TYR:CE2	26:U:81:PHE:HB3	2.49	0.48
39:i:13:LYS:NZ	39:i:15:LEU:HD21	2.28	0.48
1:1:531:A:H2'	8:C:350:LYS:HD2	1.95	0.48
1:1:1639:U:H4'	1:1:1890:A:H4'	1.96	0.48
1:1:2731:A:H5''	1:1:2732:A:H5'	1.96	0.48
6:A:50:ASP:HB3	6:A:53:ARG:HB3	1.95	0.48
9:D:126:GLU:OE1	9:D:126:GLU:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:177:ARG:H	31:a:51:GLY:HA2	1.79	0.48
26:U:10:ASN:ND2	26:U:12:TYR:OH	2.47	0.48
46:u:35:LYS:HE2	46:u:51:TRP:CZ2	2.49	0.48
1:1:590:U:H3'	1:1:591:G:H5''	1.96	0.48
1:1:1975:U:O2'	1:1:1987:A:N7	2.42	0.48
1:1:2283:C:HO2'	1:1:2359:A:HO2'	1.62	0.48
10:E:61:LEU:HD11	10:E:102:ILE:HG13	1.96	0.48
15:J:19:LEU:HB2	15:J:69:VAL:HG12	1.96	0.48
18:M:118:LYS:O	18:M:122:GLU:HG2	2.14	0.48
23:R:136:ARG:O	23:R:140:GLU:HG3	2.13	0.48
42:m:537:HIS:HB2	42:m:542:TYR:HB2	1.95	0.48
1:1:3207:U:H4'	13:H:149:LEU:HD21	1.95	0.47
7:B:56:ILE:HD12	7:B:356:LEU:HD22	1.95	0.47
15:J:122:ILE:HD12	15:J:123:TYR:H	1.79	0.47
21:P:115:LYS:HZ2	21:P:154:GLU:HA	1.79	0.47
23:R:90:PRO:HB2	23:R:93:VAL:HG23	1.94	0.47
39:i:86:GLU:HA	39:i:89:THR:HG22	1.96	0.47
1:1:1129:G:OP1	25:T:129:ARG:NH2	2.47	0.47
1:1:1470:U:O5'	1:1:1471:C:H5''	2.14	0.47
1:1:1836:U:N3	16:K:50:THR:O	2.48	0.47
1:1:2203:G:O2'	23:R:82:LYS:HD3	2.13	0.47
1:1:2240:A:H4'	6:A:244:LEU:HD22	1.96	0.47
3:3:34:VAL:CG1	3:3:52:THR:HA	2.44	0.47
10:E:97:ASN:HB3	10:E:100:TYR:HD1	1.78	0.47
21:P:115:LYS:NZ	21:P:154:GLU:HA	2.29	0.47
27:V:86:ALA:HA	27:V:96:TYR:HB3	1.95	0.47
45:p:363:ALA:HA	45:p:371:PHE:HA	1.95	0.47
1:1:518:U:H2'	1:1:519:U:C6	2.49	0.47
1:1:1370:C:OP1	35:e:58:LYS:HG3	2.14	0.47
1:1:2978:U:H2'	1:1:2979:C:C6	2.49	0.47
7:B:294:ALA:HB3	7:B:303:LYS:HG3	1.95	0.47
9:D:119:TYR:OH	9:D:139:PRO:O	2.27	0.47
10:E:173:ASN:O	10:E:173:ASN:ND2	2.47	0.47
18:M:121:ARG:O	18:M:124:VAL:HG13	2.14	0.47
21:P:48:LEU:HD22	21:P:88:VAL:HG13	1.95	0.47
44:o:6:LYS:NZ	44:o:24:ARG:HG2	2.29	0.47
1:1:85:A:H61	1:1:99:A:H3'	1.79	0.47
1:1:2285:C:H4'	1:1:2286:A:H5'	1.97	0.47
1:1:3315:A:H2	10:E:176:GLU:HG2	1.79	0.47
37:g:43:ARG:NH2	37:g:50:PRO:HB3	2.29	0.47
38:h:4:LYS:HB2	38:h:7:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:603:LYS:HE2	42:m:605:GLU:HG2	1.96	0.47
43:n:182:LEU:HD21	43:n:425:TYR:HE2	1.78	0.47
1:1:1502:A:N1	1:1:1935:U:O2'	2.40	0.47
1:1:1653:A:H2'	1:1:1654:A:C8	2.49	0.47
1:1:3280:U:H5''	13:H:24:ARG:HH22	1.79	0.47
1:1:3360:G:H4'	18:M:122:GLU:HG3	1.96	0.47
2:2:28:U:H2'	2:2:29:C:O4'	2.15	0.47
3:3:21:LYS:HG3	3:3:26:ASN:HD21	1.78	0.47
18:M:30:ASP:OD1	18:M:31:ILE:N	2.46	0.47
30:Z:84:ARG:HG2	33:c:72:TYR:OH	2.14	0.47
30:Z:109:ALA:HB2	42:m:712:ASN:HD22	1.79	0.47
1:1:216:A:H4'	1:1:218:A:C8	2.49	0.47
1:1:847:G:H5'	40:j:16:HIS:CE1	2.49	0.47
1:1:1836:U:H2'	6:A:49:HIS:CD2	2.49	0.47
1:1:3308:G:H5'	1:1:3310:A:O4'	2.14	0.47
1:1:3359:U:H5'	1:1:3361:U:H5	1.78	0.47
3:3:15:PHE:CE2	8:C:245:HIS:HB3	2.50	0.47
3:3:32:TYR:OH	3:3:50:TYR:O	2.22	0.47
7:B:262:TRP:CD1	20:O:67:PRO:HD3	2.50	0.47
21:P:8:PRO:HA	21:P:10:LEU:HD12	1.96	0.47
24:S:43:PHE:O	24:S:46:MET:HG2	2.15	0.47
33:c:97:LYS:HD3	33:c:99:PHE:CZ	2.49	0.47
1:1:316:A:H1'	1:1:2310:A:N3	2.30	0.47
1:1:948:G:H5'	1:1:949:A:OP1	2.14	0.47
1:1:1636:U:P	23:R:42:ARG:HH22	2.37	0.47
1:1:2440:A:H5''	21:P:83:TRP:O	2.15	0.47
1:1:3271:G:OP1	36:f:7:ARG:HD3	2.14	0.47
5:9:125:G:N2	5:9:150:A:OP2	2.34	0.47
7:B:123:PHE:CZ	7:B:124:LYS:HG3	2.50	0.47
8:C:329:ARG:HG2	8:C:330:LEU:HD12	1.97	0.47
9:D:78:ALA:HB3	9:D:105:VAL:HG23	1.96	0.47
13:H:11:LEU:HD13	13:H:72:TYR:HE1	1.79	0.47
19:N:145:ASP:HB3	19:N:148:ILE:HG22	1.96	0.47
37:g:13:TYR:O	37:g:15:THR:HG23	2.15	0.47
1:1:448:U:H4'	10:E:132:PRO:HG3	1.97	0.47
1:1:1095:G:N3	1:1:1098:G:O2'	2.45	0.47
1:1:1357:A:O2'	36:f:78:ASN:OD1	2.25	0.47
1:1:3395:G:O2'	1:1:3396:A:O5'	2.30	0.47
1:1:3411:A:OP1	21:P:74:LYS:NZ	2.33	0.47
14:I:45:GLU:HG2	14:I:46:PHE:CD1	2.49	0.47
18:M:63:MET:HE2	18:M:83:VAL:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:S:136:ARG:HA	24:S:136:ARG:HD3	1.68	0.47
46:u:50:ALA:HA	46:u:55:TYR:HD1	1.79	0.47
1:1:371:C:OP2	40:j:56:ARG:NH2	2.35	0.47
1:1:906:U:N3	1:1:3073:U:OP1	2.34	0.47
1:1:1177:C:H4'	1:1:1362:U:C4	2.50	0.47
1:1:1747:A:N6	1:1:1777:U:H3	2.04	0.47
3:3:86:TYR:CE2	3:3:90:LEU:HD22	2.49	0.47
9:D:153:THR:HB	9:D:160:PHE:HZ	1.79	0.47
9:D:205:ALA:HB2	9:D:236:LEU:HD12	1.95	0.47
10:E:69:ARG:O	10:E:89:ASN:ND2	2.48	0.47
11:F:227:LYS:HB2	11:F:233:GLY:HA3	1.97	0.47
12:G:90:VAL:HA	12:G:214:ILE:HD13	1.97	0.47
13:H:27:THR:HG22	13:H:36:LYS:HG3	1.97	0.47
13:H:55:PHE:CZ	13:H:75:ILE:HG21	2.50	0.47
28:X:72:MET:O	28:X:76:GLU:HG3	2.15	0.47
42:m:594:ARG:HG3	42:m:614:VAL:O	2.14	0.47
1:1:263:A:H2'	1:1:264:G:C8	2.49	0.47
1:1:294:U:O2'	19:N:179:ARG:O	2.24	0.47
1:1:1843:C:O2'	37:g:59:PRO:O	2.29	0.47
1:1:3302:U:H2'	1:1:3303:C:C6	2.50	0.47
2:2:29:C:N4	2:2:30:U:O4	2.49	0.47
12:G:227[B]:ASP:O	12:G:230:ARG:HG2	2.15	0.47
19:N:180:PHE:C	19:N:182:ASN:N	2.73	0.47
22:Q:176:ALA:O	22:Q:183:ARG:HB2	2.15	0.47
33:c:48:LEU:HD13	33:c:73:TYR:HB3	1.97	0.47
1:1:943:C:H42	6:A:3:ARG:HD3	1.79	0.46
1:1:1423:G:OP2	35:e:101:LYS:HE2	2.14	0.46
1:1:3055:C:H2'	1:1:3056:G:C8	2.50	0.46
5:9:160:G:H2'	5:9:161:C:C6	2.50	0.46
34:d:84:ARG:O	34:d:92:LEU:N	2.41	0.46
35:e:39:VAL:O	35:e:49:MET:HE2	2.14	0.46
38:h:23:LEU:HD12	38:h:56:ILE:HD12	1.97	0.46
40:j:21:ARG:HD3	40:j:39:TYR:CD1	2.50	0.46
1:1:1119:G:OP1	32:b:29:TYR:OH	2.28	0.46
1:1:1604:U:H3'	43:n:217:ARG:HH12	1.81	0.46
1:1:2511:U:H2'	1:1:2512:A:C8	2.49	0.46
1:1:3117:A:H61	1:1:3128:A:H5''	1.80	0.46
1:1:3315:A:C5	1:1:3359:U:H1'	2.50	0.46
3:3:77:TRP:HH2	8:C:138:LEU:HD11	1.79	0.46
3:3:118:TYR:HD2	35:e:112:LEU:HD23	1.80	0.46
7:B:36:ASP:OD2	7:B:38:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:43:ARG:NH1	39:i:47:GLY:O	2.43	0.46
43:n:417:ILE:HG12	43:n:436:THR:HG21	1.96	0.46
43:n:419:ILE:HG22	43:n:436:THR:HG23	1.97	0.46
1:l:372:G:OP2	40:j:52:LYS:NZ	2.48	0.46
1:l:724:A:H2'	1:l:725:U:O4'	2.15	0.46
1:l:906:U:OP2	7:B:241:LYS:NZ	2.43	0.46
1:l:1348:A:O2'	1:l:1349:A:H3'	2.15	0.46
1:l:1360:C:OP1	36:f:18:GLN:NE2	2.45	0.46
1:l:2286:A:H62	1:l:2334:G:H21	1.64	0.46
1:l:2779:C:HO2'	1:l:2780:G:P	2.39	0.46
1:l:2816:A:H5''	32:b:34:TYR:CD1	2.50	0.46
1:l:3119:U:H2'	1:l:3120:A:H8	1.80	0.46
9:D:69:VAL:HG13	25:T:28:SER:HB2	1.98	0.46
10:E:142:GLU:CG	10:E:143:ASN:H	2.29	0.46
27:V:96:TYR:OH	46:u:37:HIS:NE2	2.32	0.46
29:Y:26:ARG:HG2	29:Y:77:PHE:CZ	2.51	0.46
30:Z:105:THR:OG1	42:m:677:ASP:OD2	2.23	0.46
41:k:31:LYS:HE2	41:k:31:LYS:H	1.79	0.46
42:m:614:VAL:HG12	42:m:616:TRP:H	1.80	0.46
43:n:36:ILE:HD12	43:n:72:LEU:HD22	1.96	0.46
45:p:273:MET:H	45:p:288:GLY:HA2	1.80	0.46
1:l:110:G:OP2	17:L:73:ARG:NH2	2.48	0.46
1:l:528:G:OP1	11:F:74:ARG:NH2	2.48	0.46
5:9:167:G:OP2	9:D:255:LYS:NZ	2.38	0.46
7:B:363:SER:OG	7:B:365:PHE:O	2.25	0.46
9:D:90:TRP:NE1	9:D:229:ASP:OD2	2.47	0.46
21:P:36:ILE:HA	21:P:39:MET:HE2	1.95	0.46
30:Z:29:ILE:HD13	30:Z:40:HIS:CE1	2.51	0.46
1:l:3:U:OP1	28:X:22:ALA:N	2.49	0.46
1:l:1010:A:N3	1:l:1011:G:N2	2.64	0.46
1:l:1395:A:H2'	1:l:1396:G:C8	2.51	0.46
1:l:1679:A:N7	37:g:68:ASN:ND2	2.43	0.46
42:m:233:LYS:O	42:m:237:GLN:HG3	2.15	0.46
42:m:389:LEU:HD22	42:m:730:ALA:HB2	1.98	0.46
1:l:335:A:OP1	17:L:31:ARG:NH2	2.49	0.46
1:l:1234:A:N6	1:l:1331:G:H2'	2.29	0.46
1:l:1918:G:O3'	23:R:82:LYS:HB2	2.16	0.46
1:l:2311:A:OP2	1:l:2311:A:H8	1.99	0.46
1:l:2432:U:H2'	1:l:2433:A:C8	2.50	0.46
6:A:93:ALA:HB3	6:A:101:LEU:HG	1.98	0.46
22:Q:72:ARG:HD2	22:Q:72:ARG:HA	1.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:126:ASP:O	22:Q:130:LEU:HD22	2.15	0.46
23:R:113:GLY:C	23:R:115:ILE:N	2.74	0.46
43:n:40:LYS:HD3	43:n:118:ILE:HD12	1.98	0.46
1:1:216:A:O2'	1:1:218:A:OP2	2.26	0.46
1:1:2283:C:O2'	1:1:2359:A:O2'	2.31	0.46
1:1:2656:A:N1	12:G:32:ARG:HB2	2.30	0.46
1:1:3084:U:H5'	1:1:3085:G:OP2	2.15	0.46
5:9:51:G:N3	9:D:267:SER:OG	2.42	0.46
7:B:19:ARG:HB2	7:B:232:ARG:NH2	2.30	0.46
7:B:256:HIS:HA	7:B:257:PRO:C	2.41	0.46
31:a:75:LEU:HB3	31:a:117:LEU:HD13	1.98	0.46
32:b:52:GLU:OE2	32:b:56:GLN:HG3	2.16	0.46
37:g:92:ALA:O	37:g:96:GLU:HG2	2.16	0.46
41:k:18:LYS:C	41:k:18:LYS:HD2	2.40	0.46
1:1:1460:C:H4'	8:C:42:THR:HG23	1.96	0.46
1:1:1588:A:H4'	1:1:1589:U:H5''	1.97	0.46
1:1:1602:A:C5	42:m:334:PHE:HE2	2.34	0.46
1:1:2393:G:OP2	1:1:2393:G:N2	2.33	0.46
1:1:2650:A:H5''	6:A:86:PHE:CZ	2.50	0.46
5:9:57:G:OP1	9:D:33:ARG:HD2	2.16	0.46
7:B:373:PRO:O	7:B:377:LYS:HG2	2.15	0.46
12:G:161:GLU:CD	19:N:26:ARG:HH22	2.24	0.46
24:S:9:VAL:HB	24:S:59:ALA:HB3	1.97	0.46
26:U:39:LYS:NZ	26:U:44:THR:HB	2.31	0.46
1:1:103:G:OP1	17:L:70:ARG:NH2	2.48	0.46
1:1:1176:G:H5'	35:e:43:PHE:CE1	2.50	0.46
1:1:2856:G:N7	44:o:63:LYS:NZ	2.52	0.46
3:3:48:SER:HB3	3:3:67:ILE:HG22	1.98	0.46
8:C:314:HIS:CE1	8:C:317:LYS:HA	2.51	0.46
21:P:137:THR:OG1	21:P:138:ALA:N	2.37	0.46
30:Z:72:ILE:HD11	30:Z:107:ARG:HG3	1.98	0.46
1:1:2320:A:H1'	1:1:2517:G:H5'	1.98	0.46
13:H:75:ILE:HA	13:H:78:MET:SD	2.55	0.46
24:S:86:THR:O	24:S:87:HIS:ND1	2.49	0.46
41:k:8:ILE:HG12	41:k:46:LEU:HD21	1.98	0.46
42:m:684:PHE:CD1	42:m:700:PRO:HA	2.50	0.46
1:1:1176:G:H5'	35:e:43:PHE:CD1	2.51	0.45
1:1:1387:A:H4'	1:1:1391:G:N3	2.32	0.45
1:1:1632:C:H5'	1:1:1731:A:H1'	1.98	0.45
1:1:3042:G:N3	7:B:250:ALA:HB1	2.31	0.45
1:1:3042:G:OP1	1:1:3077:A:N6	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:266:SER:HA	8:C:279:LEU:HD12	1.98	0.45
9:D:84:PRO:HB3	9:D:89:LYS:HD3	1.98	0.45
10:E:189:ARG:O	10:E:193:MET:HG3	2.15	0.45
19:N:143:ARG:C	19:N:149:ASN:HD21	2.23	0.45
36:f:51:CYS:HB3	36:f:69:TRP:CE3	2.51	0.45
1:1:161:C:H1'	39:i:24:PRO:HB2	1.99	0.45
1:1:176:A:OP2	38:h:111:ARG:NH1	2.37	0.45
1:1:299:C:OP1	19:N:68:ARG:HB3	2.15	0.45
1:1:2809:G:H5''	1:1:2811:U:C6	2.51	0.45
7:B:216:ASP:HB2	7:B:339:ARG:HG2	1.98	0.45
8:C:159:GLN:HG3	8:C:253:THR:HG21	1.97	0.45
12:G:34:PHE:CD1	12:G:42:PRO:HD3	2.52	0.45
17:L:90:ALA:HB1	17:L:95:ILE:HB	1.98	0.45
43:n:250:ASP:OD1	43:n:251:VAL:N	2.49	0.45
1:1:311:G:O2'	1:1:312:G:OP2	2.34	0.45
1:1:787:G:H21	1:1:804:A:H62	1.64	0.45
1:1:1644:C:H2'	1:1:1645:G:C8	2.51	0.45
12:G:82:LEU:HD21	12:G:86:THR:HG22	1.98	0.45
12:G:159:PRO:HG2	12:G:162:LEU:HD22	1.99	0.45
17:L:102:ARG:HB2	39:i:20:LEU:HD22	1.98	0.45
24:S:80:TYR:CE1	24:S:115:ALA:HB2	2.51	0.45
31:a:70:ARG:HD2	31:a:128:TYR:CD2	2.51	0.45
1:1:101:G:H2'	1:1:102:C:O4'	2.16	0.45
1:1:1188:G:H2'	1:1:1189:A:O4'	2.16	0.45
1:1:1698:C:H2'	1:1:1699:G:C8	2.51	0.45
1:1:2779:C:O2'	1:1:2780:G:H8	2.00	0.45
1:1:3365:U:OP1	10:E:87:LYS:NZ	2.48	0.45
9:D:205:ALA:HB1	9:D:233:SER:HB2	1.98	0.45
11:F:46:LYS:HB3	11:F:46:LYS:HE3	1.73	0.45
32:b:25:GLN:HA	32:b:25:GLN:NE2	2.32	0.45
33:c:75:MET:HE3	33:c:76:LEU:HG	1.99	0.45
43:n:439:TYR:CE1	43:n:446:PRO:HD2	2.52	0.45
1:1:92:G:O5'	1:1:93:C:H5''	2.16	0.45
1:1:112:U:OP1	38:h:109:LYS:NZ	2.45	0.45
1:1:1396:G:H2'	1:1:1397:A:C8	2.52	0.45
1:1:2198:G:O2'	1:1:2199:G:OP1	2.31	0.45
1:1:2480:C:HO2'	7:B:266:ARG:HH12	1.62	0.45
3:3:60:LEU:HD13	3:3:112:LEU:HD11	1.98	0.45
6:A:167:ILE:HD12	6:A:167:ILE:N	2.31	0.45
30:Z:3:LYS:HD2	33:c:78:ARG:HH22	1.81	0.45
36:f:46:LEU:HD11	36:f:75:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:119:ILE:HD12	43:n:229:LEU:HD13	1.98	0.45
1:1:406:U:H5''	21:P:3:ARG:NH1	2.31	0.45
1:1:1969:G:O2'	23:R:82:LYS:O	2.32	0.45
3:3:22:GLY:O	3:3:23:GLU:HG3	2.16	0.45
8:C:301:ILE:HD11	22:Q:133:PRO:HB2	1.98	0.45
16:K:27:ARG:NH2	16:K:28:LYS:HE2	2.31	0.45
23:R:74:ARG:HB3	23:R:75:HIS:CD2	2.51	0.45
29:Y:49:VAL:HG21	29:Y:79:LEU:HD21	1.98	0.45
43:n:210:VAL:HG22	43:n:212:THR:H	1.81	0.45
1:1:353:G:O2'	2:2:33:G:N3	2.49	0.45
1:1:745:G:O6	1:1:778:G:N2	2.48	0.45
1:1:2443:G:OP2	21:P:25:HIS:NE2	2.45	0.45
1:1:2806:C:O2'	1:1:2839:U:OP1	2.32	0.45
1:1:3282:G:H2'	1:1:3283:A:O4'	2.17	0.45
1:1:3315:A:C2	10:E:176:GLU:HG2	2.52	0.45
2:2:127:U:OP1	43:n:70:GLN:NE2	2.37	0.45
33:c:23:THR:HG22	33:c:27:LYS:HE2	1.98	0.45
1:1:940:G:H4'	1:1:941:G:O5'	2.17	0.45
1:1:1559:G:H5'	1:1:1885:G:OP2	2.17	0.45
1:1:1769:A:N6	16:K:42:CYS:HA	2.31	0.45
3:3:30:ASN:HD22	3:3:31:GLU:H	1.65	0.45
8:C:60:HIS:HA	8:C:92:PHE:CE1	2.45	0.45
9:D:37:ILE:HD11	25:T:27:LEU:HD23	1.98	0.45
10:E:93:ILE:HG13	10:E:157:GLN:OE1	2.17	0.45
12:G:112:GLU:HB2	42:m:235:ILE:HD11	1.99	0.45
13:H:74:ILE:HA	13:H:77:ASN:HD22	1.81	0.45
1:1:359:A:N6	4:8:37:TYR:O	2.50	0.45
1:1:2290:C:H5''	6:A:225:PRO:HG3	1.99	0.45
3:3:15:PHE:HE2	8:C:140:ARG:HG3	1.82	0.45
28:X:59:TYR:CE1	28:X:101:LEU:HD21	2.52	0.45
37:g:41:ILE:O	37:g:43:ARG:NH2	2.50	0.45
41:k:10:GLN:NE2	42:m:646:SER:HB2	2.31	0.45
1:1:2798:A:N6	9:D:28:THR:O	2.42	0.45
1:1:3329:G:N2	18:M:122:GLU:OE1	2.49	0.45
6:A:210:HIS:ND1	6:A:218:VAL:HG13	2.32	0.45
8:C:275:LYS:NZ	8:C:275:LYS:HB3	2.32	0.45
11:F:214:LEU:HB3	11:F:249:MET:HB3	1.99	0.45
13:H:44:ILE:HD12	13:H:71:VAL:HG21	1.98	0.45
17:L:109:LEU:O	17:L:113:VAL:HG23	2.16	0.45
28:X:56:LEU:HD23	28:X:56:LEU:HA	1.84	0.45
37:g:68:ASN:OD1	37:g:68:ASN:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:10:GLN:HB2	42:m:645:PHE:O	2.17	0.45
42:m:387:ARG:HH12	42:m:451:ILE:HD12	1.82	0.45
42:m:639:CYS:HB3	42:m:641:PHE:HE1	1.82	0.45
1:1:2217:U:H2'	1:1:2218:G:C8	2.53	0.44
1:1:3271:G:H5'	36:f:4:GLN:HA	1.99	0.44
28:X:58:GLU:HG2	28:X:59:TYR:N	2.32	0.44
42:m:287:PRO:HD2	43:n:43:TYR:OH	2.16	0.44
43:n:123:TYR:OH	43:n:132:ASP:OD2	2.28	0.44
1:1:361:G:O2'	1:1:372:G:O6	2.28	0.44
1:1:536:A:H61	1:1:590:U:H3	1.63	0.44
1:1:2976:C:H2'	1:1:2977:U:C6	2.52	0.44
3:3:33:ASN:OD1	3:3:34:VAL:N	2.49	0.44
7:B:284:ARG:HB3	7:B:323:MET:HE3	1.99	0.44
13:H:5:ILE:O	13:H:58:TRP:HA	2.16	0.44
27:V:89:ARG:HD3	27:V:123:GLU:OE2	2.16	0.44
32:b:33:LYS:O	32:b:34:TYR:HB2	2.17	0.44
42:m:453:GLN:HG2	42:m:532:LYS:HA	2.00	0.44
1:1:989:C:H4'	1:1:2894:A:C5	2.52	0.44
1:1:2238:G:O2'	1:1:2277:U:OP1	2.32	0.44
3:3:105:ILE:H	3:3:105:ILE:HD12	1.80	0.44
6:A:144:LYS:HB3	6:A:156:VAL:HG13	1.99	0.44
7:B:273:MET:HE2	7:B:275:ARG:NH2	2.32	0.44
8:C:66:SER:OG	8:C:75:ARG:O	2.26	0.44
12:G:127:LYS:HD3	12:G:128:LYS:O	2.17	0.44
30:Z:29:ILE:HD12	30:Z:41:ALA:HA	1.99	0.44
1:1:541:G:H2'	1:1:542:G:H8	1.82	0.44
1:1:620:C:O2	8:C:329:ARG:HD3	2.17	0.44
1:1:2218:G:O4'	1:1:2232:A:H4'	2.17	0.44
1:1:2661:U:H3	1:1:2670:A:H61	1.65	0.44
1:1:2863:U:H2'	1:1:2864:G:C8	2.53	0.44
2:2:162:C:H2'	2:2:163:A:C8	2.53	0.44
15:J:142:LYS:HA	15:J:145:ARG:HH21	1.82	0.44
17:L:31:ARG:HG3	17:L:34:ARG:HH12	1.83	0.44
35:e:39:VAL:HG12	35:e:46:THR:HB	1.98	0.44
38:h:80:LEU:HA	38:h:83:ARG:HD2	1.99	0.44
42:m:487:ILE:O	42:m:491:LYS:HG3	2.16	0.44
1:1:37:U:O3'	1:1:967:U:H4'	2.17	0.44
1:1:616:A:H5'	10:E:35:VAL:O	2.17	0.44
1:1:1174:A:H5'	1:1:1402:U:H1'	2.00	0.44
1:1:1234:A:N3	1:1:2950:U:O2'	2.45	0.44
1:1:1648:A:OP2	41:k:38:ARG:NH1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3329:G:O2'	18:M:124:VAL:HG23	2.16	0.44
9:D:41:LYS:NZ	25:T:32:LYS:O	2.36	0.44
9:D:89:LYS:HB2	9:D:90:TRP:CD2	2.52	0.44
12:G:83:ASP:OD1	12:G:84:LYS:N	2.51	0.44
43:n:560:LEU:HD23	43:n:560:LEU:O	2.18	0.44
1:1:613:A:N6	1:1:635:G:H1'	2.32	0.44
1:1:2198:G:H1	1:1:2202:C:N4	2.15	0.44
1:1:2247:U:OP2	6:A:118:LYS:HE2	2.17	0.44
1:1:2657:A:N6	1:1:2674:G:O2'	2.50	0.44
5:9:52:U:H3	5:9:167:G:H1	1.64	0.44
5:9:54:U:H2'	5:9:55:A:H8	1.82	0.44
5:9:111:U:O3'	9:D:283:ARG:NH2	2.51	0.44
14:I:38:ARG:NH1	14:I:45:GLU:OE2	2.51	0.44
16:K:43:GLY:O	33:c:89:ILE:HD11	2.17	0.44
45:p:129:TRP:HA	45:p:135:ILE:HA	1.99	0.44
1:1:2286:A:N6	1:1:2334:G:H21	2.14	0.44
3:3:72:PHE:O	3:3:76:LEU:HB2	2.17	0.44
7:B:58:ARG:HD2	7:B:354:VAL:HG13	1.99	0.44
7:B:304:ARG:HG3	7:B:304:ARG:NH1	2.28	0.44
8:C:207:PRO:HG2	8:C:227:VAL:HG22	1.99	0.44
14:I:96:VAL:O	14:I:98:ARG:NH1	2.50	0.44
19:N:183:SER:HB3	19:N:184:PRO:CD	2.44	0.44
25:T:84:TYR:O	32:b:24:PRO:HD3	2.17	0.44
31:a:89:LYS:HG2	31:a:90:TYR:CD1	2.53	0.44
34:d:17:TYR:HD2	34:d:80:LEU:HD13	1.83	0.44
42:m:303:PRO:HD3	43:n:447:PRO:HB3	1.99	0.44
43:n:101:GLU:HG3	43:n:102:THR:N	2.33	0.44
44:o:2:VAL:N	44:o:90:HIS:O	2.51	0.44
1:1:261:A:H2'	1:1:262:A:O4'	2.18	0.44
1:1:3102:A:H2'	1:1:3103:U:O4'	2.17	0.44
1:1:3491:A:O2'	1:1:3492:G:H8	2.00	0.44
8:C:100:ARG:CZ	8:C:100:ARG:HB3	2.48	0.44
8:C:308:SER:O	8:C:309:ARG:C	2.61	0.44
17:L:25:TRP:O	19:N:199:ARG:HD2	2.18	0.44
21:P:59:PRO:HB3	21:P:78:VAL:HG21	2.00	0.44
27:V:41:VAL:HG13	27:V:60:VAL:HG12	1.99	0.44
29:Y:55:ILE:C	29:Y:55:ILE:HD12	2.42	0.44
43:n:188:TYR:CZ	43:n:201:ILE:HD12	2.52	0.44
1:1:995:G:O2'	31:a:29:PRO:O	2.35	0.44
1:1:1919:A:H5'	23:R:88:ARG:HG2	1.99	0.44
1:1:1941:A:O2'	7:B:226:ASN:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2189:C:HO2'	1:1:2190:U:C5'	2.30	0.44
1:1:3300:A:H3'	1:1:3301:C:H5''	1.99	0.44
2:2:17:A:H2'	2:2:18:G:C8	2.53	0.44
5:9:149:G:N7	24:S:51:LYS:NZ	2.47	0.44
8:C:337:TYR:HE1	8:C:339:ALA:HB2	1.82	0.44
13:H:90:MET:HB3	13:H:90:MET:HE3	1.82	0.44
28:X:56:LEU:HD11	28:X:88:LYS:HB2	1.99	0.44
31:a:148:ALA:HB2	39:i:6:VAL:HG23	1.98	0.44
42:m:236:LEU:HD23	42:m:236:LEU:HA	1.87	0.44
43:n:173:ARG:HH12	43:n:243:LEU:HD13	1.82	0.44
44:o:21:THR:O	44:o:23:HIS:ND1	2.50	0.44
1:1:1660:A:N7	43:n:565:MET:HE1	2.33	0.43
1:1:2294:G:H1	1:1:2325:C:H42	1.66	0.43
2:2:34:C:O2'	8:C:53:ALA:O	2.34	0.43
13:H:29:THR:HG22	13:H:34:THR:HG23	2.00	0.43
13:H:149:LEU:O	13:H:153:SER:OG	2.21	0.43
18:M:65:LEU:HD23	18:M:66:PRO:O	2.18	0.43
18:M:102:ARG:HD3	20:O:197:TYR:CZ	2.53	0.43
29:Y:30:MET:O	29:Y:49:VAL:HG22	2.18	0.43
43:n:561:SER:HB3	43:n:570:ARG:HH21	1.82	0.43
1:1:83:U:H2'	1:1:84:C:O4'	2.18	0.43
1:1:292:A:O2'	1:1:293:A:OP1	2.36	0.43
1:1:949:A:H62	6:A:3:ARG:HH12	1.66	0.43
1:1:2445:A:H5'	21:P:137:THR:OG1	2.18	0.43
5:9:54:U:H2'	5:9:55:A:C8	2.53	0.43
5:9:131:U:C2'	5:9:132:G:H5'	2.47	0.43
9:D:55:PHE:HE2	9:D:159:VAL:HG12	1.83	0.43
11:F:49:GLU:O	11:F:53:LYS:HE2	2.18	0.43
30:Z:103:GLU:OE1	42:m:661:ARG:NH1	2.48	0.43
31:a:75:LEU:HG	31:a:113:GLY:HA2	2.00	0.43
1:1:25:U:H4'	1:1:26:A:N7	2.33	0.43
1:1:805:G:H2'	1:1:806:G:O4'	2.19	0.43
1:1:831:G:H2'	1:1:833:A:H62	1.82	0.43
1:1:2889:G:O2'	1:1:2890:U:OP2	2.31	0.43
15:J:92:LYS:HB2	15:J:95:ASN:OD1	2.18	0.43
20:O:109:ILE:HD12	20:O:161:ARG:CZ	2.49	0.43
23:R:43:LYS:HA	23:R:43:LYS:HD2	1.77	0.43
30:Z:6:LYS:HB2	30:Z:6:LYS:HE3	1.85	0.43
43:n:244:ARG:HE	43:n:245:TYR:H	1.66	0.43
1:1:531:A:N1	8:C:349:PRO:HD2	2.34	0.43
1:1:591:G:H1'	1:1:593:A:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:892:G:O2'	1:1:927:A:H4'	2.18	0.43
1:1:1010:A:O2'	1:1:1011:G:N3	2.46	0.43
1:1:1929:A:OP2	23:R:21:LYS:NZ	2.44	0.43
1:1:2792:A:H2'	1:1:2793:G:H8	1.83	0.43
1:1:3090:A:N3	2:2:8:A:H2	2.16	0.43
1:1:3367:A:H2'	10:E:86:TYR:OH	2.19	0.43
5:9:66:U:H2'	5:9:67:A:C8	2.53	0.43
14:I:45:GLU:C	14:I:46:PHE:HD1	2.27	0.43
19:N:158:HIS:HB3	19:N:161:SER:HB3	2.01	0.43
26:U:91:LEU:HD11	26:U:103:LEU:HB3	1.99	0.43
1:1:671:A:H2'	1:1:672:A:O4'	2.18	0.43
1:1:3328:U:H6	1:1:3328:U:H2'	1.68	0.43
15:J:27:GLY:O	15:J:31:THR:HG23	2.19	0.43
24:S:11:ARG:NH1	24:S:14:PRO:HD3	2.33	0.43
42:m:705:ARG:HB3	42:m:705:ARG:CZ	2.48	0.43
3:3:59:LYS:HD2	3:3:83:SER:OG	2.18	0.43
7:B:105:VAL:HG11	7:B:148:LEU:HD11	2.01	0.43
15:J:125:MET:HE1	15:J:127:PHE:CD1	2.53	0.43
19:N:84:PRO:HA	19:N:87:GLN:HG3	2.00	0.43
26:U:13:ILE:HB	26:U:100:VAL:HG13	2.00	0.43
30:Z:18:PHE:CE1	30:Z:47:GLU:HG3	2.54	0.43
34:d:11:GLN:O	34:d:82:ARG:NH1	2.43	0.43
35:e:76:VAL:HB	35:e:108:LYS:HE3	2.01	0.43
1:1:248:G:H2'	1:1:249:G:C8	2.53	0.43
1:1:402:U:P	29:Y:86:ARG:HH22	2.42	0.43
1:1:641:G:H2'	1:1:642:A:C8	2.53	0.43
1:1:928:A:H5''	6:A:182:GLY:HA2	2.01	0.43
1:1:1000:G:N3	32:b:15:LYS:NZ	2.66	0.43
1:1:1498:G:O2'	1:1:1500:G:N7	2.49	0.43
1:1:1761:U:O2'	1:1:1763:A:N7	2.46	0.43
1:1:1944:G:H5''	7:B:245:GLY:HA3	2.01	0.43
1:1:2328:G:N2	6:A:240:ARG:O	2.37	0.43
1:1:2762:A:N6	1:1:2782:G:O2'	2.52	0.43
2:2:23:G:C6	2:2:24:G:N1	2.86	0.43
13:H:90:MET:HG3	13:H:179:VAL:HA	2.01	0.43
25:T:9:ALA:O	25:T:55:LYS:NZ	2.31	0.43
25:T:137:LYS:HD3	25:T:137:LYS:HA	1.75	0.43
27:V:98:GLU:OE2	46:u:24:ASN:N	2.51	0.43
28:X:140:PHE:HB3	38:h:32:VAL:HG13	2.01	0.43
43:n:101:GLU:O	43:n:105:ARG:HG3	2.19	0.43
45:p:151:TRP:HA	45:p:158:PHE:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:685:A:H5'	8:C:102:PHE:CD2	2.54	0.43
1:1:1332:A:H5'	1:1:1333:A:C4	2.54	0.43
1:1:2864:G:O3'	44:o:80:LYS:HB2	2.19	0.43
3:3:110:GLN:O	3:3:113:THR:HB	2.18	0.43
12:G:183:LYS:HD3	12:G:194:THR:HG23	2.00	0.43
13:H:19:VAL:HG12	13:H:19:VAL:O	2.19	0.43
24:S:47:ILE:HG13	24:S:48:ASN:N	2.34	0.43
42:m:529:SER:OG	42:m:549:THR:OG1	2.34	0.43
43:n:30:LEU:O	43:n:34:ARG:HG2	2.18	0.43
1:1:179:G:H1	1:1:253:U:H3	1.66	0.43
1:1:420:G:H5'	21:P:26:PHE:HZ	1.83	0.43
1:1:527:C:H5''	8:C:344:ASN:ND2	2.34	0.43
1:1:1163:C:H2'	1:1:1164:A:H8	1.84	0.43
1:1:1713:G:O6	26:U:72:ARG:NH2	2.52	0.43
1:1:2757:G:H2'	1:1:2758:A:C8	2.53	0.43
1:1:2784:A:N3	1:1:2784:A:H2'	2.34	0.43
1:1:3084:U:O2'	7:B:266:ARG:HB2	2.19	0.43
3:3:22:GLY:O	3:3:25:GLN:NE2	2.52	0.43
7:B:14:LEU:HA	7:B:17:LEU:HD23	2.01	0.43
8:C:297:GLU:OE1	8:C:297:GLU:N	2.47	0.43
31:a:2:PRO:HG2	31:a:5:VAL:HG22	2.01	0.43
42:m:373:THR:N	42:m:740:THR:O	2.50	0.43
43:n:181:PHE:HE2	43:n:183:SER:HB2	1.84	0.43
43:n:243:LEU:HD23	43:n:244:ARG:N	2.34	0.43
1:1:36:C:O2'	1:1:840:A:N1	2.52	0.43
1:1:311:G:O2'	1:1:2873:A:OP2	2.36	0.43
1:1:972:G:OP2	31:a:24:LYS:NZ	2.51	0.43
1:1:2890:U:OP1	44:o:62:ALA:N	2.49	0.43
1:1:2991:A:H61	1:1:3000:U:H3	1.66	0.43
3:3:54:ARG:HB3	3:3:54:ARG:HH11	1.84	0.43
6:A:117:GLU:HG2	6:A:155:LYS:NZ	2.34	0.43
8:C:183:VAL:HG11	8:C:226:GLY:HA3	2.01	0.43
29:Y:73:TYR:CE2	29:Y:75:LYS:HG2	2.52	0.43
44:o:90:HIS:CE1	44:o:92:GLU:OE2	2.72	0.43
1:1:139:U:P	1:1:140:U:H3	2.42	0.42
1:1:904:U:O2'	1:1:1963:A:OP1	2.35	0.42
1:1:1207:C:H2'	1:1:1208:G:H21	1.84	0.42
1:1:1758:G:H4'	23:R:117:LYS:HE3	2.01	0.42
1:1:2441:G:H5''	21:P:86:LYS:HB2	2.00	0.42
21:P:89:LYS:HE3	21:P:89:LYS:HB3	1.69	0.42
22:Q:73:LYS:HB3	22:Q:74:SER:H	1.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:89:ARG:NH1	27:V:95:LEU:HG	2.33	0.42
30:Z:64:ARG:NE	30:Z:67:ARG:NH1	2.67	0.42
37:g:60:ARG:HH22	43:n:4:VAL:HG11	1.84	0.42
42:m:484:ASP:HA	42:m:487:ILE:HD13	2.01	0.42
42:m:637:ARG:HA	42:m:653:LEU:O	2.19	0.42
1:1:99:A:OP2	19:N:192:HIS:NE2	2.52	0.42
1:1:283:U:H2'	1:1:284:U:C6	2.54	0.42
1:1:1834:C:OP2	16:K:49:ARG:NH2	2.52	0.42
1:1:2246:A:O2'	6:A:117:GLU:OE1	2.33	0.42
18:M:13:VAL:O	18:M:59:THR:OG1	2.23	0.42
28:X:28:SER:O	28:X:30:THR:HG23	2.18	0.42
34:d:69:ILE:HG23	34:d:70:ARG:HG3	2.00	0.42
1:1:25:U:HO2'	1:1:27:C:H41	1.62	0.42
1:1:856:C:H5''	6:A:20:ARG:HD3	2.00	0.42
1:1:921:U:H2'	1:1:922:C:O4'	2.18	0.42
1:1:1389:A:N1	22:Q:37:ARG:NH2	2.68	0.42
1:1:1650:C:H2'	1:1:1651:A:C8	2.54	0.42
1:1:3031:A:H2'	1:1:3032:G:C8	2.55	0.42
1:1:3175:U:H4'	34:d:70:ARG:HH22	1.84	0.42
3:3:114:ARG:HH21	10:E:30:ALA:H	1.67	0.42
10:E:158:LYS:HE3	10:E:158:LYS:HB2	1.83	0.42
14:I:36:LEU:HD22	14:I:73:ASN:HB2	2.00	0.42
22:Q:61:ILE:HG13	22:Q:62:SER:N	2.35	0.42
31:a:131:ARG:HH21	31:a:132:ARG:HH21	1.66	0.42
1:1:36:C:H4'	1:1:840:A:C2	2.54	0.42
1:1:275:G:OP2	1:1:326:A:N6	2.53	0.42
1:1:430:A:C2	1:1:2451:A:H4'	2.54	0.42
1:1:1791:G:O6	41:k:36:LYS:NZ	2.41	0.42
1:1:2216:C:H2'	1:1:2217:U:O4'	2.19	0.42
1:1:2284:C:O2'	1:1:2358:A:N3	2.45	0.42
1:1:2477:C:H2'	1:1:2478:A:C8	2.54	0.42
1:1:2507:A:H2'	1:1:2508:C:C6	2.54	0.42
1:1:2510:C:O5'	44:o:52:GLY:HA2	2.18	0.42
1:1:2908:A:H2'	1:1:2909:G:O4'	2.18	0.42
1:1:3083:C:O2	7:B:266:ARG:NH2	2.34	0.42
2:2:71:G:O2'	38:h:51:LYS:NZ	2.51	0.42
15:J:29:ARG:HE	15:J:123:TYR:HE1	1.67	0.42
18:M:99:LYS:O	18:M:103:SER:OG	2.31	0.42
21:P:42:LYS:O	21:P:46:ILE:HG12	2.20	0.42
21:P:141:SER:O	21:P:143:PRO:HD3	2.20	0.42
23:R:36:ASN:OD1	23:R:36:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:R:119:LEU:HD23	23:R:119:LEU:HA	1.80	0.42
24:S:26:MET:HE2	24:S:26:MET:HB3	1.70	0.42
28:X:101:LEU:HD23	28:X:101:LEU:HA	1.86	0.42
30:Z:127:SER:HB3	30:Z:130:PHE:HB3	2.01	0.42
37:g:69:LYS:HB3	37:g:69:LYS:HE2	1.90	0.42
42:m:479:PRO:HD2	42:m:482:PHE:HE2	1.83	0.42
42:m:582:HIS:HB3	42:m:585:MET:O	2.19	0.42
43:n:143:PHE:CD2	43:n:223:LEU:HD11	2.54	0.42
1:1:122:A:O2'	1:1:151:G:N2	2.53	0.42
1:1:315:A:H2'	1:1:316:A:C8	2.54	0.42
1:1:947:A:H8	1:1:2224:C:O2'	2.03	0.42
1:1:978:U:H2'	1:1:979:G:H8	1.85	0.42
1:1:1933:G:H2'	1:1:1934:A:H5'	2.01	0.42
1:1:2817:U:O2'	25:T:88:ARG:O	2.36	0.42
1:1:3302:U:O5'	1:1:3302:U:H6	2.02	0.42
1:1:3434:G:O2'	46:u:50:ALA:HB3	2.18	0.42
7:B:44:THR:HG21	7:B:184:ASN:OD1	2.20	0.42
7:B:187:SER:O	7:B:191:LYS:HG3	2.19	0.42
22:Q:61:ILE:HG13	22:Q:62:SER:H	1.84	0.42
24:S:86:THR:HG23	25:T:156:TYR:CE1	2.55	0.42
25:T:65:TYR:CE1	25:T:88:ARG:HB3	2.54	0.42
25:T:111:ALA:O	25:T:115:LYS:HG3	2.20	0.42
42:m:388:CYS:HB3	42:m:454:SER:HA	2.00	0.42
42:m:687:ARG:HD3	42:m:689:TYR:CZ	2.54	0.42
1:1:1367:C:H2'	1:1:1368:A:H8	1.84	0.42
1:1:1702:A:H2'	1:1:1703:G:C8	2.55	0.42
1:1:2620:A:N6	6:A:66:TYR:HB3	2.35	0.42
1:1:2729:U:H2'	1:1:2737:A:N6	2.34	0.42
1:1:2833:A:P	25:T:69:GLN:HE22	2.39	0.42
7:B:45:ALA:HB3	7:B:181:ILE:HG23	2.00	0.42
9:D:275:LEU:O	9:D:280:ARG:NH2	2.53	0.42
9:D:287:LYS:HE3	14:I:206:LEU:HD23	2.02	0.42
27:V:68:LYS:O	27:V:72:ARG:HG3	2.20	0.42
35:e:76:VAL:O	35:e:80:GLU:HG3	2.19	0.42
36:f:76:HIS:HB2	36:f:83:ARG:HG3	2.02	0.42
37:g:72:VAL:O	37:g:77:GLY:HA3	2.19	0.42
1:1:205:A:N3	1:1:225:G:O2'	2.52	0.42
1:1:686:G:N7	31:a:25:HIS:ND1	2.67	0.42
1:1:693:A:H5''	22:Q:165:TYR:CE1	2.55	0.42
1:1:3039:U:H1'	7:B:251:CYS:SG	2.60	0.42
1:1:3332:U:H2'	1:1:3333:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:139:GLU:HG2	7:B:140:SER:N	2.35	0.42
8:C:355:LYS:O	8:C:359:VAL:HG23	2.19	0.42
10:E:136:ASP:OD1	10:E:137:GLU:N	2.53	0.42
27:V:96:TYR:HH	46:u:37:HIS:CE1	2.31	0.42
30:Z:30:ASP:N	30:Z:30:ASP:OD1	2.53	0.42
42:m:229:LYS:O	42:m:233:LYS:HE3	2.19	0.42
44:o:24:ARG:NH1	44:o:75:VAL:HG12	2.35	0.42
1:1:168:C:H42	1:1:266:G:H1	1.67	0.42
1:1:754:A:N6	1:1:770:G:H1'	2.35	0.42
1:1:1851:A:H2'	1:1:1852:G:C8	2.55	0.42
1:1:3103:U:H2'	1:1:3104:G:C8	2.55	0.42
6:A:129:SER:OG	6:A:173:ARG:NH2	2.53	0.42
8:C:215:THR:O	8:C:215:THR:OG1	2.34	0.42
11:F:147:ASN:HD22	11:F:243:ASN:CG	2.26	0.42
27:V:68:LYS:HB3	27:V:70:ASP:OD1	2.20	0.42
33:c:32:MET:HE2	33:c:37:TYR:CE1	2.55	0.42
35:e:9:LYS:NZ	35:e:55:GLY:O	2.50	0.42
37:g:14:ASN:ND2	37:g:14:ASN:C	2.75	0.42
41:k:62:PRO:HG2	41:k:65:LEU:HB2	2.01	0.42
42:m:387:ARG:HA	42:m:716:LEU:HD23	2.00	0.42
42:m:639:CYS:HB3	42:m:641:PHE:CE1	2.54	0.42
1:1:169:U:O2'	1:1:170:G:H5'	2.19	0.42
1:1:302:U:H5'	39:i:51:TYR:CE1	2.54	0.42
1:1:511:C:H2'	1:1:512:A:C8	2.55	0.42
1:1:3004:U:O2'	1:1:3201:A:N3	2.50	0.42
7:B:143:SER:HA	7:B:146:ARG:NH1	2.34	0.42
20:O:12:ALA:HB1	20:O:42:LEU:HG	2.02	0.42
28:X:106:PRO:HB3	28:X:123:VAL:HG13	2.02	0.42
31:a:148:ALA:HB3	39:i:4:GLY:C	2.44	0.42
45:p:312:PRO:O	45:p:330:SER:N	2.50	0.42
1:1:732:A:C6	31:a:112:LEU:HD13	2.55	0.42
1:1:800:U:H2'	1:1:801:G:O4'	2.19	0.42
1:1:991:C:H5'	1:1:992:U:O5'	2.20	0.42
1:1:1344:G:O2'	1:1:1349:A:N1	2.49	0.42
14:I:58:GLU:OE2	14:I:161:GLY:HA3	2.20	0.42
19:N:35:VAL:O	19:N:64:ILE:HA	2.19	0.42
19:N:146:PRO:HA	19:N:149:ASN:OD1	2.20	0.42
25:T:8:ARG:HD2	25:T:52:MET:HE1	2.02	0.42
33:c:39:LEU:HD23	33:c:104:LEU:HB3	2.02	0.42
43:n:10:ALA:HA	43:n:14:ARG:HB2	2.01	0.42
43:n:179:LYS:HD2	43:n:451:PRO:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:248:LYS:HE2	43:n:248:LYS:H	1.84	0.42
1:1:47:C:OP2	1:1:48:A:O2'	2.34	0.41
1:1:744:U:OP1	1:1:779:A:O2'	2.33	0.41
1:1:933:G:OP1	40:j:13:ASN:ND2	2.50	0.41
1:1:1367:C:H2'	1:1:1368:A:C8	2.54	0.41
1:1:1679:A:H62	37:g:68:ASN:ND2	2.17	0.41
1:1:1728:U:O2'	1:1:1813:U:O2'	2.27	0.41
1:1:1995:G:OP1	23:R:75:HIS:ND1	2.53	0.41
1:1:2246:A:OP2	6:A:155:LYS:NZ	2.53	0.41
3:3:62:LEU:HG	3:3:64:MET:HE2	2.02	0.41
13:H:103:LEU:HD11	13:H:134:ILE:HG13	2.02	0.41
28:X:112:LEU:HD22	28:X:122:PHE:CE2	2.55	0.41
1:1:839:A:H61	1:1:966:G:H22	1.68	0.41
1:1:928:A:H5''	6:A:182:GLY:CA	2.51	0.41
1:1:1412:U:H2'	1:1:1413:G:C8	2.55	0.41
1:1:3041:A:H2'	1:1:3077:A:N7	2.36	0.41
1:1:3363:C:H2'	1:1:3364:A:H8	1.84	0.41
14:I:47:PRO:HB3	14:I:171:TRP:CZ2	2.56	0.41
21:P:9:ALA:HA	21:P:14:CYS:SG	2.60	0.41
41:k:14:ILE:HG23	41:k:17:ARG:HH21	1.85	0.41
42:m:702:LYS:HD2	42:m:702:LYS:HA	1.76	0.41
1:1:26:A:H4'	1:1:337:U:H6	1.86	0.41
1:1:775:A:O2'	32:b:29:TYR:O	2.24	0.41
1:1:943:C:OP2	6:A:9:ARG:HD2	2.19	0.41
1:1:977:C:H2'	1:1:978:U:C6	2.56	0.41
1:1:1694:U:H2'	1:1:1695:C:C6	2.55	0.41
1:1:3154:U:O4	34:d:70:ARG:NH2	2.53	0.41
2:2:57:G:O4'	38:h:43:LEU:HB3	2.20	0.41
7:B:218:ILE:HD11	7:B:339:ARG:HD3	2.00	0.41
11:F:227:LYS:HB3	11:F:231:GLU:HG3	2.02	0.41
13:H:127:LEU:HD12	13:H:151:ASN:HA	2.02	0.41
14:I:52:LEU:HD11	14:I:156:GLN:HG3	2.01	0.41
34:d:16:ASP:OD1	34:d:99:VAL:HG21	2.20	0.41
37:g:8:ARG:NH1	37:g:32:TYR:O	2.50	0.41
43:n:216:PHE:O	43:n:220:HIS:N	2.48	0.41
1:1:2361:G:O2'	1:1:2399:G:O6	2.35	0.41
1:1:2809:G:C8	1:1:2846:G:H2'	2.56	0.41
1:1:3036:A:O5'	1:1:3038:G:H4'	2.20	0.41
1:1:3368:A:H5''	10:E:64:ARG:NH1	2.35	0.41
7:B:77:THR:OG1	7:B:326:GLY:O	2.30	0.41
8:C:33:ARG:HG3	8:C:122:TYR:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:114:LYS:HG2	19:N:200:TYR:HB3	2.03	0.41
8:C:171:LEU:HD23	8:C:174:ILE:HD11	2.02	0.41
9:D:275:LEU:HB2	9:D:280:ARG:NH1	2.35	0.41
11:F:73:ALA:O	11:F:77:ARG:HG3	2.20	0.41
20:O:5:GLN:HB2	20:O:8:VAL:HG23	2.02	0.41
20:O:27:GLN:HG3	24:S:167:PHE:CZ	2.55	0.41
20:O:111:PRO:N	20:O:112:PRO:HD2	2.34	0.41
24:S:70:LYS:O	24:S:72:LYS:HE2	2.20	0.41
34:d:84:ARG:HG3	34:d:84:ARG:NH1	2.35	0.41
37:g:61:GLU:HG3	37:g:64:ARG:NH2	2.36	0.41
1:1:276:A:N1	1:1:303:A:H5'	2.35	0.41
1:1:654:U:H2'	1:1:655:C:C6	2.56	0.41
1:1:871:C:O2'	1:1:1764:U:OP1	2.35	0.41
1:1:1326:G:H2'	1:1:1327:C:C6	2.55	0.41
1:1:1748:C:OP1	16:K:60:LYS:HE3	2.19	0.41
1:1:2303:A:H3'	1:1:2304:G:H8	1.86	0.41
1:1:2863:U:H2'	1:1:2864:G:H8	1.86	0.41
1:1:2948:G:OP1	14:I:63:GLU:HB3	2.20	0.41
9:D:37:ILE:HD12	25:T:31:LEU:HD21	2.02	0.41
15:J:36:VAL:HA	15:J:39:GLN:HG2	2.03	0.41
21:P:10:LEU:HD12	21:P:10:LEU:H	1.86	0.41
26:U:91:LEU:HD12	26:U:91:LEU:HA	1.88	0.41
1:1:817:G:O6	31:a:77:ARG:HD2	2.21	0.41
1:1:992:U:H4'	1:1:995:G:C2	2.55	0.41
1:1:1549:A:H5''	4:8:43:HIS:HE2	1.86	0.41
1:1:1711:A:H4'	26:U:98:LYS:NZ	2.36	0.41
1:1:2525:G:H1	1:1:2606:U:H3	1.68	0.41
1:1:3096:G:H2'	1:1:3097:U:C6	2.56	0.41
9:D:41:LYS:HD3	9:D:41:LYS:HA	1.86	0.41
10:E:73:LEU:HD11	10:E:83:THR:HG22	2.02	0.41
23:R:140:GLU:HB3	23:R:144:ARG:HH21	1.85	0.41
42:m:463:SER:HB3	42:m:493:LEU:HD11	2.01	0.41
42:m:551:SER:O	42:m:552:SER:C	2.63	0.41
1:1:180:U:H2'	1:1:181:A:C8	2.55	0.41
1:1:590:U:H6	1:1:590:U:OP2	2.03	0.41
1:1:828:U:H2'	1:1:829:U:C6	2.56	0.41
1:1:1359:C:C2'	1:1:1360:C:H5'	2.51	0.41
1:1:1766:C:H2'	1:1:1767:G:C8	2.55	0.41
1:1:3348:U:H2'	1:1:3349:U:O4'	2.20	0.41
5:9:109:U:O2'	9:D:272:GLN:NE2	2.38	0.41
8:C:13:LYS:HE3	8:C:161:PHE:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:89:LYS:HB2	9:D:90:TRP:CE3	2.55	0.41
9:D:156:GLY:HA2	9:D:181:PRO:HD3	2.02	0.41
11:F:96:ILE:HD11	11:F:235:ALA:HB2	2.03	0.41
12:G:185:ARG:O	12:G:188:THR:HG22	2.21	0.41
15:J:30:LEU:HD12	15:J:30:LEU:HA	1.77	0.41
15:J:125:MET:HE2	15:J:126:ASP:N	2.35	0.41
17:L:69:VAL:O	17:L:157:GLN:NE2	2.54	0.41
20:O:7:VAL:HG22	20:O:33:LYS:HD2	2.02	0.41
20:O:175:LYS:HA	20:O:175:LYS:HD3	1.75	0.41
22:Q:21:GLU:CD	22:Q:26:LYS:HZ1	2.28	0.41
23:R:23:TRP:HE3	23:R:51:ILE:HB	1.86	0.41
24:S:86:THR:HG23	25:T:156:TYR:HE1	1.85	0.41
42:m:369:ARG:C	42:m:371:PHE:N	2.76	0.41
42:m:459:PRO:HG3	42:m:537:HIS:O	2.20	0.41
43:n:173:ARG:HG3	43:n:174:SER:N	2.34	0.41
1:1:94:G:H2'	1:1:95:A:C8	2.55	0.41
14:I:210:LEU:HD23	14:I:210:LEU:HA	1.95	0.41
23:R:24:MET:HB3	23:R:32:ILE:HD13	2.02	0.41
24:S:86:THR:C	24:S:87:HIS:CG	2.99	0.41
35:e:73:VAL:HG11	35:e:79:VAL:HG22	2.02	0.41
1:1:144:U:H2'	1:1:145:G:C8	2.56	0.41
1:1:148:C:H2'	1:1:149:G:O4'	2.21	0.41
1:1:443:C:O2'	1:1:444:A:O4'	2.34	0.41
1:1:609:A:O2'	36:f:85:ARG:NH2	2.53	0.41
1:1:702:A:N1	1:1:730:G:O2'	2.50	0.41
1:1:742:A:O2'	1:1:780:C:O2'	2.30	0.41
1:1:943:C:N4	6:A:3:ARG:HD3	2.36	0.41
1:1:1105:U:O2'	32:b:49:GLY:HA3	2.20	0.41
1:1:1176:G:O6	1:1:1189:A:H2	2.03	0.41
1:1:1710:G:OP1	26:U:70:SER:HB3	2.21	0.41
1:1:1751:U:HO2'	1:1:1752:G:P	2.44	0.41
1:1:2244:C:OP2	6:A:240:ARG:NH2	2.53	0.41
1:1:2309:G:N2	1:1:2311:A:H3'	2.36	0.41
1:1:2511:U:H2'	1:1:2512:A:H8	1.86	0.41
1:1:2833:A:OP1	25:T:69:GLN:NE2	2.43	0.41
3:3:30:ASN:OD1	3:3:44:PRO:HB2	2.20	0.41
5:9:89:C:H4'	15:J:44:THR:OG1	2.21	0.41
6:A:116:GLU:HG2	6:A:121:ASP:OD1	2.21	0.41
7:B:73:LEU:HD22	46:u:16:GLY:HA3	2.03	0.41
7:B:323:MET:HE1	7:B:359:ILE:HD13	2.03	0.41
8:C:205:ARG:HH21	8:C:248:ARG:HH12	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:211:LEU:HD12	9:D:223:PHE:HE2	1.86	0.41
14:I:30:LYS:HE3	14:I:30:LYS:HB3	1.92	0.41
17:L:185:TYR:O	17:L:192:ARG:NH2	2.51	0.41
19:N:160:GLU:OE1	19:N:160:GLU:N	2.48	0.41
23:R:132:PHE:CD2	23:R:138:LEU:HD13	2.56	0.41
26:U:95:SER:HB2	26:U:101:TYR:CE1	2.56	0.41
27:V:15:MET:HE2	27:V:15:MET:HB3	1.82	0.41
27:V:134:ASN:N	27:V:134:ASN:HD22	2.19	0.41
37:g:21:ARG:O	37:g:32:TYR:HA	2.20	0.41
42:m:652:ASN:O	43:n:563:MET:HB2	2.20	0.41
46:u:50:ALA:HA	46:u:55:TYR:CE1	2.56	0.41
46:u:55:TYR:CD2	46:u:55:TYR:C	2.99	0.41
1:1:258:U:N3	42:m:236:LEU:HB3	2.36	0.41
1:1:292:A:C2	1:1:314:A:H1'	2.56	0.41
1:1:946:A:C2	6:A:203:MET:HG2	2.55	0.41
1:1:953:A:N3	40:j:4:GLY:HA3	2.36	0.41
1:1:1981:C:H5''	16:K:8:VAL:HG13	2.03	0.41
1:1:3363:C:H2'	1:1:3364:A:C8	2.56	0.41
2:2:117:A:H2'	2:2:118:C:O4'	2.20	0.41
5:9:63:A:OP2	5:9:116:G:N2	2.44	0.41
9:D:246:LYS:HA	9:D:249:GLU:HG2	2.03	0.41
9:D:280:ARG:HH11	9:D:283:ARG:CZ	2.34	0.41
11:F:79:GLU:CD	11:F:81:ASN:HD22	2.29	0.41
11:F:138:GLU:HG2	11:F:236:GLY:HA2	2.03	0.41
11:F:183:TYR:CZ	11:F:204:GLN:HG2	2.56	0.41
12:G:28:VAL:HG22	12:G:29:SER:N	2.36	0.41
13:H:164:ASN:OD1	13:H:165:VAL:N	2.54	0.41
15:J:109:HIS:CE1	15:J:122:ILE:HD12	2.56	0.41
19:N:28:TRP:HA	19:N:31:ARG:HH21	1.86	0.41
26:U:12:TYR:O	26:U:13:ILE:HD13	2.20	0.41
27:V:88:ARG:HB2	27:V:94:TYR:CE2	2.56	0.41
42:m:455:LEU:HB3	42:m:468:VAL:HG13	2.02	0.41
43:n:166:GLU:OE2	43:n:247:PRO:HD2	2.21	0.41
1:1:311:G:H5'	1:1:312:G:C5'	2.48	0.40
1:1:2284:C:H2'	1:1:2330:A:H61	1.85	0.40
1:1:3180:C:H5''	46:u:38:LYS:HD3	2.03	0.40
1:1:3435:U:H1'	1:1:3471:A:C4	2.57	0.40
3:3:61:TYR:HB3	3:3:63:TYR:CE1	2.50	0.40
5:9:113:A:H5'	5:9:114:G:H5''	2.03	0.40
7:B:56:ILE:O	7:B:73:LEU:HD12	2.21	0.40
7:B:121:ASN:HD22	7:B:124:LYS:CE	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:82:GLU:OE1	9:D:108:ARG:NH2	2.45	0.40
10:E:78:ASP:OD1	10:E:78:ASP:C	2.63	0.40
12:G:73:PRO:O	12:G:77:GLN:HG2	2.21	0.40
13:H:72:TYR:HA	13:H:75:ILE:HG22	2.03	0.40
17:L:113:VAL:O	17:L:117:LYS:HG2	2.22	0.40
20:O:169:TYR:CZ	20:O:173:LEU:HD13	2.56	0.40
21:P:75:GLU:OE2	21:P:75:GLU:N	2.41	0.40
23:R:145:ALA:C	23:R:147:ALA:H	2.29	0.40
33:c:22:ASP:N	33:c:22:ASP:OD1	2.54	0.40
42:m:599:TYR:CZ	42:m:606:LEU:HD13	2.55	0.40
42:m:673:CYS:SG	42:m:720:TRP:NE1	2.95	0.40
44:o:11:TYR:HA	44:o:20:HIS:HA	2.03	0.40
1:1:292:A:N6	1:1:2880:A:O4'	2.54	0.40
1:1:680:C:OP2	35:e:24:ARG:HD3	2.21	0.40
1:1:1781:G:H8	1:1:1781:G:OP2	2.04	0.40
1:1:1916:G:H4'	23:R:63:ILE:HD12	2.02	0.40
1:1:1941:A:O4'	1:1:3408:A:H5'	2.20	0.40
1:1:2504:U:H2'	1:1:2505:U:C6	2.57	0.40
1:1:2618:G:N2	6:A:67:HIS:NE2	2.69	0.40
1:1:3234:C:H5''	7:B:274:HIS:O	2.21	0.40
1:1:3430:U:H5''	7:B:308:MET:HE3	2.03	0.40
3:3:86:TYR:O	3:3:87:ALA:C	2.65	0.40
7:B:53:MET:HB2	7:B:76:VAL:O	2.21	0.40
7:B:217:VAL:CG1	7:B:277:GLN:HB3	2.51	0.40
12:G:105:LYS:O	12:G:109:LEU:HD23	2.22	0.40
30:Z:70:PRO:HG3	30:Z:115:LYS:HB2	2.02	0.40
42:m:638:LEU:HD12	42:m:674:SER:HB3	2.02	0.40
42:m:656:HIS:HD2	42:m:660:LEU:HD12	1.87	0.40
43:n:374:ARG:CZ	43:n:377:GLY:HA2	2.51	0.40
1:1:655:C:H2'	1:1:656:A:C8	2.56	0.40
1:1:3203:C:H2'	1:1:3204:G:C8	2.56	0.40
2:2:162:C:H2'	2:2:163:A:H8	1.86	0.40
5:9:60:C:OP2	25:T:26:ARG:NE	2.45	0.40
6:A:241:ARG:HG3	6:A:241:ARG:HH11	1.86	0.40
9:D:52:VAL:HA	9:D:147:ASP:HB3	2.04	0.40
14:I:182:ILE:HD13	14:I:185:ARG:HH22	1.87	0.40
14:I:183:GLU:OE2	14:I:186:SER:OG	2.39	0.40
18:M:64:LYS:HE3	18:M:64:LYS:HB3	1.91	0.40
21:P:32:VAL:HG22	21:P:58:VAL:HG21	2.03	0.40
23:R:35:ALA:HB1	23:R:40:ASN:HB3	2.04	0.40
23:R:109:TYR:HB3	23:R:115:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:89:A:N7	22:Q:172:LYS:NZ	2.69	0.40
1:1:787:G:N2	1:1:804:A:H62	2.20	0.40
1:1:1110:U:O2'	1:1:1112:A:N7	2.51	0.40
1:1:1445:U:H2'	1:1:1446:G:H8	1.87	0.40
1:1:3242:G:H2'	1:1:3243:A:C8	2.56	0.40
22:Q:18:PRO:HD3	22:Q:52:PHE:CD1	2.55	0.40
26:U:16:ALA:HB1	26:U:19:ALA:HB3	2.03	0.40
34:d:33:ARG:HB2	34:d:69:ILE:O	2.22	0.40
42:m:660:LEU:HD21	42:m:663:VAL:HG13	2.03	0.40
46:u:6:CYS:SG	46:u:7:TYR:N	2.94	0.40
1:1:256:C:H2'	1:1:257:A:O4'	2.22	0.40
1:1:379:G:H4'	1:1:404:A:N1	2.36	0.40
1:1:746:C:O2	22:Q:72:ARG:HA	2.22	0.40
1:1:939:G:OP1	1:1:941:G:O2'	2.38	0.40
2:2:132:G:O2'	2:2:134:U:OP2	2.29	0.40
4:8:15:LYS:HG3	4:8:18:ARG:NH2	2.36	0.40
6:A:29:ARG:O	6:A:162:ARG:NH1	2.47	0.40
6:A:50:ASP:HB2	6:A:57:LEU:HG	2.04	0.40
6:A:244:LEU:HD12	6:A:245:LEU:N	2.37	0.40
7:B:232:ARG:HD3	7:B:233:TRP:NE1	2.36	0.40
7:B:374:ALA:O	7:B:378:GLN:HG2	2.21	0.40
10:E:119:PHE:HA	10:E:123:TYR:HD1	1.87	0.40
14:I:191:ILE:HD13	14:I:191:ILE:HA	1.98	0.40
19:N:162:ARG:NH1	19:N:164:LEU:HD11	2.37	0.40
20:O:90:PRO:O	20:O:96:GLY:HA3	2.21	0.40
22:Q:35:LEU:O	22:Q:39:THR:OG1	2.26	0.40
42:m:726:TRP:CD1	42:m:740:THR:HG22	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	117/302 (39%)	102 (87%)	13 (11%)	2 (2%)	7	25
4	8	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
6	A	242/253 (96%)	235 (97%)	7 (3%)	0	100	100
7	B	375/388 (97%)	365 (97%)	10 (3%)	0	100	100
8	C	357/363 (98%)	336 (94%)	20 (6%)	1 (0%)	36	66
9	D	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
10	E	170/195 (87%)	160 (94%)	9 (5%)	1 (1%)	21	51
11	F	212/250 (85%)	209 (99%)	3 (1%)	0	100	100
12	G	229/259 (88%)	219 (96%)	7 (3%)	3 (1%)	9	31
13	H	174/190 (92%)	168 (97%)	6 (3%)	0	100	100
14	I	166/221 (75%)	162 (98%)	4 (2%)	0	100	100
15	J	153/174 (88%)	151 (99%)	2 (1%)	0	100	100
16	K	88/94 (94%)	85 (97%)	3 (3%)	0	100	100
17	L	200/208 (96%)	194 (97%)	4 (2%)	2 (1%)	12	38
18	M	123/134 (92%)	118 (96%)	4 (3%)	1 (1%)	16	44
19	N	198/201 (98%)	184 (93%)	12 (6%)	2 (1%)	12	38
20	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
21	P	167/187 (89%)	161 (96%)	5 (3%)	1 (1%)	21	51
22	Q	184/187 (98%)	173 (94%)	8 (4%)	3 (2%)	7	27
23	R	144/193 (75%)	139 (96%)	4 (3%)	1 (1%)	18	47
24	S	161/176 (92%)	157 (98%)	4 (2%)	0	100	100
25	T	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
26	U	96/117 (82%)	91 (95%)	5 (5%)	0	100	100
27	V	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
28	X	118/141 (84%)	116 (98%)	2 (2%)	0	100	100
29	Y	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
30	Z	132/136 (97%)	123 (93%)	8 (6%)	1 (1%)	16	44
31	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
32	b	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
33	c	93/117 (80%)	91 (98%)	2 (2%)	0	100	100
34	d	100/113 (88%)	95 (95%)	5 (5%)	0	100	100
35	e	115/127 (91%)	114 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	f	104/108 (96%)	97 (93%)	7 (7%)	0	100	100
37	g	104/112 (93%)	99 (95%)	5 (5%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	94/99 (95%)	88 (94%)	6 (6%)	0	100	100
40	j	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
41	k	67/74 (90%)	67 (100%)	0	0	100	100
42	m	384/740 (52%)	361 (94%)	21 (6%)	2 (0%)	24	55
43	n	344/607 (57%)	329 (96%)	15 (4%)	0	100	100
44	o	95/106 (90%)	92 (97%)	3 (3%)	0	100	100
45	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
46	u	57/192 (30%)	55 (96%)	2 (4%)	0	100	100
All	All	6981/8593 (81%)	6717 (96%)	244 (4%)	20 (0%)	37	66

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	G	28	VAL
12	G	227[A]	ASP
12	G	227[B]	ASP
42	m	369	ARG
17	L	47	ALA
19	N	183	SER
22	Q	75	ALA
23	R	124	TYR
3	3	23	GLU
22	Q	73	LYS
22	Q	184	ALA
42	m	372	PRO
3	3	101	PRO
8	C	345	SER
10	E	135	LYS
17	L	3	ILE
30	Z	57	MET
19	N	181	ASN
21	P	126	ARG
18	M	124	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	3	108/271 (40%)	106 (98%)	2 (2%)	50	81
4	8	46/47 (98%)	46 (100%)	0	100	100
6	A	187/192 (97%)	186 (100%)	1 (0%)	81	93
7	B	316/326 (97%)	316 (100%)	0	100	100
8	C	296/297 (100%)	294 (99%)	2 (1%)	76	91
9	D	235/241 (98%)	234 (100%)	1 (0%)	84	94
10	E	139/155 (90%)	137 (99%)	2 (1%)	59	85
11	F	180/210 (86%)	180 (100%)	0	100	100
12	G	192/212 (91%)	192 (100%)	0	100	100
13	H	160/170 (94%)	160 (100%)	0	100	100
14	I	146/187 (78%)	146 (100%)	0	100	100
15	J	134/146 (92%)	133 (99%)	1 (1%)	76	91
16	K	71/75 (95%)	71 (100%)	0	100	100
17	L	162/167 (97%)	162 (100%)	0	100	100
18	M	108/113 (96%)	107 (99%)	1 (1%)	70	89
19	N	175/176 (99%)	175 (100%)	0	100	100
20	O	161/162 (99%)	161 (100%)	0	100	100
21	P	138/149 (93%)	138 (100%)	0	100	100
22	Q	158/159 (99%)	156 (99%)	2 (1%)	61	86
23	R	126/162 (78%)	126 (100%)	0	100	100
24	S	148/154 (96%)	146 (99%)	2 (1%)	59	85
25	T	137/139 (99%)	137 (100%)	0	100	100
26	U	85/103 (82%)	85 (100%)	0	100	100
27	V	105/107 (98%)	105 (100%)	0	100	100
28	X	106/122 (87%)	104 (98%)	2 (2%)	50	81
29	Y	110/111 (99%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Z	113/115 (98%)	113 (100%)	0	100	100
31	a	121/122 (99%)	120 (99%)	1 (1%)	73	90
32	b	47/51 (92%)	46 (98%)	1 (2%)	47	79
33	c	77/91 (85%)	76 (99%)	1 (1%)	61	86
34	d	93/102 (91%)	92 (99%)	1 (1%)	65	87
35	e	100/107 (94%)	99 (99%)	1 (1%)	68	88
36	f	89/91 (98%)	89 (100%)	0	100	100
37	g	92/97 (95%)	91 (99%)	1 (1%)	65	87
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	82/84 (98%)	82 (100%)	0	100	100
40	j	68/71 (96%)	68 (100%)	0	100	100
41	k	63/66 (96%)	63 (100%)	0	100	100
42	m	344/659 (52%)	344 (100%)	0	100	100
43	n	312/532 (59%)	312 (100%)	0	100	100
44	o	87/93 (94%)	86 (99%)	1 (1%)	65	87
46	u	52/168 (31%)	50 (96%)	2 (4%)	29	64
All	All	5775/6909 (84%)	5750 (100%)	25 (0%)	81	94

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	25	GLN
3	3	39	ASN
6	A	245	LEU
8	C	215	THR
8	C	344	ASN
9	D	163	MET
10	E	48	LEU
10	E	173	ASN
15	J	19	LEU
18	M	114	MET
22	Q	128	LEU
22	Q	130	LEU
24	S	28	LEU
24	S	89	MET
28	X	133	ASP

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Mol	Chain	Res	Type
28	X	136	ASN
31	a	120	THR
32	b	54	ILE
33	c	32	MET
34	d	51	THR
35	e	75	ASN
37	g	14	ASN
44	o	47	GLN
46	u	10	SER
46	u	13	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	25	GLN
3	3	26	ASN
3	3	104	GLN
4	8	36	HIS
6	A	215	HIS
6	A	220	HIS
7	B	259	ASN
8	C	272	GLN
8	C	286	ASN
8	C	314	HIS
8	C	323	ASN
8	C	344	ASN
9	D	178	ASN
9	D	272	GLN
11	F	69	GLN
11	F	100	ASN
11	F	166	GLN
11	F	193	HIS
11	F	204	GLN
12	G	95	ASN
13	H	49	GLN
13	H	102	ASN
13	H	158	ASN
14	I	133	GLN
15	J	20	ASN
15	J	43	GLN
15	J	161	ASN
16	K	45	ASN

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Mol	Chain	Res	Type
19	N	153	ASN
20	O	190	GLN
23	R	39	GLN
23	R	130	ASN
25	T	24	GLN
25	T	54	HIS
27	V	83	GLN
28	X	67	ASN
28	X	110	ASN
30	Z	31	GLN
30	Z	78	ASN
30	Z	91	ASN
31	a	102	ASN
37	g	29	ASN
39	i	93	GLN
40	j	12	HIS
40	j	76	ASN
41	k	10	GLN
42	m	453	GLN
42	m	712	ASN
43	n	21	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2837/3498 (81%)	600 (21%)	19 (0%)
2	2	150/165 (90%)	24 (16%)	2 (1%)
5	9	117/229 (51%)	14 (11%)	0
All	All	3104/3892 (79%)	638 (20%)	21 (0%)

All (638) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	26	A
1	1	28	G
1	1	30	G
1	1	40	A
1	1	43	A
1	1	49	A
1	1	57	A
1	1	59	G

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Mol	Chain	Res	Type
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	91	G
1	1	92	G
1	1	96	G
1	1	99	A
1	1	105	G
1	1	110	G
1	1	111	C
1	1	121	A
1	1	122	A
1	1	132	C
1	1	149	G
1	1	161	C
1	1	162	A
1	1	163	A
1	1	165	A
1	1	167	G
1	1	168	C
1	1	169	U
1	1	170	G
1	1	175	G
1	1	177	G
1	1	180	U
1	1	188	C
1	1	189	G
1	1	190	G
1	1	193	U
1	1	195	A
1	1	197	U
1	1	198	U
1	1	213	G
1	1	217	G
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	240	G
1	1	243	C
1	1	244	G

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Mol	Chain	Res	Type
1	1	247	U
1	1	253	U
1	1	257	A
1	1	258	U
1	1	259	A
1	1	260	U
1	1	261	A
1	1	266	G
1	1	269	U
1	1	270	U
1	1	277	G
1	1	289	G
1	1	292	A
1	1	293	A
1	1	303	A
1	1	310	U
1	1	311	G
1	1	312	G
1	1	313	U
1	1	319	U
1	1	321	A
1	1	331	A
1	1	337	U
1	1	345	G
1	1	347	C
1	1	350	A
1	1	357	A
1	1	359	A
1	1	360	A
1	1	377	A
1	1	378	U
1	1	382	A
1	1	384	G
1	1	403	A
1	1	405	A
1	1	406	U
1	1	410	A
1	1	411	C
1	1	415	A
1	1	429	G
1	1	430	A
1	1	437	G

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Mol	Chain	Res	Type
1	1	449	U
1	1	532	A
1	1	534	A
1	1	535	G
1	1	540	A
1	1	544	A
1	1	546	G
1	1	547	G
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	590	U
1	1	591	G
1	1	592	U
1	1	602	A
1	1	603	C
1	1	606	G
1	1	616	A
1	1	618	U
1	1	629	G
1	1	634	G
1	1	635	G
1	1	636	A
1	1	646	A
1	1	647	A
1	1	661	C
1	1	673	C
1	1	674	A
1	1	685	A
1	1	702	A
1	1	706	U
1	1	713	G
1	1	714	A
1	1	732	A
1	1	739	G
1	1	742	A
1	1	747	A
1	1	748	G

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Mol	Chain	Res	Type
1	1	749	G
1	1	765	G
1	1	766	G
1	1	768	G
1	1	769	U
1	1	771	C
1	1	774	C
1	1	775	A
1	1	778	G
1	1	788	G
1	1	789	A
1	1	792	U
1	1	794	U
1	1	795	G
1	1	796	U
1	1	797	C
1	1	798	A
1	1	802	G
1	1	803	A
1	1	806	G
1	1	808	U
1	1	809	U
1	1	812	A
1	1	813	G
1	1	816	A
1	1	817	G
1	1	839	A
1	1	847	G
1	1	849	A
1	1	862	A
1	1	877	G
1	1	878	A
1	1	879	A
1	1	882	U
1	1	889	G
1	1	893	C
1	1	902	A
1	1	903	U
1	1	906	U
1	1	911	U
1	1	916	A
1	1	939	G

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Mol	Chain	Res	Type
1	1	940	G
1	1	946	A
1	1	948	G
1	1	949	A
1	1	953	A
1	1	955	C
1	1	956	G
1	1	957	A
1	1	969	G
1	1	976	C
1	1	985	G
1	1	991	C
1	1	992	U
1	1	993	C
1	1	995	G
1	1	1006	A
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1014	C
1	1	1016	G
1	1	1023	G
1	1	1026	G
1	1	1033	G
1	1	1034	A
1	1	1042	G
1	1	1046	U
1	1	1069	C
1	1	1073	U
1	1	1079	A
1	1	1080	A
1	1	1081	C
1	1	1095	G
1	1	1096	A
1	1	1097	C
1	1	1112	A
1	1	1113	U
1	1	1119	G
1	1	1126	A
1	1	1127	U
1	1	1129	G
1	1	1130	A

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Mol	Chain	Res	Type
1	1	1135	G
1	1	1147	G
1	1	1148	G
1	1	1162	G
1	1	1166	A
1	1	1175	U
1	1	1176	G
1	1	1184	A
1	1	1185	A
1	1	1186	C
1	1	1190	A
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1217	G
1	1	1220	C
1	1	1222	U
1	1	1223	C
1	1	1224	A
1	1	1227	C
1	1	1228	A
1	1	1231	A
1	1	1232	G
1	1	1233	A
1	1	1239	U
1	1	1240	G
1	1	1322	A
1	1	1323	C
1	1	1333	A
1	1	1334	A
1	1	1336	U
1	1	1338	G
1	1	1339	A
1	1	1340	U
1	1	1360	C
1	1	1361	A
1	1	1380	A
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1421	G
1	1	1433	U

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Mol	Chain	Res	Type
1	1	1453	A
1	1	1459	U
1	1	1463	G
1	1	1468	G
1	1	1470	U
1	1	1471	C
1	1	1484	G
1	1	1487	A
1	1	1492	U
1	1	1503	C
1	1	1504	U
1	1	1515	A
1	1	1517	G
1	1	1521	G
1	1	1528	U
1	1	1536	G
1	1	1537	A
1	1	1542	C
1	1	1565	C
1	1	1571	A
1	1	1581	G
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1594	G
1	1	1600	C
1	1	1602	A
1	1	1603	U
1	1	1604	U
1	1	1606	U
1	1	1608	C
1	1	1609	G
1	1	1618	A
1	1	1622	A
1	1	1624	A
1	1	1625	G
1	1	1629	A
1	1	1640	A
1	1	1655	G
1	1	1664	A
1	1	1666	C
1	1	1674	C

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Mol	Chain	Res	Type
1	1	1677	A
1	1	1678	A
1	1	1693	G
1	1	1697	G
1	1	1713	G
1	1	1723	U
1	1	1724	U
1	1	1728	U
1	1	1730	U
1	1	1738	C
1	1	1747	A
1	1	1752	G
1	1	1754	A
1	1	1756	U
1	1	1757	C
1	1	1764	U
1	1	1780	G
1	1	1781	G
1	1	1786	U
1	1	1790	A
1	1	1791	G
1	1	1792	A
1	1	1796	C
1	1	1811	A
1	1	1819	G
1	1	1821	G
1	1	1837	G
1	1	1838	A
1	1	1839	A
1	1	1849	G
1	1	1871	U
1	1	1873	U
1	1	1874	U
1	1	1876	U
1	1	1879	C
1	1	1880	A
1	1	1897	A
1	1	1901	C
1	1	1904	C
1	1	1905	A
1	1	1913	A
1	1	1919	A

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Mol	Chain	Res	Type
1	1	1921	C
1	1	1933	G
1	1	1934	A
1	1	1935	U
1	1	1936	A
1	1	1940	C
1	1	1941	A
1	1	1948	A
1	1	1960	G
1	1	1961	G
1	1	1963	A
1	1	1990	G
1	1	1999	U
1	1	2001	A
1	1	2188	A
1	1	2189	C
1	1	2190	U
1	1	2192	A
1	1	2193	G
1	1	2194	A
1	1	2195	A
1	1	2199	G
1	1	2200	U
1	1	2202	C
1	1	2203	G
1	1	2204	G
1	1	2209	G
1	1	2210	G
1	1	2214	A
1	1	2215	U
1	1	2219	A
1	1	2228	U
1	1	2232	A
1	1	2246	A
1	1	2247	U
1	1	2248	G
1	1	2257	G
1	1	2280	C
1	1	2298	G
1	1	2311	A
1	1	2313	U
1	1	2323	C

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Mol	Chain	Res	Type
1	1	2360	G
1	1	2361	G
1	1	2364	G
1	1	2369	A
1	1	2371	G
1	1	2386	U
1	1	2395	G
1	1	2396	C
1	1	2397	A
1	1	2398	U
1	1	2401	A
1	1	2403	G
1	1	2406	U
1	1	2422	U
1	1	2423	G
1	1	2435	U
1	1	2453	C
1	1	2461	A
1	1	2462	C
1	1	2463	G
1	1	2464	G
1	1	2473	A
1	1	2477	C
1	1	2481	G
1	1	2482	G
1	1	2485	A
1	1	2486	A
1	1	2489	A
1	1	2490	A
1	1	2491	G
1	1	2492	A
1	1	2499	U
1	1	2507	A
1	1	2508	C
1	1	2523	G
1	1	2524	U
1	1	2526	A
1	1	2605	U
1	1	2610	U
1	1	2611	A
1	1	2620	A
1	1	2621	G

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Mol	Chain	Res	Type
1	1	2622	C
1	1	2647	U
1	1	2649	U
1	1	2650	A
1	1	2651	G
1	1	2654	U
1	1	2656	A
1	1	2657	A
1	1	2658	A
1	1	2668	C
1	1	2669	G
1	1	2670	A
1	1	2674	G
1	1	2675	A
1	1	2676	U
1	1	2680	C
1	1	2681	G
1	1	2686	U
1	1	2688	A
1	1	2689	C
1	1	2692	U
1	1	2696	A
1	1	2701	G
1	1	2709	G
1	1	2721	A
1	1	2722	C
1	1	2723	A
1	1	2730	A
1	1	2733	A
1	1	2746	G
1	1	2747	U
1	1	2751	A
1	1	2768	A
1	1	2769	A
1	1	2777	C
1	1	2778	U
1	1	2780	G
1	1	2781	A
1	1	2784	A
1	1	2786	A
1	1	2787	A
1	1	2789	A

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Mol	Chain	Res	Type
1	1	2799	A
1	1	2800	A
1	1	2809	G
1	1	2815	G
1	1	2823	G
1	1	2824	U
1	1	2832	C
1	1	2835	A
1	1	2847	U
1	1	2848	G
1	1	2850	C
1	1	2866	U
1	1	2867	C
1	1	2872	G
1	1	2873	A
1	1	2875	A
1	1	2889	G
1	1	2894	A
1	1	2895	G
1	1	2896	A
1	1	2897	A
1	1	2905	C
1	1	2908	A
1	1	2909	G
1	1	2912	A
1	1	2917	U
1	1	2918	G
1	1	2930	C
1	1	2932	A
1	1	2933	A
1	1	2948	G
1	1	2949	U
1	1	2966	G
1	1	2970	U
1	1	2971	C
1	1	2982	A
1	1	2991	A
1	1	3002	G
1	1	3006	A
1	1	3018	U
1	1	3021	A
1	1	3025	A

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Mol	Chain	Res	Type
1	1	3030	U
1	1	3031	A
1	1	3033	G
1	1	3037	C
1	1	3041	A
1	1	3042	G
1	1	3046	G
1	1	3050	U
1	1	3066	A
1	1	3067	G
1	1	3072	G
1	1	3075	U
1	1	3078	C
1	1	3084	U
1	1	3085	G
1	1	3108	A
1	1	3117	A
1	1	3118	G
1	1	3127	G
1	1	3135	G
1	1	3155	G
1	1	3173	A
1	1	3175	U
1	1	3182	G
1	1	3189	C
1	1	3195	C
1	1	3196	C
1	1	3197	G
1	1	3220	G
1	1	3221	C
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3237	A
1	1	3238	A
1	1	3239	A
1	1	3248	U
1	1	3269	A
1	1	3270	U
1	1	3271	G
1	1	3272	U
1	1	3273	A

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Mol	Chain	Res	Type
1	1	3275	A
1	1	3276	A
1	1	3281	A
1	1	3282	G
1	1	3283	A
1	1	3301	C
1	1	3307	U
1	1	3310	A
1	1	3313	G
1	1	3316	G
1	1	3318	A
1	1	3319	G
1	1	3328	U
1	1	3329	G
1	1	3343	A
1	1	3345	G
1	1	3347	G
1	1	3356	A
1	1	3358	U
1	1	3359	U
1	1	3360	G
1	1	3369	A
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3396	A
1	1	3404	G
1	1	3405	C
1	1	3414	U
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3435	U
1	1	3442	U
1	1	3443	A
1	1	3446	G
1	1	3470	G
1	1	3479	C
1	1	3482	U
1	1	3483	U
1	1	3484	G
1	1	3490	A

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Mol	Chain	Res	Type
1	1	3491	A
1	1	3492	G
1	1	3494	U
1	1	3497	G
2	2	9	A
2	2	42	U
2	2	43	C
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	87	A
2	2	98	U
2	2	103	G
2	2	112	A
2	2	114	C
2	2	115	G
2	2	119	A
2	2	120	U
2	2	121	U
2	2	124	G
2	2	132	G
2	2	135	C
2	2	136	U
2	2	156	G
2	2	159	U
2	2	160	G
2	2	162	C
5	9	57	G
5	9	72	A
5	9	92	A
5	9	100	A
5	9	103	U
5	9	104	A
5	9	114	G
5	9	119	U
5	9	122	U
5	9	124	A
5	9	132	G
5	9	141	C
5	9	150	A
5	9	160	G

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	269	U
1	1	310	U
1	1	311	G
1	1	628	U
1	1	672	A
1	1	770	G
1	1	805	G
1	1	948	G
1	1	1096	A
1	1	1238	G
1	1	1388	G
1	1	1628	A
1	1	1751	U
1	1	2198	G
1	1	2657	A
1	1	2673	U
1	1	3174	A
1	1	3358	U
1	1	3441	G
2	2	8	A
2	2	131	G

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

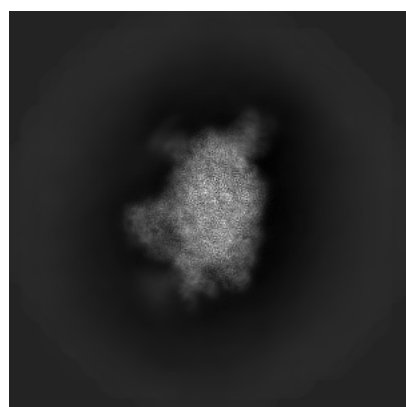
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24412. These allow visual inspection of the internal detail of the map and identification of artifacts.

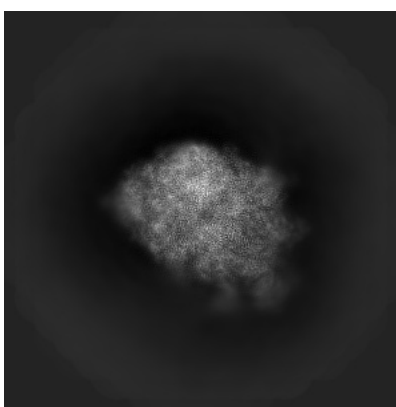
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

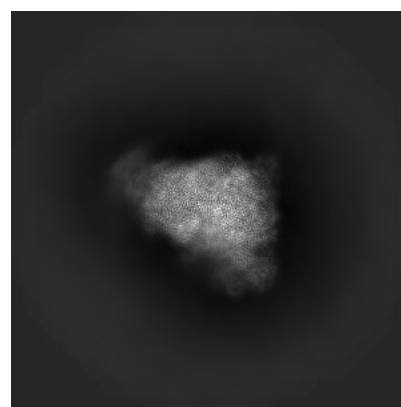
6.1.1 Primary map



X



Y

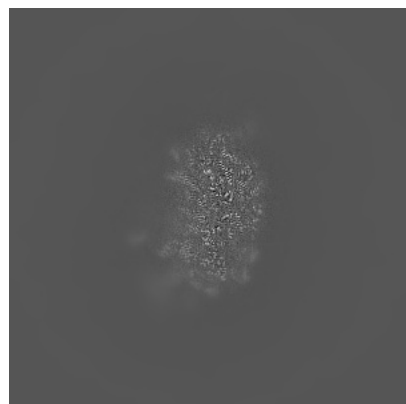


Z

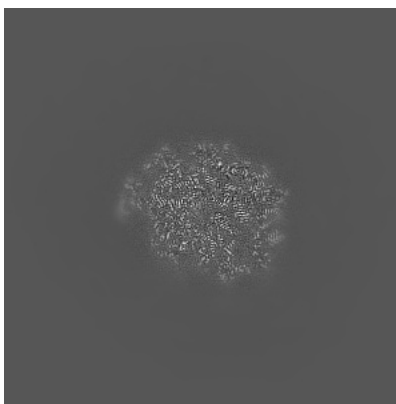
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

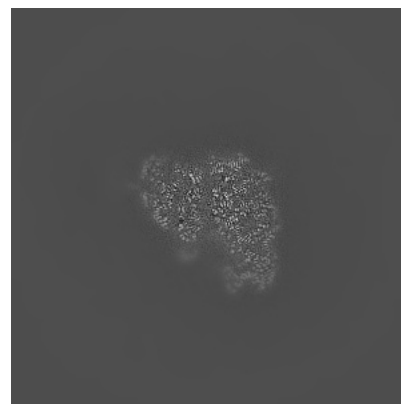
6.2.1 Primary map



X Index: 256



Y Index: 256

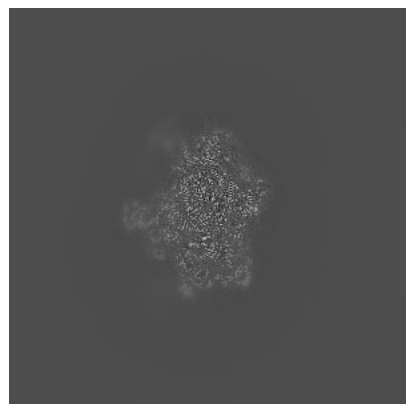


Z Index: 256

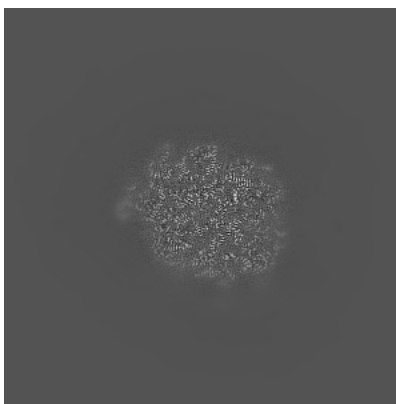
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

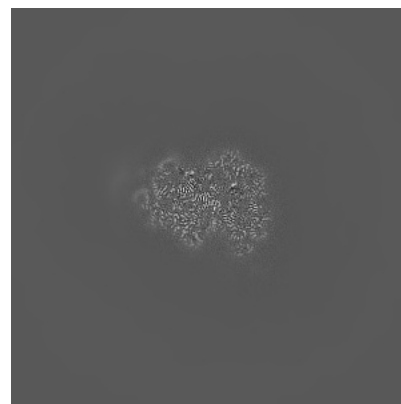
6.3.1 Primary map



X Index: 283



Y Index: 263

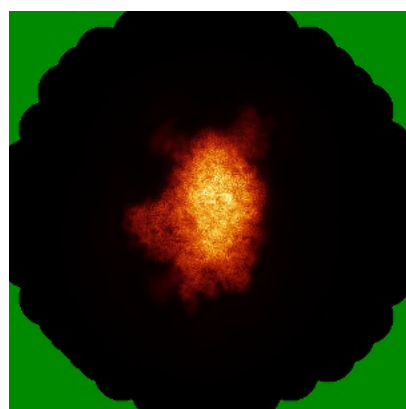


Z Index: 276

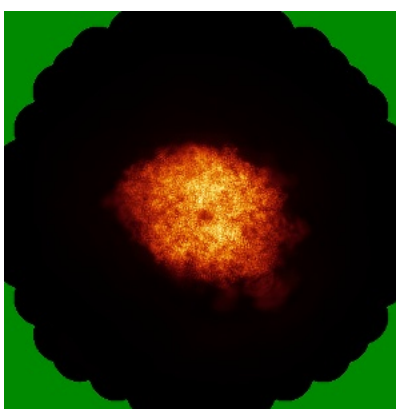
The images above show the largest variance slices of the map in three orthogonal directions.

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

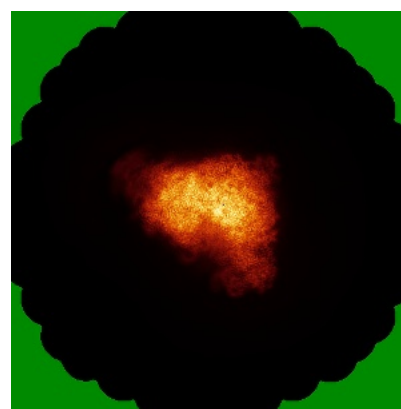
6.4.1 Primary map



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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

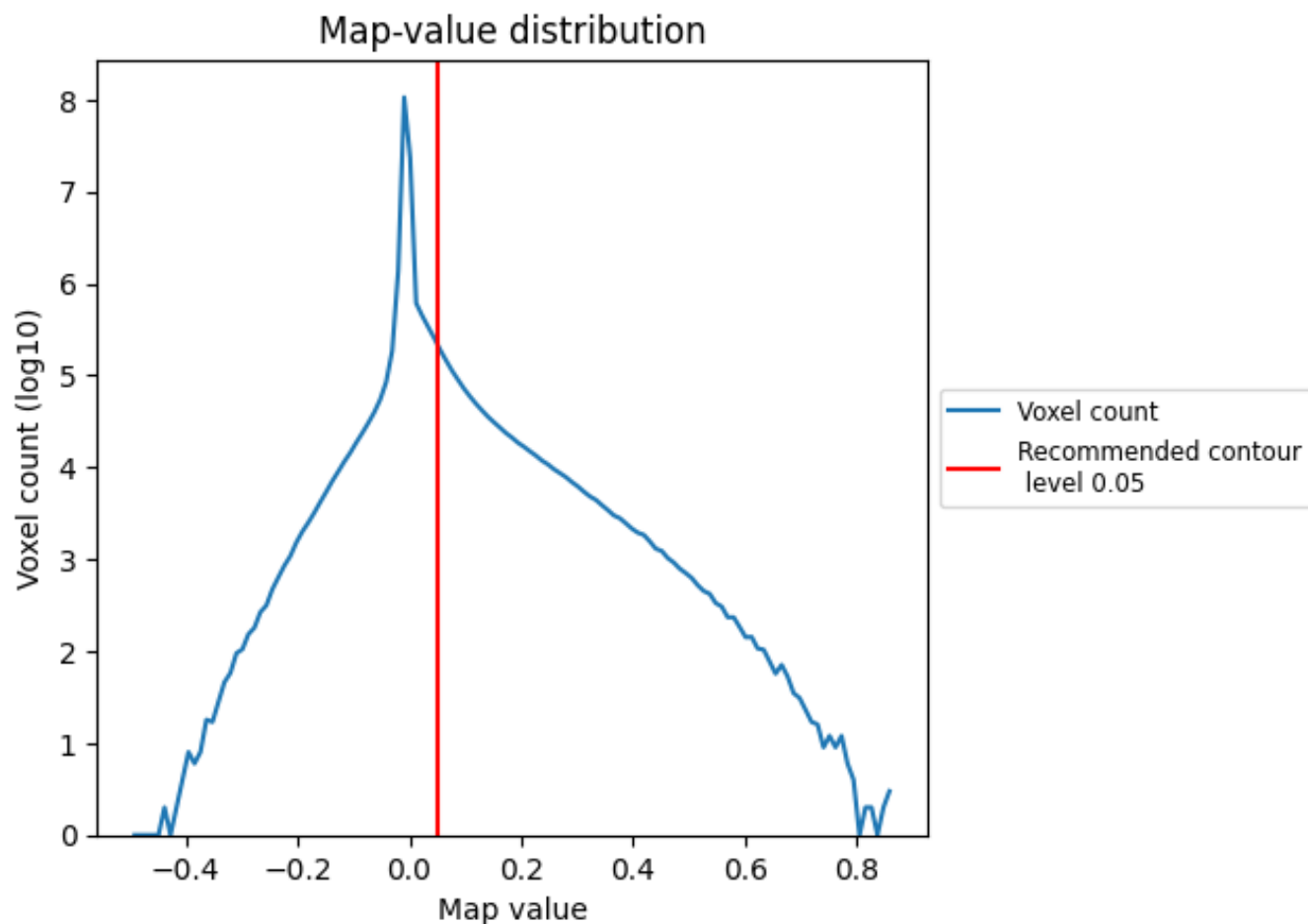
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

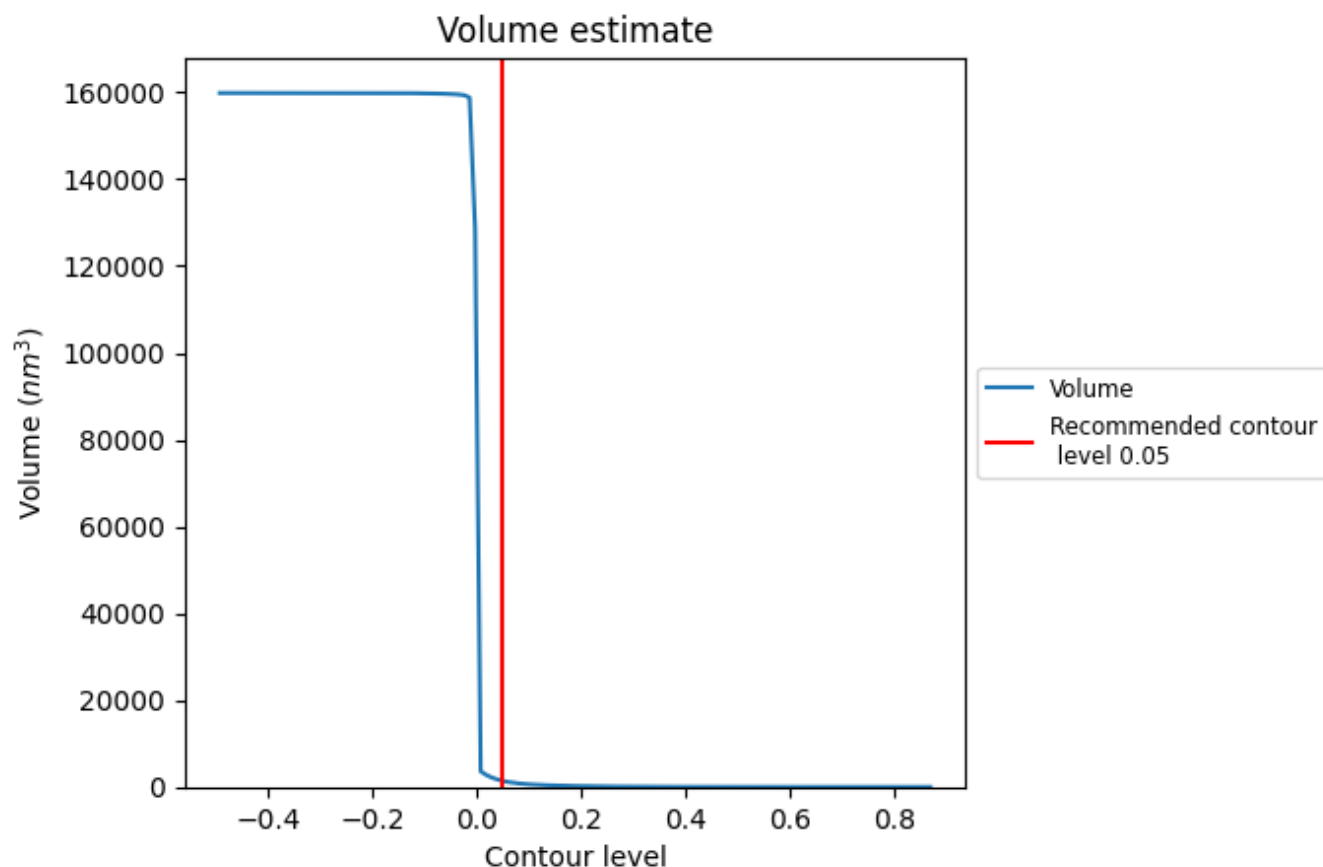
This section contains the results of statistical analysis of the map.

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.

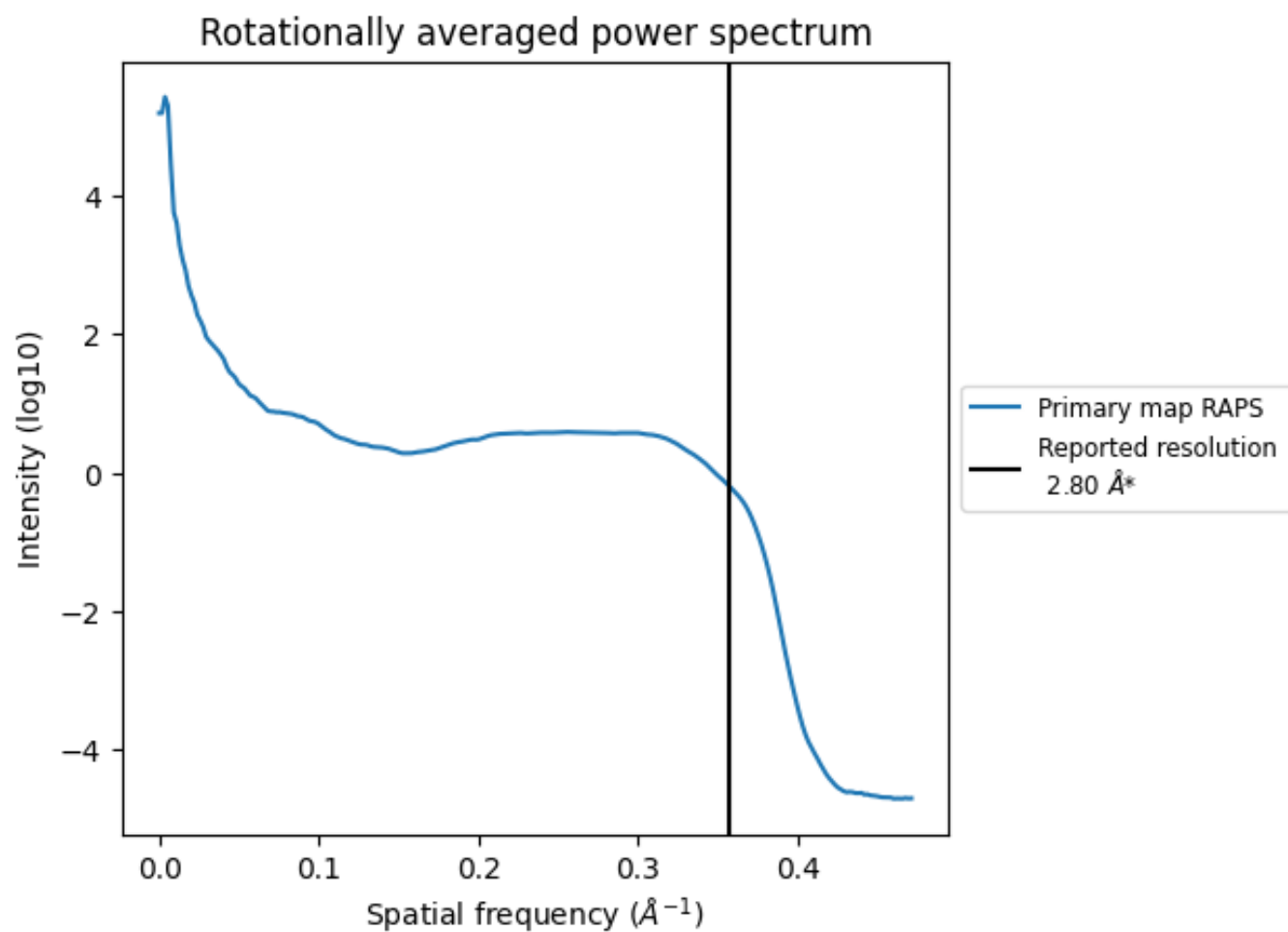
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1408 nm^3 ; this corresponds to an approximate mass of 1272 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 0.357 Å⁻¹

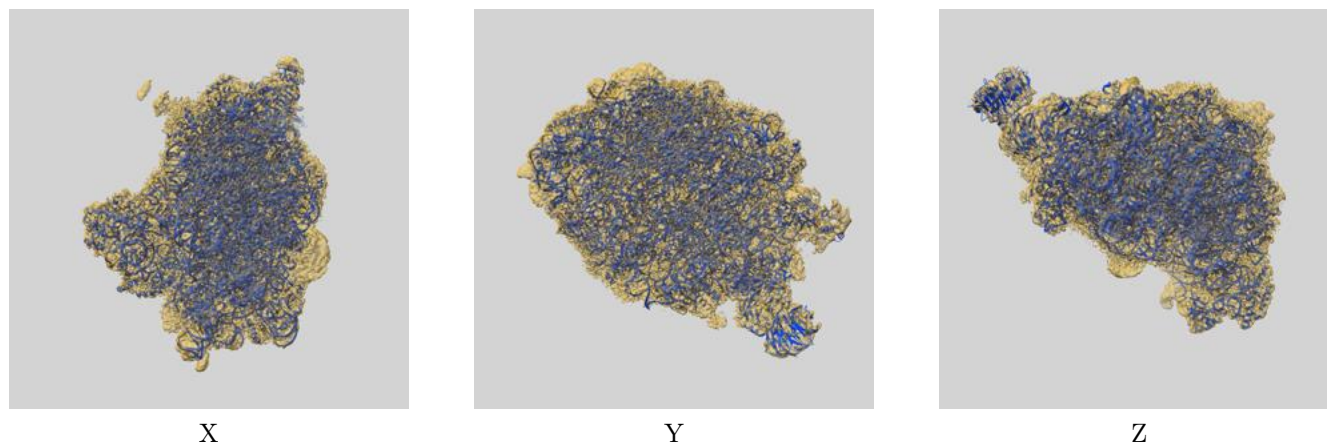
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

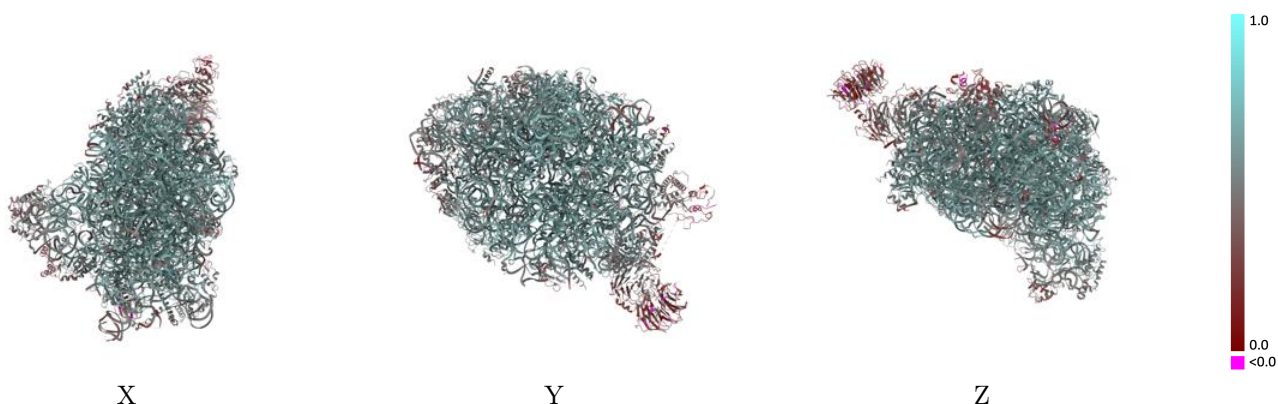
This section contains information regarding the fit between EMDB map EMD-24412 and PDB model 8EUG. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



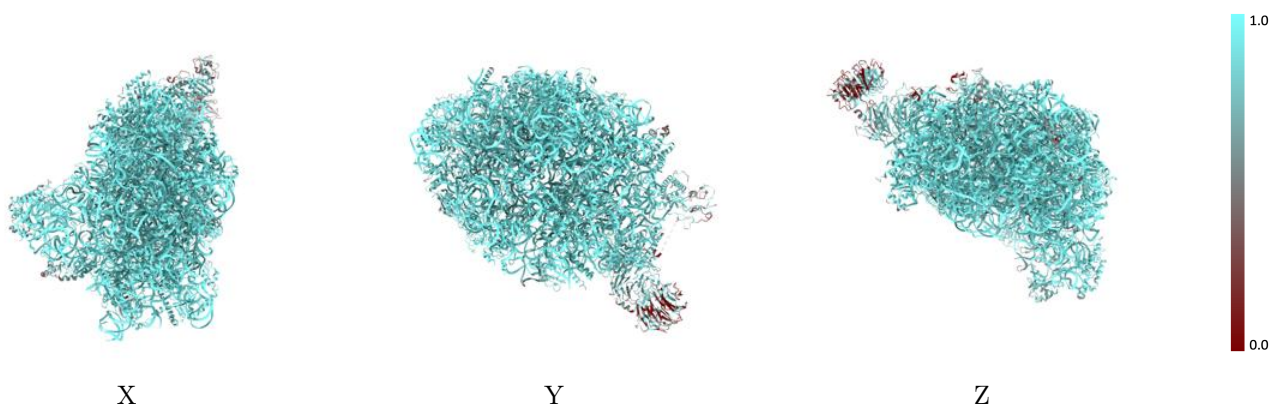
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



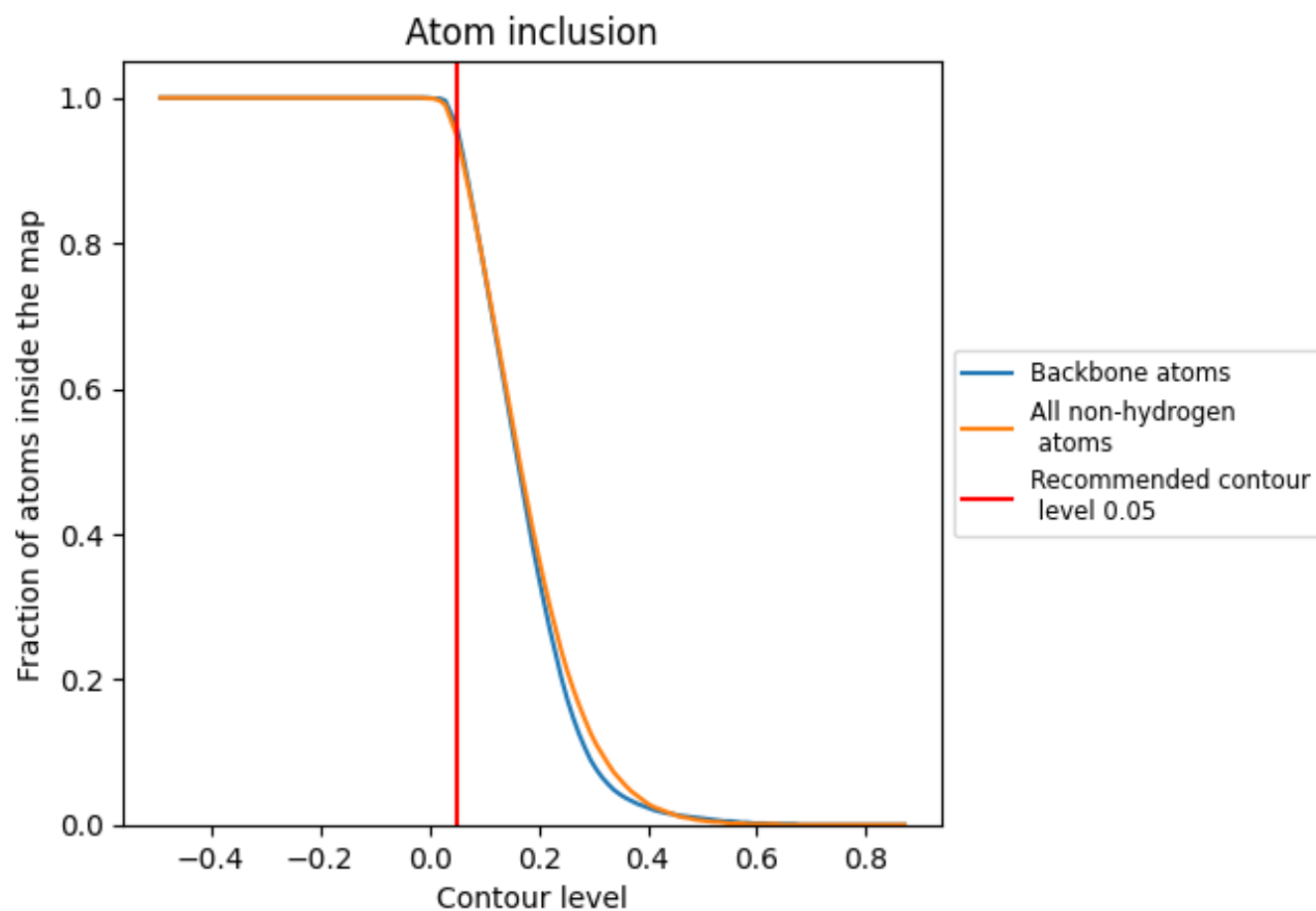
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.5670
1	 0.9860	 0.5950
2	 0.9910	 0.6210
3	 0.8360	 0.4530
8	 0.9900	 0.6190
9	 0.9920	 0.5370
A	 0.9820	 0.6130
B	 0.9730	 0.5920
C	 0.9740	 0.6030
D	 0.8880	 0.4980
E	 0.9280	 0.5250
F	 0.9620	 0.5920
G	 0.8950	 0.5310
H	 0.7750	 0.3480
I	 0.8450	 0.4870
J	 0.7800	 0.3820
K	 0.9580	 0.6010
L	 0.9580	 0.6030
M	 0.9490	 0.5140
N	 0.9890	 0.6350
O	 0.9620	 0.5810
P	 0.9500	 0.5850
Q	 0.9800	 0.6020
R	 0.9610	 0.5850
S	 0.9580	 0.5600
T	 0.9530	 0.5770
U	 0.7950	 0.4340
V	 0.9660	 0.5790
X	 0.9690	 0.6000
Y	 0.9710	 0.5930
Z	 0.9320	 0.5370
a	 0.9660	 0.6130
b	 0.9480	 0.5460
c	 0.8940	 0.5330
d	 0.9300	 0.5790



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Chain	Atom inclusion	Q-score
e	 0.9820	 0.6130
f	 0.9820	 0.6060
g	 0.9660	 0.6040
h	 0.9590	 0.5880
i	 0.9540	 0.5710
j	 0.9910	 0.6440
k	 0.8850	 0.5210
m	 0.7330	 0.3910
n	 0.7600	 0.4050
o	 0.9390	 0.5650
p	 0.4400	 0.2640
u	 0.9470	 0.5350