



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 08:03 PM JST

PDB ID : 8ZFI / pdb_00008zfi
EMDB ID : EMD-60061
Title : Structure of E.coli ribosome in complex with an engineered arrest peptide and trigger factor
Authors : Sriramoju, M.K.; Ko, T.P.; Draczkowski, P.; Hsu, S.T.D.
Deposited on : 2024-05-07
Resolution : 2.90 Å(reported)
Based on initial model : 3JBU

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

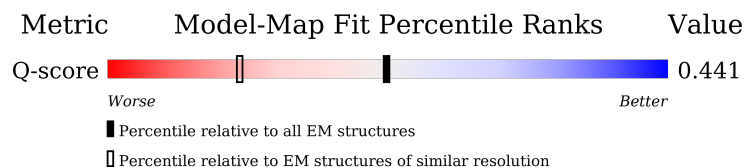
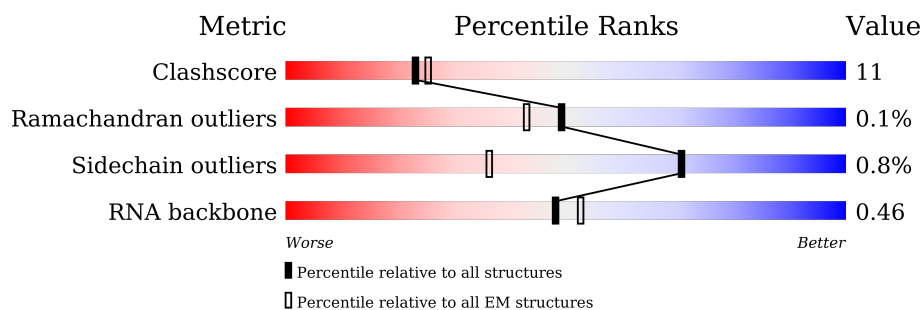
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



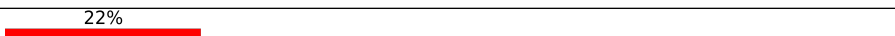
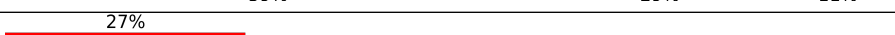
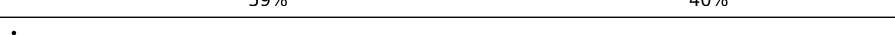
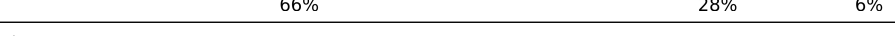
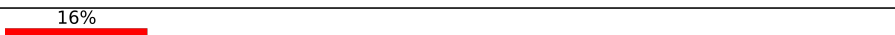
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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

Mol	Chain	Length	Quality of chain
1	0	78	
2	1	63	
3	2	59	

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Mol	Chain	Length	Quality of chain
4	4	57	
5	5	55	
6	6	46	
7	7	65	
8	8	38	
9	A	1533	
10	B	241	
11	C	233	
12	D	206	
13	E	167	
14	F	135	
15	G	179	
16	H	130	
17	I	130	
18	J	103	
19	K	129	
20	L	124	
21	M	118	
22	N	101	
23	O	89	
24	P	82	
25	Q	84	
26	R	75	
27	S	92	
28	T	87	

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Mol	Chain	Length	Quality of chain
29	U	71	
30	X	76	
31	Y	77	
31	Z	77	
32	a	120	
33	b	2904	
34	c	273	
35	d	209	
36	e	201	
37	f	179	
38	g	177	
39	h	149	
40	k	142	
41	l	123	
42	m	144	
43	n	136	
44	o	127	
45	p	117	
46	q	115	
47	r	118	
48	s	103	
49	t	110	
50	u	100	
51	v	104	
52	w	94	

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Mol	Chain	Length	Quality of chain
53	x	14	
54	y	85	
55	z	49	
56	V	432	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	PRO	Z	163	-	-	X	-

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148019 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 10 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 11 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	207	Total	C	N	O	S	0	0
			1632	1034	306	289	3		

- Molecule 12 is a protein called 30S ribosomal protein S4.

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

- Molecule 13 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 14 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 15 is a protein called 30S ribosomal protein S7.

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

- Molecule 16 is a protein called 30S ribosomal protein S8.

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

- Molecule 17 is a protein called 30S ribosomal protein S9.

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

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 21 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 22 is a protein called 30S ribosomal protein S14.

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

- Molecule 23 is a protein called 30S ribosomal protein S15.

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

- Molecule 24 is a protein called 30S ribosomal protein S16.

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

- Molecule 25 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 26 is a protein called 30S ribosomal protein S18.

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

- Molecule 27 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 28 is a protein called 30S ribosomal protein S20.

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

- Molecule 29 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	64	Total	C	N	O	S	0	0
			529	329	110	89	1		

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

- Molecule 31 is a RNA chain called P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		
31	Z	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 32 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	120	Total	C	N	O	P	0	0
			2568	1144	468	837	119		

- Molecule 33 is a RNA chain called RNA (2903-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 34 is a protein called 50S ribosomal protein L2.

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

- Molecule 35 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 36 is a protein called 50S ribosomal protein L4.

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

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 38 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 39 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 40 is a protein called 50S ribosomal protein L13.

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

- Molecule 41 is a protein called 50S ribosomal protein L14.

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

- Molecule 42 is a protein called 50S ribosomal protein L15.

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

- Molecule 43 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 44 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 45 is a protein called 50S ribosomal protein L18.

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

- Molecule 46 is a protein called 50S ribosomal protein L19.

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

- Molecule 47 is a protein called 50S ribosomal protein L20.

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

- Molecule 48 is a protein called 50S ribosomal protein L21.

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

- Molecule 49 is a protein called 50S ribosomal protein L22.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	100	Total	C	N	O	S	0	0
			786	496	146	142	2		

- Molecule 51 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 52 is a protein called 50S ribosomal protein L25.

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

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	14	Total	C	N	O	P	0	0
			299	133	55	97	14		

- Molecule 54 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 55 is a protein called eRAP-NC.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	39	Total	C	N	O	S	8	0
			398	260	72	64	2		

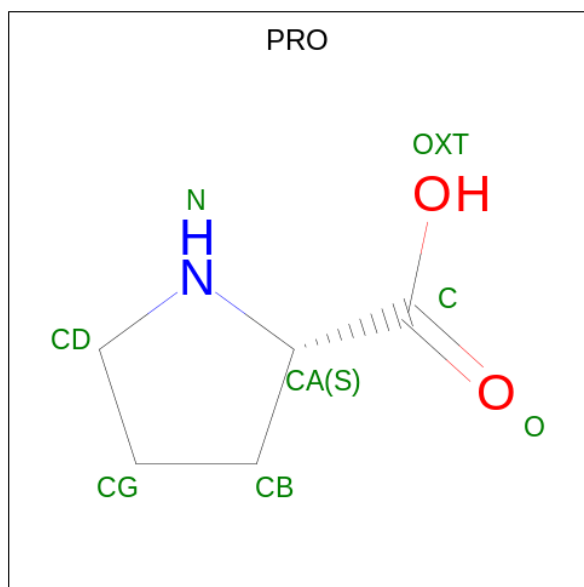
- Molecule 56 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	V	59	Total	C	N	O	S	0	0
			454	284	84	84	2		

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	8	1	Total	Zn	0
			1	1	

- Molecule 58 is PROLINE (CCD ID: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms				AltConf
58	Z	1	Total	C	N	O	0
			7	5	1	1	

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L28

Chain 0: 



- Molecule 2: 50S ribosomal protein L29

Chain 1: 



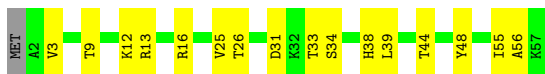
- Molecule 3: 50S ribosomal protein L30

Chain 2: 



- Molecule 4: 50S ribosomal protein L32

Chain 4: 



- Molecule 5: 50S ribosomal protein L33

Chain 5: 



- Molecule 6: 50S ribosomal protein L34

Chain 6:  85% 15%



- Molecule 7: 50S ribosomal protein L35

Chain 7:  78% 20%



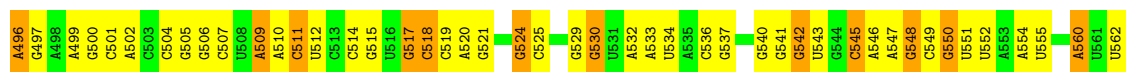
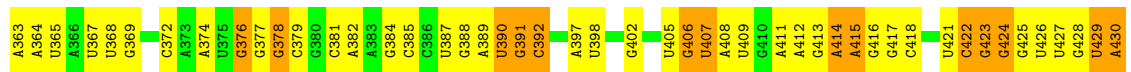
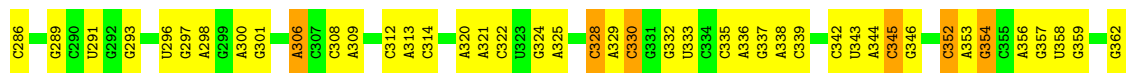
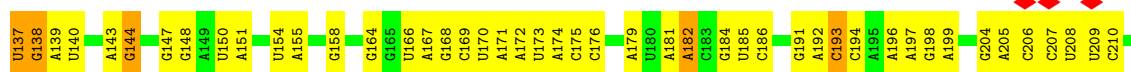
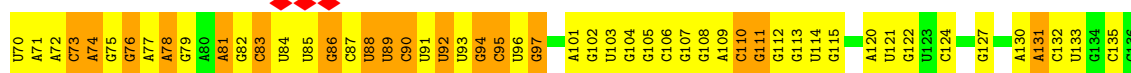
- Molecule 8: 50S ribosomal protein L36

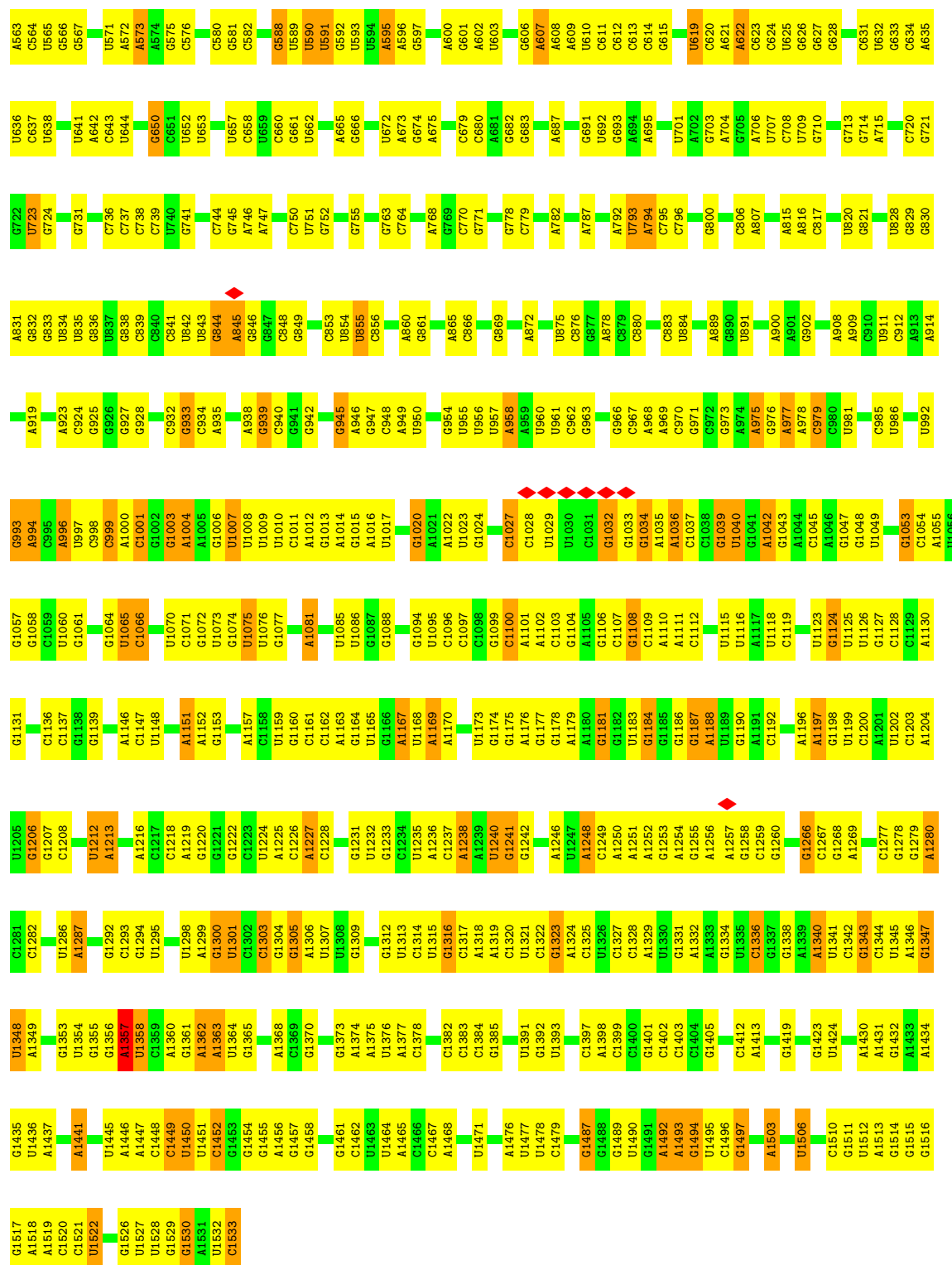
Chain 8:  82% 18%



- Molecule 9: 16S rRNA

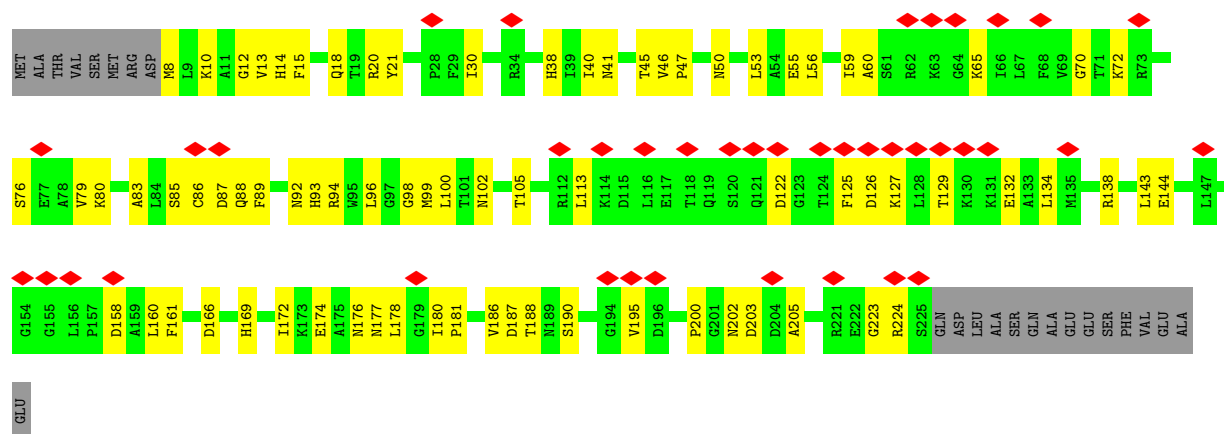
Chain A:  39% 49% 12%



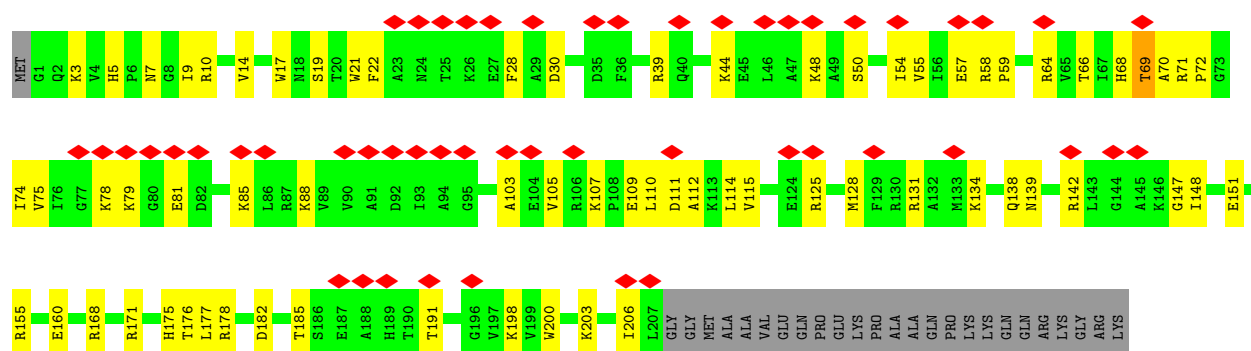


- Molecule 10: 30S ribosomal protein S2

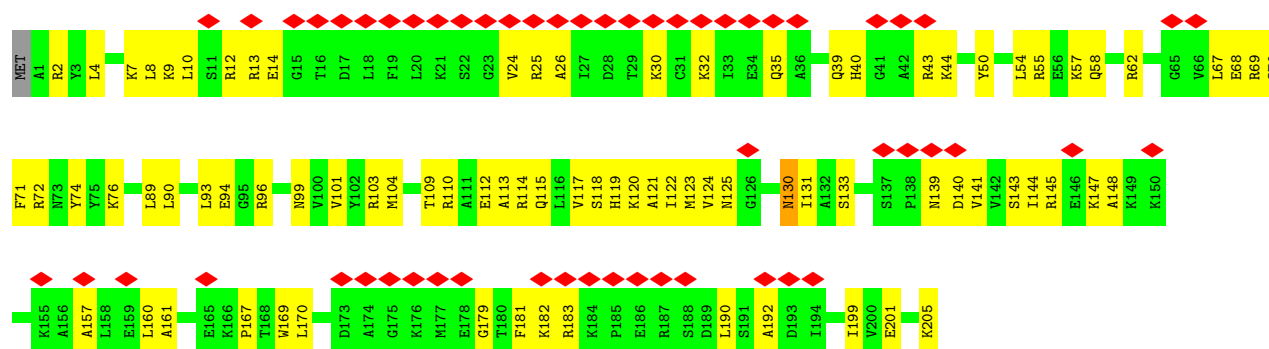




• Molecule 11: 30S ribosomal protein S3

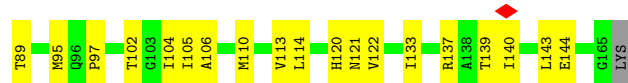


• Molecule 12: 30S ribosomal protein S4

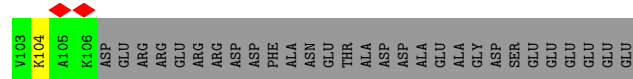


• Molecule 13: 30S ribosomal protein S5





- Molecule 14: 30S ribosomal protein S6, fully modified isoform



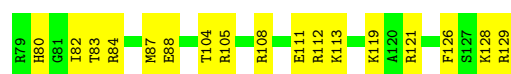
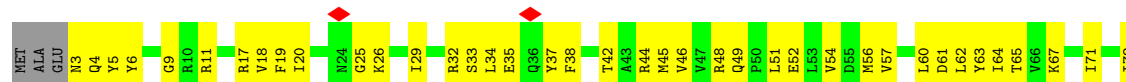
- Molecule 15: 30S ribosomal protein S7



- Molecule 16: 30S ribosomal protein S8

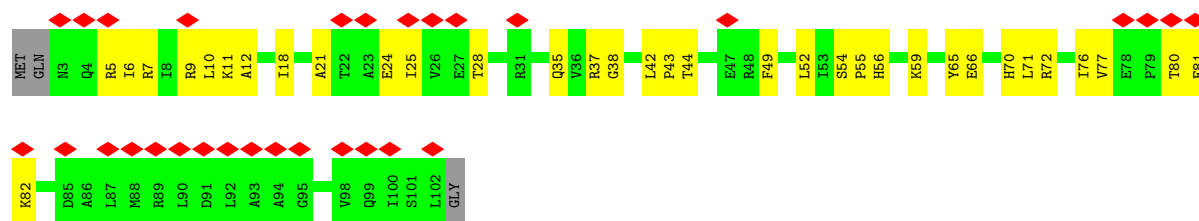


- Molecule 17: 30S ribosomal protein S9



- Molecule 18: 30S ribosomal protein S10

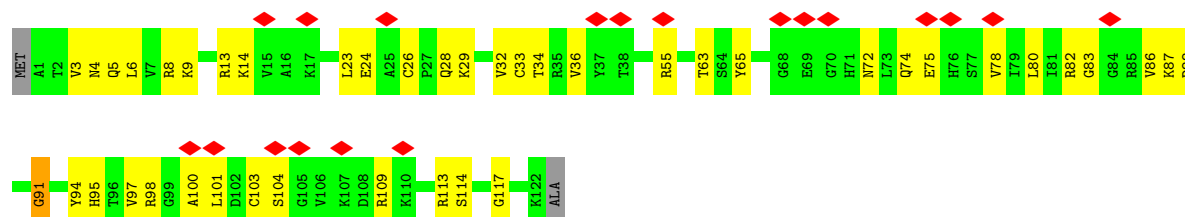




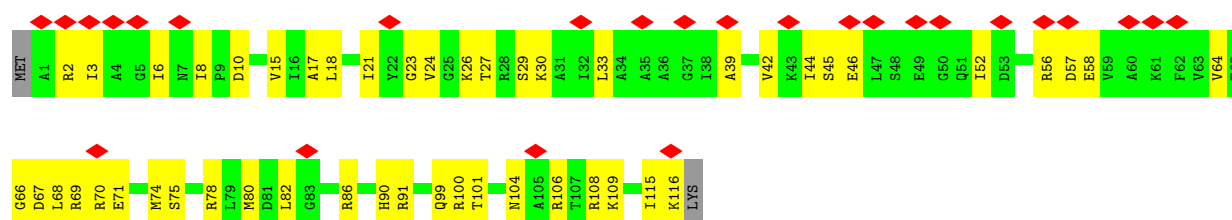
- Molecule 19: Small ribosomal subunit protein uS11



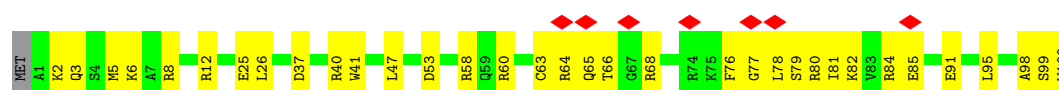
- Molecule 20: Small ribosomal subunit protein uS12



- Molecule 21: 30S ribosomal protein S13



- Molecule 22: 30S ribosomal protein S14



- Molecule 23: 30S ribosomal protein S15

Chain O:  64% 35%



- Molecule 24: 30S ribosomal protein S16

Chain P:  16% 63% 35%



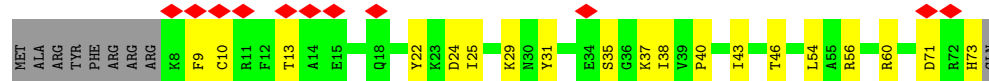
- Molecule 25: 30S ribosomal protein S17

Chain Q:  68% 27% 5%



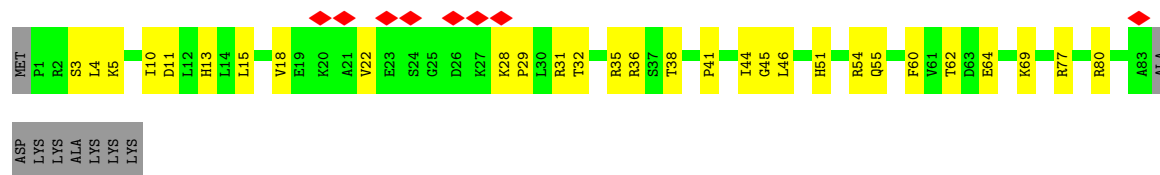
- Molecule 26: 30S ribosomal protein S18

Chain R:  15% 63% 25% 12%

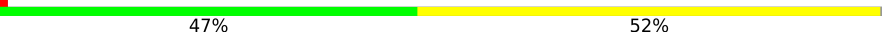


- Molecule 27: 30S ribosomal protein S19

Chain S:  9% 59% 32% 10%

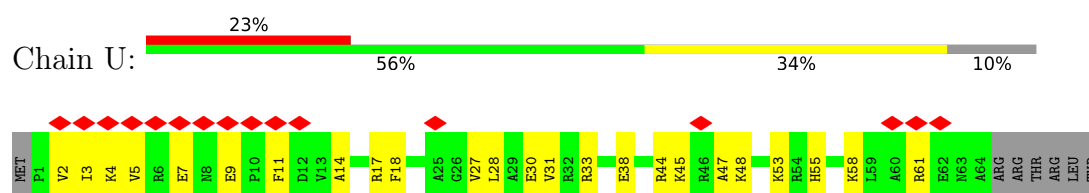


- Molecule 28: 30S ribosomal protein S20

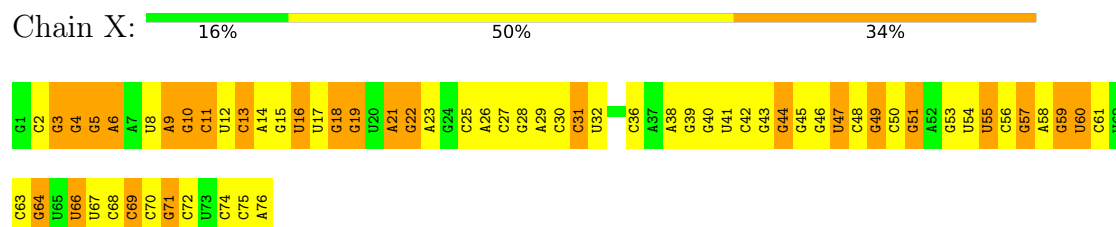
Chain T:  47% 52%



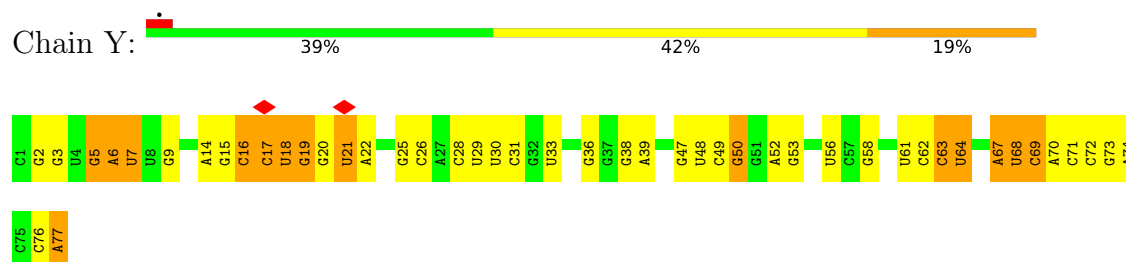
- Molecule 29: 30S ribosomal protein S21



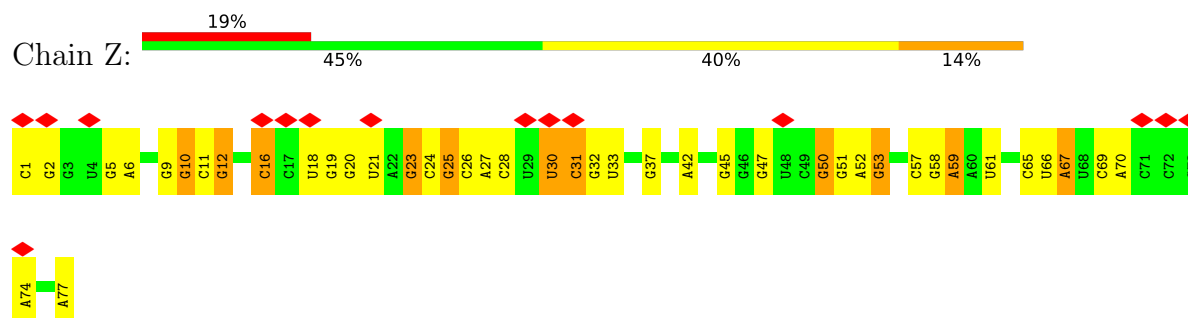
- Molecule 30: E-site tRNA



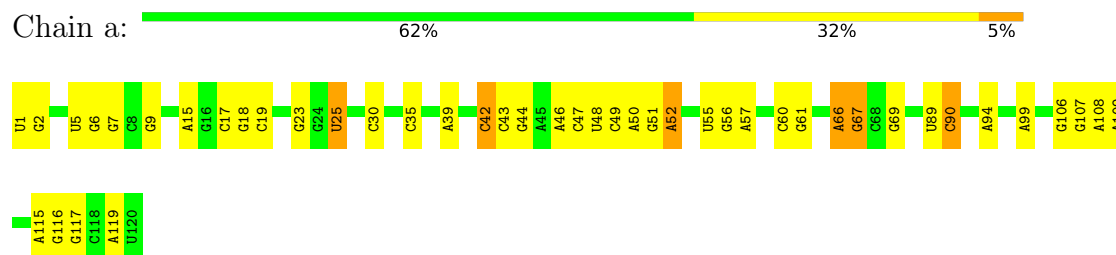
- Molecule 31: P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z)



- Molecule 31: P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z)



- Molecule 32: 5S rRNA



- Molecule 33: RNA (2903-MER)



U1506	U1412	G1300	U1173	U1081	C1007	U895	A793	C678	U573	A480	U365	G248	G110	G1
C1507	A1413	A1301	U1174	U1082	A1008	A896	A794	C679	A574	G481	U366	C249	G110	G2
A1508			A1175	U1083	A1009	C897	C795		A575	A482	G367	G250	A118	U3
A1509	G1416	A1084	U1176	A1084	U1012	C898		G682		A483	A368	A251	A119	U4
G1510	C1417	A1085	G1177	A1086	C1013	A899	G801		U580	C487	U369	A255	U120	A5
G1511	C1418	A1087	G1178	A1087	C1014	C901	G805		A582		G370		A125	G9
	A1419	U1316	G1179	G1087	A1014	C902		U686		G491	A371		A125	A10
G1514	A1420	U1317	U1180	A1088	U1019		G809	G690	A586		G372	G263	C128	G9
G1519	G1421	U1318	U1181	A1089	A1020	A910				G491	A372	C264	C128	A10
U1520	G1422	C1320		A1090	A1021	A911	C812	G701	U588	G495	G376	A265	A131	U18
	G1425	A1321	G1186	G1092	U1022	C912	U813		U589	G499	G377	G266	A131	A19
U1523	G1426	A1322	G1195	C1093	U1023	U913	C814	G704	A590	U499		C267	G133	G27
G1524	A1427		G1196	U1094	G1024	G914		A705		G500		C268	G134	A28
A1525	C1428	G1332	U1197	A1095	G1025	C915	A819	A706	U593				U135	
			U1198	A1096	G1026	G916	U826		U594	A503	G386	G271		G35
G1530			U1199	A1097	U1033	A927	U827	G713	U595	A505	G388	A272	G140	G39
C1531	A1433	G1337		A1098	U1034		U828	U714	U596	A508	U390	U276	G141	U40
A1532	A1434	G1338		G1099	U1035	G930	A845	U715	A603	C509	A391	G277	A142	C41
C1533	G1435	G1339		A1103	G1038	U931	U846	A716	G604	C510	U392	A278	A152	A42
U1534	C1436	U1340		A1104	A1039	A932		C717		C511	C393	U280	U153	G45
A1535	G1437	U1341		U1105	A1040	A933	A849	A718	A608	U511	C394	C281	U154	G46
C1536	A1438			U1106	G1041	G938	U850	C719	A609	A512	U395	A282	A155	
A1537	A1439	U1352		G1107	G1042		C851	U720		A513	G396	G283	A156	C47
G1538	U1443	C1357	G1223	G1108		A941	U852	A721	A613	U521	A404	U284		G48
U1539	G1444	G1358	U1224	U1109	G1047	C946	G856	A722	A614	A522	A405	G285	C163	G51
G1540	G1445			A1110	A1048	U932	U857	C723	U615	C523	G406	U286	A163	A52
C1541	C1461	C1362	U1234	C1109	A1053	A947	G858	G726	A621	A529	G407	U288	A165	A53
U1542			G1235	A1111	C1053	C948	G859		G622	C530		G289	A172	G61
G1543			G1236	U1112	A1054	G952	A866	G729	C623	C531	A412	U290	A173	U62
	A1469	A1365	G1237	U1113	C1055			A735	C624	A532	C413	G295	G178	A63
A1548	A1470	A1366	G1238	U1114	A1056	U955	G869	U747	A627	U534	C414	G296	G178	A64
A1549	G1471			G1115	G1057	G956	U870	G748			A415	G297	G180	U65
A1552	G1475	C1370	A1241	G1116	A1058		U871		C634	G537	U416	G298	A181	
A1553	U1476	G1371	G1250		U1059	A859	U872	G740	C635	A538	C417		A182	A71
	A1477	U1379	A1253	G1125	G1060	A960	U873	A743	G636		U418	C305	C183	
C1558	U1481	G1382	A1254	A1126	U1061	C961	U874		G637	G543	U419	U306	C208	U82
U1559	G1482	A1383	G1255	U1132	U1062		G874	U747	A637	C544	C420	G307	C209	A74
G1560	G1483	A1384	G1256	A1133	G1063	C964			G638	U545	C421		A196	G75
C1561	U1484	A1385		A1134	G1064		A877	G748	U639	U546		A310	A199	C76
U1562	U1485	C1386	U1263	C1135	G1065	G969	A878		C640	U547	G424	A311	A199	G77
	U1486	A1387		G1136	U1066	U970	G879	G757	U641	A547			C208	G81
A1566	U1487		G1266	U1141	U1067	G971	G880		U642	G548	A428	A330	C209	U82
G1567		A1392	U1267	A1142	A1067	A972	G881	C765	A643	G549	A429	A330	C209	A83
G1568	A1490	A1393	A1268	A1143	G1068	G974	G882		A644	C550	A430	A347	G215	A84
A1569	G1491	U1394	A1269	A1144	G1069	G974	G883	G774	C645	G555	C445	U349	A216	
	C1492	U1395	G1270	G1149	A1070		U884	G775	U646	A566			A216	G88
C1493	U1494	U1396	G1271	C1150	G1071	A881	C885	G776	G647	A567	U451	C353	A221	
A1495		U1397	A1272	C1153	C1072	C982	A886			C557		A354	A222	A91
C1577	U1576		U1273	A1156	G1073	A984	U887	G780	U653	C560	A457	U355	A223	G98
U1578	A1496	A1497		A1157	G1074	A984	C888	A782	A654	C561	A457	G356	C228	U99
	U1584	C1498	A1276	A1158	C1075	A986	C889	A783	A655	A563	G473	G357	C229	U100
C1585	U1585	G1407	G1281	G1159	A1077	A996	C890	G784	G656	U567	G474	U358	C229	A101
A1586	U1586	G1408	U1282	A1160	C1076	U999	C891	G785	U658	U568	C475	G359	A233	U102
G1587	G1501	U1409		A1170	A1077		A892					U360	A233	A103
U1588	A1502	G1410	G1292	C1171	C1078	C1006	A893	A792	A670			G361	G247	
A1590		A1505	C1293	A1080			U894							

U1591	U1742	C1843	G1954	G2069	G2143	A2212	U2320	C2440	U2562	G2686	G2801
G1743	C1844	C1847	U1955	A2070	A2142	A2213	U2321	U2441	U2563	U2687	G2802
A1744	A1847	A1847	U1956	A2071	G2143	C2214	A2322	G2444	A2564	G2688	G2803
A1745	A1848	A1848	C1957	C2072	G2144	C2214	G2323	G2444	A2565	U2689	U2807
U1746	U1851	U1851	C1958	U2076	C2145	G2221	U2324	G2447	G2566	U2690	G2808
U1747	U1852	U1852	U1959	A2077	C2146	C2222	C2325	A2448	G2567	U2698	
C1600	U1754	U1853	A1607	C2078	A2147	C2225	C2326	U2449	G2570	U2711	A2813
	U1758	A1854	A1608	C2079	G2148	A2225	A2327	A2450	U2571	C2712	A2814
	U1762	G1857	A1609	A2088	U2149	U2233	A2328	G2455	A2572	U2713	A2820
	A1763	A1858	A1610	C2089	U2151	G2234	U2329	C2456	G2576	G2714	A2823
	C1764	U1862	U1629	G2093	C2152	G2238	C2332	A2459	G2581	C2723	
		A1969	A1630	C2096	A2154	G2239	U2333	G2467	G2582	U2724	U2833
	U1769	A1970		C2097	U2155	U2243	A2335	A2468	G2583	A2725	G2834
	G1770	U1870		U2098	G2156	U2244	A2336	A2469	U2584	A2726	A2835
	C1771	A1871		U2099	C2157	U2245	G2345	G2476	C2591	A2727	U2836
	A1772	G1872		G2100	A2158	G2246	A2346		C2592	U2728	A2837
	A1773	G1873		C2101	C2160	A2247	C2347	G2481	U2593	G2731	G2838
	G1776	A1874		G2102	C2161	G2250	U2348	G2484	C2594	G2732	C2840
	U1779	G1875		C2103	A2162	G2251	C2349		G2595	A2733	
		A1876		U2104	C2163	G2255	C2350	G2497	A2598	G2737	G2846
		U1880		U2105	C2164	G2256	G2357	A2497	A2602	A2738	G2847
		U1783		U2106	C2165	G2257	G2361	G2502	U2609	U2739	U2848
		A1784		G2107	U2167	G2258	G2373	G2504	G2613	A2741	U2849
		A1789		A1884	G2168	A2267	C2374	U2504	U2614	G2744	G2854
		A1790		A1885	C2169	U2272	G2377	U2505	U2615	C2745	C2858
		A1791		G1888	A2170	A2273	A2377	U2506	G2616	G2746	A2860
					A2171	G2279			U2617	A2747	U2861
					U2111	C2283	A2381	U2513	U2629	C2752	G2867
					G2112	C2284	G2382	U2514	G2630	C2755	A2868
					C2113	A2285	G2383	C2515	A2635	A2758	A2873
					A2114	G2286	G2384	C2516	G2638	C2771	C2880
					G2115	A2287	G2385	C2517	U2647	C2772	A2882
					G2116	G2288	G2386	G2518	U2650	C2773	U2883
					U2117	A2289	G2387	U2519	C2651	U2776	U2884
					C2118	G2290	G2388	C2520	G2655	A2777	A2885
					U2119	U2291	G2389	C2521	U2656	A2778	A2886
					A2120	U2292	G2390	U2522	U2657	U2779	
					G2121	G2293	G2391	G2529	U2780		U2891
					U2122	U2302	G2412	G2535	G2791		G2892
					G2123	G2303	G2413	G2545	G2795		A2893
					U2124	G2304	G2422	U2546	U2897		C2896
					G2125	U2305	A2424	A2547	U2898		A2899
					A2126	G2306	A2425	U2548	U2672		U2900
					G2127	G2307	A2426	G2555	A2682		C2901
					U2128	G2308	A2427	C2556	U2684		U2903
					G2129	G2309	A2428	G2557	A2799		
					U2130	U2312	A2430	C2558			
					U2131	U2313					
					U2132	U2314					
					G2133	U2195					
					A2134	C2200					
					G2135	U2203					
					A2136	U2204					
					U2137	U2205					
					G2138	U2206					
					U2139	U2207					
					G2140	U2208					

• Molecule 34: 50S ribosomal protein L2

Chain c:  79% 20%

RET	M128	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
A2	T129	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
O6	L130	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
K7	P131	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	M132	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	I135	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	V141	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	M142	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	M143	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	M146	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	G152	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	C2902	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903
	S157	U2891	G2892	A2893	C2896	U2897	U2898	A2899	A2900	C2901	U2903



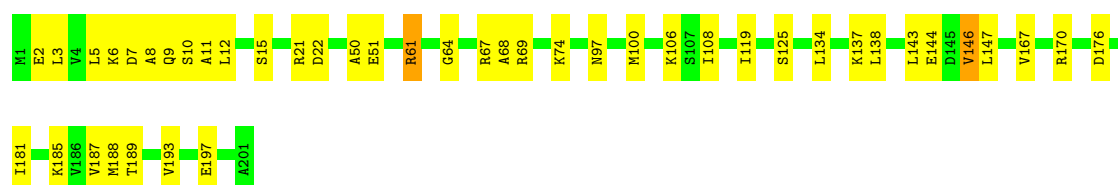
- Molecule 35: 50S ribosomal protein L3

Chain d: 85% 14%



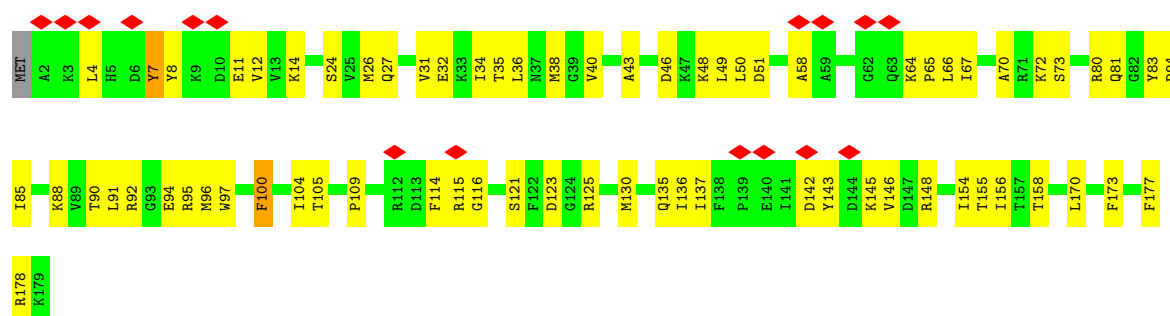
- Molecule 36: 50S ribosomal protein L4

Chain e: 78% 21%



- Molecule 37: 50S ribosomal protein L5

Chain f: 9% 60% 38%



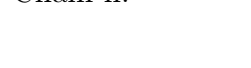
- Molecule 38: 50S ribosomal protein L6

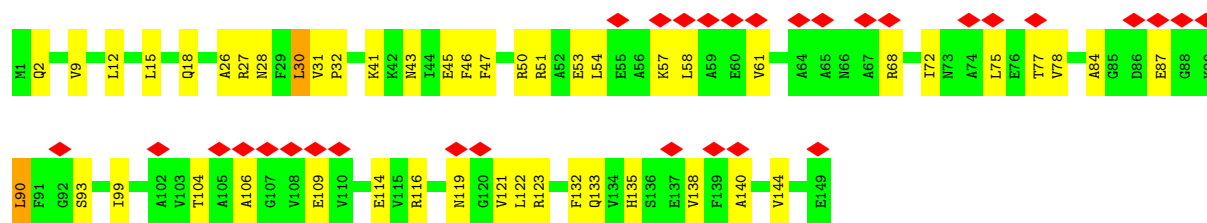
Chain g: 75% 23%



- Molecule 39: 50S ribosomal protein L9

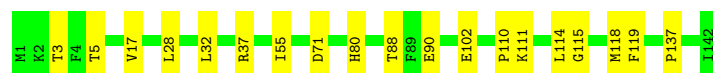
Chain h: 21% 68% 31%





- Molecule 40: 50S ribosomal protein L13

Chain k: 87% 13%



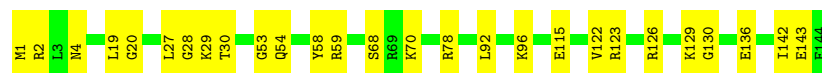
- Molecule 41: 50S ribosomal protein L14

Chain l: 92% 8%



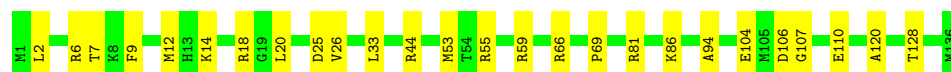
- Molecule 42: 50S ribosomal protein L15

Chain m: 81% 19%



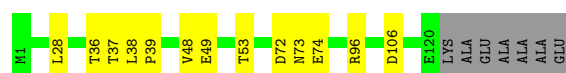
- Molecule 43: 50S ribosomal protein L16

Chain n: 81% 19%



- Molecule 44: 50S ribosomal protein L17

Chain o: 84% 10% 6%



- Molecule 45: 50S ribosomal protein L18

Chain p: 83% 16%



- Molecule 46: 50S ribosomal protein L19

Chain q:  79% 20%



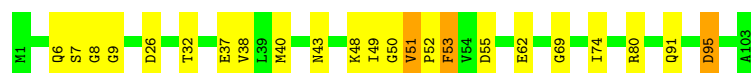
- Molecule 47: 50S ribosomal protein L20

Chain r:  85% 14%



- Molecule 48: 50S ribosomal protein L21

Chain s:  78% 19%



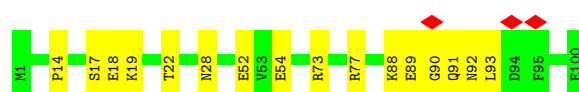
- Molecule 49: 50S ribosomal protein L22

Chain t:  82% 18%



- Molecule 50: 50S ribosomal protein L23

Chain u:  84% 16%



- Molecule 51: 50S ribosomal protein L24

Chain v:  73% 25%



- Molecule 52: 50S ribosomal protein L25

Chain w:  80% 20%



G10	C11	G12	G13	C14	C15	C16		U21	A22	A23
-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----

Method	Gene Count
MET	10
A2	10
H3	10
K4	10
K5	10
A6	10
G7	10
G8	10
S9	10
R14	10
I37	10
V38	10
K44	10
D56	10
L59	10
E70	10
R77	10
K78	10
F79	10
I80	10
E85	10

[illegible][illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145326	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.007	Depositor
Minimum map value	-0.742	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	528.0, 528.0, 528.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	0	0.28	0/635	0.34	0/848
2	1	0.25	0/496	0.37	0/660
3	2	0.29	0/453	0.37	0/605
4	4	0.33	0/450	0.37	0/599
5	5	0.22	0/433	0.32	0/576
6	6	0.33	0/380	0.36	0/498
7	7	0.31	0/513	0.31	0/676
8	8	0.32	0/303	0.29	0/397
9	A	0.16	0/36834	0.28	1/57462 (0.0%)
10	B	0.12	0/1735	0.31	0/2338
11	C	0.12	0/1659	0.29	0/2236
12	D	0.13	0/1665	0.30	0/2227
13	E	0.15	0/1169	0.34	0/1573
14	F	0.14	0/881	0.30	0/1189
15	G	0.11	0/1219	0.25	0/1635
16	H	0.17	0/989	0.34	0/1326
17	I	0.19	0/1034	0.35	0/1375
18	J	0.14	0/813	0.37	0/1100
19	K	0.16	0/893	0.31	0/1205
20	L	0.19	0/963	0.39	0/1293
21	M	0.13	0/909	0.30	0/1215
22	N	0.12	0/817	0.26	0/1088
23	O	0.14	0/722	0.28	0/964
24	P	0.11	0/653	0.27	0/877
25	Q	0.13	0/657	0.34	0/881
26	R	0.12	0/553	0.28	0/742
27	S	0.12	0/680	0.34	0/915
28	T	0.17	0/676	0.30	0/895
29	U	0.15	0/536	0.39	0/711
30	X	0.22	0/1810	0.32	0/2820
31	Y	0.15	0/1840	0.29	0/2866
31	Z	0.18	0/1840	0.28	0/2866

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	a	0.27	0/2869	0.28	0/4474
33	b	0.34	0/69800	0.32	1/108892 (0.0%)
34	c	0.32	0/2121	0.38	0/2852
35	d	0.37	1/1586 (0.1%)	0.45	2/2134 (0.1%)
36	e	0.32	0/1571	0.33	0/2113
37	f	0.25	0/1443	0.52	2/1937 (0.1%)
38	g	0.22	0/1333	0.29	0/1805
39	h	0.30	0/1121	0.42	0/1515
40	k	0.33	0/1152	0.32	0/1551
41	l	0.28	0/955	0.39	0/1279
42	m	0.29	0/1062	0.37	0/1413
43	n	0.28	0/1093	0.34	0/1460
44	o	0.30	0/973	0.33	0/1301
45	p	0.21	0/902	0.29	0/1209
46	q	0.27	0/929	0.30	0/1242
47	r	0.35	0/960	0.32	0/1278
48	s	0.31	0/829	0.43	0/1107
49	t	0.33	0/864	0.31	0/1156
50	u	0.27	0/793	0.35	0/1060
51	v	0.56	2/796 (0.3%)	0.40	0/1062
52	w	0.25	0/766	0.33	0/1025
53	x	0.13	0/333	0.28	0/517
54	y	0.31	0/642	0.33	0/848
55	z	0.36	0/416	0.61	1/569 (0.2%)
56	V	0.40	0/457	0.70	0/612
All	All	0.28	3/160976 (0.0%)	0.32	7/241069 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	v	54	GLN	C-O	-12.92	1.17	1.23
35	d	152	PRO	CG-CD	-7.24	1.26	1.50
51	v	54	GLN	CA-C	5.31	1.57	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	d	152	PRO	N-CD-CG	10.27	118.60	103.20
35	d	152	PRO	CA-N-CD	-7.25	101.85	112.00
9	A	1357	A	C2'-C3'-O3'	6.34	123.21	113.70
33	b	2571	U	C3'-C2'-O2'	5.13	118.39	110.70
37	f	4	LEU	CA-C-N	-5.11	110.76	121.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	f	4	LEU	C-N-CA	-5.11	110.76	121.64
55	z	136	SER	N-CA-C	5.04	117.16	111.11

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	0	625	0	652	14	0
2	1	495	0	526	14	0
3	2	449	0	488	7	0
4	4	444	0	458	14	0
5	5	426	0	464	6	0
6	6	377	0	418	5	0
7	7	504	0	572	7	0
8	8	302	0	341	4	0
9	A	32895	0	16553	715	0
10	B	1704	0	1732	58	0
11	C	1632	0	1710	59	0
12	D	1643	0	1710	80	0
13	E	1156	0	1199	33	0
14	F	862	0	864	33	0
15	G	1203	0	1256	39	0
16	H	979	0	1034	49	0
17	I	1022	0	1070	79	0
18	J	803	0	842	38	0
19	K	877	0	887	34	0
20	L	949	0	1014	43	0
21	M	900	0	968	38	0
22	N	805	0	847	37	0
23	O	714	0	737	27	0
24	P	643	0	661	22	0
25	Q	648	0	691	19	0
26	R	544	0	565	15	0
27	S	663	0	690	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	T	670	0	722	39	0
29	U	529	0	565	20	0
30	X	1621	0	820	63	0
31	Y	1647	0	832	43	0
31	Z	1647	0	832	32	0
32	a	2568	0	1302	35	0
33	b	62321	0	31344	686	0
34	c	2082	0	2154	43	0
35	d	1565	0	1616	27	0
36	e	1552	0	1619	57	0
37	f	1419	0	1457	73	0
38	g	1313	0	1358	34	0
39	h	1110	0	1148	44	0
40	k	1129	0	1162	14	0
41	l	946	0	1023	9	0
42	m	1053	0	1129	19	0
43	n	1074	0	1157	22	0
44	o	960	0	1000	9	0
45	p	892	0	923	15	0
46	q	917	0	962	19	0
47	r	947	0	1019	14	0
48	s	816	0	839	33	0
49	t	857	0	922	21	0
50	u	786	0	846	16	0
51	v	788	0	844	18	0
52	w	753	0	780	14	0
53	x	299	0	154	6	0
54	y	634	0	653	16	0
55	z	398	0	372	35	0
56	V	454	0	476	30	0
57	8	1	0	0	0	0
58	Z	7	0	7	4	0
All	All	148019	0	98986	2676	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (2676) 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)
36:e:5:LEU:CD2	36:e:8:ALA:HB3	1.60	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:s:51:VAL:HB	48:s:52:PRO:CD	1.60	1.29
56:V:19:ILE:HG22	56:V:23:SER:CB	1.68	1.23
31:Y:77:A:O3'	55:z:162:PRO:C	1.88	1.15
31:Z:77:A:HO3'	58:Z:163:PRO:C	1.52	1.15
20:L:87:LYS:HG3	20:L:88:ASP:H	1.13	1.13
31:Z:77:A:O3'	58:Z:163:PRO:C	1.91	1.12
39:h:31:VAL:CG1	39:h:32:PRO:HD3	1.79	1.11
12:D:109:THR:HG22	12:D:112:GLU:HG2	1.36	1.08
56:V:19:ILE:HG22	56:V:23:SER:HB2	1.10	1.07
36:e:5:LEU:HD21	36:e:8:ALA:HB3	1.27	1.07
31:Z:77:A:O3'	58:Z:163:PRO:O	1.74	1.05
33:b:2164:C:H42	33:b:2171:A:H2'	1.22	1.05
48:s:51:VAL:HB	48:s:52:PRO:HD3	1.38	1.05
33:b:2165:C:O2	33:b:2171:A:N6	1.89	1.04
17:I:51:LEU:HG	17:I:56:MET:HG3	1.41	1.02
54:y:37:ILE:HG22	54:y:59:LEU:O	1.59	1.01
17:I:56:MET:HG2	17:I:57:VAL:H	1.25	1.01
48:s:51:VAL:HB	48:s:52:PRO:HD2	1.38	0.99
39:h:31:VAL:HG12	39:h:32:PRO:HD3	1.42	0.97
12:D:119:HIS:O	12:D:130:ASN:ND2	1.98	0.97
56:V:19:ILE:CG2	56:V:23:SER:HB2	1.96	0.95
48:s:51:VAL:CB	48:s:52:PRO:CD	2.45	0.95
20:L:87:LYS:CG	20:L:88:ASP:H	1.82	0.93
9:A:418:C:HO2'	9:A:540:G:HO2'	1.07	0.93
36:e:5:LEU:CD2	36:e:8:ALA:CB	2.47	0.93
33:b:1321:A:H61	55:z:129:ARG:NH2	1.66	0.92
31:Z:27:A:H61	31:Z:45:G:H1	1.11	0.92
36:e:5:LEU:HD21	36:e:8:ALA:CB	2.00	0.92
56:V:19:ILE:CG2	56:V:23:SER:CB	2.48	0.92
31:Z:30:U:H6	31:Z:30:U:H5''	1.34	0.91
37:f:100:PHE:CE2	37:f:173:PHE:CZ	2.59	0.89
20:L:65:TYR:CD1	20:L:86:VAL:HG21	2.08	0.88
48:s:38:VAL:O	48:s:53:PHE:HA	1.73	0.88
17:I:51:LEU:CG	17:I:56:MET:HG3	2.04	0.86
38:g:133:LEU:HD11	38:g:141:ILE:HG13	1.56	0.85
36:e:143:LEU:HD23	36:e:146:VAL:HG11	1.58	0.85
20:L:87:LYS:HG3	20:L:88:ASP:N	1.87	0.84
33:b:952:G:H21	33:b:2267:A:H2	1.24	0.84
56:V:70:LEU:HD12	56:V:70:LEU:O	1.78	0.84
34:c:110:LEU:HD12	34:c:114:ASP:OD2	1.76	0.84
39:h:31:VAL:HG13	39:h:32:PRO:HD3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:76:G:H1	9:A:93:U:H3	1.25	0.83
38:g:133:LEU:CD1	38:g:141:ILE:HG13	2.08	0.82
29:U:9:GLU:HG2	29:U:14:ALA:HB2	1.62	0.82
17:I:52:GLU:HA	17:I:56:MET:HE3	1.62	0.81
49:t:85:ILE:HB	55:z:137:VAL:HG13	1.63	0.80
9:A:958:A:H62	27:S:54:ARG:HH21	1.29	0.79
55:z:125:THR:HB	55:z:129:ARG:HE	1.47	0.79
48:s:6:GLN:N	48:s:37:GLU:OE2	2.16	0.78
17:I:56:MET:CG	17:I:57:VAL:H	1.96	0.78
33:b:1069:A:H1'	33:b:1096:A:H1'	1.66	0.77
36:e:146:VAL:CG1	36:e:185:LYS:HB2	2.14	0.77
36:e:146:VAL:HG12	36:e:185:LYS:O	1.84	0.77
14:F:18:VAL:HB	14:F:19:PRO:HD3	1.67	0.76
38:g:52:PHE:CE2	38:g:72:LEU:HD12	2.20	0.76
39:h:121:VAL:O	39:h:121:VAL:HG12	1.83	0.76
17:I:51:LEU:HB3	17:I:56:MET:HE2	1.65	0.76
20:L:28:GLN:HB3	20:L:80:LEU:HD11	1.68	0.75
33:b:1433:A:H61	33:b:1560:G:H1	1.33	0.75
9:A:1347:G:H22	9:A:1373:G:H2'	1.52	0.75
33:b:2102:G:H22	33:b:2188:U:H3	1.36	0.74
9:A:546:A:H4'	9:A:548:G:H4'	1.68	0.74
17:I:51:LEU:HG	17:I:56:MET:CG	2.18	0.74
9:A:1347:G:N2	9:A:1373:G:H2'	2.03	0.73
19:K:78:ILE:O	19:K:104:PHE:HE1	1.70	0.73
17:I:56:MET:HG2	17:I:57:VAL:N	2.01	0.73
36:e:5:LEU:HD23	36:e:8:ALA:HB3	1.67	0.72
9:A:93:U:H2'	9:A:94:G:H4'	1.71	0.72
17:I:51:LEU:C	17:I:56:MET:HE3	2.15	0.72
33:b:1321:A:N6	55:z:129:ARG:NH2	2.37	0.72
33:b:1321:A:H61	55:z:129:ARG:HH21	1.36	0.72
9:A:1317:C:H4'	22:N:47:LEU:HG	1.72	0.72
30:X:15:G:H5'	30:X:16:U:H2'	1.71	0.72
33:b:1321:A:C2	55:z:125:THR:O	2.42	0.72
39:h:84:ALA:HB2	39:h:90:LEU:HD12	1.72	0.72
38:g:52:PHE:HE2	38:g:72:LEU:HD12	1.54	0.71
9:A:1405:G:O2'	9:A:1518:A:O2'	2.06	0.71
20:L:65:TYR:CG	20:L:86:VAL:HG21	2.25	0.71
39:h:26:ALA:O	39:h:31:VAL:HG12	1.90	0.71
43:n:66:ARG:HG2	43:n:66:ARG:O	1.91	0.71
33:b:2134:A:OP2	33:b:2158:A:N6	2.24	0.70
13:E:81:GLN:HA	13:E:97:PRO:HG2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:L:86:VAL:HG23	20:L:95:HIS:HE1	1.54	0.70
33:b:1321:A:N6	55:z:129:ARG:HH21	1.87	0.70
36:e:134:LEU:O	36:e:138:LEU:HD13	1.92	0.70
33:b:2164:C:N4	33:b:2171:A:H2'	2.04	0.70
12:D:109:THR:CG2	12:D:112:GLU:HG2	2.18	0.70
17:I:51:LEU:CD2	17:I:56:MET:HG3	2.21	0.70
56:V:19:ILE:HG22	56:V:23:SER:OG	1.91	0.70
17:I:51:LEU:CB	17:I:56:MET:HE2	2.21	0.69
38:g:28:GLY:HA3	38:g:79:VAL:HG11	1.75	0.69
20:L:65:TYR:CE1	20:L:86:VAL:HG21	2.28	0.69
39:h:51:ARG:HD3	39:h:54:LEU:HD12	1.75	0.69
15:G:15:PRO:HG3	17:I:42:THR:HG22	1.75	0.69
36:e:51:GLU:HG3	36:e:51:GLU:O	1.92	0.69
37:f:35:THR:HG22	37:f:155:THR:HB	1.72	0.69
9:A:1235:U:H2'	9:A:1236:A:C8	2.28	0.69
18:J:5:ARG:HA	18:J:77:VAL:HA	1.75	0.68
32:a:1:U:H2'	32:a:2:G:H8	1.58	0.68
9:A:477:C:H2'	9:A:478:A:C8	2.29	0.68
31:Y:6:A:O2'	31:Y:7:U:O4'	2.12	0.68
39:h:9:VAL:HB	39:h:12:LEU:HB2	1.76	0.68
31:Z:30:U:H5''	31:Z:30:U:C6	2.24	0.68
19:K:78:ILE:O	19:K:104:PHE:CE1	2.46	0.68
33:b:1093:G:O6	33:b:1099:G:N3	2.26	0.68
9:A:49:U:H3	9:A:362:G:H1'	1.59	0.68
9:A:407:U:H2'	9:A:408:A:C8	2.29	0.68
9:A:625:U:H2'	9:A:626:G:H8	1.59	0.68
13:E:102:THR:O	13:E:121:ASN:ND2	2.27	0.68
23:O:88:ARG:NH2	33:b:714:U:OP2	2.26	0.68
30:X:3:G:H3'	30:X:4:G:H21	1.59	0.68
31:Y:33:U:H3	31:Y:39:A:H61	1.41	0.68
29:U:30:GLU:OE1	29:U:33:ARG:NH2	2.27	0.68
37:f:109:PRO:HA	37:f:114:PHE:HE2	1.58	0.68
51:v:48:PRO:HB2	51:v:54:GLN:HG3	1.76	0.68
17:I:52:GLU:CA	17:I:56:MET:HE3	2.24	0.67
33:b:858:G:OP1	54:y:78:LYS:NZ	2.27	0.67
48:s:37:GLU:OE1	48:s:53:PHE:CE1	2.47	0.67
54:y:37:ILE:HD13	54:y:80:ILE:HG21	1.77	0.67
9:A:68:G:H22	9:A:101:A:H2	1.41	0.67
33:b:2312:U:H5'	37:f:85:ILE:HD11	1.76	0.67
33:b:445:C:OP1	47:r:2:ALA:N	2.27	0.67
48:s:37:GLU:HB2	48:s:53:PHE:CE1	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1186:G:N2	22:N:100:TRP:OXT	2.28	0.67
33:b:2571:U:H6	33:b:2571:U:O5'	1.78	0.67
10:B:30:ILE:HD11	10:B:38:HIS:HB3	1.77	0.67
11:C:78:LYS:HD2	11:C:79:LYS:HB2	1.77	0.67
9:A:1467:C:H2'	9:A:1468:A:H8	1.60	0.67
22:N:40:ARG:NH1	27:S:5:LYS:O	2.27	0.67
48:s:51:VAL:CB	48:s:52:PRO:HD2	2.17	0.67
9:A:231:U:H2'	9:A:232:G:H8	1.59	0.66
16:H:11:THR:HG22	16:H:14:ARG:HH12	1.60	0.66
33:b:1133:A:N6	33:b:2025:C:O2'	2.28	0.66
38:g:28:GLY:HA3	38:g:79:VAL:CG1	2.24	0.66
56:V:70:LEU:HD12	56:V:70:LEU:C	2.20	0.66
9:A:274:A:H4'	9:A:275:G:H5'	1.77	0.66
33:b:1057:A:N6	33:b:1081:U:O2	2.28	0.66
30:X:68:C:N3	30:X:69:C:N4	2.44	0.66
9:A:1040:U:H6	9:A:1040:U:H5''	1.61	0.66
18:J:6:ILE:HB	18:J:76:ILE:HG23	1.77	0.66
56:V:66:VAL:O	56:V:69:ASP:HB2	1.96	0.66
4:4:16:ARG:NE	33:b:1266:G:OP1	2.29	0.66
26:R:35:SER:HA	26:R:71:ASP:HB2	1.78	0.66
48:s:37:GLU:HB2	48:s:53:PHE:CD1	2.31	0.66
9:A:236:A:H2'	9:A:237:G:H8	1.60	0.66
34:c:2:ALA:N	34:c:20:VAL:O	2.29	0.66
9:A:41:G:H2'	9:A:42:G:H8	1.62	0.65
9:A:131:A:H2'	9:A:132:C:C6	2.31	0.65
12:D:96:ARG:HG3	12:D:133:SER:HA	1.79	0.65
24:P:39:PHE:HD1	24:P:50:THR:HB	1.60	0.65
14:F:11:HIS:HB3	14:F:14:GLN:HG2	1.77	0.65
16:H:28:SER:N	16:H:56:PRO:O	2.29	0.65
34:c:122:ALA:HB3	34:c:130:LEU:HD21	1.78	0.65
43:n:106:ASP:OD1	43:n:107:GLY:N	2.29	0.65
33:b:1321:A:N1	55:z:129:ARG:NH2	2.44	0.65
33:b:2148:G:H2'	33:b:2149:U:C6	2.32	0.65
36:e:125:SER:O	36:e:137:LYS:NZ	2.29	0.65
33:b:1722:A:N6	33:b:1738:G:O2'	2.30	0.65
33:b:1568:G:N7	34:c:28:LYS:NZ	2.44	0.65
36:e:5:LEU:HG	36:e:6:LYS:N	2.10	0.65
13:E:40:ASP:HB2	13:E:44:ARG:HB2	1.79	0.65
33:b:2171:A:H4'	33:b:2171:A:OP1	1.96	0.65
9:A:1222:G:H5''	27:S:77:ARG:HE	1.61	0.65
17:I:25:GLY:N	17:I:61:ASP:OD1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:L:86:VAL:HG23	20:L:95:HIS:CE1	2.32	0.65
30:X:48:C:H5''	30:X:49:G:H5''	1.76	0.65
31:Y:77:A:O3'	55:z:162:PRO:O	2.15	0.65
33:b:2184:A:H2'	33:b:2185:U:H6	1.62	0.65
33:b:2683:C:O2	41:l:70:ARG:NH2	2.29	0.65
9:A:133:U:H4'	9:A:325:A:H1'	1.79	0.65
19:K:71:ASP:HA	19:K:74:LYS:HD2	1.78	0.65
24:P:9:HIS:N	24:P:16:PHE:O	2.30	0.65
30:X:41:U:H2'	30:X:42:C:H6	1.62	0.65
33:b:1482:G:O6	33:b:1508:A:N6	2.30	0.65
9:A:1432:G:OP2	46:q:106:LYS:NZ	2.29	0.65
50:u:28:ASN:ND2	50:u:88:LYS:O	2.30	0.65
34:c:232:HIS:HA	34:c:242:LYS:HE3	1.80	0.64
36:e:5:LEU:HG	36:e:6:LYS:H	1.62	0.64
33:b:2164:C:N3	33:b:2171:A:C8	2.65	0.64
39:h:68:ARG:NH2	39:h:109:GLU:O	2.30	0.64
28:T:47:GLN:O	28:T:51:ASN:ND2	2.31	0.64
9:A:1377:A:OP1	15:G:91:ARG:NH2	2.30	0.64
33:b:878:A:H3'	33:b:879:G:H8	1.60	0.64
38:g:133:LEU:HD11	38:g:141:ILE:CG1	2.28	0.64
9:A:954:G:N2	9:A:1228:C:N3	2.46	0.64
11:C:50:SER:C	11:C:69:THR:HG23	2.23	0.64
13:E:61:LYS:O	13:E:65:LYS:NZ	2.26	0.64
33:b:1532:A:N6	33:b:1540:G:O6	2.31	0.64
33:b:1936:A:H2	33:b:1943:U:H5	1.45	0.64
13:E:95:MET:HE1	13:E:114:LEU:HD21	1.79	0.64
49:t:82:MET:CE	55:z:131:MET:HE1	2.27	0.64
9:A:580:C:O2'	23:O:57:ARG:NH2	2.31	0.64
9:A:1055:A:O2'	11:C:155:ARG:NH1	2.31	0.64
37:f:142:ASP:H	37:f:145:LYS:HZ3	1.46	0.64
31:Y:69:C:H2'	31:Y:70:A:H8	1.62	0.64
9:A:444:G:N1	9:A:491:G:O6	2.31	0.64
9:A:1424:U:H3	9:A:1476:A:H62	1.46	0.64
33:b:983:A:N6	33:b:984:A:N1	2.45	0.64
33:b:1093:G:O6	33:b:1099:G:C4	2.51	0.64
36:e:5:LEU:HD23	36:e:8:ALA:C	2.23	0.64
36:e:143:LEU:CD2	36:e:146:VAL:HG11	2.28	0.64
54:y:4:LYS:O	54:y:4:LYS:HG2	1.97	0.64
33:b:2161:C:H4'	33:b:2172:U:OP2	1.99	0.63
9:A:1467:C:H2'	9:A:1468:A:C8	2.32	0.63
16:H:63:LYS:HE2	16:H:70:VAL:HG11	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:66:A:OP2	32:a:108:A:N6	2.32	0.63
33:b:1321:A:N3	33:b:1321:A:H2'	2.14	0.63
9:A:1175:G:H2'	9:A:1176:A:H8	1.62	0.63
9:A:1179:A:H4'	17:I:104:THR:HA	1.79	0.63
32:a:1:U:H2'	32:a:2:G:C8	2.33	0.63
39:h:28:ASN:C	39:h:32:PRO:HG2	2.24	0.63
45:p:64:TYR:O	45:p:67:ASN:ND2	2.31	0.63
30:X:56:C:O2'	30:X:57:G:O4'	2.16	0.63
9:A:147:G:H2'	9:A:148:G:C8	2.34	0.63
11:C:111:ASP:O	11:C:114:LEU:N	2.30	0.63
17:I:26:LYS:HE2	17:I:61:ASP:HB3	1.81	0.63
19:K:12:ARG:O	19:K:14:GLN:NE2	2.32	0.63
33:b:849:A:H2'	33:b:850:U:H6	1.63	0.63
33:b:1796:U:H2'	33:b:1797:G:H8	1.64	0.63
9:A:518:C:H41	9:A:529:G:H3'	1.62	0.63
9:A:673:A:H2'	9:A:674:G:C8	2.31	0.63
9:A:1397:C:N4	53:x:22:A:OP2	2.31	0.63
31:Y:77:A:O3'	55:z:162:PRO:CA	2.46	0.63
9:A:1347:G:H8	17:I:108:ARG:HB3	1.64	0.63
33:b:1317:G:H1'	56:V:40:ARG:HH12	1.64	0.63
34:c:199:GLU:N	34:c:199:GLU:OE1	2.30	0.63
31:Y:77:A:H3'	55:z:162:PRO:O	1.99	0.63
39:h:2:GLN:HE21	39:h:18:GLN:HE21	1.47	0.63
41:l:4:GLU:OE1	41:l:4:GLU:N	2.32	0.63
4:4:38:HIS:ND1	4:4:39:LEU:O	2.29	0.62
30:X:16:U:OP1	30:X:59:G:N2	2.31	0.62
9:A:1321:U:OP2	9:A:1322:C:O2'	2.15	0.62
14:F:17:GLN:NE2	39:h:87:GLU:OE1	2.31	0.62
17:I:34:LEU:HD11	17:I:48:ARG:HH22	1.63	0.62
17:I:44:ARG:O	17:I:48:ARG:NH1	2.32	0.62
33:b:1080:A:H8	33:b:1081:U:H4'	1.64	0.62
48:s:38:VAL:O	48:s:53:PHE:CA	2.46	0.62
9:A:73:C:H41	9:A:97:G:H1	1.45	0.62
9:A:427:U:OP1	12:D:12:ARG:NH1	2.31	0.62
10:B:76:SER:O	10:B:92:ASN:ND2	2.28	0.62
33:b:1509:A:O2'	33:b:1510:G:O4'	2.17	0.62
46:q:2:SER:OG	46:q:3:ASN:N	2.31	0.62
9:A:378:G:H2'	9:A:379:C:C6	2.34	0.62
15:G:26:VAL:HG21	15:G:39:GLU:HG3	1.81	0.62
18:J:9:ARG:HE	18:J:42:LEU:HD21	1.65	0.62
30:X:21:A:H2'	30:X:22:G:H8	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2133:G:H1'	33:b:2157:G:H1	1.62	0.62
9:A:938:A:N3	9:A:1376:U:O2'	2.32	0.62
12:D:139:ASN:N	12:D:181:PHE:O	2.32	0.62
17:I:19:PHE:HB2	17:I:63:TYR:HD2	1.65	0.62
18:J:52:LEU:O	22:N:80:ARG:NH1	2.32	0.62
25:Q:10:ARG:NH1	25:Q:56:ASP:O	2.32	0.62
28:T:47:GLN:HE22	28:T:82:ILE:HD12	1.64	0.62
9:A:1412:C:H2'	9:A:1413:A:C8	2.34	0.62
33:b:2790:U:H2'	33:b:2893:A:N7	2.15	0.62
51:v:77:THR:O	51:v:79:LYS:NZ	2.33	0.62
9:A:389:A:N6	9:A:391:G:O6	2.32	0.62
22:N:65:GLN:HG3	22:N:78:LEU:HD11	1.82	0.62
31:Y:77:A:C3'	55:z:162:PRO:O	2.48	0.62
9:A:184:G:H2'	9:A:185:U:C6	2.35	0.62
33:b:704:G:O2'	33:b:726:G:N2	2.32	0.62
33:b:2313:C:H2'	33:b:2314:A:H8	1.64	0.62
34:c:227:PRO:HG3	34:c:234:GLY:H	1.64	0.62
9:A:236:A:H2'	9:A:237:G:C8	2.34	0.61
22:N:65:GLN:HE22	22:N:82:LYS:HG3	1.64	0.61
9:A:275:G:H2'	9:A:276:G:H8	1.65	0.61
13:E:64:GLU:OE1	13:E:64:GLU:N	2.30	0.61
33:b:1779:U:O2	33:b:1783:A:N6	2.33	0.61
37:f:24:SER:HB3	37:f:27:GLN:HB2	1.80	0.61
9:A:462:G:H2'	9:A:463:U:C5	2.35	0.61
33:b:627:A:OP1	42:m:78:ARG:NH1	2.33	0.61
9:A:514:C:H2'	9:A:515:G:C8	2.35	0.61
15:G:14:ASP:HB2	15:G:18:GLY:H	1.64	0.61
33:b:1439:A:H62	33:b:1552:A:H8	1.46	0.61
33:b:1534:U:N3	33:b:1537:G:O6	2.33	0.61
9:A:1309:G:OP1	21:M:86:ARG:NH2	2.33	0.61
12:D:90:LEU:HD13	12:D:93:LEU:HD12	1.83	0.61
13:E:104:ILE:HD12	13:E:122:VAL:HG12	1.82	0.61
33:b:1853:A:H2'	33:b:1854:A:C8	2.35	0.61
33:b:2125:G:O2'	33:b:2173:A:N1	2.33	0.61
33:b:2306:C:OP2	33:b:2307:G:O2'	2.17	0.61
38:g:27:LYS:HA	38:g:32:GLU:OE1	2.00	0.61
9:A:320:A:HO2'	9:A:1435:G:HO2'	1.46	0.61
9:A:979:C:C5	9:A:1318:A:N1	2.69	0.61
9:A:1530:G:N7	29:U:45:LYS:NZ	2.44	0.61
33:b:281:C:H2'	33:b:282:A:C8	2.35	0.61
33:b:870:U:OP1	43:n:6:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2126:A:C5	33:b:2161:C:H2'	2.36	0.61
33:b:2444:G:OP1	36:e:69:ARG:NH2	2.34	0.61
41:l:91:SER:OG	41:l:92:GLU:N	2.33	0.61
6:6:3:ARG:O	6:6:6:GLN:NE2	2.33	0.61
6:6:44:VAL:HG23	6:6:45:SER:H	1.66	0.61
33:b:713:G:H21	33:b:718:A:H2	1.46	0.61
33:b:882:G:N2	33:b:895:U:O2'	2.30	0.61
36:e:67:ARG:NH1	55:z:145:TRP:CZ3	2.69	0.61
51:v:4:LYS:O	51:v:94:ARG:NH1	2.34	0.61
9:A:1240:U:H5'	9:A:1241:G:C8	2.36	0.61
9:A:1423:G:OP1	41:l:49:ARG:NH2	2.33	0.61
22:N:79:SER:HB2	22:N:82:LYS:HG2	1.82	0.61
33:b:389:G:C8	33:b:2413:G:H4'	2.36	0.61
33:b:1038:G:H2'	33:b:1039:A:C8	2.36	0.61
33:b:2773:C:OP1	35:d:169:ARG:NH1	2.34	0.61
35:d:8:LYS:HB2	35:d:201:LEU:HD11	1.83	0.61
9:A:193:C:H2'	9:A:194:C:C6	2.35	0.61
9:A:970:C:H41	17:I:128:LYS:HD2	1.64	0.61
12:D:124:VAL:HG12	12:D:125:ASN:HD22	1.65	0.61
7:7:31:HIS:ND1	7:7:32:ILE:HG13	2.16	0.60
9:A:34:C:O4'	20:L:28:GLN:NE2	2.33	0.60
13:E:75:LEU:HA	13:E:80:LEU:HB2	1.82	0.60
33:b:495:G:OP1	49:t:6:LYS:NZ	2.29	0.60
33:b:883:G:O2'	33:b:884:U:O5'	2.19	0.60
33:b:1019:U:H3	33:b:1142:A:H62	1.48	0.60
33:b:1114:C:H2'	33:b:1115:G:C8	2.36	0.60
33:b:2682:A:H61	33:b:2728:U:H1'	1.66	0.60
12:D:104:MET:HG2	12:D:170:LEU:HD11	1.82	0.60
11:C:139:ASN:OD1	11:C:142:ARG:NH1	2.33	0.60
33:b:1996:C:OP1	41:l:31:ARG:NH1	2.34	0.60
33:b:2469:A:N6	33:b:2481:G:O2'	2.34	0.60
33:b:2515:C:H2'	33:b:2516:A:H8	1.65	0.60
28:T:3:ILE:HG12	28:T:5:SER:H	1.67	0.60
33:b:429:A:H2'	33:b:430:A:C8	2.36	0.60
33:b:1055:G:N2	33:b:1084:A:O2'	2.34	0.60
33:b:2102:G:N2	33:b:2188:U:H3	1.98	0.60
33:b:2291:U:H2'	33:b:2292:U:C6	2.36	0.60
35:d:148:GLN:OE1	35:d:148:GLN:N	2.34	0.60
22:N:63:CYS:SG	22:N:65:GLN:NE2	2.74	0.60
33:b:826:U:O2'	42:m:53:GLY:HA3	2.01	0.60
34:c:71:LYS:O	34:c:118:SER:OG	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:105:LEU:HB2	38:g:113:VAL:HG23	1.83	0.60
30:X:53:G:H2'	30:X:54:U:C6	2.36	0.60
33:b:1040:A:H61	33:b:1115:G:H1	1.49	0.60
33:b:2243:U:H2'	33:b:2244:U:C6	2.36	0.60
5:5:6:ARG:NH1	33:b:2285:C:OP2	2.31	0.60
9:A:78:A:N6	9:A:88:U:O2'	2.35	0.60
16:H:87:ARG:NH1	16:H:89:ASP:OD1	2.31	0.60
30:X:22:G:H2'	30:X:23:A:H8	1.66	0.60
12:D:125:ASN:HA	12:D:141:VAL:HG23	1.84	0.60
33:b:2126:A:N6	33:b:2162:G:O5'	2.30	0.60
1:0:37:ARG:HA	1:0:48:THR:HA	1.83	0.60
9:A:44:A:H2'	9:A:45:G:C8	2.37	0.60
9:A:462:G:H2'	9:A:463:U:H5	1.66	0.60
9:A:565:U:H3'	9:A:566:G:H2'	1.83	0.60
33:b:1339:G:H5''	50:u:19:LYS:HD3	1.83	0.60
5:5:53:LYS:NZ	5:5:55:LYS:O	2.34	0.60
9:A:768:A:N3	9:A:1512:U:O2'	2.35	0.60
9:A:1305:G:N2	9:A:1332:A:OP2	2.31	0.60
30:X:41:U:H2'	30:X:42:C:C6	2.37	0.60
32:a:116:G:H2'	32:a:117:G:H8	1.67	0.60
33:b:487:C:O2'	49:t:52:GLU:OE1	2.19	0.60
33:b:1115:G:H2'	33:b:1116:G:H8	1.67	0.60
9:A:321:A:H2'	9:A:322:C:H6	1.67	0.59
20:L:13:ARG:HE	20:L:14:LYS:H	1.50	0.59
34:c:141:VAL:HG11	34:c:190:ALA:HB1	1.83	0.59
15:G:112:ASP:HB3	15:G:118:ARG:HG2	1.83	0.59
31:Y:69:C:H2'	31:Y:70:A:C8	2.37	0.59
49:t:37:THR:OG1	49:t:48:LYS:NZ	2.34	0.59
2:1:37:LEU:HG	2:1:37:LEU:O	2.02	0.59
10:B:10:LYS:HD2	10:B:12:GLY:H	1.68	0.59
12:D:104:MET:HE2	12:D:170:LEU:HG	1.85	0.59
47:r:90:ILE:HD11	48:s:48:LYS:HE2	1.82	0.59
50:u:54:GLU:OE1	50:u:92:ASN:ND2	2.35	0.59
17:I:29:ILE:HG23	17:I:64:ILE:HG13	1.84	0.59
43:n:69:PRO:HA	43:n:94:ALA:HB2	1.84	0.59
9:A:738:C:OP1	14:F:2:ARG:NH1	2.36	0.59
9:A:1323:G:H2'	9:A:1324:A:C8	2.37	0.59
28:T:48:LYS:HA	28:T:51:ASN:HD21	1.66	0.59
33:b:1476:U:H2'	33:b:1477:A:H8	1.67	0.59
9:A:660:C:N3	9:A:746:A:N6	2.50	0.59
9:A:1307:U:O4	9:A:1331:G:N2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:68:GLU:HG3	12:D:72:ARG:HH21	1.68	0.59
33:b:310:A:O2'	33:b:311:A:H2'	2.03	0.59
36:e:5:LEU:HB3	36:e:10:SER:H	1.68	0.59
36:e:146:VAL:HG12	36:e:185:LYS:C	2.28	0.59
37:f:143:TYR:HA	37:f:146:VAL:HB	1.85	0.59
2:1:23:ARG:O	2:1:27:ASN:ND2	2.36	0.59
9:A:20:U:O2'	9:A:573:A:N6	2.35	0.59
9:A:1347:G:N7	17:I:108:ARG:CZ	2.66	0.59
28:T:16:ALA:O	28:T:20:ASN:ND2	2.34	0.59
33:b:1548:A:H2'	33:b:1549:A:C8	2.37	0.59
38:g:137:ASP:OD1	38:g:138:LYS:N	2.35	0.59
39:h:31:VAL:HG12	39:h:32:PRO:CD	2.26	0.59
9:A:602:A:H2'	9:A:603:U:C6	2.38	0.59
14:F:35:LYS:HB2	14:F:65:GLU:HB2	1.85	0.59
14:F:38:ARG:HD2	14:F:101:PRO:HD3	1.85	0.59
19:K:28:ASN:OD1	19:K:29:THR:N	2.35	0.59
33:b:2119:A:H61	33:b:2167:U:H1'	1.68	0.59
33:b:2188:U:H2'	33:b:2189:U:C6	2.38	0.59
33:b:2315:G:O2'	37:f:125:ARG:NE	2.36	0.59
37:f:64:LYS:HD3	37:f:64:LYS:H	1.67	0.59
38:g:2:SER:OG	38:g:3:ARG:N	2.36	0.59
49:t:6:LYS:HG2	49:t:104:THR:HG22	1.83	0.59
9:A:358:U:H2'	9:A:359:G:H8	1.67	0.59
10:B:10:LYS:HZ2	10:B:13:VAL:HG23	1.67	0.59
30:X:9:A:OP2	30:X:13:C:N4	2.35	0.59
31:Z:31:C:N4	31:Z:42:A:O2'	2.35	0.59
9:A:981:U:O2'	22:N:60:ARG:NH1	2.36	0.59
33:b:1509:A:O2'	33:b:1510:G:O5'	2.21	0.59
46:q:48:ILE:HG22	46:q:97:LEU:HB2	1.84	0.59
9:A:2:A:H1'	9:A:613:C:O2'	2.03	0.58
24:P:18:GLN:HA	24:P:38:PHE:HA	1.85	0.58
33:b:886:A:N3	33:b:890:C:N4	2.50	0.58
39:h:75:LEU:HD11	39:h:106:ALA:HB1	1.85	0.58
9:A:806:C:H2'	9:A:807:A:H8	1.69	0.58
11:C:110:LEU:HD23	11:C:111:ASP:H	1.68	0.58
28:T:24:ARG:O	28:T:28:ARG:HG2	2.03	0.58
31:Z:19:G:O2'	31:Z:58:G:N2	2.28	0.58
33:b:1590:A:H2'	33:b:1591:A:H8	1.67	0.58
33:b:2136:G:H22	33:b:2156:G:H1	1.48	0.58
39:h:104:THR:HG22	39:h:109:GLU:HA	1.83	0.58
9:A:1192:C:OP2	11:C:3:LYS:NZ	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1218:C:H2'	9:A:1219:A:C8	2.37	0.58
19:K:86:LYS:HA	19:K:113:THR:HG22	1.85	0.58
42:m:20:GLY:HA2	42:m:28:GLY:HA2	1.86	0.58
2:1:52:ARG:NH1	33:b:77:G:OP1	2.36	0.58
9:A:41:G:H2'	9:A:42:G:C8	2.38	0.58
11:C:30:ASP:N	11:C:30:ASP:OD1	2.35	0.58
18:J:10:LEU:O	18:J:72:ARG:N	2.35	0.58
29:U:38:GLU:OE1	29:U:38:GLU:N	2.37	0.58
33:b:1862:G:H1	33:b:1880:U:H5	1.51	0.58
36:e:5:LEU:HD22	36:e:8:ALA:HB3	1.77	0.58
45:p:18:LEU:HD21	45:p:25:ARG:HB3	1.86	0.58
17:I:51:LEU:C	17:I:56:MET:CE	2.77	0.58
30:X:49:G:H2'	30:X:50:C:C6	2.39	0.58
33:b:27:G:O2'	33:b:28:A:O5'	2.22	0.58
33:b:1443:U:H2'	33:b:1444:G:H8	1.67	0.58
1:0:31:PRO:HG2	1:0:33:LEU:CD1	2.33	0.58
31:Z:30:U:H6	31:Z:30:U:C5'	2.14	0.58
33:b:63:A:O2'	50:u:77:ARG:NH1	2.37	0.58
33:b:2840:C:H5''	44:o:53:THR:HG21	1.86	0.58
37:f:7:TYR:O	37:f:12:VAL:HG23	2.02	0.58
9:A:451:A:N1	9:A:480:U:H2'	2.19	0.58
9:A:581:G:O3'	23:O:63:ARG:NH2	2.34	0.58
17:I:51:LEU:CG	17:I:56:MET:HE2	2.33	0.58
31:Z:19:G:N2	31:Z:59:A:O4'	2.37	0.58
33:b:359:G:H2'	33:b:360:U:C6	2.39	0.58
33:b:2484:G:OP1	43:n:44:ARG:NH1	2.35	0.58
9:A:1086:U:H3	9:A:1099:G:H22	1.51	0.58
17:I:20:ILE:HD11	17:I:60:LEU:HD11	1.85	0.58
33:b:511:U:O2'	33:b:512:G:OP1	2.20	0.58
33:b:1469:A:H2'	33:b:1470:A:C8	2.39	0.58
33:b:2115:G:H4'	33:b:2166:U:H4'	1.83	0.58
38:g:155:GLU:OE1	38:g:158:LYS:N	2.36	0.58
43:n:66:ARG:NH2	43:n:104:GLU:OE2	2.36	0.58
8:8:8:LYS:NZ	33:b:2467:C:OP1	2.33	0.58
9:A:88:U:O2	9:A:90:C:N4	2.35	0.58
14:F:35:LYS:HB3	14:F:37:HIS:CE1	2.39	0.58
19:K:92:ARG:NH2	19:K:111:ASP:OD1	2.37	0.58
33:b:2514:U:H2'	33:b:2515:C:C6	2.39	0.58
9:A:1323:G:H2'	9:A:1324:A:H8	1.68	0.58
24:P:6:LEU:HD11	24:P:19:VAL:HG22	1.85	0.58
33:b:1724:G:O6	33:b:1737:G:N2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1789:A:OP2	34:c:221:ARG:NH1	2.37	0.58
36:e:5:LEU:HD23	36:e:8:ALA:CA	2.34	0.58
11:C:182:ASP:HB2	11:C:203:LYS:HE3	1.85	0.57
31:Y:77:A:C3'	55:z:162:PRO:C	2.77	0.57
33:b:404:A:N6	33:b:421:C:O2'	2.31	0.57
9:A:39:G:H2'	9:A:40:C:C6	2.39	0.57
9:A:979:C:N4	9:A:1318:A:H61	2.02	0.57
10:B:60:ALA:HB3	10:B:223:GLY:HA3	1.84	0.57
29:U:4:LYS:O	29:U:17:ARG:NH2	2.36	0.57
33:b:1425:G:O2'	33:b:1426:G:OP1	2.22	0.57
37:f:94:GLU:HA	37:f:97:TRP:NE1	2.19	0.57
42:m:136:GLU:OE1	42:m:136:GLU:N	2.37	0.57
9:A:1521:C:H2'	9:A:1522:U:C6	2.39	0.57
27:S:28:LYS:HD2	27:S:29:PRO:HD2	1.86	0.57
34:c:6:CYS:SG	34:c:13:ARG:NH2	2.77	0.57
28:T:14:GLU:HA	28:T:17:ARG:HD3	1.85	0.57
33:b:251:A:OP1	42:m:58:TYR:OH	2.22	0.57
33:b:572:A:OP2	48:s:80:ARG:NH2	2.32	0.57
48:s:69:GLY:N	48:s:91:GLN:O	2.37	0.57
49:t:77:ASP:N	49:t:77:ASP:OD1	2.37	0.57
28:T:19:HIS:O	28:T:23:ARG:HG2	2.04	0.57
33:b:1198:U:H2'	33:b:1199:U:C6	2.39	0.57
9:A:1347:G:C6	17:I:108:ARG:NH2	2.72	0.57
13:E:12:GLU:HB2	13:E:63:MET:HE1	1.86	0.57
33:b:500:G:N1	33:b:503:A:OP2	2.35	0.57
39:h:47:PHE:HA	39:h:50:ARG:HE	1.68	0.57
9:A:455:G:H2'	9:A:456:A:C8	2.40	0.57
9:A:582:C:P	23:O:63:ARG:HH22	2.27	0.57
17:I:5:TYR:HB2	17:I:20:ILE:HG22	1.87	0.57
17:I:52:GLU:N	17:I:56:MET:HE3	2.19	0.57
18:J:11:LYS:HB3	18:J:71:LEU:HD23	1.87	0.57
21:M:8:ILE:HG21	21:M:17:ALA:HB1	1.86	0.57
33:b:2848:G:O2'	33:b:2849:U:O5'	2.22	0.57
35:d:39:ASP:OD1	35:d:39:ASP:N	2.35	0.57
48:s:40:MET:HB2	48:s:48:LYS:HG3	1.84	0.57
9:A:227:G:N2	24:P:63:GLN:O	2.29	0.57
9:A:750:C:H2'	9:A:751:U:H6	1.69	0.57
15:G:110:ARG:NH2	15:G:121:ASN:OD1	2.35	0.57
33:b:276:U:O5'	33:b:276:U:H6	1.87	0.57
33:b:883:G:N2	33:b:894:U:O2'	2.38	0.57
9:A:313:A:H2'	9:A:314:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:320:A:O2'	9:A:1435:G:O2'	2.16	0.57
9:A:878:A:OP1	16:H:79:ARG:NH1	2.34	0.57
21:M:23:GLY:HA3	21:M:64:VAL:HG13	1.87	0.57
22:N:3:GLN:HA	22:N:6:LYS:HE2	1.87	0.57
28:T:74:HIS:O	28:T:78:LEU:HG	2.05	0.57
33:b:414:C:H2'	33:b:415:A:H8	1.70	0.57
33:b:549:G:H2'	33:b:550:C:C6	2.39	0.57
33:b:1105:U:H2'	33:b:1106:G:C8	2.40	0.57
33:b:2136:G:N2	33:b:2156:G:H22	2.03	0.57
36:e:138:LEU:CD2	36:e:167:VAL:HG21	2.35	0.57
9:A:40:C:H2'	9:A:41:G:H8	1.70	0.56
9:A:260:G:H2'	9:A:261:U:C6	2.40	0.56
9:A:320:A:H2'	9:A:321:A:C8	2.39	0.56
9:A:1151:A:H5''	18:J:44:THR:HG23	1.85	0.56
9:A:1242:G:H1	9:A:1295:U:H3	1.53	0.56
11:C:177:LEU:HD23	11:C:177:LEU:H	1.70	0.56
32:a:116:G:H2'	32:a:117:G:C8	2.40	0.56
38:g:75:MET:O	38:g:79:VAL:HG23	2.03	0.56
39:h:54:LEU:HA	39:h:57:LYS:HZ3	1.70	0.56
56:V:28:VAL:O	56:V:28:VAL:HG12	2.03	0.56
9:A:636:U:H2'	9:A:637:C:C6	2.40	0.56
9:A:1107:C:OP2	11:C:171:ARG:NH2	2.38	0.56
12:D:2:ARG:HE	12:D:4:LEU:HD21	1.69	0.56
13:E:140:ILE:HG23	13:E:144:GLU:OE1	2.05	0.56
22:N:37:ASP:O	22:N:41:TRP:N	2.37	0.56
33:b:1495:A:O2'	33:b:1496:A:O4'	2.23	0.56
54:y:37:ILE:HG23	54:y:38:VAL:N	2.20	0.56
9:A:714:G:H2'	9:A:715:A:C8	2.40	0.56
9:A:844:G:H2'	9:A:845:A:H2'	1.88	0.56
13:E:53:ARG:HH11	13:E:54:GLU:HB3	1.69	0.56
17:I:9:GLY:HA3	17:I:80:HIS:HB3	1.87	0.56
19:K:110:THR:HG23	29:U:2:VAL:HG22	1.88	0.56
25:Q:12:VAL:HG21	25:Q:42:LYS:HE2	1.87	0.56
30:X:54:U:H3	30:X:58:A:H62	1.52	0.56
33:b:1337:G:O2'	56:V:42:ASP:O	2.21	0.56
33:b:2292:U:H2'	33:b:2293:G:H8	1.69	0.56
36:e:146:VAL:HG12	36:e:185:LYS:HB2	1.87	0.56
39:h:135:HIS:HB3	39:h:138:VAL:HG22	1.87	0.56
43:n:55:ARG:NE	43:n:55:ARG:O	2.38	0.56
15:G:68:VAL:HG11	15:G:103:ILE:HD11	1.88	0.56
33:b:1172:C:OP2	33:b:1174:U:N3	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1802:A:H2'	33:b:1803:A:C8	2.41	0.56
33:b:2177:C:H2'	33:b:2178:C:C6	2.40	0.56
9:A:602:A:H2'	9:A:603:U:H6	1.70	0.56
33:b:2902:C:N4	33:b:2903:U:O4	2.38	0.56
46:q:31:TRP:NE1	46:q:82:ASP:OD2	2.39	0.56
17:I:3:ASN:HB3	17:I:5:TYR:HE1	1.70	0.56
28:T:15:LYS:HG2	28:T:19:HIS:HE1	1.71	0.56
33:b:845:A:H61	33:b:932:U:H3	1.52	0.56
33:b:1636:U:H2'	33:b:1637:A:H8	1.70	0.56
33:b:2187:U:H2'	33:b:2188:U:C6	2.40	0.56
33:b:2685:G:H2'	33:b:2686:G:H8	1.71	0.56
35:d:103:ASP:OD1	35:d:103:ASP:N	2.36	0.56
10:B:50:ASN:HA	10:B:53:LEU:HD12	1.88	0.56
12:D:99:ASN:OD1	12:D:110:ARG:NH2	2.39	0.56
18:J:35:GLN:OE1	18:J:35:GLN:N	2.39	0.56
37:f:100:PHE:CE2	37:f:173:PHE:CE1	2.94	0.56
46:q:106:LYS:HD3	46:q:106:LYS:H	1.69	0.56
1:0:37:ARG:NH1	33:b:2200:C:OP2	2.39	0.56
31:Y:15:G:O2'	31:Y:21:U:N3	2.38	0.56
33:b:414:C:H2'	33:b:415:A:C8	2.41	0.56
35:d:139:SER:O	35:d:139:SER:OG	2.23	0.56
9:A:104:G:H5'	9:A:172:A:H2	1.71	0.56
9:A:308:C:H2'	9:A:309:A:H8	1.70	0.56
9:A:613:C:H2'	9:A:614:C:C6	2.41	0.56
30:X:18:G:N1	30:X:58:A:C6	2.73	0.56
33:b:2246:G:H2'	33:b:2247:A:H8	1.71	0.56
33:b:2315:G:N3	37:f:125:ARG:NH2	2.54	0.56
2:1:26:PHE:HD1	2:1:29:ARG:HH21	1.52	0.56
5:5:7:GLU:N	5:5:7:GLU:OE1	2.39	0.56
9:A:166:U:H2'	9:A:167:A:C8	2.40	0.56
9:A:1081:A:H5'	13:E:22:LYS:HD2	1.88	0.56
10:B:166:ASP:O	10:B:169:HIS:ND1	2.26	0.56
14:F:104:LYS:O	14:F:104:LYS:NZ	2.28	0.56
16:H:87:ARG:HG2	16:H:90:GLU:CD	2.31	0.56
33:b:1485:U:H2'	33:b:1486:U:H6	1.70	0.56
33:b:2522:U:O2'	33:b:2647:U:OP1	2.21	0.56
35:d:13:ARG:NH1	35:d:15:PHE:CZ	2.74	0.56
35:d:88:GLU:HB3	35:d:90:PHE:HE1	1.70	0.56
9:A:10:A:HO2'	9:A:507:C:HO2'	1.53	0.55
9:A:955:U:O2'	27:S:80:ARG:NH2	2.39	0.55
9:A:1347:G:C5	17:I:108:ARG:CZ	2.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1503:A:N6	9:A:1532:U:O2'	2.39	0.55
33:b:2591:C:H2'	33:b:2592:G:H8	1.70	0.55
37:f:66:LEU:HD11	37:f:88:LYS:HB3	1.88	0.55
37:f:142:ASP:H	37:f:145:LYS:NZ	2.05	0.55
50:u:91:GLN:NE2	50:u:92:ASN:OD1	2.39	0.55
32:a:116:G:O3'	45:p:56:LYS:NZ	2.39	0.55
48:s:6:GLN:CA	48:s:37:GLU:OE2	2.55	0.55
9:A:908:A:H2'	9:A:909:A:H8	1.70	0.55
13:E:54:GLU:HG3	13:E:57:ALA:HB3	1.87	0.55
33:b:2428:G:N2	42:m:54:GLN:OE1	2.39	0.55
37:f:91:LEU:HB3	37:f:95:ARG:HG3	1.89	0.55
42:m:29:LYS:O	42:m:30:THR:OG1	2.20	0.55
48:s:49:ILE:HG12	48:s:51:VAL:HG22	1.88	0.55
9:A:337:G:H2'	9:A:338:A:H8	1.71	0.55
9:A:792:A:H4'	9:A:793:U:H5'	1.87	0.55
9:A:1202:U:O2'	22:N:66:THR:HG21	2.06	0.55
12:D:2:ARG:HG2	12:D:4:LEU:HG	1.88	0.55
14:F:30:THR:HA	14:F:34:GLY:H	1.71	0.55
22:N:2:LYS:O	22:N:6:LYS:NZ	2.35	0.55
33:b:279:A:C4	33:b:280:U:H1'	2.42	0.55
33:b:2189:U:H2'	33:b:2190:G:H8	1.71	0.55
9:A:192:A:H2'	9:A:193:C:C6	2.40	0.55
9:A:545:C:O3'	12:D:69:ARG:NH2	2.40	0.55
9:A:954:G:N2	9:A:1228:C:C4	2.74	0.55
10:B:18:GLN:HG3	10:B:20:ARG:H	1.70	0.55
10:B:46:VAL:O	10:B:50:ASN:ND2	2.32	0.55
11:C:14:VAL:HB	11:C:206:ILE:HD12	1.87	0.55
31:Y:6:A:O2'	31:Y:7:U:O5'	2.25	0.55
31:Y:14:A:N1	31:Y:22:A:O2'	2.39	0.55
33:b:45:G:H5'	33:b:46:G:OP1	2.07	0.55
37:f:34:ILE:HD12	37:f:156:ILE:HG13	1.89	0.55
51:v:96:PHE:O	51:v:100:SER:HA	2.07	0.55
9:A:591:U:H2'	9:A:592:G:H8	1.71	0.55
28:T:27:MET:HE3	28:T:28:ARG:HD3	1.89	0.55
31:Y:18:U:O2'	31:Y:19:G:O5'	2.24	0.55
33:b:1051:G:H4'	33:b:1052:C:OP1	2.05	0.55
33:b:1936:A:H2	33:b:1943:U:C5	2.25	0.55
33:b:2251:G:OP1	43:n:81:ARG:NH1	2.40	0.55
48:s:32:THR:HA	48:s:62:GLU:HA	1.88	0.55
1:0:59:ILE:HD13	1:0:67:VAL:HG21	1.87	0.55
9:A:106:C:H2'	9:A:107:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C:10:ARG:NH2	11:C:176:THR:O	2.32	0.55
30:X:26:A:H61	30:X:44:G:H1	1.54	0.55
32:a:43:C:O2	37:f:92:ARG:NH2	2.39	0.55
33:b:859:G:O2'	33:b:916:G:O6	2.24	0.55
33:b:1055:G:O2'	33:b:1056:G:O5'	2.24	0.55
33:b:845:A:N6	33:b:932:U:H3	2.04	0.55
33:b:881:G:H3'	33:b:882:G:H8	1.72	0.55
33:b:1791:A:N6	33:b:1828:G:O2'	2.33	0.55
9:A:1039:G:H2'	9:A:1040:U:C6	2.42	0.55
11:C:72:PRO:HA	11:C:75:VAL:HB	1.89	0.55
21:M:66:GLY:HA2	21:M:69:ARG:HH11	1.71	0.55
28:T:43:LYS:HG3	28:T:86:ALA:HA	1.88	0.55
30:X:27:C:N3	30:X:44:G:N2	2.55	0.55
49:t:82:MET:SD	55:z:131:MET:HE1	2.47	0.55
51:v:101:GLU:OE1	51:v:101:GLU:N	2.38	0.55
9:A:430:A:P	12:D:7:LYS:HG2	2.46	0.55
9:A:875:U:O2'	16:H:14:ARG:NH1	2.40	0.55
9:A:1015:G:H2'	9:A:1016:A:C8	2.42	0.55
9:A:1227:A:OP2	21:M:109:LYS:NZ	2.36	0.55
16:H:38:VAL:HG21	16:H:109:VAL:HG12	1.88	0.55
51:v:54:GLN:N	51:v:55:PRO:HD3	2.21	0.55
8:8:11:CYS:SG	8:8:33:HIS:HE1	2.29	0.54
9:A:337:G:H2'	9:A:338:A:C8	2.42	0.54
16:H:11:THR:O	16:H:15:ASN:ND2	2.40	0.54
16:H:12:ARG:HA	16:H:15:ASN:HD21	1.71	0.54
29:U:5:VAL:HA	29:U:9:GLU:OE1	2.07	0.54
39:h:41:LYS:O	39:h:45:GLU:HG3	2.07	0.54
9:A:339:C:OP2	41:l:98:ARG:NH2	2.39	0.54
9:A:1175:G:H2'	9:A:1176:A:C8	2.41	0.54
10:B:126:ASP:N	10:B:126:ASP:OD1	2.36	0.54
14:F:90:MET:SD	26:R:60:ARG:NH2	2.80	0.54
18:J:54:SER:O	22:N:80:ARG:NH2	2.40	0.54
20:L:32:VAL:HA	20:L:78:VAL:HA	1.90	0.54
33:b:1854:A:H62	33:b:1888:G:H8	1.54	0.54
38:g:166:ASP:N	38:g:166:ASP:OD1	2.40	0.54
39:h:121:VAL:O	39:h:121:VAL:CG1	2.52	0.54
9:A:486:U:H2'	9:A:487:A:C8	2.43	0.54
9:A:600:A:P	16:H:87:ARG:HB2	2.47	0.54
9:A:779:C:H1'	19:K:121:ARG:NH2	2.22	0.54
10:B:83:ALA:HA	10:B:88:GLN:HG2	1.88	0.54
18:J:5:ARG:HD2	18:J:5:ARG:C	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:21:ALA:O	18:J:25:ILE:HG12	2.07	0.54
28:T:52:GLU:N	28:T:52:GLU:OE1	2.40	0.54
30:X:22:G:H2'	30:X:23:A:C8	2.41	0.54
33:b:1019:U:OP1	33:b:1035:U:O2'	2.23	0.54
33:b:1487:U:O4	33:b:1502:A:N6	2.33	0.54
33:b:1965:C:H5''	33:b:1966:A:H2'	1.89	0.54
33:b:2307:G:H5'	33:b:2308:G:C4	2.42	0.54
33:b:2859:G:H2'	33:b:2860:A:C8	2.42	0.54
37:f:35:THR:CG2	37:f:155:THR:HB	2.37	0.54
4:4:31:ASP:OD1	4:4:34:SER:N	2.40	0.54
12:D:167:PRO:HB2	12:D:169:TRP:CD1	2.42	0.54
17:I:129:ARG:NH2	31:Y:36:G:OP2	2.36	0.54
26:R:37:LYS:HG2	26:R:38:ILE:H	1.73	0.54
33:b:288:U:H2'	33:b:289:G:C8	2.42	0.54
33:b:307:G:N1	33:b:310:A:OP2	2.38	0.54
33:b:1796:U:H2'	33:b:1797:G:C8	2.42	0.54
33:b:1858:A:N6	33:b:1884:G:O2'	2.41	0.54
9:A:456:A:H2'	9:A:457:G:C8	2.42	0.54
9:A:1347:G:C8	17:I:108:ARG:HB3	2.43	0.54
33:b:1089:A:H1'	33:b:1090:A:N1	2.22	0.54
33:b:1589:U:H2'	33:b:1590:A:H8	1.73	0.54
33:b:2130:U:H5'	33:b:2131:U:H2'	1.90	0.54
33:b:2595:G:N2	33:b:2598:A:OP2	2.31	0.54
9:A:693:G:N2	30:X:38:A:O2'	2.40	0.54
9:A:745:G:H2'	9:A:746:A:H8	1.71	0.54
9:A:1320:C:H42	27:S:35:ARG:HG3	1.71	0.54
12:D:109:THR:HG22	12:D:112:GLU:CG	2.23	0.54
33:b:289:G:H2'	33:b:290:U:C6	2.43	0.54
33:b:1082:U:H2'	33:b:1083:U:H4'	1.89	0.54
33:b:1485:U:H2'	33:b:1486:U:C6	2.43	0.54
33:b:2529:G:O4'	38:g:175:LYS:NZ	2.33	0.54
35:d:30:GLU:OE1	35:d:30:GLU:N	2.39	0.54
48:s:40:MET:HE3	48:s:48:LYS:HB2	1.89	0.54
9:A:36:C:H5'	20:L:117:GLY:HA2	1.87	0.54
9:A:148:G:H1	9:A:174:A:H61	1.55	0.54
9:A:426:U:H1'	12:D:39:GLN:HG2	1.90	0.54
10:B:102:ASN:O	10:B:105:THR:OG1	2.26	0.54
33:b:2345:G:N3	33:b:2381:A:H2'	2.22	0.54
33:b:2591:C:H2'	33:b:2592:G:C8	2.42	0.54
36:e:143:LEU:HD23	36:e:146:VAL:CG1	2.33	0.54
37:f:88:LYS:NZ	37:f:90:THR:CG2	2.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:2:LEU:H	43:n:2:LEU:HD12	1.73	0.54
9:A:10:A:O2'	9:A:507:C:O2'	2.25	0.54
9:A:977:A:N6	9:A:1224:U:OP1	2.41	0.54
9:A:1251:A:H2'	9:A:1252:A:C8	2.43	0.54
9:A:1253:G:H2'	9:A:1254:A:H8	1.73	0.54
9:A:1254:A:H2'	9:A:1255:G:C8	2.42	0.54
9:A:1300:G:N2	9:A:1301:U:O4	2.38	0.54
9:A:1317:C:H2'	9:A:1318:A:O4'	2.08	0.54
14:F:15:SER:O	14:F:18:VAL:HG23	2.08	0.54
16:H:86:LYS:HB2	16:H:124:ILE:HD11	1.89	0.54
17:I:29:ILE:N	17:I:32:ARG:O	2.28	0.54
33:b:2858:C:O2'	33:b:2859:G:O5'	2.25	0.54
9:A:459:A:H2'	9:A:460:A:H8	1.72	0.54
9:A:713:G:H2'	9:A:714:G:C8	2.42	0.54
9:A:1435:G:H2'	9:A:1436:U:C6	2.43	0.54
12:D:145:ARG:HB2	12:D:148:ALA:H	1.73	0.54
28:T:15:LYS:O	28:T:19:HIS:ND1	2.31	0.54
33:b:2102:G:C2	33:b:2187:U:O2	2.61	0.54
37:f:173:PHE:CG	37:f:173:PHE:O	2.61	0.54
49:t:85:ILE:CD1	55:z:140:THR:HB	2.38	0.54
9:A:1237:C:H3'	9:A:1336:C:H41	1.73	0.54
21:M:57:ASP:OD1	21:M:58:GLU:N	2.41	0.54
33:b:65:U:H1'	50:u:73:ARG:HG2	1.89	0.54
33:b:172:A:H2'	33:b:173:A:C8	2.42	0.54
33:b:549:G:H2'	33:b:550:C:H6	1.73	0.54
33:b:2279:G:N7	54:y:14:ARG:NH2	2.51	0.54
35:d:149:ASN:O	35:d:152:PRO:HD2	2.08	0.54
9:A:86:G:OP1	9:A:86:G:N2	2.40	0.53
9:A:384:G:H2'	9:A:385:C:C6	2.42	0.53
9:A:830:G:O3'	10:B:20:ARG:NH1	2.40	0.53
16:H:6:ILE:HB	16:H:76:ARG:NH1	2.23	0.53
28:T:28:ARG:HA	28:T:31:ILE:HG22	1.90	0.53
33:b:1433:A:N6	33:b:1560:G:H1	2.03	0.53
37:f:7:TYR:H	37:f:7:TYR:HD1	1.54	0.53
2:l:5:GLU:OE1	2:l:5:GLU:N	2.41	0.53
7:7:6:THR:HG22	7:7:63:PRO:HD2	1.89	0.53
9:A:82:G:N7	9:A:83:C:N4	2.56	0.53
9:A:682:G:H2'	9:A:683:G:H8	1.72	0.53
9:A:1445:U:H3	9:A:1457:G:H1	1.56	0.53
11:C:160:GLU:HG3	53:x:23:A:H5''	1.90	0.53
12:D:122:ILE:HD12	12:D:144:ILE:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:15:SER:HA	14:F:18:VAL:HG23	1.88	0.53
18:J:66:GLU:OE1	22:N:98:ALA:N	2.41	0.53
19:K:75:GLU:OE1	19:K:75:GLU:N	2.39	0.53
28:T:15:LYS:HG2	28:T:19:HIS:CE1	2.43	0.53
33:b:1099:G:H8	33:b:1099:G:OP1	1.90	0.53
33:b:1506:U:H5'	33:b:1507:C:OP2	2.09	0.53
37:f:8:TYR:HA	37:f:12:VAL:HB	1.90	0.53
44:o:72:ASP:OD1	44:o:73:ASN:N	2.40	0.53
9:A:425:G:N2	12:D:39:GLN:OE1	2.41	0.53
9:A:582:C:H5''	23:O:63:ARG:HH12	1.72	0.53
9:A:1299:A:C8	9:A:1301:U:H1'	2.43	0.53
9:A:1401:G:H2'	9:A:1402:C:C6	2.43	0.53
19:K:97:ARG:HA	29:U:11:PHE:HE2	1.72	0.53
9:A:691:G:H2'	9:A:692:U:C6	2.43	0.53
9:A:994:A:N1	9:A:1216:A:H4'	2.23	0.53
9:A:1320:C:H2'	9:A:1321:U:C6	2.43	0.53
9:A:1356:G:H2'	9:A:1357:A:H8	1.73	0.53
20:L:101:LEU:HD23	20:L:101:LEU:H	1.73	0.53
24:P:69:ASP:OD1	24:P:69:ASP:N	2.42	0.53
31:Y:56:U:O2'	31:Y:58:G:N7	2.36	0.53
33:b:740:C:H5	33:b:757:G:H22	1.56	0.53
33:b:2123:G:O6	33:b:2176:A:N6	2.41	0.53
46:q:65:SER:OG	46:q:66:ASN:OD1	2.27	0.53
9:A:215:C:H2'	9:A:216:U:C6	2.44	0.53
10:B:46:VAL:HG23	10:B:47:PRO:HD3	1.91	0.53
13:E:113:VAL:HG11	13:E:139:THR:HG22	1.90	0.53
19:K:92:ARG:HH12	29:U:27:VAL:HG21	1.74	0.53
30:X:18:G:C6	30:X:58:A:N1	2.77	0.53
33:b:613:A:H5'	33:b:614:A:H2	1.71	0.53
33:b:2062:A:C6	55:z:158:ARG:HD2	2.44	0.53
1:0:61:LYS:NZ	33:b:372:G:O4'	2.32	0.53
9:A:185:U:H2'	9:A:186:C:H6	1.74	0.53
9:A:623:C:H2'	9:A:624:C:H6	1.74	0.53
11:C:185:THR:HB	11:C:198:LYS:HZ3	1.73	0.53
25:Q:10:ARG:O	25:Q:23:ALA:N	2.38	0.53
31:Z:1:C:H2'	31:Z:2:G:H8	1.73	0.53
33:b:1703:G:H2'	33:b:1704:C:C6	2.44	0.53
33:b:2112:G:OP2	33:b:2114:A:N6	2.42	0.53
36:e:143:LEU:HD23	36:e:146:VAL:HG21	1.91	0.53
1:0:28:ARG:HH22	33:b:1365:A:H5''	1.73	0.53
5:5:7:GLU:OE2	5:5:27:LYS:NZ	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:514:C:H2'	9:A:515:G:H8	1.72	0.53
9:A:993:G:O2'	9:A:994:A:N7	2.41	0.53
17:I:18:VAL:HG22	17:I:64:ILE:HG22	1.91	0.53
33:b:1013:C:H2'	33:b:1014:A:H8	1.73	0.53
33:b:1538:G:H2'	33:b:1539:U:H6	1.72	0.53
33:b:2847:U:OP1	46:q:96:LYS:NZ	2.42	0.53
41:l:85:VAL:HG11	41:l:115:ILE:HD11	1.90	0.53
43:n:20:LEU:HD13	52:w:81:PRO:HG2	1.90	0.53
49:t:2:GLU:OE1	49:t:2:GLU:N	2.41	0.53
56:V:39:VAL:HB	56:V:58:TYR:OH	2.08	0.53
2:l:47:ARG:NH2	33:b:61:C:OP2	2.41	0.53
9:A:35:G:H1'	20:L:114:SER:O	2.09	0.53
9:A:481:G:H1'	9:A:483:C:N4	2.24	0.53
9:A:542:G:O3'	12:D:13:ARG:NH2	2.42	0.53
9:A:1009:U:H3	9:A:1020:G:H1	1.56	0.53
9:A:1130:A:H2'	9:A:1131:G:H8	1.73	0.53
27:S:38:THR:HG22	27:S:69:LYS:HG2	1.91	0.53
32:a:44:G:H21	32:a:47:C:H5	1.56	0.53
46:q:11:GLU:OE1	46:q:11:GLU:N	2.42	0.53
9:A:113:G:N3	9:A:353:A:O2'	2.41	0.53
9:A:363:A:N6	20:L:26:CYS:SG	2.82	0.53
9:A:1300:G:C4	9:A:1334:G:O6	2.62	0.53
9:A:1343:G:H2'	9:A:1344:C:C6	2.44	0.53
33:b:581:C:H2'	33:b:582:A:C8	2.44	0.53
33:b:1475:G:H1'	33:b:1476:U:H5	1.73	0.53
33:b:2328:A:H2'	33:b:2329:U:C6	2.43	0.53
50:u:54:GLU:HB2	50:u:88:LYS:HG3	1.91	0.53
9:A:1106:G:H3'	11:C:171:ARG:HH21	1.74	0.53
9:A:1199:U:H4'	18:J:56:HIS:NE2	2.23	0.53
32:a:52:A:N7	45:p:33:ARG:NH1	2.57	0.53
33:b:1820:U:H3	34:c:159:GLY:HA3	1.73	0.53
34:c:75:PRO:HD2	34:c:97:LYS:HD3	1.91	0.53
38:g:133:LEU:HD12	38:g:133:LEU:C	2.33	0.53
9:A:269:C:H2'	9:A:270:A:C8	2.44	0.52
9:A:458:U:H2'	9:A:459:A:C8	2.44	0.52
9:A:625:U:H2'	9:A:626:G:C8	2.43	0.52
9:A:1219:A:H2'	9:A:1220:G:C8	2.43	0.52
20:L:74:GLN:HG3	20:L:75:GLU:H	1.74	0.52
23:O:60:SER:O	23:O:63:ARG:HG3	2.08	0.52
54:y:56:ASP:OD1	54:y:56:ASP:N	2.42	0.52
3:2:45:ARG:NH2	3:2:59:GLU:OE1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:104:G:H2'	9:A:105:G:H8	1.73	0.52
9:A:778:G:H21	19:K:121:ARG:CZ	2.21	0.52
9:A:973:G:H5'	18:J:59:LYS:HE2	1.91	0.52
9:A:1287:A:H2	9:A:1353:G:H1'	1.74	0.52
9:A:1300:G:C4	9:A:1334:G:C6	2.98	0.52
9:A:1303:C:H2'	9:A:1304:G:O4'	2.09	0.52
9:A:1349:A:H1'	9:A:1374:A:H61	1.74	0.52
31:Z:24:C:H2'	31:Z:25:G:C8	2.43	0.52
33:b:2521:C:C2	33:b:2545:G:N2	2.77	0.52
9:A:74:A:H2'	9:A:75:G:H8	1.74	0.52
9:A:975:A:H5''	9:A:1365:G:H22	1.75	0.52
12:D:101:VAL:HG23	12:D:113:ALA:HB1	1.92	0.52
12:D:119:HIS:C	12:D:130:ASN:HD21	2.16	0.52
19:K:88:PRO:HG3	29:U:31:VAL:HG11	1.91	0.52
23:O:12:SER:OG	23:O:13:GLU:OE1	2.27	0.52
31:Y:63:C:H2'	31:Y:64:U:C6	2.45	0.52
31:Z:1:C:H2'	31:Z:2:G:C8	2.44	0.52
31:Z:23:G:N7	31:Z:47:G:N2	2.50	0.52
33:b:271:G:H1'	33:b:272:A:C8	2.44	0.52
33:b:955:U:OP1	43:n:86:LYS:NZ	2.42	0.52
33:b:1924:C:H2'	33:b:1925:C:C6	2.44	0.52
33:b:2100:G:H2'	33:b:2101:A:C8	2.45	0.52
33:b:2164:C:H4'	33:b:2165:C:H5'	1.90	0.52
33:b:2731:G:H2'	33:b:2732:G:C8	2.44	0.52
36:e:97:ASN:HB2	36:e:100:MET:HG2	1.91	0.52
52:w:76:ASP:OD1	52:w:77:VAL:N	2.42	0.52
9:A:741:G:OP1	23:O:1:SER:N	2.42	0.52
12:D:10:LEU:HG	12:D:62:ARG:HE	1.71	0.52
15:G:115:MET:SD	15:G:115:MET:N	2.77	0.52
51:v:14:LEU:HD11	51:v:71:ALA:HB2	1.91	0.52
9:A:472:U:H2'	9:A:473:U:H6	1.75	0.52
9:A:946:A:H2'	9:A:947:G:H8	1.74	0.52
9:A:1100:C:H3'	10:B:94:ARG:HH12	1.74	0.52
9:A:1346:A:N6	9:A:1375:A:N7	2.48	0.52
12:D:114:ARG:HA	12:D:117:VAL:HG22	1.91	0.52
33:b:306:U:H3	33:b:310:A:H62	1.57	0.52
33:b:406:G:H2'	33:b:407:G:H8	1.74	0.52
33:b:721:A:H2'	33:b:722:A:C8	2.45	0.52
33:b:2315:G:H21	37:f:125:ARG:HH22	1.56	0.52
33:b:2635:A:O2'	35:d:81:GLU:OE2	2.26	0.52
37:f:100:PHE:O	37:f:104:ILE:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:427:U:H5''	12:D:9:LYS:HD2	1.91	0.52
27:S:41:PRO:HA	27:S:44:ILE:HD11	1.91	0.52
33:b:1443:U:H2'	33:b:1444:G:C8	2.44	0.52
47:r:50:ARG:HH12	48:s:74:ILE:HG13	1.74	0.52
1:0:42:SER:OG	1:0:43:GLU:OE1	2.27	0.52
9:A:135:C:O2	24:P:1:MET:HB2	2.10	0.52
9:A:171:A:H2'	9:A:172:A:C8	2.44	0.52
9:A:591:U:H2'	9:A:592:G:C8	2.45	0.52
9:A:691:G:N2	9:A:695:A:C8	2.74	0.52
24:P:23:ASP:OD1	24:P:24:SER:N	2.43	0.52
33:b:413:C:HO2'	33:b:1880:U:HO2'	1.57	0.52
33:b:1115:G:H2'	33:b:1116:G:C8	2.44	0.52
33:b:2183:A:H2'	33:b:2184:A:C8	2.45	0.52
49:t:84:ARG:HA	55:z:137:VAL:HG21	1.91	0.52
9:A:127:G:O2'	25:Q:5:ARG:NH1	2.43	0.52
9:A:438:U:OP2	12:D:147:LYS:NZ	2.43	0.52
9:A:945:G:N2	9:A:1334:G:O2'	2.43	0.52
9:A:978:A:N7	9:A:1318:A:N6	2.58	0.52
9:A:1162:C:H2'	9:A:1163:A:H8	1.73	0.52
12:D:96:ARG:HB3	12:D:99:ASN:HB3	1.91	0.52
33:b:1417:C:HO2'	33:b:1587:G:HO2'	1.57	0.52
43:n:81:ARG:NH2	54:y:4:LYS:HB2	2.24	0.52
9:A:110:C:OP1	9:A:111:G:N2	2.43	0.52
9:A:137:U:H2'	9:A:138:G:H8	1.75	0.52
9:A:335:C:H2'	9:A:336:A:H8	1.75	0.52
9:A:950:U:OP2	21:M:100:ARG:HD2	2.10	0.52
9:A:1147:C:H2'	9:A:1148:U:H6	1.74	0.52
9:A:1374:A:O3'	15:G:27:ASN:ND2	2.43	0.52
12:D:123:MET:SD	12:D:145:ARG:HG2	2.49	0.52
33:b:959:A:H2'	33:b:960:A:C8	2.45	0.52
33:b:1321:A:C6	55:z:129:ARG:NH2	2.78	0.52
52:w:6:ALA:HB3	52:w:65:VAL:HG22	1.92	0.52
9:A:263:A:H2'	9:A:264:C:C6	2.45	0.52
9:A:674:G:H2'	9:A:675:A:C8	2.45	0.52
33:b:1585:C:H2'	33:b:1586:A:O4'	2.10	0.52
33:b:2109:U:O2	33:b:2180:U:N3	2.43	0.52
50:u:17:SER:OG	50:u:18:GLU:N	2.42	0.52
52:w:7:GLU:OE1	52:w:7:GLU:N	2.43	0.52
9:A:948:C:H3'	21:M:104:ASN:HD22	1.76	0.51
9:A:1376:U:H2'	9:A:1377:A:C8	2.45	0.51
9:A:1458:G:OP1	28:T:25:SER:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:X:44:G:H2'	30:X:45:G:C4	2.45	0.51
30:X:47:U:H4'	30:X:48:C:H5'	1.91	0.51
30:X:55:U:H2'	30:X:56:C:H2'	1.92	0.51
33:b:2302:U:O2'	37:f:123:ASP:O	2.26	0.51
36:e:146:VAL:HG13	36:e:185:LYS:HB2	1.92	0.51
38:g:86:LYS:HG2	38:g:132:VAL:HG12	1.92	0.51
9:A:308:C:H2'	9:A:309:A:C8	2.45	0.51
9:A:500:G:P	9:A:500:G:H8	2.34	0.51
10:B:122:ASP:N	10:B:122:ASP:OD1	2.42	0.51
16:H:9:MET:HE1	16:H:26:MET:CE	2.40	0.51
33:b:1332:G:N7	33:b:1609:A:O2'	2.37	0.51
33:b:1406:U:H2'	33:b:1407:G:H8	1.75	0.51
33:b:2133:G:O3'	33:b:2157:G:N2	2.44	0.51
9:A:175:C:H2'	9:A:176:C:C6	2.45	0.51
9:A:1048:G:H5''	22:N:2:LYS:HG2	1.92	0.51
17:I:80:HIS:HA	17:I:83:THR:HG22	1.92	0.51
20:L:34:THR:OG1	20:L:55:ARG:HG3	2.11	0.51
21:M:18:LEU:O	21:M:21:ILE:HG12	2.10	0.51
33:b:475:C:O2	33:b:479:A:N6	2.43	0.51
33:b:878:A:H3'	33:b:879:G:C8	2.45	0.51
11:C:110:LEU:HD23	11:C:111:ASP:N	2.26	0.51
16:H:76:ARG:NH2	16:H:78:SER:O	2.44	0.51
17:I:60:LEU:HD22	17:I:61:ASP:H	1.76	0.51
18:J:52:LEU:HD23	18:J:52:LEU:H	1.75	0.51
25:Q:13:SER:OG	25:Q:21:VAL:N	2.41	0.51
33:b:411:G:OP2	33:b:2406:A:O2'	2.28	0.51
9:A:392:C:OP2	24:P:8:ARG:NH2	2.40	0.51
9:A:1212:U:H5'	9:A:1213:A:N7	2.26	0.51
9:A:1450:U:H2'	9:A:1452:C:C4	2.46	0.51
10:B:65:LYS:HG3	10:B:89:PHE:HE2	1.76	0.51
15:G:142:ARG:NH2	30:X:41:U:O2'	2.43	0.51
19:K:17:ASP:OD2	19:K:36:ARG:NH1	2.44	0.51
19:K:23:HIS:HB3	19:K:30:ILE:HG13	1.91	0.51
20:L:97:VAL:O	20:L:103:CYS:SG	2.67	0.51
30:X:18:G:C8	30:X:60:U:C5	2.99	0.51
33:b:84:A:OP1	51:v:6:ARG:NH2	2.42	0.51
33:b:521:U:H2'	33:b:522:A:H8	1.76	0.51
33:b:718:A:H5''	33:b:719:C:C5	2.46	0.51
33:b:1361:G:H2'	33:b:1362:C:C6	2.46	0.51
33:b:2100:G:C6	33:b:2101:A:C6	2.99	0.51
36:e:5:LEU:CD2	36:e:8:ALA:CA	2.89	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:f:46:ASP:OD2	37:f:49:LEU:N	2.43	0.51
39:h:15:LEU:HD21	39:h:54:LEU:HD13	1.92	0.51
39:h:31:VAL:N	39:h:32:PRO:CD	2.73	0.51
9:A:218:U:H5''	9:A:219:U:H5	1.75	0.51
9:A:378:G:H2'	9:A:379:C:H6	1.75	0.51
9:A:475:C:H2'	9:A:476:U:C6	2.46	0.51
15:G:74:VAL:HA	15:G:87:PRO:HA	1.91	0.51
27:S:11:ASP:OD2	27:S:13:HIS:NE2	2.44	0.51
30:X:9:A:H1'	30:X:45:G:N7	2.25	0.51
33:b:705:A:N6	33:b:726:G:H1'	2.25	0.51
56:V:22:ASP:O	56:V:26:THR:OG1	2.27	0.51
9:A:543:U:OP1	12:D:13:ARG:NE	2.44	0.51
9:A:876:C:H1'	16:H:11:THR:HG21	1.92	0.51
9:A:1147:C:H4'	17:I:6:TYR:CZ	2.45	0.51
27:S:31:ARG:NH1	27:S:32:THR:O	2.44	0.51
32:a:48:U:OP1	45:p:30:ARG:NH2	2.43	0.51
32:a:51:G:OP1	45:p:63:LYS:NZ	2.44	0.51
33:b:1597:A:H5''	33:b:1598:A:H5'	1.91	0.51
33:b:2313:C:H2'	33:b:2314:A:C8	2.46	0.51
9:A:430:A:P	12:D:7:LYS:H	2.33	0.51
9:A:1178:G:N2	9:A:1181:G:OP2	2.42	0.51
9:A:1237:C:H4'	9:A:1300:G:H22	1.76	0.51
29:U:28:LEU:HD23	29:U:28:LEU:H	1.75	0.51
30:X:19:G:H5'	30:X:57:G:H21	1.75	0.51
31:Y:76:C:H5	54:y:3:HIS:ND1	2.09	0.51
31:Z:6:A:N3	31:Z:6:A:H5''	2.26	0.51
33:b:721:A:H2'	33:b:722:A:H8	1.75	0.51
39:h:114:GLU:O	39:h:116:ARG:NH2	2.44	0.51
9:A:275:G:H2'	9:A:276:G:C8	2.46	0.51
9:A:1115:U:H2'	9:A:1116:U:C6	2.46	0.51
17:I:87:MET:N	17:I:87:MET:SD	2.83	0.51
18:J:21:ALA:O	18:J:24:GLU:HG3	2.10	0.51
31:Y:17:C:OP2	31:Y:18:U:O2'	2.20	0.51
31:Y:76:C:H41	54:y:3:HIS:HA	1.74	0.51
32:a:49:C:H2'	32:a:50:A:H8	1.76	0.51
33:b:134:G:H2'	33:b:135:U:C6	2.45	0.51
33:b:580:U:H2'	33:b:581:C:C6	2.46	0.51
37:f:40:VAL:HG11	37:f:43:ALA:HB2	1.92	0.51
39:h:114:GLU:OE2	39:h:133:GLN:N	2.42	0.51
47:r:49:ASP:HA	47:r:52:GLN:HG3	1.91	0.51
49:t:85:ILE:HD12	55:z:140:THR:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:56:LYS:HD3	3:2:57:VAL:N	2.26	0.51
9:A:673:A:H2'	9:A:674:G:H8	1.76	0.51
9:A:1192:C:P	11:C:3:LYS:HZ1	2.32	0.51
9:A:1489:G:H2'	9:A:1490:U:C6	2.46	0.51
15:G:13:PRO:HB2	15:G:18:GLY:HA2	1.93	0.51
15:G:142:ARG:NH2	30:X:42:C:O5'	2.34	0.51
16:H:13:ILE:HD11	16:H:60:LEU:HD12	1.93	0.51
18:J:5:ARG:HD2	18:J:5:ARG:O	2.11	0.51
31:Z:59:A:O2'	31:Z:61:U:OP2	2.28	0.51
33:b:1087:G:H4'	33:b:1089:A:H4'	1.93	0.51
33:b:1395:A:O2'	33:b:1396:U:H5''	2.11	0.51
38:g:52:PHE:HE2	38:g:72:LEU:CD1	2.23	0.51
1:0:31:PRO:HG2	1:0:33:LEU:HD11	1.92	0.50
9:A:31:G:N3	9:A:306:A:O2'	2.42	0.50
9:A:486:U:H2'	9:A:487:A:H8	1.75	0.50
9:A:622:A:H5''	9:A:623:C:H5	1.75	0.50
9:A:1072:G:H2'	9:A:1073:U:C6	2.46	0.50
15:G:121:ASN:O	15:G:124:SER:OG	2.27	0.50
16:H:77:VAL:HG12	16:H:84:ILE:HD13	1.92	0.50
20:L:26:CYS:HB2	20:L:29:LYS:HE3	1.93	0.50
28:T:51:ASN:HA	28:T:54:GLN:HE22	1.76	0.50
31:Y:72:C:H2'	31:Y:73:G:H8	1.76	0.50
33:b:1496:A:H2'	33:b:1498:C:C5	2.46	0.50
33:b:1590:A:H2'	33:b:1591:A:C8	2.45	0.50
33:b:1762:A:O2'	33:b:1763:G:OP1	2.27	0.50
33:b:2246:G:H2'	33:b:2247:A:C8	2.46	0.50
33:b:2839:G:O2'	44:o:49:GLU:OE1	2.22	0.50
36:e:119:ILE:O	36:e:187:VAL:HA	2.12	0.50
44:o:72:ASP:OD1	44:o:74:GLU:N	2.44	0.50
45:p:88:LYS:HZ3	45:p:116:GLN:HE21	1.60	0.50
9:A:59:A:H2	9:A:330:C:H42	1.59	0.50
9:A:144:G:C2	9:A:179:A:C8	2.99	0.50
9:A:338:A:H2'	9:A:339:C:H6	1.75	0.50
9:A:978:A:C2	9:A:1319:A:C4	2.99	0.50
9:A:1164:G:H2'	9:A:1165:U:C6	2.46	0.50
13:E:59:ILE:O	13:E:63:MET:HG2	2.11	0.50
17:I:33:SER:O	17:I:37:TYR:N	2.40	0.50
20:L:5:GLN:HG2	20:L:8:ARG:HH12	1.76	0.50
25:Q:66:LEU:HD23	25:Q:66:LEU:H	1.76	0.50
27:S:28:LYS:NZ	27:S:29:PRO:O	2.44	0.50
30:X:5:G:H2'	30:X:6:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1484:U:H2'	33:b:1485:U:C6	2.45	0.50
49:t:29:VAL:HG21	49:t:55:ILE:HD11	1.93	0.50
9:A:601:G:OP2	16:H:87:ARG:NH2	2.44	0.50
9:A:606:G:H21	9:A:631:C:H3'	1.77	0.50
11:C:22:PHE:HE2	18:J:12:ALA:HA	1.76	0.50
13:E:81:GLN:HA	13:E:97:PRO:CG	2.42	0.50
18:J:25:ILE:HA	18:J:28:THR:HG22	1.93	0.50
19:K:32:THR:OG1	19:K:42:GLY:O	2.25	0.50
23:O:11:VAL:HG21	23:O:21:THR:HG22	1.93	0.50
28:T:37:ALA:HB1	28:T:46:ALA:HA	1.92	0.50
33:b:645:C:N4	33:b:2349:G:N3	2.59	0.50
33:b:874:G:O6	33:b:899:A:N6	2.45	0.50
33:b:1386:C:H2'	33:b:1387:A:H8	1.76	0.50
36:e:5:LEU:CG	36:e:6:LYS:H	2.24	0.50
37:f:173:PHE:O	37:f:173:PHE:CD2	2.64	0.50
1:0:67:VAL:O	1:0:70:GLU:HG3	2.12	0.50
9:A:54:C:H2'	9:A:352:C:H41	1.76	0.50
9:A:623:C:H2'	9:A:624:C:C6	2.46	0.50
9:A:958:A:N7	27:S:54:ARG:NH2	2.60	0.50
9:A:1349:A:H5''	17:I:119:LYS:HE3	1.92	0.50
10:B:122:ASP:HA	10:B:125:PHE:HD2	1.76	0.50
10:B:186:VAL:HG13	10:B:190:SER:HB2	1.93	0.50
13:E:139:THR:OG1	13:E:140:ILE:N	2.44	0.50
33:b:172:A:H2'	33:b:173:A:H8	1.76	0.50
33:b:2154:A:H2'	33:b:2155:U:C6	2.47	0.50
33:b:2813:A:H2'	33:b:2814:A:H8	1.76	0.50
35:d:88:GLU:N	35:d:88:GLU:OE1	2.43	0.50
36:e:7:ASP:OD1	36:e:7:ASP:N	2.42	0.50
37:f:40:VAL:HG21	37:f:50:LEU:HD23	1.94	0.50
45:p:61:GLN:N	45:p:61:GLN:OE1	2.44	0.50
55:z:140:THR:O	55:z:144:ALA:HB2	2.11	0.50
9:A:92:U:H2'	9:A:93:U:C2	2.46	0.50
9:A:237:G:H5''	25:Q:26:ARG:HH22	1.77	0.50
9:A:580:C:O3'	23:O:57:ARG:NH1	2.45	0.50
9:A:830:G:O2'	10:B:20:ARG:NH2	2.37	0.50
9:A:1007:U:N3	9:A:1023:U:O2	2.44	0.50
9:A:1036:A:H2'	9:A:1037:C:C6	2.46	0.50
9:A:1124:G:H5'	18:J:37:ARG:NH1	2.27	0.50
15:G:142:ARG:HH12	30:X:42:C:P	2.33	0.50
22:N:5:MET:SD	22:N:6:LYS:HG3	2.51	0.50
33:b:608:A:H2'	33:b:609:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1087:G:H5'	33:b:1090:A:N7	2.26	0.50
39:h:31:VAL:N	39:h:32:PRO:HD2	2.27	0.50
56:V:19:ILE:CG2	56:V:23:SER:OG	2.55	0.50
2:1:10:SER:OG	2:1:13:GLU:OE1	2.23	0.50
4:4:3:VAL:HG12	33:b:2015:A:C2	2.47	0.50
9:A:101:A:H2'	9:A:102:G:C8	2.47	0.50
9:A:255:G:H4'	25:Q:18:LYS:HE3	1.92	0.50
9:A:642:A:C5	16:H:106:SER:HA	2.46	0.50
9:A:1435:G:H2'	9:A:1436:U:H6	1.76	0.50
11:C:28:PHE:HE2	22:N:76:PHE:HA	1.76	0.50
27:S:80:ARG:HD3	27:S:80:ARG:H	1.77	0.50
30:X:21:A:C8	30:X:21:A:H5''	2.47	0.50
31:Y:67:A:H2'	31:Y:68:U:C4'	2.42	0.50
33:b:1589:U:H2'	33:b:1590:A:C8	2.46	0.50
39:h:31:VAL:CG1	39:h:32:PRO:CD	2.71	0.50
8:8:30:GLU:HG2	8:8:32:LYS:H	1.75	0.50
9:A:475:C:H2'	9:A:476:U:H6	1.75	0.50
9:A:483:C:H2'	9:A:484:G:C8	2.47	0.50
9:A:1102:A:H2'	9:A:1103:C:C6	2.47	0.50
14:F:96:VAL:HG23	14:F:98:GLU:HG2	1.94	0.50
33:b:278:A:O2'	33:b:279:A:N7	2.44	0.50
33:b:878:A:N6	33:b:900:A:OP1	2.44	0.50
33:b:996:A:OP2	47:r:93:LYS:NZ	2.30	0.50
40:k:88:THR:OG1	40:k:90:GLU:OE1	2.27	0.50
9:A:31:G:O4'	9:A:306:A:H1'	2.12	0.50
9:A:746:A:H5'	9:A:836:G:H21	1.76	0.50
9:A:1312:G:H5'	27:S:4:LEU:HD21	1.94	0.50
23:O:68:TYR:OH	23:O:72:LYS:NZ	2.32	0.50
28:T:30:PHE:HD2	28:T:53:MET:HB3	1.77	0.50
31:Z:65:C:N4	31:Z:66:U:O4	2.44	0.50
33:b:546:U:H2'	33:b:547:A:N3	2.26	0.50
33:b:593:U:H2'	33:b:594:U:C6	2.46	0.50
33:b:635:C:OP2	42:m:126:ARG:NH1	2.44	0.50
33:b:1808:A:H3'	33:b:1809:A:C8	2.47	0.50
33:b:1820:U:O2	34:c:158:ALA:HB3	2.11	0.50
36:e:67:ARG:CZ	55:z:145:TRP:CH2	2.94	0.50
9:A:3:A:N3	9:A:613:C:H1'	2.26	0.50
9:A:231:U:H2'	9:A:232:G:C8	2.45	0.50
9:A:634:C:H2'	9:A:635:A:H8	1.77	0.50
9:A:1106:G:H2'	9:A:1107:C:C6	2.47	0.50
9:A:1187:G:O2'	9:A:1188:A:OP1	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1345:U:H5''	17:I:121:ARG:HH11	1.77	0.50
11:C:39:ARG:NH1	11:C:54:ILE:O	2.33	0.50
12:D:104:MET:HA	12:D:170:LEU:HD21	1.94	0.50
16:H:27:PRO:HA	16:H:57:GLU:HA	1.93	0.50
30:X:5:G:H2'	30:X:6:A:C8	2.46	0.50
33:b:1596:A:H2'	33:b:1597:A:C8	2.47	0.50
33:b:2192:U:H2'	33:b:2193:G:C8	2.47	0.50
40:k:3:THR:HG21	47:r:61:TRP:HE1	1.76	0.50
2:1:38:GLN:OE1	2:1:38:GLN:N	2.43	0.49
9:A:416:G:H2'	9:A:417:G:H8	1.77	0.49
9:A:1203:C:H2'	9:A:1204:A:C8	2.46	0.49
9:A:1464:U:H2'	9:A:1465:A:H8	1.77	0.49
9:A:1477:U:H2'	9:A:1478:U:C6	2.47	0.49
31:Z:57:C:OP2	43:n:59:ARG:NH2	2.45	0.49
32:a:49:C:H2'	32:a:50:A:C8	2.47	0.49
33:b:1255:U:C5	36:e:68:ALA:HA	2.46	0.49
33:b:2184:A:H2'	33:b:2185:U:C6	2.45	0.49
49:t:17:VAL:HG11	49:t:103:ILE:HD11	1.93	0.49
56:V:19:ILE:CB	56:V:23:SER:CB	2.88	0.49
9:A:222:C:H2'	9:A:223:A:C8	2.47	0.49
9:A:1027:C:N3	9:A:1035:A:N6	2.60	0.49
9:A:1106:G:H2'	9:A:1107:C:H6	1.77	0.49
9:A:1328:C:H5''	21:M:27:THR:HG21	1.94	0.49
12:D:104:MET:SD	12:D:179:GLY:HA3	2.52	0.49
15:G:114:SER:O	15:G:117:LEU:N	2.42	0.49
29:U:44:ARG:O	29:U:48:LYS:HG2	2.13	0.49
38:g:31:GLY:H	38:g:79:VAL:HG13	1.76	0.49
18:J:80:THR:OG1	18:J:81:GLU:N	2.45	0.49
26:R:40:PRO:HG2	26:R:43:ILE:HG12	1.94	0.49
28:T:59:ARG:HG2	28:T:63:LYS:HE2	1.94	0.49
33:b:52:A:H2'	33:b:53:A:C8	2.48	0.49
33:b:1403:A:HO2'	33:b:1471:G:HO2'	1.60	0.49
33:b:1656:C:H2'	33:b:1657:U:H6	1.78	0.49
33:b:1735:A:H2'	33:b:1736:U:C6	2.47	0.49
33:b:2112:G:H5'	33:b:2113:U:C5	2.47	0.49
40:k:17:VAL:HG12	40:k:55:ILE:HB	1.94	0.49
45:p:2:ASP:OD1	45:p:2:ASP:N	2.44	0.49
48:s:95:ASP:N	48:s:95:ASP:OD1	2.45	0.49
4:4:25:VAL:HG23	4:4:26:THR:H	1.76	0.49
9:A:1004:A:H61	9:A:1024:G:H1'	1.78	0.49
12:D:43:ARG:CZ	12:D:44:LYS:H	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:28:VAL:HG22	25:Q:29:LYS:H	1.78	0.49
30:X:3:G:H3'	30:X:4:G:N2	2.24	0.49
33:b:722:A:H2'	33:b:723:C:C6	2.48	0.49
33:b:1361:G:H2'	33:b:1362:C:H6	1.77	0.49
33:b:1548:A:H2'	33:b:1549:A:H8	1.75	0.49
33:b:1779:U:H5	33:b:1784:A:N7	2.10	0.49
33:b:2036:C:H2'	33:b:2037:A:C8	2.48	0.49
56:V:61:SER:O	56:V:65:ASP:HB2	2.12	0.49
9:A:1100:C:OP2	10:B:94:ARG:NH1	2.45	0.49
9:A:1164:G:H2'	9:A:1165:U:H6	1.78	0.49
10:B:8:MET:HA	10:B:46:VAL:HG11	1.93	0.49
22:N:53:ASP:OD1	22:N:58:ARG:NE	2.39	0.49
22:N:64:ARG:NE	22:N:77:GLY:O	2.45	0.49
22:N:81:ILE:O	22:N:85:GLU:HG2	2.13	0.49
30:X:15:G:N3	30:X:15:G:H2'	2.27	0.49
34:c:158:ALA:O	34:c:195:VAL:HG12	2.13	0.49
9:A:218:U:H4'	9:A:218:U:OP1	2.12	0.49
9:A:415:A:H2'	9:A:416:G:O4'	2.11	0.49
9:A:456:A:H2'	9:A:457:G:H8	1.77	0.49
9:A:1112:C:N4	11:C:175:HIS:O	2.45	0.49
9:A:1147:C:H2'	9:A:1148:U:C6	2.47	0.49
11:C:134:LYS:O	11:C:138:GLN:HG2	2.13	0.49
21:M:26:LYS:O	21:M:30:LYS:HG2	2.12	0.49
33:b:748:G:OP1	49:t:88:ARG:NH2	2.41	0.49
33:b:1149:G:H2'	33:b:1150:C:C6	2.47	0.49
33:b:1769:U:O2'	33:b:1958:C:OP1	2.30	0.49
33:b:2323:G:H2'	33:b:2324:U:C6	2.47	0.49
6:6:41:ARG:O	6:6:41:ARG:HG3	2.13	0.49
9:A:476:U:H2'	9:A:477:C:C6	2.48	0.49
12:D:32:LYS:HA	12:D:35:GLN:HE22	1.77	0.49
17:I:45:MET:HE3	17:I:45:MET:H	1.77	0.49
21:M:80:MET:HG2	21:M:91:ARG:HG3	1.95	0.49
24:P:3:THR:HG21	24:P:24:SER:HB3	1.94	0.49
28:T:13:SER:O	28:T:17:ARG:HG3	2.13	0.49
30:X:14:A:N6	30:X:21:A:C2	2.78	0.49
33:b:483:A:O2'	51:v:57:GLY:N	2.44	0.49
33:b:2096:C:H2'	33:b:2097:A:H8	1.76	0.49
33:b:2581:G:OP2	33:b:2581:G:N2	2.44	0.49
36:e:5:LEU:CD2	36:e:8:ALA:H	2.26	0.49
37:f:36:LEU:HD22	37:f:154:ILE:HG22	1.93	0.49
9:A:181:A:O2'	9:A:194:C:N4	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:332:G:OP2	28:T:1:ALA:N	2.38	0.49
9:A:335:C:H2'	9:A:336:A:C8	2.48	0.49
9:A:1254:A:H2'	9:A:1255:G:H8	1.78	0.49
9:A:1515:G:H2'	9:A:1516:G:C8	2.47	0.49
10:B:88:GLN:H	10:B:88:GLN:CD	2.20	0.49
14:F:42:TRP:HB2	14:F:59:TYR:HB2	1.94	0.49
17:I:51:LEU:HA	17:I:54:VAL:HG22	1.94	0.49
33:b:1083:U:O2	33:b:1085:A:H2'	2.12	0.49
33:b:1656:C:H2'	33:b:1657:U:C6	2.48	0.49
33:b:2139:U:H5'	33:b:2140:G:OP1	2.13	0.49
33:b:2192:U:H2'	33:b:2193:G:H8	1.78	0.49
56:V:24:ILE:HD11	56:V:70:LEU:HD23	1.95	0.49
9:A:22:G:H2'	9:A:23:C:C6	2.48	0.49
9:A:113:G:H2'	9:A:114:U:C6	2.48	0.49
9:A:405:U:OP2	12:D:2:ARG:NH1	2.45	0.49
9:A:1391:U:H2'	9:A:1392:G:C8	2.48	0.49
18:J:10:LEU:HB2	18:J:72:ARG:HB2	1.94	0.49
19:K:52:ARG:HD3	19:K:56:LYS:HD3	1.94	0.49
33:b:1056:G:O2'	33:b:1104:C:N4	2.41	0.49
33:b:1281:G:H2'	33:b:1282:U:C6	2.48	0.49
33:b:2159:G:H2'	33:b:2160:C:C6	2.48	0.49
43:n:110:GLU:OE1	43:n:110:GLU:N	2.42	0.49
3:2:5:ILE:N	3:2:38:ARG:O	2.45	0.49
9:A:683:G:H1	9:A:707:U:H3	1.61	0.49
9:A:1267:C:N3	9:A:1327:C:H4'	2.28	0.49
9:A:1306:A:N6	9:A:1331:G:H1'	2.28	0.49
15:G:30:MET:HE2	15:G:35:LYS:HG2	1.93	0.49
21:M:68:LEU:HA	21:M:71:GLU:CD	2.38	0.49
27:S:31:ARG:HH12	27:S:51:HIS:HB2	1.78	0.49
33:b:849:A:H2'	33:b:850:U:C6	2.46	0.49
33:b:871:U:H2'	33:b:872:U:H6	1.78	0.49
33:b:1704:C:H2'	33:b:1705:A:C8	2.48	0.49
33:b:1847:A:H2'	33:b:1848:A:C8	2.48	0.49
33:b:2686:G:H2'	33:b:2687:U:C6	2.47	0.49
37:f:34:ILE:HG12	37:f:96:MET:HE2	1.95	0.49
47:r:98:ILE:HG22	47:r:106:PHE:HD1	1.76	0.49
9:A:833:G:H2'	9:A:834:U:C6	2.47	0.48
9:A:1346:A:N7	9:A:1375:A:N6	2.60	0.48
12:D:54:LEU:O	12:D:58:GLN:HG2	2.13	0.48
12:D:103:ARG:HB2	12:D:170:LEU:HD13	1.95	0.48
18:J:5:ARG:NH1	18:J:7:ARG:HG3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:77:A:C3'	58:Z:163:PRO:O	2.60	0.48
33:b:1090:A:H8	33:b:1103:A:P	2.36	0.48
33:b:2135:A:N6	33:b:2156:G:O2'	2.46	0.48
35:d:12:THR:HB	46:q:5:ILE:HD11	1.95	0.48
53:x:13:G:H4'	53:x:14:C:OP1	2.13	0.48
9:A:328:C:H4'	9:A:329:A:H5'	1.94	0.48
9:A:608:A:H3'	9:A:609:A:H8	1.78	0.48
9:A:707:U:H4'	19:K:21:HIS:CD2	2.48	0.48
9:A:1119:C:OP1	17:I:84:ARG:NH1	2.38	0.48
9:A:1152:A:OP1	18:J:70:HIS:ND1	2.46	0.48
13:E:120:HIS:O	13:E:121:ASN:ND2	2.46	0.48
14:F:40:GLU:OE2	14:F:42:TRP:NE1	2.47	0.48
16:H:10:LEU:HD11	16:H:126:CYS:SG	2.54	0.48
21:M:71:GLU:HA	21:M:74:MET:HG3	1.93	0.48
32:a:5:U:H2'	32:a:6:G:H8	1.78	0.48
33:b:740:C:H5	33:b:757:G:H1	1.60	0.48
33:b:801:G:C8	36:e:50:ALA:HB2	2.48	0.48
33:b:2096:C:H2'	33:b:2097:A:C8	2.48	0.48
36:e:61:ARG:NH2	36:e:64:GLY:HA3	2.28	0.48
56:V:19:ILE:HB	56:V:23:SER:HB3	1.95	0.48
9:A:184:G:H2'	9:A:185:U:H6	1.74	0.48
9:A:1492:A:O2'	9:A:1493:A:O4'	2.24	0.48
11:C:57:GLU:HG2	11:C:64:ARG:HB3	1.96	0.48
12:D:170:LEU:HD12	12:D:181:PHE:CZ	2.48	0.48
17:I:51:LEU:HD21	17:I:57:VAL:HG23	1.96	0.48
31:Z:32:G:H2'	31:Z:32:G:N3	2.27	0.48
33:b:310:A:O2'	33:b:311:A:O5'	2.28	0.48
33:b:596:U:H2'	33:b:597:G:H8	1.77	0.48
33:b:1406:U:H2'	33:b:1407:G:C8	2.47	0.48
34:c:93:LEU:HD11	34:c:101:ARG:HB3	1.95	0.48
36:e:5:LEU:CG	36:e:6:LYS:N	2.77	0.48
9:A:312:C:H2'	9:A:313:A:C8	2.48	0.48
9:A:672:U:H2'	9:A:673:A:H8	1.78	0.48
9:A:1402:C:H2'	9:A:1403:C:O4'	2.13	0.48
9:A:1441:A:H62	9:A:1461:G:H21	1.61	0.48
10:B:72:LYS:NZ	10:B:203:ASP:O	2.40	0.48
12:D:94:GLU:HA	12:D:99:ASN:ND2	2.28	0.48
16:H:94:VAL:HG11	16:H:100:ILE:C	2.38	0.48
17:I:3:ASN:OD1	17:I:4:GLN:N	2.47	0.48
17:I:52:GLU:N	17:I:56:MET:CE	2.76	0.48
33:b:2848:G:H1'	33:b:2868:A:H61	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:15:SER:N	36:e:197:GLU:OE2	2.43	0.48
37:f:80:ARG:HB2	37:f:83:TYR:CE2	2.48	0.48
55:z:136:SER:O	55:z:139:VAL:HG22	2.14	0.48
9:A:1032:G:H2'	9:A:1033:G:C8	2.48	0.48
13:E:35:LEU:HD22	13:E:133:ILE:HG12	1.95	0.48
31:Y:77:A:N6	54:y:2:ALA:O	2.38	0.48
33:b:2137:U:H5''	33:b:2138:G:C8	2.48	0.48
33:b:2292:U:H2'	33:b:2293:G:C8	2.49	0.48
39:h:72:ILE:HD11	39:h:140:ALA:HB1	1.96	0.48
44:o:28:LEU:HD23	44:o:48:VAL:HG21	1.94	0.48
9:A:256:U:H2'	9:A:257:G:C8	2.48	0.48
9:A:626:G:H2'	9:A:627:G:C8	2.48	0.48
9:A:1042:A:H2'	9:A:1043:G:C4	2.49	0.48
9:A:1152:A:H2'	9:A:1153:G:C8	2.48	0.48
9:A:1506:U:O2	19:K:127:ARG:HD3	2.14	0.48
15:G:112:ASP:OD1	15:G:113:LYS:N	2.40	0.48
18:J:37:ARG:NH1	18:J:38:GLY:H	2.12	0.48
31:Z:50:G:O6	31:Z:67:A:N6	2.47	0.48
33:b:640:C:H2'	33:b:641:U:H6	1.78	0.48
33:b:1826:G:OP1	34:c:223:THR:HG23	2.13	0.48
33:b:2136:G:H22	33:b:2156:G:H22	1.60	0.48
34:c:23:GLU:OE1	34:c:23:GLU:N	2.47	0.48
2:1:20:ASN:O	2:1:24:GLU:HG2	2.14	0.48
9:A:40:C:H2'	9:A:41:G:C8	2.48	0.48
9:A:234:C:H2'	9:A:235:C:C6	2.49	0.48
11:C:112:ALA:HA	11:C:115:VAL:HG12	1.95	0.48
16:H:125:ILE:HG22	16:H:126:CYS:SG	2.53	0.48
18:J:42:LEU:HB3	18:J:71:LEU:HB3	1.96	0.48
28:T:79:THR:HA	28:T:82:ILE:HG12	1.95	0.48
31:Y:50:G:C5	31:Y:67:A:C6	3.02	0.48
32:a:51:G:H2'	32:a:52:A:C8	2.49	0.48
33:b:996:A:H4'	47:r:91:ASP:OD2	2.14	0.48
33:b:1063:G:O6	33:b:1070:A:H5'	2.13	0.48
33:b:1771:C:H2'	33:b:1772:A:C8	2.48	0.48
34:c:117:GLN:N	34:c:128:ASN:OD1	2.41	0.48
37:f:31:VAL:HG22	37:f:158:THR:HG22	1.96	0.48
50:u:89:GLU:OE1	50:u:89:GLU:N	2.44	0.48
9:A:438:U:O2'	9:A:493:A:N6	2.46	0.48
9:A:501:C:H2'	9:A:502:A:H8	1.78	0.48
9:A:620:C:C4	12:D:131:ILE:HG13	2.48	0.48
9:A:865:A:H2'	9:A:866:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:975:A:H5''	9:A:1365:G:N2	2.28	0.48
9:A:985:C:H2'	9:A:986:U:C6	2.48	0.48
16:H:94:VAL:HG13	16:H:94:VAL:O	2.14	0.48
31:Z:5:G:H2'	31:Z:6:A:N3	2.29	0.48
33:b:1060:U:H1'	33:b:1062:G:P	2.54	0.48
33:b:1084:A:H2'	33:b:1084:A:N3	2.29	0.48
35:d:181:ASP:HB3	35:d:186:LEU:HB2	1.96	0.48
47:r:41:LYS:HB3	47:r:45:TYR:HE2	1.78	0.48
9:A:333:U:P	28:T:1:ALA:H1	2.37	0.48
9:A:346:G:OP1	46:q:39:ARG:NH2	2.40	0.48
9:A:474:G:H2'	9:A:475:C:C6	2.49	0.48
9:A:744:C:H2'	9:A:745:G:C8	2.49	0.48
9:A:985:C:H2'	9:A:986:U:H6	1.79	0.48
9:A:1076:U:H2'	9:A:1077:G:C8	2.48	0.48
9:A:1130:A:H2'	9:A:1131:G:C8	2.48	0.48
10:B:20:ARG:HG3	10:B:21:TYR:CD1	2.49	0.48
16:H:95:MET:HB3	16:H:99:GLY:HA3	1.96	0.48
21:M:74:MET:SD	21:M:75:SER:N	2.87	0.48
31:Y:30:U:H2'	31:Y:31:C:H6	1.79	0.48
33:b:416:U:H2'	33:b:417:C:C6	2.49	0.48
33:b:2186:G:H2'	33:b:2187:U:C5	2.48	0.48
33:b:2304:G:H5'	37:f:121:SER:HB2	1.95	0.48
34:c:141:VAL:N	34:c:162:VAL:O	2.39	0.48
56:V:24:ILE:O	56:V:28:VAL:HG23	2.14	0.48
9:A:17:U:H2'	9:A:18:C:C6	2.49	0.48
9:A:946:A:H2'	9:A:947:G:C8	2.48	0.48
9:A:1169:A:H3'	9:A:1170:A:C8	2.49	0.48
33:b:27:G:H1'	33:b:513:A:H62	1.78	0.48
33:b:871:U:H2'	33:b:872:U:C6	2.48	0.48
33:b:2014:A:H2'	33:b:2015:A:C8	2.47	0.48
34:c:268:VAL:HG12	34:c:269:ARG:HG2	1.95	0.48
9:A:17:U:H2'	9:A:18:C:H6	1.79	0.47
9:A:472:U:H2'	9:A:473:U:C6	2.49	0.47
9:A:1197:A:H2'	9:A:1198:G:H8	1.79	0.47
9:A:1246:A:N6	9:A:1292:G:O6	2.47	0.47
28:T:50:PHE:HD2	28:T:82:ILE:HG21	1.79	0.47
29:U:5:VAL:HG12	29:U:7:GLU:H	1.77	0.47
33:b:46:G:C6	33:b:180:G:C2	3.02	0.47
33:b:964:C:O2'	33:b:2273:A:N3	2.42	0.47
33:b:1070:A:OP2	33:b:1075:C:N4	2.47	0.47
33:b:1481:U:H3	33:b:1510:G:H1	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2076:U:OP2	33:b:2238:G:N2	2.40	0.47
33:b:2111:U:OP1	33:b:2119:A:H5'	2.13	0.47
33:b:2175:C:H3'	33:b:2176:A:H2	1.78	0.47
9:A:143:A:H5''	9:A:144:G:H5'	1.95	0.47
9:A:198:G:H2'	9:A:199:A:C8	2.48	0.47
9:A:588:G:H2'	9:A:589:U:C6	2.49	0.47
9:A:958:A:N6	27:S:54:ARG:HE	2.12	0.47
9:A:1000:A:H2'	9:A:1001:C:C6	2.50	0.47
11:C:39:ARG:NE	22:N:91:GLU:OE2	2.47	0.47
13:E:76:ASN:N	13:E:79:THR:O	2.43	0.47
17:I:46:VAL:HA	17:I:49:GLN:CD	2.39	0.47
23:O:33:ALA:HA	23:O:36:ASN:HD21	1.78	0.47
28:T:24:ARG:HD2	28:T:28:ARG:HH21	1.77	0.47
33:b:521:U:H2'	33:b:522:A:C8	2.49	0.47
33:b:947:A:H2'	33:b:948:C:C6	2.49	0.47
33:b:2132:U:O2'	33:b:2133:G:O4'	2.31	0.47
33:b:2180:U:H2'	33:b:2181:U:C6	2.49	0.47
33:b:2668:G:H1'	38:g:110:SER:OG	2.14	0.47
53:x:13:G:H2'	53:x:14:C:C6	2.49	0.47
5:5:23:THR:OG1	5:5:24:THR:N	2.47	0.47
9:A:67:C:H4'	9:A:172:A:O4'	2.14	0.47
9:A:923:A:H2'	9:A:924:C:C6	2.49	0.47
9:A:1318:A:H1'	27:S:36:ARG:HH11	1.79	0.47
10:B:45:THR:HG22	10:B:200:PRO:HB2	1.96	0.47
20:L:4:ASN:OD1	20:L:5:GLN:N	2.46	0.47
23:O:57:ARG:NH1	23:O:60:SER:OG	2.47	0.47
26:R:56:ARG:HE	26:R:60:ARG:HH11	1.61	0.47
33:b:2:G:O2'	33:b:3:U:H5'	2.14	0.47
33:b:827:U:H4'	33:b:828:U:C2	2.49	0.47
33:b:900:A:H2'	33:b:901:C:C6	2.49	0.47
35:d:13:ARG:NH1	35:d:15:PHE:HZ	2.12	0.47
7:7:55:LEU:O	7:7:59:ILE:HD12	2.15	0.47
9:A:30:U:O4	9:A:32:A:N6	2.48	0.47
9:A:660:C:H2'	9:A:661:G:C8	2.49	0.47
9:A:1363:A:O2'	9:A:1365:G:N7	2.42	0.47
9:A:1492:A:H2'	9:A:1493:A:C8	2.50	0.47
11:C:151:GLU:HB3	11:C:198:LYS:HB2	1.96	0.47
22:N:5:MET:SD	22:N:6:LYS:N	2.87	0.47
23:O:73:ASP:HB3	23:O:76:ARG:HB2	1.96	0.47
31:Y:16:C:H5''	31:Y:17:C:C5	2.49	0.47
31:Y:16:C:O2'	31:Y:61:U:O3'	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:90:C:H5'	43:n:18:ARG:HG2	1.95	0.47
33:b:250:G:H5''	42:m:59:ARG:CZ	2.44	0.47
36:e:119:ILE:HB	36:e:187:VAL:HG12	1.96	0.47
48:s:7:SER:OG	48:s:8:GLY:N	2.47	0.47
9:A:237:G:H2'	9:A:238:A:C8	2.49	0.47
9:A:298:A:H8	9:A:298:A:OP1	1.98	0.47
9:A:501:C:P	20:L:113:ARG:HH21	2.37	0.47
9:A:908:A:H2'	9:A:909:A:C8	2.50	0.47
9:A:962:C:H2'	9:A:963:G:H8	1.79	0.47
9:A:978:A:C5	9:A:1318:A:C6	3.03	0.47
9:A:1340:A:H2'	9:A:1341:U:O4'	2.15	0.47
13:E:53:ARG:NH1	13:E:54:GLU:HB3	2.29	0.47
32:a:66:A:H4'	32:a:67:G:O5'	2.15	0.47
33:b:2745:C:H2'	33:b:2746:U:C6	2.49	0.47
38:g:86:LYS:HB2	38:g:165:ALA:HB2	1.97	0.47
9:A:104:G:H2'	9:A:105:G:C8	2.49	0.47
9:A:1187:G:N3	22:N:99:SER:OG	2.28	0.47
10:B:113:LEU:HB2	10:B:143:LEU:HD23	1.96	0.47
11:C:128:MET:HE1	11:C:131:ARG:HG3	1.96	0.47
12:D:54:LEU:HD11	12:D:55:ARG:HH21	1.80	0.47
13:E:82:HIS:HB3	13:E:84:VAL:HG13	1.95	0.47
20:L:97:VAL:O	20:L:98:ARG:HD2	2.15	0.47
21:M:116:LYS:HD2	21:M:116:LYS:HA	1.78	0.47
29:U:47:ALA:HB3	29:U:48:LYS:HE2	1.97	0.47
33:b:581:C:H2'	33:b:582:A:H8	1.78	0.47
33:b:827:U:O2'	33:b:2068:U:N3	2.48	0.47
33:b:2114:A:C6	33:b:2115:G:H1'	2.49	0.47
33:b:2901:C:H2'	33:b:2902:C:C6	2.50	0.47
36:e:61:ARG:HH21	36:e:64:GLY:HA3	1.80	0.47
2:l:30:MET:HE3	50:u:14:PRO:HD3	1.97	0.47
7:7:51:SER:OG	7:7:52:LYS:N	2.47	0.47
9:A:424:G:H2'	9:A:425:G:H8	1.79	0.47
9:A:1096:C:H2'	9:A:1097:C:C6	2.49	0.47
9:A:1266:G:N2	9:A:1269:A:OP2	2.39	0.47
9:A:1324:A:H2'	9:A:1325:C:H6	1.80	0.47
9:A:1357:A:H2'	9:A:1358:U:C6	2.49	0.47
9:A:1391:U:H2'	9:A:1392:G:H8	1.79	0.47
10:B:70:GLY:HA3	10:B:79:VAL:HG11	1.96	0.47
12:D:139:ASN:H	12:D:182:LYS:HA	1.79	0.47
16:H:26:MET:O	16:H:57:GLU:HG2	2.14	0.47
17:I:51:LEU:HG	17:I:56:MET:HE2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:5:ARG:HH11	18:J:7:ARG:HG3	1.80	0.47
20:L:23:LEU:O	20:L:24:GLU:HG3	2.14	0.47
22:N:65:GLN:HE21	22:N:78:LEU:HG	1.78	0.47
23:O:56:LEU:HG	23:O:57:ARG:HH21	1.78	0.47
30:X:18:G:C6	30:X:58:A:C6	3.02	0.47
30:X:58:A:N3	30:X:60:U:H5''	2.29	0.47
33:b:713:G:H2'	33:b:714:U:C6	2.50	0.47
33:b:1541:C:H2'	33:b:1542:U:C6	2.49	0.47
33:b:1607:C:H4'	33:b:1608:A:H5'	1.96	0.47
33:b:1954:G:O2'	33:b:1956:U:O4	2.20	0.47
33:b:2136:G:N2	33:b:2156:G:H1	2.11	0.47
33:b:2137:U:H5''	33:b:2138:G:N7	2.30	0.47
33:b:2373:G:H2'	33:b:2374:C:C6	2.50	0.47
33:b:2684:U:C4	33:b:2685:G:N7	2.83	0.47
43:n:25:ASP:OD1	43:n:26:VAL:N	2.48	0.47
46:q:4:ILE:H	46:q:4:ILE:HD12	1.80	0.47
46:q:88:ARG:NH2	46:q:112:GLU:OE1	2.48	0.47
56:V:53:ILE:H	56:V:53:ILE:HD12	1.79	0.47
9:A:338:A:H2'	9:A:339:C:C6	2.49	0.47
9:A:1203:C:H5'	22:N:66:THR:HG23	1.97	0.47
11:C:50:SER:O	11:C:69:THR:HG23	2.13	0.47
11:C:55:VAL:HB	11:C:66:THR:HB	1.95	0.47
33:b:596:U:H2'	33:b:597:G:C8	2.49	0.47
33:b:1051:G:OP1	33:b:2752:C:H1'	2.15	0.47
33:b:2102:G:N1	33:b:2187:U:C2	2.83	0.47
9:A:1250:A:C2	9:A:1370:G:H1'	2.49	0.47
9:A:1277:C:H1'	9:A:1282:C:O2	2.15	0.47
9:A:1347:G:C5	17:I:108:ARG:NH2	2.82	0.47
10:B:56:LEU:HA	10:B:59:ILE:HB	1.97	0.47
15:G:45:ALA:HB2	15:G:116:ALA:HA	1.97	0.47
15:G:110:ARG:HH12	15:G:122:GLU:HB3	1.79	0.47
17:I:52:GLU:HA	17:I:56:MET:CE	2.39	0.47
25:Q:20:ILE:HG13	25:Q:45:VAL:HB	1.97	0.47
33:b:288:U:H2'	33:b:289:G:H8	1.79	0.47
33:b:1386:C:H2'	33:b:1387:A:C8	2.49	0.47
33:b:1746:A:H2'	33:b:1747:U:C6	2.50	0.47
33:b:2132:U:H2'	33:b:2133:G:C8	2.49	0.47
33:b:2849:U:N3	33:b:2867:G:O4'	2.48	0.47
36:e:67:ARG:CZ	55:z:145:TRP:CZ3	2.97	0.47
9:A:60:A:N7	9:A:110:C:N4	2.63	0.47
9:A:1314:C:H2'	9:A:1315:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:88:HIS:CE1	13:E:137:ARG:HG3	2.50	0.47
19:K:59:PRO:HD3	19:K:90:PRO:HB2	1.97	0.47
21:M:15:VAL:O	21:M:29:SER:OG	2.33	0.47
30:X:71:G:O2'	33:b:1851:U:O2'	2.30	0.47
33:b:9:G:O2'	33:b:10:A:O5'	2.32	0.47
33:b:1168:G:H1	33:b:1181:U:H3	1.62	0.47
38:g:42:GLU:OE1	38:g:55:ARG:HG2	2.14	0.47
47:r:86:ALA:O	48:s:50:GLY:O	2.33	0.47
9:A:179:A:H2'	9:A:179:A:N3	2.30	0.46
9:A:520:A:H61	9:A:529:G:H1'	1.79	0.46
11:C:107:LYS:HE3	11:C:109:GLU:HG2	1.96	0.46
12:D:71:PHE:HE1	12:D:89:LEU:HD11	1.79	0.46
33:b:956:G:N7	43:n:14:LYS:NZ	2.63	0.46
33:b:2514:U:H2'	33:b:2515:C:H6	1.79	0.46
35:d:181:ASP:OD1	35:d:184:ARG:N	2.39	0.46
45:p:58:ILE:O	45:p:58:ILE:HG22	2.14	0.46
56:V:24:ILE:CD1	56:V:70:LEU:CD2	2.93	0.46
9:A:93:U:C2'	9:A:94:G:H4'	2.44	0.46
9:A:285:C:H2'	9:A:286:C:H6	1.79	0.46
9:A:505:G:H2'	9:A:506:G:H8	1.79	0.46
9:A:674:G:H2'	9:A:675:A:H8	1.80	0.46
9:A:1314:C:H2'	9:A:1315:U:H6	1.79	0.46
12:D:143:SER:OG	12:D:144:ILE:N	2.48	0.46
15:G:115:MET:HA	15:G:118:ARG:HD3	1.97	0.46
30:X:66:U:H2'	30:X:67:U:C6	2.51	0.46
33:b:52:A:H2'	33:b:53:A:H8	1.80	0.46
33:b:494:G:OP1	49:t:8:ARG:HD3	2.15	0.46
9:A:320:A:H2'	9:A:321:A:H8	1.81	0.46
9:A:1461:G:H2'	9:A:1462:C:C6	2.50	0.46
11:C:22:PHE:CE2	18:J:12:ALA:HA	2.50	0.46
14:F:23:GLU:OE1	14:F:23:GLU:N	2.47	0.46
20:L:32:VAL:O	20:L:55:ARG:N	2.47	0.46
23:O:24:THR:HG21	23:O:69:LEU:HD13	1.97	0.46
27:S:10:ILE:O	27:S:15:LEU:HD23	2.15	0.46
31:Y:73:G:H2'	31:Y:74:A:C8	2.49	0.46
37:f:170:LEU:HB3	37:f:177:PHE:HZ	1.80	0.46
51:v:98:SER:O	51:v:99:ASN:HB3	2.16	0.46
56:V:24:ILE:CD1	56:V:70:LEU:HD23	2.44	0.46
9:A:185:U:H2'	9:A:186:C:C6	2.51	0.46
9:A:501:C:H2'	9:A:502:A:C8	2.49	0.46
15:G:141:HIS:O	15:G:145:GLU:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:6:G:H2'	32:a:7:G:H8	1.80	0.46
33:b:1056:G:H2'	33:b:1102:C:N4	2.30	0.46
33:b:1059:G:H2'	33:b:1060:U:O4'	2.15	0.46
33:b:1093:G:N7	33:b:1099:G:C2	2.83	0.46
33:b:1425:G:H2'	33:b:1426:G:C8	2.50	0.46
33:b:1530:G:H2'	33:b:1531:C:C6	2.51	0.46
33:b:1820:U:O2'	34:c:157:SER:OG	2.30	0.46
33:b:2164:C:O2	33:b:2171:A:N7	2.48	0.46
33:b:2193:G:H2'	33:b:2194:U:H6	1.80	0.46
36:e:5:LEU:HD23	36:e:8:ALA:CB	2.31	0.46
9:A:74:A:H2'	9:A:75:G:C8	2.50	0.46
9:A:1324:A:H2'	9:A:1325:C:C6	2.49	0.46
9:A:1513:A:H2'	9:A:1514:G:C8	2.51	0.46
16:H:31:LEU:O	16:H:35:ILE:HG13	2.15	0.46
18:J:12:ALA:HB3	18:J:18:ILE:HB	1.98	0.46
20:L:72:ASN:HB3	20:L:104:SER:H	1.80	0.46
21:M:21:ILE:C	21:M:23:GLY:H	2.23	0.46
31:Y:72:C:H2'	31:Y:73:G:C8	2.50	0.46
33:b:1024:G:C6	33:b:1025:G:C6	3.03	0.46
33:b:1068:G:N1	33:b:1097:U:O4	2.48	0.46
33:b:1969:A:O2'	33:b:1972:G:N3	2.45	0.46
36:e:3:LEU:HD12	36:e:3:LEU:HA	1.81	0.46
37:f:48:LYS:HA	37:f:51:ASP:HB3	1.98	0.46
9:A:8:A:C6	12:D:205:LYS:HG3	2.50	0.46
9:A:60:A:OP2	9:A:60:A:H8	1.99	0.46
9:A:214:C:H2'	9:A:215:C:C6	2.51	0.46
9:A:417:G:N2	9:A:426:U:O2	2.43	0.46
9:A:1187:G:HO2'	9:A:1188:A:P	2.37	0.46
10:B:14:HIS:HB3	10:B:202:ASN:ND2	2.30	0.46
11:C:71:ARG:HH22	11:C:74:ILE:HG13	1.81	0.46
13:E:37:VAL:HG23	13:E:47:PHE:HB3	1.97	0.46
28:T:43:LYS:O	28:T:47:GLN:HG2	2.15	0.46
31:Y:20:G:O6	37:f:80:ARG:NH2	2.48	0.46
31:Z:52:A:O2'	31:Z:53:G:H8	1.98	0.46
33:b:9:G:H4'	33:b:10:A:OP1	2.16	0.46
33:b:365:U:H2'	33:b:366:C:C6	2.51	0.46
33:b:580:U:H2'	33:b:581:C:H6	1.80	0.46
33:b:1771:C:H2'	33:b:1772:A:H8	1.80	0.46
33:b:2119:A:N6	33:b:2167:U:H1'	2.31	0.46
39:h:119:ASN:N	39:h:119:ASN:OD1	2.48	0.46
50:u:90:GLY:O	50:u:93:LEU:HD13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:13:ARG:NH1	33:b:1263:U:OP1	2.48	0.46
9:A:439:U:H5'	12:D:120:LYS:H	1.81	0.46
9:A:490:C:H2'	9:A:491:G:C8	2.51	0.46
9:A:1147:C:H4'	17:I:6:TYR:CE2	2.51	0.46
10:B:160:LEU:HD22	10:B:161:PHE:H	1.81	0.46
12:D:57:LYS:HB2	12:D:199:ILE:HD12	1.98	0.46
20:L:65:TYR:N	20:L:94:TYR:O	2.48	0.46
23:O:38:LEU:HD13	23:O:42:PHE:HE2	1.81	0.46
26:R:10:CYS:HB2	26:R:46:THR:HA	1.96	0.46
33:b:560:C:O2'	47:r:48:ARG:NH1	2.48	0.46
33:b:608:A:H2'	33:b:609:A:H8	1.80	0.46
33:b:1501:G:OP1	34:c:101:ARG:NH2	2.46	0.46
33:b:1636:U:H2'	33:b:1637:A:C8	2.50	0.46
33:b:2088:A:H2'	33:b:2089:C:C6	2.51	0.46
38:g:29:LYS:HB3	38:g:29:LYS:HE2	1.44	0.46
52:w:9:ARG:HG2	52:w:41:GLU:CD	2.41	0.46
9:A:1008:U:H2'	9:A:1009:U:C6	2.50	0.46
18:J:35:GLN:HG2	18:J:77:VAL:HG13	1.97	0.46
33:b:1741:C:H2'	33:b:1742:U:C6	2.50	0.46
33:b:2233:U:H2'	33:b:2234:G:H8	1.81	0.46
33:b:2802:G:H2'	33:b:2803:G:H8	1.80	0.46
9:A:76:G:C6	9:A:95:C:N4	2.83	0.46
9:A:637:C:H2'	9:A:638:U:C6	2.50	0.46
9:A:738:C:H2'	9:A:739:C:H6	1.80	0.46
9:A:1399:C:C2	9:A:1401:G:C6	3.04	0.46
12:D:121:ALA:HA	12:D:145:ARG:CD	2.46	0.46
14:F:33:GLU:O	14:F:35:LYS:NZ	2.36	0.46
33:b:639:U:H2'	33:b:640:C:C6	2.51	0.46
33:b:969:G:H2'	33:b:970:U:C6	2.50	0.46
33:b:1315:C:O2'	33:b:1392:A:H8	1.99	0.46
33:b:1469:A:H2'	33:b:1470:A:H8	1.79	0.46
33:b:1535:A:O2'	33:b:1536:C:O4'	2.34	0.46
33:b:1873:G:H2'	33:b:1874:C:C6	2.51	0.46
33:b:2813:A:H2'	33:b:2814:A:C8	2.51	0.46
45:p:33:ARG:NH1	45:p:64:TYR:OH	2.49	0.46
9:A:71:A:C8	9:A:72:A:C8	3.04	0.46
9:A:1368:A:OP1	17:I:112:ARG:NH1	2.45	0.46
11:C:68:HIS:HA	11:C:103:ALA:HB3	1.97	0.46
12:D:125:ASN:ND2	12:D:140:ASP:OD1	2.40	0.46
14:F:5:GLU:OE2	26:R:22:TYR:OH	2.21	0.46
28:T:59:ARG:O	28:T:63:LYS:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:X:50:C:H2'	30:X:51:G:C8	2.51	0.46
33:b:499:U:H5''	51:v:43:LYS:HE2	1.97	0.46
33:b:900:A:H2'	33:b:901:C:H6	1.81	0.46
33:b:1267:U:O2	33:b:1267:U:H2'	2.15	0.46
33:b:2187:U:H3'	33:b:2187:U:H6	1.80	0.46
33:b:2332:C:OP1	54:y:77:ARG:NH2	2.49	0.46
36:e:170:ARG:NH2	36:e:176:ASP:OD2	2.48	0.46
39:h:99:ILE:HD11	39:h:122:LEU:CD1	2.46	0.46
48:s:37:GLU:OE1	48:s:53:PHE:HE1	1.96	0.46
49:t:82:MET:SD	49:t:82:MET:N	2.88	0.46
9:A:31:G:C6	9:A:306:A:H4'	2.51	0.45
9:A:335:C:H1'	9:A:1434:A:H1'	1.98	0.45
9:A:763:G:H2'	9:A:764:C:C6	2.51	0.45
9:A:1109:C:C2	9:A:1110:A:C8	3.05	0.45
9:A:1319:A:C4	9:A:1323:G:C8	3.04	0.45
10:B:10:LYS:NZ	10:B:13:VAL:HG23	2.30	0.45
12:D:169:TRP:N	12:D:183:ARG:HH21	2.13	0.45
17:I:26:LYS:HB3	17:I:61:ASP:HB3	1.98	0.45
30:X:5:G:C6	30:X:68:C:C2	3.05	0.45
32:a:42:C:OP1	37:f:64:LYS:HE2	2.16	0.45
33:b:27:G:HO2'	33:b:28:A:P	2.38	0.45
33:b:2305:U:H2'	33:b:2306:C:C6	2.51	0.45
33:b:2615:U:H2'	33:b:2616:C:H6	1.81	0.45
36:e:61:ARG:HD3	55:z:150[A]:TYR:HE1	1.81	0.45
47:r:99:ALA:HB2	47:r:106:PHE:CE1	2.50	0.45
9:A:344:A:H3'	9:A:345:C:C6	2.51	0.45
9:A:524:G:H2'	9:A:525:C:H6	1.82	0.45
9:A:580:C:H4'	23:O:57:ARG:CZ	2.46	0.45
9:A:911:U:H2'	9:A:912:C:C6	2.50	0.45
9:A:1162:C:H2'	9:A:1163:A:C8	2.51	0.45
9:A:1392:G:H2'	9:A:1393:U:C6	2.51	0.45
10:B:41:ASN:O	10:B:45:THR:HG23	2.16	0.45
15:G:68:VAL:HG23	15:G:137:ARG:HG2	1.98	0.45
19:K:58:THR:HG22	19:K:60:PHE:H	1.80	0.45
26:R:9:PHE:CZ	26:R:13:THR:HB	2.51	0.45
27:S:46:LEU:HD12	27:S:46:LEU:HA	1.84	0.45
32:a:9:G:P	45:p:25:ARG:HH22	2.38	0.45
33:b:289:G:H2'	33:b:290:U:H6	1.80	0.45
33:b:873:C:N4	33:b:899:A:H62	2.14	0.45
33:b:1021:A:H62	33:b:1141:U:H3	1.63	0.45
33:b:1435:G:H2'	33:b:1436:G:H8	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1667:G:O2'	33:b:1991:U:O4	2.22	0.45
33:b:2071:A:H2'	33:b:2072:C:C6	2.51	0.45
36:e:22:ASP:OD1	36:e:22:ASP:N	2.37	0.45
37:f:114:PHE:HE1	37:f:116:GLY:HA2	1.80	0.45
39:h:75:LEU:HD23	39:h:77:THR:H	1.81	0.45
9:A:723:U:O4	29:U:55:HIS:ND1	2.44	0.45
9:A:1014:A:C2	9:A:1219:A:H1'	2.51	0.45
16:H:51:GLU:OE2	16:H:57:GLU:HB3	2.17	0.45
17:I:111:GLU:OE1	17:I:111:GLU:N	2.49	0.45
21:M:10:ASP:HA	21:M:44:ILE:HB	1.98	0.45
21:M:90:HIS:HA	21:M:108:ARG:HH21	1.81	0.45
26:R:25:ILE:O	26:R:29:LYS:HG2	2.16	0.45
31:Z:10:G:H2'	31:Z:11:C:C6	2.52	0.45
33:b:1721:G:N2	33:b:1738:G:H2'	2.31	0.45
33:b:2521:C:H2'	33:b:2522:U:C6	2.52	0.45
33:b:2554:U:C2	33:b:2555:U:C5	3.05	0.45
33:b:2737:G:H2'	33:b:2738:A:C8	2.51	0.45
33:b:2740:A:H2'	33:b:2741:A:C8	2.51	0.45
34:c:89:ALA:HB2	34:c:158:ALA:HA	1.98	0.45
39:h:93:SER:HB2	39:h:123:ARG:HH11	1.81	0.45
46:q:78:SER:OG	46:q:80:VAL:HG12	2.16	0.45
9:A:8:A:N6	12:D:201:GLU:O	2.49	0.45
9:A:746:A:H2'	9:A:747:A:C8	2.51	0.45
9:A:962:C:H2'	9:A:963:G:C8	2.52	0.45
9:A:1240:U:O5'	15:G:115:MET:HE1	2.17	0.45
9:A:1256:A:H2'	9:A:1278:G:H1	1.81	0.45
9:A:1334:G:H8	9:A:1334:G:O5'	1.99	0.45
18:J:10:LEU:HB3	18:J:18:ILE:HD11	1.99	0.45
24:P:6:LEU:HD23	24:P:17:TYR:HB3	1.96	0.45
24:P:39:PHE:CD1	24:P:50:THR:HB	2.47	0.45
28:T:24:ARG:HB3	28:T:28:ARG:HH21	1.81	0.45
33:b:1062:G:H2'	33:b:1063:G:C8	2.51	0.45
33:b:1387:A:H5'	33:b:1469:A:H1'	1.98	0.45
44:o:36:THR:OG1	44:o:37:THR:N	2.50	0.45
3:2:30:ARG:NH2	33:b:931:U:OP1	2.26	0.45
11:C:85:LYS:HD3	11:C:88:LYS:HE2	1.98	0.45
13:E:22:LYS:HD3	13:E:29:ILE:HD11	1.99	0.45
21:M:33:LEU:HD23	21:M:33:LEU:HA	1.81	0.45
30:X:4:G:N2	30:X:4:G:OP2	2.42	0.45
32:a:60:C:H2'	32:a:61:G:H8	1.82	0.45
33:b:2:G:H2'	33:b:3:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:643:A:O2'	33:b:644:A:O4'	2.35	0.45
35:d:13:ARG:O	35:d:13:ARG:HG2	2.12	0.45
37:f:67:ILE:HG21	37:f:84:PRO:HB3	1.99	0.45
40:k:90:GLU:OE1	40:k:90:GLU:N	2.50	0.45
56:V:39:VAL:CB	56:V:58:TYR:OH	2.65	0.45
9:A:439:U:O4'	12:D:119:HIS:HA	2.16	0.45
9:A:562:U:H2'	20:L:13:ARG:CZ	2.46	0.45
9:A:661:G:H2'	9:A:662:U:H6	1.81	0.45
9:A:1003:G:H21	9:A:1037:C:H2'	1.82	0.45
9:A:1109:C:H2'	9:A:1110:A:H8	1.80	0.45
9:A:1238:A:H2	9:A:1241:G:N3	2.15	0.45
9:A:1306:A:H61	9:A:1331:G:H1'	1.81	0.45
9:A:1346:A:H61	9:A:1374:A:H3'	1.82	0.45
13:E:73:VAL:HG21	13:E:143:LEU:HB3	1.98	0.45
14:F:2:ARG:HD2	14:F:68:GLN:HB3	1.97	0.45
21:M:74:MET:O	21:M:78:ARG:HG2	2.16	0.45
27:S:18:VAL:O	27:S:22:VAL:HG23	2.16	0.45
33:b:133:U:H2'	33:b:134:G:H8	1.82	0.45
33:b:2167:U:C2	33:b:2170:A:N6	2.84	0.45
33:b:2335:A:H5'	45:p:13:ARG:NH2	2.32	0.45
33:b:2655:G:O2'	33:b:2656:U:P	2.75	0.45
9:A:28:A:H2	9:A:296:U:H4'	1.82	0.45
9:A:738:C:H2'	9:A:739:C:C6	2.52	0.45
9:A:738:C:H5''	14:F:2:ARG:HH12	1.82	0.45
9:A:782:A:H62	9:A:800:G:H21	1.63	0.45
9:A:1455:G:H2'	9:A:1456:A:H8	1.82	0.45
10:B:85:SER:OG	10:B:88:GLN:NE2	2.50	0.45
10:B:99:MET:HG2	10:B:100:LEU:HD12	1.98	0.45
18:J:49:PHE:HB2	18:J:65:TYR:HB2	1.99	0.45
21:M:39:ALA:HB3	21:M:42:VAL:HG13	1.99	0.45
23:O:14:PHE:HB3	23:O:26:VAL:HG22	1.99	0.45
31:Y:52:A:O2'	31:Y:53:G:H5''	2.16	0.45
33:b:1315:C:HO2'	33:b:1392:A:H8	1.63	0.45
33:b:1434:A:H1'	33:b:1435:G:C8	2.52	0.45
33:b:1844:C:O3'	34:c:256:LYS:NZ	2.44	0.45
9:A:150:U:H2'	9:A:151:A:H8	1.82	0.45
9:A:475:C:O5'	9:A:475:C:H6	2.00	0.45
9:A:494:G:C8	9:A:496:A:H1'	2.51	0.45
9:A:932:C:H2'	9:A:933:G:C8	2.51	0.45
9:A:958:A:N6	27:S:54:ARG:HH21	2.06	0.45
9:A:1065:U:H4'	9:A:1066:C:O5'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:10:ARG:HA	25:Q:10:ARG:HH11	1.82	0.45
28:T:35:TYR:HA	28:T:38:ILE:HD12	1.99	0.45
33:b:1741:C:H2'	33:b:1742:U:H6	1.81	0.45
33:b:2180:U:O2'	33:b:2181:U:O5'	2.20	0.45
37:f:7:TYR:HD1	37:f:7:TYR:N	2.11	0.45
40:k:17:VAL:HG13	40:k:137:PRO:HB2	1.98	0.45
56:V:67:LEU:O	56:V:70:LEU:HB3	2.17	0.45
3:2:39:GLU:OE1	3:2:39:GLU:N	2.31	0.45
9:A:198:G:H2'	9:A:199:A:H8	1.82	0.45
9:A:220:G:H2'	9:A:221:C:H6	1.82	0.45
9:A:746:A:H2'	9:A:747:A:H8	1.82	0.45
9:A:1413:A:H2	9:A:1487:G:H22	1.62	0.45
14:F:26:THR:HA	14:F:29:ILE:HG12	1.99	0.45
23:O:64:LYS:HA	23:O:67:ASP:OD2	2.17	0.45
32:a:57:A:C2	37:f:26:MET:HE1	2.52	0.45
33:b:155:A:H2'	33:b:156:A:H8	1.82	0.45
33:b:1412:U:H2'	33:b:1413:A:C8	2.51	0.45
33:b:2062:A:N7	55:z:158:ARG:NH1	2.65	0.45
33:b:2121:G:OP1	33:b:2169:A:O2'	2.35	0.45
33:b:2405:G:O2'	33:b:2406:A:OP1	2.30	0.45
39:h:26:ALA:HA	39:h:30:LEU:HD12	1.99	0.45
56:V:28:VAL:O	56:V:28:VAL:CG1	2.65	0.45
9:A:45:G:H2'	9:A:46:G:O4'	2.17	0.45
9:A:191:G:H2'	9:A:192:A:C8	2.52	0.45
9:A:465:A:H2'	9:A:466:A:C8	2.52	0.45
9:A:524:G:H2'	9:A:525:C:C6	2.52	0.45
9:A:1495:U:H2'	9:A:1496:C:C6	2.52	0.45
11:C:44:LYS:HE2	11:C:44:LYS:HB3	1.87	0.45
13:E:79:THR:OG1	13:E:80:LEU:N	2.50	0.45
33:b:952:G:N2	33:b:2267:A:H2	2.03	0.45
33:b:974:G:H2'	33:b:974:G:N3	2.32	0.45
33:b:1341:G:H5''	33:b:1397:U:O2	2.17	0.45
33:b:1907:G:O6	33:b:1924:C:N4	2.50	0.45
33:b:2062:A:N1	55:z:158:ARG:HB3	2.32	0.45
33:b:2062:A:O2'	33:b:2063:C:O5'	2.35	0.45
37:f:11:GLU:HA	37:f:14:LYS:HE3	1.99	0.45
37:f:73:SER:OG	37:f:81:GLN:N	2.50	0.45
42:m:1:MET:SD	42:m:2:ARG:N	2.90	0.45
46:q:48:ILE:HG13	46:q:60:THR:OG1	2.17	0.45
9:A:389:A:N3	9:A:390:U:H5''	2.32	0.44
9:A:402:G:H4'	9:A:620:C:H42	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:511:C:O2	12:D:40:HIS:NE2	2.50	0.44
9:A:845:A:C2	26:R:9:PHE:HB3	2.52	0.44
9:A:1496:C:H2'	9:A:1497:G:C8	2.52	0.44
10:B:187:ASP:OD1	10:B:188:THR:N	2.42	0.44
17:I:64:ILE:HD12	17:I:78:ILE:HD12	1.98	0.44
20:L:100:ALA:HB3	20:L:103:CYS:SG	2.57	0.44
24:P:67:ILE:HG22	24:P:71:VAL:HG13	1.99	0.44
33:b:522:A:H2'	33:b:523:C:C6	2.52	0.44
33:b:718:A:H5''	33:b:719:C:H5	1.81	0.44
33:b:1435:G:H2'	33:b:1436:G:C8	2.52	0.44
33:b:1524:G:H2'	33:b:1525:A:C8	2.53	0.44
33:b:1649:G:O2'	44:o:106:ASP:OD2	2.22	0.44
33:b:2183:A:H8	33:b:2184:A:N7	2.15	0.44
33:b:2684:U:O4'	41:l:70:ARG:NH1	2.50	0.44
36:e:5:LEU:HD23	36:e:9:GLN:N	2.32	0.44
46:q:68:GLU:OE1	46:q:68:GLU:N	2.50	0.44
48:s:6:GLN:H	48:s:37:GLU:CD	2.21	0.44
52:w:11:GLU:OE1	52:w:11:GLU:N	2.51	0.44
56:V:19:ILE:HD12	56:V:20:ALA:H	1.82	0.44
9:A:1009:U:H2'	9:A:1010:U:C6	2.52	0.44
9:A:1246:A:C6	9:A:1292:G:C6	3.05	0.44
9:A:1516:G:H2'	9:A:1518:A:OP2	2.17	0.44
11:C:17:TRP:HH2	22:N:95:LEU:H	1.64	0.44
12:D:14:GLU:OE1	12:D:62:ARG:NH1	2.50	0.44
12:D:25:ARG:HG2	12:D:26:ALA:H	1.82	0.44
12:D:67:LEU:HB2	12:D:70:GLN:CD	2.43	0.44
12:D:157:ALA:O	12:D:161:ALA:N	2.50	0.44
16:H:10:LEU:HD22	16:H:74:ILE:HD11	2.00	0.44
16:H:12:ARG:HA	16:H:15:ASN:ND2	2.32	0.44
30:X:70:C:H2'	30:X:71:G:C8	2.52	0.44
31:Z:11:C:H2'	31:Z:12:G:C8	2.52	0.44
32:a:51:G:O2'	32:a:52:A:OP1	2.33	0.44
33:b:1:G:H8	33:b:1:G:O5'	2.00	0.44
33:b:1779:U:OP2	33:b:1784:A:N6	2.47	0.44
33:b:2267:A:H62	33:b:2272:U:H3	1.64	0.44
37:f:148:ARG:HA	37:f:148:ARG:NH1	2.32	0.44
43:n:7:THR:OG1	43:n:9:PHE:O	2.35	0.44
4:4:55:ILE:HG23	4:4:56:ALA:H	1.82	0.44
9:A:154:U:H2'	9:A:155:A:C8	2.52	0.44
9:A:237:G:H5''	25:Q:39:ARG:NH2	2.33	0.44
9:A:560:A:N1	9:A:566:G:H5'	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:949:A:N6	9:A:1233:G:C6	2.85	0.44
9:A:1060:U:OP1	22:N:84:ARG:NH2	2.50	0.44
9:A:1111:A:H2'	9:A:1112:C:C6	2.53	0.44
9:A:1253:G:H2'	9:A:1254:A:C8	2.52	0.44
11:C:57:GLU:OE1	11:C:57:GLU:N	2.50	0.44
12:D:72:ARG:O	12:D:76:LYS:HG3	2.17	0.44
15:G:91:ARG:O	15:G:95:ARG:HG3	2.17	0.44
32:a:39:A:C2	32:a:44:G:C2	3.06	0.44
33:b:882:G:O2'	33:b:883:G:H5'	2.17	0.44
33:b:1292:G:H2'	33:b:1293:C:C6	2.53	0.44
52:w:24:ASN:OD1	52:w:44:HIS:HB3	2.18	0.44
9:A:463:U:H2'	9:A:464:U:C6	2.52	0.44
9:A:592:G:H2'	9:A:593:U:C6	2.52	0.44
9:A:592:G:H2'	9:A:593:U:H6	1.82	0.44
9:A:660:C:H2'	9:A:661:G:H8	1.82	0.44
9:A:778:G:N3	19:K:121:ARG:NH1	2.65	0.44
9:A:967:C:OP2	9:A:968:A:O2'	2.28	0.44
16:H:41:GLU:H	16:H:41:GLU:CD	2.25	0.44
31:Y:22:A:C6	31:Y:47:G:H2'	2.52	0.44
31:Y:30:U:H2'	31:Y:31:C:C6	2.52	0.44
31:Y:76:C:H5''	31:Y:77:A:OP2	2.17	0.44
31:Z:10:G:C6	31:Z:27:A:C5	3.06	0.44
33:b:1019:U:H3	33:b:1142:A:N6	2.14	0.44
33:b:1712:U:OP2	33:b:1713:A:O2'	2.30	0.44
36:e:2:GLU:HG3	36:e:11:ALA:HB1	1.99	0.44
54:y:37:ILE:HG12	54:y:38:VAL:HG23	2.00	0.44
9:A:31:G:O2'	9:A:48:C:N4	2.51	0.44
9:A:33:A:H2'	20:L:28:GLN:HE22	1.83	0.44
9:A:137:U:H2'	9:A:138:G:C8	2.53	0.44
9:A:206:C:H2'	9:A:207:C:C6	2.53	0.44
11:C:28:PHE:CE2	22:N:76:PHE:HA	2.52	0.44
24:P:68:SER:OG	24:P:69:ASP:N	2.50	0.44
25:Q:16:MET:HB2	25:Q:19:SER:O	2.17	0.44
32:a:115:A:H2'	32:a:116:G:H8	1.81	0.44
33:b:548:G:H2'	33:b:549:G:C4'	2.47	0.44
33:b:1599:U:H2'	33:b:1600:C:C6	2.51	0.44
33:b:2450:A:OP1	33:b:2497:A:O2'	2.22	0.44
36:e:3:LEU:HB3	36:e:12:LEU:HB2	1.98	0.44
37:f:88:LYS:HZ2	37:f:90:THR:HG23	1.83	0.44
37:f:170:LEU:HA	37:f:173:PHE:HB3	2.00	0.44
39:h:53:GLU:OE1	39:h:53:GLU:N	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:s:6:GLN:CB	48:s:37:GLU:OE2	2.66	0.44
9:A:62:U:H3	9:A:105:G:H1	1.65	0.44
9:A:582:C:C5'	23:O:63:ARG:HH12	2.31	0.44
9:A:595:A:N6	9:A:641:U:O2'	2.51	0.44
9:A:855:U:H2'	9:A:856:C:C6	2.52	0.44
9:A:1249:C:H1'	17:I:71:ILE:HD11	1.99	0.44
9:A:1304:G:H8	9:A:1304:G:O5'	2.01	0.44
9:A:1356:G:H2'	9:A:1357:A:C8	2.50	0.44
17:I:78:ILE:O	17:I:82:ILE:HG12	2.18	0.44
19:K:34:THR:OG1	19:K:35:ASP:N	2.50	0.44
21:M:67:ASP:HA	21:M:70:ARG:HG3	2.00	0.44
28:T:14:GLU:O	28:T:18:LYS:HG2	2.18	0.44
30:X:14:A:C2	30:X:15:G:H1'	2.53	0.44
31:Y:16:C:O2'	31:Y:17:C:OP1	2.36	0.44
33:b:285:G:H2'	33:b:286:U:C6	2.52	0.44
33:b:900:A:H2'	33:b:901:C:O4'	2.17	0.44
33:b:1744:A:C2	33:b:1745:A:H1'	2.52	0.44
33:b:1790:C:H2'	33:b:1791:A:C8	2.52	0.44
33:b:2136:G:H1	33:b:2156:G:H1	1.66	0.44
34:c:141:VAL:CG1	34:c:190:ALA:HB1	2.47	0.44
35:d:85:ALA:O	35:d:86:GLU:HG3	2.17	0.44
39:h:58:LEU:HA	39:h:61:VAL:HG12	1.98	0.44
55:z:125:THR:HB	55:z:129:ARG:NE	2.24	0.44
9:A:230:G:H2'	9:A:231:U:O4'	2.18	0.44
9:A:504:C:H1'	9:A:510:A:H2'	1.99	0.44
9:A:519:C:H2'	9:A:520:A:O4'	2.18	0.44
9:A:590:U:H5'	16:H:30:LYS:HE3	1.99	0.44
15:G:99:ALA:O	15:G:103:ILE:HG12	2.18	0.44
16:H:47:ASP:OD1	16:H:48:PHE:N	2.51	0.44
30:X:10:G:N7	30:X:45:G:C2	2.86	0.44
30:X:31:C:H2'	30:X:32:U:H6	1.82	0.44
33:b:155:A:H2'	33:b:156:A:C8	2.53	0.44
33:b:813:U:H2'	33:b:814:C:H6	1.82	0.44
33:b:892:A:O2'	33:b:893:C:O4'	2.30	0.44
33:b:1510:G:H2'	33:b:1511:G:H8	1.83	0.44
33:b:1827:U:H2'	33:b:1828:G:O4'	2.17	0.44
33:b:2194:U:H2'	33:b:2195:U:C6	2.52	0.44
33:b:2547:A:H2'	33:b:2548:U:C6	2.52	0.44
37:f:142:ASP:O	37:f:146:VAL:N	2.48	0.44
2:1:51:ALA:O	2:1:55:THR:OG1	2.26	0.44
4:4:9:THR:CG2	33:b:2020:A:H5'	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:285:C:H2'	9:A:286:C:C6	2.53	0.44
9:A:518:C:H2'	9:A:530:G:C8	2.53	0.44
9:A:1455:G:H2'	9:A:1456:A:C8	2.53	0.44
17:I:51:LEU:HG	17:I:56:MET:CE	2.48	0.44
30:X:18:G:H5'	30:X:60:U:C2	2.52	0.44
33:b:48:G:C2	33:b:178:G:C6	3.06	0.44
33:b:208:C:H2'	33:b:209:C:H6	1.82	0.44
33:b:353:C:H2'	33:b:354:A:C8	2.53	0.44
33:b:1475:G:H2'	33:b:1475:G:N3	2.32	0.44
33:b:1727:C:H2'	33:b:1728:C:H6	1.83	0.44
33:b:2671:G:H2'	33:b:2672:U:C6	2.53	0.44
33:b:2898:U:H2'	33:b:2899:A:H8	1.81	0.44
34:c:269:ARG:CZ	34:c:269:ARG:HB3	2.48	0.44
36:e:188:MET:HE3	36:e:193:VAL:HG22	2.00	0.44
39:h:78:VAL:HG13	39:h:144:VAL:HG23	2.00	0.44
9:A:48:C:H6	9:A:365:U:H5	1.65	0.44
9:A:166:U:H2'	9:A:167:A:H8	1.82	0.44
9:A:736:C:H2'	9:A:737:C:C6	2.53	0.44
9:A:1034:G:H2'	9:A:1035:A:H8	1.82	0.44
9:A:1088:G:H1'	9:A:1167:A:H61	1.83	0.44
9:A:1118:U:H2'	9:A:1119:C:C6	2.53	0.44
9:A:1222:G:OP2	9:A:1322:C:N4	2.40	0.44
9:A:1322:C:OP1	27:S:77:ARG:NH2	2.41	0.44
9:A:1434:A:H2'	9:A:1435:G:O4'	2.18	0.44
10:B:127:LYS:HE3	10:B:132:GLU:HG2	2.00	0.44
14:F:44:ARG:HA	14:F:57:ALA:O	2.18	0.44
16:H:93:LYS:HG3	16:H:97:GLY:N	2.33	0.44
33:b:430:A:H8	33:b:430:A:OP2	2.01	0.44
33:b:2109:U:H1'	33:b:2180:U:H3	1.83	0.44
35:d:74:GLU:CD	35:d:74:GLU:H	2.26	0.44
40:k:114:LEU:HG	40:k:118:MET:HE3	1.99	0.44
55:z:133:LEU:HD23	55:z:133:LEU:C	2.42	0.44
6:6:10:LEU:HD13	33:b:125:A:C6	2.53	0.43
9:A:27:G:H2'	9:A:28:A:C8	2.53	0.43
9:A:424:G:H2'	9:A:425:G:C8	2.53	0.43
9:A:745:G:H2'	9:A:746:A:C8	2.51	0.43
9:A:1023:U:H6	9:A:1023:U:O5'	2.00	0.43
9:A:1064:G:H21	9:A:1190:G:H1'	1.83	0.43
9:A:1116:U:H3	9:A:1184:G:H1	1.66	0.43
10:B:138:ARG:CZ	10:B:138:ARG:HA	2.48	0.43
15:G:137:ARG:O	15:G:141:HIS:ND1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:6:G:H2'	32:a:7:G:C8	2.53	0.43
33:b:265:A:N6	33:b:428:A:C8	2.84	0.43
33:b:1561:C:H2'	33:b:1562:U:C6	2.53	0.43
33:b:2564:A:C2	33:b:2647:U:H4'	2.53	0.43
40:k:111:LYS:N	40:k:111:LYS:HD2	2.33	0.43
9:A:31:G:C5	9:A:306:A:H4'	2.53	0.43
9:A:661:G:H2'	9:A:662:U:C6	2.53	0.43
9:A:778:G:H21	19:K:121:ARG:NH1	2.17	0.43
14:F:3:HIS:HB2	14:F:92:THR:HB	1.99	0.43
20:L:36:VAL:HG23	20:L:75:GLU:OE1	2.18	0.43
27:S:54:ARG:HG3	27:S:55:GLN:OE1	2.19	0.43
28:T:54:GLN:N	28:T:55:PRO:HD2	2.33	0.43
30:X:69:C:H2'	30:X:70:C:C6	2.53	0.43
32:a:94:A:OP1	52:w:19:ARG:NH1	2.44	0.43
33:b:134:G:H2'	33:b:135:U:H6	1.80	0.43
33:b:640:C:H2'	33:b:641:U:C6	2.54	0.43
33:b:1406:U:C2	33:b:1407:G:C8	3.06	0.43
33:b:2025:C:H2'	33:b:2026:U:C6	2.53	0.43
34:c:183:LYS:HB3	34:c:183:LYS:HE2	1.83	0.43
36:e:51:GLU:O	36:e:51:GLU:CG	2.63	0.43
37:f:31:VAL:HG12	37:f:96:MET:HE1	2.00	0.43
38:g:18:LYS:HG3	38:g:20:ASN:OD1	2.18	0.43
38:g:133:LEU:CD1	38:g:141:ILE:CG1	2.90	0.43
43:n:53:MET:HB3	43:n:120:ALA:HB2	1.99	0.43
9:A:33:A:N1	9:A:552:U:C5	2.85	0.43
9:A:237:G:C5'	25:Q:26:ARG:HH12	2.31	0.43
9:A:1010:U:H2'	9:A:1011:C:H6	1.82	0.43
9:A:1513:A:H2'	9:A:1514:G:H8	1.83	0.43
13:E:37:VAL:HA	13:E:47:PHE:HA	2.00	0.43
16:H:4:ASP:OD2	16:H:76:ARG:NH1	2.51	0.43
24:P:39:PHE:HE2	24:P:70:ARG:NH2	2.17	0.43
31:Y:70:A:H2'	31:Y:71:C:H6	1.82	0.43
33:b:881:G:H3'	33:b:882:G:C8	2.53	0.43
33:b:1370:C:H2'	33:b:1371:G:O4'	2.18	0.43
33:b:2836:U:H2'	33:b:2837:A:C8	2.53	0.43
34:c:141:VAL:O	34:c:162:VAL:N	2.44	0.43
36:e:21:ARG:HD3	36:e:106:LYS:HB3	2.01	0.43
48:s:43:ASN:N	48:s:43:ASN:OD1	2.51	0.43
4:4:9:THR:HG22	33:b:2020:A:H5'	2.00	0.43
9:A:139:A:H2'	9:A:140:U:C6	2.53	0.43
9:A:949:A:OP1	21:M:99:GLN:NE2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1011:C:H2'	9:A:1012:A:H8	1.82	0.43
9:A:1048:G:OP1	22:N:2:LYS:HA	2.18	0.43
9:A:1256:A:H62	9:A:1279:G:N2	2.16	0.43
9:A:1345:U:OP1	17:I:121:ARG:NH1	2.51	0.43
9:A:1494:G:P	33:b:1913:A:H62	2.41	0.43
12:D:169:TRP:HE3	12:D:181:PHE:HE1	1.64	0.43
20:L:63:THR:HG22	20:L:91:GLY:O	2.18	0.43
33:b:152:A:H2'	33:b:153:U:C6	2.53	0.43
33:b:706:A:OP1	34:c:7:LYS:NZ	2.51	0.43
33:b:2052:A:H4'	35:d:148:GLN:O	2.18	0.43
33:b:2545:G:H2'	33:b:2546:U:O4'	2.18	0.43
33:b:2771:C:H2'	33:b:2772:C:H6	1.83	0.43
33:b:2847:U:H2'	33:b:2848:G:O4'	2.18	0.43
37:f:114:PHE:HD1	37:f:115:ARG:N	2.16	0.43
37:f:148:ARG:HA	37:f:148:ARG:CZ	2.49	0.43
9:A:148:G:H1'	9:A:1447:A:N3	2.34	0.43
9:A:406:G:N3	12:D:115:GLN:NE2	2.67	0.43
9:A:433:G:OP2	9:A:433:G:H8	2.02	0.43
9:A:589:U:H3	9:A:650:G:H1	1.66	0.43
11:C:148:ILE:HD12	11:C:200:TRP:O	2.17	0.43
12:D:124:VAL:HG12	12:D:125:ASN:ND2	2.31	0.43
14:F:18:VAL:HG21	14:F:58:HIS:CE1	2.53	0.43
19:K:27:ASN:O	19:K:56:LYS:HE3	2.18	0.43
31:Y:5:G:N1	31:Y:6:A:N1	2.67	0.43
33:b:2088:A:H2'	33:b:2089:C:H6	1.84	0.43
46:q:2:SER:OG	46:q:5:ILE:HG22	2.18	0.43
49:t:96:ILE:HD13	49:t:96:ILE:HA	1.91	0.43
50:u:54:GLU:OE1	50:u:54:GLU:N	2.51	0.43
52:w:5:ASN:OD1	52:w:5:ASN:N	2.51	0.43
9:A:114:U:H2'	9:A:115:G:C8	2.54	0.43
9:A:124:C:H4'	9:A:291:U:O2'	2.18	0.43
9:A:590:U:OP2	16:H:29:SER:HB2	2.19	0.43
9:A:627:G:H2'	9:A:628:G:C8	2.54	0.43
9:A:838:G:H2'	9:A:839:C:C6	2.54	0.43
9:A:939:G:H4'	15:G:101:ARG:HH12	1.83	0.43
9:A:1226:C:H2'	21:M:101:THR:HG23	1.99	0.43
9:A:1250:A:H2'	9:A:1251:A:C8	2.53	0.43
10:B:134:LEU:O	10:B:138:ARG:HG2	2.19	0.43
17:I:52:GLU:CA	17:I:56:MET:CE	2.96	0.43
18:J:55:PRO:HA	22:N:80:ARG:NH2	2.33	0.43
19:K:60:PHE:O	19:K:64:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:53:GLY:N	25:Q:56:ASP:OD2	2.36	0.43
33:b:555:G:O2'	33:b:556:A:H8	2.01	0.43
33:b:1197:G:H2'	33:b:1198:U:H6	1.83	0.43
33:b:1444:G:C4	33:b:1445:G:C8	3.06	0.43
33:b:1509:A:H2'	33:b:1510:G:C8	2.54	0.43
33:b:2307:G:H5'	33:b:2308:G:N3	2.34	0.43
38:g:2:SER:O	38:g:6:LYS:HG2	2.18	0.43
52:w:24:ASN:O	52:w:25:LYS:HG3	2.18	0.43
9:A:254:G:O3'	25:Q:70:LYS:NZ	2.45	0.43
9:A:703:G:H4'	9:A:704:A:H5'	2.00	0.43
9:A:845:A:H5'	26:R:9:PHE:CZ	2.54	0.43
11:C:79:LYS:N	11:C:81:GLU:OE2	2.51	0.43
13:E:106:ALA:HB1	13:E:110:MET:HB3	2.01	0.43
17:I:32:ARG:NH2	17:I:37:TYR:HA	2.34	0.43
21:M:45:SER:OG	21:M:46:GLU:OE1	2.31	0.43
33:b:851:C:H2'	33:b:852:U:H6	1.83	0.43
33:b:1930:G:HO2'	33:b:1931:U:H6	1.62	0.43
33:b:2194:U:H2'	33:b:2195:U:H6	1.83	0.43
33:b:2291:U:H2'	33:b:2292:U:H6	1.81	0.43
42:m:19:LEU:HD23	42:m:27:LEU:HB3	2.00	0.43
46:q:11:GLU:H	46:q:11:GLU:CD	2.26	0.43
54:y:70:GLU:OE1	54:y:70:GLU:N	2.51	0.43
56:V:58:TYR:CD2	56:V:58:TYR:O	2.72	0.43
3:2:45:ARG:O	3:2:48:ILE:HG13	2.18	0.43
9:A:214:C:H2'	9:A:215:C:H6	1.84	0.43
9:A:414:A:H2'	9:A:414:A:N3	2.33	0.43
9:A:606:G:P	9:A:607:A:H5'	2.58	0.43
9:A:999:C:N4	9:A:1042:A:H61	2.17	0.43
9:A:1060:U:H2'	9:A:1061:G:H8	1.82	0.43
9:A:1074:G:H2'	9:A:1075:U:C6	2.54	0.43
9:A:1176:A:H2'	9:A:1177:G:C8	2.54	0.43
9:A:1227:A:H2'	21:M:115:ILE:HD11	2.00	0.43
10:B:113:LEU:HD11	10:B:144:GLU:HB3	2.01	0.43
15:G:12:LEU:HD12	15:G:13:PRO:HD2	2.00	0.43
15:G:102:TRP:O	15:G:105:GLU:HG3	2.19	0.43
30:X:70:C:O5'	30:X:70:C:H6	2.02	0.43
31:Y:28:C:H2'	31:Y:29:U:C6	2.54	0.43
33:b:627:A:C6	33:b:637:A:C8	3.07	0.43
33:b:2130:U:N3	33:b:2158:A:OP1	2.50	0.43
34:c:143:ASN:OD1	34:c:152:GLY:HA3	2.19	0.43
35:d:35:THR:HG22	35:d:73:VAL:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:61:LYS:HD3	33:b:372:G:C8	2.54	0.43
3:2:24:LEU:HD23	3:2:24:LEU:HA	1.84	0.43
9:A:269:C:H2'	9:A:270:A:H8	1.83	0.43
9:A:478:A:H3'	9:A:479:U:H5''	2.01	0.43
9:A:613:C:H2'	9:A:614:C:H6	1.82	0.43
9:A:627:G:H2'	9:A:628:G:H8	1.83	0.43
9:A:1241:G:H2'	9:A:1242:G:H8	1.84	0.43
10:B:86:CYS:SG	10:B:87:ASP:N	2.91	0.43
10:B:224:ARG:HE	10:B:224:ARG:H	1.67	0.43
12:D:24:VAL:HG22	12:D:160:LEU:HD22	2.00	0.43
12:D:101:VAL:HA	12:D:104:MET:HB2	2.00	0.43
16:H:75:GLN:NE2	16:H:127:TYR:HB2	2.34	0.43
19:K:74:LYS:HD3	19:K:75:GLU:OE1	2.18	0.43
33:b:851:C:H2'	33:b:852:U:C6	2.54	0.43
33:b:971:G:OP2	33:b:974:G:N2	2.52	0.43
33:b:1009:A:N3	33:b:1153:C:O2'	2.51	0.43
33:b:1099:G:OP1	33:b:1099:G:C8	2.71	0.43
33:b:1176:U:H3'	33:b:1177:G:H8	1.84	0.43
33:b:2112:G:P	33:b:2114:A:H62	2.41	0.43
33:b:2307:G:H4'	33:b:2308:G:O5'	2.19	0.43
34:c:246:THR:HG23	34:c:250:VAL:O	2.19	0.43
36:e:189:THR:O	36:e:193:VAL:HG23	2.19	0.43
41:l:111:LYS:O	41:l:111:LYS:HD3	2.18	0.43
48:s:26:ASP:OD1	48:s:26:ASP:N	2.38	0.43
48:s:32:THR:HG22	48:s:62:GLU:HB3	2.01	0.43
9:A:112:G:H21	9:A:354:G:C4'	2.32	0.43
9:A:461:A:H2'	9:A:462:G:N7	2.34	0.43
9:A:855:U:H2'	9:A:856:C:H6	1.83	0.43
9:A:1309:G:C6	9:A:1329:A:C6	3.07	0.43
30:X:10:G:H2'	30:X:11:C:C6	2.53	0.43
33:b:28:A:N6	33:b:512:G:O2'	2.51	0.43
33:b:48:G:N1	33:b:178:G:O6	2.51	0.43
33:b:263:G:O2'	33:b:429:A:N3	2.52	0.43
33:b:972:A:OP2	33:b:973:A:O2'	2.36	0.43
33:b:2557:G:H2'	33:b:2558:C:C6	2.53	0.43
35:d:16:THR:HG22	35:d:20:VAL:O	2.19	0.43
37:f:88:LYS:NZ	37:f:90:THR:HG23	2.33	0.43
42:m:4:ASN:O	42:m:4:ASN:ND2	2.52	0.43
49:t:95:ARG:NH1	55:z:137:VAL:HG12	2.33	0.43
51:v:88:GLU:C	51:v:89:ASP:OD1	2.62	0.43
9:A:264:C:H2'	9:A:265:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:473:U:H2'	9:A:474:G:C8	2.54	0.42
9:A:549:C:OP1	12:D:69:ARG:NH1	2.41	0.42
9:A:1163:A:H2'	9:A:1164:G:C8	2.54	0.42
9:A:1298:U:C4	15:G:113:LYS:HD3	2.53	0.42
12:D:114:ARG:O	12:D:118:SER:HB3	2.19	0.42
14:F:49:TYR:HB3	26:R:73:HIS:CE1	2.54	0.42
30:X:71:G:O2'	33:b:1852:U:H5'	2.19	0.42
31:Y:67:A:H2'	31:Y:68:U:O4'	2.19	0.42
31:Z:50:G:H2'	31:Z:51:G:H8	1.84	0.42
33:b:279:A:N3	33:b:280:U:H1'	2.34	0.42
33:b:533:G:H2'	33:b:534:U:C6	2.54	0.42
33:b:930:G:C2	33:b:933:A:C2	3.07	0.42
33:b:1917:U:O4	33:b:1918:A:N6	2.52	0.42
33:b:2711:A:N6	33:b:2714:G:N7	2.67	0.42
35:d:157:LYS:HG2	40:k:80:HIS:CD2	2.53	0.42
42:m:129:LYS:HG3	42:m:130:GLY:N	2.33	0.42
50:u:91:GLN:OE1	50:u:91:GLN:N	2.46	0.42
52:w:63:ILE:HG22	52:w:65:VAL:HG23	2.01	0.42
8:8:16:ILE:HG13	8:8:25:VAL:HG22	2.01	0.42
9:A:102:G:H2'	9:A:103:U:C6	2.55	0.42
9:A:461:A:H1'	9:A:471:U:O4	2.19	0.42
9:A:509:A:C4	12:D:50:TYR:HE2	2.37	0.42
9:A:619:U:OP1	9:A:621:A:N6	2.52	0.42
9:A:1103:C:H4'	10:B:96:LEU:HD13	2.00	0.42
9:A:1112:C:O2'	11:C:178:ARG:HD3	2.19	0.42
9:A:1231:G:H2'	9:A:1232:U:C6	2.54	0.42
12:D:123:MET:HG2	12:D:144:ILE:C	2.44	0.42
15:G:42:VAL:HG12	15:G:46:LEU:HD23	2.00	0.42
16:H:40:LYS:HD3	16:H:48:PHE:CE2	2.54	0.42
17:I:38:PHE:O	17:I:44:ARG:NH1	2.52	0.42
18:J:42:LEU:HG	18:J:71:LEU:HD13	2.01	0.42
30:X:56:C:O2'	30:X:57:G:O5'	2.32	0.42
32:a:17:C:C2	32:a:18:G:C8	3.07	0.42
33:b:28:A:HO2'	33:b:582:A:HO2'	1.66	0.42
33:b:555:G:HO2'	33:b:556:A:P	2.42	0.42
33:b:1475:G:O2'	33:b:1514:G:O6	2.37	0.42
33:b:2078:C:H2'	33:b:2079:U:C6	2.54	0.42
33:b:2174:C:H2'	33:b:2175:C:C6	2.54	0.42
33:b:2711:A:N6	33:b:2714:G:C8	2.87	0.42
33:b:2795:C:H2'	33:b:2796:U:O4'	2.18	0.42
36:e:147:LEU:HD11	36:e:170:ARG:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:f:7:TYR:CD1	37:f:7:TYR:C	2.90	0.42
37:f:70:ALA:HB2	37:f:83:TYR:H	1.83	0.42
39:h:9:VAL:HG11	39:h:12:LEU:HG	2.00	0.42
45:p:60:GLU:H	45:p:60:GLU:CD	2.27	0.42
55:z:133:LEU:HD23	55:z:133:LEU:O	2.20	0.42
2:l:8:GLU:OE1	2:l:8:GLU:N	2.31	0.42
9:A:104:G:H5'	9:A:172:A:C2	2.54	0.42
9:A:779:C:H1'	19:K:121:ARG:HH22	1.84	0.42
9:A:794:A:H2'	9:A:795:C:C6	2.54	0.42
9:A:1126:U:O2	9:A:1280:A:H3'	2.19	0.42
9:A:1384:C:H2'	9:A:1385:G:C8	2.54	0.42
9:A:1436:U:H2'	9:A:1437:A:C8	2.54	0.42
10:B:172:ILE:O	10:B:176:ASN:ND2	2.50	0.42
10:B:181:PRO:HA	10:B:195:VAL:HG11	2.00	0.42
11:C:70:ALA:HB2	11:C:105:VAL:HB	2.00	0.42
15:G:55:LYS:HB3	15:G:59:GLU:HG3	2.00	0.42
17:I:17:ARG:HG3	17:I:65:THR:OG1	2.19	0.42
33:b:1198:U:H2'	33:b:1199:U:H6	1.83	0.42
33:b:1204:A:O2'	33:b:1205:A:OP2	2.33	0.42
33:b:1417:C:H2'	33:b:1418:G:O4'	2.19	0.42
33:b:2391:G:O2'	33:b:2424:C:N4	2.46	0.42
34:c:157:SER:O	34:c:195:VAL:HG11	2.20	0.42
9:A:191:G:H2'	9:A:192:A:H8	1.84	0.42
9:A:321:A:H4'	9:A:1436:U:H5'	2.02	0.42
9:A:643:C:H2'	9:A:644:U:C6	2.54	0.42
9:A:942:G:O6	9:A:1342:C:N4	2.52	0.42
9:A:1163:A:H2'	9:A:1164:G:H8	1.83	0.42
10:B:55:GLU:O	10:B:59:ILE:N	2.52	0.42
18:J:81:GLU:OE1	18:J:82:LYS:N	2.39	0.42
21:M:3:ILE:CD1	21:M:56:ARG:HG2	2.49	0.42
25:Q:23:ALA:HA	25:Q:42:LYS:HD3	2.02	0.42
28:T:56:ILE:O	28:T:60:GLN:HG2	2.18	0.42
33:b:228:C:H4'	33:b:229:C:O5'	2.19	0.42
33:b:1727:C:H2'	33:b:1728:C:C6	2.54	0.42
33:b:1831:G:H2'	33:b:1832:C:C6	2.55	0.42
33:b:2097:A:H2'	33:b:2098:U:C6	2.54	0.42
35:d:88:GLU:HB3	35:d:90:PHE:CE1	2.53	0.42
9:A:390:U:H4'	24:P:28:ARG:NH2	2.35	0.42
9:A:505:G:H4'	9:A:534:U:C2	2.54	0.42
9:A:1477:U:H2'	9:A:1478:U:H6	1.84	0.42
10:B:10:LYS:HD2	10:B:12:GLY:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:158:ASP:O	10:B:180:ILE:HG23	2.19	0.42
16:H:95:MET:HB3	16:H:99:GLY:H	1.84	0.42
22:N:25:GLU:HG2	22:N:26:LEU:HD12	2.01	0.42
27:S:62:THR:OG1	27:S:64:GLU:OE1	2.34	0.42
33:b:263:G:H2'	33:b:264:C:O4'	2.20	0.42
33:b:2255:G:N2	54:y:8:GLY:O	2.34	0.42
33:b:2547:A:H5''	33:b:2566:A:C2	2.54	0.42
34:c:30:PHE:CE2	34:c:32:PRO:HD2	2.55	0.42
34:c:200:HIS:O	34:c:200:HIS:CD2	2.72	0.42
39:h:27:ARG:O	39:h:32:PRO:CG	2.68	0.42
40:k:102:GLU:HB2	40:k:119:PHE:CZ	2.55	0.42
42:m:115:GLU:OE1	42:m:115:GLU:N	2.53	0.42
51:v:27:ASN:OD1	51:v:27:ASN:N	2.52	0.42
51:v:81:ASP:OD1	51:v:82:ARG:N	2.46	0.42
1:0:57:ARG:HA	1:0:60:ASP:OD2	2.20	0.42
9:A:131:A:OP2	9:A:131:A:H8	2.03	0.42
9:A:750:C:O2'	23:O:20:ASP:O	2.26	0.42
9:A:834:U:H2'	9:A:835:U:C6	2.54	0.42
9:A:1054:C:H4'	9:A:1055:A:H5''	2.01	0.42
21:M:2:ARG:HH21	37:f:136:ILE:HD12	1.84	0.42
33:b:208:C:H2'	33:b:209:C:C6	2.55	0.42
33:b:740:C:H41	33:b:757:G:H1	1.68	0.42
33:b:850:U:H3	33:b:927:A:H61	1.67	0.42
33:b:1410:G:H2'	33:b:1411:U:C6	2.54	0.42
33:b:1742:U:H2'	33:b:1743:G:O4'	2.19	0.42
33:b:2055:C:O2'	33:b:2504:U:H4'	2.19	0.42
33:b:2155:U:H5''	33:b:2156:G:OP2	2.20	0.42
34:c:210:ALA:HA	34:c:213:TRP:CE3	2.54	0.42
38:g:133:LEU:HD12	38:g:133:LEU:O	2.19	0.42
39:h:43:ASN:O	39:h:47:PHE:HB2	2.20	0.42
48:s:51:VAL:CG2	48:s:52:PRO:HD2	2.49	0.42
51:v:47:LYS:HE3	51:v:47:LYS:HB3	1.80	0.42
56:V:58:TYR:O	56:V:58:TYR:CG	2.72	0.42
4:4:12:LYS:HA	4:4:12:LYS:HD2	1.78	0.42
9:A:181:A:H1'	9:A:182:A:C8	2.54	0.42
9:A:217:C:H5'	9:A:218:U:OP2	2.19	0.42
9:A:284:C:H2'	9:A:285:C:C6	2.54	0.42
9:A:356:A:H2'	9:A:357:G:C8	2.54	0.42
9:A:376:G:H4'	24:P:5:ARG:HE	1.85	0.42
9:A:417:G:H2'	9:A:418:C:C6	2.53	0.42
9:A:608:A:C2	9:A:609:A:H1'	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:883:C:H2'	9:A:884:U:C6	2.54	0.42
9:A:1111:A:N1	11:C:176:THR:OG1	2.47	0.42
9:A:1293:C:H2'	9:A:1294:G:C8	2.54	0.42
17:I:26:LYS:HE3	17:I:62:LEU:C	2.44	0.42
17:I:51:LEU:O	17:I:56:MET:HE3	2.18	0.42
21:M:21:ILE:HB	21:M:24:VAL:HG23	2.01	0.42
28:T:14:GLU:OE1	28:T:18:LYS:NZ	2.53	0.42
31:Z:69:C:H2'	31:Z:70:A:H8	1.83	0.42
33:b:39:G:H2'	33:b:40:U:O2	2.20	0.42
33:b:153:U:H2'	33:b:154:U:C6	2.54	0.42
33:b:417:C:H2'	33:b:418:C:C6	2.55	0.42
33:b:418:C:H2'	33:b:419:U:C6	2.55	0.42
33:b:1417:C:C4	33:b:1418:G:C5	3.07	0.42
33:b:1575:C:H2'	33:b:1576:U:C6	2.55	0.42
33:b:2104:C:H2'	33:b:2105:U:C2	2.54	0.42
33:b:2723:C:H2'	33:b:2724:U:O4'	2.20	0.42
34:c:132:MET:HA	34:c:135:ILE:HG12	2.01	0.42
37:f:170:LEU:O	37:f:173:PHE:HB3	2.20	0.42
37:f:178:ARG:NE	37:f:178:ARG:O	2.53	0.42
43:n:33:LEU:HG	43:n:128:THR:HG21	2.02	0.42
48:s:7:SER:O	48:s:9:GLY:N	2.50	0.42
52:w:41:GLU:N	52:w:41:GLU:OE1	2.52	0.42
4:4:31:ASP:OD1	4:4:33:THR:N	2.52	0.42
9:A:220:G:H2'	9:A:221:C:C6	2.54	0.42
9:A:672:U:H2'	9:A:673:A:C8	2.54	0.42
9:A:939:G:H4'	15:G:101:ARG:NH1	2.35	0.42
9:A:939:G:H2'	9:A:940:C:C6	2.54	0.42
9:A:1107:C:H5'	11:C:168:ARG:NH2	2.34	0.42
9:A:1382:C:H2'	9:A:1383:C:H6	1.84	0.42
10:B:202:ASN:HD22	10:B:205:ALA:HB2	1.85	0.42
12:D:30:LYS:HE3	12:D:30:LYS:HB3	1.91	0.42
15:G:82:SER:HB2	15:G:84:TYR:CE1	2.55	0.42
16:H:29:SER:H	16:H:32:LYS:HB2	1.85	0.42
16:H:35:ILE:HG22	16:H:102:VAL:HG11	2.02	0.42
17:I:35:GLU:HA	17:I:44:ARG:NH2	2.35	0.42
21:M:3:ILE:HD12	21:M:3:ILE:HA	1.91	0.42
23:O:66:LEU:HD23	23:O:66:LEU:HA	1.86	0.42
31:Y:16:C:H4'	31:Y:17:C:OP2	2.19	0.42
33:b:18:U:H2'	33:b:19:A:H8	1.85	0.42
33:b:678:C:H2'	33:b:679:C:H6	1.84	0.42
33:b:1047:G:O2'	33:b:1110:G:N2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1407:G:H2'	33:b:1408:G:H8	1.85	0.42
33:b:1754:A:O3'	46:q:103:ARG:NH2	2.48	0.42
35:d:106:LYS:HD3	35:d:175:LEU:O	2.19	0.42
39:h:46:PHE:CE2	39:h:50:ARG:HD2	2.55	0.42
42:m:123:ARG:NH1	42:m:143:GLU:OE2	2.52	0.42
43:n:66:ARG:O	43:n:66:ARG:CG	2.64	0.42
9:A:32:A:N1	9:A:552:U:C5	2.88	0.42
9:A:261:U:P	28:T:70:LYS:HZ3	2.42	0.42
9:A:324:G:H8	9:A:324:G:O5'	2.03	0.42
9:A:427:U:O5'	9:A:427:U:H6	2.02	0.42
9:A:623:C:O5'	9:A:623:C:H6	2.03	0.42
9:A:770:C:H2'	9:A:771:G:H8	1.84	0.42
9:A:971:G:P	9:A:1231:G:H21	2.42	0.42
9:A:1197:A:H2'	9:A:1198:G:C8	2.54	0.42
9:A:1316:G:N1	9:A:1319:A:OP2	2.46	0.42
10:B:18:GLN:HG3	10:B:20:ARG:HB3	2.01	0.42
12:D:120:LYS:HE2	12:D:145:ARG:NH1	2.35	0.42
12:D:123:MET:H	12:D:144:ILE:HA	1.85	0.42
12:D:190:LEU:HD12	12:D:192:ALA:H	1.84	0.42
20:L:28:GLN:O	20:L:29:LYS:HE2	2.19	0.42
30:X:36:C:H5	53:x:12:G:H22	1.68	0.42
33:b:866:A:C8	33:b:914:G:C6	3.08	0.42
33:b:2066:C:H2'	33:b:2067:G:C8	2.55	0.42
33:b:2148:G:H2'	33:b:2149:U:C5	2.55	0.42
34:c:45:ASN:OD1	34:c:45:ASN:N	2.53	0.42
2:1:50:VAL:O	2:1:54:LYS:HG2	2.20	0.42
9:A:222:C:H2'	9:A:223:A:H8	1.85	0.42
9:A:979:C:H41	9:A:1318:A:H61	1.66	0.42
9:A:1430:A:H2'	9:A:1431:A:C8	2.55	0.42
10:B:59:ILE:HD13	10:B:59:ILE:HA	1.89	0.42
12:D:120:LYS:HE2	12:D:145:ARG:HH12	1.85	0.42
16:H:9:MET:HE1	16:H:26:MET:HE3	2.01	0.42
21:M:52:ILE:O	21:M:56:ARG:HG3	2.20	0.42
33:b:305:C:H2'	33:b:306:U:C6	2.54	0.42
33:b:813:U:H2'	33:b:814:C:C6	2.54	0.42
33:b:1357:C:H2'	33:b:1358:G:O4'	2.19	0.42
49:t:85:ILE:HD13	55:z:140:THR:HG21	2.02	0.42
50:u:52:GLU:OE1	50:u:52:GLU:N	2.53	0.42
51:v:62:GLU:OE1	51:v:62:GLU:N	2.43	0.42
52:w:80:HIS:HB2	52:w:85:LYS:HB2	2.02	0.42
4:4:38:HIS:CG	4:4:44:THR:HG22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:652:U:O4	9:A:752:G:O2'	2.38	0.41
9:A:1096:C:H2'	9:A:1097:C:H6	1.83	0.41
9:A:1109:C:H2'	9:A:1110:A:C8	2.54	0.41
9:A:1206:G:H4'	11:C:191:THR:O	2.20	0.41
9:A:1343:G:OP1	17:I:126:PHE:HB3	2.19	0.41
9:A:1349:A:H1'	9:A:1374:A:N6	2.35	0.41
16:H:94:VAL:HG13	16:H:99:GLY:O	2.19	0.41
30:X:3:G:H2'	30:X:4:G:H5'	2.01	0.41
30:X:11:C:H2'	30:X:12:U:C6	2.55	0.41
30:X:19:G:H5'	30:X:57:G:N2	2.35	0.41
32:a:25:U:N3	32:a:55:U:O4	2.53	0.41
32:a:66:A:H61	32:a:107:G:H2'	1.85	0.41
33:b:623:C:H2'	33:b:624:C:C6	2.55	0.41
33:b:639:U:H2'	33:b:640:C:H6	1.83	0.41
33:b:1319:C:H2'	33:b:1320:C:C6	2.54	0.41
33:b:1930:G:O2'	33:b:1931:U:H6	2.02	0.41
33:b:2036:C:H2'	33:b:2037:A:H8	1.83	0.41
33:b:2314:A:OP1	37:f:88:LYS:HE3	2.20	0.41
33:b:2327:A:H2'	33:b:2328:A:C8	2.55	0.41
33:b:2867:G:O2'	33:b:2868:A:OP2	2.35	0.41
37:f:32:GLU:OE1	37:f:32:GLU:N	2.53	0.41
40:k:110:PRO:O	40:k:115:GLY:HA3	2.20	0.41
42:m:122:VAL:HG22	42:m:142:ILE:HA	2.02	0.41
9:A:263:A:OP1	28:T:73:ARG:NH1	2.53	0.41
9:A:710:G:OP1	14:F:53:LYS:NZ	2.48	0.41
9:A:1013:G:H2'	9:A:1015:G:OP2	2.20	0.41
9:A:1287:A:C2	9:A:1353:G:H1'	2.54	0.41
9:A:1313:U:H2'	9:A:1314:C:C6	2.55	0.41
9:A:1348:U:H3'	9:A:1348:U:OP2	2.20	0.41
9:A:1354:U:H2'	9:A:1355:G:H8	1.84	0.41
10:B:15:PHE:HD1	10:B:40:ILE:HG22	1.84	0.41
14:F:45:ARG:HB3	14:F:59:TYR:HE1	1.85	0.41
17:I:5:TYR:CD2	17:I:88:GLU:HB3	2.56	0.41
20:L:3:VAL:HA	20:L:6:LEU:HB2	2.02	0.41
20:L:9:LYS:HE3	20:L:9:LYS:HB3	1.88	0.41
25:Q:17:GLU:O	25:Q:18:LYS:HG3	2.20	0.41
26:R:56:ARG:HB3	26:R:56:ARG:NH1	2.35	0.41
27:S:3:SER:HB3	27:S:5:LYS:NZ	2.35	0.41
30:X:18:G:H2'	30:X:18:G:OP2	2.20	0.41
30:X:71:G:HO2'	33:b:1851:U:HO2'	1.64	0.41
31:Y:70:A:H2'	31:Y:71:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:2290:G:H2'	33:b:2291:U:C6	2.55	0.41
33:b:2455:G:H2'	33:b:2456:C:C6	2.55	0.41
33:b:2650:U:H2'	33:b:2651:C:H6	1.86	0.41
33:b:2846:G:H2'	33:b:2847:U:C6	2.55	0.41
37:f:58:ALA:HB2	37:f:65:PRO:HD3	2.02	0.41
38:g:24:ILE:HD13	38:g:37:LEU:HG	2.02	0.41
42:m:2:ARG:HD3	42:m:2:ARG:HA	1.79	0.41
42:m:68:SER:C	42:m:70:LYS:H	2.27	0.41
44:o:38:LEU:HB3	44:o:39:PRO:HD3	2.02	0.41
9:A:549:C:H2'	9:A:550:G:C8	2.55	0.41
9:A:945:G:H21	9:A:1334:G:H4'	1.85	0.41
11:C:5:HIS:HE1	11:C:7:ASN:OD1	2.03	0.41
12:D:71:PHE:HA	12:D:74:TYR:CD2	2.55	0.41
22:N:8:ARG:HB3	22:N:12:ARG:NH2	2.35	0.41
23:O:2:LEU:HD12	23:O:2:LEU:HA	1.90	0.41
29:U:58:LYS:HA	29:U:61:ARG:NH2	2.35	0.41
33:b:64:A:H2'	33:b:65:U:C6	2.56	0.41
33:b:152:A:H2'	33:b:153:U:H6	1.86	0.41
33:b:589:U:H2'	33:b:590:A:C8	2.55	0.41
33:b:877:A:H2'	33:b:878:A:C8	2.55	0.41
33:b:1425:G:HO2'	33:b:1426:G:P	2.42	0.41
34:c:146:MET:HE2	34:c:146:MET:HB3	1.87	0.41
39:h:2:GLN:HB3	39:h:18:GLN:NE2	2.35	0.41
48:s:6:GLN:O	48:s:37:GLU:OE2	2.38	0.41
51:v:100:SER:O	51:v:100:SER:OG	2.37	0.41
9:A:33:A:C6	9:A:552:U:C5	3.09	0.41
9:A:796:C:O3'	19:K:126:ARG:NH2	2.52	0.41
9:A:816:A:OP1	9:A:1526:G:O2'	2.39	0.41
9:A:1248:A:O2'	9:A:1249:C:H5''	2.20	0.41
10:B:18:GLN:HG3	10:B:20:ARG:N	2.35	0.41
15:G:114:SER:O	15:G:116:ALA:N	2.53	0.41
19:K:17:ASP:N	19:K:17:ASP:OD1	2.53	0.41
23:O:9:LYS:O	23:O:12:SER:OG	2.27	0.41
25:Q:30:HIS:HB3	25:Q:34:GLY:H	1.85	0.41
26:R:31:TYR:CG	26:R:54:LEU:HD21	2.55	0.41
31:Z:6:A:H5'	31:Z:16:C:H42	1.85	0.41
32:a:66:A:H5'	32:a:108:A:H61	1.84	0.41
32:a:106:G:H2'	32:a:107:G:O4'	2.21	0.41
33:b:181:A:H2'	33:b:182:A:H8	1.85	0.41
33:b:182:A:H2'	33:b:183:C:H6	1.85	0.41
33:b:690:G:O2'	33:b:780:G:OP1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:983:A:C6	33:b:984:A:N1	2.88	0.41
33:b:1519:G:H2'	33:b:1520:U:C6	2.56	0.41
33:b:2166:U:O2'	33:b:2167:U:O4'	2.32	0.41
38:g:4:VAL:HG12	38:g:69:ARG:HD2	2.02	0.41
1:0:77:LYS:HD3	1:0:77:LYS:HA	1.77	0.41
9:A:219:U:H2'	9:A:220:G:C8	2.55	0.41
9:A:314:C:H6	9:A:314:C:O5'	2.03	0.41
9:A:537:G:H5''	20:L:109:ARG:NH1	2.36	0.41
9:A:554:A:H2'	9:A:555:U:C6	2.55	0.41
9:A:657:U:H2'	9:A:658:C:H6	1.86	0.41
9:A:956:U:H2'	9:A:957:U:C2	2.55	0.41
9:A:1057:G:H2'	9:A:1058:G:O4'	2.20	0.41
9:A:1070:U:H2'	9:A:1071:C:H6	1.85	0.41
11:C:59:PRO:HG3	11:C:64:ARG:HH22	1.84	0.41
14:F:3:HIS:CD2	14:F:3:HIS:H	2.37	0.41
16:H:13:ILE:HD11	16:H:60:LEU:CD1	2.49	0.41
17:I:51:LEU:HD21	17:I:56:MET:HG3	1.97	0.41
21:M:86:ARG:O	21:M:90:HIS:ND1	2.40	0.41
28:T:29:THR:O	28:T:33:LYS:HG3	2.20	0.41
32:a:60:C:H2'	32:a:61:G:C8	2.56	0.41
33:b:27:G:O2'	33:b:28:A:H8	2.02	0.41
33:b:376:G:H2'	33:b:377:G:H8	1.85	0.41
33:b:1170:C:H2'	33:b:1171:G:C8	2.56	0.41
33:b:1524:G:H2'	33:b:1525:A:H8	1.85	0.41
33:b:2320:U:H1'	33:b:2322:A:C8	2.55	0.41
36:e:138:LEU:HD21	36:e:167:VAL:HG21	2.03	0.41
37:f:100:PHE:CE2	37:f:173:PHE:HZ	2.32	0.41
37:f:135:GLN:C	37:f:137:ILE:H	2.28	0.41
38:g:54:PRO:HG3	38:g:62:TRP:CE2	2.55	0.41
42:m:92:LEU:O	42:m:96:LYS:HG3	2.21	0.41
50:u:77:ARG:H	50:u:77:ARG:HG2	1.57	0.41
7:7:4:ILE:HD12	7:7:4:ILE:H	1.86	0.41
9:A:8:A:C8	13:E:105:ILE:HG23	2.56	0.41
9:A:505:G:H2'	9:A:506:G:C8	2.55	0.41
9:A:1494:G:H2'	9:A:1494:G:N3	2.35	0.41
9:A:1495:U:H2'	9:A:1496:C:H6	1.86	0.41
9:A:1510:C:H2'	9:A:1511:G:C8	2.55	0.41
10:B:92:ASN:HB3	10:B:93:HIS:CE1	2.54	0.41
16:H:39:LEU:HG	16:H:45:ILE:HG12	2.02	0.41
17:I:4:GLN:HA	17:I:20:ILE:O	2.20	0.41
20:L:82:ARG:HG2	20:L:83:GLY:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:78:ARG:O	21:M:82:LEU:HD13	2.20	0.41
29:U:53:LYS:HE3	29:U:53:LYS:HB3	1.91	0.41
30:X:18:G:H5'	30:X:60:U:N1	2.36	0.41
33:b:285:G:H2'	33:b:286:U:N1	2.35	0.41
33:b:1020:A:C2	33:b:1141:U:C2	3.09	0.41
33:b:1199:U:H1'	47:r:4:VAL:HG22	2.01	0.41
33:b:2105:U:O2	33:b:2184:A:N6	2.53	0.41
33:b:2132:U:O2'	33:b:2133:G:O5'	2.36	0.41
33:b:2193:G:H2'	33:b:2194:U:C6	2.56	0.41
43:n:12:MET:HE3	43:n:12:MET:HB2	1.87	0.41
48:s:51:VAL:CB	48:s:52:PRO:HD3	2.24	0.41
56:V:32:LEU:HD12	56:V:33:VAL:N	2.35	0.41
1:0:52:SER:OG	1:0:53:ALA:N	2.53	0.41
2:1:56:LEU:O	2:1:59:GLU:HG3	2.21	0.41
4:4:44:THR:HG23	4:4:48:TYR:O	2.20	0.41
9:A:103:U:O2'	9:A:171:A:N1	2.43	0.41
9:A:422:C:H4'	9:A:423:G:C4	2.55	0.41
9:A:429:U:H5'	12:D:8:LEU:HD12	2.02	0.41
9:A:996:A:H2'	9:A:997:U:C6	2.56	0.41
9:A:1053:G:O6	9:A:1200:C:H5''	2.20	0.41
9:A:1107:C:H5'	11:C:168:ARG:HH22	1.85	0.41
10:B:129:THR:O	10:B:132:GLU:HG3	2.21	0.41
11:C:198:LYS:HB3	11:C:200:TRP:CH2	2.56	0.41
14:F:102:MET:HG3	26:R:24:ASP:OD2	2.20	0.41
24:P:46:LYS:HE2	24:P:46:LYS:HB2	1.83	0.41
31:Z:50:G:C6	31:Z:67:A:C6	3.08	0.41
33:b:543:G:H2'	33:b:544:C:C6	2.55	0.41
33:b:1537:G:H2'	33:b:1538:G:O4'	2.20	0.41
33:b:1542:U:H2'	33:b:1543:G:O4'	2.21	0.41
33:b:2100:G:C6	33:b:2190:G:C6	3.08	0.41
33:b:2771:C:H2'	33:b:2772:C:C6	2.56	0.41
37:f:94:GLU:HA	37:f:97:TRP:CD1	2.55	0.41
40:k:28:LEU:O	40:k:32:LEU:HD23	2.21	0.41
50:u:18:GLU:O	50:u:22:THR:HG23	2.20	0.41
7:7:14:PHE:O	7:7:15:LYS:HD2	2.21	0.41
9:A:1300:G:C2	9:A:1334:G:C6	3.09	0.41
9:A:1448:C:H2'	9:A:1449:C:C6	2.55	0.41
10:B:80:LYS:HA	10:B:83:ALA:HB3	2.03	0.41
11:C:48:LYS:HB2	11:C:48:LYS:HE2	1.80	0.41
16:H:48:PHE:HB2	16:H:58:LEU:HD11	2.03	0.41
17:I:112:ARG:NH1	17:I:113:LYS:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:3:ILE:O	21:M:6:ILE:HG13	2.20	0.41
22:N:68:ARG:HH22	22:N:81:ILE:HD12	1.85	0.41
23:O:7:THR:HA	23:O:10:ILE:HG22	2.03	0.41
33:b:221:A:C4	33:b:266:G:N7	2.88	0.41
33:b:247:G:N2	33:b:250:G:O2'	2.54	0.41
33:b:657:U:H2'	33:b:658:U:C6	2.56	0.41
33:b:743:A:OP1	35:d:135:GLY:HA2	2.21	0.41
33:b:1069:A:O2'	33:b:1072:C:OP2	2.33	0.41
33:b:1484:U:H2'	33:b:1485:U:H6	1.83	0.41
33:b:1629:U:N3	33:b:1630:A:N7	2.69	0.41
33:b:1883:U:H2'	33:b:1884:G:O4'	2.21	0.41
33:b:2897:U:H2'	33:b:2898:U:C6	2.56	0.41
37:f:100:PHE:HE2	37:f:173:PHE:CE1	2.38	0.41
39:h:30:LEU:H	39:h:30:LEU:HG	1.56	0.41
54:y:37:ILE:HG23	54:y:38:VAL:H	1.85	0.41
7:7:54:ASP:O	7:7:58:VAL:HG23	2.20	0.41
9:A:89:U:H2'	9:A:90:C:C5	2.55	0.41
9:A:101:A:H2'	9:A:102:G:H8	1.84	0.41
9:A:131:A:H2'	9:A:132:C:H6	1.83	0.41
9:A:426:U:O2	12:D:39:GLN:NE2	2.54	0.41
9:A:500:G:H2'	9:A:501:C:H6	1.84	0.41
9:A:679:C:H2'	9:A:680:C:C6	2.56	0.41
9:A:706:A:H2'	9:A:707:U:C6	2.56	0.41
9:A:860:A:H2'	9:A:861:G:O4'	2.20	0.41
9:A:924:C:H2'	9:A:925:G:C8	2.56	0.41
9:A:928:G:O2'	9:A:1533:C:OP1	2.27	0.41
10:B:177:ASN:OD1	10:B:178:LEU:N	2.54	0.41
11:C:19:SER:O	11:C:19:SER:OG	2.39	0.41
16:H:73:SER:OG	16:H:129:ALA:OXT	2.31	0.41
17:I:17:ARG:HD3	17:I:67:LYS:NZ	2.36	0.41
17:I:45:MET:HA	17:I:48:ARG:HD3	2.03	0.41
19:K:81:LEU:HD23	19:K:81:LEU:HA	1.96	0.41
19:K:100:ASN:HB2	19:K:106:ILE:HD13	2.02	0.41
20:L:6:LEU:HD23	20:L:6:LEU:HA	1.81	0.41
20:L:33:CYS:SG	20:L:34:THR:N	2.94	0.41
24:P:12:LYS:HD2	24:P:13:LYS:HE2	2.02	0.41
29:U:3:ILE:HD13	29:U:18:PHE:HB2	2.02	0.41
29:U:58:LYS:HA	29:U:61:ARG:HH21	1.86	0.41
30:X:63:C:H5'	30:X:64:G:OP2	2.21	0.41
33:b:491:G:O6	49:t:49:LYS:NZ	2.52	0.41
33:b:586:A:H2	33:b:809:G:N3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1042:G:H1	33:b:1113:U:H3	1.68	0.41
33:b:1412:U:H2'	33:b:1413:A:H8	1.85	0.41
33:b:2107:G:H2'	33:b:2108:A:O4'	2.21	0.41
33:b:2547:A:H2'	33:b:2548:U:H6	1.86	0.41
33:b:2570:G:H2'	33:b:2571:U:C6	2.56	0.41
33:b:2655:G:O2'	33:b:2656:U:O5'	2.38	0.41
34:c:175:ARG:O	34:c:175:ARG:HG3	2.20	0.41
36:e:108:ILE:HD13	36:e:181:ILE:HD11	2.02	0.41
37:f:7:TYR:N	37:f:7:TYR:CD1	2.74	0.41
37:f:72:LYS:HG2	37:f:73:SER:H	1.86	0.41
37:f:91:LEU:HB3	37:f:95:ARG:CG	2.50	0.41
37:f:94:GLU:HG2	37:f:97:TRP:CD1	2.55	0.41
38:g:71:LEU:HD23	38:g:71:LEU:HA	1.91	0.41
46:q:110:ILE:HG22	46:q:111:LYS:O	2.21	0.41
9:A:81:A:H2'	9:A:82:G:C8	2.56	0.41
9:A:296:U:H2'	9:A:297:G:C8	2.55	0.41
9:A:880:C:P	20:L:4:ASN:HD21	2.43	0.41
9:A:1043:G:H8	9:A:1043:G:O5'	2.03	0.41
9:A:1047:G:H5''	22:N:3:GLN:OE1	2.21	0.41
11:C:85:LYS:O	11:C:88:LYS:HG3	2.20	0.41
11:C:125:ARG:NE	11:C:125:ARG:HA	2.36	0.41
14:F:3:HIS:ND1	14:F:65:GLU:OE2	2.54	0.41
14:F:15:SER:C	14:F:18:VAL:HG23	2.46	0.41
18:J:55:PRO:HA	22:N:80:ARG:HH22	1.86	0.41
24:P:7:ALA:O	24:P:17:TYR:HA	2.20	0.41
30:X:36:C:H41	53:x:12:G:H1	1.69	0.41
33:b:74:A:O2'	33:b:88:G:OP2	2.36	0.41
33:b:81:G:H2'	33:b:82:U:O4'	2.21	0.41
33:b:1007:C:OP1	40:k:37:ARG:NH1	2.54	0.41
33:b:1038:G:H2'	33:b:1039:A:H8	1.85	0.41
33:b:1114:C:H2'	33:b:1115:G:H8	1.84	0.41
33:b:1156:A:C8	47:r:51:ARG:HG2	2.56	0.41
33:b:1884:G:H8	33:b:1884:G:OP2	2.04	0.41
33:b:1901:A:OP2	34:c:253:LYS:NZ	2.35	0.41
33:b:2142:A:H2'	33:b:2143:C:C2	2.56	0.41
33:b:2638:G:H1'	33:b:2778:A:N6	2.36	0.41
33:b:2808:G:N2	33:b:2891:U:C6	2.88	0.41
34:c:31:ALA:HB3	34:c:32:PRO:HD3	2.02	0.41
38:g:35:ARG:HB2	38:g:75:MET:HE1	2.03	0.41
38:g:60:ASP:OD1	38:g:61:GLY:N	2.47	0.41
51:v:5:ILE:C	51:v:6:ARG:HD2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:w:46:LYS:HE3	52:w:46:LYS:HB2	1.88	0.41
9:A:1:A:H2'	9:A:2:A:N3	2.36	0.40
9:A:517:G:N2	9:A:529:G:O3'	2.54	0.40
9:A:611:C:H2'	9:A:612:C:H6	1.86	0.40
9:A:691:G:H22	9:A:695:A:H5''	1.86	0.40
9:A:1014:A:N3	9:A:1219:A:H1'	2.36	0.40
9:A:1161:C:C2	9:A:1162:C:C5	3.09	0.40
9:A:1161:C:H2'	9:A:1162:C:C6	2.56	0.40
13:E:88:HIS:CG	13:E:89:THR:H	2.38	0.40
14:F:18:VAL:HG11	14:F:58:HIS:HE1	1.86	0.40
15:G:48:THR:HA	15:G:51:GLN:HE22	1.86	0.40
15:G:75:LYS:HE2	15:G:75:LYS:HB3	1.93	0.40
23:O:38:LEU:HD12	23:O:55:LEU:HD13	2.03	0.40
31:Y:25:G:H2'	31:Y:26:C:C6	2.56	0.40
31:Z:27:A:H2'	31:Z:28:C:H5'	2.03	0.40
33:b:278:A:H2	33:b:361:G:H1'	1.85	0.40
33:b:1095:A:OP1	33:b:1096:A:H5''	2.20	0.40
33:b:1713:A:N6	33:b:1746:A:N1	2.69	0.40
33:b:2055:C:O2'	33:b:2056:G:OP2	2.37	0.40
33:b:2616:C:H2'	33:b:2617:U:H6	1.85	0.40
33:b:2747:G:O6	33:b:2755:C:H5''	2.21	0.40
37:f:104:ILE:HG22	37:f:105:THR:OG1	2.21	0.40
37:f:170:LEU:CB	37:f:177:PHE:HZ	2.33	0.40
39:h:54:LEU:HA	39:h:54:LEU:HD23	1.86	0.40
9:A:168:G:H2'	9:A:169:C:H6	1.85	0.40
9:A:169:C:H2'	9:A:170:U:C6	2.56	0.40
9:A:739:C:P	14:F:2:ARG:HH22	2.44	0.40
9:A:924:C:H2'	9:A:925:G:H8	1.86	0.40
9:A:1107:C:C4	9:A:1108:G:C8	3.09	0.40
9:A:1109:C:OP2	11:C:175:HIS:ND1	2.54	0.40
9:A:1127:G:C2	9:A:1128:C:C5	3.10	0.40
9:A:1151:A:H5'	18:J:43:PRO:HA	2.02	0.40
9:A:1240:U:C6	15:G:115:MET:HE3	2.56	0.40
13:E:67:ARG:O	13:E:70:MET:HG2	2.20	0.40
21:M:15:VAL:HG23	21:M:33:LEU:HD12	2.02	0.40
30:X:2:C:N4	30:X:72:C:H42	2.20	0.40
33:b:133:U:H2'	33:b:134:G:C8	2.55	0.40
33:b:532:A:N3	33:b:532:A:H2'	2.35	0.40
33:b:1064:C:O2'	33:b:1069:A:N7	2.52	0.40
33:b:1098:A:H3'	33:b:1099:G:C8	2.57	0.40
33:b:1321:A:N3	33:b:1321:A:C2'	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:1830:C:H2'	33:b:1831:G:H8	1.87	0.40
33:b:2097:A:H2'	33:b:2098:U:H6	1.86	0.40
33:b:2113:U:H3'	33:b:2115:G:N2	2.36	0.40
33:b:2175:C:N4	33:b:2176:A:H61	2.19	0.40
37:f:130:MET:HE2	37:f:130:MET:HB2	1.90	0.40
38:g:99:LYS:HB3	38:g:99:LYS:HE3	1.85	0.40
39:h:47:PHE:HD1	39:h:50:ARG:HH21	1.69	0.40
56:V:33:VAL:HG13	56:V:34:ASN:N	2.36	0.40
6:6:26:ASN:CG	33:b:682:G:H5'	2.47	0.40
9:A:19:A:H2'	9:A:20:U:C6	2.56	0.40
9:A:32:A:N1	9:A:552:U:H5	2.20	0.40
9:A:562:U:H2'	20:L:13:ARG:NH2	2.36	0.40
9:A:707:U:H2'	9:A:708:C:H6	1.86	0.40
9:A:1124:G:O2'	9:A:1127:G:N1	2.55	0.40
10:B:98:GLY:N	10:B:174:GLU:OE2	2.54	0.40
11:C:147:GLY:HA3	11:C:171:ARG:O	2.22	0.40
20:L:34:THR:O	20:L:75:GLU:HB3	2.21	0.40
24:P:40:ASN:N	24:P:49:GLY:O	2.47	0.40
24:P:71:VAL:O	24:P:75:ILE:N	2.54	0.40
29:U:4:LYS:HB3	29:U:4:LYS:HE2	1.79	0.40
31:Y:38:G:H3'	31:Y:39:A:H8	1.87	0.40
31:Z:23:G:H8	31:Z:23:G:OP2	2.03	0.40
33:b:393:C:O2	33:b:393:C:H2'	2.22	0.40
33:b:537:G:H5''	40:k:5:THR:HG21	2.02	0.40
33:b:794:A:H2'	33:b:795:C:C6	2.57	0.40
33:b:856:G:H2'	33:b:857:G:C8	2.57	0.40
33:b:1057:A:C4	33:b:1086:A:N6	2.90	0.40
33:b:1061:U:N3	33:b:1068:G:N3	2.69	0.40
33:b:1321:A:C2	33:b:1322:A:C8	3.09	0.40
33:b:1437:C:H2'	33:b:1438:U:C6	2.57	0.40
33:b:1725:U:H2'	33:b:1726:C:C6	2.57	0.40
33:b:2221:G:H2'	33:b:2222:C:C6	2.56	0.40
33:b:2858:C:O2'	33:b:2859:G:O4'	2.40	0.40
33:b:2882:A:OP1	44:o:96:ARG:NH1	2.55	0.40
36:e:144:GLU:N	36:e:144:GLU:OE1	2.54	0.40
39:h:132:PHE:HB2	39:h:140:ALA:HB3	2.04	0.40
45:p:98:GLN:HB3	45:p:100:HIS:CE1	2.56	0.40
9:A:143:A:H8	9:A:143:A:O5'	2.03	0.40
9:A:185:U:C2	9:A:186:C:C5	3.09	0.40
9:A:691:G:N2	9:A:695:A:H8	2.16	0.40
9:A:1130:A:C8	9:A:1146:A:C5	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1161:C:H2'	9:A:1162:C:H6	1.87	0.40
9:A:1347:G:C5	17:I:108:ARG:NH1	2.90	0.40
12:D:109:THR:HG23	12:D:112:GLU:H	1.86	0.40
17:I:11:ARG:HA	17:I:105:ARG:HH12	1.86	0.40
19:K:85:VAL:HG11	19:K:92:ARG:HB2	2.03	0.40
21:M:106:ARG:HH22	21:M:109:LYS:HD3	1.84	0.40
28:T:75:LYS:HE2	28:T:75:LYS:HB3	1.96	0.40
32:a:18:G:H2'	32:a:19:C:C6	2.56	0.40
33:b:1125:G:C6	33:b:1126:A:N6	2.89	0.40
33:b:1482:G:H2'	33:b:1483:G:H8	1.87	0.40
33:b:1561:C:H2'	33:b:1562:U:H6	1.85	0.40
33:b:1712:U:C4	33:b:1713:A:C5	3.09	0.40
33:b:2078:C:H2'	33:b:2079:U:H6	1.85	0.40
33:b:2153:C:H2'	33:b:2154:A:N7	2.37	0.40
33:b:2183:A:H2'	33:b:2184:A:N7	2.36	0.40
33:b:2303:G:O2'	37:f:121:SER:O	2.36	0.40
34:c:34:LEU:HD23	34:c:34:LEU:HA	1.89	0.40
40:k:71:ASP:OD1	40:k:71:ASP:N	2.53	0.40
55:z:153[A]:SER:OG	55:z:154[A]:TRP:N	2.55	0.40
1:0:74:ARG:HB3	1:0:76:GLU:OE1	2.21	0.40
4:4:25:VAL:O	4:4:26:THR:OG1	2.32	0.40
5:5:44:ARG:NH2	33:b:643:A:C8	2.90	0.40
9:A:56:U:H2'	9:A:57:G:C8	2.57	0.40
9:A:108:G:N3	9:A:108:G:H5''	2.36	0.40
9:A:600:A:OP1	16:H:88:LYS:HG2	2.22	0.40
9:A:853:C:H2'	9:A:854:U:H6	1.86	0.40
9:A:1123:U:O3'	18:J:37:ARG:NH1	2.54	0.40
9:A:1246:A:N1	9:A:1292:G:C6	2.90	0.40
9:A:1256:A:H62	9:A:1279:G:H21	1.70	0.40
9:A:1318:A:O2'	27:S:36:ARG:HD2	2.21	0.40
9:A:1361:G:O6	9:A:1362:A:N6	2.54	0.40
9:A:1368:A:OP2	17:I:113:LYS:NZ	2.48	0.40
9:A:1527:U:H2'	9:A:1528:U:C6	2.56	0.40
11:C:9:ILE:HD12	11:C:9:ILE:HA	1.95	0.40
11:C:21:TRP:HB3	11:C:58:ARG:H	1.86	0.40
13:E:64:GLU:HG2	13:E:68:ARG:HH22	1.87	0.40
22:N:64:ARG:HH21	22:N:78:LEU:HD13	1.87	0.40
27:S:3:SER:O	27:S:5:LYS:HG2	2.22	0.40
27:S:45:GLY:HA2	27:S:60:PHE:CZ	2.56	0.40
30:X:21:A:H2'	30:X:22:G:C8	2.50	0.40
32:a:115:A:H2'	32:a:116:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:297:G:H2'	33:b:298:G:O4'	2.21	0.40
33:b:1292:G:H2'	33:b:1293:C:H6	1.87	0.40
33:b:1422:G:C6	33:b:1577:C:N3	2.90	0.40
33:b:1558:C:C2	33:b:1560:G:C5	3.10	0.40
33:b:1843:C:H2'	33:b:1844:C:H6	1.87	0.40
33:b:1857:G:O2'	33:b:1885:A:N6	2.54	0.40
33:b:2144:G:H21	33:b:2147:A:H8	1.70	0.40
33:b:2173:A:H2'	33:b:2174:C:C6	2.56	0.40
33:b:2848:G:H1'	33:b:2868:A:N6	2.37	0.40
35:d:74:GLU:OE1	35:d:74:GLU:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
2	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
3	2	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
4	4	54/57 (95%)	45 (83%)	9 (17%)	0	100	100
5	5	50/55 (91%)	48 (96%)	2 (4%)	0	100	100
6	6	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
7	7	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
10	B	216/241 (90%)	198 (92%)	18 (8%)	0	100	100
11	C	205/233 (88%)	192 (94%)	13 (6%)	0	100	100
12	D	203/206 (98%)	183 (90%)	20 (10%)	0	100	100
13	E	155/167 (93%)	142 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	F	104/135 (77%)	98 (94%)	6 (6%)	0	100	100
15	G	151/179 (84%)	144 (95%)	7 (5%)	0	100	100
16	H	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
17	I	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
18	J	98/103 (95%)	84 (86%)	14 (14%)	0	100	100
19	K	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
20	L	120/124 (97%)	105 (88%)	14 (12%)	1 (1%)	16	44
21	M	114/118 (97%)	104 (91%)	10 (9%)	0	100	100
22	N	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
23	O	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
24	P	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
25	Q	78/84 (93%)	72 (92%)	6 (8%)	0	100	100
26	R	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
27	S	81/92 (88%)	72 (89%)	9 (11%)	0	100	100
28	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
29	U	62/71 (87%)	53 (86%)	9 (14%)	0	100	100
34	c	269/273 (98%)	248 (92%)	21 (8%)	0	100	100
35	d	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
36	e	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
37	f	176/179 (98%)	156 (89%)	20 (11%)	0	100	100
38	g	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
39	h	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
40	k	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
41	l	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
42	m	142/144 (99%)	125 (88%)	17 (12%)	0	100	100
43	n	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
44	o	118/127 (93%)	110 (93%)	8 (7%)	0	100	100
45	p	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
46	q	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
47	r	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
48	s	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	t	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
50	u	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
51	v	101/104 (97%)	88 (87%)	13 (13%)	0	100	100
52	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
54	y	82/85 (96%)	80 (98%)	2 (2%)	0	100	100
55	z	45/49 (92%)	32 (71%)	13 (29%)	0	100	100
56	V	57/432 (13%)	52 (91%)	5 (9%)	0	100	100
All	All	5652/6324 (89%)	5216 (92%)	433 (8%)	3 (0%)	49	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	s	51	VAL
20	L	91	GLY
48	s	53	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	48/49 (98%)	48 (100%)	0	100	100
4	4	47/48 (98%)	47 (100%)	0	100	100
5	5	47/49 (96%)	47 (100%)	0	100	100
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/34 (100%)	34 (100%)	0	100	100
10	B	180/199 (90%)	180 (100%)	0	100	100
11	C	171/190 (90%)	170 (99%)	1 (1%)	78	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	D	172/173 (99%)	171 (99%)	1 (1%)	78	93
13	E	119/126 (94%)	119 (100%)	0	100	100
14	F	92/116 (79%)	92 (100%)	0	100	100
15	G	126/147 (86%)	126 (100%)	0	100	100
16	H	104/105 (99%)	103 (99%)	1 (1%)	68	89
17	I	105/107 (98%)	105 (100%)	0	100	100
18	J	88/90 (98%)	88 (100%)	0	100	100
19	K	90/99 (91%)	90 (100%)	0	100	100
20	L	103/104 (99%)	103 (100%)	0	100	100
21	M	94/96 (98%)	94 (100%)	0	100	100
22	N	83/84 (99%)	83 (100%)	0	100	100
23	O	76/77 (99%)	76 (100%)	0	100	100
24	P	65/65 (100%)	65 (100%)	0	100	100
25	Q	74/78 (95%)	74 (100%)	0	100	100
26	R	57/65 (88%)	57 (100%)	0	100	100
27	S	72/79 (91%)	72 (100%)	0	100	100
28	T	65/66 (98%)	65 (100%)	0	100	100
29	U	54/61 (88%)	54 (100%)	0	100	100
34	c	216/218 (99%)	216 (100%)	0	100	100
35	d	164/164 (100%)	162 (99%)	2 (1%)	63	86
36	e	165/165 (100%)	162 (98%)	3 (2%)	51	80
37	f	149/150 (99%)	146 (98%)	3 (2%)	48	78
38	g	136/138 (99%)	134 (98%)	2 (2%)	57	84
39	h	114/114 (100%)	112 (98%)	2 (2%)	51	80
40	k	116/116 (100%)	116 (100%)	0	100	100
41	l	104/104 (100%)	104 (100%)	0	100	100
42	m	103/103 (100%)	103 (100%)	0	100	100
43	n	109/109 (100%)	109 (100%)	0	100	100
44	o	100/103 (97%)	100 (100%)	0	100	100
45	p	86/87 (99%)	84 (98%)	2 (2%)	44	76
46	q	99/100 (99%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	r	89/90 (99%)	89 (100%)	0	100	100
48	s	84/84 (100%)	82 (98%)	2 (2%)	43	75
49	t	93/93 (100%)	92 (99%)	1 (1%)	65	88
50	u	84/84 (100%)	84 (100%)	0	100	100
51	v	84/85 (99%)	82 (98%)	2 (2%)	43	75
52	w	78/78 (100%)	77 (99%)	1 (1%)	61	86
54	y	62/63 (98%)	61 (98%)	1 (2%)	55	83
55	z	39/43 (91%)	34 (87%)	5 (13%)	4	14
56	V	49/359 (14%)	40 (82%)	9 (18%)	1	6
All	All	4699/5170 (91%)	4661 (99%)	38 (1%)	70	90

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	C	69	THR
12	D	130	ASN
16	H	26	MET
35	d	11	MET
35	d	13	ARG
36	e	61	ARG
36	e	74	LYS
36	e	146	VAL
37	f	7	TYR
37	f	38	MET
37	f	100	PHE
38	g	26	ILE
38	g	29	LYS
39	h	30	LEU
39	h	90	LEU
45	p	47	VAL
45	p	83	LEU
48	s	55	ASP
48	s	95	ASP
49	t	72	THR
51	v	7	ARG
51	v	52	LEU
52	w	64	VAL
54	y	44	LYS
55	z	124	MET

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Mol	Chain	Res	Type
55	z	131	MET
55	z	134	SER
55	z	143	GLU
55	z	146	ARG
56	V	19	ILE
56	V	22	ASP
56	V	24	ILE
56	V	25	GLU
56	V	26	THR
56	V	66	VAL
56	V	67	LEU
56	V	70	LEU
56	V	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	23	ASN
3	2	34	HIS
5	5	19	HIS
8	8	35	GLN
10	B	35	ASN
10	B	202	ASN
11	C	68	HIS
12	D	125	ASN
12	D	130	ASN
12	D	135	GLN
13	E	88	HIS
13	E	121	ASN
14	F	46	GLN
14	F	52	ASN
14	F	58	HIS
15	G	129	ASN
17	I	49	GLN
18	J	58	ASN
19	K	21	HIS
19	K	100	ASN
20	L	95	HIS
21	M	104	ASN
22	N	48	GLN
22	N	65	GLN
23	O	34	GLN

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Mol	Chain	Res	Type
28	T	2	ASN
28	T	47	GLN
28	T	51	ASN
28	T	81	GLN
35	d	49	GLN
38	g	30	ASN
39	h	2	GLN
39	h	145	ASN
41	l	3	GLN
41	l	9	ASN
45	p	116	GLN
48	s	66	HIS
52	w	87	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	75/76 (98%)	40 (53%)	1 (1%)
31	Y	76/77 (98%)	20 (26%)	2 (2%)
31	Z	76/77 (98%)	19 (25%)	0
32	a	119/120 (99%)	17 (14%)	0
33	b	2902/2904 (99%)	603 (20%)	0
53	x	13/14 (92%)	5 (38%)	0
9	A	1532/1533 (99%)	371 (24%)	9 (0%)
All	All	4793/4801 (99%)	1075 (22%)	12 (0%)

All (1075) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	2	A
9	A	4	U
9	A	6	G
9	A	9	G
9	A	16	A
9	A	31	G
9	A	32	A
9	A	39	G
9	A	47	C
9	A	48	C
9	A	51	A
9	A	65	A

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Mol	Chain	Res	Type
9	A	66	A
9	A	70	U
9	A	73	C
9	A	74	A
9	A	76	G
9	A	77	A
9	A	78	A
9	A	79	G
9	A	81	A
9	A	83	C
9	A	84	U
9	A	85	U
9	A	86	G
9	A	87	C
9	A	88	U
9	A	89	U
9	A	90	C
9	A	91	U
9	A	92	U
9	A	94	G
9	A	95	C
9	A	96	U
9	A	97	G
9	A	109	A
9	A	110	C
9	A	111	G
9	A	120	A
9	A	121	U
9	A	122	G
9	A	130	A
9	A	131	A
9	A	137	U
9	A	138	G
9	A	144	G
9	A	158	G
9	A	164	G
9	A	173	U
9	A	182	A
9	A	193	C
9	A	196	A
9	A	197	A
9	A	204	G

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Mol	Chain	Res	Type
9	A	205	A
9	A	208	U
9	A	209	U
9	A	210	C
9	A	214	C
9	A	216	U
9	A	217	C
9	A	218	U
9	A	219	U
9	A	222	C
9	A	224	U
9	A	231	U
9	A	239	U
9	A	240	G
9	A	244	U
9	A	245	U
9	A	246	A
9	A	247	G
9	A	251	G
9	A	253	A
9	A	256	U
9	A	262	A
9	A	266	G
9	A	267	C
9	A	279	A
9	A	283	U
9	A	289	G
9	A	293	G
9	A	300	A
9	A	301	G
9	A	306	A
9	A	328	C
9	A	330	C
9	A	342	C
9	A	343	U
9	A	345	C
9	A	352	C
9	A	354	G
9	A	364	A
9	A	367	U
9	A	368	U
9	A	369	G

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Mol	Chain	Res	Type
9	A	372	C
9	A	374	A
9	A	376	G
9	A	377	G
9	A	378	G
9	A	381	C
9	A	382	A
9	A	387	U
9	A	388	G
9	A	390	U
9	A	391	G
9	A	392	C
9	A	397	A
9	A	398	U
9	A	406	G
9	A	407	U
9	A	409	U
9	A	411	A
9	A	412	A
9	A	413	G
9	A	414	A
9	A	415	A
9	A	421	U
9	A	422	C
9	A	423	G
9	A	424	G
9	A	428	G
9	A	429	U
9	A	430	A
9	A	431	A
9	A	433	G
9	A	435	A
9	A	438	U
9	A	439	U
9	A	445	G
9	A	446	G
9	A	448	A
9	A	449	G
9	A	452	A
9	A	461	A
9	A	462	G
9	A	463	U

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Mol	Chain	Res	Type
9	A	465	A
9	A	467	U
9	A	468	A
9	A	471	U
9	A	474	G
9	A	479	U
9	A	480	U
9	A	482	A
9	A	483	C
9	A	485	U
9	A	486	U
9	A	488	C
9	A	491	G
9	A	493	A
9	A	495	A
9	A	496	A
9	A	497	G
9	A	499	A
9	A	509	A
9	A	511	C
9	A	512	U
9	A	517	G
9	A	518	C
9	A	521	G
9	A	524	G
9	A	530	G
9	A	532	A
9	A	533	A
9	A	536	C
9	A	541	G
9	A	542	G
9	A	545	C
9	A	547	A
9	A	548	G
9	A	550	G
9	A	551	U
9	A	560	A
9	A	563	A
9	A	564	C
9	A	567	G
9	A	571	U
9	A	572	A

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Mol	Chain	Res	Type
9	A	573	A
9	A	575	G
9	A	576	C
9	A	588	G
9	A	590	U
9	A	591	U
9	A	595	A
9	A	596	A
9	A	597	G
9	A	607	A
9	A	610	U
9	A	615	G
9	A	619	U
9	A	622	A
9	A	632	U
9	A	633	G
9	A	650	G
9	A	653	U
9	A	665	A
9	A	666	G
9	A	687	A
9	A	701	U
9	A	709	U
9	A	720	C
9	A	721	G
9	A	723	U
9	A	724	G
9	A	731	G
9	A	755	G
9	A	787	A
9	A	793	U
9	A	794	A
9	A	815	A
9	A	817	C
9	A	820	U
9	A	821	G
9	A	828	U
9	A	829	G
9	A	831	A
9	A	832	G
9	A	841	C
9	A	842	U

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Mol	Chain	Res	Type
9	A	843	U
9	A	844	G
9	A	845	A
9	A	846	G
9	A	848	C
9	A	849	G
9	A	855	U
9	A	869	G
9	A	872	A
9	A	889	A
9	A	891	U
9	A	900	A
9	A	902	G
9	A	914	A
9	A	919	A
9	A	927	G
9	A	933	G
9	A	934	C
9	A	935	A
9	A	939	G
9	A	945	G
9	A	958	A
9	A	960	U
9	A	961	U
9	A	966	G
9	A	969	A
9	A	975	A
9	A	976	G
9	A	977	A
9	A	979	C
9	A	992	U
9	A	993	G
9	A	994	A
9	A	996	A
9	A	998	C
9	A	999	C
9	A	1001	C
9	A	1003	G
9	A	1004	A
9	A	1006	G
9	A	1007	U
9	A	1017	U

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Mol	Chain	Res	Type
9	A	1020	G
9	A	1022	A
9	A	1027	C
9	A	1028	C
9	A	1029	U
9	A	1032	G
9	A	1034	G
9	A	1036	A
9	A	1039	G
9	A	1040	U
9	A	1042	A
9	A	1045	C
9	A	1049	U
9	A	1053	G
9	A	1065	U
9	A	1066	C
9	A	1075	U
9	A	1081	A
9	A	1085	U
9	A	1094	G
9	A	1095	U
9	A	1100	C
9	A	1101	A
9	A	1104	G
9	A	1108	G
9	A	1124	G
9	A	1125	U
9	A	1136	C
9	A	1137	C
9	A	1139	G
9	A	1151	A
9	A	1157	A
9	A	1159	U
9	A	1160	G
9	A	1167	A
9	A	1168	U
9	A	1169	A
9	A	1173	U
9	A	1174	G
9	A	1181	G
9	A	1183	U
9	A	1184	G

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Mol	Chain	Res	Type
9	A	1188	A
9	A	1196	A
9	A	1197	A
9	A	1206	G
9	A	1207	G
9	A	1208	C
9	A	1212	U
9	A	1213	A
9	A	1225	A
9	A	1227	A
9	A	1238	A
9	A	1240	U
9	A	1241	G
9	A	1248	A
9	A	1257	A
9	A	1258	G
9	A	1259	C
9	A	1260	G
9	A	1266	G
9	A	1268	G
9	A	1280	A
9	A	1286	U
9	A	1287	A
9	A	1300	G
9	A	1301	U
9	A	1303	C
9	A	1305	G
9	A	1316	G
9	A	1323	G
9	A	1336	C
9	A	1338	G
9	A	1340	A
9	A	1343	G
9	A	1347	G
9	A	1348	U
9	A	1358	U
9	A	1360	A
9	A	1362	A
9	A	1363	A
9	A	1364	U
9	A	1378	C
9	A	1398	A

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Mol	Chain	Res	Type
9	A	1419	G
9	A	1441	A
9	A	1446	A
9	A	1449	C
9	A	1450	U
9	A	1451	U
9	A	1452	C
9	A	1454	G
9	A	1471	U
9	A	1479	C
9	A	1487	G
9	A	1492	A
9	A	1494	G
9	A	1497	G
9	A	1503	A
9	A	1506	U
9	A	1517	G
9	A	1519	A
9	A	1520	C
9	A	1522	U
9	A	1529	G
9	A	1530	G
9	A	1533	C
30	X	3	G
30	X	4	G
30	X	5	G
30	X	6	A
30	X	8	U
30	X	9	A
30	X	10	G
30	X	11	C
30	X	13	C
30	X	16	U
30	X	17	U
30	X	18	G
30	X	19	G
30	X	21	A
30	X	22	G
30	X	25	C
30	X	28	G
30	X	29	A
30	X	30	C

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Mol	Chain	Res	Type
30	X	31	C
30	X	39	G
30	X	40	G
30	X	43	G
30	X	44	G
30	X	46	G
30	X	47	U
30	X	49	G
30	X	51	G
30	X	55	U
30	X	57	G
30	X	59	G
30	X	60	U
30	X	61	C
30	X	64	G
30	X	66	U
30	X	69	C
30	X	71	G
30	X	74	C
30	X	75	C
30	X	76	A
31	Y	2	G
31	Y	3	G
31	Y	5	G
31	Y	7	U
31	Y	9	G
31	Y	16	C
31	Y	17	C
31	Y	18	U
31	Y	19	G
31	Y	21	U
31	Y	48	U
31	Y	49	C
31	Y	50	G
31	Y	62	C
31	Y	63	C
31	Y	64	U
31	Y	67	A
31	Y	68	U
31	Y	69	C
31	Y	77	A
31	Z	9	G

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Mol	Chain	Res	Type
31	Z	10	G
31	Z	12	G
31	Z	16	C
31	Z	18	U
31	Z	20	G
31	Z	21	U
31	Z	23	G
31	Z	25	G
31	Z	26	C
31	Z	30	U
31	Z	31	C
31	Z	33	U
31	Z	37	G
31	Z	50	G
31	Z	53	G
31	Z	59	A
31	Z	67	A
31	Z	74	A
32	a	15	A
32	a	23	G
32	a	25	U
32	a	30	C
32	a	35	C
32	a	42	C
32	a	46	A
32	a	52	A
32	a	56	G
32	a	66	A
32	a	67	G
32	a	69	G
32	a	89	U
32	a	90	C
32	a	99	A
32	a	109	A
32	a	119	A
33	b	3	U
33	b	5	A
33	b	10	A
33	b	28	A
33	b	35	G
33	b	39	G
33	b	40	U

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Mol	Chain	Res	Type
33	b	42	A
33	b	45	G
33	b	46	G
33	b	51	G
33	b	71	A
33	b	74	A
33	b	75	G
33	b	84	A
33	b	88	G
33	b	91	A
33	b	98	G
33	b	100	U
33	b	101	A
33	b	102	U
33	b	103	A
33	b	110	G
33	b	118	A
33	b	120	U
33	b	128	C
33	b	131	A
33	b	133	U
33	b	140	C
33	b	142	A
33	b	163	C
33	b	165	A
33	b	181	A
33	b	196	A
33	b	199	A
33	b	215	G
33	b	216	A
33	b	222	A
33	b	223	A
33	b	228	C
33	b	229	C
33	b	233	A
33	b	248	G
33	b	250	G
33	b	251	A
33	b	255	A
33	b	265	A
33	b	266	G
33	b	267	C

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Mol	Chain	Res	Type
33	b	268	C
33	b	271	G
33	b	272	A
33	b	276	U
33	b	278	A
33	b	279	A
33	b	280	U
33	b	282	A
33	b	284	U
33	b	286	U
33	b	295	G
33	b	310	A
33	b	330	A
33	b	347	A
33	b	349	U
33	b	356	G
33	b	357	C
33	b	359	G
33	b	361	G
33	b	368	A
33	b	369	U
33	b	371	A
33	b	372	G
33	b	385	C
33	b	386	G
33	b	387	U
33	b	391	A
33	b	395	U
33	b	396	G
33	b	404	A
33	b	405	U
33	b	406	G
33	b	411	G
33	b	412	A
33	b	417	C
33	b	420	C
33	b	424	G
33	b	428	A
33	b	430	A
33	b	451	U
33	b	457	A
33	b	473	G

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Mol	Chain	Res	Type
33	b	481	G
33	b	491	G
33	b	505	A
33	b	508	A
33	b	509	C
33	b	510	C
33	b	512	G
33	b	529	A
33	b	530	G
33	b	531	C
33	b	532	A
33	b	538	A
33	b	546	U
33	b	548	G
33	b	549	G
33	b	556	A
33	b	557	C
33	b	563	A
33	b	568	U
33	b	573	U
33	b	574	A
33	b	575	A
33	b	587	C
33	b	595	C
33	b	603	A
33	b	604	G
33	b	613	A
33	b	614	A
33	b	615	U
33	b	621	A
33	b	627	A
33	b	634	C
33	b	637	A
33	b	639	U
33	b	644	A
33	b	645	C
33	b	646	U
33	b	647	G
33	b	653	U
33	b	654	A
33	b	655	A
33	b	670	A

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Mol	Chain	Res	Type
33	b	686	U
33	b	701	G
33	b	709	U
33	b	713	G
33	b	716	A
33	b	717	C
33	b	718	A
33	b	719	C
33	b	729	G
33	b	730	A
33	b	735	A
33	b	747	U
33	b	748	G
33	b	757	G
33	b	765	C
33	b	774	G
33	b	775	G
33	b	776	G
33	b	782	A
33	b	784	G
33	b	785	G
33	b	792	A
33	b	805	G
33	b	812	C
33	b	819	A
33	b	827	U
33	b	828	U
33	b	845	A
33	b	846	U
33	b	859	G
33	b	869	G
33	b	877	A
33	b	879	G
33	b	880	G
33	b	881	G
33	b	883	G
33	b	884	U
33	b	885	C
33	b	886	A
33	b	887	U
33	b	888	C
33	b	889	C

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Mol	Chain	Res	Type
33	b	890	C
33	b	891	G
33	b	892	A
33	b	893	C
33	b	894	U
33	b	895	U
33	b	896	A
33	b	897	C
33	b	898	C
33	b	899	A
33	b	900	A
33	b	902	C
33	b	910	A
33	b	912	C
33	b	927	A
33	b	932	U
33	b	938	G
33	b	941	A
33	b	946	C
33	b	959	A
33	b	961	C
33	b	972	A
33	b	974	G
33	b	981	A
33	b	983	A
33	b	996	A
33	b	999	U
33	b	1006	C
33	b	1009	A
33	b	1012	U
33	b	1013	C
33	b	1022	G
33	b	1026	G
33	b	1033	U
33	b	1040	A
33	b	1047	G
33	b	1048	A
33	b	1051	G
33	b	1052	C
33	b	1053	C
33	b	1056	G
33	b	1057	A

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Mol	Chain	Res	Type
33	b	1058	U
33	b	1059	G
33	b	1060	U
33	b	1061	U
33	b	1062	G
33	b	1064	C
33	b	1065	U
33	b	1066	U
33	b	1067	A
33	b	1068	G
33	b	1070	A
33	b	1072	C
33	b	1073	A
33	b	1076	C
33	b	1078	U
33	b	1080	A
33	b	1081	U
33	b	1083	U
33	b	1084	A
33	b	1085	A
33	b	1086	A
33	b	1087	G
33	b	1088	A
33	b	1090	A
33	b	1092	C
33	b	1093	G
33	b	1094	U
33	b	1095	A
33	b	1096	A
33	b	1099	G
33	b	1102	C
33	b	1103	A
33	b	1104	C
33	b	1105	U
33	b	1106	G
33	b	1108	U
33	b	1110	G
33	b	1111	A
33	b	1112	G
33	b	1132	U
33	b	1133	A
33	b	1134	A

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Mol	Chain	Res	Type
33	b	1135	C
33	b	1136	G
33	b	1141	U
33	b	1142	A
33	b	1174	U
33	b	1175	A
33	b	1179	G
33	b	1186	G
33	b	1195	G
33	b	1205	A
33	b	1206	G
33	b	1210	G
33	b	1223	G
33	b	1224	U
33	b	1234	U
33	b	1236	G
33	b	1238	G
33	b	1241	A
33	b	1250	G
33	b	1253	A
33	b	1255	U
33	b	1256	G
33	b	1266	G
33	b	1267	U
33	b	1269	A
33	b	1271	G
33	b	1272	A
33	b	1273	U
33	b	1276	A
33	b	1300	G
33	b	1301	A
33	b	1314	C
33	b	1341	G
33	b	1352	U
33	b	1365	A
33	b	1366	A
33	b	1379	U
33	b	1382	G
33	b	1383	A
33	b	1384	A
33	b	1386	C
33	b	1393	A

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Mol	Chain	Res	Type
33	b	1395	A
33	b	1409	U
33	b	1416	G
33	b	1420	A
33	b	1421	G
33	b	1426	G
33	b	1427	A
33	b	1428	C
33	b	1433	A
33	b	1461	C
33	b	1482	G
33	b	1484	U
33	b	1487	U
33	b	1490	A
33	b	1491	G
33	b	1493	C
33	b	1494	A
33	b	1496	A
33	b	1497	U
33	b	1505	A
33	b	1506	U
33	b	1507	C
33	b	1509	A
33	b	1510	G
33	b	1520	U
33	b	1523	U
33	b	1532	A
33	b	1534	U
33	b	1535	A
33	b	1536	C
33	b	1540	G
33	b	1541	C
33	b	1552	A
33	b	1553	A
33	b	1560	G
33	b	1562	U
33	b	1566	A
33	b	1568	G
33	b	1569	A
33	b	1576	U
33	b	1578	U
33	b	1584	U

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Mol	Chain	Res	Type
33	b	1585	C
33	b	1607	C
33	b	1609	A
33	b	1610	A
33	b	1646	C
33	b	1647	U
33	b	1648	U
33	b	1674	G
33	b	1675	C
33	b	1713	A
33	b	1716	U
33	b	1729	U
33	b	1730	C
33	b	1733	G
33	b	1738	G
33	b	1744	A
33	b	1745	A
33	b	1758	U
33	b	1763	G
33	b	1764	C
33	b	1773	A
33	b	1776	G
33	b	1799	G
33	b	1800	C
33	b	1801	A
33	b	1802	A
33	b	1805	A
33	b	1808	A
33	b	1810	A
33	b	1811	G
33	b	1816	C
33	b	1829	A
33	b	1847	A
33	b	1857	G
33	b	1870	C
33	b	1871	A
33	b	1872	A
33	b	1875	G
33	b	1876	A
33	b	1901	A
33	b	1906	G
33	b	1913	A

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Mol	Chain	Res	Type
33	b	1914	C
33	b	1916	A
33	b	1919	A
33	b	1927	A
33	b	1929	G
33	b	1930	G
33	b	1931	U
33	b	1936	A
33	b	1937	A
33	b	1938	A
33	b	1955	U
33	b	1960	A
33	b	1963	U
33	b	1967	C
33	b	1970	A
33	b	1971	U
33	b	1972	G
33	b	1977	A
33	b	1992	G
33	b	1993	U
33	b	1997	C
33	b	2023	C
33	b	2031	A
33	b	2032	G
33	b	2033	A
33	b	2043	C
33	b	2055	C
33	b	2056	G
33	b	2060	A
33	b	2061	G
33	b	2062	A
33	b	2063	C
33	b	2069	G
33	b	2093	G
33	b	2102	G
33	b	2103	C
33	b	2105	U
33	b	2106	U
33	b	2107	G
33	b	2109	U
33	b	2110	G
33	b	2111	U

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Mol	Chain	Res	Type
33	b	2112	G
33	b	2113	U
33	b	2114	A
33	b	2115	G
33	b	2116	G
33	b	2118	U
33	b	2119	A
33	b	2120	G
33	b	2121	G
33	b	2122	U
33	b	2123	G
33	b	2124	G
33	b	2126	A
33	b	2127	G
33	b	2128	G
33	b	2129	C
33	b	2130	U
33	b	2131	U
33	b	2132	U
33	b	2133	G
33	b	2134	A
33	b	2136	G
33	b	2138	G
33	b	2140	G
33	b	2143	C
33	b	2144	G
33	b	2145	C
33	b	2146	C
33	b	2149	U
33	b	2150	C
33	b	2151	U
33	b	2152	G
33	b	2153	C
33	b	2154	A
33	b	2156	G
33	b	2157	G
33	b	2158	A
33	b	2159	G
33	b	2161	C
33	b	2164	C
33	b	2165	C
33	b	2166	U

Continued on next page...

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Mol	Chain	Res	Type
33	b	2170	A
33	b	2171	A
33	b	2172	U
33	b	2173	A
33	b	2174	C
33	b	2175	C
33	b	2178	C
33	b	2180	U
33	b	2181	U
33	b	2182	U
33	b	2186	G
33	b	2187	U
33	b	2188	U
33	b	2191	A
33	b	2192	U
33	b	2203	U
33	b	2204	G
33	b	2212	A
33	b	2213	U
33	b	2214	C
33	b	2222	C
33	b	2225	A
33	b	2238	G
33	b	2239	G
33	b	2247	A
33	b	2250	G
33	b	2279	G
33	b	2283	C
33	b	2284	A
33	b	2286	G
33	b	2287	A
33	b	2288	A
33	b	2305	U
33	b	2307	G
33	b	2309	A
33	b	2320	U
33	b	2322	A
33	b	2325	G
33	b	2333	A
33	b	2336	A
33	b	2345	G
33	b	2347	C

Continued on next page...

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Mol	Chain	Res	Type
33	b	2350	C
33	b	2357	G
33	b	2361	G
33	b	2377	A
33	b	2383	G
33	b	2385	C
33	b	2402	U
33	b	2406	A
33	b	2407	A
33	b	2412	A
33	b	2422	C
33	b	2423	U
33	b	2424	C
33	b	2425	A
33	b	2427	C
33	b	2429	G
33	b	2430	A
33	b	2440	C
33	b	2441	U
33	b	2447	G
33	b	2448	A
33	b	2450	A
33	b	2459	A
33	b	2476	A
33	b	2502	G
33	b	2503	A
33	b	2505	G
33	b	2506	U
33	b	2513	A
33	b	2518	A
33	b	2520	C
33	b	2529	G
33	b	2535	G
33	b	2547	A
33	b	2554	U
33	b	2561	U
33	b	2562	U
33	b	2566	A
33	b	2567	G
33	b	2572	A
33	b	2576	G
33	b	2582	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
33	b	2584	U
33	b	2593	U
33	b	2602	A
33	b	2609	U
33	b	2613	U
33	b	2615	U
33	b	2629	U
33	b	2630	G
33	b	2656	U
33	b	2689	U
33	b	2690	U
33	b	2698	U
33	b	2713	U
33	b	2714	G
33	b	2726	A
33	b	2728	U
33	b	2733	A
33	b	2744	G
33	b	2748	A
33	b	2758	A
33	b	2776	A
33	b	2778	A
33	b	2779	U
33	b	2790	U
33	b	2791	G
33	b	2797	U
33	b	2798	U
33	b	2800	A
33	b	2801	G
33	b	2807	U
33	b	2808	G
33	b	2820	A
33	b	2823	A
33	b	2833	U
33	b	2834	G
33	b	2835	A
33	b	2849	U
33	b	2854	G
33	b	2859	G
33	b	2861	U
33	b	2867	G
33	b	2873	A

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Mol	Chain	Res	Type
33	b	2880	C
33	b	2883	A
33	b	2885	G
33	b	2886	A
33	b	2896	C
33	b	2900	A
33	b	2901	C
33	b	2903	U
53	x	14	C
53	x	16	C
53	x	21	U
53	x	22	A
53	x	23	A

All (12) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	66	A
9	A	223	A
9	A	238	A
9	A	429	U
9	A	1003	G
9	A	1065	U
9	A	1187	G
9	A	1357	A
9	A	1493	A
30	X	21	A
31	Y	6	A
31	Y	16	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	PRO	Z	163	-	5,7,8	0.56	0	7,8,10	1.31	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PRO	Z	163	-	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Z	163	PRO	O-C-CA	-2.38	118.55	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Z	163	PRO	4	0

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.

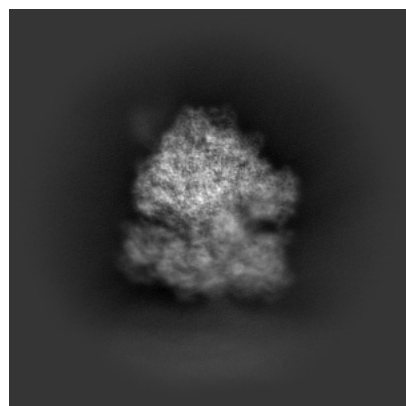
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60061. These allow visual inspection of the internal detail of the map and identification of artifacts.

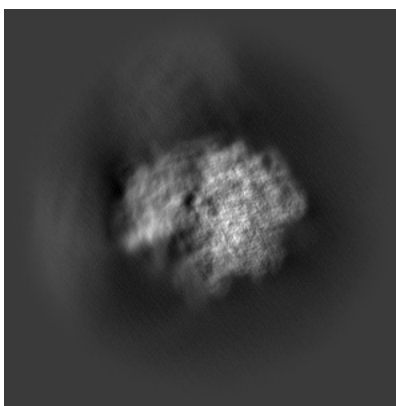
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

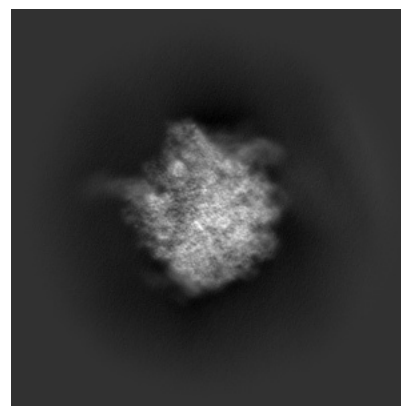
6.1.1 Primary map



X

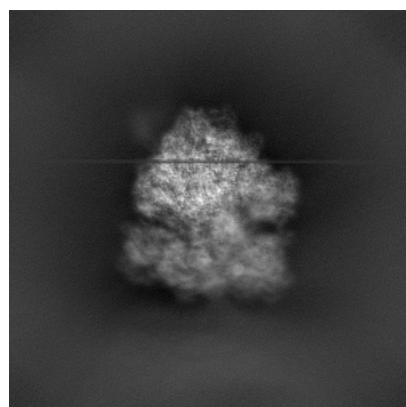


Y

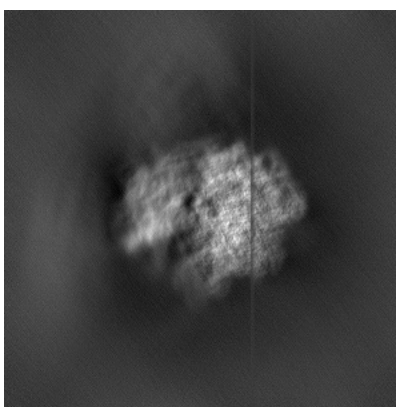


Z

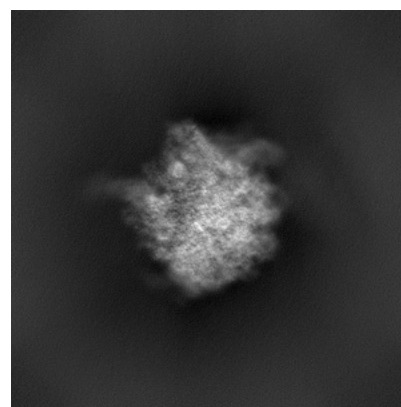
6.1.2 Raw map



X



Y

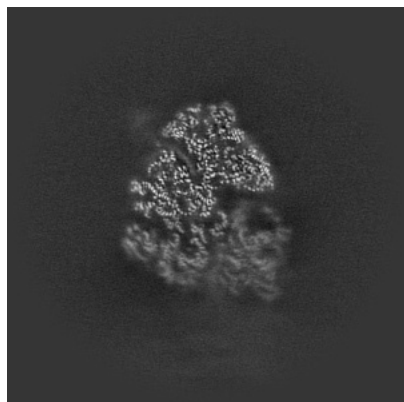


Z

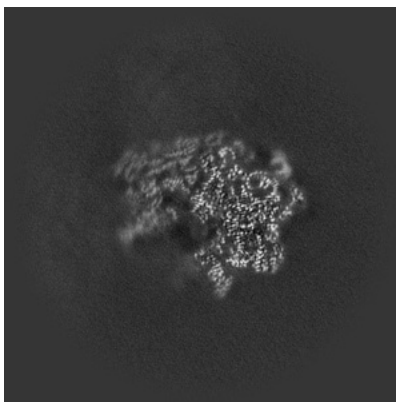
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

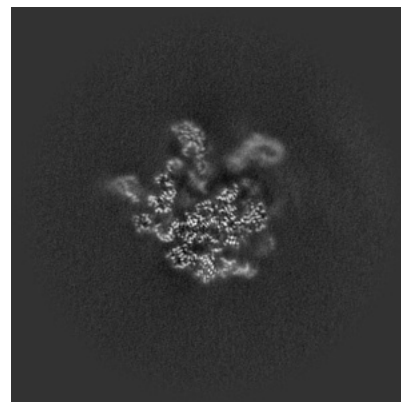
6.2.1 Primary map



X Index: 240

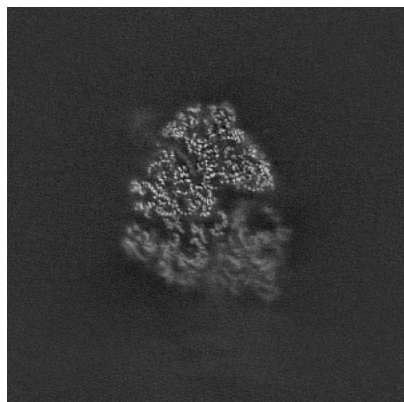


Y Index: 240

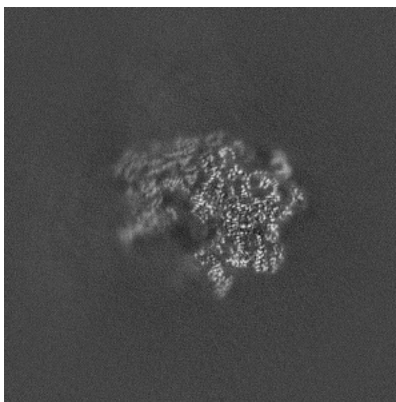


Z Index: 240

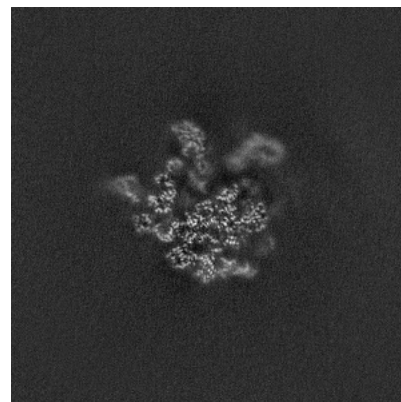
6.2.2 Raw map



X Index: 240



Y Index: 240

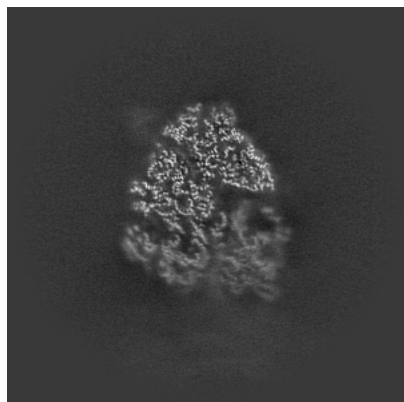


Z Index: 240

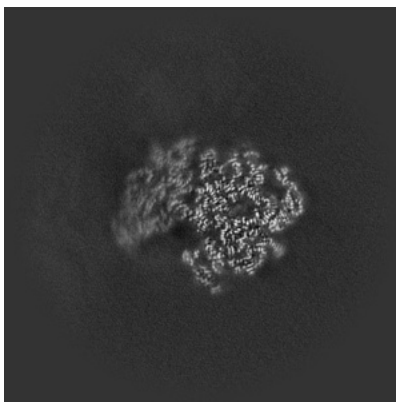
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

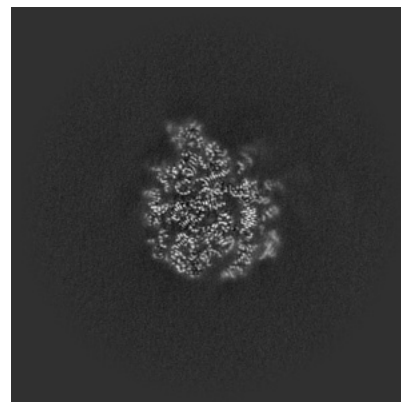
6.3.1 Primary map



X Index: 238

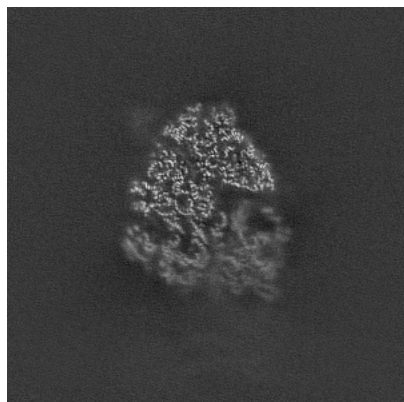


Y Index: 223

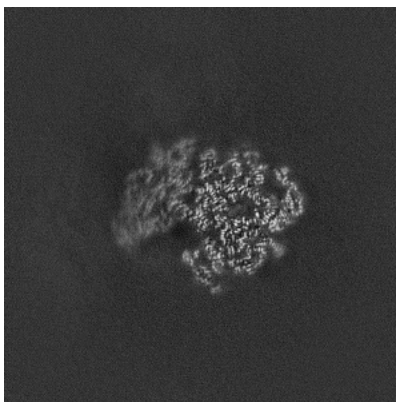


Z Index: 280

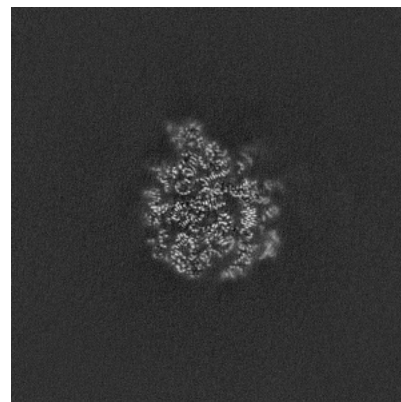
6.3.2 Raw map



X Index: 238



Y Index: 223

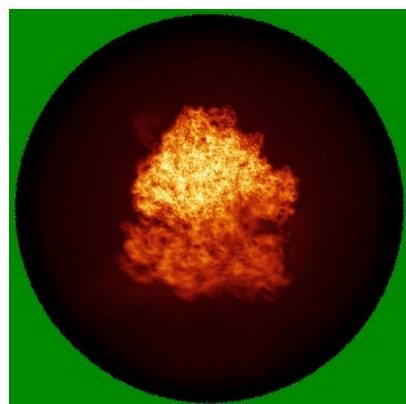


Z Index: 280

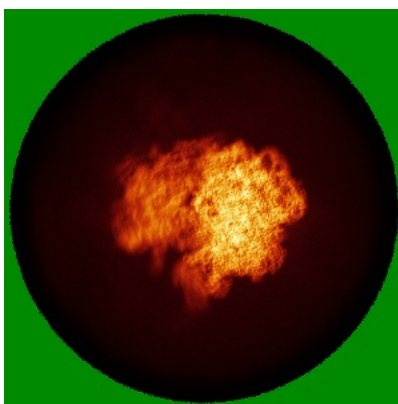
The images above show the largest variance slices of the map in three orthogonal directions.

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

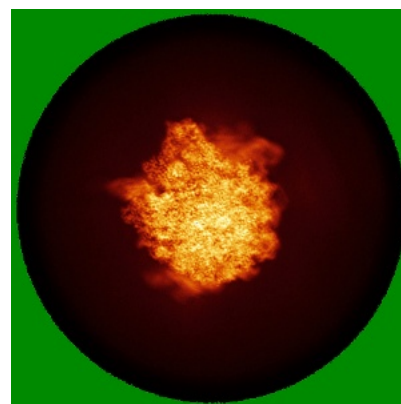
6.4.1 Primary map



X

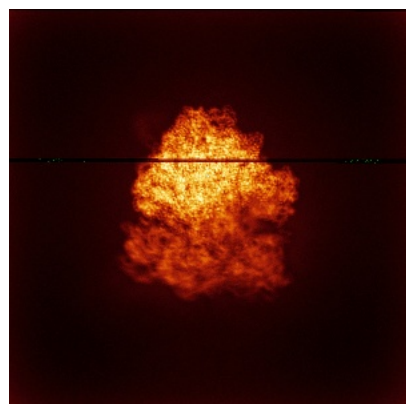


Y

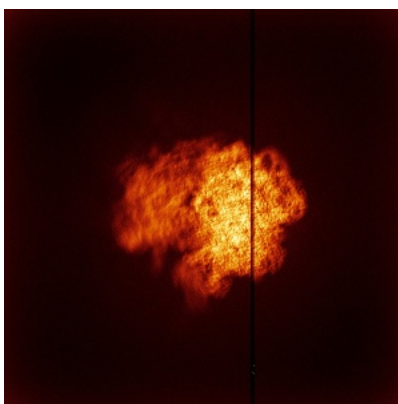


Z

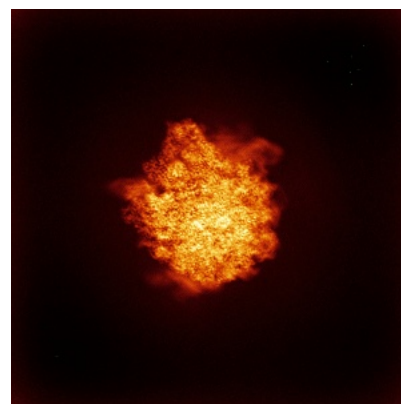
6.4.2 Raw map



X



Y



Z

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

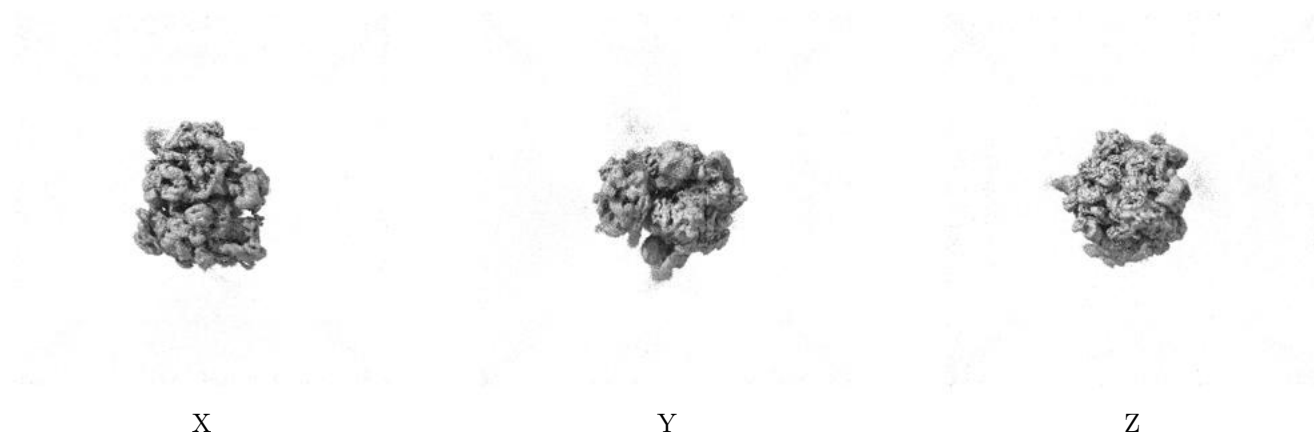
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

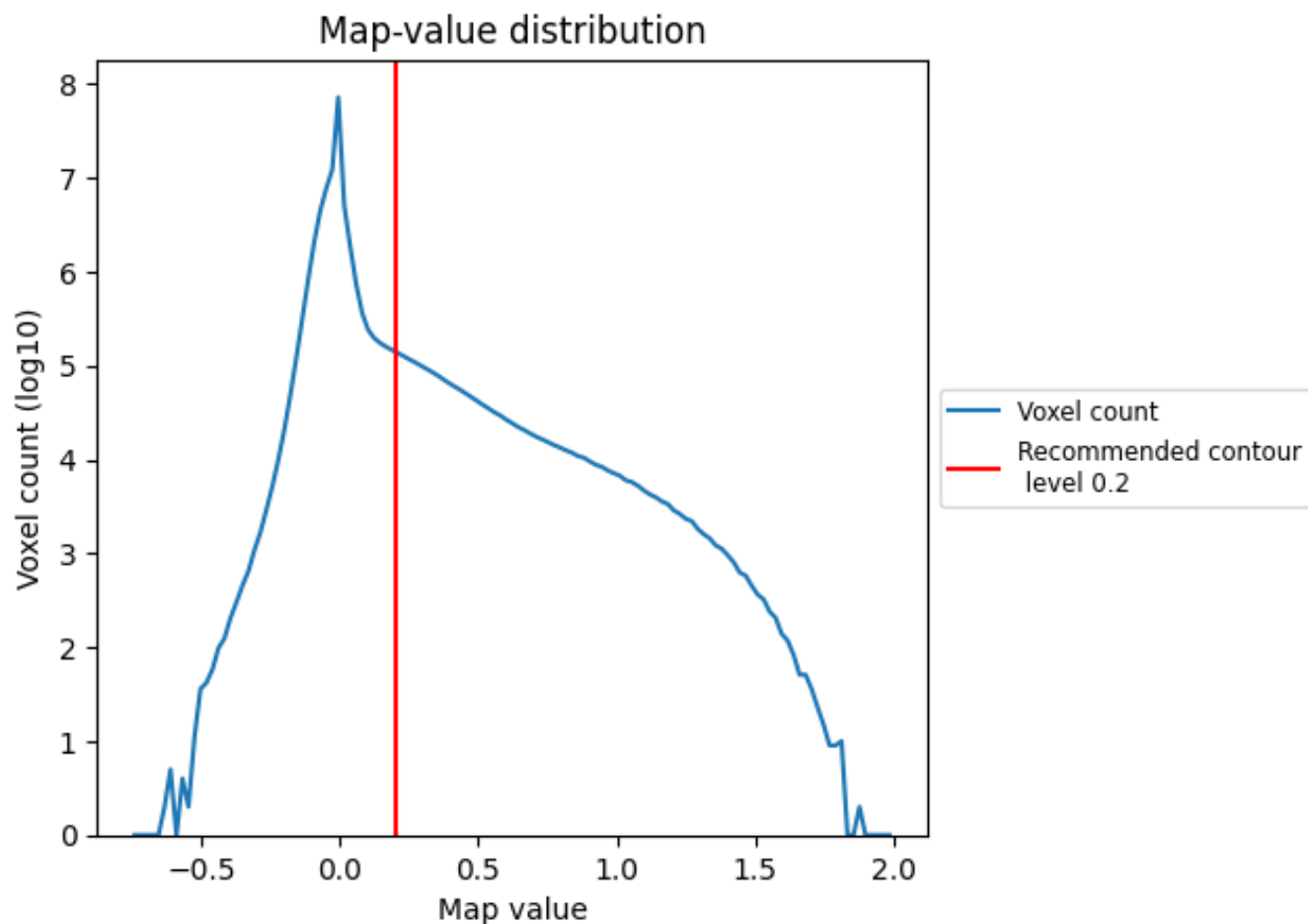
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

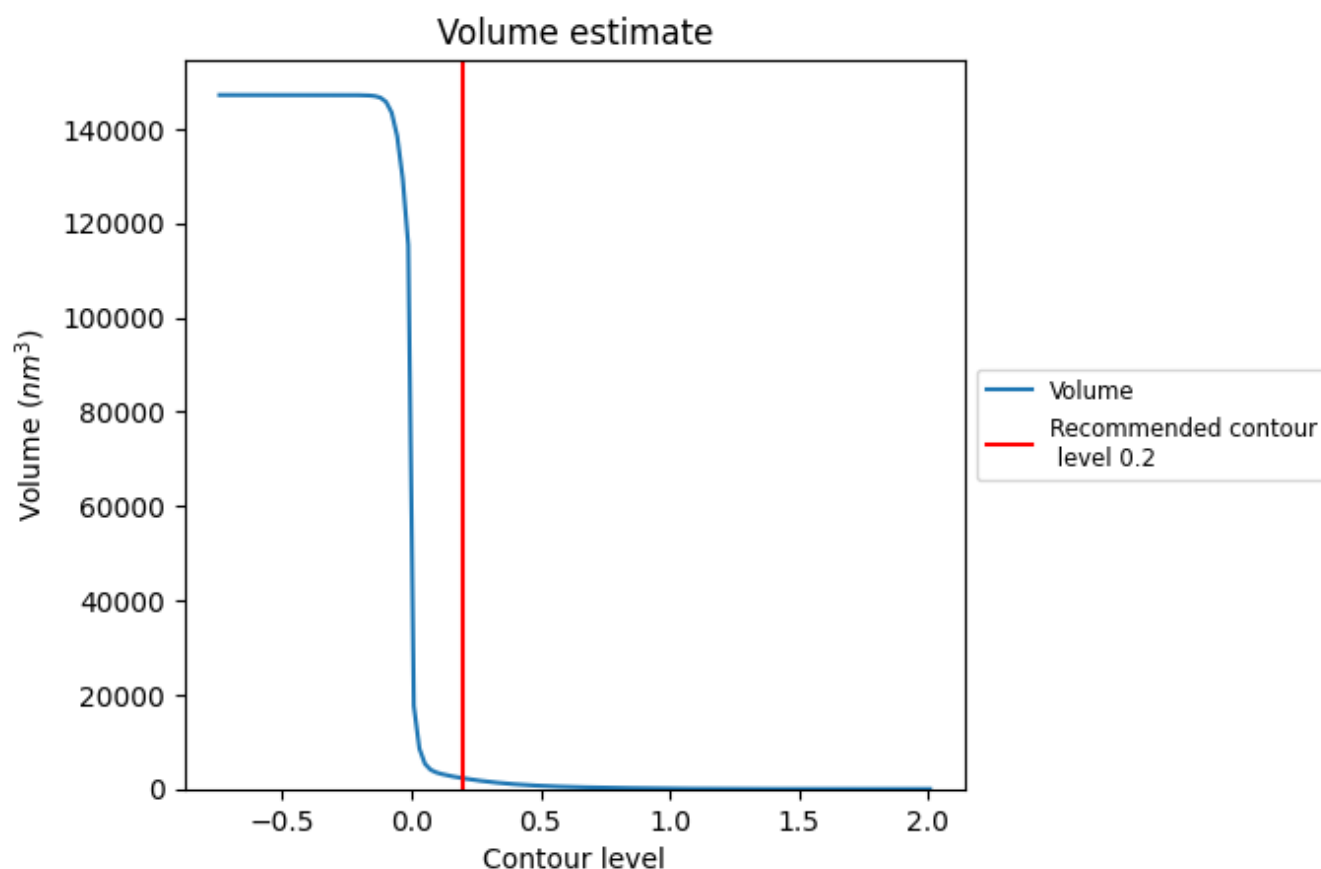
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

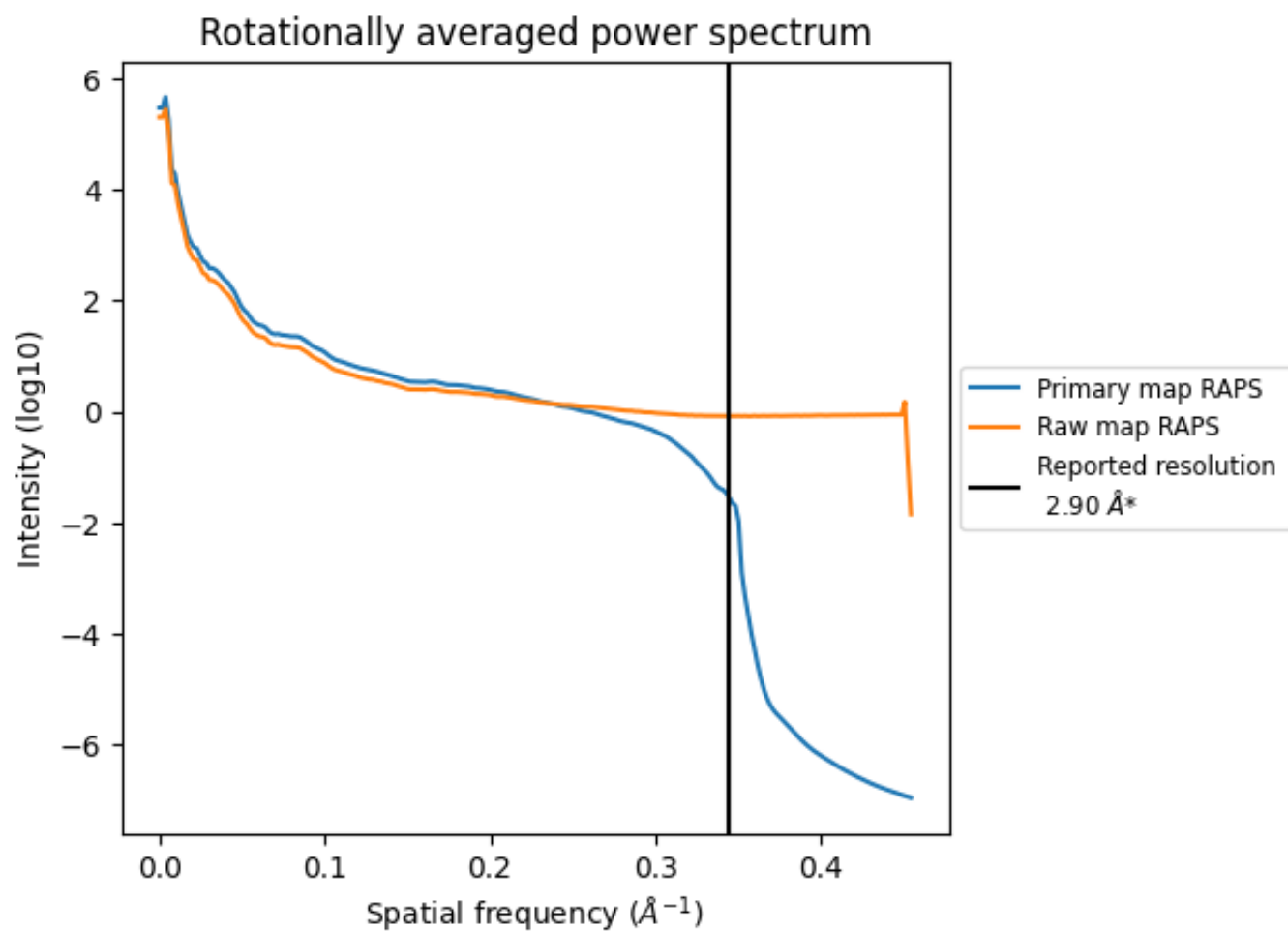
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2269 nm^3 ; this corresponds to an approximate mass of 2050 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

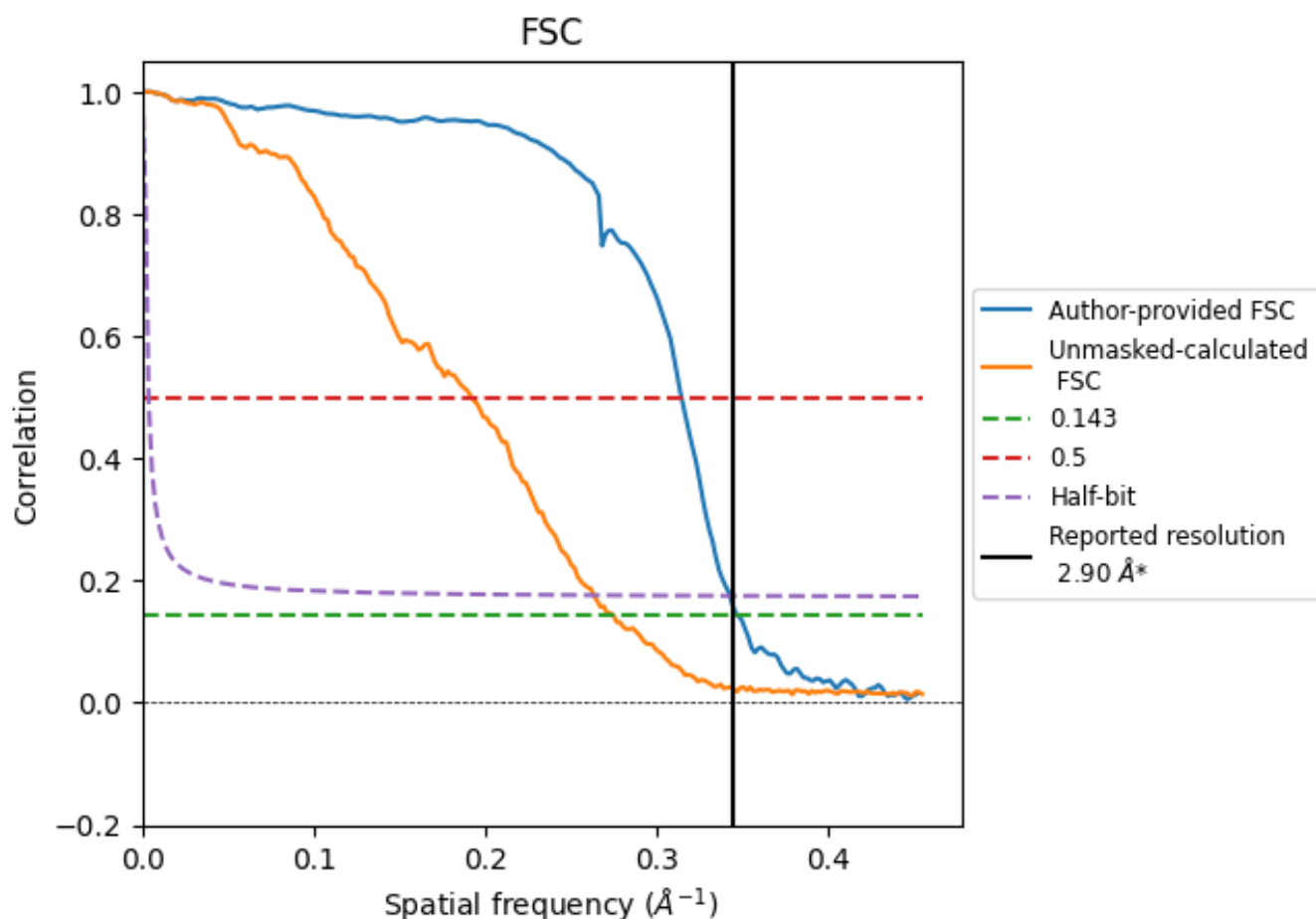


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

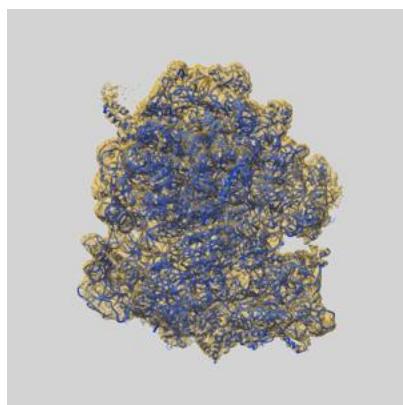
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.88	3.18	2.92
Unmasked-calculated*	3.64	5.21	3.80

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.64 differs from the reported value 2.9 by more than 10 %

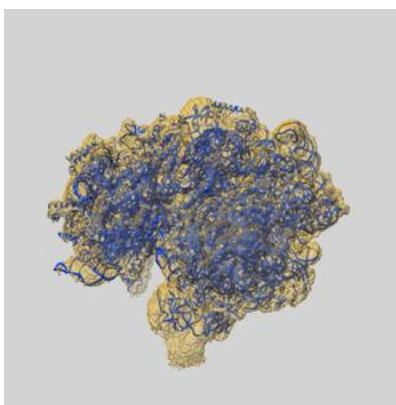
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60061 and PDB model 8ZFI. Per-residue inclusion information can be found in section 3 on page 15.

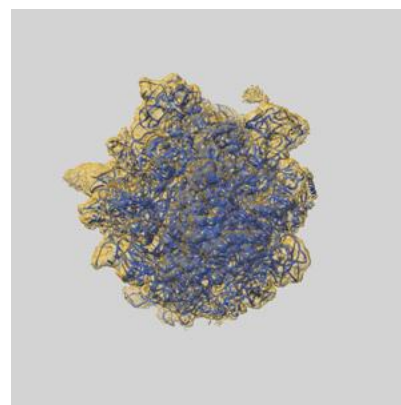
9.1 Map-model overlay [i](#)



X



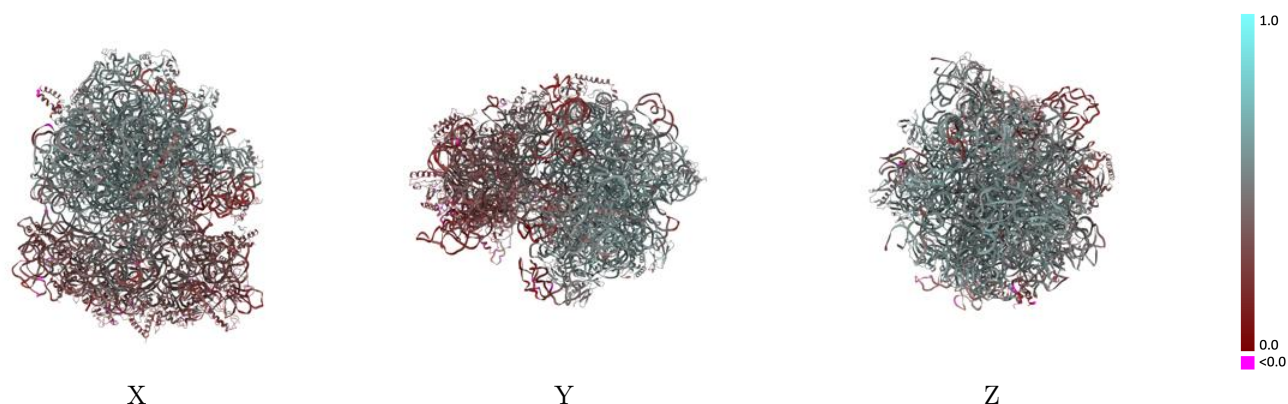
Y



Z

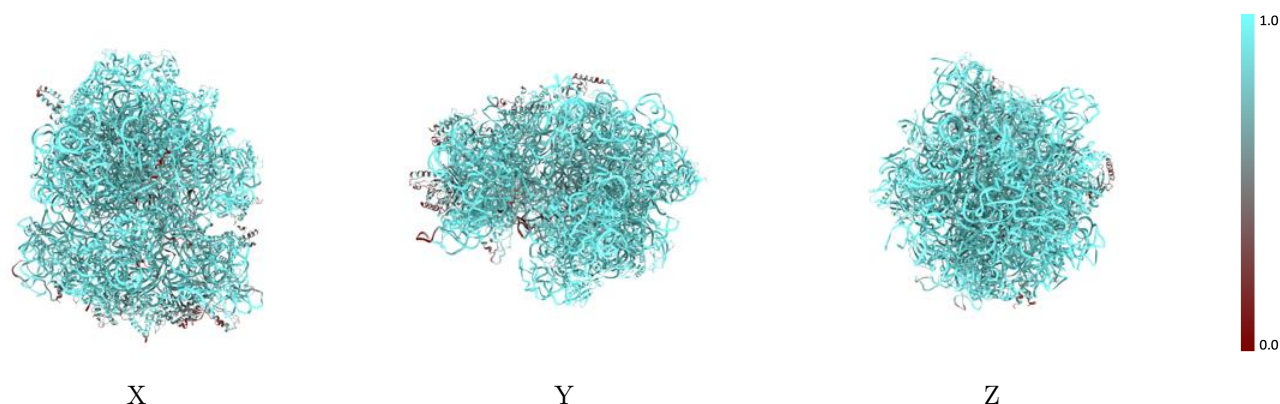
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



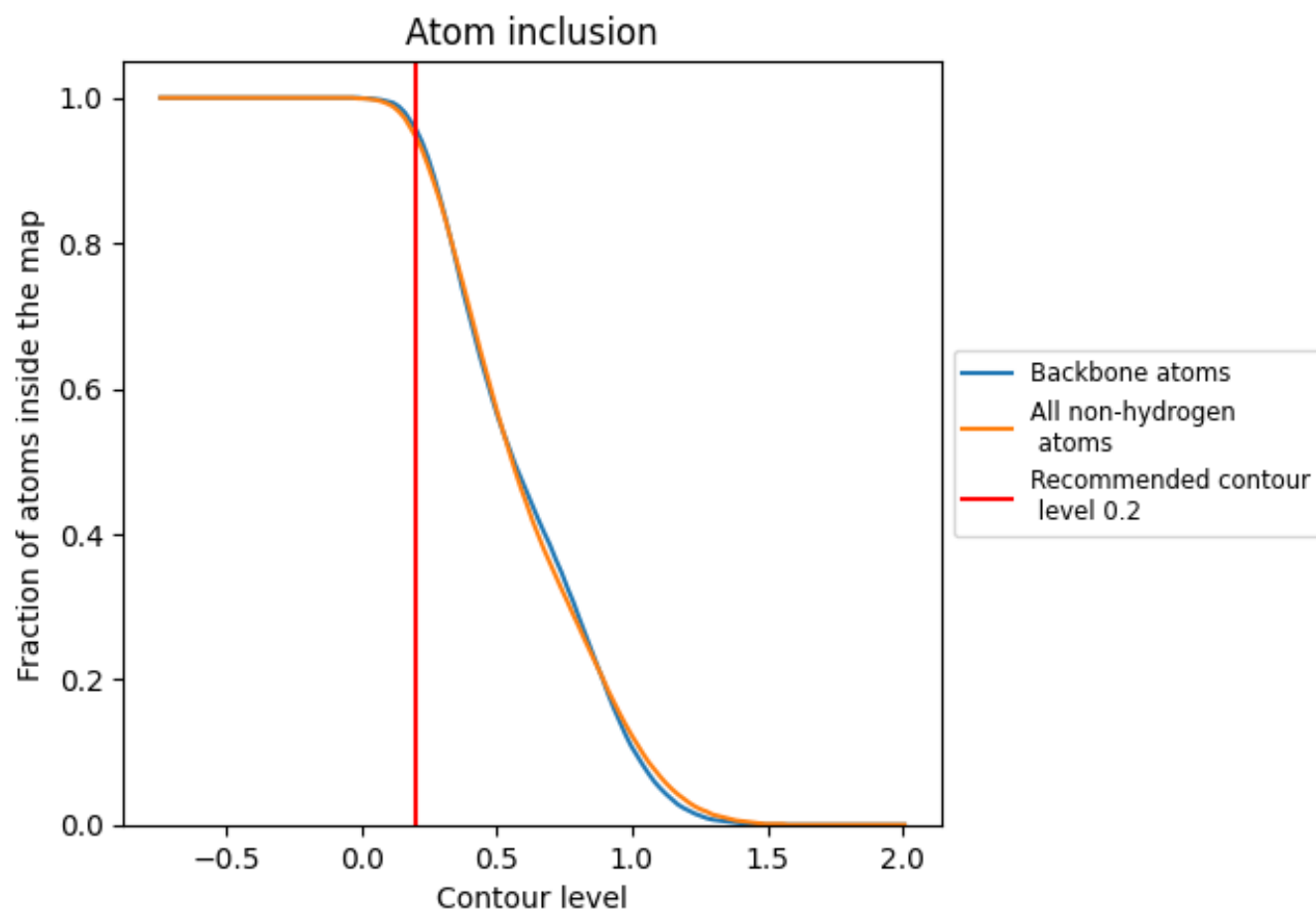
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion ⓘ



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

Chain	Atom inclusion	Q-score
All	 0.9470	 0.4410
0	 0.9980	 0.5010
1	 0.9900	 0.4730
2	 0.9730	 0.5430
4	 0.9700	 0.5400
5	 0.9500	 0.5100
6	 0.9970	 0.5680
7	 0.9760	 0.5700
8	 0.9900	 0.5500
A	 0.9680	 0.3400
B	 0.6660	 0.3070
C	 0.6200	 0.3200
D	 0.6430	 0.1970
E	 0.8770	 0.3710
F	 0.9330	 0.3760
G	 0.9030	 0.3000
H	 0.8860	 0.3760
I	 0.9060	 0.2590
J	 0.6270	 0.2650
K	 0.8510	 0.3980
L	 0.7120	 0.2850
M	 0.6600	 0.2880
N	 0.8590	 0.2440
O	 0.9480	 0.4050
P	 0.7870	 0.3160
Q	 0.8690	 0.3130
R	 0.7710	 0.3560
S	 0.8360	 0.2420
T	 0.8700	 0.2700
U	 0.6170	 0.3470
V	 0.6430	 0.2910
X	 0.9460	 0.2420
Y	 0.8890	 0.3530
Z	 0.6520	 0.3790
a	 0.9980	 0.5120



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Chain	Atom inclusion	Q-score
b	 0.9960	 0.5150
c	 0.9890	 0.5490
d	 0.9770	 0.5530
e	 0.9720	 0.5170
f	 0.8420	 0.3280
g	 0.9850	 0.4950
h	 0.7010	 0.3980
k	 0.9780	 0.5560
l	 0.9030	 0.5420
m	 0.9770	 0.5370
n	 0.9790	 0.5480
o	 0.9880	 0.5560
p	 0.9760	 0.4790
q	 0.9190	 0.5330
r	 0.9840	 0.5460
s	 0.9850	 0.5340
t	 0.9770	 0.5360
u	 0.9510	 0.4870
v	 0.9850	 0.4930
w	 0.9770	 0.5210
x	 0.8960	 0.3890
y	 0.8900	 0.5140
z	 0.5540	 0.3540