



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 11:26 PM UTC

PDB ID : 6S0X / pdb_00006s0x
EMDB ID : EMD-10076
Title : Erythromycin Resistant Staphylococcus aureus 70S ribosome (delta R88 A89 uL22) in complex with erythromycin.
Authors : Halfon, Y.; Matozv, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Kjeldgaard, J.; Ingmer, H.; Yonath, A.
Deposited on : 2019-06-18
Resolution : 2.42 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

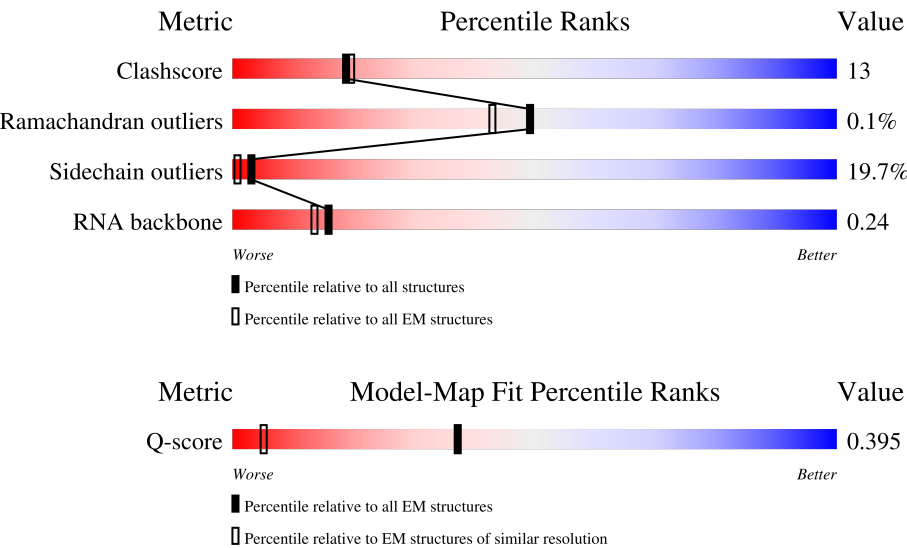
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.42 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.



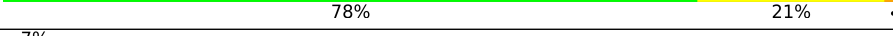
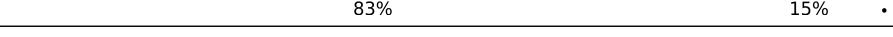
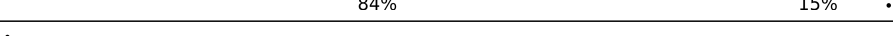
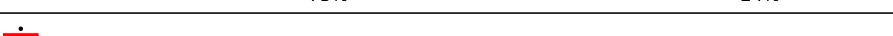
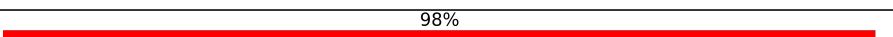
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5720 (1.93 - 2.92)

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

Mol	Chain	Length	Quality of chain
1	A	2905	16% 38% 32% 21% 9%
2	B	115	62% 27% 11%
3	C	274	76% 20%

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Mol	Chain	Length	Quality of chain
4	D	215	
5	E	206	
6	F	173	
7	G	173	
8	H	145	
9	I	122	
10	J	146	
11	K	137	
12	L	120	
13	M	118	
14	N	114	
15	O	116	
16	P	102	
17	Q	110	
18	R	89	
19	S	103	
20	T	94	
21	U	77	
22	V	49	
23	W	67	
24	X	58	
25	Y	59	
26	Z	48	
27	1	47	
28	2	43	

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Mol	Chain	Length	Quality of chain
29	3	64	
30	4	37	
31	a	1539	
32	b	226	
33	c	202	
34	d	198	
35	e	156	
36	f	95	
37	g	152	
38	h	131	
39	i	127	
40	j	97	
41	k	114	
42	l	135	
43	m	104	
44	n	60	
45	o	88	
46	p	89	
47	q	80	
48	r	54	
49	s	80	
50	t	81	
51	u	52	
52	v	162	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
53	ERY	A	3001	X	-	-	-

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 140672 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2905	Total	C	N	O	P	0	0
			62277	27803	11387	20182	2905		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	115	Total	C	N	O	P	0	0
			2445	1094	436	801	114		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	274	Total	C	N	O	S	0	0
			2090	1301	415	369	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	173	Total	C	N	O	S	0	0
			1315	831	225	253	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	173	Total	C	N	O	S	0	0
			1248	780	236	229	3		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	145	Total	C	N	O	S	0	0
			1149	717	211	218	3		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	137	Total	C	N	O	S	0	0
			1079	694	204	177	4		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	118	Total	C	N	O	0	0
			883	552	173	158		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	114	Total	C	N	O	0	0
			889	563	175	151		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	110	Total	C	N	O	S	0	0
			838	525	159	151	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	?	-	ARG	deletion	UNP A0A077UKF9
Q	?	-	ALA	deletion	UNP A0A077UKF9

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	77	Total	C	N	O	0	0
			587	363	115	109		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	58	Total	C	N	O	0	0
			449	280	85	84		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	59	Total	C	N	O	S	0	0
			370	225	68	76	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	48	Total	C	N	O	S	0	0
			360	222	77	59	2		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	47	Total	C	N	O	S	0	0
			390	238	78	70	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

- Molecule 31 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1539	Total	C	N	O	P	0	0
			32969	14719	6017	10694	1539		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	226	Total	C	N	O	S	0	0
			1819	1159	317	335	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	202	Total	C	N	O	S	0	0
			1501	945	284	271	1		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	198	Total	C	N	O	S	0	0
			1497	952	275	268	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	156	Total	C	N	O	S	0	0
			1145	723	211	209	2		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	95	Total	C	N	O	S	0	0
			778	493	138	145	2		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	152	Total	C	N	O	S	0	0
			1161	722	218	217	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	131	Total	C	N	O	S	0	0
			1026	650	183	189	4		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			922	576	179	166	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	97	Total	C	N	O	S	0	0
			752	475	140	136	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	114	Total	C	N	O	S	0	0
			810	498	151	159	2		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	135	Total	C	N	O	S	0	0
			1037	646	211	178	2		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	104	Total	C	N	O	S	0	0
			727	453	139	135			

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	60	Total	C	N	O	S	0	0
			487	307	98	77	5		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			723	448	150	124	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	89	Total	C	N	O	S	0	0
			694	436	128	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	80	Total	C	N	O	S	0	0
			621	392	112	117			

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	54	Total	C	N	O	S	0	0
			445	284	86	73	2		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	80	Total	C	N	O	S	0	0
			636	410	113	111	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	81	Total	C	N	O	S	0	0
			591	358	117	115	1		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	52	Total	C	N	O	0	0
			400	249	79	72		

- Molecule 52 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	162	Total	C	N	O	S	0	0
			1333	835	242	254	2		

There are 24 discrepancies between the modelled and reference sequences:

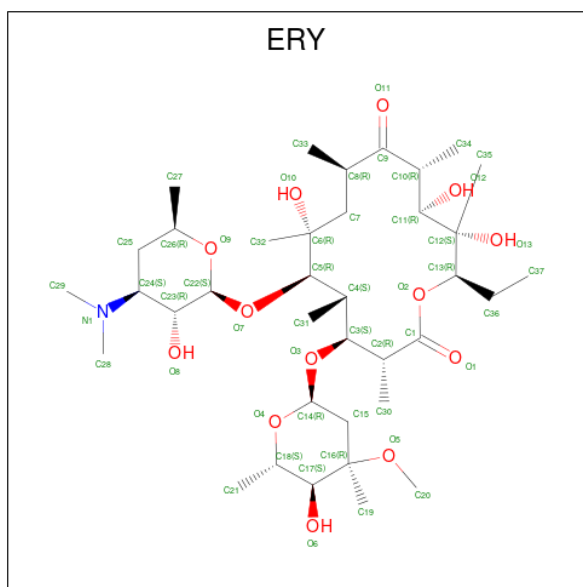
Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	PHE	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	LEU	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	MET	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

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Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	THR	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	TYR	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

- Molecule 53 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$).

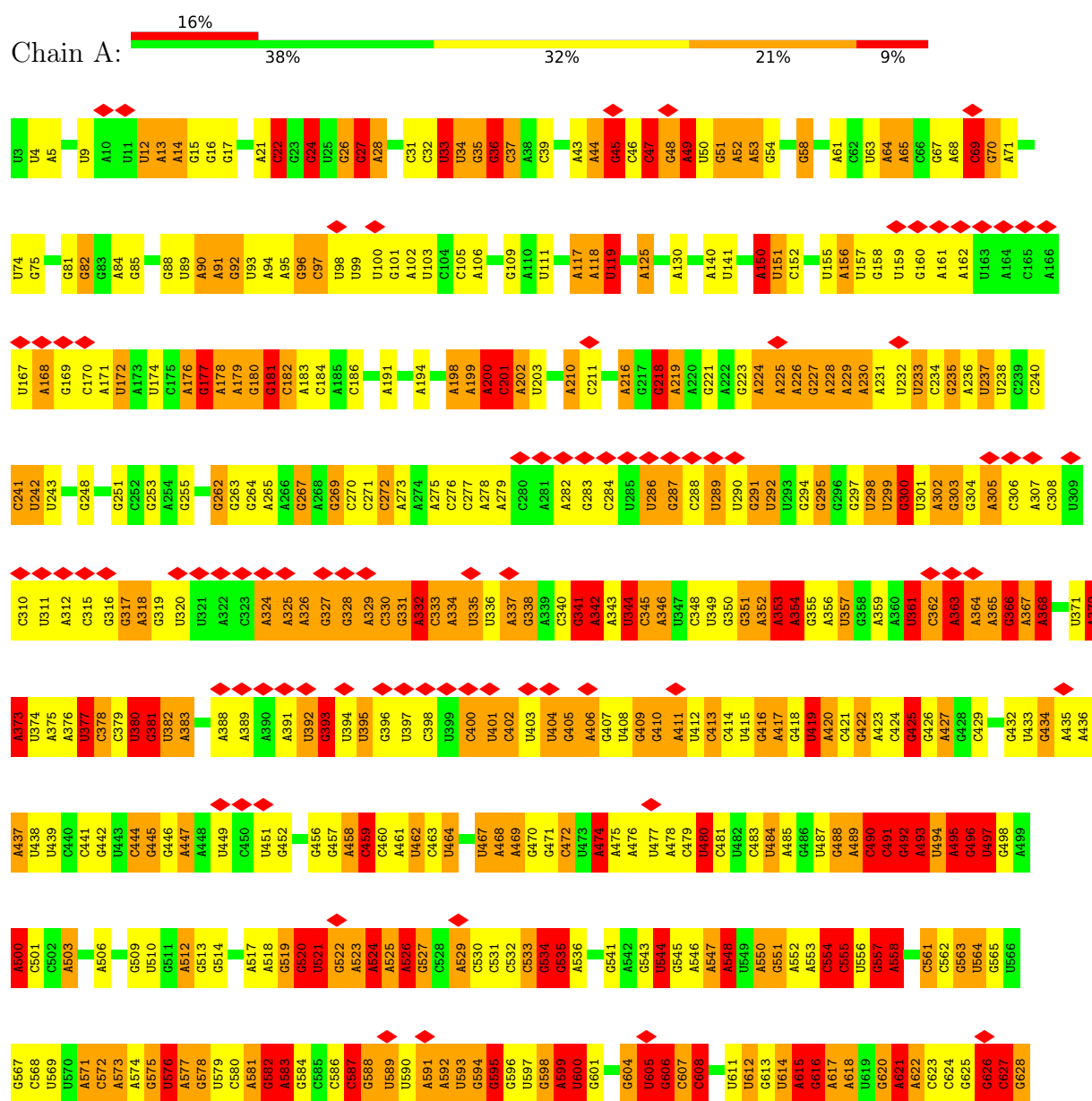


Mol	Chain	Residues	Atoms				AltConf
53	A	1	Total	C	N	O	0
			51	37	1	13	

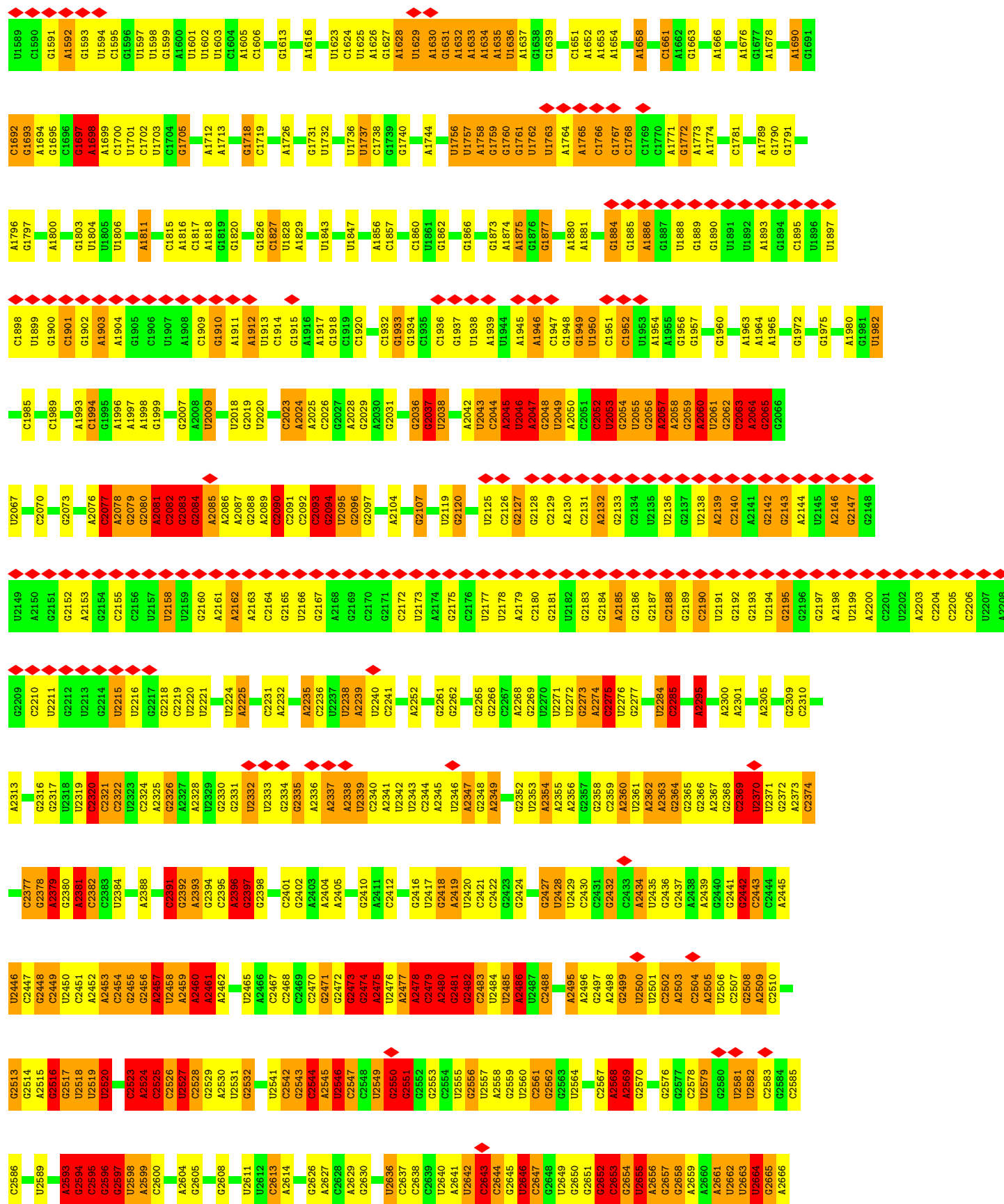
3 Residue-property plots

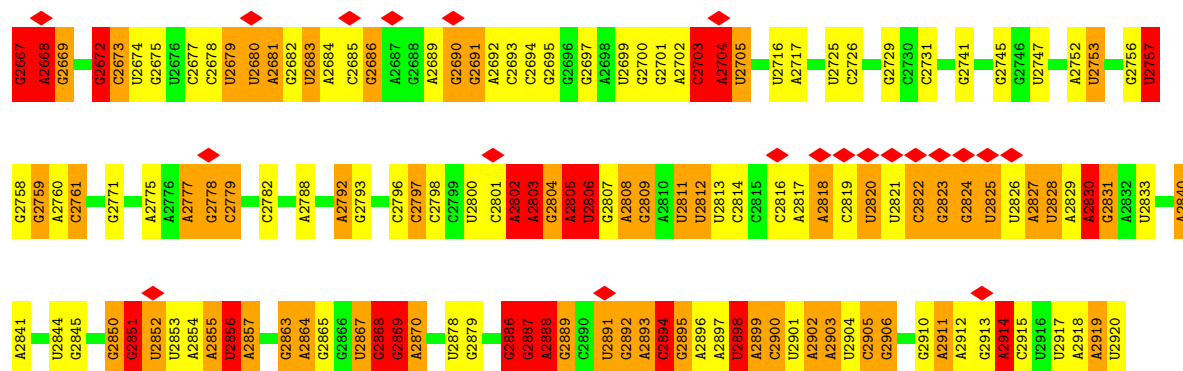
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S ribosomal RNA

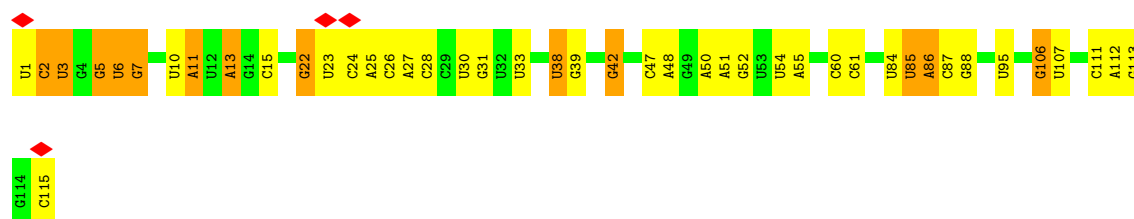




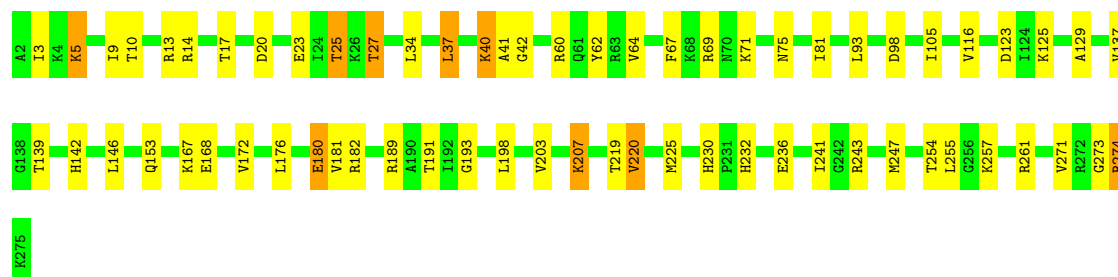
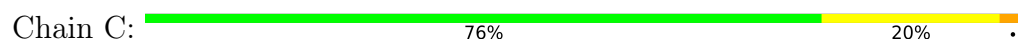




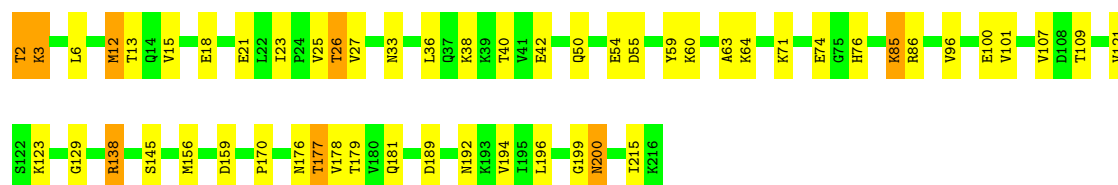
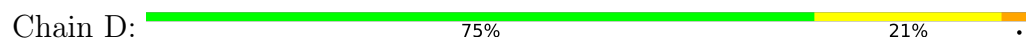
• Molecule 2: 5S ribosomal RNA



• Molecule 3: 50S ribosomal protein L2

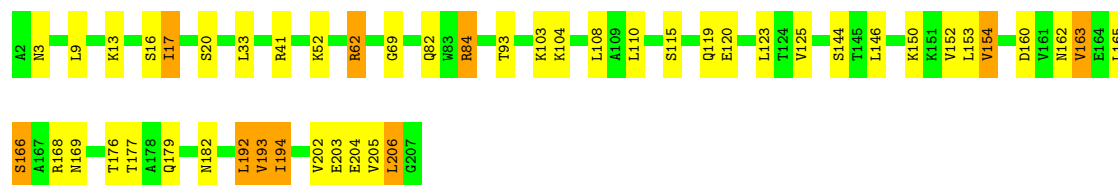


• Molecule 4: 50S ribosomal protein L3

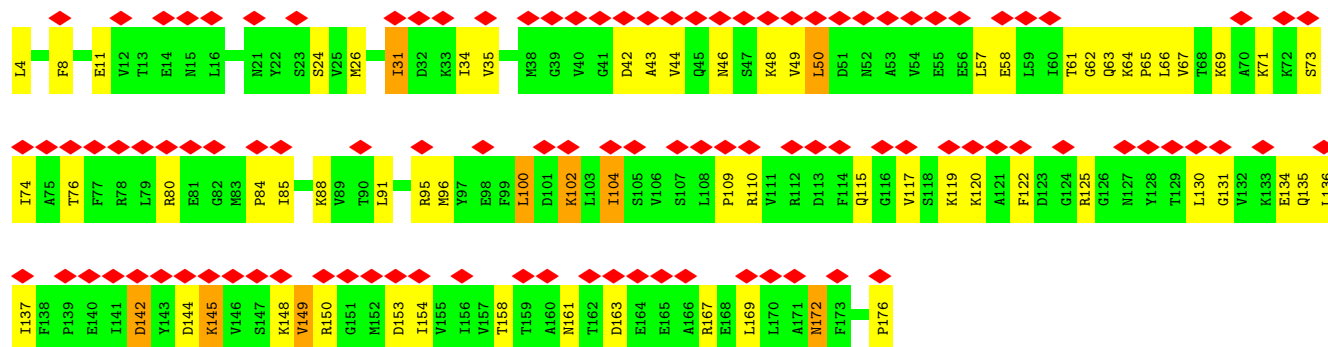


• Molecule 5: 50S ribosomal protein L4

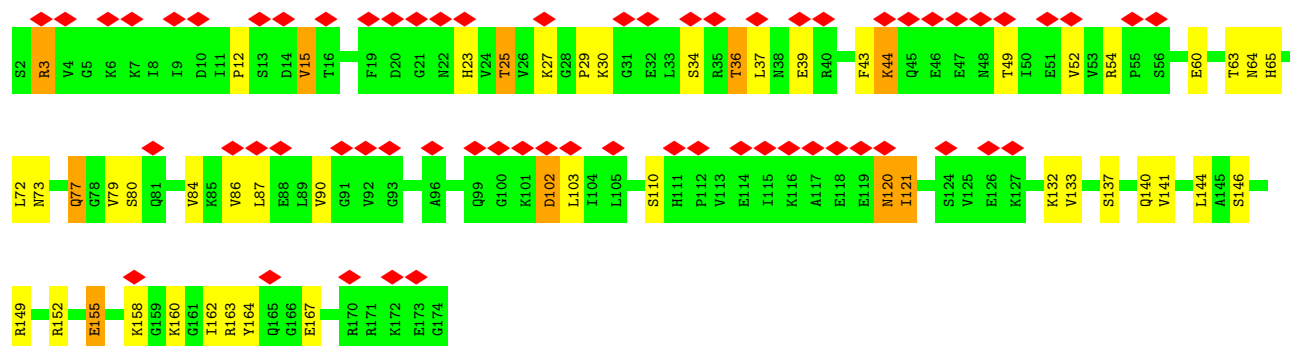




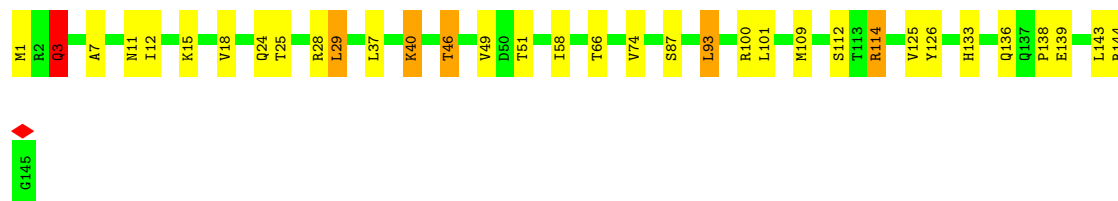
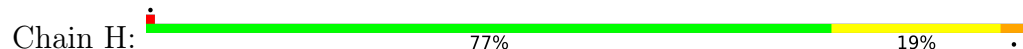
• Molecule 6: 50S ribosomal protein L5



• Molecule 7: 50S ribosomal protein L6



• Molecule 8: 50S ribosomal protein L13

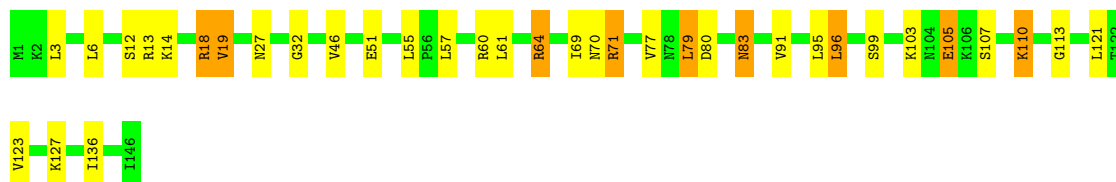


• Molecule 9: 50S ribosomal protein L14

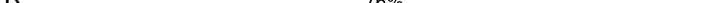


- Molecule 10: 50S ribosomal protein L15

Chain J:  75% 18% 6%

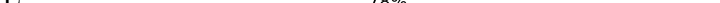


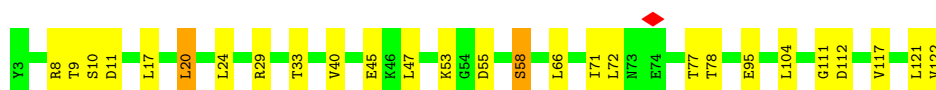
- Molecule 11: 50S ribosomal protein L16

Chain K:  76% 24%

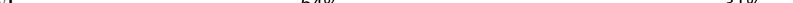


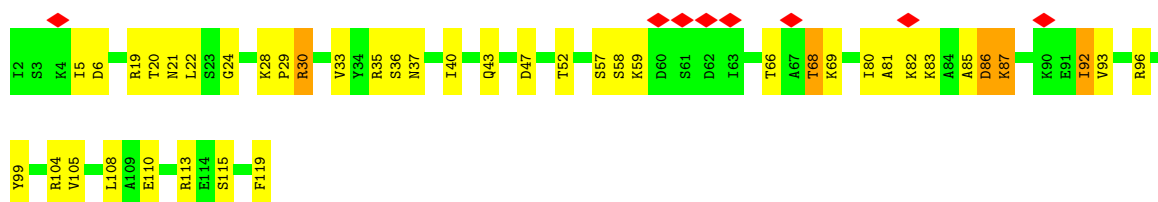
- Molecule 12: 50S ribosomal protein L17

Chain L:  78% 21%



- Molecule 13: 50S ribosomal protein L18

Chain M:  7% 64% 31% .

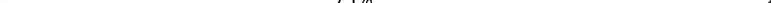


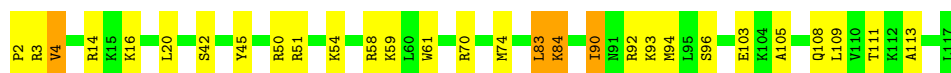
- Molecule 14: 50S ribosomal protein L19

Chain N: 83% 15%



- Molecule 15: 50S ribosomal protein L20

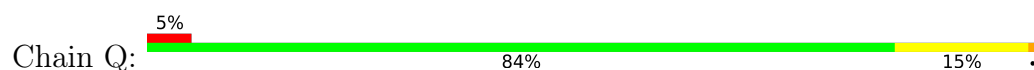
Chain O:  75% 22% .



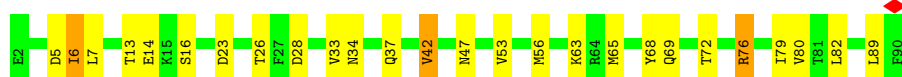
- Molecule 16: 50S ribosomal protein L21



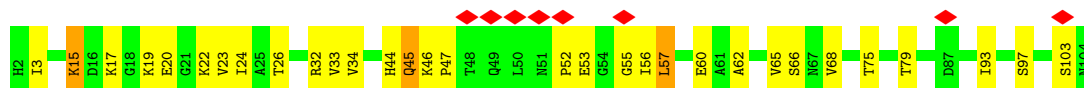
- Molecule 17: 50S ribosomal protein L22



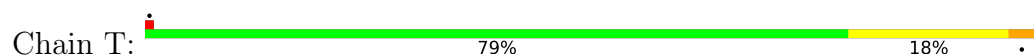
- Molecule 18: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L24



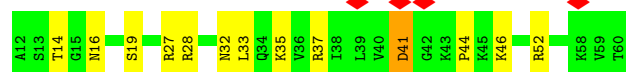
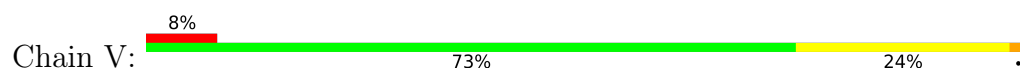
- Molecule 20: 50S ribosomal protein L25



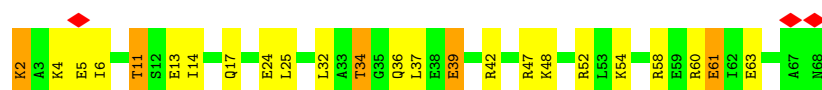
- Molecule 21: 50S ribosomal protein L27



- Molecule 22: 50S ribosomal protein L28



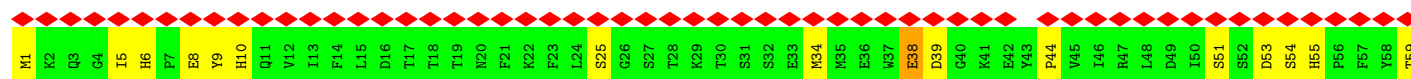
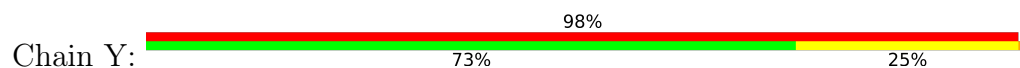
- Molecule 23: 50S ribosomal protein L29



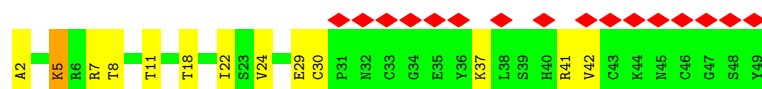
- Molecule 24: 50S ribosomal protein L30



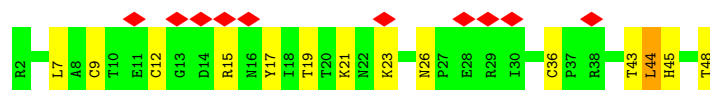
- Molecule 25: 50S ribosomal protein L31 type B



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33

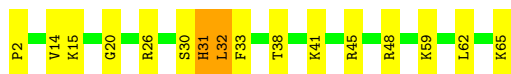


- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35

Chain 3:  75% 22% .

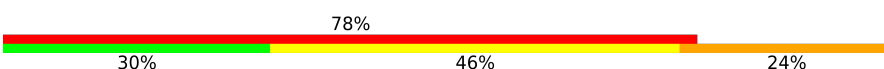


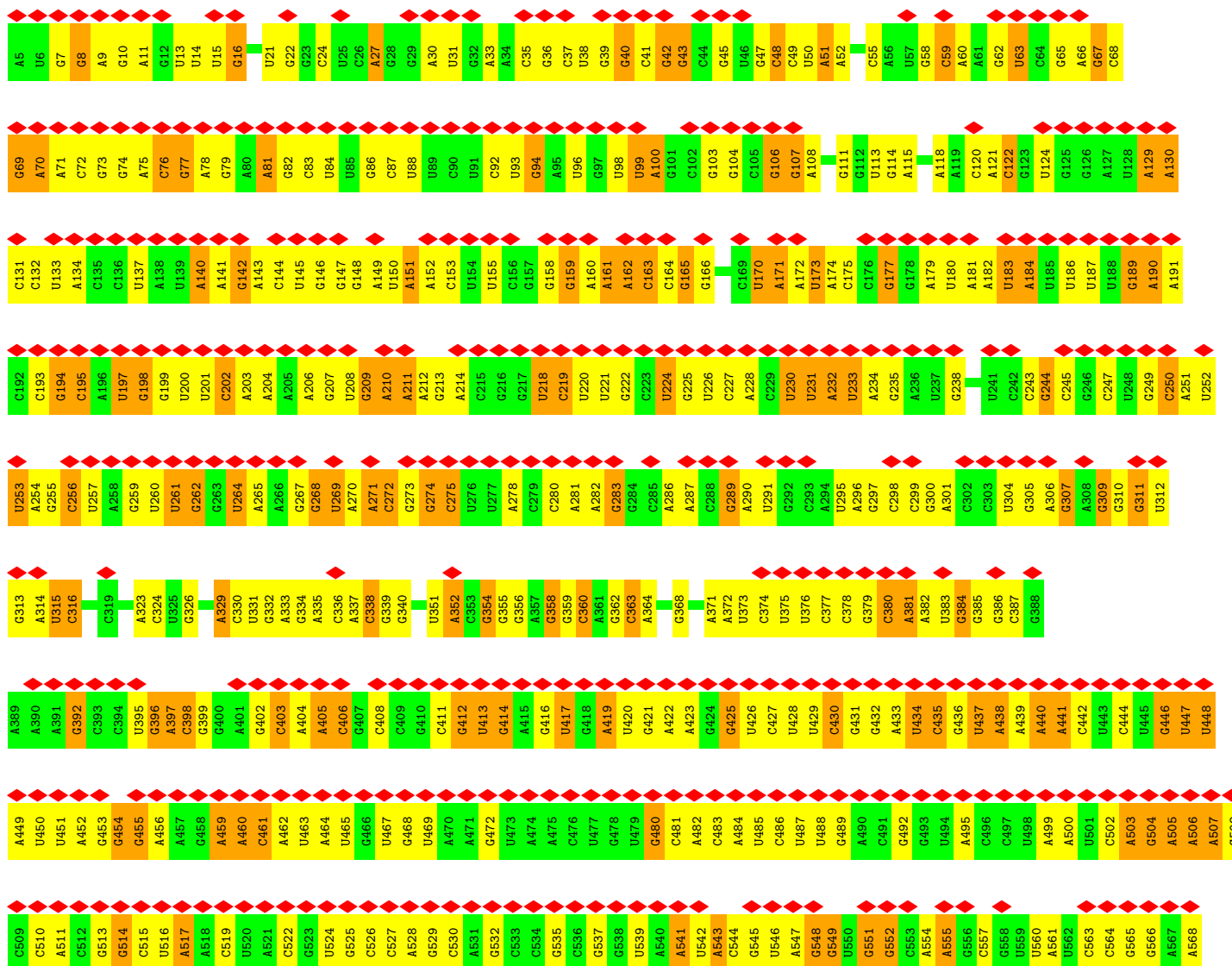
- Molecule 30: 50S ribosomal protein L36

Chain 4:  76% 19% 5%

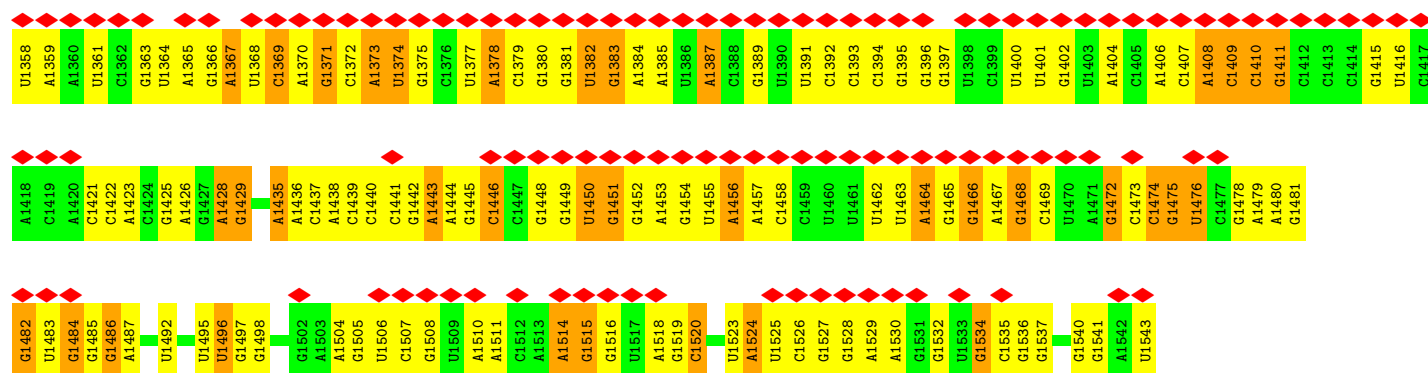


- Molecule 31: 16S ribosomal RNA

Chain a:  30% 78% 46% 24%



A1298	C1238	G1058	U998	A938	U872	U812	C752	U692	C632	U569
A1299	A1239	G1059	C999	C939	C875	C814	U753	G693	C632	U570
G1300	C1240	U1060	U1000	C940	C876	C815	G754	U694		A571
U1301	G1241	G1061	U1001	C941	C877	C816	U755	A695		U572
U1302	U1242	G1062	G1002	G942	A878	C916	U756	G696		U573
G1303	C1243	U1063	A1003	C943	U879	G817	A757	G697		G574
U1304	C1244	G1064	C1004	A944	U880	C818	C758	G698		G575
U1305	U1245	C1065	A1005	C945	U881	G819	U759	G699		C577
C1306	U1246	A1066	U1006	A946	A882	G820	U760	U700		
U1307	C1247	U1067	C1007	A947	G883	U821	A761	G701		A581
C1308	A1248	G1068	C1008	G948	C884	A822	C762	G702		A582
A1309	U1249	G1069	U1009	C949	G885	A823	A763	A703		G583
G1310	U1250	U1070	U1010	G950	A886	A824	C764	A704		C584
U1311	G1251	U1071	G1011	G951	U887	C826	U765	U705		G585
U1312	G1252	U1072	G1012	U952	C888	A827	G766	G706		C586
C1313	U1133	U1073	A1013	G953	C889	G828	A767	C707		C588
G1314	A1254	C1074	C1014	G954	C890	G829	U768	G708		G589
G1315	C1255	U1075	A1015	A955	C891	A830	G769	C709		U590
A1316	A1256	U1076	A1016	G956	C892	G831	U770	C710		A591
U1317	U1257	C1077	C1017	C957	G893	U832	C772	A711		G592
U1318	A1258	A1078	U1018	A958	G894	G833	G773	A712		C594
G1319	C1259	G1079	C1019	U959	A898	C834	A774	A714		G595
U1320	A1260	C1080	U1020	G960	G899	U835	A775	U715		G596
G1321	A1261	U1081	A1021	U961	U900	A836	A776	A716		U597
U1322	A1262	C1082	G1022	G962	A901	A837	C777	U717		U598
C1323	G1263	U1083	A1023	G963	A904	G838	G778	U718		U599
C1324	G1264	U1084	G1024	U964	A905	U839	U779	G719		U600
U1325	G1265	U1085	A1025	U965	C906	G840	U780	G720		U601
G1326	C1266	U1086	U1026	U966	G907	U841	G781	U660		U602
C1327	A1267	C1087	A1027	A967	C908	U842	G782	U661		A603
A1328	G1268	U1088	G1028	A968	C909	A843	G783	G662		A604
U1329	C1269	U1089	A1029	U969	C910	G844	G784	A663		G605
C1330	G1270	U1090	U1030	U970	G911	G845	A785	G664		U606
U1331	A1271	A1091	C1031	C971	U914	G846	U786	C725		C607
G1332	A1272	G1092	C1032	G972	G915	U847	C787	A726		U608
A1333	A1273	A1093	U1033	A973	A916	G848	A788	C727		G609
C1335	C1274	U1094	C1034	A974	A917	U849	A789	A610		A610
U1336	C1275	G1095	U1035	G975	A918	U850	A790	C728		U611
A1337	G1276	U1096	C1036	C976	C921	U851	C791	A729		G612
C1338	C1277	U1097	C1037	A977	A922	C852	A792	G730		U613
U1339	U1278	G1098	U1038	A978	A923	C853	G793	G731		G614
A1340	A1279	U1099	C1039	C979	A924	G854	A794	G732		A615
G1341	G1280	U1100	U1040	G980	G925	C855	U795	C733		A616
A1342	U1281	U1101	C1041	C981	G926	C856	U796	G734		A617
C1343	U1282	A1102	G1042	G982	G927	C857	A797	A675		G618
G1344	C1283	A1103	G1043	A983	A928	C858	U798	A677		C619
A1345	A1284	U1104	U1044	A984	U929	U859	G799	A678		C620
U1346	U1285	G1105	G1045	G985	U930	U860	G739	G679		C621
G1347	C1286	U1106	G1046	A986	G931	A961	C740	U680		A622
A1348	U1287	C1107	A1047	A987	A932	G862	G741	G681		C623
U1349	A1288	C1108	C1048	C988	G934	U863	A742	G682		G624
A1350	U1289	C1109	A1049	C989	G935	G864	C743	A683		G625
G1351	A1290	G1110	U1050	U990	G936	C865	C904	G684		C626
C1352	U1291	C1111	A1051	U991	G937	U866	U806	U685		U627
U1353	C1292	A1112	G1052	A992	C937	G867	G507	U686		C628
G1354	C1293	A1113	U1053	C993	A938	A868	G608	C687		A629
U1355	C1294	C1114	G1054	C994	A939	A869	U809	C688		U630
A1356	U1295	G1115	A1055	A995	G940	G870	A810	U689		
G1357	U1296	G1116	C1056	A996	G941	C871	G611	U690		
	A1297	G1117	A1057	A997	G942			G691		
		A1177								



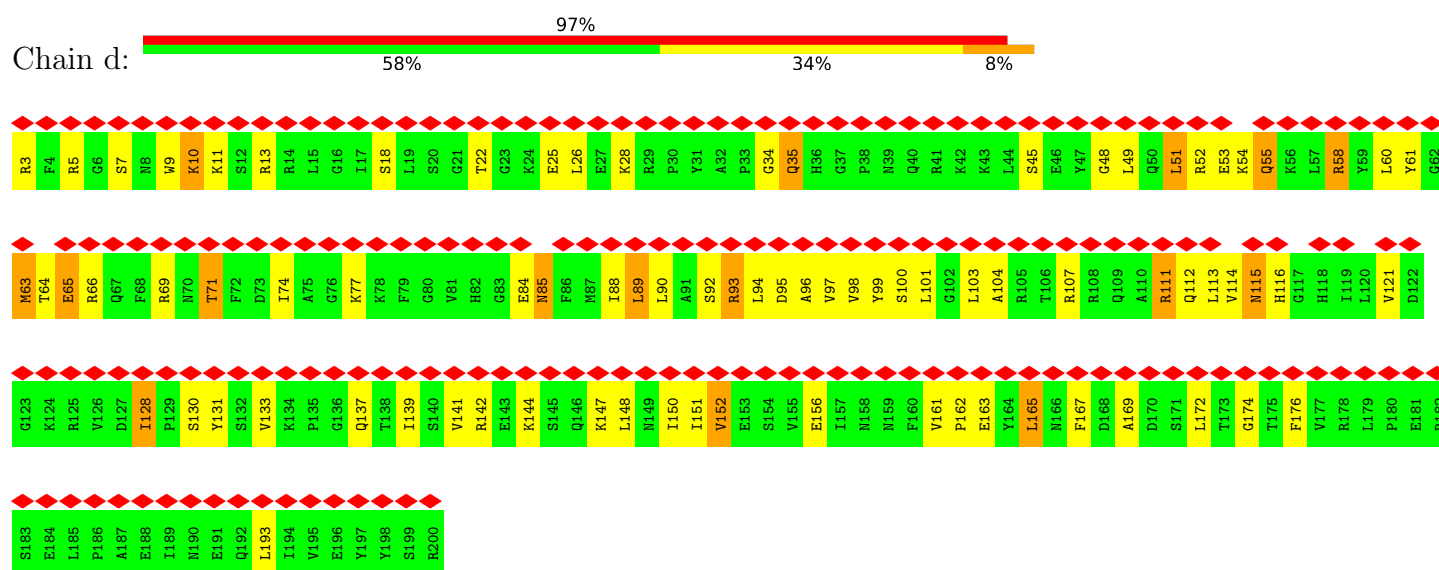
• Molecule 32: 30S ribosomal protein S2



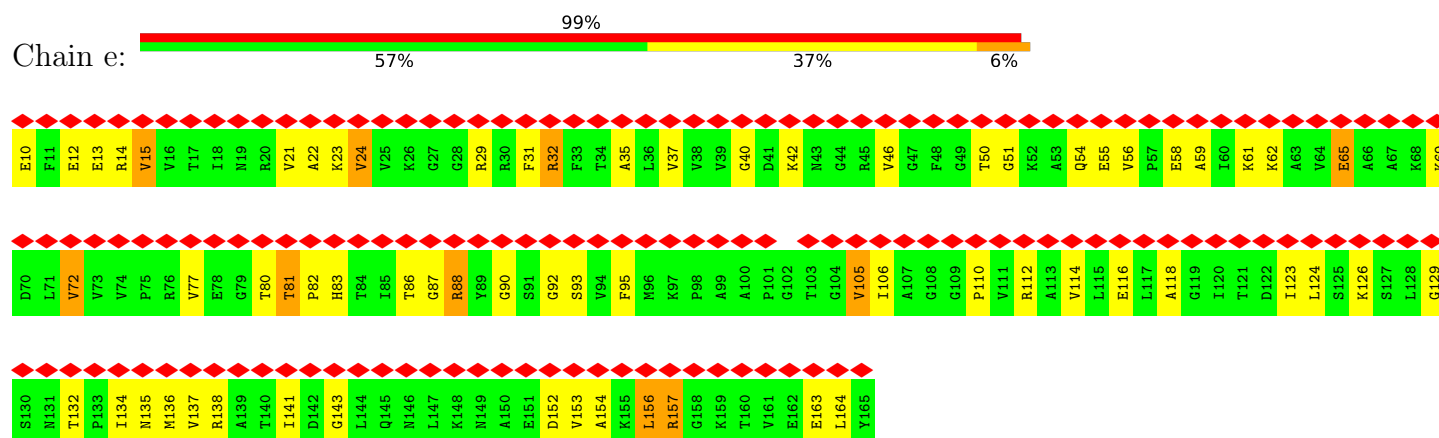
• Molecule 33: 30S ribosomal protein S3



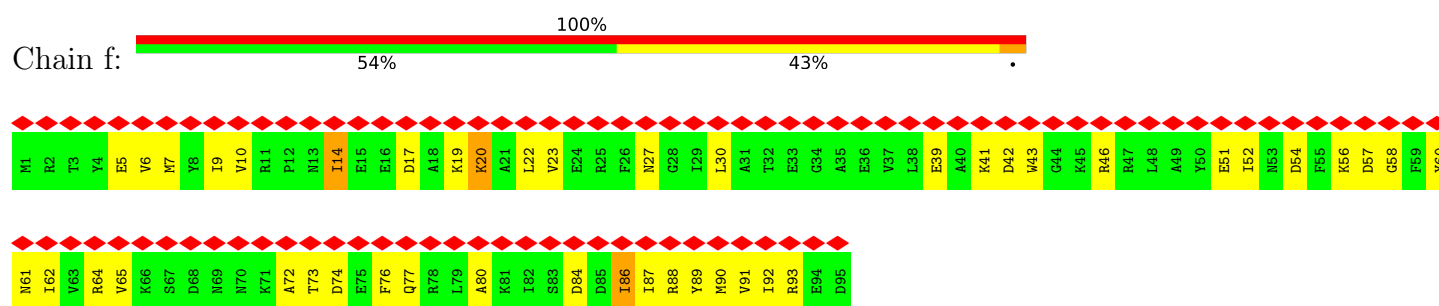
• Molecule 34: 30S ribosomal protein S4



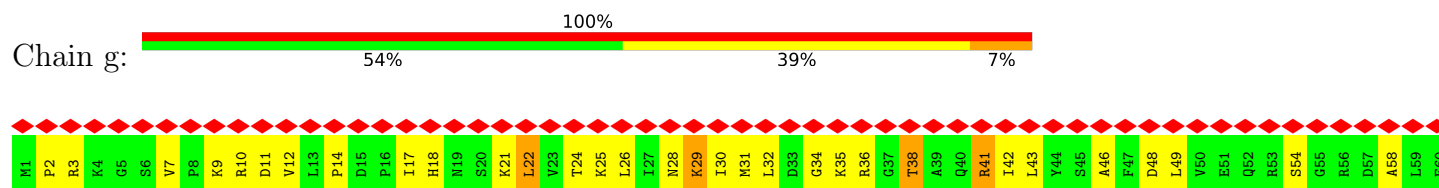
• Molecule 35: 30S ribosomal protein S5

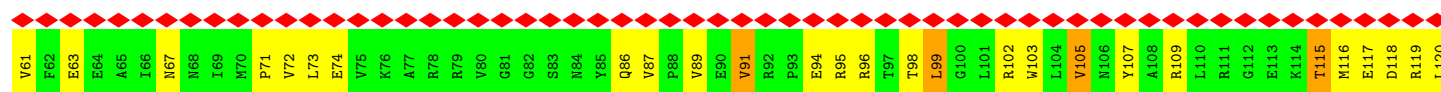


• Molecule 36: 30S ribosomal protein S6

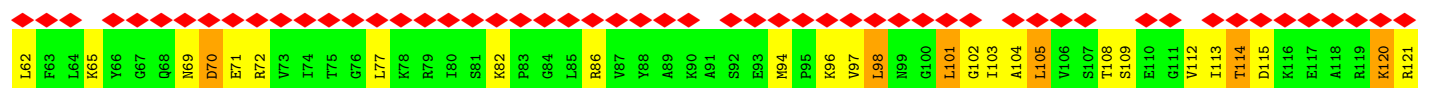


• Molecule 37: 30S ribosomal protein S7

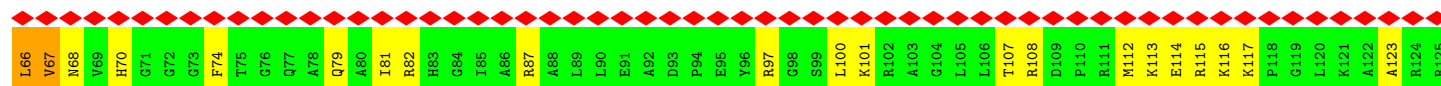
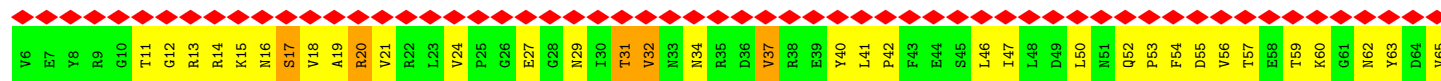




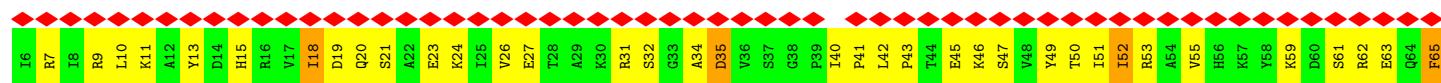
• Molecule 38: 30S ribosomal protein S8



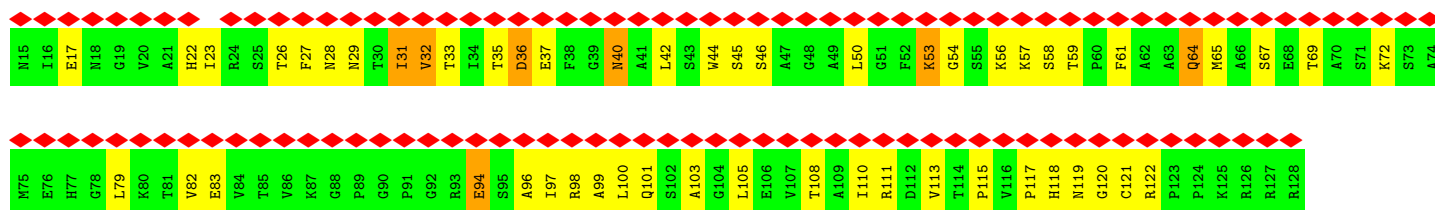
• Molecule 39: 30S ribosomal protein S9



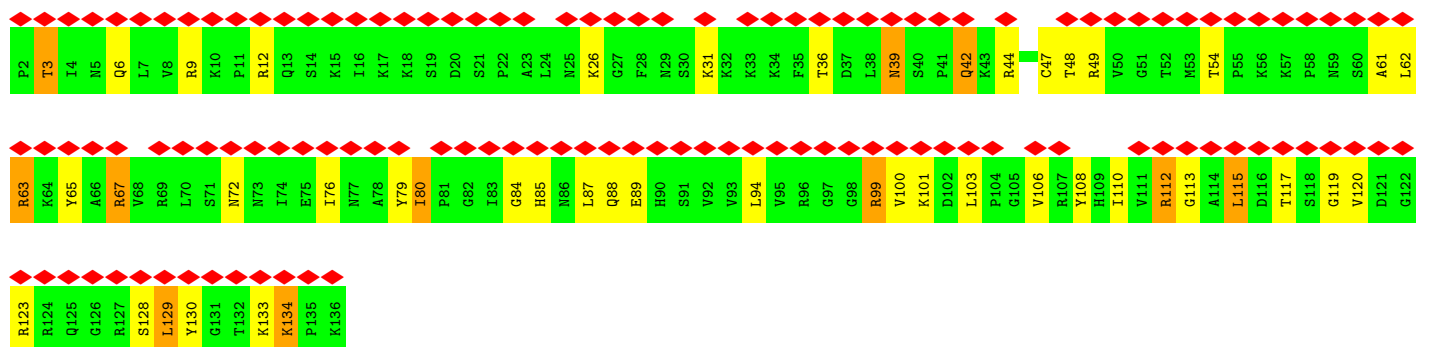
• Molecule 40: 30S ribosomal protein S10



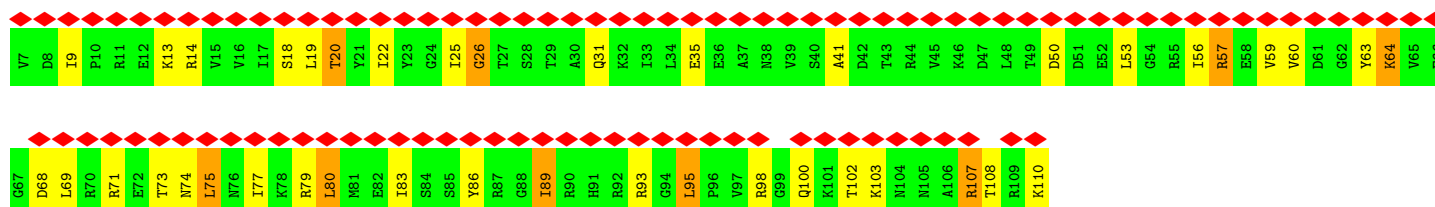
• Molecule 41: 30S ribosomal protein S11



• Molecule 42: 30S ribosomal protein S12



• Molecule 43: 30S ribosomal protein S13



• Molecule 44: 30S ribosomal protein S14 type Z

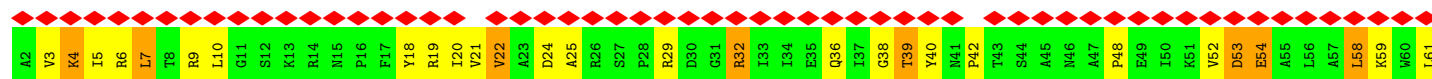
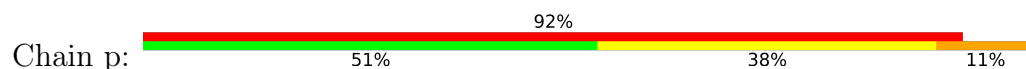


• Molecule 45: 30S ribosomal protein S15

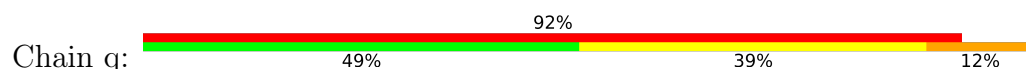




• Molecule 46: 30S ribosomal protein S16



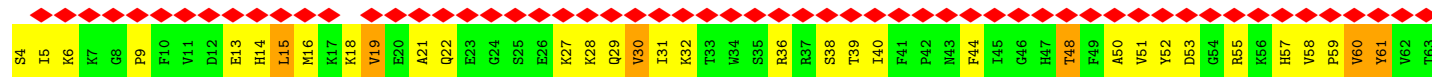
• Molecule 47: 30S ribosomal protein S17



• Molecule 48: 30S ribosomal protein S18

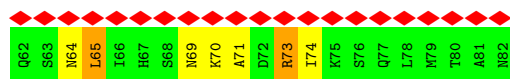


• Molecule 49: 30S ribosomal protein S19

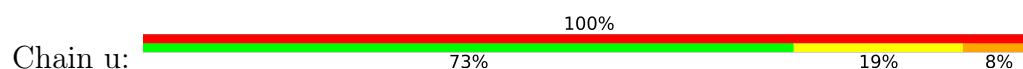


• Molecule 50: 30S ribosomal protein S20

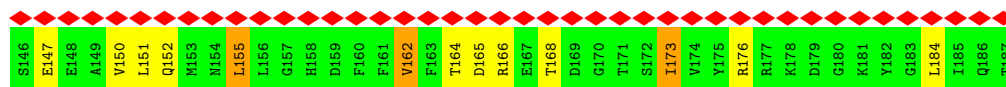
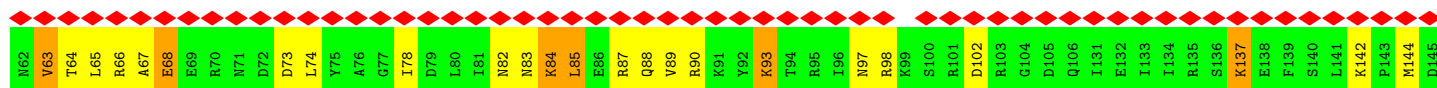




- Molecule 51: 30S ribosomal protein S21



- Molecule 52: Ribosome hibernation promoting factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	378309	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.076	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.320	Depositor
Minimum map value	-0.137	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	426.80002, 426.80002, 426.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.067, 1.067, 1.067	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.45	258/69740 (0.4%)	1.25	862/108755 (0.8%)
2	B	0.78	0/2733	0.66	1/4257 (0.0%)
3	C	1.17	0/2125	0.88	0/2853
4	D	1.19	0/1651	0.97	1/2215 (0.0%)
5	E	1.15	0/1595	0.98	2/2154 (0.1%)
6	F	0.36	0/1329	0.68	1/1791 (0.1%)
7	G	0.35	0/1266	0.56	0/1717
8	H	1.18	1/1171 (0.1%)	0.98	4/1577 (0.3%)
9	I	1.16	1/925 (0.1%)	0.98	3/1242 (0.2%)
10	J	1.11	0/1100	0.91	0/1467
11	K	1.02	1/1103 (0.1%)	0.78	0/1481
12	L	1.13	0/936	0.85	0/1253
13	M	0.64	0/892	0.71	0/1195
14	N	1.14	0/901	0.81	0/1209
15	O	1.30	0/955	0.93	0/1265
16	P	1.19	0/800	1.02	5/1070 (0.5%)
17	Q	1.11	0/846	0.89	0/1140
18	R	0.97	0/723	0.84	0/966
19	S	0.82	0/779	0.88	1/1043 (0.1%)
20	T	0.75	0/730	0.74	0/981
21	U	1.20	0/593	0.89	0/788
22	V	0.99	0/384	0.81	0/515
23	W	0.79	0/542	0.85	0/722
24	X	1.21	1/451 (0.2%)	0.90	0/606
25	Y	0.29	0/378	0.59	0/521
26	Z	1.12	0/366	0.96	0/489
27	1	0.45	0/395	0.55	0/530
28	2	1.35	0/371	1.00	0/484
29	3	1.12	0/526	0.85	0/690
30	4	0.72	0/298	0.73	0/392
31	a	0.30	0/36913	0.54	6/57564 (0.0%)
32	b	0.23	0/1846	0.59	2/2477 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.23	0/1523	0.60	0/2062
34	d	0.25	0/1526	0.67	1/2063 (0.0%)
35	e	0.25	0/1159	0.60	0/1566
36	f	0.26	0/789	0.65	0/1060
37	g	0.51	4/1176 (0.3%)	0.67	4/1588 (0.3%)
38	h	0.23	0/1038	0.56	0/1395
39	i	0.25	0/937	0.65	0/1269
40	j	0.23	0/764	0.60	0/1034
41	k	0.29	0/824	0.69	1/1119 (0.1%)
42	l	0.27	0/1054	0.57	0/1415
43	m	0.24	0/732	0.67	0/991
44	n	0.30	0/497	0.64	0/662
45	o	0.23	0/732	0.60	0/979
46	p	0.23	0/705	0.59	0/952
47	q	0.25	0/629	0.58	0/849
48	r	0.23	0/452	0.61	0/604
49	s	0.29	0/654	0.66	0/879
50	t	0.22	0/591	0.52	0/793
51	u	0.22	0/403	0.56	0/535
52	v	0.21	0/1350	0.56	0/1812
All	All	1.08	266/152898 (0.2%)	0.98	894/229036 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	15
5	E	0	3
9	I	0	1
11	K	0	1
13	M	0	1
16	P	0	2
19	S	0	1
23	W	0	1
26	Z	0	1
29	3	0	1
43	m	0	1
49	s	0	3
All	All	3	31

All (266) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	393	G	C1'-N9	77.54	2.64	1.48
1	A	332	A	N9-C8	58.30	2.54	1.37
1	A	332	A	N7-C5	57.70	2.54	1.39
1	A	332	A	C8-N7	55.93	2.43	1.31
1	A	332	A	N9-C4	54.45	2.46	1.37
1	A	332	A	C5-C4	47.16	2.33	1.38
1	A	393	G	N9-C4	12.70	1.63	1.38
37	g	87	VAL	CA-C	10.17	1.61	1.53
1	A	1029	C	P-O5'	9.33	1.73	1.59
1	A	1029	C	O5'-C5'	8.98	1.55	1.42
1	A	639	U	C3'-O3'	8.87	1.55	1.42
1	A	606	G	C2-N2	-8.66	1.17	1.34
1	A	707	G	O3'-P	8.64	1.74	1.61
1	A	2024	A	C5'-C4'	8.59	1.64	1.51
1	A	1017	A	C5-C6	-8.56	1.24	1.41
1	A	1029	C	C5'-C4'	8.53	1.64	1.51
1	A	1028	G	C3'-O3'	8.45	1.55	1.43
1	A	639	U	O3'-P	8.25	1.73	1.61
1	A	708	G	C5'-C4'	8.06	1.63	1.51
1	A	2024	A	O5'-C5'	8.04	1.54	1.42
1	A	707	G	C3'-O3'	8.02	1.54	1.42
1	A	2023	C	C3'-O3'	8.00	1.55	1.43
1	A	1034	A	N9-C8	-7.71	1.22	1.37
1	A	2094	G	N9-C4	7.54	1.53	1.38
1	A	1286	G	C5-C6	-7.52	1.27	1.42
1	A	640	G	O5'-C5'	7.49	1.53	1.42
1	A	990	G	C4'-C3'	-7.46	1.41	1.52
1	A	1027	A	N1-C2	-7.39	1.19	1.34
1	A	2064	A	O5'-C5'	7.36	1.53	1.42
1	A	1698	A	P-O5'	7.34	1.70	1.59
1	A	708	G	P-O5'	7.34	1.70	1.59
1	A	544	U	C2-O2	-7.31	1.07	1.22
1	A	2811	U	C3'-O3'	7.31	1.53	1.42
1	A	607	C	C2-O2	-7.29	1.09	1.24
1	A	2064	A	P-O5'	7.27	1.70	1.59
11	K	13	HIS	C-N	-7.26	1.10	1.33
1	A	2064	A	O3'-P	7.16	1.71	1.61
1	A	2024	A	P-O5'	7.15	1.70	1.59
1	A	668	C	C3'-O3'	7.13	1.52	1.42
37	g	132	GLY	C-O	-7.08	1.14	1.23
1	A	1286	G	C1'-N9	-7.08	1.36	1.47
1	A	2646	U	C3'-O3'	7.07	1.52	1.42
1	A	1295	C	C2-N3	-7.05	1.21	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	640	G	C5'-C4'	7.02	1.61	1.51
1	A	2077	C	O5'-C5'	6.95	1.52	1.42
1	A	607	C	N3-C4	-6.95	1.20	1.33
1	A	640	G	P-O5'	6.95	1.70	1.59
1	A	2077	C	P-O5'	6.93	1.70	1.59
1	A	1016	G	N7-C5	-6.92	1.25	1.39
1	A	668	C	O3'-P	6.91	1.71	1.61
1	A	708	G	O5'-C5'	6.88	1.52	1.42
1	A	1698	A	O5'-C5'	6.80	1.52	1.42
1	A	544	U	N3-C4	-6.77	1.25	1.38
1	A	2481	G	O3'-P	6.76	1.71	1.61
1	A	2064	A	C3'-O3'	6.74	1.52	1.42
1	A	2895	G	O5'-C5'	6.74	1.52	1.42
1	A	1016	G	C1'-N9	6.71	1.58	1.48
1	A	2894	C	C3'-O3'	6.70	1.52	1.42
1	A	2031	G	N1-C2	-6.69	1.24	1.37
1	A	2077	C	C5'-C4'	6.65	1.61	1.51
1	A	2647	C	O5'-C5'	6.63	1.52	1.42
1	A	2663	U	O5'-C5'	6.61	1.52	1.42
1	A	607	C	C2-N3	-6.61	1.22	1.35
1	A	606	G	C2-N3	-6.57	1.19	1.32
1	A	2064	A	C4'-C3'	6.55	1.62	1.52
1	A	1198	G	N7-C5	-6.54	1.26	1.39
1	A	2811	U	O3'-P	6.54	1.71	1.61
1	A	2065	G	C5-C6	-6.50	1.29	1.42
1	A	2894	C	O3'-P	6.49	1.70	1.61
1	A	488	G	C3'-O3'	6.47	1.52	1.43
1	A	2471	G	C5-C6	-6.46	1.29	1.42
1	A	2025	A	N9-C4	-6.46	1.25	1.37
1	A	2077	C	C4'-C3'	6.45	1.62	1.52
1	A	2597	G	N9-C8	-6.41	1.25	1.37
1	A	534	G	O3'-P	6.40	1.70	1.61
1	A	198	A	C6-N6	-6.38	1.21	1.33
1	A	363	A	C5-C6	-6.38	1.28	1.41
1	A	1029	C	C4'-C3'	6.38	1.62	1.52
1	A	2653	C	C1'-N1	6.37	1.58	1.48
1	A	2031	G	C2-N3	-6.36	1.20	1.32
24	X	14	GLY	C-N	-6.35	1.15	1.33
1	A	2704	A	N7-C5	-6.34	1.26	1.39
1	A	863	G	C5-C6	-6.34	1.29	1.42
1	A	2056	G	C6-N1	-6.33	1.26	1.39
1	A	2473	G	C2-N3	-6.33	1.20	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2868	G	C3'-O3'	6.32	1.51	1.42
1	A	2063	C	O3'-P	6.30	1.70	1.61
1	A	1228	A	C5-C6	-6.30	1.28	1.41
1	A	1010	G	C5-C6	-6.28	1.29	1.42
1	A	2812	U	O5'-C5'	6.28	1.51	1.42
1	A	606	G	N9-C4	-6.27	1.25	1.38
1	A	2647	C	C5'-C4'	6.22	1.60	1.51
1	A	1283	G	N9-C4	-6.20	1.25	1.38
1	A	488	G	O3'-P	6.19	1.70	1.61
1	A	2364	G	O5'-C5'	6.19	1.51	1.42
1	A	2481	G	N9-C4	6.16	1.50	1.38
1	A	2863	G	N9-C4	6.15	1.50	1.38
1	A	1046	G	C8-N7	-6.13	1.18	1.30
1	A	2668	A	N9-C4	6.12	1.50	1.37
1	A	1188	A	P-O5'	6.11	1.69	1.59
1	A	27	G	N9-C4	6.09	1.50	1.38
1	A	2597	G	C8-N7	-6.09	1.18	1.30
1	A	520	G	C2-N3	-6.08	1.20	1.32
1	A	626	G	C6-N1	-6.06	1.27	1.39
1	A	2642	U	N3-C4	-6.06	1.26	1.38
1	A	1187	A	C3'-O3'	6.04	1.51	1.42
1	A	1022	G	O3'-P	6.04	1.70	1.61
1	A	2080	G	C2-N3	-6.03	1.20	1.32
1	A	2471	G	C1'-N9	-6.03	1.39	1.48
1	A	1296	C	C2-O2	-6.02	1.12	1.24
1	A	2364	G	P-O5'	6.02	1.68	1.59
1	A	707	G	C5-C6	6.02	1.54	1.42
1	A	2868	G	O3'-P	6.02	1.70	1.61
1	A	1175	G	C1'-N9	-6.02	1.38	1.47
1	A	2023	C	O3'-P	6.01	1.70	1.61
1	A	2454	C	C1'-N1	5.99	1.57	1.48
1	A	620	G	C6-O6	-5.99	1.12	1.24
1	A	1179	C	P-OP2	-5.99	1.36	1.49
1	A	1236	G	C5-C6	-5.99	1.30	1.42
1	A	2895	G	C5'-C4'	5.98	1.60	1.51
1	A	2519	U	P-O5'	5.97	1.68	1.59
1	A	2546	U	C1'-N1	5.97	1.56	1.47
1	A	2664	U	P-O5'	5.96	1.68	1.59
1	A	1011	U	C4-C5	-5.94	1.31	1.43
1	A	1049	C	C1'-N1	5.94	1.57	1.48
1	A	2065	G	C5'-C4'	5.93	1.60	1.51
1	A	2568	A	C5-C6	-5.92	1.29	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2482	G	C4'-C3'	-5.89	1.43	1.52
1	A	2646	U	O3'-P	5.87	1.70	1.61
1	A	1027	A	N3-C4	-5.86	1.23	1.34
1	A	1697	G	O3'-P	5.86	1.70	1.61
1	A	2527	U	N3-C4	5.86	1.50	1.38
1	A	1698	A	C5'-C4'	5.82	1.59	1.51
1	A	378	C	C5'-C4'	5.77	1.59	1.51
1	A	1175	G	C5-C6	-5.76	1.30	1.42
1	A	2812	U	P-O5'	5.75	1.68	1.59
1	A	1020	G	C8-N7	-5.75	1.19	1.30
1	A	27	G	C1'-N9	5.74	1.55	1.47
1	A	2481	G	C3'-O3'	5.74	1.50	1.42
1	A	2856	U	N3-C4	-5.73	1.26	1.38
1	A	2094	G	C6-N1	-5.73	1.28	1.39
1	A	606	G	N3-C4	-5.72	1.24	1.35
1	A	378	C	P-O5'	5.72	1.68	1.59
1	A	1049	C	N1-C2	5.71	1.51	1.40
1	A	905	U	O3'-P	5.70	1.69	1.61
8	H	109	MET	C-N	-5.70	1.18	1.33
1	A	378	C	O5'-C5'	5.69	1.50	1.42
1	A	393	G	N9-C8	5.68	1.49	1.37
1	A	1198	G	N9-C8	-5.67	1.26	1.37
1	A	1269	A	C5-C6	-5.67	1.29	1.41
1	A	373	A	N9-C4	5.66	1.49	1.37
37	g	87	VAL	CA-CB	-5.64	1.47	1.53
1	A	2461	A	N7-C5	-5.64	1.27	1.39
1	A	2895	G	P-O5'	5.63	1.68	1.59
1	A	2047	A	N7-C5	-5.63	1.27	1.39
1	A	712	U	C2-N3	-5.62	1.26	1.37
1	A	1201	G	C5-C6	-5.62	1.31	1.42
1	A	241	C	O3'-P	5.60	1.69	1.61
1	A	1289	A	C3'-O3'	5.60	1.50	1.42
1	A	2664	U	C1'-N1	5.60	1.55	1.47
1	A	606	G	C6-N1	-5.58	1.28	1.39
1	A	1227	U	N3-C4	-5.58	1.27	1.38
1	A	612	U	C4-O4	-5.57	1.12	1.23
1	A	533	C	O3'-P	5.57	1.69	1.61
1	A	2457	A	C1'-N9	5.56	1.55	1.47
1	A	1188	A	O5'-C5'	5.56	1.50	1.42
1	A	2025	A	C5-C6	-5.53	1.29	1.41
1	A	2047	A	C5-C6	-5.53	1.29	1.41
1	A	582	G	P-O5'	5.53	1.68	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	954	A	C1'-N9	-5.52	1.39	1.48
1	A	907	G	C8-N7	-5.51	1.20	1.30
1	A	2473	G	C1'-N9	5.50	1.56	1.48
1	A	669	C	O5'-C5'	5.49	1.50	1.42
1	A	2646	U	C4'-C3'	5.49	1.60	1.52
1	A	622	A	C5-C6	-5.48	1.30	1.41
1	A	2382	C	O5'-C5'	5.46	1.50	1.42
1	A	669	C	P-O5'	5.46	1.68	1.59
1	A	2044	C	O3'-P	5.45	1.69	1.61
1	A	496	G	P-O5'	-5.44	1.51	1.59
1	A	2888	A	O5'-C5'	5.44	1.50	1.42
1	A	377	U	C3'-O3'	5.44	1.50	1.42
1	A	363	A	N7-C5	-5.42	1.28	1.39
1	A	1241	A	N7-C5	-5.42	1.28	1.39
1	A	1198	G	C2-N2	-5.41	1.23	1.34
1	A	1697	G	C3'-O3'	5.41	1.51	1.43
1	A	2056	G	C2-N2	-5.41	1.23	1.34
1	A	2757	U	C2-N3	-5.40	1.26	1.37
1	A	1050	C	C1'-N1	5.39	1.56	1.48
1	A	639	U	C4'-C3'	5.37	1.60	1.52
1	A	1014	U	C1'-N1	5.36	1.56	1.48
1	A	2544	C	C3'-O3'	5.36	1.50	1.42
1	A	2663	U	O3'-P	5.34	1.69	1.61
1	A	1308	C	C4-N4	-5.32	1.23	1.33
1	A	1705	G	C6-O6	-5.32	1.13	1.24
1	A	2544	C	O3'-P	5.32	1.69	1.61
1	A	70	G	N9-C8	-5.31	1.27	1.37
1	A	70	G	N7-C5	-5.31	1.28	1.39
1	A	612	U	C2-N3	-5.31	1.27	1.37
1	A	650	U	N3-C4	-5.30	1.27	1.38
1	A	1034	A	C1'-N9	-5.30	1.40	1.48
1	A	2887	G	N9-C4	5.30	1.48	1.38
1	A	632	U	N3-C4	-5.30	1.27	1.38
37	g	86	GLN	C-N	-5.29	1.28	1.33
1	A	547	A	C5-C6	-5.28	1.30	1.41
1	A	1028	G	O3'-P	5.28	1.69	1.61
1	A	242	U	C5'-C4'	5.27	1.59	1.51
1	A	1207	G	C5-C6	-5.26	1.31	1.42
1	A	2063	C	C3'-O3'	5.26	1.50	1.42
1	A	864	A	C6-N1	-5.25	1.25	1.35
1	A	1014	U	C4'-C3'	-5.25	1.44	1.52
1	A	2473	G	C5-C6	-5.25	1.31	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2597	G	N7-C5	-5.24	1.28	1.39
1	A	2419	A	P-O5'	5.24	1.67	1.59
1	A	905	U	C3'-O3'	5.24	1.50	1.42
1	A	2475	A	P-OP2	-5.23	1.38	1.49
1	A	2664	U	N1-C2	5.22	1.49	1.38
9	I	6	THR	CB-CG2	-5.21	1.35	1.52
1	A	1185	U	C1'-N1	5.20	1.55	1.47
1	A	990	G	C5-C6	-5.20	1.31	1.42
1	A	24	G	C2-N3	-5.19	1.22	1.32
1	A	669	C	C5'-C4'	5.19	1.59	1.51
1	A	2596	G	C2'-C1'	-5.18	1.45	1.53
1	A	643	G	C2-N2	-5.18	1.24	1.34
1	A	2284	U	N1-C2	5.18	1.49	1.38
1	A	2024	A	O3'-P	5.17	1.69	1.61
1	A	2663	U	C5'-C4'	5.17	1.59	1.51
1	A	2065	G	O5'-C5'	5.17	1.50	1.42
1	A	903	G	C6-O6	-5.17	1.13	1.24
1	A	1374	G	N7-C5	-5.16	1.28	1.39
1	A	2471	G	N9-C4	-5.16	1.27	1.38
1	A	595	G	C1'-N9	5.16	1.55	1.48
1	A	1018	A	N9-C4	-5.16	1.27	1.37
1	A	1174	U	C1'-N1	-5.15	1.40	1.48
1	A	1174	U	C2'-C1'	-5.14	1.45	1.53
1	A	1199	A	C1'-N9	5.13	1.55	1.48
1	A	868	A	C5-C6	-5.12	1.30	1.41
1	A	198	A	C6-N1	-5.12	1.25	1.35
1	A	608	C	C4'-C3'	-5.12	1.44	1.52
1	A	2542	C	N1-C2	5.12	1.50	1.40
1	A	1046	G	N7-C5	-5.11	1.29	1.39
1	A	2869	G	O5'-C5'	5.11	1.50	1.42
1	A	22	C	C4-C5	-5.10	1.32	1.43
1	A	883	C	P-O5'	-5.10	1.52	1.59
1	A	2551	G	N7-C5	-5.10	1.29	1.39
1	A	198	A	N1-C2	-5.10	1.24	1.34
1	A	2667	G	N3-C4	-5.10	1.25	1.35
1	A	1044	A	C1'-N9	5.09	1.55	1.48
1	A	2519	U	O5'-C5'	5.08	1.50	1.42
1	A	1014	U	C2-N3	5.08	1.48	1.37
1	A	1187	A	O3'-P	5.08	1.68	1.61
1	A	626	G	N9-C4	5.07	1.48	1.38
1	A	1288	G	N9-C4	5.04	1.48	1.38
1	A	533	C	C3'-O3'	5.04	1.49	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1804	U	N3-C4	-5.04	1.28	1.38
1	A	884	U	C4-C5	-5.03	1.33	1.43
1	A	640	G	C4'-C3'	5.03	1.60	1.52
1	A	2064	A	N1-C2	-5.03	1.24	1.34
1	A	1010	G	N9-C4	-5.02	1.27	1.38
1	A	1049	C	C4-C5	-5.02	1.32	1.43
1	A	2056	G	N7-C5	-5.02	1.29	1.39
1	A	1050	C	O3'-P	5.02	1.68	1.61
1	A	2046	U	C1'-N1	5.02	1.55	1.48
1	A	2080	G	C5-C4	-5.02	1.28	1.38
1	A	1015	C	C3'-O3'	5.01	1.49	1.42
1	A	1374	G	C6-N1	-5.01	1.29	1.39
1	A	17	G	C5-C6	-5.01	1.32	1.42

All (894) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	G	C8-N9-C4	-22.05	40.24	106.40
1	A	393	G	C5-N7-C8	-16.87	53.69	104.30
1	A	990	G	C5'-C4'-O4'	15.37	132.85	109.80
1	A	644	C	O4'-C1'-N1	12.94	127.91	108.50
1	A	393	G	N9-C1'-C2'	12.30	130.45	112.00
1	A	644	C	C5'-C4'-O4'	12.26	128.19	109.80
1	A	2525	C	C5'-C4'-O4'	11.74	127.42	109.80
37	g	87	VAL	CA-C-O	-11.53	112.35	119.15
1	A	627	C	O4'-C1'-N1	11.44	125.36	108.20
1	A	1049	C	C2-N1-C1'	11.42	153.05	118.80
1	A	1289	A	N9-C1'-C2'	11.41	129.11	112.00
1	A	393	G	C8-N9-C1'	11.19	160.56	127.00
1	A	1014	U	N1-C1'-C2'	11.18	128.77	112.00
1	A	650	U	N3-C2-O2	-11.07	88.98	122.20
1	A	1197	C	OP1-P-OP2	-10.96	86.73	119.60
1	A	534	G	C4'-C3'-O3'	10.94	129.41	113.00
1	A	393	G	C4-N9-C1'	10.90	159.20	126.50
1	A	634	C	O4'-C1'-N1	10.88	124.82	108.50
1	A	858	U	O5'-C5'-C4'	-10.74	95.39	111.50
1	A	1288	G	O4'-C1'-N9	10.70	124.25	108.20
1	A	557	G	O4'-C1'-N9	10.65	124.48	108.50
1	A	2672	G	N9-C1'-C2'	10.64	127.96	112.00
1	A	1197	C	O5'-P-OP2	10.58	139.75	108.00
1	A	2856	U	O4'-C1'-N1	10.49	124.23	108.50
1	A	770	G	OP1-P-O3'	-10.42	76.75	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2519	U	C4'-C3'-O3'	10.37	128.55	113.00
1	A	1028	G	C4'-C3'-O3'	10.31	124.87	109.40
1	A	1028	G	O3'-P-O5'	10.27	119.40	104.00
1	A	648	G	O4'-C1'-N9	10.17	123.75	108.50
1	A	2023	C	N1-C1'-C2'	10.07	129.11	114.00
1	A	366	G	N9-C1'-C2'	9.97	128.96	114.00
1	A	1241	A	O4'-C1'-N9	9.86	123.29	108.50
1	A	626	G	C4-N9-C1'	9.77	155.81	126.50
1	A	707	G	C4'-C3'-O3'	9.76	127.64	113.00
1	A	2043	U	C4'-C3'-O3'	9.69	127.54	113.00
1	A	2077	C	N1-C1'-C2'	9.62	126.42	112.00
1	A	2079	G	O5'-P-OP2	-9.56	79.31	108.00
1	A	650	U	N1-C1'-C2'	9.53	126.30	112.00
1	A	2662	U	C4'-C3'-O3'	9.53	127.29	113.00
1	A	2542	C	OP1-P-OP2	-9.46	91.22	119.60
1	A	1015	C	O4'-C1'-N1	9.42	122.63	108.50
31	a	745	U	OP1-P-O3'	-9.41	79.76	108.00
1	A	2397	G	O4'-C1'-N9	9.38	122.56	108.50
1	A	1022	G	C4'-C3'-O3'	9.34	127.00	113.00
1	A	1289	A	O4'-C1'-N9	9.31	122.46	108.50
1	A	639	U	O3'-P-O5'	9.30	117.95	104.00
1	A	896	U	O3'-P-O5'	9.18	117.77	104.00
1	A	1256	U	C4'-C3'-O3'	9.18	126.77	113.00
1	A	707	G	O3'-P-O5'	9.17	117.75	104.00
1	A	2672	G	O4'-C1'-N9	9.15	122.23	108.50
1	A	1369	G	C4-N9-C1'	9.14	153.93	126.50
1	A	1289	A	P-O3'-C3'	9.11	133.87	120.20
1	A	2482	G	O5'-P-OP1	-9.10	80.70	108.00
1	A	341	G	C4'-C3'-O3'	9.08	126.62	113.00
1	A	2481	G	P-O3'-C3'	9.07	133.81	120.20
1	A	561	C	C2-N1-C1'	9.06	145.98	118.80
1	A	2045	A	N9-C1'-C2'	9.05	127.57	114.00
1	A	607	C	N3-C4-N4	-9.05	90.86	118.00
1	A	1051	C	N1-C1'-C2'	9.04	125.56	112.00
1	A	2568	A	OP1-P-O3'	-9.04	80.88	108.00
1	A	2052	C	C4'-C3'-O3'	9.03	126.54	113.00
1	A	2664	U	O4'-C1'-N1	8.99	121.68	108.20
1	A	2379	A	OP1-P-OP2	-8.88	92.95	119.60
1	A	639	U	C4'-C3'-O3'	8.87	126.30	113.00
1	A	1014	U	C2-N1-C1'	8.87	144.30	117.70
1	A	2064	A	O3'-P-O5'	8.86	117.29	104.00
1	A	1028	G	OP1-P-O3'	-8.85	81.47	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	990	G	N9-C1'-C2'	-8.84	98.74	112.00
1	A	490	C	O4'-C1'-N1	8.82	121.44	108.20
1	A	860	U	O5'-C5'-C4'	-8.80	98.30	111.50
1	A	626	G	C8-N9-C1'	-8.73	100.80	127.00
1	A	1028	G	P-O3'-C3'	8.72	133.28	120.20
1	A	667	G	C5'-C4'-O4'	8.71	122.87	109.80
1	A	864	A	O4'-C1'-N9	8.69	121.54	108.50
1	A	587	C	O4'-C1'-N1	8.66	121.19	108.20
1	A	2042	A	O3'-P-O5'	8.63	116.95	104.00
1	A	2077	C	O4'-C1'-N1	8.60	121.40	108.50
1	A	2856	U	C4'-C3'-O3'	8.60	125.89	113.00
1	A	1199	A	O4'-C1'-N9	8.57	121.36	108.50
1	A	2663	U	C2'-C3'-O3'	-8.56	100.85	113.70
1	A	607	C	N3-C2-O2	-8.56	96.22	121.90
1	A	626	G	N1-C2-N2	-8.55	90.55	116.20
1	A	2024	A	C4'-C3'-O3'	8.49	125.74	113.00
1	A	2525	C	O5'-C5'-C4'	8.49	124.23	111.50
1	A	2543	G	OP1-P-OP2	-8.48	94.16	119.60
1	A	1034	A	O4'-C1'-N9	-8.48	95.78	108.50
1	A	1016	G	C4-N9-C1'	8.47	151.90	126.50
1	A	2482	G	O5'-P-OP2	-8.38	82.86	108.00
1	A	2454	C	O3'-P-O5'	8.36	116.55	104.00
1	A	1227	U	N3-C4-O4	-8.36	94.32	119.40
1	A	668	C	O3'-P-O5'	8.32	116.47	104.00
1	A	2894	C	O3'-P-O5'	8.27	116.40	104.00
1	A	1027	A	C4'-C3'-O3'	8.22	125.34	113.00
1	A	2655	U	N1-C1'-C2'	8.21	126.32	114.00
1	A	907	G	C4-N9-C1'	8.21	151.13	126.50
1	A	2481	G	C4-N9-C1'	8.15	150.95	126.50
1	A	1055	A	C2'-C3'-O3'	8.14	121.70	109.50
1	A	640	G	O5'-C5'-C4'	8.12	123.68	111.50
1	A	2894	C	C4'-C3'-O3'	8.11	125.17	113.00
1	A	1187	A	O3'-P-O5'	8.11	116.16	104.00
1	A	2898	U	N1-C1'-C2'	8.09	124.13	112.00
1	A	1036	C	O5'-P-OP1	-8.07	83.80	108.00
1	A	2663	U	O3'-P-O5'	8.05	116.08	104.00
1	A	987	U	C2'-C3'-O3'	8.05	125.77	113.70
1	A	2044	C	C2-N1-C1'	8.03	142.87	118.80
1	A	2486	A	C4-N9-C1'	8.01	150.33	126.30
1	A	2542	C	C2-N1-C1'	8.01	142.82	118.80
1	A	1019	A	O5'-P-OP1	-8.00	84.00	108.00
1	A	615	A	C2'-C3'-O3'	8.00	121.49	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1288	G	P-O3'-C3'	7.99	132.18	120.20
1	A	526	A	C4-N9-C1'	7.99	150.26	126.30
1	A	2419	A	C4'-C3'-O3'	7.96	124.94	113.00
1	A	1197	C	C2-N1-C1'	7.96	142.67	118.80
1	A	2418	G	N9-C1'-C2'	7.95	125.92	114.00
1	A	2646	U	O3'-P-O5'	7.90	115.85	104.00
1	A	1240	U	N1-C1'-C2'	7.89	125.84	114.00
1	A	1256	U	O3'-P-O5'	7.89	115.83	104.00
1	A	354	A	O3'-P-O5'	7.89	115.83	104.00
1	A	36	G	C2'-C3'-O3'	-7.88	101.87	113.70
1	A	474	A	O4'-C1'-N9	7.87	120.31	108.50
1	A	990	G	C4'-C3'-C2'	-7.87	94.73	102.60
1	A	2320	C	N1-C1'-C2'	7.86	123.79	112.00
1	A	2481	G	N1-C2-N2	-7.86	92.62	116.20
1	A	607	C	N1-C2-O2	7.85	142.45	118.90
1	A	650	U	O4'-C1'-N1	7.84	120.26	108.50
1	A	634	C	C5'-C4'-O4'	7.84	121.56	109.80
1	A	1029	C	O5'-C5'-C4'	7.83	123.25	111.50
1	A	2043	U	C5'-C4'-C3'	7.83	127.75	116.00
1	A	2363	A	O3'-P-O5'	7.80	115.70	104.00
1	A	1261	G	P-O3'-C3'	7.80	131.90	120.20
1	A	2031	G	N1-C6-O6	-7.78	96.56	119.90
1	A	2076	A	O3'-P-O5'	7.78	115.67	104.00
1	A	990	G	P-O5'-C5'	7.77	132.55	120.90
1	A	576	U	O4'-C1'-N1	7.75	119.82	108.20
1	A	650	U	C2-N1-C1'	7.72	140.85	117.70
1	A	393	G	N7-C8-N9	7.70	136.20	113.10
1	A	2523	C	O4'-C1'-N1	7.69	119.74	108.20
1	A	1042	C	O3'-P-O5'	7.68	115.53	104.00
1	A	905	U	OP2-P-O3'	7.66	130.98	108.00
1	A	2811	U	C4'-C3'-O3'	7.66	124.48	113.00
1	A	2585	C	N1-C1'-C2'	7.65	123.48	112.00
1	A	1228	A	C8-N9-C1'	-7.65	104.75	127.70
1	A	2805	A	C2'-C3'-O3'	7.65	120.98	109.50
1	A	2419	A	C5'-C4'-C3'	7.63	127.45	116.00
1	A	1057	A	O4'-C1'-N9	7.63	119.64	108.20
1	A	2647	C	O5'-C5'-C4'	7.61	122.92	111.50
1	A	1001	A	O4'-C1'-N9	7.61	119.62	108.20
1	A	893	G	N9-C1'-C2'	7.58	123.38	112.00
1	A	627	C	O5'-C5'-C4'	-7.58	100.34	111.70
1	A	2369	C	N1-C1'-C2'	7.56	123.34	112.00
1	A	1023	A	O4'-C4'-C3'	-7.56	96.44	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	627	C	C5'-C4'-O4'	7.54	120.41	109.10
1	A	2812	U	P-O5'-C5'	7.53	132.19	120.90
1	A	533	C	P-O3'-C3'	7.51	131.47	120.20
1	A	1034	A	OP1-P-O3'	7.50	130.49	108.00
1	A	488	G	C4'-C3'-O3'	7.48	120.62	109.40
1	A	640	G	P-O5'-C5'	7.46	132.10	120.90
1	A	2663	U	C4'-C3'-O3'	7.46	124.20	113.00
1	A	2053	U	N1-C1'-C2'	7.45	125.18	114.00
1	A	2668	A	OP2-P-O3'	7.45	130.33	108.00
1	A	2056	G	N1-C2-N2	-7.41	93.98	116.20
1	A	2379	A	O5'-P-OP1	7.39	130.17	108.00
1	A	1015	C	OP1-P-O3'	7.38	130.14	108.00
1	A	1049	C	C6-N1-C1'	-7.37	98.68	120.80
1	A	1057	A	P-O3'-C3'	7.36	131.25	120.20
1	A	905	U	P-O3'-C3'	7.31	131.16	120.20
1	A	2457	A	C4-N9-C1'	7.25	148.06	126.30
1	A	644	C	C1'-O4'-C4'	-7.22	102.68	109.90
1	A	1056	U	OP1-P-OP2	-7.21	97.97	119.60
1	A	1185	U	O5'-P-OP2	7.21	129.63	108.00
1	A	2023	C	O3'-P-O5'	7.21	114.81	104.00
1	A	669	C	P-O5'-C5'	7.20	131.69	120.90
1	A	2285	C	N3-C2-O2	-7.19	100.33	121.90
16	P	78	ARG	N-CA-C	7.17	118.88	111.14
34	d	34	GLY	N-CA-C	7.17	121.03	110.63
1	A	1046	G	C4'-C3'-O3'	7.17	123.75	113.00
1	A	883	C	O5'-C5'-C4'	-7.16	100.76	111.50
1	A	1251	A	C4'-C3'-C2'	-7.16	95.44	102.60
1	A	2811	U	O3'-P-O5'	7.15	114.73	104.00
1	A	1227	U	C4'-C3'-O3'	7.14	123.71	113.00
1	A	353	A	O4'-C1'-N9	7.13	119.19	108.50
1	A	621	A	O3'-P-O5'	7.11	114.67	104.00
1	A	2084	G	N9-C1'-C2'	7.09	124.63	114.00
1	A	1029	C	C4'-C3'-O3'	7.09	123.63	113.00
1	A	668	C	C4'-C3'-O3'	7.08	123.62	113.00
1	A	667	G	C4'-C3'-C2'	-7.08	95.52	102.60
1	A	600	U	P-O3'-C3'	7.08	130.81	120.20
1	A	626	G	C4'-C3'-O3'	7.06	123.59	113.00
1	A	867	U	C5'-C4'-O4'	-7.06	99.21	109.80
1	A	1174	U	O4'-C1'-N1	7.04	119.06	108.50
1	A	667	G	C5'-C4'-C3'	7.04	126.55	116.00
1	A	1036	C	O5'-C5'-C4'	-7.04	100.95	111.50
1	A	859	C	C4'-C3'-O3'	7.03	123.55	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2090	C	P-O3'-C3'	7.03	130.75	120.20
1	A	2381	A	O3'-P-O5'	7.03	114.54	104.00
1	A	1263	A	C3'-C2'-O2'	-7.00	104.11	114.60
1	A	1182	G	OP2-P-O3'	-6.99	87.02	108.00
1	A	897	A	O5'-P-OP1	-6.99	87.03	108.00
1	A	2023	C	P-O3'-C3'	6.98	130.67	120.20
1	A	2544	C	N1-C1'-C2'	-6.98	101.53	112.00
1	A	2543	G	P-O5'-C5'	6.97	131.36	120.90
1	A	1225	G	O5'-P-OP1	-6.97	87.09	108.00
1	A	576	U	N1-C1'-C2'	6.97	124.45	114.00
1	A	1029	C	O3'-P-O5'	6.96	114.44	104.00
1	A	2064	A	P-O5'-C5'	6.96	131.34	120.90
1	A	526	A	C8-N9-C1'	-6.96	106.83	127.70
1	A	2544	C	C4'-C3'-O3'	6.96	123.44	113.00
1	A	907	G	C6-C5-N7	-6.95	109.55	130.40
1	A	1023	A	C4'-C3'-O3'	6.95	123.42	113.00
1	A	497	U	O4'-C1'-N1	6.95	118.92	108.50
1	A	1297	G	C4-N9-C1'	6.93	147.31	126.50
1	A	621	A	C2'-C3'-O3'	-6.92	103.32	113.70
1	A	861	C	O5'-C5'-C4'	-6.91	101.14	111.50
1	A	1042	C	C4'-C3'-O3'	6.90	123.36	113.00
1	A	2077	C	O5'-C5'-C4'	6.90	121.85	111.50
1	A	2455	G	OP2-P-O3'	6.89	128.68	108.00
1	A	872	U	P-O3'-C3'	6.89	130.53	120.20
1	A	1044	A	OP2-P-O3'	6.88	128.65	108.00
1	A	2419	A	O3'-P-O5'	6.88	114.32	104.00
1	A	1050	C	C2'-C3'-O3'	6.88	124.01	113.70
1	A	226	A	OP1-P-O3'	6.87	128.62	108.00
1	A	1053	A	OP2-P-O3'	6.87	128.62	108.00
1	A	2543	G	C5'-C4'-C3'	6.86	126.30	116.00
1	A	2060	A	O4'-C1'-N9	6.86	118.48	108.20
1	A	1196	C	N1-C1'-C2'	6.85	122.27	112.00
1	A	1291	A	O5'-P-OP2	-6.85	87.46	108.00
1	A	2668	A	C4-N9-C1'	6.84	146.82	126.30
1	A	633	A	C4-N9-C1'	6.83	146.80	126.30
1	A	593	U	C2'-C3'-O3'	6.83	119.75	109.50
1	A	615	A	P-O3'-C3'	6.83	130.44	120.20
1	A	544	U	C6-N1-C2	-6.82	100.55	121.00
1	A	119	U	N1-C1'-C2'	6.81	124.21	114.00
1	A	467	U	N1-C1'-C2'	6.81	124.21	114.00
1	A	2065	G	O5'-C5'-C4'	6.81	121.71	111.50
1	A	28	A	O5'-P-OP2	-6.80	87.59	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1020	G	C4'-N9-C1'	6.80	146.90	126.50
1	A	495	A	O5'-P-OP2	-6.79	87.62	108.00
1	A	557	G	P-O5'-C5'	6.78	131.07	120.90
1	A	2868	G	C4'-C3'-O3'	6.78	123.17	113.00
1	A	2053	U	C4'-C3'-O3'	6.78	119.56	109.40
1	A	2887	G	O3'-P-O5'	6.77	114.16	104.00
1	A	368	A	C4'-N9-C1'	6.77	146.61	126.30
1	A	1013	U	C2'-C3'-O3'	6.77	123.85	113.70
1	A	1027	A	P-O3'-C3'	6.77	130.35	120.20
37	g	87	VAL	O-C-N	6.76	127.45	121.57
1	A	489	A	O4'-C1'-N9	6.74	118.61	108.50
1	A	1049	C	N1-C1'-C2'	6.73	122.10	112.00
1	A	1251	A	C4'-C3'-O3'	6.73	123.09	113.00
1	A	262	G	C5'-C4'-C3'	6.72	126.08	116.00
1	A	647	G	O3'-P-O5'	6.72	114.07	104.00
1	A	864	A	N1-C6-N6	-6.70	98.50	118.60
1	A	669	C	O5'-C5'-C4'	6.70	121.54	111.50
1	A	2569	A	C2'-C3'-O3'	6.69	119.54	109.50
1	A	521	U	N1-C1'-C2'	6.68	122.03	112.00
1	A	1035	C	N1-C1'-C2'	6.68	122.02	112.00
1	A	2056	G	P-O3'-C3'	-6.67	110.19	120.20
1	A	1188	A	C4'-C3'-O3'	6.67	123.00	113.00
1	A	2550	G	O4'-C1'-N9	6.65	118.18	108.20
1	A	2914	A	N9-C1'-C2'	6.65	121.98	112.00
1	A	2455	G	O5'-P-OP1	-6.65	88.06	108.00
31	a	745	U	OP2-P-O3'	-6.64	88.08	108.00
1	A	488	G	O3'-P-O5'	6.63	113.94	104.00
1	A	2830	A	O3'-P-O5'	6.62	113.93	104.00
1	A	1049	C	N1-C2-O2	6.62	138.76	118.90
1	A	1251	A	C2'-C3'-O3'	6.61	123.62	113.70
1	A	1188	A	O3'-P-O5'	6.59	113.89	104.00
1	A	1046	G	C4'-N9-C1'	6.59	146.27	126.50
1	A	2664	U	N1-C1'-C2'	6.58	123.88	114.00
1	A	1015	C	C1'-C2'-O2'	-6.58	98.52	108.40
1	A	2064	A	C5'-C4'-C3'	6.58	125.88	116.00
1	A	378	C	O5'-C5'-C4'	6.58	121.37	111.50
1	A	1003	A	OP2-P-O3'	-6.58	88.26	108.00
1	A	990	G	O4'-C1'-N9	6.58	118.36	108.50
1	A	1184	C	N1-C1'-C2'	6.58	121.86	112.00
1	A	872	U	C3'-C2'-O2'	6.57	120.56	110.70
1	A	704	U	N1-C1'-C2'	6.57	121.85	112.00
1	A	644	C	C4'-C3'-C2'	-6.56	96.04	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2804	G	O5'-P-OP1	6.55	127.64	108.00
1	A	1261	G	O5'-P-OP2	-6.54	88.37	108.00
1	A	1369	G	C8-N9-C1'	-6.54	107.38	127.00
1	A	2396	A	C4-N9-C1'	6.53	145.89	126.30
1	A	2064	A	C5'-C4'-O4'	-6.53	100.01	109.80
1	A	1367	C	O5'-C5'-C4'	6.53	121.29	111.50
1	A	2840	A	P-O3'-C3'	6.53	129.99	120.20
1	A	218	G	P-O3'-C3'	6.52	129.99	120.20
1	A	1057	A	C4'-C3'-O3'	6.52	119.19	109.40
1	A	1261	G	OP2-P-O3'	6.51	127.53	108.00
1	A	957	C	N1-C1'-C2'	6.51	121.77	112.00
1	A	2285	C	N1-C2-O2	6.51	138.43	118.90
1	A	650	U	N1-C2-O2	6.51	142.32	122.80
1	A	2052	C	N1-C1'-C2'	-6.50	102.25	112.00
1	A	1268	C	O3'-P-O5'	6.49	113.74	104.00
1	A	69	C	C5'-C4'-C3'	6.49	124.94	115.20
1	A	45	G	C4-N9-C1'	6.49	145.96	126.50
1	A	1364	C	N1-C1'-C2'	6.49	123.73	114.00
1	A	2646	U	C4'-C3'-O3'	6.49	122.73	113.00
1	A	708	G	O5'-C5'-C4'	6.49	121.23	111.50
1	A	2061	U	OP1-P-OP2	-6.48	100.16	119.60
1	A	990	G	C1'-O4'-C4'	-6.47	103.43	109.90
1	A	1016	G	N7-C8-N9	6.46	132.49	113.10
19	S	103	SER	N-CA-C	-6.46	106.36	114.56
1	A	2094	G	C4-N9-C1'	6.46	145.87	126.50
1	A	1185	U	O5'-P-OP1	-6.45	88.66	108.00
1	A	242	U	O4'-C1'-N1	6.44	118.17	108.50
1	A	1043	U	C4'-C3'-O3'	6.44	122.66	113.00
1	A	2454	C	N1-C1'-C2'	6.44	121.65	112.00
1	A	2886	G	P-O3'-C3'	6.44	129.85	120.20
1	A	1268	C	C4'-C3'-O3'	6.43	122.65	113.00
1	A	639	U	C5'-C4'-O4'	-6.43	100.15	109.80
1	A	2082	C	OP1-P-O3'	-6.42	88.72	108.00
1	A	2797	C	C4'-C3'-O3'	6.41	122.62	113.00
1	A	2595	C	O4'-C1'-N1	6.39	118.09	108.50
1	A	634	C	C1'-O4'-C4'	-6.39	103.51	109.90
1	A	1274	G	O4'-C1'-N9	6.38	117.77	108.20
1	A	1020	G	C8-N9-C1'	-6.38	107.87	127.00
1	A	2486	A	O5'-P-OP2	-6.38	88.86	108.00
1	A	884	U	OP1-P-OP2	-6.37	100.50	119.60
1	A	1228	A	N9-C1'-C2'	-6.37	102.45	112.00
1	A	607	C	C5-C4-N4	6.36	139.26	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1019	A	OP2-P-O3'	6.36	127.06	108.00
1	A	2094	G	O5'-P-OP2	-6.36	88.93	108.00
1	A	2474	G	OP2-P-O3'	-6.35	88.94	108.00
1	A	961	G	N9-C1'-C2'	6.35	121.52	112.00
1	A	36	G	C5'-C4'-C3'	6.33	125.49	116.00
1	A	991	A	OP1-P-OP2	-6.33	100.61	119.60
1	A	2597	G	C4-N9-C1'	6.33	145.48	126.50
1	A	2914	A	C4-N9-C1'	6.32	145.26	126.30
1	A	1235	C	C2-N1-C1'	6.32	137.76	118.80
1	A	2525	C	P-O5'-C5'	-6.32	111.42	120.90
1	A	1016	G	C8-N9-C4	-6.32	87.45	106.40
1	A	198	A	N1-C6-N6	-6.31	99.67	118.60
1	A	2594	G	O4'-C1'-N9	6.31	117.97	108.50
1	A	626	G	N3-C2-N2	6.30	138.79	119.90
1	A	445	G	N9-C1'-C2'	6.29	121.44	112.00
1	A	872	U	P-O5'-C5'	6.28	130.32	120.90
1	A	1162	C	C5'-C4'-O4'	6.28	118.52	109.10
1	A	2523	C	N1-C1'-C2'	6.28	123.42	114.00
1	A	594	G	P-O3'-C3'	6.27	129.61	120.20
1	A	2024	A	O3'-P-O5'	6.27	113.41	104.00
1	A	535	G	O3'-P-O5'	6.27	113.40	104.00
1	A	872	U	O4'-C1'-N1	6.26	117.90	108.50
1	A	2895	G	O5'-C5'-C4'	6.26	120.89	111.50
1	A	344	U	N1-C1'-C2'	6.26	123.39	114.00
1	A	2661	A	O3'-P-O5'	6.26	113.39	104.00
1	A	1302	G	OP1-P-O3'	6.25	126.75	108.00
1	A	2863	G	C4-N9-C1'	6.25	145.25	126.50
1	A	1181	G	C4'-C3'-C2'	-6.25	96.35	102.60
1	A	1224	U	P-O3'-C3'	6.24	129.56	120.20
1	A	534	G	O3'-P-O5'	6.24	113.36	104.00
1	A	45	G	N9-C1'-C2'	6.24	123.36	114.00
1	A	650	U	C5'-C4'-O4'	6.24	119.16	109.80
1	A	1035	C	P-O5'-C5'	-6.23	111.56	120.90
1	A	496	G	C4'-C3'-O3'	6.23	122.34	113.00
1	A	69	C	C5'-C4'-O4'	6.22	118.43	109.10
1	A	2803	A	C8-N9-C1'	-6.22	109.04	127.70
1	A	2094	G	O4'-C1'-N9	6.22	117.53	108.20
1	A	557	G	C2'-C3'-O3'	-6.21	104.39	113.70
1	A	2525	C	N3-C2-O2	-6.21	103.27	121.90
1	A	576	U	P-O3'-C3'	6.20	129.50	120.20
1	A	583	A	C5'-C4'-C3'	6.20	125.29	116.00
1	A	700	A	O4'-C1'-N9	6.20	117.49	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1062	U	C4'-C3'-O3'	6.20	122.29	113.00
1	A	1302	G	OP2-P-O3'	-6.19	89.43	108.00
1	A	2042	A	OP1-P-O3'	-6.19	89.43	108.00
1	A	2024	A	O5'-C5'-C4'	6.18	120.77	111.50
1	A	866	A	OP1-P-O3'	-6.18	89.47	108.00
1	A	2473	G	C8-N9-C1'	6.17	145.51	127.00
1	A	2486	A	O5'-P-OP1	6.17	126.51	108.00
1	A	1274	G	C4-N9-C1'	6.17	145.00	126.50
1	A	713	A	P-O3'-C3'	6.17	129.45	120.20
1	A	2797	C	P-O3'-C3'	6.17	129.45	120.20
1	A	864	A	C8-N9-C1'	6.17	146.19	127.70
1	A	2082	C	C2'-C3'-O3'	6.16	122.95	113.70
1	A	627	C	P-O5'-C5'	6.16	130.14	120.90
1	A	857	C	OP1-P-OP2	-6.16	101.12	119.60
8	H	11	ASN	N-CA-C	-6.16	106.99	114.75
1	A	1016	G	O5'-P-OP1	-6.16	89.53	108.00
1	A	2516	G	O4'-C1'-N9	6.15	117.43	108.20
1	A	373	A	C4-N9-C1'	6.15	144.75	126.30
1	A	2083	G	C4-N9-C1'	6.15	144.94	126.50
1	A	2364	G	O3'-P-O5'	6.15	113.22	104.00
1	A	2863	G	C8-N9-C1'	-6.13	108.62	127.00
1	A	1228	A	O4'-C1'-N9	6.12	117.68	108.50
1	A	547	A	O3'-P-O5'	6.12	113.18	104.00
1	A	1228	A	C4-N9-C1'	6.12	144.65	126.30
1	A	2868	G	C5'-C4'-O4'	-6.12	100.62	109.80
1	A	300	G	O5'-P-OP1	-6.11	89.67	108.00
1	A	893	G	C4'-C3'-O3'	6.11	122.17	113.00
1	A	2803	A	C4-N9-C1'	6.11	144.62	126.30
1	A	1030	C	O5'-C5'-C4'	6.10	120.66	111.50
1	A	1198	G	C4-N9-C1'	6.10	144.80	126.50
1	A	1263	A	OP1-P-O3'	-6.09	89.72	108.00
1	A	1289	A	C3'-C2'-O2'	6.09	119.84	110.70
1	A	125	A	N9-C1'-C2'	6.09	121.14	112.00
1	A	557	G	C1'-C2'-O2'	6.09	117.53	108.40
1	A	1020	G	C6-C5-N7	-6.08	112.15	130.40
1	A	2899	A	N9-C1'-C2'	6.07	123.11	114.00
1	A	599	A	OP2-P-O3'	-6.07	89.79	108.00
1	A	2090	C	C4'-C3'-O3'	6.07	122.10	113.00
1	A	1297	G	C8-N9-C1'	-6.06	108.81	127.00
1	A	1188	A	O5'-C5'-C4'	6.06	120.58	111.50
1	A	2479	C	P-O5'-C5'	6.06	129.98	120.90
1	A	2419	A	P-O5'-C5'	6.05	129.97	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1182	G	O3'-P-O5'	6.04	113.06	104.00
1	A	1697	G	C4'-C3'-O3'	6.04	118.46	109.40
1	A	393	G	O4'-C1'-N9	6.03	117.54	108.50
1	A	1264	A	O5'-P-OP2	-6.03	89.92	108.00
1	A	1184	C	O3'-P-O5'	6.03	113.04	104.00
1	A	1006	G	O5'-C5'-C4'	6.02	120.53	111.50
1	A	2056	G	C4'-C3'-C2'	6.02	108.62	102.60
1	A	908	A	C4-N9-C1'	6.02	144.35	126.30
1	A	36	G	O3'-P-O5'	6.01	113.02	104.00
1	A	1026	C	O3'-P-O5'	6.01	113.02	104.00
41	k	120	GLY	N-CA-C	6.01	119.47	112.50
1	A	262	G	N9-C1'-C2'	-6.01	102.99	112.00
1	A	2544	C	C3'-C2'-C1'	6.01	107.31	101.30
1	A	1054	A	C2'-C3'-O3'	6.01	122.71	113.70
16	P	78	ARG	CA-C-N	-6.01	111.57	122.50
16	P	78	ARG	C-N-CA	-6.01	111.57	122.50
1	A	242	U	O5'-P-OP2	-5.99	90.03	108.00
4	D	123	LYS	N-CA-C	5.99	117.50	110.97
1	A	668	C	C5'-C4'-O4'	-5.99	100.82	109.80
1	A	1046	G	C6-C5-N7	-5.98	112.45	130.40
1	A	2480	A	O4'-C1'-N9	5.98	117.17	108.20
1	A	1014	U	N3-C4-O4	5.98	137.34	119.40
1	A	708	G	P-O5'-C5'	5.97	129.86	120.90
1	A	344	U	C6-N1-C1'	5.97	139.11	121.20
1	A	2863	G	N9-C1'-C2'	5.97	120.95	112.00
1	A	2453	A	P-O3'-C3'	5.97	129.15	120.20
1	A	2851	G	C5'-C4'-C3'	-5.97	107.05	116.00
16	P	80	LYS	CA-C-N	-5.96	113.59	123.37
16	P	80	LYS	C-N-CA	-5.96	113.59	123.37
1	A	999	U	N3-C2-O2	-5.96	104.32	122.20
8	H	3	GLN	N-CA-C	5.96	119.42	108.58
1	A	1043	U	O5'-P-OP2	-5.95	90.14	108.00
1	A	2542	C	N3-C2-O2	-5.95	104.04	121.90
1	A	2868	G	O3'-P-O5'	5.95	112.93	104.00
1	A	1185	U	OP1-P-OP2	-5.95	101.76	119.60
1	A	2455	G	C5'-C4'-C3'	5.94	124.11	115.20
1	A	2295	A	C5'-C4'-C3'	5.94	124.11	115.20
1	A	1275	A	N9-C1'-C2'	5.94	122.91	114.00
1	A	52	A	N9-C1'-C2'	5.93	120.89	112.00
1	A	2520	U	N3-C2-O2	-5.93	104.41	122.20
1	A	1001	A	P-O3'-C3'	5.93	129.09	120.20
1	A	2043	U	O5'-C5'-C4'	5.93	120.39	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	600	U	C5'-C4'-C3'	5.90	124.05	115.20
1	A	994	A	N9-C1'-C2'	-5.89	103.16	112.00
1	A	1197	C	N1-C1'-C2'	5.89	120.84	112.00
1	A	607	C	C4'-C3'-O3'	5.89	121.83	113.00
1	A	707	G	N1-C6-O6	-5.88	102.27	119.90
1	A	496	G	C4-N9-C1'	5.87	144.12	126.50
1	A	2568	A	C5-C6-N6	-5.87	106.08	123.70
1	A	2093	C	C2-N1-C1'	-5.87	101.19	118.80
1	A	1016	G	N9-C1'-C2'	5.87	120.80	112.00
1	A	1046	G	O5'-P-OP2	5.86	125.58	108.00
1	A	2642	U	N3-C2-O2	-5.86	104.62	122.20
1	A	521	U	C2-N1-C1'	5.86	135.26	117.70
1	A	1045	A	O5'-P-OP2	-5.86	90.43	108.00
1	A	2869	G	P-O3'-C3'	5.85	128.98	120.20
1	A	1035	C	C4'-C3'-O3'	5.84	121.75	113.00
2	B	6	U	C4'-C3'-O3'	5.83	121.75	113.00
1	A	2664	U	N3-C2-O2	-5.83	104.72	122.20
1	A	368	A	C8-N9-C1'	-5.83	110.22	127.70
1	A	2065	G	O5'-P-OP1	-5.83	90.52	108.00
1	A	2481	G	C8-N9-C1'	-5.83	109.53	127.00
1	A	1051	C	O5'-P-OP2	-5.82	90.55	108.00
1	A	2914	A	C8-N9-C1'	-5.82	110.25	127.70
1	A	1049	C	N3-C4-N4	5.81	135.43	118.00
1	A	354	A	C4-N9-C1'	5.81	143.72	126.30
1	A	595	G	C5'-C4'-O4'	5.81	118.51	109.80
1	A	377	U	O3'-P-O5'	5.80	112.70	104.00
1	A	858	U	O4'-C1'-N1	5.80	117.20	108.50
1	A	896	U	P-O3'-C3'	5.80	128.90	120.20
1	A	2704	A	C4-N9-C1'	5.80	143.70	126.30
1	A	1299	U	N3-C2-O2	-5.80	104.81	122.20
1	A	1302	G	P-O3'-C3'	5.80	128.90	120.20
1	A	2044	C	OP2-P-O3'	5.80	125.39	108.00
1	A	906	A	OP1-P-OP2	-5.79	102.22	119.60
1	A	858	U	C1'-O4'-C4'	-5.79	104.11	109.90
1	A	1230	G	C4-N9-C1'	5.79	143.85	126.50
1	A	2482	G	O3'-P-O5'	-5.78	95.33	104.00
1	A	1274	G	N9-C1'-C2'	5.78	122.67	114.00
1	A	497	U	C1'-O4'-C4'	-5.78	104.12	109.90
1	A	857	C	O3'-P-O5'	-5.78	95.34	104.00
1	A	995	U	P-O3'-C3'	5.77	128.86	120.20
1	A	1362	C	OP1-P-O3'	-5.77	90.69	108.00
1	A	2460	A	C5-C6-N6	-5.77	106.39	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1301	U	C2-N1-C1'	5.77	135.00	117.70
1	A	905	U	N1-C1'-C2'	5.77	120.65	112.00
1	A	2063	C	N1-C1'-C2'	5.76	120.65	112.00
1	A	489	A	C5'-C4'-C3'	5.76	124.64	116.00
1	A	667	G	O5'-C5'-C4'	-5.75	102.88	111.50
1	A	1363	U	C5'-C4'-C3'	5.74	124.61	116.00
1	A	2473	G	O4'-C1'-N9	5.74	117.12	108.50
1	A	583	A	O3'-P-O5'	5.74	112.61	104.00
1	A	1072	A	C4-N9-C1'	5.74	143.52	126.30
1	A	2056	G	C4-N9-C1'	5.74	143.72	126.50
32	b	20	THR	CA-C-N	5.74	132.50	121.54
32	b	20	THR	C-N-CA	5.74	132.50	121.54
1	A	467	U	C5'-C4'-C3'	5.74	123.81	115.20
1	A	1298	G	C5'-C4'-O4'	5.73	118.40	109.80
1	A	200	A	OP2-P-O3'	-5.73	90.82	108.00
1	A	650	U	OP1-P-OP2	-5.73	102.42	119.60
1	A	2812	U	O5'-C5'-C4'	5.72	120.09	111.50
1	A	907	G	C8-N9-C1'	-5.72	109.83	127.00
1	A	503	A	O4'-C1'-N9	5.72	116.78	108.20
1	A	2830	A	C4'-C3'-O3'	5.72	121.58	113.00
1	A	2474	G	OP1-P-O3'	5.72	125.15	108.00
1	A	1174	U	C1'-O4'-C4'	-5.71	104.19	109.90
1	A	2516	G	C5'-C4'-O4'	5.71	117.67	109.10
1	A	1033	G	N9-C1'-C2'	5.71	122.57	114.00
1	A	616	G	C4'-C3'-O3'	-5.71	100.84	109.40
1	A	500	A	C4-N9-C1'	5.70	143.40	126.30
1	A	1015	C	C4'-C3'-O3'	5.70	121.54	113.00
1	A	1174	U	O4'-C1'-C2'	-5.70	101.91	107.60
1	A	1287	U	C2-N1-C1'	5.70	134.78	117.70
1	A	1286	G	C1'-O4'-C4'	-5.69	104.01	109.70
1	A	497	U	C5'-C4'-O4'	5.69	118.34	109.80
1	A	45	G	C8-N9-C1'	-5.69	109.93	127.00
1	A	2295	A	O4'-C1'-N9	5.69	116.73	108.20
1	A	241	C	C2-N1-C1'	5.68	135.85	118.80
1	A	1049	C	N3-C2-O2	-5.68	104.84	121.90
1	A	582	G	O5'-C5'-C4'	5.68	120.22	111.70
1	A	2549	U	OP2-P-O3'	5.68	125.05	108.00
1	A	1031	C	O4'-C1'-N1	5.68	117.02	108.50
1	A	2523	C	O5'-C5'-C4'	-5.68	103.18	111.70
1	A	627	C	O3'-P-O5'	5.68	112.52	104.00
1	A	2830	A	O5'-C5'-C4'	5.68	120.02	111.50
1	A	2523	C	C1'-O4'-C4'	-5.67	104.03	109.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	708	G	C5'-C4'-C3'	5.67	124.51	116.00
1	A	1073	A	C4-N9-C1'	5.67	143.30	126.30
1	A	2812	U	O5'-P-OP1	5.67	125.00	108.00
1	A	2653	C	N1-C1'-C2'	5.66	120.49	112.00
1	A	2036	G	C4'-C3'-O3'	-5.65	104.52	113.00
1	A	893	G	C2'-C3'-O3'	5.65	122.18	113.70
1	A	65	A	O3'-P-O5'	5.65	112.47	104.00
1	A	1369	G	O3'-P-O5'	5.65	112.48	104.00
1	A	2295	A	C5'-C4'-O4'	5.65	117.58	109.10
1	A	492	G	OP1-P-O3'	5.64	124.93	108.00
1	A	2594	G	O3'-P-O5'	5.64	112.46	104.00
1	A	987	U	P-O3'-C3'	5.64	128.66	120.20
9	I	64	ARG	CA-C-N	-5.64	112.96	123.05
9	I	64	ARG	C-N-CA	-5.64	112.96	123.05
1	A	458	A	O3'-P-O5'	5.63	112.45	104.00
1	A	2370	U	N1-C1'-C2'	5.63	120.45	112.00
1	A	593	U	C5'-C4'-O4'	5.63	117.55	109.10
1	A	2887	G	N9-C1'-C2'	5.63	122.44	114.00
1	A	201	C	N1-C1'-C2'	5.63	122.44	114.00
1	A	561	C	N3-C4-N4	5.63	134.88	118.00
1	A	1034	A	N9-C1'-C2'	5.63	120.44	112.00
1	A	1063	U	N1-C1'-C2'	5.62	120.44	112.00
1	A	608	C	P-O5'-C5'	5.62	129.33	120.90
1	A	1295	C	N3-C2-O2	-5.62	105.03	121.90
1	A	2516	G	C1'-O4'-C4'	-5.61	104.09	109.70
1	A	1263	A	OP2-P-O3'	5.61	124.83	108.00
1	A	1035	C	O4'-C1'-N1	5.61	116.91	108.50
1	A	2703	C	C5'-C4'-O4'	5.61	117.51	109.10
5	E	103	LYS	CA-C-N	-5.60	113.86	122.60
5	E	103	LYS	C-N-CA	-5.60	113.86	122.60
1	A	1369	G	C4'-C3'-O3'	5.60	117.80	109.40
1	A	419	U	N1-C1'-C2'	5.60	122.40	114.00
1	A	242	U	O5'-C5'-C4'	5.60	119.89	111.50
1	A	622	A	O5'-C5'-C4'	5.59	119.89	111.50
1	A	459	C	O5'-C5'-C4'	5.59	119.89	111.50
1	A	1044	A	C4-N9-C1'	5.59	143.07	126.30
1	A	2090	C	O5'-C5'-C4'	5.59	119.89	111.50
1	A	151	U	O5'-C5'-C4'	5.59	119.88	111.50
1	A	1054	A	C4'-C3'-O3'	5.58	121.38	113.00
1	A	1002	U	O4'-C1'-N1	5.58	116.87	108.50
1	A	2363	A	C4'-C3'-O3'	5.58	117.77	109.40
1	A	608	C	C5'-C4'-O4'	5.57	118.16	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	558	A	O5'-P-OP1	5.57	124.71	108.00
1	A	2044	C	P-O3'-C3'	5.57	128.56	120.20
1	A	2802	A	N9-C1'-C2'	5.57	120.35	112.00
1	A	605	U	O3'-P-O5'	5.57	112.35	104.00
1	A	2024	A	C2'-C3'-O3'	-5.56	105.36	113.70
1	A	27	G	N9-C1'-C2'	5.56	122.34	114.00
1	A	555	C	C4'-C3'-C2'	-5.56	97.04	102.60
1	A	554	C	C4'-C3'-O3'	5.56	121.33	113.00
1	A	1022	G	O5'-P-OP2	5.55	124.66	108.00
1	A	241	C	C4'-C3'-O3'	5.55	121.32	113.00
1	A	2061	U	O4'-C1'-N1	5.54	116.51	108.20
1	A	2443	C	C2-N1-C1'	5.54	135.43	118.80
1	A	1073	A	N9-C1'-C2'	5.54	120.30	112.00
1	A	2527	U	C4'-C3'-O3'	5.54	121.30	113.00
1	A	2856	U	P-O3'-C3'	5.54	128.50	120.20
1	A	1363	U	C3'-C2'-O2'	5.53	119.00	110.70
1	A	1181	G	C5'-C4'-C3'	5.53	124.29	116.00
1	A	2043	U	O5'-P-OP1	-5.53	91.42	108.00
1	A	2397	G	C1'-O4'-C4'	-5.53	104.38	109.90
1	A	1023	A	O4'-C1'-N9	5.52	116.78	108.50
6	F	144	ASP	N-CA-C	-5.52	107.55	114.56
1	A	495	A	P-O3'-C3'	-5.52	111.92	120.20
1	A	2455	G	O5'-C5'-C4'	5.52	119.98	111.70
1	A	1257	G	O5'-P-OP2	-5.52	91.45	108.00
1	A	36	G	C3'-C2'-O2'	-5.51	102.43	110.70
1	A	2811	U	C5'-C4'-O4'	-5.51	101.53	109.80
1	A	1251	A	O4'-C4'-C3'	-5.51	98.49	104.00
1	A	770	G	OP2-P-O3'	-5.50	91.50	108.00
1	A	1698	A	P-O5'-C5'	5.50	129.15	120.90
1	A	2396	A	C8-N9-C1'	-5.50	111.20	127.70
1	A	37	C	C2-N1-C1'	5.50	135.30	118.80
1	A	2046	U	N1-C1'-C2'	5.50	120.25	112.00
1	A	496	G	O4'-C4'-C3'	-5.49	98.51	104.00
1	A	1015	C	N3-C2-O2	-5.49	105.43	121.90
1	A	381	G	N9-C1'-C2'	5.49	120.23	112.00
1	A	2044	C	C2'-C3'-O3'	5.49	117.73	109.50
1	A	996	G	N9-C1'-C2'	5.49	120.23	112.00
1	A	381	G	C4-N9-C1'	5.49	142.96	126.50
1	A	703	A	P-O5'-C5'	5.48	129.13	120.90
1	A	1366	U	O3'-P-O5'	5.48	112.22	104.00
1	A	640	G	C4'-C3'-O3'	5.48	121.22	113.00
1	A	52	A	O3'-P-O5'	5.48	112.22	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1241	A	N9-C1'-C2'	-5.48	103.78	112.00
1	A	860	U	C4'-C3'-O3'	5.47	121.21	113.00
1	A	872	U	C5'-C4'-C3'	5.47	124.21	116.00
1	A	1258	A	OP2-P-O3'	5.47	124.40	108.00
1	A	860	U	C2'-C3'-O3'	5.46	121.89	113.70
1	A	2093	C	C6-N1-C1'	5.45	137.16	120.80
1	A	627	C	P-O3'-C3'	5.45	128.38	120.20
1	A	903	G	N1-C6-O6	-5.45	103.55	119.90
1	A	1051	C	C3'-C2'-O2'	-5.45	102.52	110.70
1	A	668	C	N3-C2-O2	-5.45	105.56	121.90
1	A	2031	G	C8-N9-C1'	5.44	143.32	127.00
1	A	583	A	C2'-C3'-O3'	-5.44	105.54	113.70
1	A	644	C	C5'-C4'-C3'	5.44	124.16	116.00
1	A	1027	A	N1-C6-N6	-5.44	102.28	118.60
1	A	544	U	C4'-C3'-O3'	5.44	121.15	113.00
1	A	2888	A	C5'-C4'-C3'	5.43	124.15	116.00
1	A	620	G	N1-C6-O6	-5.43	103.61	119.90
1	A	1062	U	OP1-P-O3'	5.43	124.29	108.00
8	H	58	ILE	CA-C-N	-5.43	111.87	121.81
8	H	58	ILE	C-N-CA	-5.43	111.87	121.81
1	A	2812	U	C4'-C3'-O3'	5.43	121.14	113.00
1	A	36	G	C4'-C3'-O3'	5.43	121.14	113.00
1	A	241	C	O3'-P-O5'	5.43	112.14	104.00
1	A	867	U	O3'-P-O5'	5.43	112.14	104.00
1	A	1162	C	O4'-C1'-N1	5.43	116.34	108.20
1	A	1698	A	C5'-C4'-C3'	5.42	124.14	116.00
1	A	2485	U	C2'-C3'-O3'	-5.42	105.57	113.70
1	A	1269	A	O3'-P-O5'	5.42	112.12	104.00
1	A	480	U	C6-N1-C1'	5.41	137.44	121.20
1	A	489	A	O4'-C4'-C3'	-5.41	98.59	104.00
1	A	1016	G	N3-C4-C5	-5.41	112.36	128.60
1	A	2083	G	O5'-C5'-C4'	5.41	119.62	111.50
1	A	496	G	C3'-C2'-C1'	-5.41	95.89	101.30
1	A	721	A	O4'-C1'-N9	5.41	116.61	108.50
1	A	2094	G	OP1-P-O3'	5.41	124.23	108.00
1	A	978	A	C3'-C2'-O2'	5.41	118.81	110.70
1	A	2544	C	O3'-P-O5'	5.41	112.11	104.00
1	A	874	A	O5'-P-OP1	-5.41	91.78	108.00
1	A	2595	C	P-O5'-C5'	5.41	129.01	120.90
1	A	907	G	N3-C4-N9	5.40	142.21	126.00
1	A	2594	G	C4'-C3'-O3'	5.40	121.10	113.00
1	A	1286	G	C5-C6-O6	-5.40	112.41	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2364	G	O5'-C5'-C4'	5.39	119.59	111.50
1	A	805	G	OP1-P-O3'	5.39	124.18	108.00
1	A	908	A	C8-N9-C1'	-5.39	111.52	127.70
1	A	2543	G	C5'-C4'-O4'	5.39	117.89	109.80
1	A	2663	U	C5'-C4'-C3'	5.39	124.09	116.00
1	A	1056	U	O5'-P-OP1	5.39	124.17	108.00
1	A	892	U	C2-N1-C1'	-5.39	101.54	117.70
1	A	666	A	C3'-C2'-O2'	-5.38	102.62	110.70
1	A	1017	A	C5-N7-C8	-5.38	87.75	103.90
1	A	1029	C	P-O5'-C5'	5.38	128.98	120.90
1	A	1251	A	O4'-C1'-N9	5.38	116.58	108.50
1	A	2023	C	C4'-C3'-C2'	-5.38	97.22	102.60
1	A	2453	A	OP2-P-O3'	5.38	124.15	108.00
1	A	1197	C	P-O5'-C5'	5.38	128.97	120.90
1	A	262	G	C4'-C3'-O3'	5.38	121.07	113.00
1	A	2364	G	C4'-C3'-O3'	5.38	121.06	113.00
1	A	2047	A	C4-N9-C1'	5.37	142.42	126.30
1	A	2518	U	O3'-P-O5'	5.37	112.06	104.00
1	A	2593	A	N9-C1'-C2'	5.37	122.06	114.00
1	A	49	A	OP1-P-OP2	-5.37	103.49	119.60
1	A	1049	C	C5-C4-N4	-5.37	104.11	120.20
1	A	1168	C	O3'-P-O5'	5.37	112.05	104.00
1	A	2478	A	P-O3'-C3'	5.36	128.25	120.20
1	A	2643	C	N1-C2-O2	5.36	134.99	118.90
1	A	1056	U	O5'-P-OP2	-5.36	91.92	108.00
1	A	497	U	O5'-C5'-C4'	5.36	119.54	111.50
1	A	500	A	P-O3'-C3'	5.36	128.24	120.20
1	A	372	A	O3'-P-O5'	5.36	112.04	104.00
1	A	626	G	OP1-P-O3'	5.36	124.07	108.00
1	A	2705	U	O5'-P-OP2	-5.36	91.93	108.00
1	A	150	A	O3'-P-O5'	5.35	112.02	104.00
1	A	198	A	C8-N9-C1'	5.35	143.74	127.70
1	A	993	C	O5'-P-OP1	-5.35	91.96	108.00
1	A	2442	G	C5'-C4'-O4'	5.34	117.82	109.80
1	A	177	G	C4-N9-C1'	5.33	142.50	126.50
1	A	1029	C	C2'-C3'-O3'	-5.33	105.70	113.70
1	A	1261	G	C5'-C4'-C3'	5.33	124.00	116.00
1	A	629	A	O3'-P-O5'	5.33	112.00	104.00
1	A	427	A	C4-N9-C1'	-5.33	110.32	126.30
1	A	1035	C	O3'-P-O5'	5.32	111.98	104.00
31	a	65	G	P-O3'-C3'	5.32	128.18	120.20
1	A	632	U	C6-N1-C1'	5.32	137.15	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1034	A	C5'-C4'-C3'	5.31	123.97	116.00
1	A	2391	C	O3'-P-O5'	5.31	111.97	104.00
1	A	707	G	C5'-C4'-C3'	5.30	123.95	116.00
1	A	1016	G	P-O3'-C3'	5.30	128.15	120.20
1	A	2568	A	N9-C1'-C2'	5.30	119.95	112.00
1	A	1698	A	O3'-P-O5'	5.30	111.95	104.00
1	A	2658	G	N9-C1'-C2'	5.30	119.95	112.00
1	A	987	U	OP2-P-O3'	-5.30	92.11	108.00
1	A	2653	C	C6-N1-C2	-5.30	104.31	120.20
1	A	2867	U	O3'-P-O5'	5.30	111.94	104.00
1	A	1028	G	C5'-C4'-O4'	-5.29	101.16	109.10
1	A	474	A	C5'-C4'-O4'	5.29	117.74	109.80
1	A	865	A	C5'-C4'-C3'	5.29	123.94	116.00
1	A	2077	C	OP2-P-O3'	-5.29	92.13	108.00
1	A	2391	C	O5'-C5'-C4'	5.29	119.43	111.50
1	A	488	G	C5'-C4'-O4'	-5.29	101.17	109.10
1	A	990	G	O5'-P-OP1	5.29	123.86	108.00
1	A	1168	C	O5'-C5'-C4'	5.29	119.43	111.50
1	A	2488	C	C2-N1-C1'	5.29	134.66	118.80
1	A	989	A	OP1-P-O3'	-5.28	92.15	108.00
1	A	2856	U	O4'-C4'-C3'	-5.28	98.72	104.00
1	A	1257	G	O5'-C5'-C4'	5.28	119.41	111.50
1	A	1007	U	O5'-P-OP1	-5.27	92.18	108.00
1	A	1248	U	O4'-C1'-N1	5.27	116.11	108.20
1	A	1005	G	O3'-P-O5'	5.27	111.90	104.00
1	A	380	U	O4'-C1'-N1	5.27	116.40	108.50
1	A	948	U	O3'-P-O5'	5.27	111.90	104.00
1	A	520	G	N7-C8-N9	5.26	128.89	113.10
1	A	2455	G	OP1-P-O3'	-5.26	92.21	108.00
1	A	897	A	N9-C1'-C2'	5.26	119.89	112.00
1	A	2542	C	C4-C5-C6	5.26	133.19	117.40
1	A	458	A	C4'-C3'-O3'	5.26	120.89	113.00
1	A	489	A	C4'-C3'-O3'	5.26	120.89	113.00
1	A	2652	G	O3'-P-O5'	5.26	111.89	104.00
1	A	1049	C	P-O5'-C5'	5.26	128.79	120.90
1	A	707	G	C4'-C3'-C2'	-5.25	97.35	102.60
1	A	1045	A	OP2-P-O3'	-5.25	92.24	108.00
1	A	342	A	N9-C1'-C2'	5.25	119.87	112.00
1	A	857	C	C5'-C4'-O4'	5.25	117.67	109.80
1	A	524	A	P-O3'-C3'	5.24	128.06	120.20
1	A	2093	C	C2'-C3'-O3'	-5.24	105.84	113.70
1	A	2550	G	C5'-C4'-O4'	5.23	116.95	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1017	A	N7-C8-N9	5.22	129.45	113.80
1	A	990	G	N3-C2-N2	5.22	135.55	119.90
1	A	2457	A	N7-C8-N9	5.22	129.45	113.80
1	A	1006	G	C4'-C3'-O3'	5.21	120.82	113.00
1	A	631	U	O5'-P-OP2	-5.21	92.36	108.00
1	A	2812	U	O5'-P-OP2	-5.21	92.37	108.00
1	A	299	U	N1-C1'-C2'	5.21	121.81	114.00
1	A	1004	A	C8-N9-C1'	5.21	143.32	127.70
1	A	2363	A	OP1-P-O3'	-5.21	92.38	108.00
1	A	706	U	O3'-P-O5'	5.21	111.81	104.00
1	A	594	G	N9-C1'-C2'	5.20	119.81	112.00
1	A	2056	G	O5'-C5'-C4'	5.20	119.31	111.50
1	A	582	G	O3'-P-O5'	5.20	111.80	104.00
1	A	211	C	C5'-C4'-O4'	-5.20	102.00	109.80
1	A	1295	C	N3-C4-N4	-5.20	102.40	118.00
9	I	64	ARG	N-CA-C	5.20	121.87	110.80
1	A	561	C	N1-C2-O2	5.20	134.49	118.90
1	A	2081	A	C8-N9-C1'	5.20	143.28	127.70
1	A	1369	G	N9-C1'-C2'	5.19	121.79	114.00
1	A	1697	G	N9-C1'-C2'	-5.19	106.21	114.00
1	A	2542	C	N1-C1'-C2'	5.19	119.79	112.00
1	A	1023	A	P-O5'-C5'	5.19	128.69	120.90
1	A	494	U	C3'-C2'-C1'	5.19	106.49	101.30
1	A	707	G	OP2-P-O3'	-5.19	92.44	108.00
1	A	1189	C	O5'-C5'-C4'	5.19	119.28	111.50
1	A	1700	C	N3-C2-O2	-5.18	106.35	121.90
1	A	2646	U	C3'-C2'-C1'	5.18	106.48	101.30
37	g	86	GLN	CA-C-N	5.18	126.32	122.59
37	g	86	GLN	C-N-CA	5.18	126.32	122.59
1	A	378	C	P-O5'-C5'	5.18	128.67	120.90
1	A	634	C	C4'-C3'-C2'	-5.18	97.42	102.60
1	A	1050	C	C2-N1-C1'	5.18	134.35	118.80
1	A	2761	C	N1-C1'-C2'	5.18	119.77	112.00
1	A	200	A	C5'-C4'-O4'	5.18	117.57	109.80
1	A	2090	C	C2-N1-C1'	5.18	134.34	118.80
1	A	544	U	N1-C2-N3	5.18	130.44	114.90
1	A	864	A	O5'-C5'-C4'	5.18	119.27	111.50
1	A	561	C	N1-C1'-C2'	5.18	119.77	112.00
1	A	65	A	C4'-C3'-O3'	5.18	120.77	113.00
1	A	69	C	P-O3'-C3'	5.17	127.96	120.20
1	A	1180	G	C4-N9-C1'	5.17	142.02	126.50
1	A	361	U	P-O3'-C3'	5.17	127.96	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	491	C	C1'-C2'-O2'	5.17	116.16	108.40
1	A	1183	G	C4'-C3'-O3'	5.17	120.76	113.00
1	A	2064	A	C4'-C3'-O3'	5.17	120.75	113.00
1	A	33	U	O4'-C1'-N1	5.17	115.95	108.20
1	A	2078	A	P-O3'-C3'	5.17	127.95	120.20
1	A	548	A	N7-C8-N9	5.16	129.28	113.80
1	A	561	C	C5-C6-N1	5.16	136.47	121.00
1	A	857	C	O5'-P-OP2	5.15	123.45	108.00
1	A	1250	G	P-O3'-C3'	-5.15	112.47	120.20
1	A	2056	G	N9-C1'-C2'	5.15	119.73	112.00
1	A	2806	U	P-O3'-C3'	-5.15	112.47	120.20
1	A	1700	C	N1-C1'-C2'	5.15	119.72	112.00
1	A	557	G	C1'-O4'-C4'	-5.15	104.75	109.90
1	A	2830	A	C5'-C4'-C3'	5.14	123.72	116.00
1	A	1030	C	O3'-P-O5'	5.14	111.71	104.00
1	A	500	A	C3'-C2'-C1'	5.13	106.63	101.50
1	A	1289	A	C1'-C2'-O2'	5.13	116.10	108.40
1	A	2663	U	O5'-C5'-C4'	5.13	119.20	111.50
1	A	2044	C	N1-C1'-C2'	5.13	121.69	114.00
1	A	600	U	O3'-P-O5'	5.13	111.69	104.00
1	A	2057	A	N9-C1'-C2'	5.13	121.69	114.00
1	A	2664	U	C2-N1-C1'	5.13	133.09	117.70
1	A	2094	G	C8-N9-C1'	-5.12	111.63	127.00
1	A	47	C	C2'-C3'-O3'	-5.12	106.01	113.70
1	A	911	A	O4'-C1'-N9	-5.12	100.82	108.50
1	A	2652	G	P-O3'-C3'	5.12	127.88	120.20
1	A	1007	U	OP1-P-OP2	5.12	134.95	119.60
1	A	648	G	P-O5'-C5'	5.12	128.57	120.90
1	A	583	A	C4'-C3'-O3'	5.11	120.67	113.00
1	A	1247	G	N9-C1'-C2'	-5.11	104.33	112.00
1	A	1013	U	OP2-P-O3'	5.11	123.33	108.00
1	A	1174	U	C3'-C2'-C1'	-5.11	96.19	101.30
1	A	1368	C	C4'-C3'-O3'	5.11	120.66	113.00
1	A	2379	A	C4-N9-C1'	5.11	141.62	126.30
1	A	2546	U	C6-N1-C2	-5.11	105.68	121.00
1	A	2542	C	N1-C2-O2	5.10	134.21	118.90
1	A	1014	U	C5'-C4'-O4'	-5.10	102.14	109.80
1	A	2527	U	C2'-C3'-O3'	5.10	121.35	113.70
1	A	45	G	P-O3'-C3'	5.10	127.85	120.20
1	A	642	U	N3-C2-O2	-5.10	106.90	122.20
1	A	1015	C	C3'-C2'-C1'	5.10	106.40	101.30
1	A	2636	U	C2-N1-C1'	5.10	133.00	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2647	C	P-O5'-C5'	5.10	128.55	120.90
1	A	598	G	C2'-C3'-O3'	-5.09	106.06	113.70
1	A	2812	U	O3'-P-O5'	5.09	111.64	104.00
1	A	957	C	N3-C2-O2	-5.09	106.63	121.90
1	A	1014	U	C6-N1-C1'	-5.09	105.93	121.20
1	A	958	U	O3'-P-O5'	5.09	111.63	104.00
1	A	1277	C	C5'-C4'-C3'	-5.09	108.37	116.00
1	A	2802	A	C4-N9-C1'	5.09	141.56	126.30
1	A	1046	G	C8-N9-C1'	-5.08	111.75	127.00
1	A	520	G	C8-N9-C4	-5.08	91.16	106.40
1	A	2481	G	O4'-C4'-C3'	-5.08	98.92	104.00
1	A	2523	C	O5'-P-OP2	-5.08	92.77	108.00
1	A	1082	C	C2'-C3'-O3'	5.08	121.31	113.70
1	A	1224	U	C5'-C4'-O4'	-5.08	102.19	109.80
1	A	1360	G	N9-C1'-C2'	5.07	119.61	112.00
1	A	2024	A	C5'-C4'-C3'	5.07	123.61	116.00
1	A	640	G	O3'-P-O5'	5.07	111.61	104.00
1	A	956	A	O3'-P-O5'	5.07	111.61	104.00
1	A	1255	A	O3'-P-O5'	5.07	111.60	104.00
1	A	1274	G	C5'-C4'-O4'	5.07	116.70	109.10
1	A	2806	U	C5'-C4'-C3'	-5.07	107.60	115.20
1	A	494	U	O5'-P-OP2	5.07	123.20	108.00
1	A	52	A	C4-N9-C1'	5.06	141.49	126.30
1	A	1180	G	O3'-P-O5'	5.06	111.59	104.00
1	A	1203	U	C5'-C4'-O4'	-5.06	102.21	109.80
1	A	2524	A	C2'-C3'-O3'	-5.06	106.11	113.70
1	A	2868	G	OP1-P-OP2	-5.06	104.42	119.60
1	A	2275	C	C4'-C3'-O3'	5.06	116.99	109.40
1	A	2644	C	P-O5'-C5'	-5.06	113.32	120.90
1	A	2023	C	C3'-C2'-C1'	-5.05	96.45	101.50
1	A	70	G	C4-N9-C1'	5.05	141.66	126.50
1	A	70	G	C8-N9-C1'	-5.05	111.85	127.00
1	A	2486	A	C8-N9-C1'	-5.05	112.54	127.70
31	a	437	U	P-O3'-C3'	5.05	127.77	120.20
1	A	425	G	N9-C1'-C2'	5.05	119.57	112.00
1	A	872	U	N1-C1'-C2'	5.04	119.57	112.00
1	A	1185	U	N1-C1'-C2'	5.04	121.56	114.00
1	A	378	C	C5'-C4'-C3'	5.04	123.56	116.00
1	A	1207	G	C4'-C3'-O3'	5.04	120.56	113.00
31	a	711	G	P-O3'-C3'	5.04	127.76	120.20
1	A	896	U	O5'-P-OP2	5.04	123.12	108.00
1	A	1006	G	O3'-P-O5'	5.04	111.56	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1290	G	P-O3'-C3'	5.04	127.76	120.20
1	A	2481	G	OP2-P-O3'	5.04	123.12	108.00
1	A	493	A	P-O3'-C3'	-5.04	112.64	120.20
1	A	496	G	C4'-C3'-C2'	-5.04	97.56	102.60
1	A	864	A	O3'-P-O5'	5.04	111.55	104.00
1	A	1175	G	O4'-C1'-N9	-5.04	100.65	108.20
1	A	1020	G	N3-C4-N9	5.03	141.10	126.00
1	A	858	U	C5'-C4'-O4'	5.03	117.34	109.80
1	A	2482	G	O4'-C4'-C3'	-5.03	98.97	104.00
1	A	587	C	C2-N1-C1'	-5.03	103.72	118.80
1	A	2055	U	O4'-C1'-N1	5.02	116.03	108.50
1	A	2093	C	N3-C4-N4	-5.02	102.93	118.00
1	A	2519	U	C5'-C4'-C3'	5.02	123.53	116.00
1	A	489	A	C4-N9-C1'	5.02	141.36	126.30
1	A	1207	G	N1-C6-O6	5.02	134.96	119.90
1	A	867	U	C5'-C4'-C3'	5.02	123.53	116.00
1	A	1039	C	O4'-C4'-C3'	5.02	109.02	104.00
1	A	2515	A	OP1-P-O3'	-5.02	92.95	108.00
1	A	1698	A	C2'-C3'-O3'	-5.01	106.18	113.70
1	A	2594	G	C5'-C4'-C3'	5.01	123.52	116.00
1	A	640	G	C2'-C3'-O3'	-5.01	106.18	113.70
31	a	460	A	P-O3'-C3'	5.01	127.72	120.20
1	A	1227	U	N3-C4-C5	5.01	129.62	114.60
1	A	1287	U	C6-N1-C1'	-5.01	106.18	121.20
1	A	638	U	O3'-P-O5'	5.01	111.51	104.00
1	A	864	A	N9-C1'-C2'	5.01	119.51	112.00
1	A	181	G	O4'-C4'-C3'	-5.00	99.00	104.00
1	A	990	G	C5'-C4'-C3'	5.00	123.50	116.00
1	A	2037	G	C4-N9-C1'	5.00	141.51	126.50

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	990	G	C4'
1	A	1289	A	C1'
1	A	2077	C	C1'

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	3	31	HIS	Peptide
1	A	1241	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1324	A	Sidechain
1	A	1705	G	Sidechain
1	A	2026	C	Sidechain
1	A	2045	A	Sidechain
1	A	2060	A	Sidechain
1	A	2275	C	Sidechain
1	A	2544	C	Sidechain
1	A	2646	U	Sidechain
1	A	490	C	Sidechain
1	A	557	G	Sidechain
1	A	627	C	Sidechain
1	A	644	C	Sidechain
1	A	648	G	Sidechain
1	A	902	A	Sidechain
5	E	104	LYS	Peptide
5	E	169	ASN	Peptide
5	E	69	GLY	Peptide
9	I	119	PRO	Peptide
11	K	42	ILE	Peptide
13	M	68	THR	Peptide
16	P	50	ALA	Peptide
16	P	55	GLY	Peptide
19	S	55	GLY	Peptide
23	W	34	THR	Peptide
26	Z	41	ARG	Peptide
43	m	26	GLY	Peptide
49	s	14	HIS	Peptide
49	s	80	PHE	Peptide
49	s	9	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62277	0	30925	1220	0
2	B	2445	0	1240	16	0
3	C	2090	0	2201	26	0
4	D	1627	0	1667	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1572	0	1619	19	0
6	F	1315	0	1338	35	0
7	G	1248	0	1205	28	0
8	H	1149	0	1144	11	0
9	I	918	0	981	11	0
10	J	1086	0	1125	18	0
11	K	1079	0	1137	11	0
12	L	932	0	983	7	0
13	M	883	0	913	20	0
14	N	889	0	937	9	0
15	O	943	0	1014	23	0
16	P	790	0	830	13	0
17	Q	838	0	896	8	0
18	R	715	0	748	8	0
19	S	770	0	809	10	0
20	T	722	0	766	7	0
21	U	587	0	600	12	0
22	V	379	0	400	9	0
23	W	541	0	563	10	0
24	X	449	0	490	4	0
25	Y	370	0	243	9	0
26	Z	360	0	358	5	0
27	1	390	0	394	8	0
28	2	367	0	415	1	0
29	3	521	0	586	4	0
30	4	295	0	340	4	0
31	a	32969	0	16595	703	0
32	b	1819	0	1886	71	0
33	c	1501	0	1464	35	0
34	d	1497	0	1449	49	0
35	e	1145	0	1202	37	0
36	f	778	0	775	23	0
37	g	1161	0	1165	38	0
38	h	1026	0	1078	25	0
39	i	922	0	890	36	0
40	j	752	0	775	30	0
41	k	810	0	784	35	0
42	l	1037	0	1091	32	0
43	m	727	0	674	23	0
44	n	487	0	492	15	0
45	o	723	0	752	20	0
46	p	694	0	709	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	q	621	0	615	29	0
48	r	445	0	482	8	0
49	s	636	0	626	27	0
50	t	591	0	616	25	0
51	u	400	0	407	9	0
52	v	1333	0	1349	38	0
53	A	51	0	66	4	0
All	All	140672	0	92809	2714	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 13.

All (2714) 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)
1:A:582:G:N2	1:A:599:A:H8	1.18	1.39
1:A:1055:A:C6	1:A:1194:U:O4	1.77	1.37
1:A:272:C:O2	1:A:416:G:N2	1.59	1.34
1:A:583:A:N7	1:A:598:G:N2	1.75	1.31
1:A:1078:G:N2	1:A:1165:C:O2	1.63	1.31
1:A:900:G:N2	1:A:967:C:O2	1.65	1.29
1:A:362:C:O2	1:A:366:G:N2	1.66	1.27
1:A:2379:A:N7	1:A:2392:G:N2	1.82	1.27
1:A:27:G:N2	1:A:558:A:C8	2.02	1.26
1:A:1055:A:N1	1:A:1194:U:C4	2.05	1.25
1:A:1055:A:N6	1:A:1194:U:O4	1.72	1.21
1:A:2830:A:N7	1:A:2910:G:N2	1.90	1.20
1:A:31:C:O2	1:A:520:G:N2	1.77	1.18
1:A:582:G:N2	1:A:599:A:C8	1.95	1.18
31:a:161:A:N6	31:a:354:G:C6	2.13	1.17
1:A:422:G:N2	1:A:444:C:O2	1.76	1.17
1:A:2052:C:N3	1:A:2065:G:N1	1.91	1.16
1:A:332:A:C4	1:A:332:A:C5	2.33	1.15
1:A:2499:G:N2	1:A:2505:A:H62	1.46	1.14
1:A:1073:A:N6	1:A:1169:G:H21	1.46	1.13
31:a:27:A:N6	31:a:566:G:N3	1.97	1.13
1:A:2496:A:C8	1:A:2508:G:N2	2.17	1.12
1:A:583:A:C5	1:A:598:G:N2	2.08	1.11
1:A:2319:U:O4	1:A:2367:A:C6	2.05	1.09
1:A:2499:G:H21	1:A:2505:A:N6	1.51	1.09
1:A:1041:G:O6	1:A:1202:C:N4	1.87	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:U:N3	1:A:169:G:O6	1.87	1.08
1:A:2496:A:H8	1:A:2508:G:N2	1.48	1.07
1:A:646:A:N6	1:A:699:U:H3	1.53	1.06
1:A:1352:C:O2	1:A:1374:G:N2	1.88	1.04
1:A:2379:A:N6	1:A:2392:G:N3	2.06	1.04
1:A:2658:G:N2	1:A:2814:C:O2	1.88	1.04
1:A:686:U:N3	1:A:692:G:O6	1.90	1.03
31:a:987:A:N1	31:a:1326:G:N2	2.07	1.03
1:A:889:U:O4	1:A:978:A:N6	1.89	1.03
1:A:583:A:N6	1:A:598:G:N3	2.06	1.02
1:A:425:G:N2	1:A:441:C:O2	1.93	1.02
1:A:2053:U:N3	1:A:2064:A:C2	2.27	1.02
1:A:522:G:H21	1:A:526:A:N6	1.58	1.01
1:A:272:C:C2	1:A:416:G:N2	2.29	1.01
1:A:332:A:C8	1:A:393:G:N9	2.27	1.01
1:A:996:G:N1	1:A:1009:C:N3	2.09	1.01
1:A:2868:G:N2	1:A:2888:A:H62	1.58	1.01
31:a:1444:A:H62	31:a:1478:G:N2	1.59	1.00
1:A:889:U:N3	1:A:978:A:N1	2.09	1.00
31:a:1444:A:H62	31:a:1478:G:H21	1.07	1.00
1:A:1514:A:N6	1:A:1566:G:H1	1.59	0.99
1:A:272:C:N3	1:A:416:G:N1	2.08	0.99
31:a:1435:A:N6	31:a:1486:G:H1	1.59	0.98
1:A:1235:C:N4	1:A:1288:G:O6	1.96	0.98
31:a:695:A:N6	31:a:711:G:H21	1.58	0.98
31:a:790:A:H62	31:a:808:G:N2	1.60	0.97
1:A:9:U:H3	1:A:2656:A:N6	1.62	0.97
31:a:304:U:H3	31:a:309:G:H1	1.00	0.97
1:A:1884:G:N2	1:A:1912:A:H62	1.61	0.97
1:A:859:C:N4	1:A:1232:G:O6	1.96	0.96
1:A:12:U:N3	1:A:571:A:N7	2.12	0.96
1:A:332:A:C5	1:A:393:G:N9	2.33	0.96
1:A:1055:A:C6	1:A:1194:U:C4	2.47	0.96
1:A:1056:U:O4	1:A:1187:A:N6	1.99	0.96
1:A:2052:C:O2	1:A:2065:G:N2	1.99	0.96
31:a:69:G:H1	31:a:100:A:H2	1.00	0.96
31:a:257:U:H3	31:a:283:G:H1	1.06	0.96
1:A:332:A:C4	1:A:393:G:N9	2.33	0.95
1:A:2095:U:N3	1:A:2457:A:N7	2.13	0.95
1:A:27:G:N2	1:A:558:A:H8	1.47	0.95
1:A:2828:U:O2	1:A:2911:A:N6	2.00	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1055:A:N1	1:A:1194:U:N3	2.14	0.94
1:A:2125:U:H3	1:A:2218:G:H1	1.08	0.94
31:a:953:G:H21	31:a:1349:A:H62	1.11	0.94
1:A:341:G:N2	1:A:383:A:N7	2.14	0.94
1:A:1040:A:N1	1:A:1203:U:N3	2.16	0.94
1:A:2046:U:H2'	1:A:2047:A:H8	1.33	0.94
1:A:994:A:N1	1:A:1011:U:N3	2.11	0.93
1:A:2828:U:H3	1:A:2911:A:H62	1.05	0.93
31:a:836:A:N6	31:a:867:G:N3	2.15	0.93
1:A:16:G:H1	1:A:569:U:H3	1.13	0.93
1:A:1884:G:H21	1:A:1912:A:H62	1.10	0.93
31:a:695:A:H62	31:a:711:G:N2	1.65	0.93
1:A:1036:C:O2	1:A:1206:G:N2	2.02	0.93
1:A:584:G:N1	1:A:597:U:O2	2.02	0.93
1:A:332:A:C4	1:A:393:G:H1'	2.04	0.92
1:A:2665:G:H21	1:A:2805:A:H62	1.09	0.92
1:A:2868:G:H21	1:A:2888:A:N6	1.66	0.92
1:A:583:A:N6	1:A:598:G:C2	2.38	0.92
1:A:883:C:N4	1:A:984:G:O6	2.03	0.92
1:A:1079:U:H3	1:A:1164:G:H1	0.92	0.92
31:a:1527:G:N2	31:a:1530:A:N7	2.18	0.92
31:a:592:G:H1	31:a:765:U:H3	0.99	0.92
31:a:836:A:H62	31:a:867:G:N2	1.68	0.91
1:A:1085:U:H3	1:A:1158:G:H1	0.92	0.91
31:a:1423:A:C2	31:a:1498:G:N1	2.38	0.91
1:A:332:A:N7	1:A:393:G:N9	2.17	0.91
1:A:27:G:H21	1:A:558:A:H8	0.93	0.91
1:A:2553:G:H1	1:A:2564:U:H3	1.13	0.91
31:a:161:A:C6	31:a:354:G:C6	2.58	0.91
31:a:987:A:C2	31:a:1326:G:N2	2.39	0.91
1:A:2378:G:H21	1:A:2393:A:N6	1.70	0.90
31:a:684:A:C2	31:a:722:G:N1	2.38	0.90
1:A:583:A:N6	1:A:598:G:H21	1.68	0.90
1:A:583:A:H62	1:A:598:G:N2	1.68	0.90
31:a:790:A:N6	31:a:808:G:H21	1.68	0.90
1:A:1073:A:H62	1:A:1169:G:N2	1.69	0.90
31:a:840:G:H1	31:a:863:U:H3	0.91	0.90
1:A:332:A:N9	1:A:393:G:N9	2.20	0.89
1:A:2432:G:H22	1:A:2439:A:H61	1.21	0.89
1:A:642:U:H3	1:A:703:A:H61	0.95	0.89
1:A:2868:G:N2	1:A:2888:A:N6	2.21	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2052:C:N3	1:A:2065:G:C6	2.35	0.88
31:a:695:A:H62	31:a:711:G:H21	1.14	0.88
1:A:35:G:N2	1:A:491:C:O2	2.06	0.88
31:a:790:A:H62	31:a:808:G:H21	0.88	0.87
31:a:1444:A:N6	31:a:1478:G:H21	1.72	0.87
31:a:1127:U:H3	31:a:1194:G:H1	0.88	0.87
1:A:332:A:C8	1:A:332:A:N7	2.43	0.87
1:A:35:G:N2	1:A:496:G:N7	2.23	0.87
31:a:934:G:H1	31:a:1401:U:H3	0.88	0.87
1:A:1884:G:H21	1:A:1912:A:N6	1.73	0.86
1:A:2544:C:O2	1:A:2594:G:N2	2.07	0.86
1:A:12:U:C4	1:A:571:A:N7	2.44	0.86
1:A:159:U:C4	1:A:169:G:O6	2.29	0.85
1:A:902:A:C2	1:A:965:G:N1	2.43	0.85
31:a:1435:A:H61	31:a:1486:G:H1	0.86	0.85
1:A:910:C:H42	1:A:954:A:H8	1.23	0.85
1:A:2378:G:N2	1:A:2393:A:N6	2.23	0.85
1:A:2674:U:H3	1:A:2700:G:H1	1.22	0.85
31:a:151:A:N7	31:a:170:U:C2	2.44	0.85
31:a:161:A:N6	31:a:354:G:C5	2.44	0.85
1:A:642:U:H3	1:A:703:A:N6	1.74	0.85
31:a:609:G:H1	31:a:645:U:H3	0.86	0.85
1:A:607:C:N4	1:A:620:G:H1	1.74	0.85
1:A:272:C:O2	1:A:416:G:C2	2.29	0.84
1:A:583:A:N6	1:A:598:G:N2	2.23	0.84
31:a:953:G:N2	31:a:1349:A:H62	1.76	0.84
31:a:1455:U:H3	31:a:1468:G:H1	1.19	0.83
1:A:332:A:C4	1:A:332:A:N9	2.46	0.83
1:A:1073:A:H62	1:A:1169:G:H21	0.88	0.83
1:A:913:U:O4	1:A:954:A:N6	2.11	0.83
1:A:2828:U:H3	1:A:2911:A:N6	1.76	0.83
1:A:2667:G:N2	1:A:2668:A:N7	2.27	0.82
1:A:498:G:H21	1:A:503:A:H8	1.24	0.82
1:A:2127:G:H1	1:A:2216:U:H3	1.27	0.82
1:A:2273:G:O6	1:A:2285:C:N4	2.12	0.82
1:A:9:U:N3	1:A:2656:A:N6	2.23	0.82
1:A:900:G:N1	1:A:967:C:N3	2.28	0.82
1:A:27:G:N3	1:A:558:A:N7	2.28	0.82
1:A:341:G:N2	1:A:383:A:C5	2.46	0.82
31:a:953:G:H21	31:a:1349:A:N6	1.78	0.81
1:A:1466:G:H1	1:A:1623:U:H3	0.88	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2496:A:H8	1:A:2508:G:H21	0.84	0.81
31:a:1423:A:H2	31:a:1498:G:H1	1.16	0.81
1:A:367:A:C5	1:A:381:G:N2	2.34	0.81
1:A:2378:G:C2	1:A:2393:A:N6	2.49	0.81
1:A:2550:G:H21	1:A:2792:A:H61	1.26	0.81
1:A:522:G:N2	1:A:526:A:N6	2.28	0.81
1:A:1044:A:N6	1:A:1198:G:O2'	2.14	0.81
1:A:2550:G:N2	1:A:2567:C:O2	2.14	0.81
1:A:1934:G:O6	1:A:1950:U:C2	2.34	0.81
31:a:300:G:N2	31:a:617:A:N6	2.29	0.81
1:A:2424:G:H1	1:A:2446:U:H3	0.86	0.80
1:A:2054:G:N2	1:A:2063:C:O2	2.14	0.80
31:a:839:U:O2	31:a:864:G:N1	2.14	0.80
1:A:1040:A:N1	1:A:1203:U:C2	2.49	0.80
1:A:13:A:N3	1:A:14:A:N6	2.29	0.80
1:A:2377:C:O2	1:A:2394:G:N2	2.15	0.79
1:A:2703:C:N3	1:A:2704:A:N6	2.30	0.79
1:A:2488:C:N4	1:A:2516:G:O6	2.15	0.79
1:A:1017:A:HO2'	1:A:1225:G:N2	1.81	0.79
1:A:1514:A:H61	1:A:1566:G:H1	0.85	0.79
31:a:16:G:H1	31:a:929:U:H3	1.27	0.79
1:A:890:G:H21	1:A:977:A:H62	1.30	0.79
1:A:1035:C:N3	1:A:1207:G:N1	2.31	0.79
1:A:606:G:N2	1:A:620:G:O6	2.16	0.78
1:A:582:G:C2	1:A:599:A:C8	2.70	0.78
1:A:582:G:N3	1:A:599:A:N7	2.32	0.78
1:A:2273:G:H3'	1:A:2274:A:H8	1.47	0.78
1:A:1078:G:N1	1:A:1165:C:N3	2.30	0.78
1:A:721:A:H8	1:A:2096:G:H21	1.30	0.78
1:A:883:C:N3	1:A:984:G:N1	2.32	0.78
1:A:422:G:N2	1:A:444:C:C2	2.51	0.77
3:C:230:HIS:HD2	3:C:232:HIS:H	1.31	0.77
7:G:90:VAL:O	7:G:160:LYS:HA	1.83	0.77
1:A:276:C:O2	1:A:295:G:N2	2.12	0.77
1:A:864:A:N6	1:A:1227:U:O4	2.18	0.77
1:A:2828:U:C2	1:A:2911:A:N6	2.50	0.77
1:A:45:G:N2	1:A:480:U:O2	2.17	0.77
31:a:1314:G:N2	31:a:1343:A:N6	2.32	0.77
1:A:1018:A:OP1	1:A:1225:G:N2	2.17	0.77
1:A:1499:U:O4	1:A:2731:C:N4	2.18	0.77
1:A:2596:G:H2'	1:A:2597:G:H8	1.50	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:161:A:N6	31:a:354:G:O6	2.17	0.77
31:a:1297:A:H62	31:a:1380:G:H21	1.32	0.77
1:A:2319:U:C4	1:A:2367:A:N1	2.53	0.77
1:A:200:A:C5	1:A:201:C:H1'	2.20	0.76
31:a:601:U:H3	31:a:654:G:H1	1.34	0.76
31:a:684:A:N1	31:a:722:G:C6	2.54	0.76
1:A:583:A:C6	1:A:598:G:N2	2.37	0.76
1:A:152:C:N4	1:A:177:G:O6	2.14	0.76
1:A:9:U:O4	1:A:2656:A:N7	2.19	0.76
1:A:1449:A:N7	1:A:1635:A:N6	2.34	0.76
1:A:1017:A:O2'	1:A:1225:G:N2	2.18	0.76
1:A:1086:G:H1	1:A:1157:U:H3	0.80	0.76
31:a:954:G:H1	31:a:1246:A:N6	1.84	0.75
1:A:332:A:C5	1:A:332:A:N7	2.54	0.75
21:U:34:ALA:H	21:U:37:GLN:HE21	1.35	0.75
1:A:893:G:O6	1:A:975:U:O2	2.02	0.75
1:A:1055:A:C2	1:A:1194:U:N3	2.53	0.75
1:A:2480:A:H2'	1:A:2481:G:H8	1.51	0.75
31:a:147:G:N2	31:a:175:C:C2	2.54	0.75
1:A:332:A:C8	1:A:332:A:N9	2.54	0.75
1:A:857:C:O2	1:A:1264:A:O2'	2.03	0.75
1:A:521:U:O4	1:A:526:A:N6	2.19	0.75
1:A:354:A:N3	1:A:373:A:O2'	2.20	0.75
1:A:362:C:C2	1:A:366:G:N2	2.53	0.75
31:a:1314:G:N2	31:a:1343:A:H62	1.85	0.75
1:A:2319:U:O4	1:A:2367:A:N1	2.18	0.74
1:A:2480:A:N6	1:A:2527:U:H3	1.83	0.74
1:A:752:G:H1	1:A:769:U:H3	1.33	0.74
31:a:836:A:H62	31:a:867:G:H21	1.31	0.74
1:A:27:G:N2	1:A:558:A:OP2	2.20	0.74
1:A:526:A:N3	1:A:544:U:N3	2.35	0.74
1:A:1014:U:H3'	1:A:1015:C:H4'	1.70	0.74
31:a:959:U:N3	31:a:1241:G:N1	2.35	0.74
1:A:614:U:OP2	16:P:79:ARG:NH1	2.20	0.73
1:A:2036:G:H5''	17:Q:42:ALA:HB2	1.70	0.73
1:A:346:A:N6	1:A:357:U:O4	2.20	0.73
1:A:1514:A:N1	1:A:1566:G:N2	2.35	0.73
1:A:1253:G:O6	1:A:1272:U:O2	2.07	0.73
31:a:528:A:N1	31:a:541:A:N6	2.35	0.73
1:A:35:G:N1	1:A:491:C:N3	2.33	0.73
1:A:503:A:H2	1:A:517:A:H62	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:C:O2'	1:A:1291:A:N7	2.23	0.72
1:A:648:G:N2	1:A:669:C:OP1	2.22	0.72
31:a:27:A:H62	31:a:566:G:N2	1.86	0.72
1:A:219:A:OP2	1:A:478:A:N6	2.23	0.72
1:A:607:C:N4	1:A:620:G:N1	2.37	0.72
1:A:1018:A:HO2'	1:A:1033:G:H1	1.37	0.72
1:A:2053:U:C4	1:A:2064:A:N1	2.58	0.72
1:A:2480:A:H61	1:A:2527:U:H3	1.35	0.72
31:a:181:A:N6	31:a:209:G:N7	2.37	0.72
1:A:12:U:N3	1:A:571:A:C5	2.31	0.72
1:A:1087:C:O2	1:A:1156:G:N2	2.17	0.72
8:H:7:ALA:H	8:H:46:THR:HG21	1.54	0.72
1:A:1975:G:O2'	31:a:1428:A:N6	2.22	0.72
1:A:584:G:O6	1:A:597:U:N3	2.15	0.72
1:A:2496:A:N7	1:A:2508:G:N3	2.37	0.72
1:A:12:U:O4	1:A:571:A:N7	2.22	0.71
1:A:850:G:N2	1:A:874:A:OP1	2.23	0.71
1:A:2868:G:C2	1:A:2888:A:N6	2.58	0.71
1:A:36:G:O2'	1:A:496:G:N3	2.23	0.71
1:A:586:C:O2	1:A:595:G:N2	2.22	0.71
31:a:1423:A:N1	31:a:1498:G:C6	2.58	0.71
1:A:2053:U:N3	1:A:2064:A:H2	1.88	0.71
1:A:2679:U:H3	1:A:2695:G:H1	1.36	0.71
1:A:519:G:H3'	1:A:520:G:H8	1.55	0.71
31:a:69:G:N1	31:a:100:A:H2	1.84	0.71
1:A:1265:G:OP1	1:A:1288:G:N2	2.20	0.71
1:A:2046:U:H2'	1:A:2047:A:C8	2.23	0.71
31:a:836:A:N6	31:a:867:G:C2	2.56	0.71
1:A:497:U:OP2	5:E:52:LYS:NZ	2.22	0.71
1:A:1174:U:H4'	1:A:2542:C:H1'	1.71	0.71
1:A:2473:G:H2'	1:A:2528:C:H5	1.56	0.71
32:b:18:HIS:HA	32:b:38:ILE:HG13	1.71	0.71
1:A:660:A:H8	5:E:182:ASN:HB3	1.55	0.71
1:A:2127:G:N2	1:A:2216:U:O2	2.24	0.71
31:a:161:A:C6	31:a:354:G:O6	2.43	0.71
1:A:1174:U:OP2	1:A:2597:G:N2	2.24	0.71
31:a:602:U:H3	31:a:653:G:H1	1.36	0.71
31:a:1450:U:N3	31:a:1472:G:N1	2.38	0.71
1:A:267:G:O2'	1:A:474:A:N6	2.24	0.70
1:A:1286:G:H2'	15:O:3:ARG:HA	1.73	0.70
31:a:1525:U:O2	31:a:1532:G:N2	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:900:G:N2	1:A:967:C:C2	2.53	0.70
1:A:923:A:N1	1:A:944:G:C6	2.59	0.70
1:A:1055:A:N6	1:A:1194:U:C4	2.56	0.70
1:A:2486:A:H61	1:A:2520:U:H3	1.39	0.70
1:A:332:A:C5	1:A:393:G:H1'	2.26	0.70
1:A:1452:C:N4	1:A:1633:A:N7	2.40	0.70
1:A:656:G:H21	1:A:660:A:H2	1.37	0.70
1:A:2703:C:N4	1:A:2757:U:O4	2.25	0.70
1:A:1177:A:N6	1:A:2053:U:OP2	2.24	0.70
1:A:1047:G:N2	1:A:1054:A:O2'	2.17	0.70
31:a:841:U:H3	31:a:862:G:H1	1.38	0.70
31:a:300:G:N2	31:a:617:A:H61	1.90	0.70
1:A:13:A:O2'	1:A:15:G:N7	2.24	0.70
2:B:1:U:O2	2:B:2:C:N4	2.25	0.70
31:a:836:A:H61	31:a:867:G:H2'	1.57	0.69
1:A:1053:A:OP2	1:A:1054:A:N6	2.25	0.69
1:A:2422:C:O2	1:A:2448:G:N2	2.20	0.69
31:a:270:A:H4'	50:t:69:ASN:HD22	1.57	0.69
1:A:2093:C:N4	1:A:2094:G:O6	2.24	0.69
1:A:2828:U:N3	1:A:2911:A:N6	2.36	0.69
31:a:108:A:H62	31:a:332:G:H21	1.41	0.69
1:A:616:G:OP2	1:A:2045:A:N6	2.25	0.69
31:a:150:U:O2	31:a:171:A:N7	2.25	0.69
1:A:874:A:N6	1:A:2274:A:O2'	2.26	0.69
1:A:1015:C:OP2	1:A:1018:A:O2'	2.11	0.69
1:A:1082:C:H2'	1:A:1083:G:H8	1.58	0.69
1:A:1086:G:N2	1:A:1157:U:O2	2.23	0.69
1:A:2855:A:O2'	1:A:2857:A:N7	2.26	0.69
1:A:2499:G:H21	1:A:2505:A:H62	0.75	0.69
1:A:22:C:N3	1:A:563:G:N1	2.40	0.68
1:A:648:G:O2'	1:A:703:A:O4'	2.10	0.68
1:A:688:A:H61	1:A:2396:A:H2'	1.57	0.68
1:A:2643:C:N4	26:Z:5:LYS:H	1.91	0.68
31:a:1315:G:H21	31:a:1342:A:H8	1.39	0.68
31:a:151:A:N7	31:a:170:U:O2	2.25	0.68
31:a:1000:U:C2	31:a:1223:A:N7	2.61	0.68
1:A:1240:U:H3'	1:A:1241:A:H3'	1.73	0.68
1:A:1692:C:H2'	1:A:1693:G:H4'	1.74	0.68
1:A:2851:G:O2'	1:A:2903:A:N6	2.26	0.68
31:a:148:G:O6	31:a:174:A:N1	2.26	0.68
1:A:2680:U:H3'	1:A:2681:A:H2'	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:987:A:N7	31:a:1370:A:N6	2.40	0.68
1:A:1175:G:N3	1:A:2052:C:O2'	2.25	0.68
1:A:2128:G:N2	1:A:2215:U:O2	2.25	0.68
1:A:444:C:H41	22:V:52:ARG:HH22	1.42	0.68
31:a:1066:A:C8	31:a:1210:C:N4	2.61	0.68
1:A:1073:A:N6	1:A:1169:G:N2	2.31	0.67
6:F:130:LEU:HB3	6:F:154:ILE:O	1.93	0.67
31:a:673:A:N7	31:a:732:G:O6	2.26	0.67
1:A:643:G:N2	1:A:649:U:O5'	2.27	0.67
31:a:151:A:C5	31:a:170:U:O2	2.47	0.67
46:p:52:VAL:HG11	46:p:80:ILE:HG12	1.75	0.67
1:A:714:G:O2'	1:A:846:G:N2	2.26	0.67
1:A:2649:U:O2'	1:A:2845:G:N2	2.28	0.67
31:a:684:A:N1	31:a:722:G:O6	2.28	0.67
1:A:152:C:N3	1:A:177:G:N1	2.37	0.67
1:A:2472:G:H2'	1:A:2473:G:C8	2.30	0.67
1:A:2665:G:N2	1:A:2805:A:H62	1.89	0.67
31:a:73:G:H22	31:a:96:U:H3	1.42	0.67
31:a:75:A:N6	31:a:94:G:O2'	2.28	0.67
1:A:589:U:OP1	1:A:1258:A:N6	2.28	0.67
1:A:1044:A:O5'	1:A:1198:G:N2	2.28	0.67
31:a:994:C:H2'	31:a:995:A:H8	1.60	0.67
1:A:1022:G:O2'	1:A:1053:A:N6	2.24	0.67
52:v:43:LYS:HB2	52:v:55:GLU:HB2	1.76	0.67
1:A:332:A:C8	1:A:393:G:C1'	2.77	0.67
1:A:1048:U:H1'	1:A:1054:A:H2'	1.77	0.67
7:G:29:PRO:HB2	7:G:30:LYS:HE2	1.76	0.67
31:a:1423:A:N1	31:a:1498:G:O6	2.27	0.67
1:A:901:G:N7	1:A:902:A:N6	2.43	0.66
31:a:954:G:N1	31:a:1246:A:N6	2.42	0.66
1:A:267:G:N2	1:A:269:G:OP2	2.25	0.66
1:A:1692:C:N4	1:A:2037:G:N7	2.40	0.66
1:A:1862:G:H1	1:A:1932:C:H5	1.42	0.66
1:A:436:A:O2'	1:A:437:A:N7	2.29	0.66
18:R:7:LEU:HD21	18:R:42:VAL:HG12	1.77	0.66
31:a:676:A:H1'	45:o:46:HIS:HB3	1.78	0.66
31:a:836:A:N6	31:a:867:G:H21	1.94	0.66
31:a:1525:U:N3	31:a:1532:G:N1	2.42	0.66
1:A:615:A:N6	1:A:2056:G:O2'	2.29	0.66
3:C:180:GLU:HB2	3:C:273:GLY:HA2	1.76	0.66
31:a:58:G:N1	31:a:364:A:C2	2.64	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:602:U:OP2	31:a:603:A:N6	2.29	0.66
31:a:1315:G:HO2'	31:a:1341:G:H1	1.43	0.66
1:A:444:C:H5	22:V:52:ARG:HH12	1.42	0.66
1:A:2864:A:H61	1:A:2894:C:H42	1.43	0.66
31:a:682:G:O6	31:a:724:A:N1	2.29	0.66
46:p:4:LYS:HD3	46:p:25:ALA:HB2	1.78	0.66
1:A:1781:C:OP1	14:N:96:ARG:NH2	2.29	0.66
1:A:2060:A:O2'	1:A:2063:C:N4	2.28	0.66
19:S:46:LYS:HD3	19:S:47:PRO:HD2	1.77	0.66
4:D:2:THR:OG1	4:D:3:LYS:N	2.27	0.65
21:U:72:ASP:OD1	21:U:72:ASP:N	2.29	0.65
13:M:29:PRO:HD2	13:M:92:ILE:HG22	1.78	0.65
31:a:1429:G:H1	31:a:1492:U:H3	1.42	0.65
1:A:9:U:C2	1:A:2656:A:N6	2.64	0.65
1:A:582:G:C2	1:A:599:A:N7	2.64	0.65
1:A:1056:U:H4'	1:A:1057:A:H5'	1.78	0.65
36:f:7:MET:HG3	36:f:62:ILE:HG12	1.78	0.65
1:A:572:C:H5''	1:A:2806:U:H3	1.60	0.65
1:A:574:A:N3	1:A:575:G:N2	2.43	0.65
1:A:650:U:O2	1:A:651:A:N6	2.30	0.65
31:a:1314:G:N2	31:a:1343:A:C5	2.65	0.65
1:A:612:U:O3'	1:A:1027:A:N6	2.29	0.65
1:A:645:A:O2'	1:A:700:A:N6	2.29	0.65
1:A:1053:A:H5''	15:O:59:LYS:HD3	1.79	0.65
1:A:2424:G:N2	1:A:2446:U:O2	2.27	0.65
31:a:161:A:N7	31:a:354:G:C2	2.65	0.65
1:A:589:U:O4	1:A:592:A:N7	2.30	0.65
1:A:27:G:C2	1:A:558:A:N7	2.65	0.65
1:A:33:U:O2	1:A:493:A:N7	2.29	0.65
1:A:425:G:N1	1:A:441:C:N3	2.44	0.65
31:a:159:G:N2	31:a:162:A:OP2	2.30	0.65
31:a:836:A:N6	31:a:867:G:N2	2.43	0.65
1:A:393:G:N2	1:A:395:U:O2'	2.30	0.65
1:A:1016:G:H8	1:A:1016:G:O5'	1.80	0.65
1:A:2036:G:N2	1:A:2037:G:O6	2.29	0.65
31:a:455:G:O2'	31:a:495:A:N6	2.30	0.65
1:A:1138:U:H2'	1:A:1140:A:H5''	1.78	0.64
1:A:576:U:N3	1:A:605:U:O2'	2.26	0.64
1:A:702:U:O2'	1:A:703:A:N7	2.30	0.64
1:A:2549:U:H3'	1:A:2550:G:H4'	1.78	0.64
1:A:373:A:N3	1:A:1248:U:O2'	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:A:C6	1:A:201:C:H1'	2.32	0.64
31:a:839:U:O2	31:a:864:G:C2	2.51	0.64
1:A:859:C:N3	1:A:1232:G:N1	2.46	0.64
1:A:2820:U:O2'	1:A:2823:G:N7	2.30	0.64
31:a:589:G:H21	31:a:768:U:H5	1.45	0.64
1:A:272:C:C2	1:A:416:G:C2	2.84	0.64
1:A:548:A:H8	1:A:550:A:C8	2.16	0.64
1:A:1079:U:O4	1:A:1164:G:O6	2.16	0.64
1:A:2485:U:O2	1:A:2486:A:N6	2.31	0.64
31:a:1455:U:O2	31:a:1468:G:N2	2.30	0.64
1:A:1035:C:N3	1:A:1207:G:C6	2.61	0.64
1:A:1947:C:H2'	1:A:1948:G:H8	1.62	0.64
1:A:2052:C:C2	1:A:2065:G:N1	2.63	0.64
31:a:108:A:H62	31:a:332:G:N2	1.96	0.64
31:a:155:U:O2	31:a:166:G:N2	2.30	0.64
1:A:332:A:C5	1:A:393:G:C1'	2.81	0.63
1:A:1763:U:N3	1:A:1766:C:OP2	2.31	0.63
1:A:2689:A:H3'	1:A:2690:G:H8	1.63	0.63
18:R:33:VAL:O	18:R:76:ARG:NH2	2.31	0.63
1:A:927:G:H22	1:A:939:U:H2'	1.63	0.63
1:A:2273:G:C6	1:A:2285:C:N4	2.65	0.63
15:O:83:LEU:HD13	15:O:113:ALA:HB2	1.80	0.63
31:a:300:G:H21	31:a:617:A:N6	1.97	0.63
1:A:1080:G:O6	1:A:1162:C:N4	2.31	0.63
1:A:2053:U:O4	1:A:2064:A:N1	2.31	0.63
31:a:753:U:O2'	31:a:844:G:N3	2.31	0.63
1:A:923:A:N1	1:A:944:G:O6	2.31	0.63
31:a:190:A:N6	31:a:202:C:O2	2.31	0.63
1:A:1510:U:H3	1:A:1571:G:H1	1.45	0.63
31:a:1270:G:N2	31:a:1285:A:N6	2.46	0.63
34:d:93:ARG:HA	34:d:133:VAL:H	1.63	0.63
1:A:1032:A:O2'	1:A:1034:A:OP1	2.17	0.63
1:A:2397:G:O2'	1:A:2398:G:O4'	2.17	0.63
1:A:2482:G:H2'	1:A:2483:C:C6	2.34	0.63
1:A:2665:G:H21	1:A:2805:A:N6	1.90	0.63
39:i:59:THR:HA	39:i:62:ASN:HB3	1.80	0.63
1:A:1014:U:OP1	1:A:1032:A:N6	2.32	0.63
1:A:2675:G:N2	1:A:2699:U:O2	2.24	0.63
34:d:66:ARG:H	34:d:69:ARG:HB3	1.64	0.63
10:J:79:LEU:HD22	10:J:113:GLY:HA2	1.80	0.63
39:i:21:VAL:HG12	39:i:67:VAL:HG13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:905:U:H1'	1:A:2295:A:H4'	1.81	0.63
1:A:2675:G:O6	1:A:2699:U:O4	2.17	0.63
19:S:47:PRO:HB3	19:S:53:GLU:HA	1.80	0.63
1:A:526:A:H1'	1:A:544:U:H1'	1.79	0.62
1:A:649:U:O3'	1:A:703:A:O2'	2.15	0.62
1:A:2084:G:H21	1:A:2085:A:H62	1.46	0.62
1:A:2856:U:H2'	1:A:2857:A:C8	2.34	0.62
31:a:8:G:H1'	35:e:126:LYS:HD3	1.79	0.62
31:a:1452:G:N2	31:a:1466:G:OP1	2.32	0.62
1:A:182:C:N4	1:A:216:A:N7	2.43	0.62
1:A:2686:G:N2	1:A:2689:A:OP2	2.32	0.62
31:a:213:G:H1	31:a:226:U:H3	1.46	0.62
31:a:575:G:N7	42:l:12:ARG:NH1	2.47	0.62
1:A:1079:U:O2	1:A:1164:G:N2	2.33	0.62
1:A:1501:G:H22	1:A:2729:G:H22	1.48	0.62
1:A:2524:A:O2'	1:A:2526:C:OP1	2.17	0.62
31:a:218:U:H2'	31:a:219:C:H2'	1.81	0.62
31:a:1366:G:H2'	31:a:1367:A:H8	1.64	0.62
36:f:7:MET:H	36:f:90:MET:H	1.47	0.62
1:A:27:G:C2	1:A:558:A:C8	2.86	0.62
1:A:416:G:OP2	1:A:469:A:N6	2.31	0.62
1:A:2559:G:N2	1:A:2690:G:O2'	2.32	0.62
31:a:214:A:N1	31:a:225:G:O6	2.33	0.62
31:a:1423:A:H2	31:a:1498:G:N1	1.89	0.62
1:A:226:A:N6	1:A:420:A:O2'	2.32	0.62
1:A:1087:C:N3	1:A:1156:G:N1	2.40	0.62
1:A:2477:A:N7	1:A:2528:C:N3	2.48	0.62
31:a:150:U:H2'	31:a:170:U:H3	1.64	0.62
31:a:160:A:N6	31:a:351:U:O2'	2.32	0.62
31:a:507:A:N6	31:a:555:A:OP2	2.33	0.62
31:a:725:C:H4'	41:k:119:ASN:HB2	1.81	0.62
31:a:802:A:OP2	31:a:804:C:N4	2.33	0.62
1:A:640:G:H1	1:A:705:U:H3	1.46	0.62
1:A:1450:A:H61	1:A:1635:A:H62	1.45	0.62
1:A:2317:G:H1	1:A:2368:G:H1	1.45	0.62
31:a:194:G:H1	47:q:7:ARG:HH21	1.47	0.62
31:a:527:C:N4	31:a:537:G:O2'	2.29	0.62
31:a:680:U:O2	48:r:69:HIS:NE2	2.31	0.62
1:A:427:A:OP1	22:V:16:ASN:ND2	2.28	0.62
1:A:2557:U:O2'	1:A:2561:C:N4	2.25	0.62
31:a:592:G:N2	31:a:765:U:O2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2596:G:N1	1:A:2597:G:O6	2.33	0.62
31:a:961:U:OP1	31:a:981:C:N4	2.32	0.62
33:c:155:ARG:NH1	33:c:192:TYR:O	2.33	0.62
31:a:69:G:O6	31:a:100:A:N1	2.32	0.62
31:a:684:A:H2	31:a:722:G:N1	1.96	0.62
31:a:1314:G:N2	31:a:1343:A:C6	2.67	0.62
49:s:39:THR:HA	49:s:70:LYS:HA	1.80	0.62
1:A:581:A:N6	1:A:600:U:C5	2.68	0.62
1:A:2581:U:H3'	1:A:2583:C:H41	1.63	0.62
1:A:860:U:H1'	1:A:1232:G:C2	2.35	0.61
1:A:2486:A:N6	1:A:2520:U:H3	1.97	0.61
31:a:900:U:O2	31:a:916:A:N7	2.33	0.61
36:f:9:ILE:HG12	36:f:88:ARG:HB2	1.82	0.61
1:A:522:G:N2	1:A:525:A:O5'	2.31	0.61
1:A:1240:U:O4	1:A:1241:A:N6	2.33	0.61
1:A:2865:G:O6	1:A:2891:U:O2	2.18	0.61
1:A:2867:U:O2	1:A:2889:G:N2	2.21	0.61
31:a:672:G:N2	31:a:734:C:O2'	2.32	0.61
1:A:1138:U:O2'	1:A:1142:A:N6	2.33	0.61
1:A:2162:A:N6	1:A:2184:G:O2'	2.33	0.61
18:R:34:ASN:H	18:R:37:GLN:HE21	1.47	0.61
23:W:2:LYS:O	23:W:6:ILE:N	2.33	0.61
31:a:666:G:H1	31:a:755:U:H3	1.47	0.61
31:a:1429:G:N2	31:a:1492:U:O2	2.32	0.61
34:d:104:ALA:HA	34:d:150:ILE:HB	1.82	0.61
37:g:116:MET:HA	37:g:119:ARG:HB2	1.83	0.61
1:A:1034:A:OP1	1:A:1200:A:O2'	2.17	0.61
1:A:2055:U:O2	1:A:2060:A:N7	2.33	0.61
1:A:2338:A:OP1	1:A:2340:C:N4	2.34	0.61
6:F:34:ILE:HB	6:F:91:LEU:HB2	1.82	0.61
31:a:1258:A:N6	31:a:1299:A:OP2	2.32	0.61
41:k:32:VAL:HG11	41:k:67:SER:HA	1.81	0.61
41:k:50:LEU:HD11	41:k:65:MET:HB2	1.83	0.61
1:A:159:U:O4	1:A:169:G:O6	2.18	0.61
1:A:352:A:H2'	1:A:373:A:N7	2.14	0.61
1:A:521:U:O4	1:A:522:G:N2	2.32	0.61
1:A:608:C:O2'	1:A:1291:A:N1	2.33	0.61
1:A:1078:G:N2	1:A:1165:C:C2	2.42	0.61
1:A:1960:G:H1	1:A:1994:C:H5	1.46	0.61
1:A:2480:A:N1	1:A:2527:U:C2	2.68	0.61
1:A:2679:U:N3	1:A:2695:G:N1	2.44	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:120:LYS:HZ1	38:h:121:ARG:HE	1.47	0.61
1:A:1934:G:O6	1:A:1950:U:O2	2.18	0.61
31:a:38:U:H5'	42:l:134:LYS:HB3	1.83	0.61
1:A:564:U:H2'	1:A:565:G:C8	2.36	0.61
1:A:26:G:O2'	1:A:27:G:O4'	2.17	0.61
1:A:898:U:O4	1:A:968:A:N6	2.20	0.61
1:A:1491:C:H1'	1:A:1509:G:H22	1.66	0.61
1:A:2679:U:O2	1:A:2695:G:N2	2.30	0.61
31:a:59:C:N4	31:a:363:C:O2	2.28	0.61
31:a:69:G:N1	31:a:100:A:C2	2.55	0.61
1:A:329:A:H62	1:A:331:G:H22	1.48	0.61
1:A:2081:A:N7	1:A:2604:A:N6	2.49	0.61
31:a:959:U:O2	31:a:1241:G:N2	2.32	0.61
46:p:20:ILE:HG12	46:p:38:GLY:H	1.66	0.61
1:A:48:G:H4'	1:A:51:G:H5'	1.82	0.61
1:A:393:G:N9	1:A:393:G:C1'	2.64	0.61
1:A:1756:U:O2	1:A:1757:U:N3	2.34	0.61
31:a:967:A:N6	49:s:77:THR:O	2.34	0.61
38:h:30:SER:HG	38:h:33:LYS:H	1.48	0.61
50:t:29:ARG:HA	50:t:32:VAL:HG22	1.82	0.61
1:A:1283:G:O6	1:A:1284:A:N6	2.34	0.60
1:A:1509:G:H21	1:A:1593:G:H8	1.49	0.60
1:A:1886:A:H62	1:A:1910:G:H21	1.47	0.60
1:A:2048:G:OP2	1:A:2049:U:N3	2.34	0.60
1:A:2822:C:O2'	1:A:2824:G:O6	2.17	0.60
2:B:7:G:OP1	13:M:30:ARG:NH1	2.34	0.60
31:a:16:G:H1'	35:e:24:VAL:HG11	1.82	0.60
31:a:1361:U:O2	31:a:1381:G:N2	2.33	0.60
1:A:47:C:H2'	1:A:48:G:C8	2.36	0.60
1:A:330:C:O2'	1:A:331:G:N2	2.34	0.60
1:A:2120:G:N3	1:A:2225:A:N6	2.48	0.60
31:a:681:G:H2'	31:a:682:G:H8	1.65	0.60
1:A:2477:A:OP1	1:A:2524:A:N6	2.34	0.60
31:a:1003:A:N7	31:a:1226:A:O2'	2.33	0.60
31:a:1261:A:N3	31:a:1379:C:O2'	2.31	0.60
40:j:15:HIS:O	40:j:19:ASP:N	2.34	0.60
46:p:6:ARG:NH2	46:p:24:ASP:O	2.34	0.60
1:A:231:A:C6	1:A:233:U:H1'	2.36	0.60
1:A:904:G:O2'	1:A:961:G:O6	2.17	0.60
1:A:1287:U:H2'	1:A:1288:G:C8	2.36	0.60
1:A:2800:U:O4	1:A:2801:C:N4	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1416:U:O2'	31:a:1528:G:N2	2.34	0.60
1:A:300:G:H1	1:A:415:U:H3	1.47	0.60
1:A:1105:U:H3	1:A:1108:C:H41	1.49	0.60
1:A:2642:U:O2	1:A:2643:C:N4	2.35	0.60
31:a:898:A:N6	31:a:917:A:OP2	2.33	0.60
31:a:1436:A:N1	31:a:1485:G:O6	2.34	0.60
45:o:61:GLY:HA2	45:o:64:ARG:HB3	1.84	0.60
1:A:2381:A:O2'	21:U:42:GLY:O	2.19	0.60
1:A:2504:C:O2'	30:4:4:ARG:NH2	2.34	0.60
1:A:2546:U:O2	1:A:2547:C:N4	2.34	0.60
31:a:256:C:OP1	31:a:290:A:N6	2.35	0.60
31:a:1356:A:H62	31:a:1384:A:H5''	1.67	0.60
31:a:1435:A:N1	31:a:1486:G:N2	2.43	0.60
1:A:1034:A:H2'	1:A:1225:G:OP2	2.02	0.60
16:P:26:ASP:OD1	16:P:26:ASP:N	2.27	0.60
31:a:48:C:H5''	31:a:373:U:H2'	1.83	0.60
31:a:155:U:H3	31:a:166:G:H1	1.49	0.60
31:a:446:G:O2'	31:a:502:C:N4	2.34	0.60
31:a:447:U:O2'	34:d:115:ASN:ND2	2.34	0.60
31:a:1077:C:O2	31:a:1201:A:N6	2.35	0.60
1:A:325:A:H1'	1:A:400:C:H42	1.66	0.60
1:A:1236:G:H21	15:O:4:VAL:HG21	1.65	0.60
31:a:674:G:N1	31:a:748:U:N3	2.48	0.60
1:A:332:A:C4	1:A:393:G:C1'	2.81	0.60
1:A:1041:G:N1	1:A:1202:C:N3	2.46	0.60
1:A:1362:C:O2'	1:A:2037:G:N2	2.35	0.60
1:A:1767:G:OP2	1:A:1768:C:N4	2.34	0.60
10:J:70:ASN:OD1	10:J:70:ASN:N	2.35	0.60
46:p:42:PRO:HA	46:p:48:PRO:HA	1.82	0.60
17:Q:73:GLU:HB2	17:Q:104:VAL:HG13	1.84	0.60
31:a:603:A:O2'	31:a:648:A:N7	2.34	0.60
31:a:1410:C:H5''	52:v:84:LYS:HD2	1.84	0.60
35:e:77:VAL:HB	35:e:82:PRO:HB3	1.84	0.60
1:A:324:A:N6	1:A:402:C:O2	2.32	0.59
1:A:365:A:H3'	1:A:366:G:H3'	1.84	0.59
31:a:323:A:HO2'	31:a:338:C:HO2'	1.49	0.59
33:c:141:MET:HA	33:c:145:ALA:H	1.66	0.59
1:A:202:A:N1	1:A:2460:A:N6	2.51	0.59
1:A:2532:G:O6	1:A:2637:C:O2	2.20	0.59
1:A:2582:U:OP2	1:A:2583:C:N4	2.35	0.59
31:a:37:C:H5''	42:l:133:LYS:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1515:G:N3	52:v:87:ARG:NH2	2.50	0.59
1:A:757:G:OP2	1:A:759:U:N3	2.33	0.59
1:A:1053:A:H8	1:A:1197:C:H2'	1.66	0.59
31:a:164:C:H2'	31:a:165:G:H8	1.66	0.59
31:a:674:G:O6	31:a:748:U:C4	2.54	0.59
1:A:225:A:H61	1:A:237:U:H5'	1.68	0.59
1:A:326:A:N6	1:A:401:U:O2	2.36	0.59
1:A:1457:U:OP2	1:A:1628:A:N6	2.35	0.59
6:F:102:LYS:NZ	25:Y:25:SER:O	2.35	0.59
31:a:996:A:N3	31:a:1023:A:N6	2.50	0.59
38:h:105:LEU:HA	38:h:114:THR:HA	1.85	0.59
42:l:42:GLN:HE21	42:l:94:LEU:HD11	1.67	0.59
1:A:89:U:H2'	1:A:90:A:H8	1.67	0.59
31:a:587:G:H1	31:a:770:U:H3	1.50	0.59
37:g:99:LEU:HB3	37:g:137:LYS:HE2	1.85	0.59
47:q:62:LYS:HB3	47:q:79:GLU:HB3	1.84	0.59
1:A:34:U:O2	1:A:500:A:O2'	2.20	0.59
1:A:1195:A:OP1	15:O:84:LYS:NZ	2.30	0.59
1:A:1452:C:O2	1:A:1459:A:N6	2.36	0.59
1:A:2496:A:N6	1:A:2508:G:O3'	2.36	0.59
31:a:962:G:OP1	31:a:974:A:N6	2.35	0.59
31:a:1124:C:O2'	44:n:57:ARG:NH2	2.36	0.59
42:l:84:GLY:O	42:l:112:ARG:NH2	2.36	0.59
1:A:303:G:O6	1:A:413:C:N4	2.31	0.59
1:A:2056:G:N7	1:A:2058:A:H4'	2.17	0.59
1:A:2384:U:OP1	21:U:28:ARG:NH1	2.35	0.59
1:A:2500:U:OP1	1:A:2502:C:N4	2.36	0.59
31:a:40:G:H1	31:a:555:A:H2'	1.67	0.59
31:a:307:G:N2	31:a:573:U:O2	2.36	0.59
31:a:1166:G:H2'	31:a:1189:A:H62	1.67	0.59
31:a:1261:A:N6	31:a:1364:U:O2'	2.33	0.59
41:k:36:ASP:OD1	41:k:36:ASP:N	2.36	0.59
1:A:615:A:H2'	1:A:616:G:C2	2.37	0.59
31:a:1000:U:O2	31:a:1223:A:N7	2.35	0.59
31:a:1002:G:OP2	31:a:1004:C:N4	2.35	0.59
31:a:1270:G:N2	31:a:1285:A:H62	2.01	0.59
31:a:1441:C:H42	31:a:1480:A:H61	1.51	0.59
43:m:19:LEU:HB3	43:m:25:ILE:HD13	1.85	0.59
31:a:1036:C:N4	31:a:1044:G:O6	2.36	0.59
34:d:63:MET:SD	34:d:93:ARG:NH2	2.75	0.59
1:A:1395:G:H8	1:A:1410:A:H62	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2319:U:O2'	1:A:2402:G:O2'	2.20	0.58
6:F:46:ASN:O	6:F:50:LEU:N	2.36	0.58
25:Y:51:SER:O	25:Y:55:HIS:NE2	2.36	0.58
31:a:130:A:H1'	31:a:271:A:H1'	1.84	0.58
36:f:51:GLU:HG3	36:f:54:ASP:HA	1.84	0.58
49:s:48:THR:HA	49:s:61:TYR:HA	1.84	0.58
1:A:2142:G:N2	1:A:2188:C:OP1	2.37	0.58
1:A:2867:U:H3	1:A:2889:G:H1	0.79	0.58
45:o:36:ILE:HG12	45:o:56:LEU:HD13	1.83	0.58
1:A:1886:A:H62	1:A:1910:G:N2	2.01	0.58
1:A:2532:G:H22	1:A:2637:C:H42	1.50	0.58
6:F:142:ASP:N	6:F:142:ASP:OD1	2.33	0.58
32:b:83:GLU:HG2	32:b:210:VAL:HG12	1.86	0.58
1:A:645:A:O2'	1:A:647:G:O2'	2.21	0.58
1:A:362:C:N3	1:A:366:G:N1	2.50	0.58
1:A:1463:A:N7	1:A:1625:U:O2	2.35	0.58
1:A:2852:U:OP2	4:D:64:LYS:NZ	2.31	0.58
20:T:10:GLN:O	20:T:13:GLN:NE2	2.36	0.58
31:a:144:C:N3	31:a:179:A:N6	2.51	0.58
31:a:936:G:N2	31:a:1400:U:O2	2.33	0.58
31:a:1270:G:H21	31:a:1285:A:N6	2.02	0.58
37:g:14:PRO:HG3	37:g:21:LYS:HG2	1.84	0.58
1:A:589:U:O2'	1:A:591:A:OP2	2.20	0.58
1:A:2828:U:O4	1:A:2911:A:N7	2.36	0.58
13:M:36:SER:OG	13:M:37:ASN:N	2.36	0.58
24:X:11:SER:OG	24:X:12:VAL:N	2.36	0.58
31:a:469:U:H3	31:a:480:G:H1	1.52	0.58
39:i:13:ARG:HA	39:i:18:VAL:HA	1.85	0.58
1:A:24:G:H1	1:A:561:C:N4	2.01	0.58
1:A:1137:G:N2	1:A:1143:G:N7	2.52	0.58
1:A:2474:G:N7	1:A:2528:C:H5'	2.18	0.58
1:A:2680:U:H3	1:A:2694:C:H42	1.50	0.58
13:M:96:ARG:NH2	13:M:99:TYR:O	2.36	0.58
31:a:387:C:H41	31:a:392:G:H1	1.52	0.58
6:F:64:LYS:NZ	6:F:65:PRO:O	2.37	0.58
31:a:823:A:N7	31:a:1520:C:O2'	2.33	0.58
35:e:110:PRO:HG2	35:e:136:MET:HE3	1.86	0.58
1:A:1448:U:N3	1:A:1635:A:N1	2.39	0.58
1:A:1758:A:O2'	1:A:1761:G:O6	2.22	0.58
1:A:2918:A:H2'	1:A:2919:A:H8	1.69	0.58
31:a:841:U:O2	31:a:862:G:N2	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:907:G:N2	31:a:910:A:OP2	2.37	0.58
32:b:32:PHE:HB3	32:b:40:ILE:HB	1.86	0.58
41:k:110:ILE:HB	51:u:18:ARG:HH12	1.69	0.58
1:A:2081:A:H2'	1:A:2083:G:H4'	1.85	0.58
31:a:572:U:OP2	42:l:12:ARG:NH1	2.35	0.58
31:a:1016:A:N6	31:a:1033:U:OP1	2.35	0.58
31:a:1058:G:N2	31:a:1220:C:O2'	2.32	0.58
34:d:95:ASP:O	34:d:107:ARG:NH2	2.37	0.58
1:A:474:A:H2'	1:A:475:A:C8	2.39	0.57
1:A:1252:A:N6	1:A:1273:G:O2'	2.37	0.57
1:A:1874:A:H61	1:A:1920:C:H42	1.51	0.57
2:B:52:G:H21	6:F:26:MET:HE3	1.69	0.57
11:K:99:PRO:HB2	20:T:82:LEU:HD21	1.85	0.57
31:a:962:G:H2'	31:a:963:G:H8	1.68	0.57
31:a:1252:G:N1	31:a:1305:U:N3	2.51	0.57
27:1:21:LYS:NZ	27:1:26:ASN:O	2.36	0.57
31:a:145:U:O2	31:a:177:G:N2	2.36	0.57
41:k:96:ALA:O	41:k:100:LEU:N	2.36	0.57
52:v:57:THR:HB	52:v:66:ARG:HG2	1.86	0.57
1:A:1072:A:OP2	1:A:1169:G:N1	2.34	0.57
31:a:175:C:O2'	31:a:1457:A:N6	2.37	0.57
31:a:383:U:O2	46:p:29:ARG:NH2	2.37	0.57
32:b:34:GLU:HG3	32:b:37:GLY:H	1.69	0.57
46:p:84:PHE:HA	46:p:87:GLN:HB2	1.86	0.57
1:A:332:A:N9	1:A:393:G:C1'	2.68	0.57
1:A:351:G:N2	1:A:373:A:OP1	2.35	0.57
1:A:790:G:HO2'	1:A:793:G:HO2'	1.50	0.57
1:A:1100:G:N2	1:A:1130:A:N3	2.52	0.57
1:A:1162:C:H2'	1:A:1163:U:C6	2.39	0.57
1:A:1515:G:H22	1:A:1565:U:H3	1.52	0.57
1:A:2693:C:N4	7:G:110:SER:OG	2.34	0.57
31:a:106:G:OP1	31:a:333:A:N6	2.35	0.57
31:a:414:G:O6	31:a:446:G:N2	2.37	0.57
31:a:546:U:O4	31:a:547:A:N6	2.38	0.57
31:a:587:G:O6	31:a:770:U:O4	2.23	0.57
32:b:61:SER:HA	32:b:65:GLY:H	1.69	0.57
1:A:422:G:N1	1:A:444:C:N3	2.52	0.57
1:A:1239:C:H42	1:A:1282:A:H61	1.51	0.57
1:A:2093:C:O2	1:A:2472:G:N2	2.37	0.57
1:A:2850:G:O2'	1:A:2856:U:O2	2.22	0.57
2:B:38:U:N3	2:B:42:G:OP2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:609:G:N2	31:a:645:U:O2	2.35	0.57
31:a:1450:U:C2	31:a:1472:G:N1	2.73	0.57
38:h:50:GLU:HB2	38:h:61:ARG:HB2	1.85	0.57
1:A:70:G:OP2	1:A:111:U:N3	2.34	0.57
1:A:1465:G:O2'	1:A:1537:A:N6	2.38	0.57
31:a:985:G:O2'	31:a:1372:C:N4	2.38	0.57
31:a:1260:A:H61	31:a:1364:U:H4'	1.69	0.57
35:e:154:ALA:HB2	35:e:164:LEU:HD11	1.85	0.57
11:K:21:SER:OG	11:K:25:ASN:ND2	2.34	0.57
31:a:1252:G:O6	31:a:1305:U:C4	2.58	0.57
33:c:109:ASP:OD1	33:c:109:ASP:N	2.37	0.57
1:A:492:G:H4'	1:A:493:A:H5'	1.86	0.57
1:A:495:A:H5'	1:A:1286:G:O6	2.04	0.57
1:A:2125:U:O2	1:A:2218:G:N2	2.35	0.57
14:N:31:HIS:HB3	14:N:42:ILE:HD11	1.86	0.57
1:A:1056:U:O2'	1:A:1058:U:OP1	2.23	0.57
1:A:1064:A:N1	1:A:1185:U:O2'	2.29	0.57
1:A:1762:U:O4	1:A:1765:A:O2'	2.23	0.57
7:G:164:TYR:HB2	7:G:167:GLU:HB2	1.86	0.57
23:W:2:LYS:HD2	23:W:6:ILE:HD11	1.86	0.57
31:a:304:U:O4	31:a:309:G:O6	2.23	0.57
31:a:954:G:N2	31:a:1246:A:N1	2.51	0.57
33:c:51:VAL:HG13	33:c:69:THR:H	1.69	0.57
40:j:52:ILE:HA	40:j:62:ARG:HA	1.87	0.57
1:A:1081:G:N2	1:A:1163:U:O2	2.38	0.57
1:A:2870:A:N7	1:A:2886:G:N1	2.38	0.57
3:C:123:ASP:OD1	3:C:123:ASP:N	2.38	0.57
31:a:570:U:H4'	31:a:571:A:H5'	1.86	0.57
47:q:14:VAL:HA	47:q:25:VAL:HA	1.86	0.57
1:A:651:A:H61	1:A:666:A:H61	1.52	0.56
1:A:1175:G:C5	1:A:2052:C:H4'	2.40	0.56
1:A:1933:G:H1	1:A:1952:C:H42	1.51	0.56
31:a:1319:G:O6	31:a:1338:C:N4	2.39	0.56
41:k:94:GLU:HB3	51:u:16:LEU:HD21	1.87	0.56
47:q:29:THR:OG1	47:q:30:TYR:N	2.37	0.56
1:A:352:A:H5'	19:S:17:LYS:HD2	1.86	0.56
1:A:1311:A:N7	1:A:1690:A:O2'	2.37	0.56
5:E:177:THR:HG22	5:E:179:GLN:H	1.70	0.56
1:A:901:G:H1'	21:U:35:ASP:HB3	1.87	0.56
1:A:1004:A:H5''	1:A:1005:G:H5'	1.86	0.56
4:D:3:LYS:NZ	4:D:109:THR:O	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:295:U:H2'	31:a:296:A:H8	1.71	0.56
31:a:385:G:H2'	31:a:386:G:H8	1.71	0.56
31:a:1011:U:O2'	31:a:1012:G:N7	2.35	0.56
31:a:1066:A:O2'	33:c:155:ARG:NH1	2.39	0.56
31:a:1261:A:O2'	39:i:16:ASN:ND2	2.38	0.56
35:e:83:HIS:ND1	38:h:98:LEU:O	2.38	0.56
36:f:23:VAL:O	36:f:27:ASN:N	2.38	0.56
39:i:32:VAL:HG21	39:i:37:VAL:HG13	1.86	0.56
1:A:155:U:O4	1:A:156:A:N6	2.38	0.56
1:A:1085:U:O2	1:A:1158:G:N2	2.34	0.56
31:a:680:U:O2'	36:f:88:ARG:NH1	2.39	0.56
31:a:1272:A:N1	31:a:1284:A:N6	2.53	0.56
31:a:1314:G:C2	31:a:1343:A:N6	2.68	0.56
1:A:1196:C:OP1	15:O:84:LYS:NZ	2.31	0.56
31:a:13:U:O2'	31:a:923:A:OP2	2.24	0.56
31:a:453:G:H2'	31:a:454:G:H8	1.71	0.56
1:A:1466:G:O6	1:A:1623:U:O4	2.24	0.56
1:A:1917:A:H3'	1:A:1918:G:H8	1.70	0.56
2:B:113:G:O2'	13:M:59:LYS:NZ	2.39	0.56
21:U:83:ASP:N	21:U:83:ASP:OD1	2.37	0.56
31:a:598:U:H5''	38:h:30:SER:HA	1.88	0.56
31:a:867:G:N1	31:a:879:U:OP1	2.36	0.56
32:b:173:ILE:HG21	32:b:196:ILE:HG12	1.88	0.56
51:u:5:VAL:O	51:u:18:ARG:NH2	2.38	0.56
52:v:45:LYS:HG2	52:v:53:LYS:HB3	1.87	0.56
1:A:267:G:H21	1:A:269:G:P	2.29	0.56
1:A:2473:G:H2'	1:A:2528:C:C5	2.40	0.56
1:A:2656:A:O2'	1:A:2914:A:N7	2.38	0.56
32:b:109:LYS:O	32:b:113:ARG:N	2.36	0.56
43:m:57:ARG:NH1	43:m:57:ARG:O	2.38	0.56
1:A:2053:U:C2	1:A:2064:A:H2	2.24	0.56
1:A:2550:G:N2	1:A:2792:A:H61	2.01	0.56
31:a:27:A:H62	31:a:566:G:H21	1.52	0.56
31:a:995:A:N3	49:s:52:TYR:OH	2.38	0.56
40:j:41:PRO:HA	40:j:72:ARG:HA	1.87	0.56
49:s:36:ARG:NH2	49:s:75:ALA:O	2.39	0.56
52:v:5:GLU:O	52:v:41:HIS:ND1	2.38	0.56
1:A:954:A:H3'	1:A:957:C:C4	2.41	0.56
1:A:2166:U:H2'	1:A:2167:G:H8	1.69	0.56
1:A:2542:C:N4	1:A:2596:G:O6	2.36	0.56
31:a:161:A:C5	31:a:354:G:N1	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1385:A:OP2	37:g:10:ARG:NH1	2.39	0.56
31:a:1411:G:OP2	52:v:84:LYS:NZ	2.37	0.56
31:a:1450:U:O2	31:a:1472:G:N2	2.39	0.56
36:f:14:ILE:HD12	36:f:19:LYS:HB2	1.86	0.56
50:t:26:SER:O	50:t:30:THR:N	2.37	0.56
1:A:318:A:O2'	1:A:402:C:N3	2.37	0.56
31:a:899:G:N2	31:a:900:U:O4	2.38	0.56
31:a:1278:G:N2	31:a:1337:A:N3	2.52	0.56
34:d:45:SER:O	34:d:49:LEU:N	2.39	0.56
1:A:543:G:O2'	1:A:544:U:O4'	2.24	0.55
1:A:2142:G:O2'	1:A:2192:G:N1	2.40	0.55
1:A:2428:U:O2	1:A:2442:G:O6	2.23	0.55
6:F:69:LYS:HA	6:F:84:PRO:HA	1.89	0.55
31:a:257:U:O4	31:a:283:G:O6	2.24	0.55
1:A:363:A:O2'	1:A:364:A:O5'	2.23	0.55
1:A:1013:U:H2'	1:A:1014:U:O4'	2.06	0.55
1:A:1533:A:N6	3:C:98:ASP:OD1	2.39	0.55
1:A:2273:G:H3'	1:A:2274:A:C8	2.36	0.55
1:A:2368:G:N2	1:A:2401:C:H4'	2.21	0.55
1:A:2596:G:H2'	1:A:2597:G:C8	2.36	0.55
3:C:25:THR:HG22	3:C:81:ILE:H	1.71	0.55
31:a:1109:C:H1'	31:a:1179:A:H4'	1.88	0.55
1:A:368:A:H61	1:A:380:U:H3	1.52	0.55
1:A:616:G:H1'	1:A:617:A:H5'	1.87	0.55
1:A:649:U:O2	1:A:667:G:O6	2.23	0.55
1:A:1082:C:N4	1:A:1083:G:O6	2.39	0.55
1:A:1357:G:O2'	1:A:1359:A:N6	2.39	0.55
1:A:1422:A:O2'	1:A:1433:U:O2	2.24	0.55
1:A:2189:G:H21	1:A:2190:C:H41	1.54	0.55
31:a:947:A:N6	31:a:948:G:O6	2.39	0.55
1:A:759:U:H2'	1:A:760:A:C4	2.41	0.55
1:A:1035:C:H2'	1:A:1036:C:O4'	2.07	0.55
1:A:1540:U:O2'	1:A:1624:C:O3'	2.23	0.55
1:A:2340:C:H2'	1:A:2341:A:H8	1.71	0.55
1:A:2379:A:H62	1:A:2392:G:N2	2.04	0.55
1:A:2668:A:H2'	1:A:2669:G:H4'	1.88	0.55
31:a:682:G:C6	31:a:724:A:N1	2.73	0.55
52:v:57:THR:HA	52:v:66:ARG:HA	1.89	0.55
1:A:179:A:H3'	1:A:180:G:C8	2.41	0.55
1:A:1197:C:H3'	1:A:1198:G:C8	2.41	0.55
16:P:1:MET:HB3	16:P:43:GLY:HA3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:194:G:N2	47:q:66:THR:OG1	2.39	0.55
43:m:53:LEU:O	43:m:57:ARG:N	2.39	0.55
1:A:529:A:H8	19:S:44:HIS:CG	2.24	0.55
1:A:575:G:O2'	1:A:577:A:N6	2.39	0.55
1:A:590:U:OP1	1:A:1257:G:N2	2.39	0.55
1:A:1462:G:O2'	1:A:1626:A:N6	2.40	0.55
1:A:2347:A:O2'	1:A:2349:A:N6	2.28	0.55
1:A:2471:G:O6	1:A:2472:G:N1	2.40	0.55
1:A:2475:A:OP2	1:A:2524:A:O2'	2.23	0.55
11:K:51:ARG:HG3	11:K:66:ILE:HD11	1.89	0.55
31:a:124:U:O2	31:a:244:G:O6	2.24	0.55
31:a:1249:A:N6	31:a:1311:U:O4	2.39	0.55
31:a:1329:A:OP2	49:s:4:SER:OG	2.25	0.55
41:k:17:GLU:H	41:k:79:LEU:HA	1.72	0.55
1:A:521:U:H2'	1:A:522:G:H4'	1.88	0.55
1:A:614:U:O2'	1:A:618:A:N6	2.40	0.55
1:A:1324:A:N7	12:L:111:GLY:HA3	2.22	0.55
1:A:2480:A:H2'	1:A:2481:G:C8	2.37	0.55
31:a:664:G:H4'	45:o:62:ARG:HD3	1.87	0.55
31:a:1085:G:O6	31:a:1094:U:O2	2.25	0.55
39:i:117:LYS:H	39:i:123:ALA:H	1.53	0.55
40:j:42:LEU:HB2	40:j:71:LYS:HB2	1.89	0.55
46:p:53:ASP:N	46:p:53:ASP:OD1	2.40	0.55
47:q:13:LYS:NZ	47:q:14:VAL:O	2.39	0.55
1:A:332:A:N9	1:A:393:G:C8	2.75	0.55
1:A:1214:C:H42	1:A:1217:U:H3	1.53	0.55
37:g:67:ASN:O	37:g:138:ARG:NH2	2.39	0.55
1:A:626:G:O3'	15:O:3:ARG:NH2	2.39	0.55
1:A:1266:G:O6	1:A:1267:A:N6	2.39	0.55
4:D:55:ASP:HB3	4:D:85:LYS:HE2	1.88	0.55
19:S:3:ILE:HD11	19:S:33:VAL:HG11	1.88	0.55
31:a:1065:C:H41	52:v:45:LYS:HE2	1.72	0.55
1:A:425:G:N2	1:A:441:C:C2	2.72	0.55
1:A:573:A:OP2	8:H:114:ARG:NH2	2.36	0.55
1:A:1004:A:H2'	1:A:1006:G:H8	1.72	0.55
1:A:2608:G:H1	1:A:2637:C:HO2'	1.53	0.55
31:a:753:U:H1'	31:a:844:G:H1'	1.88	0.55
31:a:959:U:N3	31:a:1241:G:C6	2.75	0.55
37:g:58:ALA:HA	37:g:61:VAL:HG12	1.89	0.55
46:p:54:GLU:HB3	46:p:80:ILE:HG23	1.89	0.55
1:A:332:A:N7	1:A:393:G:C1'	2.69	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:909:G:N2	1:A:958:U:O2	2.40	0.54
1:A:1133:G:N2	1:A:1145:U:O4	2.40	0.54
3:C:37:LEU:HG	3:C:62:TYR:HB2	1.89	0.54
1:A:923:A:C2	1:A:944:G:N1	2.60	0.54
1:A:1130:A:O2'	1:A:1147:A:N7	2.38	0.54
1:A:1458:A:N6	1:A:1629:U:O4	2.40	0.54
1:A:2664:U:H1'	1:A:2809:G:C2	2.41	0.54
1:A:2672:G:N3	1:A:2672:G:O2'	2.30	0.54
1:A:2685:C:H3'	1:A:2686:G:H8	1.72	0.54
8:H:29:LEU:HD12	8:H:143:LEU:HD11	1.87	0.54
31:a:1209:U:O2'	31:a:1212:U:OP1	2.24	0.54
32:b:12:ALA:O	52:v:166:ARG:NH2	2.40	0.54
41:k:29:ASN:HB2	41:k:57:LYS:HD3	1.88	0.54
1:A:44:A:N6	1:A:480:U:O4	2.26	0.54
1:A:434:G:O2'	1:A:436:A:OP2	2.25	0.54
1:A:687:G:H22	1:A:690:U:H3'	1.72	0.54
1:A:1658:A:OP1	1:A:1661:C:N4	2.34	0.54
1:A:2146:A:N6	1:A:2197:G:O6	2.40	0.54
1:A:2683:U:OP2	1:A:2691:G:N2	2.40	0.54
1:A:2555:U:H3	1:A:2562:G:H1	1.55	0.54
11:K:34:LEU:HB2	11:K:118:LEU:HD22	1.89	0.54
42:l:26:LYS:O	42:l:72:ASN:ND2	2.40	0.54
1:A:518:A:OP1	1:A:1297:G:O2'	2.18	0.54
1:A:788:A:O2'	1:A:1703:U:OP1	2.24	0.54
1:A:1015:C:OP2	1:A:1033:G:N1	2.32	0.54
1:A:1109:U:N3	1:A:1113:A:OP2	2.41	0.54
1:A:2055:U:C2	1:A:2060:A:N7	2.75	0.54
4:D:189:ASP:OD2	4:D:192:ASN:ND2	2.35	0.54
31:a:254:A:O2'	31:a:287:A:N6	2.40	0.54
31:a:613:U:N3	31:a:640:G:OP2	2.39	0.54
31:a:626:C:H2'	31:a:629:A:H62	1.73	0.54
31:a:819:C:O2'	31:a:909:A:N6	2.41	0.54
31:a:1064:G:H4'	31:a:1065:C:H2'	1.89	0.54
31:a:1523:U:O2	31:a:1534:G:N2	2.35	0.54
1:A:316:G:H3'	1:A:317:G:H8	1.73	0.54
1:A:405:G:H1'	1:A:406:A:H4'	1.89	0.54
1:A:625:G:N1	1:A:626:G:O6	2.40	0.54
1:A:735:C:O2'	1:A:825:G:OP1	2.25	0.54
1:A:1044:A:OP2	1:A:1198:G:N1	2.41	0.54
1:A:1362:C:O3'	1:A:2037:G:N2	2.40	0.54
31:a:819:C:O2'	31:a:910:A:N1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1125:C:H5'	44:n:57:ARG:HH22	1.73	0.54
32:b:47:VAL:O	32:b:51:ASP:N	2.38	0.54
44:n:6:MET:SD	44:n:19:ARG:NH1	2.80	0.54
1:A:344:U:H1'	1:A:345:C:H5'	1.90	0.54
1:A:1175:G:C4	1:A:2052:C:H4'	2.43	0.54
1:A:1365:G:N2	1:A:1367:C:O5'	2.41	0.54
1:A:2152:G:N2	1:A:2189:G:O2'	2.41	0.54
1:A:2272:U:H5''	1:A:2273:G:H4'	1.89	0.54
1:A:2319:U:C2	1:A:2320:C:H1'	2.43	0.54
31:a:517:A:N7	31:a:551:G:O2'	2.38	0.54
31:a:824:A:H5'	31:a:825:C:H2'	1.90	0.54
47:q:23:ILE:HG12	47:q:50:ASP:HB2	1.88	0.54
1:A:995:U:H2'	1:A:996:G:H8	1.72	0.54
1:A:2508:G:O2'	1:A:2509:A:N7	2.30	0.54
16:P:36:ASP:OD1	16:P:36:ASP:N	2.40	0.54
25:Y:8:GLU:OE1	25:Y:10:HIS:ND1	2.40	0.54
31:a:1313:C:N4	31:a:1314:G:O6	2.40	0.54
33:c:22:TRP:HB3	33:c:58:ARG:H	1.72	0.54
35:e:32:ARG:HA	35:e:54:GLN:HG3	1.89	0.54
39:i:15:LYS:HE2	39:i:113:LYS:HB2	1.89	0.54
1:A:902:A:C2	1:A:965:G:C2	2.96	0.54
31:a:1330:C:H5'	49:s:69:HIS:HE1	1.72	0.54
35:e:86:THR:HA	35:e:95:PHE:HA	1.90	0.54
42:l:85:HIS:HD2	42:l:87:LEU:H	1.55	0.54
1:A:522:G:H3'	1:A:523:A:H5''	1.89	0.54
4:D:6:LEU:H	4:D:33:ASN:HD21	1.55	0.54
29:3:26:ARG:HD3	29:3:48:ARG:HG3	1.90	0.54
31:a:77:G:H3'	31:a:78:A:H8	1.73	0.54
31:a:587:G:O6	31:a:770:U:C4	2.61	0.54
31:a:608:U:O2	31:a:646:G:O6	2.25	0.54
33:c:11:ARG:HH21	33:c:179:ALA:HB3	1.73	0.54
33:c:16:ARG:NH1	33:c:180:ASP:OD1	2.41	0.54
34:d:142:ARG:HG2	34:d:144:LYS:H	1.73	0.54
35:e:50:THR:OG1	35:e:51:GLY:N	2.40	0.54
1:A:351:G:N2	1:A:372:A:O2'	2.34	0.53
1:A:1251:A:H2'	1:A:1252:A:O4'	2.07	0.53
1:A:1283:G:N1	1:A:1284:A:N1	2.55	0.53
1:A:2125:U:O4	1:A:2218:G:O6	2.26	0.53
6:F:119:LYS:O	6:F:167:ARG:NH1	2.42	0.53
13:M:30:ARG:NH2	13:M:47:ASP:OD2	2.40	0.53
33:c:149:LYS:HB3	33:c:200:TRP:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:12:GLU:N	35:e:40:GLY:O	2.39	0.53
48:r:61:THR:HG22	48:r:65:LYS:HD3	1.89	0.53
1:A:294:G:H2'	1:A:295:G:C8	2.43	0.53
1:A:332:A:C5	1:A:393:G:C4	2.95	0.53
1:A:703:A:H3'	1:A:704:U:H4'	1.90	0.53
1:A:1827:C:OP2	3:C:182:ARG:NH2	2.41	0.53
3:C:40:LYS:O	3:C:42:GLY:N	2.41	0.53
13:M:86:ASP:N	13:M:86:ASP:OD1	2.39	0.53
15:O:50:ARG:O	15:O:54:LYS:NZ	2.41	0.53
31:a:160:A:N7	31:a:352:A:O2'	2.34	0.53
31:a:614:G:H1	31:a:641:U:H2'	1.74	0.53
31:a:681:G:H2'	31:a:682:G:C8	2.43	0.53
40:j:15:HIS:HA	40:j:18:ILE:HG22	1.91	0.53
50:t:30:THR:O	50:t:34:ASN:ND2	2.42	0.53
1:A:235:G:H1	1:A:265:A:N6	2.07	0.53
1:A:1040:A:C6	1:A:1203:U:N3	2.74	0.53
1:A:1193:U:H2'	1:A:1194:U:C6	2.44	0.53
10:J:55:LEU:O	10:J:60:ARG:NH1	2.42	0.53
31:a:310:G:H2'	31:a:311:G:C8	2.43	0.53
31:a:1016:A:N1	31:a:1031:C:O2'	2.42	0.53
31:a:1132:U:N3	31:a:1163:G:N1	2.56	0.53
52:v:162:VAL:HA	52:v:173:ILE:HG13	1.90	0.53
1:A:420:A:H3'	1:A:421:C:H6	1.74	0.53
1:A:604:G:O2'	15:O:45:TYR:OH	2.27	0.53
1:A:1128:A:N6	1:A:1150:A:N7	2.56	0.53
1:A:1352:C:N3	1:A:1374:G:N1	2.55	0.53
1:A:1463:A:H2'	1:A:1465:G:C8	2.44	0.53
1:A:1481:A:O2'	1:A:1520:A:N6	2.41	0.53
17:Q:25:ARG:NH1	17:Q:74:ALA:O	2.42	0.53
31:a:118:A:N7	31:a:295:U:O2	2.41	0.53
31:a:197:U:N3	31:a:198:G:O6	2.38	0.53
31:a:299:C:H2'	31:a:300:G:H8	1.73	0.53
31:a:405:A:N7	31:a:555:A:O2'	2.35	0.53
31:a:685:U:H3	31:a:721:G:H22	1.57	0.53
34:d:147:LYS:NZ	34:d:148:LEU:O	2.41	0.53
1:A:1099:G:N2	1:A:1129:A:N1	2.56	0.53
1:A:2140:C:N3	1:A:2195:G:O2'	2.41	0.53
1:A:2477:A:N6	1:A:2528:C:O2	2.36	0.53
31:a:304:U:O2	31:a:309:G:N2	2.37	0.53
31:a:411:C:H5'	34:d:128:ILE:HD11	1.91	0.53
40:j:47:SER:HB3	40:j:67:GLN:HG3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:3:VAL:HA	46:p:24:ASP:HA	1.90	0.53
46:p:58:LEU:O	46:p:62:ASN:ND2	2.41	0.53
1:A:334:A:H3'	1:A:335:U:H4'	1.91	0.53
1:A:864:A:H5'	1:A:1226:G:N1	2.24	0.53
1:A:1103:G:N1	1:A:1124:A:N7	2.56	0.53
1:A:2053:U:C2	1:A:2064:A:C2	2.95	0.53
1:A:2869:G:OP2	1:A:2887:G:N2	2.42	0.53
13:M:28:LYS:HB3	13:M:93:VAL:HG23	1.91	0.53
31:a:300:G:H3'	31:a:301:A:H8	1.73	0.53
31:a:840:G:N2	31:a:863:U:O2	2.36	0.53
31:a:1075:G:H5'	31:a:1077:C:H5''	1.90	0.53
1:A:47:C:O4'	1:A:181:G:N2	2.41	0.53
1:A:424:C:O2	1:A:442:G:N2	2.31	0.53
1:A:426:G:N7	1:A:427:A:N6	2.57	0.53
1:A:891:A:H1'	1:A:892:U:H5''	1.90	0.53
1:A:2477:A:H5''	1:A:2478:A:H8	1.74	0.53
3:C:69:ARG:O	3:C:189:ARG:NH1	2.41	0.53
6:F:62:GLY:H	6:F:95:ARG:HH11	1.54	0.53
17:Q:86:ARG:HG2	17:Q:89:GLY:H	1.73	0.53
31:a:209:G:OP1	50:t:59:LYS:NZ	2.40	0.53
1:A:491:C:H1'	1:A:495:A:O2'	2.08	0.53
1:A:1963:A:OP2	1:A:1989:C:N4	2.37	0.53
1:A:2830:A:H2'	1:A:2831:G:O4'	2.09	0.53
25:Y:54:SER:HA	25:Y:59:THR:HA	1.91	0.53
31:a:459:A:N6	31:a:489:G:O2'	2.40	0.53
31:a:1058:G:O3'	44:n:2:ALA:N	2.42	0.53
33:c:7:PRO:HA	33:c:10:LEU:HD23	1.91	0.53
34:d:167:PHE:HA	34:d:174:GLY:HA2	1.91	0.53
41:k:83:GLU:O	41:k:111:ARG:NH1	2.42	0.53
52:v:14:THR:OG1	52:v:15:ASP:N	2.41	0.53
1:A:1004:A:H5''	1:A:1005:G:H8	1.73	0.53
1:A:2544:C:H2'	1:A:2569:A:N7	2.24	0.53
1:A:2778:G:OP1	1:A:2778:G:N2	2.41	0.53
22:V:37:ARG:HD3	22:V:44:PRO:HB2	1.90	0.53
31:a:936:G:H1	31:a:1400:U:H3	1.55	0.53
32:b:94:GLN:HB2	32:b:147:PHE:HA	1.90	0.53
1:A:273:A:N6	1:A:298:U:C2	2.77	0.53
1:A:2589:U:H3	1:A:2593:A:H62	1.57	0.53
31:a:959:U:C2	31:a:1241:G:N1	2.75	0.53
45:o:36:ILE:HA	45:o:56:LEU:HD22	1.91	0.53
1:A:759:U:O2'	1:A:763:A:N6	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:900:G:C2	1:A:967:C:O2	2.54	0.52
1:A:1285:A:O2'	1:A:1287:U:O4'	2.27	0.52
1:A:2502:C:C2	1:A:2556:G:N1	2.77	0.52
7:G:60:GLU:O	7:G:63:THR:OG1	2.28	0.52
22:V:14:THR:HG22	22:V:28:ARG:HD2	1.91	0.52
31:a:944:A:H2	31:a:1393:C:H42	1.57	0.52
31:a:1000:U:N3	31:a:1223:A:C8	2.76	0.52
31:a:1329:A:C2	31:a:1371:G:N2	2.73	0.52
31:a:1456:A:OP1	31:a:1464:A:N6	2.43	0.52
45:o:42:HIS:O	45:o:45:THR:OG1	2.26	0.52
1:A:362:C:O2	1:A:366:G:C2	2.52	0.52
1:A:883:C:O2	1:A:984:G:N2	2.42	0.52
1:A:2803:A:O2'	1:A:2808:A:O2'	2.17	0.52
31:a:1325:U:H1'	31:a:1371:G:H5'	1.92	0.52
31:a:1357:G:N2	31:a:1358:U:O4	2.41	0.52
32:b:103:ASN:ND2	32:b:106:THR:OG1	2.43	0.52
1:A:52:A:H3'	1:A:53:A:H8	1.74	0.52
1:A:2569:A:OP1	1:A:2569:A:H4'	2.09	0.52
6:F:42:ASP:O	6:F:46:ASN:ND2	2.42	0.52
31:a:666:G:O6	31:a:755:U:O4	2.27	0.52
31:a:1379:C:H2'	31:a:1380:G:H8	1.73	0.52
31:a:1455:U:O4	31:a:1468:G:O6	2.27	0.52
32:b:30:TYR:HB3	32:b:201:PRO:HG3	1.91	0.52
34:d:148:LEU:HB2	34:d:151:ILE:HG13	1.92	0.52
47:q:9:VAL:O	47:q:62:LYS:NZ	2.39	0.52
1:A:1453:G:N3	1:A:1631:G:N1	2.58	0.52
1:A:2353:U:H3	1:A:2416:G:H1	1.56	0.52
7:G:23:HIS:HA	7:G:36:THR:HA	1.92	0.52
27:1:9:CYS:SG	27:1:12:CYS:N	2.79	0.52
31:a:412:G:HO2'	31:a:447:U:H3	1.55	0.52
31:a:651:C:O2'	38:h:86:ARG:NH1	2.43	0.52
31:a:691:G:N1	31:a:715:U:C2	2.77	0.52
1:A:605:U:H2'	16:P:78:ARG:NH2	2.24	0.52
1:A:1215:U:O2'	1:A:1217:U:OP2	2.26	0.52
1:A:2342:U:O2	6:F:125:ARG:NH2	2.42	0.52
1:A:2432:G:N2	1:A:2439:A:H61	2.01	0.52
6:F:115:GLN:NE2	6:F:176:PRO:O	2.42	0.52
31:a:726:A:N7	41:k:118:HIS:ND1	2.57	0.52
31:a:1263:G:H2'	31:a:1264:G:H8	1.75	0.52
32:b:184:VAL:HB	32:b:198:TYR:HB2	1.90	0.52
37:g:29:LYS:HE2	37:g:102:ARG:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:52:ASN:OD1	47:q:52:ASN:N	2.41	0.52
1:A:284:C:N3	1:A:286:U:C4	2.77	0.52
1:A:702:U:O2	1:A:703:A:N6	2.24	0.52
1:A:1018:A:O3'	1:A:1019:A:H8	1.93	0.52
1:A:1308:C:H5''	1:A:1309:G:H5'	1.90	0.52
1:A:1915:G:OP2	1:A:1915:G:N2	2.42	0.52
1:A:2319:U:H1'	1:A:2402:G:H4'	1.90	0.52
9:I:115:VAL:HG13	9:I:121:VAL:HG21	1.91	0.52
12:L:55:ASP:OD1	12:L:58:SER:OG	2.27	0.52
31:a:775:A:O2'	31:a:1535:C:O2	2.25	0.52
50:t:18:GLU:HA	50:t:21:ASN:HB2	1.92	0.52
1:A:342:A:N6	1:A:365:A:O2'	2.42	0.52
1:A:2082:C:H2'	1:A:2531:U:H4'	1.90	0.52
10:J:83:ASN:OD1	10:J:83:ASN:N	2.42	0.52
31:a:273:G:H2'	31:a:275:C:H5	1.74	0.52
31:a:380:C:O2	31:a:397:A:N6	2.43	0.52
31:a:577:C:H1'	31:a:582:A:H2'	1.90	0.52
31:a:1258:A:N6	31:a:1299:A:N7	2.58	0.52
31:a:1318:U:OP2	43:m:98:ARG:NH1	2.42	0.52
44:n:23:ARG:NH2	44:n:28:GLY:O	2.43	0.52
51:u:33:ARG:HH21	51:u:34:LYS:HB2	1.74	0.52
1:A:91:A:H2'	1:A:92:G:C8	2.45	0.52
1:A:2627:A:N6	3:C:236:GLU:OE1	2.37	0.52
31:a:592:G:O6	31:a:765:U:O4	2.27	0.52
1:A:1115:G:N1	1:A:1136:C:OP2	2.34	0.52
31:a:1161:A:H4'	40:j:43:PRO:HG3	1.92	0.52
31:a:1325:U:H5	31:a:1329:A:H62	1.56	0.52
34:d:58:ARG:NH2	34:d:65:GLU:OE1	2.43	0.52
38:h:21:ARG:NH1	38:h:70:ASP:O	2.42	0.52
1:A:223:G:O2'	1:A:224:A:O4'	2.26	0.52
1:A:524:A:H2'	1:A:526:A:N7	2.24	0.52
1:A:1247:G:O2'	1:A:1251:A:O4'	2.19	0.52
1:A:2483:C:H2'	1:A:2484:U:C6	2.45	0.52
4:D:54:GLU:O	4:D:86:ARG:N	2.39	0.52
31:a:382:A:N1	31:a:398:C:O2'	2.42	0.52
31:a:1369:C:OP2	44:n:35:ARG:NH1	2.43	0.52
1:A:883:C:H2'	1:A:884:U:C6	2.45	0.51
1:A:1297:G:O5'	1:A:1298:G:H5''	2.10	0.51
1:A:1363:U:O3'	1:A:2037:G:O2'	2.22	0.51
1:A:1462:G:H22	1:A:1625:U:H3'	1.75	0.51
1:A:2090:C:H3'	1:A:2477:A:C2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:41:ASP:N	22:V:41:ASP:OD1	2.42	0.51
31:a:1197:G:H21	44:n:61:TRP:HB2	1.73	0.51
47:q:64:GLN:HB3	47:q:76:ARG:HH21	1.75	0.51
51:u:31:GLU:OE2	51:u:35:ARG:NH1	2.42	0.51
52:v:34:ASP:N	52:v:34:ASP:OD1	2.35	0.51
1:A:1015:C:H3'	1:A:1016:G:N7	2.25	0.51
1:A:2502:C:O2	1:A:2556:G:C6	2.63	0.51
31:a:806:U:H2'	31:a:807:G:H8	1.76	0.51
31:a:985:G:H1	31:a:1373:A:H5''	1.76	0.51
31:a:1140:C:OP1	39:i:68:ASN:ND2	2.43	0.51
36:f:43:TRP:N	36:f:60:TYR:O	2.37	0.51
38:h:15:ARG:NH2	38:h:77:LEU:O	2.36	0.51
1:A:1455:U:O2'	1:A:1631:G:OP2	2.27	0.51
31:a:39:G:O2'	31:a:40:G:N2	2.39	0.51
31:a:435:C:H4'	31:a:549:G:H5'	1.92	0.51
31:a:675:G:O2'	45:o:48:LYS:O	2.25	0.51
36:f:42:ASP:HA	36:f:61:ASN:HA	1.92	0.51
1:A:2546:U:H2'	1:A:2568:A:N6	2.25	0.51
31:a:959:U:C4	31:a:1241:G:O6	2.64	0.51
31:a:1168:C:O2'	31:a:1191:G:N2	2.39	0.51
31:a:1378:A:OP2	39:i:115:ARG:NH2	2.43	0.51
41:k:26:THR:OG1	41:k:28:ASN:O	2.28	0.51
46:p:61:LEU:HD13	46:p:81:MET:HE2	1.91	0.51
1:A:200:A:C4	1:A:201:C:H1'	2.45	0.51
1:A:304:G:H2'	1:A:305:A:H8	1.75	0.51
1:A:2544:C:HO2'	1:A:2545:A:P	2.34	0.51
4:D:60:LYS:HG2	4:D:63:ALA:HB2	1.92	0.51
6:F:34:ILE:HG12	6:F:96:MET:HE2	1.91	0.51
18:R:26:THR:HG23	18:R:79:ILE:HG12	1.91	0.51
31:a:943:C:H4'	31:a:945:C:H41	1.75	0.51
32:b:114:ILE:HG12	32:b:145:ILE:HG23	1.92	0.51
50:t:25:LYS:HB2	50:t:65:LEU:HD21	1.93	0.51
1:A:961:G:H8	1:A:961:G:O5'	1.92	0.51
1:A:1000:G:H21	1:A:1004:A:N6	2.09	0.51
1:A:2717:A:OP2	12:L:10:SER:OG	2.29	0.51
7:G:37:LEU:HD11	7:G:72:LEU:HD13	1.91	0.51
31:a:55:C:H2'	31:a:360:C:H41	1.76	0.51
38:h:29:ALA:H	38:h:57:GLN:HB3	1.75	0.51
40:j:23:GLU:HA	40:j:26:VAL:HG12	1.93	0.51
1:A:89:U:H2'	1:A:90:A:C8	2.46	0.51
1:A:756:A:N1	1:A:764:C:N4	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:58:G:C2	31:a:364:A:C2	2.99	0.51
31:a:639:G:O2'	31:a:641:U:OP2	2.26	0.51
31:a:934:G:N2	31:a:1401:U:O2	2.33	0.51
34:d:3:ARG:O	34:d:5:ARG:NH2	2.41	0.51
37:g:30:ILE:HA	37:g:105:VAL:HG11	1.92	0.51
42:l:80:ILE:HG12	42:l:110:ILE:HD12	1.91	0.51
46:p:20:ILE:N	46:p:38:GLY:O	2.40	0.51
1:A:650:U:H2'	1:A:651:A:C8	2.46	0.51
1:A:1104:U:O2	1:A:1123:C:N4	2.44	0.51
6:F:58:GLU:HG3	6:F:65:PRO:HD3	1.93	0.51
13:M:40:ILE:H	13:M:58:SER:HB3	1.75	0.51
30:4:11:CYS:SG	30:4:12:GLU:N	2.84	0.51
31:a:1422:C:H2'	31:a:1423:A:C8	2.46	0.51
1:A:333:C:OP2	1:A:392:U:O2'	2.22	0.51
1:A:809:A:H61	1:A:1816:A:H8	1.58	0.51
1:A:996:G:N1	1:A:1009:C:C2	2.75	0.51
6:F:100:LEU:HD13	6:F:104:ILE:HD13	1.93	0.51
6:F:148:LYS:NZ	6:F:149:VAL:O	2.37	0.51
31:a:171:A:H2'	31:a:172:A:C8	2.45	0.51
32:b:53:ALA:HA	32:b:56:PHE:HB3	1.93	0.51
37:g:42:ILE:HG12	37:g:117:GLU:HA	1.92	0.51
39:i:52:GLN:HA	39:i:55:ASP:HB2	1.93	0.51
43:m:64:LYS:O	43:m:69:LEU:N	2.44	0.51
1:A:229:A:N6	1:A:464:U:O2'	2.44	0.51
1:A:1186:A:H1'	1:A:1187:A:H2'	1.93	0.51
31:a:384:G:H2'	31:a:385:G:H8	1.75	0.51
31:a:385:G:OP1	46:p:4:LYS:NZ	2.44	0.51
31:a:890:G:OP2	42:l:9:ARG:NH1	2.43	0.51
31:a:1015:A:N6	31:a:1029:A:N7	2.59	0.51
35:e:105:VAL:O	35:e:112:ARG:NH2	2.44	0.51
43:m:20:THR:HG22	43:m:26:GLY:HA2	1.92	0.51
46:p:19:ARG:HA	46:p:39:THR:HA	1.92	0.51
1:A:626:G:H3'	1:A:627:C:H3'	1.93	0.50
1:A:1712:A:O2'	1:A:1718:G:N7	2.38	0.50
1:A:1796:A:O2'	1:A:1985:C:OP1	2.28	0.50
1:A:2855:A:H2	1:A:2900:C:H41	1.58	0.50
31:a:749:G:H3'	31:a:750:G:H8	1.75	0.50
31:a:1141:A:H61	31:a:1155:C:H2'	1.76	0.50
32:b:118:GLU:OE1	32:b:152:ARG:NH1	2.44	0.50
33:c:153:SER:HA	33:c:164:ALA:HA	1.93	0.50
41:k:27:PHE:O	41:k:58:SER:OG	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:14:ARG:NE	43:m:41:ALA:O	2.41	0.50
52:v:10:ASN:O	52:v:46:THR:OG1	2.28	0.50
1:A:21:A:H2'	1:A:22:C:C6	2.47	0.50
1:A:1092:A:N6	1:A:1154:G:O2'	2.25	0.50
1:A:2080:G:H1	1:A:2643:C:H42	1.60	0.50
1:A:2195:G:N1	1:A:2197:G:N7	2.58	0.50
31:a:1139:C:H1'	31:a:1159:C:H42	1.76	0.50
32:b:67:VAL:HG22	32:b:160:ALA:HB3	1.92	0.50
34:d:99:TYR:HB2	34:d:107:ARG:HE	1.76	0.50
1:A:618:A:O2'	1:A:2527:U:OP1	2.23	0.50
1:A:872:U:H4'	1:A:873:U:C2	2.46	0.50
1:A:2458:U:H3	1:A:2460:A:H62	1.59	0.50
31:a:264:U:O4	31:a:274:G:N2	2.45	0.50
31:a:691:G:O6	31:a:716:A:N6	2.44	0.50
31:a:1316:A:N6	31:a:1341:G:O2'	2.44	0.50
40:j:20:GLN:HA	40:j:23:GLU:HB2	1.93	0.50
43:m:73:THR:O	43:m:77:ILE:N	2.43	0.50
48:r:57:GLN:O	48:r:61:THR:OG1	2.29	0.50
1:A:634:C:H2'	1:A:635:G:H8	1.77	0.50
4:D:38:LYS:HD2	4:D:96:VAL:HG22	1.93	0.50
5:E:154:VAL:HB	5:E:193:VAL:HG22	1.94	0.50
32:b:59:GLN:HA	32:b:62:GLU:HB2	1.92	0.50
33:c:23:TYR:HB2	40:j:95:GLY:HA2	1.92	0.50
34:d:98:VAL:HG23	34:d:107:ARG:HB2	1.94	0.50
36:f:20:LYS:HA	36:f:23:VAL:HG22	1.94	0.50
40:j:97:ASP:N	40:j:97:ASP:OD1	2.45	0.50
42:l:49:ARG:NH2	42:l:65:TYR:OH	2.45	0.50
52:v:30:ARG:HH12	52:v:38:ALA:HB3	1.74	0.50
1:A:1053:A:H4'	15:O:59:LYS:HB2	1.94	0.50
1:A:1085:U:O4	1:A:1158:G:O6	2.30	0.50
1:A:2059:G:N7	1:A:2481:G:O2'	2.25	0.50
1:A:2905:C:N4	26:Z:29:GLU:O	2.35	0.50
3:C:67:PHE:HE1	3:C:105:ILE:HD11	1.77	0.50
40:j:18:ILE:HD12	40:j:21:SER:HB2	1.93	0.50
1:A:642:U:O2	1:A:703:A:N1	2.44	0.50
1:A:714:G:H1'	1:A:846:G:N2	2.27	0.50
1:A:1182:G:C6	1:A:1183:G:H1'	2.46	0.50
1:A:2496:A:C8	1:A:2508:G:C2	2.97	0.50
2:B:11:A:O2'	2:B:13:A:OP2	2.27	0.50
9:I:35:ILE:HD11	9:I:65:THR:H	1.76	0.50
31:a:38:U:O2'	31:a:555:A:N1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1013:A:O2'	31:a:1048:C:N3	2.44	0.50
34:d:165:LEU:HA	34:d:176:PHE:HA	1.94	0.50
42:l:63:ARG:HB3	42:l:79:TYR:HE1	1.77	0.50
47:q:70:SER:OG	47:q:71:ALA:N	2.42	0.50
1:A:52:A:H3'	1:A:53:A:C8	2.47	0.50
1:A:613:G:H1	1:A:2525:C:H5'	1.77	0.50
1:A:621:A:C2	1:A:2045:A:H1'	2.47	0.50
1:A:957:C:O2'	1:A:958:U:O4'	2.28	0.50
1:A:1440:A:H1'	1:A:1513:A:H2	1.77	0.50
1:A:1501:G:N2	1:A:2729:G:H22	2.09	0.50
1:A:2654:G:H21	1:A:2808:A:H2	1.58	0.50
1:A:2891:U:O5'	1:A:2892:G:H5'	2.12	0.50
25:Y:34:MET:H	25:Y:44:PRO:HG3	1.77	0.50
31:a:404:A:H2'	31:a:406:C:H5	1.76	0.50
31:a:934:G:O6	31:a:1401:U:O4	2.30	0.50
31:a:944:A:H62	37:g:2:PRO:HD2	1.77	0.50
31:a:1263:G:H2'	31:a:1264:G:C8	2.46	0.50
32:b:218:ALA:HA	32:b:221:ILE:HG23	1.94	0.50
33:c:154:GLY:H	33:c:195:LEU:HD23	1.76	0.50
36:f:19:LYS:NZ	36:f:43:TRP:O	2.45	0.50
1:A:64:A:N6	1:A:90:A:O4'	2.45	0.50
1:A:885:C:O2'	1:A:1230:G:O2'	2.29	0.50
1:A:1174:U:N3	1:A:2052:C:OP1	2.31	0.50
1:A:1283:G:C6	1:A:1284:A:C6	2.99	0.50
1:A:1488:A:H61	1:A:1595:C:H42	1.59	0.50
13:M:81:ALA:O	13:M:85:ALA:HB2	2.12	0.50
17:Q:41:LYS:HE2	26:Z:22:ILE:HD11	1.92	0.50
31:a:81:A:N6	31:a:86:G:N7	2.59	0.50
31:a:754:G:H5'	31:a:844:G:H21	1.77	0.50
32:b:101:LEU:HD11	32:b:158:PRO:HG2	1.91	0.50
1:A:337:A:H3'	1:A:338:G:H4'	1.94	0.50
1:A:1477:U:H2'	1:A:1478:A:C8	2.46	0.50
1:A:2830:A:C5	1:A:2910:G:N2	2.64	0.50
8:H:15:LYS:NZ	8:H:139:GLU:OE2	2.41	0.50
16:P:15:GLU:H	16:P:18:GLN:HE21	1.58	0.50
31:a:419:A:H8	31:a:439:A:H61	1.60	0.50
31:a:703:A:H2	31:a:795:A:H1'	1.76	0.50
31:a:1295:A:N6	31:a:1364:U:O2'	2.45	0.50
33:c:107:LYS:HG3	33:c:143:LEU:HG	1.94	0.50
1:A:651:A:N6	1:A:666:A:H61	2.10	0.49
1:A:1287:U:O2	10:J:18:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:121:CYS:SG	41:k:122:ARG:N	2.85	0.49
43:m:53:LEU:HA	43:m:56:ILE:HG12	1.94	0.49
1:A:587:C:O2'	1:A:588:G:N7	2.45	0.49
1:A:923:A:C6	1:A:944:G:O6	2.64	0.49
1:A:993:C:H1'	1:A:1028:G:H8	1.77	0.49
1:A:1209:U:H2'	1:A:1210:U:C6	2.47	0.49
31:a:129:A:H62	31:a:193:C:H4'	1.76	0.49
31:a:775:A:O3'	31:a:1535:C:O2'	2.28	0.49
31:a:1128:A:H2'	31:a:1129:A:H8	1.77	0.49
31:a:1169:U:H1'	31:a:1171:C:H41	1.77	0.49
31:a:1252:G:O6	31:a:1305:U:O4	2.30	0.49
31:a:1275:C:H2'	31:a:1276:G:C8	2.47	0.49
31:a:1450:U:O4	31:a:1472:G:O6	2.31	0.49
32:b:68:LEU:O	32:b:162:PHE:N	2.43	0.49
47:q:11:VAL:HA	47:q:62:LYS:HA	1.92	0.49
49:s:60:VAL:HG11	49:s:74:PHE:HB3	1.94	0.49
1:A:24:G:H1	1:A:561:C:H42	1.59	0.49
1:A:366:G:OP1	1:A:382:U:O2'	2.29	0.49
1:A:524:A:C2	1:A:544:U:H2'	2.47	0.49
1:A:643:G:C6	1:A:703:A:C5	3.00	0.49
1:A:1064:A:N3	1:A:1065:A:N6	2.58	0.49
1:A:1111:A:N1	1:A:1139:A:O2'	2.43	0.49
1:A:1197:C:H3'	1:A:1198:G:H8	1.76	0.49
1:A:1702:C:N4	1:A:2028:A:H61	2.10	0.49
1:A:2825:U:H2'	1:A:2826:U:C6	2.46	0.49
4:D:129:GLY:HA2	4:D:170:PRO:HB3	1.92	0.49
21:U:40:THR:HA	21:U:72:ASP:HB3	1.94	0.49
31:a:130:A:H5'	47:q:67:ARG:HD3	1.93	0.49
31:a:381:A:H61	31:a:399:G:H1'	1.78	0.49
31:a:1175:U:O2	31:a:1176:G:O2'	2.30	0.49
31:a:1258:A:N6	31:a:1300:G:N7	2.60	0.49
33:c:109:ASP:OD2	33:c:139:ARG:NH2	2.45	0.49
37:g:30:ILE:HG21	37:g:43:LEU:HD13	1.95	0.49
48:r:53:SER:OG	48:r:54:ALA:N	2.44	0.49
1:A:49:A:N7	1:A:119:U:O4	2.45	0.49
1:A:1552:U:O2'	1:A:1553:A:O4'	2.30	0.49
1:A:1982:U:H3	1:A:2579:U:HO2'	1.60	0.49
1:A:2090:C:H3'	1:A:2477:A:H2	1.77	0.49
10:J:110:LYS:HD3	10:J:127:LYS:HB3	1.93	0.49
31:a:1329:A:H61	31:a:1371:G:H1'	1.76	0.49
32:b:23:TRP:HE1	32:b:31:ILE:HD11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:24:ASN:HD22	32:b:27:MET:HG2	1.77	0.49
41:k:32:VAL:HG13	41:k:45:SER:HB3	1.95	0.49
47:q:48:THR:HA	47:q:75:PHE:HB2	1.94	0.49
1:A:885:C:H4'	1:A:1230:G:H1'	1.94	0.49
1:A:1240:U:O2	1:A:1283:G:N2	2.45	0.49
1:A:2355:A:H2'	1:A:2356:A:C8	2.47	0.49
1:A:2689:A:H3'	1:A:2690:G:C8	2.47	0.49
31:a:35:C:H2'	31:a:36:G:H8	1.77	0.49
31:a:1425:G:N2	31:a:1496:U:O2	2.42	0.49
32:b:117:ILE:HD11	32:b:137:LEU:HD22	1.93	0.49
37:g:74:GLU:HG2	37:g:91:VAL:HG22	1.94	0.49
47:q:26:LEU:HA	47:q:45:LYS:HG2	1.94	0.49
1:A:620:G:O2'	1:A:1292:A:OP1	2.30	0.49
1:A:2486:A:N1	1:A:2520:U:O2	2.46	0.49
3:C:243:ARG:HH11	3:C:247:MET:HE3	1.77	0.49
31:a:969:U:O2'	31:a:1235:A:N7	2.41	0.49
31:a:1259:C:O2'	39:i:74:PHE:N	2.46	0.49
32:b:134:VAL:HA	32:b:137:LEU:HB2	1.94	0.49
39:i:112:MET:N	39:i:112:MET:SD	2.86	0.49
1:A:89:U:H3'	1:A:90:A:H3'	1.94	0.49
1:A:646:A:N6	1:A:699:U:N3	2.33	0.49
1:A:1353:A:H61	1:A:1372:C:N4	2.10	0.49
2:B:22:G:N7	2:B:54:U:O2'	2.45	0.49
31:a:1001:U:C2	31:a:1055:A:N7	2.80	0.49
31:a:1309:A:O2'	31:a:1311:U:N3	2.46	0.49
31:a:1450:U:H2'	31:a:1451:G:H8	1.78	0.49
42:l:112:ARG:HG3	42:l:119:GLY:HA2	1.94	0.49
44:n:7:VAL:HG23	44:n:23:ARG:HB2	1.94	0.49
1:A:332:A:C8	1:A:393:G:C8	3.01	0.49
1:A:365:A:O2'	1:A:366:G:H5'	2.12	0.49
1:A:945:A:H2'	1:A:946:A:H8	1.78	0.49
11:K:116:GLU:OE2	11:K:119:ARG:NH2	2.33	0.49
15:O:108:GLN:O	15:O:111:THR:OG1	2.30	0.49
31:a:111:G:H21	31:a:362:G:H5'	1.78	0.49
31:a:235:G:O2'	46:p:63:ASP:OD2	2.29	0.49
31:a:684:A:H5'	41:k:115:PRO:HB3	1.94	0.49
31:a:1484:G:H2'	31:a:1485:G:C8	2.47	0.49
31:a:1507:C:OP1	52:v:20:TYR:OH	2.31	0.49
43:m:14:ARG:O	43:m:18:SER:N	2.40	0.49
46:p:58:LEU:HD21	46:p:87:GLN:HB3	1.93	0.49
1:A:33:U:C2	1:A:493:A:N7	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:A:H1'	1:A:404:U:H5'	1.94	0.49
1:A:2128:G:H1	1:A:2215:U:H3	1.61	0.49
3:C:167:LYS:HG2	3:C:172:VAL:HG12	1.94	0.49
31:a:440:A:H5''	31:a:441:A:C8	2.48	0.49
31:a:1259:C:N4	31:a:1298:A:O5'	2.45	0.49
31:a:1271:A:H3'	31:a:1272:A:H8	1.78	0.49
37:g:30:ILE:HG12	37:g:43:LEU:HD22	1.94	0.49
41:k:61:PHE:HA	41:k:64:GLN:HB2	1.94	0.49
42:l:61:ALA:HB3	42:l:63:ARG:HD2	1.95	0.49
1:A:380:U:H2'	1:A:381:G:C8	2.48	0.49
1:A:903:G:N3	1:A:2295:A:H2'	2.28	0.49
1:A:926:G:O2'	1:A:941:A:N1	2.46	0.49
1:A:1017:A:HO2'	1:A:1018:A:P	2.33	0.49
1:A:2472:G:H2'	1:A:2473:G:N9	2.27	0.49
1:A:2509:A:N1	11:K:124:LYS:NZ	2.46	0.49
1:A:2757:U:O2'	4:D:181:GLN:O	2.29	0.49
31:a:98:U:H2'	31:a:99:U:H1'	1.93	0.49
35:e:15:VAL:HA	35:e:37:VAL:HG12	1.93	0.49
45:o:34:ALA:O	45:o:38:ALA:N	2.44	0.49
45:o:39:VAL:HA	45:o:42:HIS:HB3	1.94	0.49
46:p:6:ARG:HH11	46:p:29:ARG:HA	1.77	0.49
49:s:15:LEU:HD22	49:s:38:SER:HB2	1.95	0.49
1:A:168:A:H3'	1:A:169:G:H8	1.77	0.48
1:A:584:G:C2	1:A:597:U:O2	2.64	0.48
1:A:1574:G:O6	1:A:1592:A:O2'	2.29	0.48
1:A:1737:U:O2'	3:C:14:ARG:NH2	2.46	0.48
1:A:2369:C:C2	1:A:2370:U:H1'	2.48	0.48
1:A:2481:G:H5''	1:A:2599:A:N3	2.28	0.48
29:3:33:PHE:HB3	29:3:41:LYS:HE2	1.95	0.48
31:a:700:U:H3	41:k:54:GLY:HA2	1.78	0.48
33:c:94:THR:OG1	33:c:95:ASP:N	2.44	0.48
35:e:21:VAL:HB	35:e:32:ARG:HG3	1.95	0.48
43:m:86:TYR:HA	43:m:89:ILE:HB	1.95	0.48
51:u:14:ASP:HA	51:u:17:ARG:HB2	1.95	0.48
1:A:893:G:O4'	1:A:978:A:O2'	2.31	0.48
1:A:1240:U:O2'	5:E:41:ARG:NE	2.47	0.48
1:A:2525:C:H5''	1:A:2526:C:OP1	2.13	0.48
1:A:2800:U:C4	1:A:2801:C:N4	2.81	0.48
20:T:34:TYR:OH	20:T:95:ASN:O	2.31	0.48
31:a:151:A:H62	31:a:170:U:H1'	1.78	0.48
31:a:783:G:O2'	31:a:812:U:O4	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:86:THR:OG1	35:e:87:GLY:N	2.44	0.48
37:g:17:ILE:HG22	37:g:18:HIS:HD2	1.78	0.48
52:v:43:LYS:N	52:v:55:GLU:O	2.41	0.48
1:A:1053:A:H3'	1:A:1054:A:C8	2.49	0.48
1:A:2456:G:O2'	1:A:2459:A:OP1	2.21	0.48
1:A:2501:U:OP2	1:A:2502:C:N4	2.38	0.48
1:A:2546:U:H1'	1:A:2547:C:H5	1.78	0.48
19:S:32:ARG:HB3	19:S:62:ALA:HB1	1.95	0.48
31:a:1077:C:C2	31:a:1201:A:N6	2.81	0.48
31:a:1186:A:H61	31:a:1191:G:H8	1.59	0.48
31:a:1289:A:O2'	31:a:1291:U:OP2	2.30	0.48
31:a:1345:C:H5'	31:a:1347:G:H21	1.78	0.48
32:b:92:ILE:HG12	32:b:151:ILE:HD11	1.94	0.48
34:d:97:VAL:HG13	34:d:101:LEU:HD11	1.95	0.48
45:o:26:GLU:HB3	45:o:81:LEU:HD21	1.95	0.48
1:A:225:A:N1	1:A:237:U:H4'	2.28	0.48
1:A:1240:U:O2	5:E:41:ARG:NH2	2.46	0.48
1:A:1353:A:H61	1:A:1372:C:H42	1.60	0.48
31:a:980:G:N1	31:a:1374:U:O2'	2.46	0.48
35:e:14:ARG:NH1	35:e:116:GLU:OE1	2.44	0.48
43:m:89:ILE:O	43:m:93:ARG:N	2.45	0.48
45:o:28:GLN:HA	45:o:31:VAL:HB	1.94	0.48
46:p:5:ILE:HB	46:p:71:VAL:HG21	1.95	0.48
1:A:219:A:O4'	1:A:478:A:N6	2.46	0.48
1:A:521:U:H4'	1:A:555:C:OP2	2.14	0.48
1:A:529:A:O2'	19:S:45:GLN:O	2.21	0.48
1:A:2594:G:O2'	1:A:2595:C:H5'	2.13	0.48
31:a:63:U:H1'	31:a:387:C:H1'	1.94	0.48
31:a:453:G:H2'	31:a:454:G:C8	2.48	0.48
31:a:889:C:H5''	42:l:9:ARG:HH22	1.78	0.48
31:a:953:G:N1	31:a:1348:G:OP2	2.39	0.48
31:a:1268:G:N2	31:a:1288:A:N1	2.62	0.48
34:d:54:LYS:HD3	34:d:55:GLN:HE22	1.79	0.48
45:o:64:ARG:HA	45:o:67:LEU:HD12	1.96	0.48
50:t:30:THR:HG22	50:t:34:ASN:HD21	1.78	0.48
1:A:36:G:H1'	1:A:496:G:C4	2.49	0.48
1:A:2319:U:C4	1:A:2320:C:C2	3.02	0.48
1:A:2542:C:O2	1:A:2597:G:N1	2.46	0.48
4:D:121:VAL:HG12	4:D:177:THR:HG22	1.96	0.48
31:a:1525:U:O2	31:a:1532:G:C2	2.66	0.48
32:b:64:GLY:O	32:b:66:GLN:NE2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:135:VAL:HG12	37:g:139:GLU:HB2	1.96	0.48
46:p:9:ARG:HA	46:p:18:TYR:HA	1.94	0.48
1:A:420:A:H4'	1:A:468:A:H2	1.78	0.48
1:A:1088:C:C2	1:A:1092:A:H8	2.30	0.48
31:a:231:U:H2'	31:a:232:A:C8	2.48	0.48
33:c:113:ARG:HD2	33:c:116:ALA:HB3	1.96	0.48
40:j:13:TYR:HE1	40:j:67:GLN:HB2	1.77	0.48
50:t:57:VAL:HG11	50:t:74:ILE:HG21	1.96	0.48
52:v:28:LEU:HD13	52:v:31:TYR:HE2	1.77	0.48
52:v:30:ARG:HH22	52:v:38:ALA:H	1.61	0.48
1:A:176:A:H1'	1:A:177:G:C8	2.48	0.48
1:A:333:C:H3'	1:A:334:A:C8	2.49	0.48
1:A:442:G:H5''	22:V:32:ASN:HB2	1.95	0.48
1:A:534:G:N2	1:A:535:G:H3'	2.28	0.48
1:A:644:C:H2'	1:A:645:A:H8	1.79	0.48
1:A:1092:A:O3'	1:A:1156:G:N2	2.45	0.48
1:A:1453:G:H1'	1:A:1631:G:H22	1.78	0.48
1:A:2092:C:H2'	1:A:2093:C:C6	2.49	0.48
1:A:2507:C:H2'	1:A:2508:G:O4'	2.13	0.48
1:A:2654:G:H3'	1:A:2655:U:H6	1.78	0.48
31:a:137:U:H5'	46:p:66:LYS:HD3	1.95	0.48
31:a:140:A:H2'	31:a:141:A:H8	1.79	0.48
31:a:326:G:O2'	31:a:1479:A:O2'	2.31	0.48
31:a:692:U:H2'	31:a:693:G:C4	2.48	0.48
31:a:1245:U:O2'	31:a:1315:G:OP1	2.30	0.48
31:a:1272:A:H2'	31:a:1273:A:H8	1.79	0.48
31:a:1381:G:OP2	39:i:15:LYS:NZ	2.34	0.48
31:a:1384:A:O2'	37:g:28:ASN:O	2.31	0.48
34:d:48:GLY:HA2	34:d:51:LEU:HB3	1.95	0.48
47:q:66:THR:OG1	47:q:67:ARG:N	2.47	0.48
1:A:230:A:H61	1:A:456:G:H21	1.62	0.48
5:E:3:ASN:HA	5:E:17:ILE:O	2.14	0.48
10:J:80:ASP:OD1	10:J:80:ASP:N	2.44	0.48
31:a:142:G:N2	31:a:230:U:H3	2.12	0.48
31:a:789:A:N7	31:a:809:U:C2	2.82	0.48
31:a:955:A:HO2'	31:a:956:G:H8	1.60	0.48
31:a:1092:G:H2'	31:a:1093:A:H8	1.78	0.48
42:l:72:ASN:N	42:l:72:ASN:OD1	2.45	0.48
1:A:342:A:N6	1:A:365:A:HO2'	2.12	0.48
1:A:919:G:N1	1:A:949:C:OP2	2.47	0.48
1:A:2339:U:H5'	6:F:71:LYS:HD3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:50:GLN:HE22	4:D:76:HIS:HE1	1.62	0.48
7:G:84:VAL:HA	7:G:133:VAL:O	2.14	0.48
31:a:842:U:H2'	31:a:843:A:C8	2.48	0.48
31:a:1357:G:H5'	39:i:114:GLU:H	1.78	0.48
33:c:131:ARG:HH12	33:c:135:GLN:HE21	1.62	0.48
34:d:13:ARG:HH22	34:d:28:LYS:H	1.61	0.48
42:l:113:GLY:H	42:l:117:THR:HG23	1.79	0.48
1:A:35:G:N2	1:A:491:C:C2	2.81	0.47
1:A:866:A:H2'	1:A:990:G:C8	2.49	0.47
1:A:2391:C:H2'	1:A:2392:G:C8	2.49	0.47
1:A:2471:G:C6	1:A:2472:G:C2	3.02	0.47
1:A:2652:G:H2'	1:A:2653:C:C6	2.49	0.47
1:A:2682:G:N2	1:A:2691:G:H2'	2.29	0.47
1:A:2801:C:C6	1:A:2802:A:H1'	2.49	0.47
1:A:2905:C:H2'	1:A:2906:G:H4'	1.95	0.47
6:F:66:LEU:HB3	6:F:88:LYS:HZ2	1.79	0.47
9:I:67:SER:O	9:I:67:SER:OG	2.30	0.47
31:a:384:G:H2'	31:a:385:G:C8	2.49	0.47
31:a:1024:G:H2'	31:a:1025:A:C8	2.49	0.47
31:a:1273:A:H61	31:a:1282:U:H3	1.60	0.47
32:b:41:ILE:HG12	32:b:201:PRO:HG2	1.95	0.47
32:b:47:VAL:HA	32:b:50:VAL:HG12	1.95	0.47
32:b:176:ALA:HA	32:b:181:ILE:HD12	1.95	0.47
35:e:80:THR:OG1	35:e:81:THR:N	2.47	0.47
36:f:74:ASP:HA	36:f:77:GLN:HB2	1.95	0.47
39:i:53:PRO:HG3	39:i:82:ARG:HE	1.79	0.47
1:A:1202:C:H2'	1:A:1203:U:N1	2.28	0.47
1:A:2391:C:H2'	1:A:2392:G:H8	1.78	0.47
31:a:510:C:H42	31:a:552:G:H1	1.62	0.47
31:a:705:U:H3'	31:a:706:G:H8	1.79	0.47
32:b:68:LEU:HB2	32:b:158:PRO:HB3	1.95	0.47
47:q:70:SER:HB3	47:q:73:LYS:HE2	1.96	0.47
1:A:304:G:H2'	1:A:305:A:C8	2.49	0.47
1:A:329:A:N6	1:A:397:U:O4	2.40	0.47
1:A:579:U:H5'	15:O:42:SER:HB2	1.95	0.47
1:A:863:G:H22	1:A:1226:G:H3'	1.79	0.47
1:A:1241:A:H5'	5:E:41:ARG:HD3	1.97	0.47
1:A:1283:G:C6	1:A:1284:A:N6	2.83	0.47
31:a:464:A:N7	31:a:465:U:N3	2.62	0.47
31:a:737:A:H2'	31:a:738:G:C8	2.49	0.47
31:a:1146:U:O2	31:a:1148:A:O2'	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1278:G:H21	31:a:1337:A:H1'	1.78	0.47
32:b:15:HIS:HB2	32:b:40:ILE:HG23	1.95	0.47
39:i:42:PRO:HD3	39:i:74:PHE:HE2	1.79	0.47
42:l:39:ASN:N	42:l:39:ASN:OD1	2.47	0.47
49:s:18:LYS:HA	49:s:21:ALA:HB3	1.96	0.47
50:t:10:ARG:HA	50:t:13:THR:HG22	1.96	0.47
1:A:302:A:N6	1:A:414:C:H42	2.11	0.47
1:A:527:G:HO2'	1:A:552:A:H61	1.59	0.47
1:A:1512:U:H2'	1:A:1513:A:C8	2.48	0.47
1:A:1936:C:N4	1:A:1949:G:O6	2.46	0.47
1:A:2918:A:H2'	1:A:2919:A:C8	2.50	0.47
53:A:3001:ERY:H362	53:A:3001:ERY:H351	1.69	0.47
12:L:55:ASP:OD1	12:L:55:ASP:N	2.41	0.47
31:a:459:A:O4'	31:a:489:G:N1	2.47	0.47
31:a:664:G:H21	45:o:23:GLY:HA3	1.78	0.47
31:a:682:G:H21	41:k:118:HIS:H	1.61	0.47
31:a:1115:G:H4'	32:b:113:ARG:HH22	1.79	0.47
32:b:100:LEU:HA	32:b:107:ILE:HB	1.97	0.47
34:d:49:LEU:O	34:d:53:GLU:N	2.40	0.47
34:d:111:ARG:NH2	34:d:115:ASN:OD1	2.47	0.47
37:g:31:MET:HE1	37:g:36:ARG:HH11	1.78	0.47
40:j:35:ASP:N	40:j:35:ASP:OD1	2.47	0.47
1:A:31:C:N3	1:A:520:G:N1	2.59	0.47
1:A:1490:G:O2'	1:A:1491:C:O4'	2.33	0.47
1:A:1520:A:H61	1:A:1561:G:H2'	1.79	0.47
1:A:1625:U:H2'	1:A:1626:A:H8	1.79	0.47
7:G:63:THR:OG1	7:G:64:ASN:N	2.47	0.47
31:a:8:G:H22	31:a:568:A:H62	1.63	0.47
31:a:411:C:O2'	31:a:447:U:O2	2.29	0.47
31:a:748:U:H2'	31:a:749:G:H8	1.79	0.47
31:a:1345:C:H4'	31:a:1346:U:H5'	1.95	0.47
36:f:5:GLU:HG2	36:f:64:ARG:HG2	1.96	0.47
36:f:41:LYS:HB2	36:f:62:ILE:HB	1.97	0.47
37:g:49:LEU:HB2	37:g:121:ALA:HB1	1.96	0.47
37:g:71:PRO:HD3	37:g:137:LYS:HE3	1.96	0.47
1:A:858:U:H1'	1:A:1234:G:N2	2.29	0.47
1:A:1040:A:N6	1:A:1203:U:C4	2.79	0.47
1:A:1299:U:H2'	1:A:1300:G:O4'	2.14	0.47
1:A:2424:G:O6	1:A:2446:U:O4	2.33	0.47
1:A:2778:G:H1'	7:G:3:ARG:HB2	1.97	0.47
31:a:925:G:H2'	31:a:926:G:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1151:U:H2'	31:a:1152:G:H8	1.80	0.47
35:e:42:LYS:HA	35:e:118:ALA:HA	1.95	0.47
1:A:117:A:H5'	1:A:118:A:H8	1.80	0.47
1:A:615:A:N3	1:A:616:G:N2	2.57	0.47
1:A:1044:A:H2'	1:A:1045:A:H1'	1.97	0.47
1:A:2421:C:H42	1:A:2449:C:N4	2.12	0.47
1:A:2541:U:O2	1:A:2542:C:H5	1.98	0.47
1:A:2682:G:O2'	1:A:2691:G:N1	2.46	0.47
6:F:163:ASP:OD1	6:F:163:ASP:N	2.48	0.47
31:a:27:A:N6	31:a:566:G:H21	2.12	0.47
31:a:106:G:C2	31:a:107:G:H1'	2.49	0.47
31:a:330:C:O2'	50:t:18:GLU:OE1	2.33	0.47
31:a:403:C:H2'	31:a:404:A:C8	2.49	0.47
31:a:609:G:O6	31:a:645:U:O4	2.33	0.47
31:a:723:A:H2'	31:a:724:A:C8	2.49	0.47
31:a:917:A:H2'	31:a:918:A:H8	1.79	0.47
31:a:947:A:H1'	31:a:1387:A:H5''	1.97	0.47
31:a:994:C:H2'	31:a:995:A:C8	2.46	0.47
31:a:1001:U:N3	31:a:1055:A:C8	2.83	0.47
31:a:1094:U:O2'	31:a:1113:A:OP2	2.28	0.47
31:a:1195:G:H2'	31:a:1196:G:C8	2.49	0.47
40:j:49:TYR:HB2	40:j:65:PHE:HB2	1.96	0.47
50:t:57:VAL:HB	50:t:74:ILE:HD13	1.97	0.47
1:A:954:A:O2'	1:A:956:A:OP2	2.32	0.47
1:A:1086:G:O6	1:A:1157:U:O4	2.33	0.47
1:A:1228:A:H5''	10:J:32:GLY:HA2	1.96	0.47
1:A:1453:G:H1'	1:A:1631:G:H1	1.79	0.47
1:A:1454:U:H2'	1:A:1456:U:C4	2.50	0.47
1:A:1877:G:H22	1:A:1918:G:H1	1.62	0.47
1:A:2219:C:H2'	1:A:2220:U:C6	2.50	0.47
1:A:2332:U:H5''	6:F:131:GLY:HA3	1.97	0.47
1:A:2675:G:H1	1:A:2699:U:H3	0.64	0.47
31:a:333:A:H5'	50:t:64:ASN:HD21	1.80	0.47
31:a:795:A:N6	31:a:802:A:OP2	2.44	0.47
31:a:991:U:N3	31:a:1233:C:N3	2.56	0.47
31:a:1422:C:H2'	31:a:1423:A:H8	1.79	0.47
33:c:189:ASP:HA	33:c:194:LYS:HA	1.97	0.47
36:f:30:LEU:HD23	36:f:72:ALA:HB1	1.96	0.47
49:s:30:VAL:HB	49:s:59:PRO:HG3	1.97	0.47
49:s:53:ASP:HB2	49:s:77:THR:HA	1.97	0.47
52:v:38:ALA:HB2	52:v:60:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:A:C2	1:A:45:G:C4	3.03	0.47
1:A:759:U:O4	1:A:762:C:N4	2.47	0.47
1:A:1274:G:H4'	1:A:1275:A:H8	1.79	0.47
1:A:1282:A:C6	1:A:1283:G:C6	3.03	0.47
1:A:2107:G:H5'	22:V:19:SER:HB2	1.97	0.47
25:Y:38:GLU:OE1	25:Y:39:ASP:N	2.48	0.47
31:a:590:U:OP2	31:a:766:G:N1	2.46	0.47
31:a:1205:C:H2'	31:a:1207:A:H8	1.80	0.47
35:e:157:ARG:O	38:h:65:LYS:NZ	2.47	0.47
37:g:74:GLU:HG3	37:g:89:VAL:HB	1.96	0.47
38:h:129:ALA:HB1	38:h:131:VAL:HG23	1.97	0.47
41:k:44:TRP:HZ3	41:k:46:SER:HB3	1.80	0.47
42:l:99:ARG:HH11	42:l:101:LYS:HA	1.80	0.47
45:o:38:ALA:O	45:o:42:HIS:N	2.46	0.47
1:A:2374:C:O2'	27:1:17:TYR:OH	2.27	0.47
1:A:2421:C:H42	1:A:2449:C:H42	1.63	0.47
2:B:106:G:H2'	2:B:107:U:C6	2.50	0.47
31:a:261:U:H2'	31:a:262:G:C8	2.49	0.47
32:b:93:ASN:HD22	32:b:94:GLN:HE21	1.62	0.47
34:d:35:GLN:HE21	34:d:35:GLN:HB3	1.56	0.47
36:f:80:ALA:HA	36:f:86:ILE:HD12	1.97	0.47
50:t:69:ASN:HB3	50:t:73:ARG:HH22	1.78	0.47
1:A:1078:G:C2	1:A:1165:C:O2	2.56	0.46
1:A:1593:G:N2	1:A:1593:G:OP2	2.48	0.46
9:I:23:LYS:HD3	9:I:23:LYS:HA	1.77	0.46
30:4:2:LYS:HG3	30:4:34:GLN:HG2	1.97	0.46
31:a:682:G:O6	31:a:724:A:C6	2.68	0.46
31:a:1149:G:H21	31:a:1150:U:H4'	1.80	0.46
31:a:1443:A:H2'	31:a:1444:A:C8	2.50	0.46
34:d:7:SER:O	34:d:10:LYS:NZ	2.48	0.46
34:d:18:SER:HA	34:d:60:LEU:HD12	1.98	0.46
42:l:49:ARG:HH21	42:l:67:ARG:HD2	1.80	0.46
42:l:67:ARG:NE	42:l:76:ILE:O	2.49	0.46
42:l:85:HIS:HA	42:l:112:ARG:HH12	1.80	0.46
47:q:32:THR:HA	47:q:39:ARG:HA	1.97	0.46
50:t:71:ALA:HA	50:t:74:ILE:HD12	1.97	0.46
1:A:548:A:H2	1:A:551:G:C6	2.33	0.46
1:A:1456:U:H3'	1:A:1457:U:H6	1.80	0.46
1:A:1980:A:H8	1:A:2576:G:H21	1.60	0.46
1:A:2273:G:N1	1:A:2285:C:N4	2.63	0.46
1:A:2604:A:O2'	1:A:2641:A:N6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:123:VAL:HG21	10:J:136:ILE:HD13	1.97	0.46
31:a:235:G:N2	46:p:63:ASP:O	2.40	0.46
31:a:732:G:OP2	31:a:863:U:O2'	2.23	0.46
31:a:1525:U:C2	31:a:1532:G:N1	2.84	0.46
32:b:17:GLY:N	32:b:39:TYR:O	2.48	0.46
33:c:155:ARG:HD3	33:c:193:GLY:HA3	1.97	0.46
1:A:676:A:OP1	10:J:64:ARG:NH1	2.48	0.46
1:A:1081:G:H2'	1:A:1082:C:C2	2.50	0.46
1:A:1185:U:H5'	8:H:28:ARG:NH2	2.30	0.46
9:I:112:MET:O	9:I:116:SER:OG	2.33	0.46
23:W:11:THR:OG1	23:W:60:ARG:NH2	2.48	0.46
23:W:32:LEU:HD13	23:W:37:LEU:HD23	1.97	0.46
31:a:70:A:O2'	31:a:152:A:N3	2.47	0.46
31:a:1315:G:O2'	31:a:1341:G:N1	2.43	0.46
31:a:1401:U:H2'	31:a:1402:G:C8	2.50	0.46
32:b:111:ILE:HA	32:b:114:ILE:HG22	1.96	0.46
35:e:55:GLU:O	35:e:59:ALA:N	2.39	0.46
49:s:36:ARG:HH21	49:s:75:ALA:HB3	1.81	0.46
1:A:1701:U:H3	1:A:2029:G:H1	1.63	0.46
1:A:2673:C:N4	1:A:2702:A:H2	2.13	0.46
2:B:47:C:H2'	2:B:48:A:H8	1.81	0.46
4:D:12:MET:HE1	4:D:200:ASN:HB3	1.97	0.46
31:a:1141:A:OP1	39:i:68:ASN:ND2	2.49	0.46
31:a:1301:U:OP1	37:g:41:ARG:NE	2.49	0.46
31:a:1339:A:H5'	43:m:26:GLY:H	1.79	0.46
31:a:1441:C:H2'	31:a:1442:G:O4'	2.16	0.46
32:b:186:ILE:H	32:b:186:ILE:HG13	1.46	0.46
36:f:41:LYS:O	36:f:62:ILE:N	2.46	0.46
1:A:1004:A:C5'	1:A:1005:G:H5'	2.45	0.46
1:A:1761:G:O2'	1:A:1763:U:O4'	2.32	0.46
1:A:2354:A:H2'	1:A:2355:A:C8	2.50	0.46
1:A:2360:A:C8	1:A:2362:A:H1'	2.50	0.46
1:A:2523:C:H3'	1:A:2524:A:O4'	2.16	0.46
18:R:23:ASP:HB3	18:R:82:LEU:HB2	1.96	0.46
21:U:57:GLU:HB2	21:U:88:SER:HB3	1.96	0.46
31:a:300:G:N7	31:a:313:G:N2	2.64	0.46
31:a:448:U:H3'	31:a:449:A:C8	2.51	0.46
31:a:1151:U:H2'	31:a:1152:G:C8	2.51	0.46
31:a:1507:C:H2'	31:a:1508:G:C8	2.50	0.46
38:h:12:THR:HG22	38:h:15:ARG:HH22	1.81	0.46
42:l:79:TYR:N	42:l:108:TYR:O	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:17:ASP:HA	47:q:23:ILE:HA	1.97	0.46
1:A:300:G:H1'	1:A:302:A:OP2	2.16	0.46
1:A:640:G:H5''	1:A:640:G:H8	1.80	0.46
1:A:646:A:H62	1:A:699:U:H3	0.71	0.46
1:A:988:C:H4'	1:A:990:G:H5''	1.98	0.46
1:A:1484:G:H1	1:A:1599:G:H22	1.64	0.46
1:A:2672:G:O2'	1:A:2673:C:H4'	2.16	0.46
1:A:2911:A:H2'	1:A:2912:A:C8	2.50	0.46
3:C:232:HIS:CE1	3:C:247:MET:H	2.34	0.46
8:H:126:TYR:OH	8:H:133:HIS:NE2	2.43	0.46
21:U:18:THR:OG1	21:U:19:LYS:N	2.47	0.46
31:a:530:C:H41	42:l:63:ARG:HH12	1.62	0.46
31:a:661:U:OP2	31:a:663:A:N6	2.49	0.46
31:a:1093:A:OP2	35:e:23:LYS:NZ	2.37	0.46
31:a:1129:A:H5''	39:i:108:ARG:HA	1.98	0.46
31:a:1377:U:OP1	40:j:62:ARG:NH2	2.48	0.46
32:b:76:ALA:HB2	32:b:164:VAL:HG21	1.98	0.46
41:k:53:LYS:HE2	41:k:53:LYS:HB2	1.75	0.46
47:q:13:LYS:O	47:q:26:LEU:N	2.46	0.46
1:A:332:A:N7	1:A:393:G:C4	2.84	0.46
1:A:342:A:H2'	1:A:343:A:O4'	2.16	0.46
1:A:1100:G:O2'	1:A:1101:A:O4'	2.29	0.46
1:A:2801:C:C4	1:A:2802:A:C4	3.04	0.46
13:M:110:GLU:OE2	13:M:113:ARG:NH1	2.49	0.46
31:a:22:G:H5'	31:a:581:A:H61	1.81	0.46
31:a:262:G:O6	31:a:281:A:N6	2.49	0.46
31:a:1523:U:H3	31:a:1534:G:H1	1.63	0.46
32:b:173:ILE:H	32:b:173:ILE:HG12	1.54	0.46
39:i:14:ARG:O	39:i:17:SER:OG	2.29	0.46
40:j:15:HIS:CD2	40:j:72:ARG:HH21	2.34	0.46
49:s:22:GLN:HB3	49:s:27:LYS:HG3	1.97	0.46
1:A:591:A:H1'	1:A:592:A:C8	2.51	0.46
1:A:629:A:H8	1:A:854:G:H21	1.63	0.46
1:A:1043:U:H3'	1:A:1198:G:N1	2.30	0.46
1:A:2496:A:N7	1:A:2508:G:C2	2.83	0.46
5:E:153:LEU:HB3	5:E:192:LEU:HD22	1.97	0.46
7:G:121:ILE:HD11	7:G:140:GLN:HB3	1.97	0.46
31:a:280:C:H2'	31:a:281:A:C8	2.51	0.46
31:a:921:C:H2'	31:a:922:A:C8	2.51	0.46
31:a:1305:U:O2'	43:m:14:ARG:NH2	2.48	0.46
31:a:1450:U:N3	31:a:1472:G:C6	2.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:s:13:GLU:H	49:s:16:MET:HB3	1.81	0.46
1:A:22:C:C4	1:A:563:G:N1	2.83	0.46
1:A:1138:U:H4'	1:A:1142:A:H61	1.81	0.46
1:A:2668:A:H61	1:A:2800:U:H3	1.64	0.46
1:A:2758:G:H2'	1:A:2759:G:C8	2.51	0.46
31:a:611:U:H2'	31:a:612:G:H8	1.81	0.46
31:a:935:G:O2'	52:v:98:ARG:NH1	2.49	0.46
31:a:987:A:N6	31:a:1328:A:N7	2.63	0.46
31:a:1056:C:N4	31:a:1221:U:O2	2.49	0.46
31:a:1251:G:OP2	37:g:35:LYS:NZ	2.46	0.46
32:b:50:VAL:HG21	32:b:213:LEU:HD11	1.98	0.46
32:b:205:ASP:HB3	52:v:152:GLN:HG3	1.98	0.46
1:A:226:A:OP1	1:A:468:A:H4'	2.16	0.46
1:A:521:U:H1'	1:A:554:C:H2'	1.98	0.46
1:A:650:U:C4	1:A:664:G:H2'	2.51	0.46
1:A:1199:A:H2'	1:A:1200:A:C5'	2.46	0.46
1:A:1261:G:O6	15:O:16:LYS:NZ	2.49	0.46
1:A:1452:C:H2'	1:A:1453:G:C4	2.51	0.46
1:A:1495:C:H42	1:A:1504:U:H3	1.64	0.46
1:A:2300:A:H2'	1:A:2301:A:C8	2.51	0.46
1:A:2483:C:H2'	1:A:2484:U:H6	1.79	0.46
1:A:2598:U:O3'	4:D:159:ASP:HB2	2.16	0.46
31:a:413:U:H5'	31:a:506:A:C5	2.51	0.46
31:a:462:A:O3'	46:p:73:ASN:ND2	2.49	0.46
31:a:689:A:H2	31:a:718:G:H22	1.62	0.46
31:a:789:A:N7	31:a:809:U:O2	2.49	0.46
31:a:900:U:C2	31:a:916:A:N7	2.84	0.46
31:a:1523:U:H2'	31:a:1524:A:C8	2.50	0.46
34:d:113:LEU:HD12	34:d:116:HIS:HD1	1.80	0.46
40:j:53:ARG:N	40:j:61:SER:O	2.42	0.46
48:r:55:LYS:HE3	48:r:55:LYS:HB2	1.85	0.46
50:t:24:GLN:O	50:t:28:MET:N	2.42	0.46
52:v:11:LEU:HD13	52:v:44:VAL:HB	1.97	0.46
1:A:517:A:OP1	5:E:84:ARG:NH2	2.41	0.45
1:A:633:A:C2	29:3:2:PRO:HD3	2.50	0.45
1:A:953:C:H2'	1:A:954:A:H1'	1.98	0.45
1:A:978:A:H2'	1:A:979:C:C6	2.51	0.45
1:A:1373:U:C2	1:A:1374:G:N7	2.84	0.45
1:A:1827:C:O2'	3:C:153:GLN:NE2	2.49	0.45
2:B:112:A:H2'	2:B:113:G:C8	2.51	0.45
3:C:27:THR:O	3:C:27:THR:OG1	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:172:ASN:OD1	6:F:172:ASN:N	2.47	0.45
21:U:22:ARG:HE	21:U:22:ARG:HB2	1.43	0.45
31:a:425:G:O6	31:a:434:U:O2	2.34	0.45
31:a:1000:U:OP2	31:a:1222:U:N3	2.49	0.45
31:a:1236:C:H5'	43:m:95:LEU:HD22	1.99	0.45
31:a:1442:G:N1	31:a:1478:G:N7	2.64	0.45
44:n:7:VAL:HG22	44:n:11:GLN:HE21	1.81	0.45
1:A:272:C:C2	1:A:416:G:N1	2.76	0.45
1:A:859:C:O2	1:A:1232:G:N2	2.49	0.45
1:A:994:A:H2'	1:A:995:U:C6	2.52	0.45
1:A:1465:G:H2'	1:A:1466:G:H8	1.81	0.45
1:A:2460:A:O2'	1:A:2461:A:N3	2.40	0.45
4:D:196:LEU:HD21	14:N:10:VAL:HG11	1.98	0.45
21:U:73:GLY:HA3	21:U:90:TYR:O	2.16	0.45
31:a:104:G:N2	31:a:387:C:O3'	2.49	0.45
31:a:683:A:H1'	41:k:117:PRO:HA	1.96	0.45
31:a:781:G:H2'	31:a:782:G:C8	2.51	0.45
31:a:933:C:H2'	31:a:934:G:C8	2.50	0.45
31:a:975:G:H22	52:v:64:THR:HB	1.81	0.45
32:b:18:HIS:HE1	32:b:22:ARG:HE	1.64	0.45
33:c:8:ILE:HB	33:c:183:TYR:HB3	1.98	0.45
37:g:43:LEU:HA	37:g:46:ALA:HB3	1.97	0.45
37:g:118:ASP:O	37:g:122:ASN:ND2	2.36	0.45
39:i:31:THR:HB	39:i:66:LEU:HA	1.97	0.45
41:k:111:ARG:HB3	41:k:113:VAL:HG23	1.98	0.45
46:p:75:LEU:HA	46:p:80:ILE:HD12	1.98	0.45
1:A:31:C:C2	1:A:520:G:N2	2.58	0.45
1:A:44:A:H2'	1:A:45:G:O4'	2.17	0.45
1:A:589:U:N3	1:A:591:A:O4'	2.49	0.45
1:A:893:G:C4	1:A:894:A:H1'	2.50	0.45
1:A:1214:C:N4	1:A:1217:U:H3	2.13	0.45
1:A:1888:U:H2'	1:A:1889:G:H8	1.81	0.45
1:A:2471:G:O6	1:A:2472:G:C6	2.69	0.45
1:A:2502:C:C2	1:A:2556:G:C6	3.04	0.45
9:I:110:ASN:N	9:I:110:ASN:OD1	2.49	0.45
12:L:71:ILE:O	12:L:78:THR:HA	2.16	0.45
15:O:16:LYS:HB3	15:O:16:LYS:HE2	1.68	0.45
31:a:814:C:H2'	31:a:815:A:C8	2.51	0.45
31:a:1136:U:H4'	40:j:7:ARG:HH22	1.81	0.45
31:a:1165:U:H2'	31:a:1166:G:C8	2.51	0.45
32:b:79:SER:HB3	32:b:210:VAL:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:84:ALA:HA	32:b:87:ALA:HB3	1.98	0.45
32:b:91:TYR:HE2	32:b:93:ASN:HB2	1.82	0.45
32:b:114:ILE:O	32:b:152:ARG:NH1	2.50	0.45
35:e:46:VAL:O	35:e:72:VAL:N	2.46	0.45
37:g:54:SER:HB2	37:g:125:LEU:HD11	1.97	0.45
37:g:103:TRP:HE3	37:g:107:TYR:HE2	1.63	0.45
38:h:97:VAL:O	38:h:102:GLY:N	2.50	0.45
39:i:27:GLU:HG3	39:i:29:ASN:HD21	1.81	0.45
39:i:47:ILE:HA	39:i:50:LEU:HB2	1.98	0.45
49:s:15:LEU:O	49:s:19:VAL:N	2.46	0.45
52:v:56:VAL:N	52:v:67:ALA:O	2.43	0.45
52:v:60:LEU:HD12	52:v:63:VAL:HG23	1.98	0.45
1:A:341:G:N2	1:A:383:A:C6	2.54	0.45
1:A:842:U:OP1	5:E:62:ARG:NH2	2.50	0.45
1:A:1697:G:O2'	1:A:1698:A:OP2	2.32	0.45
1:A:2667:G:H1	1:A:2668:A:H62	1.65	0.45
1:A:2801:C:N4	1:A:2802:A:C4	2.85	0.45
9:I:21:THR:HB	9:I:39:ILE:HD12	1.98	0.45
31:a:358:G:H2'	31:a:359:G:C8	2.51	0.45
31:a:362:G:N2	31:a:396:G:O2'	2.46	0.45
31:a:737:A:H2'	31:a:738:G:H8	1.82	0.45
34:d:64:THR:OG1	34:d:65:GLU:O	2.35	0.45
36:f:17:ASP:OD1	36:f:17:ASP:N	2.49	0.45
1:A:223:G:H4'	1:A:225:A:C2	2.51	0.45
1:A:317:G:H1	1:A:402:C:HO2'	1.63	0.45
1:A:522:G:N1	1:A:525:A:OP2	2.48	0.45
1:A:889:U:C4	1:A:978:A:N6	2.69	0.45
1:A:922:G:H22	1:A:945:A:H2	1.64	0.45
1:A:1097:U:H2'	1:A:1098:A:C8	2.52	0.45
31:a:21:U:O2'	31:a:581:A:N6	2.50	0.45
31:a:159:G:H1	31:a:163:C:N4	2.15	0.45
31:a:398:C:O2'	46:p:29:ARG:NH2	2.43	0.45
31:a:454:G:H3'	31:a:455:G:H8	1.81	0.45
31:a:1394:C:H41	37:g:3:ARG:HH11	1.65	0.45
39:i:12:GLY:O	39:i:19:ALA:N	2.50	0.45
40:j:35:ASP:OD2	40:j:78:ASN:ND2	2.50	0.45
1:A:527:G:O6	1:A:554:C:N4	2.50	0.45
1:A:2427:G:H3'	1:A:2428:U:H6	1.80	0.45
3:C:5:LYS:HG3	3:C:17:THR:HG22	1.98	0.45
6:F:8:PHE:HA	6:F:11:GLU:HB2	1.97	0.45
13:M:82:LYS:HD3	13:M:82:LYS:HA	1.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:35:LYS:HD3	22:V:46:LYS:HD3	1.97	0.45
23:W:34:THR:O	23:W:36:GLN:N	2.47	0.45
23:W:58:ARG:O	23:W:61:GLU:HB2	2.16	0.45
31:a:398:C:O3'	46:p:29:ARG:NH1	2.50	0.45
31:a:585:G:H2'	31:a:586:C:C6	2.51	0.45
31:a:980:G:OP2	39:i:130:SER:OG	2.31	0.45
31:a:1238:C:H41	43:m:103:LYS:HA	1.81	0.45
35:e:32:ARG:H	35:e:32:ARG:HG2	1.51	0.45
37:g:115:THR:O	37:g:119:ARG:N	2.50	0.45
38:h:54:ASP:HB2	38:h:58:GLY:HA2	1.99	0.45
39:i:59:THR:HG22	39:i:62:ASN:HD22	1.81	0.45
41:k:98:ARG:HH22	51:u:13:GLU:HG2	1.80	0.45
47:q:18:LYS:N	47:q:22:THR:O	2.44	0.45
1:A:963:A:H2	1:A:2295:A:H5''	1.82	0.45
1:A:1050:C:OP1	8:H:40:LYS:NZ	2.50	0.45
1:A:2527:U:O2'	1:A:2531:U:OP1	2.26	0.45
31:a:72:C:H2'	31:a:73:G:C8	2.51	0.45
31:a:103:G:H2'	31:a:104:G:H8	1.81	0.45
31:a:209:G:H3'	31:a:210:A:H2'	1.99	0.45
31:a:1089:U:H4'	35:e:138:ARG:HH22	1.81	0.45
31:a:1474:C:H2'	31:a:1475:G:C8	2.52	0.45
40:j:53:ARG:HG3	40:j:63:GLU:HB2	1.98	0.45
41:k:72:LYS:HE3	41:k:103:ALA:HB1	1.98	0.45
1:A:2685:C:H3'	1:A:2686:G:C8	2.52	0.45
8:H:18:VAL:HG23	8:H:138:PRO:HB2	1.99	0.45
10:J:14:LYS:HB3	10:J:14:LYS:HE3	1.72	0.45
18:R:6:ILE:HB	18:R:33:VAL:HG11	1.98	0.45
27:1:7:LEU:HB3	27:1:45:HIS:HB3	1.98	0.45
31:a:113:U:H2'	31:a:114:G:C8	2.52	0.45
31:a:674:G:C6	31:a:748:U:N3	2.85	0.45
31:a:1059:G:N1	31:a:1220:C:O2	2.49	0.45
31:a:1251:G:H2'	31:a:1252:G:H8	1.82	0.45
31:a:1251:G:H2'	31:a:1252:G:C8	2.51	0.45
31:a:1437:C:H2'	31:a:1438:A:H8	1.81	0.45
33:c:7:PRO:HG2	33:c:200:TRP:HZ2	1.82	0.45
35:e:135:ASN:HA	35:e:138:ARG:HB2	1.98	0.45
40:j:24:LYS:HE3	40:j:24:LYS:HB3	1.80	0.45
52:v:137:LYS:HD2	52:v:137:LYS:HA	1.78	0.45
52:v:142:LYS:HE2	52:v:142:LYS:HB2	1.80	0.45
1:A:226:A:P	1:A:468:A:H4'	2.57	0.45
1:A:1010:G:H8	1:A:1010:G:O5'	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:C:O2'	1:A:1028:G:N2	2.50	0.45
1:A:2886:G:O2'	1:A:2887:G:OP2	2.35	0.45
11:K:1:MET:HE2	11:K:1:MET:HB3	1.85	0.45
14:N:41:ARG:CZ	31:a:354:G:H5''	2.46	0.45
31:a:103:G:H2'	31:a:104:G:C8	2.51	0.45
31:a:268:G:H4'	31:a:269:U:H5'	1.98	0.45
31:a:461:C:OP1	46:p:40:TYR:OH	2.32	0.45
31:a:797:U:O2'	52:v:97:ASN:ND2	2.38	0.45
31:a:1167:A:H61	31:a:1190:A:H3'	1.82	0.45
31:a:1452:G:H2'	31:a:1453:A:C8	2.52	0.45
1:A:617:A:H5''	1:A:617:A:C8	2.52	0.45
1:A:902:A:H2'	1:A:903:G:C8	2.52	0.45
1:A:1018:A:H2	1:A:1034:A:N7	2.15	0.45
1:A:1489:A:H4'	1:A:1490:G:H21	1.82	0.45
1:A:1634:A:H1'	1:A:1635:A:C8	2.52	0.45
7:G:146:SER:HA	7:G:149:ARG:HG2	1.99	0.45
17:Q:22:ASP:OD1	17:Q:25:ARG:NH2	2.50	0.45
23:W:2:LYS:O	23:W:5:GLU:N	2.50	0.45
31:a:164:C:H2'	31:a:165:G:C8	2.50	0.45
31:a:180:U:H2'	31:a:181:A:C5	2.51	0.45
31:a:378:C:H2'	31:a:379:G:C8	2.52	0.45
31:a:889:C:OP1	42:l:9:ARG:NH2	2.50	0.45
31:a:1425:G:H1	31:a:1496:U:H3	1.65	0.45
41:k:40:ASN:HD22	41:k:40:ASN:HA	1.61	0.45
50:t:33:LYS:O	50:t:37:THR:OG1	2.26	0.45
52:v:60:LEU:HD22	52:v:61:LYS:H	1.81	0.45
1:A:365:A:H1'	1:A:382:U:O2	2.17	0.44
9:I:63:VAL:HG12	9:I:106:LEU:HD21	1.97	0.44
10:J:79:LEU:HD12	10:J:79:LEU:HA	1.86	0.44
11:K:68:ILE:HD13	11:K:68:ILE:HA	1.78	0.44
31:a:76:C:OP2	31:a:78:A:N6	2.49	0.44
31:a:385:G:H2'	31:a:386:G:C8	2.52	0.44
31:a:980:G:N2	31:a:1375:G:O4'	2.49	0.44
35:e:88:ARG:NH2	35:e:90:GLY:O	2.44	0.44
42:l:48:THR:OG1	42:l:67:ARG:O	2.31	0.44
1:A:372:A:H61	19:S:15:LYS:HB2	1.82	0.44
1:A:527:G:O2'	1:A:552:A:N6	2.36	0.44
1:A:689:A:C6	1:A:2396:A:H1'	2.52	0.44
1:A:890:G:N2	1:A:977:A:H62	2.07	0.44
1:A:1636:U:O4	1:A:1637:A:N6	2.50	0.44
1:A:1772:G:N3	1:A:1773:A:H1'	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1773:A:H2'	1:A:1774:A:H8	1.83	0.44
1:A:2470:C:H2'	1:A:2471:G:C8	2.53	0.44
31:a:459:A:H5'	31:a:489:G:H22	1.81	0.44
31:a:936:G:O2'	31:a:1514:A:N6	2.44	0.44
33:c:21:LYS:O	40:j:94:SER:OG	2.34	0.44
34:d:128:ILE:HG23	34:d:131:TYR:H	1.82	0.44
37:g:71:PRO:HD2	37:g:96:ARG:HG3	2.00	0.44
1:A:910:C:N3	1:A:954:A:N7	2.64	0.44
31:a:35:C:H2'	31:a:36:G:C8	2.51	0.44
31:a:839:U:H2'	31:a:840:G:C8	2.53	0.44
31:a:959:U:O4	31:a:1241:G:O6	2.36	0.44
31:a:999:C:H2'	31:a:1000:U:C6	2.52	0.44
32:b:9:LEU:HD21	32:b:43:LEU:HD13	2.00	0.44
33:c:46:LEU:HD13	33:c:69:THR:HG22	2.00	0.44
38:h:70:ASP:OD1	38:h:70:ASP:N	2.49	0.44
41:k:98:ARG:HE	51:u:16:LEU:HD12	1.83	0.44
43:m:14:ARG:H	43:m:14:ARG:HG3	1.64	0.44
43:m:50:ASP:N	43:m:50:ASP:OD1	2.50	0.44
47:q:12:GLY:N	47:q:61:VAL:O	2.48	0.44
1:A:589:U:O2'	1:A:590:U:H3'	2.17	0.44
1:A:2127:G:C2	1:A:2216:U:O2	2.70	0.44
24:X:8:LEU:HB2	24:X:28:LEU:HD13	2.00	0.44
25:Y:53:ASP:OD1	25:Y:54:SER:N	2.50	0.44
31:a:503:A:N1	34:d:112:GLN:NE2	2.60	0.44
31:a:725:C:H2'	31:a:742:A:C8	2.53	0.44
32:b:111:ILE:HD11	32:b:148:LEU:HD22	2.00	0.44
38:h:54:ASP:H	38:h:58:GLY:HA3	1.82	0.44
41:k:33:THR:HG23	41:k:44:TRP:HB3	1.98	0.44
47:q:39:ARG:H	47:q:39:ARG:HG3	1.59	0.44
1:A:327:G:H21	1:A:328:G:H1'	1.80	0.44
1:A:2045:A:H2'	1:A:2046:U:C2	2.53	0.44
1:A:2139:A:OP2	1:A:2172:C:N4	2.47	0.44
1:A:2360:A:H4'	1:A:2361:U:H5'	2.00	0.44
6:F:95:ARG:HD3	25:Y:9:TYR:CZ	2.53	0.44
7:G:23:HIS:CE1	7:G:25:THR:HG22	2.52	0.44
19:S:57:LEU:HD22	19:S:57:LEU:HA	1.78	0.44
31:a:43:G:H21	31:a:630:A:H1'	1.82	0.44
31:a:161:A:N7	31:a:354:G:N1	2.66	0.44
31:a:549:G:O2'	34:d:35:GLN:NE2	2.51	0.44
31:a:995:A:O2'	49:s:55:ARG:O	2.34	0.44
31:a:1369:C:OP1	44:n:35:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:155:ARG:HH21	33:c:160:ASP:HA	1.82	0.44
1:A:361:U:H2'	1:A:366:G:H1	1.83	0.44
1:A:543:G:N3	1:A:544:U:H5	2.15	0.44
1:A:1365:G:H4'	1:A:1366:U:H2'	1.99	0.44
1:A:2054:G:H2'	1:A:2055:U:O4'	2.18	0.44
1:A:2516:G:O2'	1:A:2517:G:H5'	2.17	0.44
18:R:63:LYS:HB3	18:R:63:LYS:HE2	1.76	0.44
31:a:134:A:H1'	31:a:333:A:C8	2.53	0.44
31:a:984:A:H4'	31:a:1373:A:H61	1.82	0.44
31:a:1305:U:O2'	31:a:1312:U:O4	2.36	0.44
33:c:84:GLU:O	33:c:88:ASN:N	2.50	0.44
45:o:36:ILE:O	45:o:40:ASN:N	2.34	0.44
1:A:863:G:O3'	1:A:884:U:H5'	2.18	0.44
1:A:1297:G:P	1:A:1298:G:H5''	2.57	0.44
1:A:1372:C:H2'	1:A:1373:U:H1'	2.00	0.44
8:H:3:GLN:H	8:H:3:GLN:HG2	1.34	0.44
10:J:71:ARG:HE	10:J:71:ARG:HB2	1.57	0.44
31:a:507:A:H1'	31:a:555:A:C6	2.52	0.44
31:a:971:C:H2'	31:a:972:G:H8	1.83	0.44
31:a:1357:G:O2'	31:a:1383:G:O6	2.29	0.44
32:b:75:GLN:O	32:b:79:SER:OG	2.31	0.44
32:b:90:PHE:CG	32:b:154:MET:HB2	2.53	0.44
35:e:92:GLY:HA2	35:e:129:GLY:HA3	2.00	0.44
1:A:343:A:N6	1:A:377:U:O5'	2.50	0.44
1:A:995:U:HO2'	1:A:996:G:P	2.40	0.44
1:A:1014:U:H2'	1:A:1027:A:O3'	2.18	0.44
1:A:1195:A:H2'	1:A:1196:C:H1'	1.99	0.44
1:A:2138:U:H3	1:A:2146:A:H5''	1.83	0.44
1:A:2650:G:O5'	1:A:2845:G:N2	2.51	0.44
1:A:2801:C:N1	1:A:2802:A:H1'	2.33	0.44
14:N:50:ILE:HD13	14:N:50:ILE:HA	1.73	0.44
31:a:728:C:O2'	48:r:57:GLN:OE1	2.35	0.44
31:a:1129:A:H61	31:a:1165:U:H3	1.66	0.44
32:b:18:HIS:NE2	32:b:188:ASP:OD2	2.46	0.44
37:g:72:VAL:HG23	37:g:73:LEU:HG	1.98	0.44
45:o:42:HIS:NE2	45:o:49:ASP:OD2	2.51	0.44
1:A:85:G:H1	1:A:96:G:H1	1.65	0.44
1:A:484:U:H2'	1:A:485:A:C8	2.53	0.44
1:A:630:G:H22	10:J:19:VAL:HG12	1.83	0.44
1:A:774:G:C6	3:C:207:LYS:HB2	2.53	0.44
1:A:1078:G:C2	1:A:1165:C:C2	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1209:U:H2'	1:A:1210:U:H6	1.82	0.44
1:A:1274:G:H4'	1:A:1275:A:C8	2.53	0.44
1:A:1630:A:H2'	1:A:1631:G:H2'	2.00	0.44
1:A:2503:A:H2'	1:A:2504:C:C4	2.53	0.44
13:M:69:LYS:HB3	13:M:104:ARG:HD3	2.00	0.44
31:a:332:G:O2'	31:a:334:G:O6	2.34	0.44
31:a:535:G:O2'	31:a:543:A:N1	2.46	0.44
31:a:1132:U:O4	31:a:1163:G:O6	2.35	0.44
36:f:86:ILE:H	36:f:86:ILE:HG13	1.47	0.44
1:A:1206:G:H2'	1:A:1207:G:N7	2.33	0.43
1:A:1817:C:H2'	1:A:1818:A:C5	2.53	0.43
1:A:2503:A:N6	11:K:119:ARG:HH22	2.16	0.43
1:A:2745:G:O2'	1:A:2868:G:OP1	2.33	0.43
31:a:628:C:H4'	34:d:131:TYR:HD1	1.83	0.43
31:a:636:G:H2'	31:a:637:A:O4'	2.18	0.43
31:a:1177:A:O5'	31:a:1179:A:N6	2.51	0.43
34:d:128:ILE:HA	34:d:128:ILE:HD12	1.77	0.43
44:n:19:ARG:HD2	44:n:21:TYR:HB2	1.99	0.43
1:A:45:G:O6	1:A:218:G:O2'	2.37	0.43
1:A:49:A:N1	1:A:180:G:H1'	2.33	0.43
1:A:58:G:H1	1:A:68:A:N6	2.16	0.43
1:A:159:U:H3'	1:A:160:G:C8	2.53	0.43
1:A:579:U:H2'	1:A:580:C:C6	2.53	0.43
1:A:686:U:C4	1:A:692:G:O6	2.66	0.43
1:A:1625:U:H2'	1:A:1626:A:C8	2.53	0.43
1:A:2395:C:C2	1:A:2396:A:N7	2.85	0.43
1:A:2505:A:OP2	30:4:2:LYS:NZ	2.52	0.43
1:A:2747:U:H5	1:A:2893:A:N7	2.16	0.43
1:A:2752:A:H1'	1:A:2753:U:H2'	2.00	0.43
1:A:2818:A:N6	1:A:2826:U:O4	2.52	0.43
1:A:2855:A:H61	1:A:2898:U:H3'	1.82	0.43
4:D:42:GLU:H	4:D:42:GLU:HG3	1.57	0.43
16:P:1:MET:HE2	16:P:43:GLY:HA2	2.00	0.43
31:a:383:U:H5''	46:p:7:LEU:HD13	1.99	0.43
31:a:806:U:H2'	31:a:807:G:C8	2.52	0.43
32:b:9:LEU:HD11	32:b:43:LEU:HB3	1.99	0.43
1:A:106:A:O2'	1:A:337:A:O2'	2.33	0.43
1:A:621:A:N1	1:A:2045:A:H1'	2.33	0.43
1:A:893:G:N3	1:A:978:A:H4'	2.34	0.43
1:A:919:G:O6	1:A:948:U:C2	2.71	0.43
1:A:1028:G:N2	1:A:1028:G:OP2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2093:C:H3'	1:A:2094:G:H2'	1.99	0.43
1:A:2190:C:H5''	1:A:2191:U:H5	1.83	0.43
7:G:120:ASN:OD1	7:G:120:ASN:N	2.51	0.43
27:1:44:LEU:HD22	27:1:44:LEU:HA	1.88	0.43
29:3:32:LEU:H	29:3:32:LEU:HG	1.40	0.43
31:a:78:A:H5''	31:a:79:G:H5'	2.00	0.43
31:a:189:G:H2'	31:a:190:A:C8	2.53	0.43
31:a:1061:G:H2'	31:a:1062:G:C8	2.53	0.43
31:a:1247:C:O2	31:a:1344:G:O2'	2.36	0.43
31:a:1358:U:H3	31:a:1384:A:H2	1.67	0.43
34:d:63:MET:HE1	34:d:90:LEU:HD11	2.00	0.43
34:d:66:ARG:HE	34:d:66:ARG:HB3	1.63	0.43
46:p:58:LEU:HA	46:p:84:PHE:HE1	1.83	0.43
52:v:37:ASN:N	52:v:37:ASN:OD1	2.50	0.43
1:A:521:U:C5	1:A:522:G:H1'	2.53	0.43
1:A:535:G:H8	1:A:535:G:O5'	2.01	0.43
1:A:613:G:H5'	1:A:1027:A:N7	2.33	0.43
1:A:1055:A:H5'	1:A:1195:A:H2	1.82	0.43
1:A:1127:U:N3	1:A:1130:A:OP2	2.40	0.43
1:A:1806:U:H5	1:A:1811:A:N7	2.16	0.43
1:A:2368:G:H2'	1:A:2369:C:H1'	2.00	0.43
53:A:3001:ERY:H203	53:A:3001:ERY:H192	1.66	0.43
31:a:195:C:C5	47:q:76:ARG:HD2	2.53	0.43
31:a:753:U:H2'	31:a:754:G:C8	2.53	0.43
31:a:1166:G:C2	31:a:1189:A:N6	2.86	0.43
31:a:1351:U:H2'	31:a:1352:C:C6	2.53	0.43
33:c:123:LEU:HD13	33:c:195:LEU:HD22	2.01	0.43
34:d:131:TYR:OH	34:d:137:GLN:NE2	2.50	0.43
38:h:104:ALA:HB1	38:h:127:ILE:HD11	1.99	0.43
45:o:29:ILE:HG12	45:o:63:ARG:HD2	2.01	0.43
1:A:179:A:H3'	1:A:180:G:H8	1.80	0.43
1:A:1056:U:H5'	15:O:70:ARG:NH2	2.33	0.43
1:A:1452:C:H1'	1:A:1459:A:N6	2.34	0.43
1:A:1538:A:N3	1:A:1625:U:O2'	2.44	0.43
1:A:2077:C:O2	1:A:2077:C:O2'	2.36	0.43
1:A:2471:G:H2'	1:A:2472:G:O4'	2.17	0.43
1:A:2869:G:C6	1:A:2887:G:H1'	2.53	0.43
3:C:20:ASP:N	3:C:20:ASP:OD1	2.43	0.43
7:G:102:ASP:OD1	7:G:102:ASP:N	2.49	0.43
31:a:59:C:O2	31:a:362:G:N2	2.51	0.43
31:a:251:A:N6	31:a:291:U:O4	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:930:U:H5'	31:a:1092:G:H4'	2.00	0.43
31:a:1108:C:O2	31:a:1179:A:O2'	2.35	0.43
32:b:133:GLU:HG2	32:b:137:LEU:HG	2.00	0.43
33:c:89:LYS:HA	33:c:92:ALA:HB3	1.99	0.43
34:d:169:ALA:HA	34:d:172:LEU:HD23	2.00	0.43
35:e:87:GLY:HA2	35:e:143:GLY:HA3	1.99	0.43
42:l:103:LEU:HD23	42:l:103:LEU:HA	1.87	0.43
44:n:29:ARG:HG3	44:n:31:HIS:H	1.83	0.43
45:o:37:ASN:HA	45:o:40:ASN:HB3	2.01	0.43
46:p:84:PHE:O	46:p:88:LYS:N	2.40	0.43
1:A:200:A:N1	1:A:201:C:O2'	2.39	0.43
1:A:613:G:OP1	1:A:1027:A:N6	2.51	0.43
1:A:1040:A:C2	1:A:1203:U:C2	3.04	0.43
1:A:1239:C:H2'	1:A:1240:U:C1'	2.48	0.43
1:A:1873:G:H2'	1:A:1874:A:C8	2.53	0.43
1:A:2037:G:O5'	1:A:2038:U:H5''	2.18	0.43
1:A:2128:G:C2	1:A:2215:U:O2	2.70	0.43
1:A:2142:G:H2'	1:A:2143:G:C8	2.54	0.43
1:A:2177:U:OP1	1:A:2187:G:O2'	2.26	0.43
1:A:2317:G:H22	1:A:2368:G:N2	2.17	0.43
3:C:274:ARG:HD3	3:C:274:ARG:HA	1.69	0.43
6:F:43:ALA:HA	6:F:46:ASN:HB2	1.99	0.43
6:F:63:GLN:HA	25:Y:6:HIS:CD2	2.54	0.43
31:a:438:A:H2'	31:a:439:A:O4'	2.18	0.43
31:a:524:U:O2'	31:a:527:C:N3	2.42	0.43
31:a:1415:G:HO2'	31:a:1529:A:HO2'	1.63	0.43
32:b:24:ASN:HB3	32:b:27:MET:HG2	2.00	0.43
49:s:51:VAL:HB	49:s:75:ALA:HB2	1.99	0.43
1:A:522:G:C4	1:A:524:A:H5''	2.54	0.43
1:A:990:G:OP1	1:A:991:A:H5'	2.19	0.43
1:A:2325:A:H3'	1:A:2326:G:C8	2.54	0.43
1:A:2656:A:O2'	1:A:2657:G:OP2	2.37	0.43
1:A:2778:G:C8	7:G:3:ARG:HB2	2.53	0.43
6:F:145:LYS:HB2	6:F:145:LYS:HE3	1.74	0.43
20:T:21:LEU:HD11	20:T:42:LYS:HD3	2.00	0.43
27:1:23:LYS:HE3	27:1:23:LYS:HB2	1.80	0.43
27:1:48:THR:O	27:1:48:THR:OG1	2.33	0.43
31:a:545:G:H5''	42:l:123:ARG:HH12	1.83	0.43
31:a:823:A:O2'	31:a:1537:G:N2	2.40	0.43
31:a:1129:A:O3'	39:i:87:ARG:NH2	2.51	0.43
31:a:1373:A:O2'	31:a:1375:G:N7	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1450:U:H2'	31:a:1451:G:C8	2.54	0.43
32:b:78:GLU:OE1	32:b:82:SER:OG	2.36	0.43
34:d:88:ILE:O	34:d:92:SER:OG	2.33	0.43
35:e:24:VAL:HA	35:e:29:ARG:HG2	2.00	0.43
39:i:97:ARG:HA	39:i:100:LEU:HB2	2.01	0.43
40:j:32:SER:HB3	40:j:83:THR:HB	2.01	0.43
43:m:71:ARG:HA	43:m:74:ASN:HB3	2.00	0.43
45:o:43:LEU:O	45:o:47:LYS:NZ	2.38	0.43
50:t:36:LYS:HB2	50:t:36:LYS:HE3	1.85	0.43
1:A:344:U:H5'	1:A:361:U:H4'	2.01	0.43
1:A:367:A:OP1	5:E:168:ARG:NE	2.45	0.43
1:A:707:G:N2	1:A:708:G:OP1	2.50	0.43
1:A:787:U:H2'	1:A:788:A:C8	2.54	0.43
1:A:1040:A:H3'	1:A:1041:G:C8	2.54	0.43
1:A:1946:A:H2'	1:A:1947:C:C2	2.54	0.43
1:A:2057:A:C2	1:A:2526:C:H4'	2.54	0.43
1:A:2343:U:H2'	1:A:2344:C:C6	2.54	0.43
1:A:2855:A:H2'	1:A:2898:U:C4	2.54	0.43
1:A:2869:G:O2'	1:A:2870:A:OP2	2.32	0.43
31:a:714:A:H2'	31:a:715:U:C2	2.54	0.43
31:a:941:C:H2'	31:a:942:G:C8	2.54	0.43
37:g:95:ARG:HA	37:g:98:THR:HB	2.01	0.43
41:k:56:LYS:HA	41:k:56:LYS:HD3	1.90	0.43
1:A:61:A:N6	1:A:93:U:O4	2.52	0.43
1:A:171:A:H2'	1:A:172:U:O4'	2.19	0.43
1:A:278:A:H2'	1:A:279:A:C8	2.53	0.43
1:A:459:C:N4	1:A:2436:G:O6	2.52	0.43
1:A:864:A:H4'	1:A:883:C:O3'	2.19	0.43
1:A:926:G:N1	1:A:939:U:OP1	2.52	0.43
1:A:1176:U:O2'	1:A:1177:A:H5'	2.18	0.43
1:A:1456:U:H3'	1:A:1457:U:C6	2.54	0.43
6:F:134:GLU:O	6:F:135:GLN:NE2	2.52	0.43
9:I:2:ILE:HG12	9:I:8:LEU:HD21	2.01	0.43
31:a:145:U:O2	31:a:177:G:C2	2.72	0.43
31:a:161:A:C5	31:a:354:G:C6	3.07	0.43
31:a:211:A:H1'	31:a:212:A:C4	2.53	0.43
31:a:269:U:N3	31:a:272:C:OP2	2.52	0.43
31:a:738:G:H4'	31:a:822:A:H61	1.83	0.43
33:c:5:ILE:HD12	40:j:53:ARG:HH11	1.83	0.43
40:j:34:ALA:HB1	40:j:76:ILE:HB	2.00	0.43
1:A:47:C:O2	1:A:52:A:O2'	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:A:H4'	1:A:404:U:C6	2.53	0.43
1:A:794:A:H4'	1:A:1309:G:N3	2.33	0.43
1:A:903:G:C8	1:A:2295:A:C2	3.07	0.43
1:A:1035:C:H5'	1:A:1224:U:C6	2.54	0.43
1:A:1626:A:H3'	1:A:1627:G:H8	1.84	0.43
53:A:3001:ERY:H8	53:A:3001:ERY:H321	1.61	0.43
10:J:13:ARG:HA	10:J:13:ARG:HD3	1.87	0.43
31:a:183:U:H3	31:a:233:U:H4'	1.84	0.43
31:a:995:A:H2'	31:a:996:A:C8	2.54	0.43
32:b:136:GLU:HA	32:b:139:LYS:HB2	2.01	0.43
46:p:5:ILE:HA	46:p:22:VAL:HA	2.00	0.43
46:p:61:LEU:HD22	46:p:67:PRO:HD3	2.01	0.43
49:s:50:ALA:HA	49:s:59:PRO:HA	2.00	0.43
52:v:45:LYS:HE3	52:v:45:LYS:HB3	1.92	0.43
1:A:229:A:H3'	1:A:230:A:C8	2.54	0.42
1:A:342:A:H1'	1:A:365:A:C6	2.54	0.42
1:A:395:U:O2'	1:A:396:G:N7	2.49	0.42
1:A:491:C:H2'	1:A:492:G:N9	2.34	0.42
1:A:1632:A:H2'	1:A:1633:A:C5	2.54	0.42
1:A:2167:G:H22	1:A:2178:U:H3	1.65	0.42
1:A:2235:A:H2'	1:A:2236:C:C6	2.54	0.42
4:D:12:MET:HE2	4:D:12:MET:HB2	1.73	0.42
31:a:408:C:O2	31:a:630:A:O2'	2.37	0.42
31:a:1177:A:H4'	31:a:1179:A:H62	1.83	0.42
31:a:1212:U:H1'	44:n:29:ARG:HD3	2.00	0.42
31:a:1379:C:H2'	31:a:1380:G:C8	2.54	0.42
33:c:94:THR:OG1	33:c:95:ASP:OD1	2.37	0.42
34:d:161:VAL:HA	34:d:162:PRO:HD3	1.89	0.42
35:e:153:VAL:HG21	38:h:101:LEU:HD11	2.00	0.42
42:l:112:ARG:HB3	42:l:130:TYR:HA	2.00	0.42
1:A:287:G:H2'	1:A:288:C:O4'	2.19	0.42
1:A:289:U:H2'	1:A:290:U:C6	2.54	0.42
1:A:326:A:H5''	1:A:327:G:C2	2.54	0.42
1:A:627:C:H4'	1:A:628:G:H5'	2.01	0.42
1:A:888:G:H2'	1:A:889:U:C6	2.54	0.42
1:A:2404:A:H2'	1:A:2405:A:C8	2.53	0.42
1:A:2495:A:H2	1:A:2509:A:H62	1.65	0.42
1:A:2823:G:H3'	1:A:2824:G:H8	1.85	0.42
1:A:2855:A:H2'	1:A:2898:U:O4	2.18	0.42
7:G:155:GLU:OE1	7:G:158:LYS:N	2.46	0.42
14:N:18:ASP:OD1	14:N:18:ASP:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:22:LYS:HE2	19:S:22:LYS:HB2	1.89	0.42
28:2:23:MET:HE3	28:2:23:MET:HB3	1.92	0.42
31:a:547:A:H2'	31:a:548:G:C8	2.54	0.42
31:a:660:U:N3	31:a:761:A:C8	2.78	0.42
31:a:689:A:H2'	31:a:690:U:C6	2.54	0.42
31:a:1315:G:N2	31:a:1342:A:OP2	2.47	0.42
32:b:133:GLU:O	32:b:137:LEU:N	2.43	0.42
35:e:22:ALA:HB1	35:e:29:ARG:HD2	2.01	0.42
40:j:9:ARG:H	40:j:9:ARG:HG2	1.63	0.42
43:m:80:LEU:HD12	43:m:83:ILE:HD12	2.00	0.42
1:A:684:U:H2'	1:A:685:C:C6	2.54	0.42
1:A:1070:A:H2'	1:A:1170:A:N6	2.34	0.42
6:F:73:SER:HA	6:F:80:ARG:HA	2.02	0.42
31:a:504:G:H2'	31:a:505:A:C5	2.54	0.42
31:a:660:U:O4	31:a:760:G:O2'	2.30	0.42
31:a:819:C:H1'	31:a:909:A:H61	1.84	0.42
31:a:843:A:OP1	48:r:58:ARG:NH2	2.53	0.42
31:a:1080:C:O2'	31:a:1202:C:O2	2.30	0.42
31:a:1144:A:N6	31:a:1152:G:O6	2.52	0.42
31:a:1366:G:H2'	31:a:1367:A:C8	2.50	0.42
51:u:18:ARG:HE	51:u:18:ARG:HB3	1.52	0.42
1:A:606:G:N2	1:A:607:C:N4	2.67	0.42
1:A:1082:C:H2'	1:A:1083:G:C8	2.45	0.42
1:A:1499:U:O4	1:A:2731:C:N3	2.52	0.42
1:A:2080:G:H1	1:A:2643:C:N4	2.17	0.42
53:A:3001:ERY:H202	53:A:3001:ERY:H151	1.75	0.42
3:C:142:HIS:ND1	3:C:193:GLY:O	2.34	0.42
3:C:220:VAL:HG22	3:C:225:MET:HE3	2.02	0.42
11:K:68:ILE:HD11	11:K:101:ARG:HD2	2.01	0.42
31:a:148:G:O6	31:a:174:A:C6	2.72	0.42
31:a:254:A:H8	31:a:289:G:H21	1.68	0.42
31:a:315:U:H3'	31:a:316:C:H6	1.85	0.42
31:a:332:G:N1	31:a:335:A:OP2	2.52	0.42
31:a:967:A:C6	49:s:55:ARG:HB2	2.55	0.42
31:a:1195:G:H2'	31:a:1196:G:H8	1.83	0.42
31:a:1273:A:N6	31:a:1282:U:H3	2.17	0.42
34:d:152:VAL:HG13	34:d:172:LEU:HD11	2.02	0.42
42:l:3:THR:HG1	42:l:6:GLN:H	1.63	0.42
49:s:40:ILE:HG23	49:s:44:PHE:HE2	1.83	0.42
52:v:58:ILE:HB	52:v:65:LEU:HB2	2.02	0.42
1:A:272:C:H5	1:A:298:U:N3	2.16	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:G:C2	1:A:444:C:O2	2.60	0.42
1:A:577:A:C2	1:A:2047:A:H2'	2.55	0.42
1:A:759:U:HO2'	1:A:763:A:H62	1.64	0.42
1:A:944:G:H2'	1:A:945:A:C8	2.55	0.42
1:A:1048:U:O2'	1:A:1055:A:OP2	2.18	0.42
1:A:2131:C:H3'	1:A:2132:A:H2'	2.01	0.42
1:A:2480:A:C4	1:A:2481:G:N7	2.87	0.42
2:B:111:C:H2'	2:B:112:A:C8	2.55	0.42
4:D:189:ASP:HB3	4:D:194:VAL:HG22	2.01	0.42
5:E:123:LEU:HD11	5:E:194:ILE:HD11	2.02	0.42
6:F:122:PHE:HD2	6:F:163:ASP:HB2	1.84	0.42
7:G:133:VAL:HG12	7:G:141:VAL:HG12	2.01	0.42
10:J:96:LEU:HD12	10:J:96:LEU:HA	1.91	0.42
23:W:39:GLU:OE2	23:W:42:ARG:NH2	2.52	0.42
31:a:260:U:O2	31:a:283:G:N2	2.52	0.42
31:a:380:C:C2	31:a:397:A:N6	2.87	0.42
31:a:765:U:O3'	31:a:829:G:N2	2.45	0.42
31:a:1012:G:N1	31:a:1013:A:O2'	2.49	0.42
31:a:1446:C:N3	31:a:1476:U:O4	2.51	0.42
31:a:1525:U:H2'	31:a:1526:C:C6	2.54	0.42
32:b:112:LYS:HE3	32:b:112:LYS:HB2	1.89	0.42
33:c:139:ARG:HA	33:c:142:LYS:HB2	2.01	0.42
36:f:46:ARG:O	36:f:58:GLY:N	2.52	0.42
41:k:64:GLN:HA	41:k:99:ALA:HB1	2.00	0.42
1:A:221:G:N2	1:A:238:U:O2'	2.46	0.42
1:A:614:U:H6	1:A:614:U:H2'	1.54	0.42
1:A:2007:G:O2'	1:A:2009:U:OP2	2.38	0.42
1:A:2062:G:O2'	1:A:2063:C:OP1	2.38	0.42
1:A:2158:U:P	1:A:2185:A:H61	2.42	0.42
8:H:24:GLN:HE21	8:H:24:GLN:HB3	1.70	0.42
24:X:43:ILE:HD13	24:X:43:ILE:HA	1.84	0.42
31:a:41:C:H2'	31:a:42:G:C8	2.55	0.42
31:a:425:G:O6	31:a:434:U:C2	2.72	0.42
31:a:647:G:H2'	31:a:648:A:C8	2.55	0.42
31:a:695:A:N6	31:a:711:G:N2	2.33	0.42
31:a:847:G:H2'	31:a:848:G:C8	2.54	0.42
31:a:906:C:H2'	31:a:907:G:H8	1.85	0.42
31:a:1160:U:H5'	39:i:18:VAL:HG21	2.00	0.42
31:a:1258:A:H2'	31:a:1259:C:C2	2.55	0.42
31:a:1479:A:H2'	31:a:1480:A:O4'	2.20	0.42
35:e:152:ASP:OD1	35:e:152:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:153:VAL:HA	35:e:156:LEU:HB2	2.01	0.42
47:q:9:VAL:HA	47:q:64:GLN:HA	2.02	0.42
1:A:922:G:H2'	1:A:923:A:C8	2.55	0.42
1:A:1032:A:O2'	1:A:1200:A:O2'	2.37	0.42
1:A:1197:C:P	15:O:58:ARG:HH22	2.41	0.42
1:A:1197:C:OP1	15:O:92:ARG:NH1	2.53	0.42
1:A:2474:G:N2	1:A:2477:A:O5'	2.53	0.42
1:A:2550:G:H2'	1:A:2551:G:N7	2.35	0.42
1:A:2613:C:H2'	1:A:2614:A:C8	2.54	0.42
1:A:2891:U:O2'	1:A:2894:C:N4	2.44	0.42
7:G:12:PRO:HB3	7:G:15:VAL:HG13	2.00	0.42
31:a:374:C:H1'	31:a:402:G:H22	1.85	0.42
31:a:614:G:N1	31:a:641:U:H2'	2.34	0.42
31:a:637:A:H3'	31:a:638:G:H8	1.84	0.42
31:a:817:G:C2	31:a:818:C:H1'	2.55	0.42
31:a:910:A:C5	31:a:911:G:H1'	2.54	0.42
31:a:917:A:H2'	31:a:918:A:C8	2.54	0.42
31:a:1213:C:H4'	44:n:28:GLY:H	1.85	0.42
37:g:22:LEU:O	37:g:26:LEU:N	2.52	0.42
39:i:11:THR:HG22	39:i:20:ARG:HB2	2.02	0.42
1:A:36:G:O2'	1:A:496:G:H2'	2.19	0.42
1:A:757:G:H3'	1:A:758:G:C8	2.55	0.42
1:A:1356:G:C6	1:A:1357:G:C4	3.08	0.42
1:A:1901:C:O2	1:A:1903:A:O2'	2.38	0.42
1:A:2163:A:N6	1:A:2183:G:H21	2.18	0.42
1:A:2335:G:H5''	1:A:2337:A:N7	2.35	0.42
1:A:2513:G:H2'	1:A:2514:G:C8	2.54	0.42
1:A:2641:A:C4	26:Z:2:ALA:HA	2.55	0.42
1:A:2704:A:N1	1:A:2757:U:O2	2.52	0.42
1:A:2831:G:OP2	4:D:71:LYS:HG3	2.20	0.42
3:C:129:ALA:HB2	3:C:191:THR:HG22	2.01	0.42
4:D:138:ARG:H	4:D:138:ARG:HG2	1.58	0.42
16:P:4:ILE:HD12	16:P:40:PHE:HB3	2.01	0.42
31:a:67:G:O2'	31:a:173:U:O2	2.31	0.42
31:a:310:G:H2'	31:a:311:G:H8	1.84	0.42
31:a:1127:U:O4	31:a:1194:G:O6	2.38	0.42
32:b:148:LEU:HD23	32:b:151:ILE:HG13	2.00	0.42
34:d:96:ALA:O	34:d:100:SER:OG	2.28	0.42
37:g:63:GLU:O	37:g:67:ASN:ND2	2.53	0.42
50:t:50:VAL:HA	50:t:53:ALA:HB3	2.01	0.42
1:A:68:A:O2'	1:A:70:G:OP1	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:A:H3'	1:A:199:A:H4'	2.02	0.42
1:A:225:A:C8	1:A:227:G:C8	3.07	0.42
1:A:277:C:H2'	1:A:278:A:C8	2.55	0.42
1:A:367:A:P	5:E:168:ARG:HE	2.42	0.42
1:A:522:G:H2'	1:A:524:A:O5'	2.20	0.42
1:A:644:C:H2'	1:A:645:A:C8	2.55	0.42
1:A:1131:G:H2'	1:A:1133:G:H4'	2.01	0.42
1:A:1658:A:H2	17:Q:87:PRO:HA	1.84	0.42
1:A:2558:A:H1'	1:A:2686:G:H5''	2.01	0.42
5:E:160:ASP:HB2	5:E:163:VAL:HG22	2.01	0.42
6:F:31:ILE:HA	6:F:158:THR:HA	2.02	0.42
6:F:46:ASN:HB3	6:F:49:VAL:HB	2.02	0.42
9:I:59:LYS:HE2	9:I:59:LYS:HB3	1.87	0.42
18:R:65:MET:O	18:R:68:TYR:HB2	2.20	0.42
31:a:182:A:OP2	31:a:184:A:N6	2.42	0.42
31:a:674:G:H2'	31:a:675:G:C8	2.54	0.42
31:a:985:G:H5''	31:a:1373:A:H61	1.85	0.42
31:a:1127:U:O2	31:a:1194:G:N2	2.39	0.42
38:h:59:VAL:O	38:h:61:ARG:NH2	2.52	0.42
43:m:79:ARG:HE	43:m:79:ARG:HB3	1.60	0.42
1:A:291:G:H2'	1:A:292:U:H6	1.85	0.42
1:A:498:G:N2	1:A:503:A:H8	2.05	0.42
1:A:588:G:H4'	1:A:1258:A:N1	2.35	0.42
1:A:923:A:H2	1:A:944:G:H1	1.51	0.42
1:A:1287:U:C2	1:A:1288:G:N7	2.88	0.42
1:A:1365:G:O2'	1:A:1367:C:OP2	2.38	0.42
1:A:1424:A:H5'	1:A:1512:U:H1'	2.02	0.42
1:A:2335:G:H5''	1:A:2337:A:C8	2.54	0.42
1:A:2482:G:O2'	1:A:2483:C:O4'	2.33	0.42
1:A:2830:A:C5	1:A:2910:G:C2	3.04	0.42
7:G:44:LYS:HE2	7:G:44:LYS:HB2	1.90	0.42
23:W:48:LYS:HA	23:W:48:LYS:HD3	1.87	0.42
31:a:329:A:N1	31:a:340:G:O6	2.53	0.42
31:a:417:U:OP2	34:d:9:TRP:NE1	2.53	0.42
31:a:930:U:O2'	35:e:24:VAL:O	2.31	0.42
31:a:1119:G:H1'	31:a:1201:A:H1'	2.02	0.42
32:b:74:LYS:HB2	52:v:155:LEU:HB3	2.02	0.42
47:q:61:VAL:HG22	47:q:80:ILE:HG22	2.01	0.42
1:A:627:C:H4'	1:A:628:G:C5'	2.50	0.41
1:A:917:U:H2'	1:A:918:G:C8	2.55	0.41
1:A:1040:A:O3'	16:P:10:LYS:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2094:G:C5	1:A:2096:G:C8	3.08	0.41
3:C:40:LYS:HE3	3:C:40:LYS:HB3	1.63	0.41
6:F:95:ARG:HD2	6:F:95:ARG:HA	1.83	0.41
13:M:57:SER:OG	13:M:58:SER:N	2.53	0.41
21:U:33:ARG:HD3	21:U:33:ARG:HA	1.91	0.41
31:a:299:C:H2'	31:a:300:G:C8	2.55	0.41
31:a:682:G:H1	31:a:724:A:H2	1.58	0.41
31:a:684:A:C6	31:a:722:G:O6	2.72	0.41
31:a:1252:G:C6	31:a:1305:U:N3	2.88	0.41
36:f:5:GLU:HB2	36:f:92:ILE:HG22	2.01	0.41
36:f:90:MET:HE1	36:f:92:ILE:HD12	2.02	0.41
47:q:71:ALA:O	47:q:74:ARG:NH1	2.49	0.41
49:s:19:VAL:HA	49:s:22:GLN:HB2	2.02	0.41
1:A:81:G:H3'	1:A:82:G:H8	1.85	0.41
1:A:999:U:O4	1:A:1006:G:O6	2.37	0.41
1:A:1490:G:O2'	1:A:1491:C:O5'	2.35	0.41
1:A:1759:G:H2'	1:A:1760:G:C8	2.55	0.41
1:A:2321:C:H3'	1:A:2322:C:H6	1.85	0.41
4:D:194:VAL:HG21	14:N:10:VAL:HG21	2.00	0.41
6:F:169:LEU:HA	6:F:169:LEU:HD23	1.80	0.41
31:a:428:U:C4	31:a:430:C:N3	2.88	0.41
31:a:1270:G:C2	31:a:1285:A:N6	2.87	0.41
32:b:20:THR:HA	32:b:23:TRP:HB2	2.02	0.41
34:d:71:THR:HG22	34:d:89:LEU:HD11	2.01	0.41
38:h:120:LYS:HZ2	38:h:120:LYS:HG3	1.81	0.41
41:k:57:LYS:HE2	41:k:57:LYS:HB3	1.84	0.41
47:q:52:ASN:OD1	47:q:54:SER:OG	2.38	0.41
1:A:33:U:N3	1:A:493:A:C8	2.88	0.41
1:A:319:G:OP1	1:A:324:A:N6	2.52	0.41
1:A:410:G:H5''	1:A:411:A:H5'	2.02	0.41
1:A:955:A:H2'	1:A:956:A:C8	2.56	0.41
1:A:1374:G:C4	1:A:1375:G:H1'	2.55	0.41
1:A:1423:C:O2'	1:A:1512:U:O2	2.27	0.41
1:A:1466:G:H2'	1:A:1467:G:C8	2.56	0.41
2:B:2:C:H2'	2:B:3:U:O4'	2.21	0.41
3:C:125:LYS:HE2	3:C:125:LYS:HB3	1.84	0.41
7:G:27:LYS:HE2	7:G:27:LYS:HB3	1.76	0.41
9:I:73:ASP:OD1	9:I:73:ASP:N	2.40	0.41
15:O:93:LYS:HG2	15:O:94:MET:HE2	2.01	0.41
23:W:13:GLU:O	23:W:17:GLN:HB2	2.20	0.41
31:a:1189:A:O2'	39:i:107:THR:O	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1191:G:H4'	31:a:1192:G:H5'	2.02	0.41
32:b:58:LYS:HE3	32:b:58:LYS:HB2	1.78	0.41
36:f:77:GLN:HG2	36:f:89:TYR:CZ	2.55	0.41
38:h:108:THR:OG1	38:h:109:SER:N	2.54	0.41
47:q:65:GLU:HA	47:q:75:PHE:HA	2.01	0.41
1:A:267:G:HO2'	1:A:474:A:N6	2.17	0.41
1:A:906:A:H2'	1:A:907:G:C8	2.55	0.41
1:A:922:G:H2'	1:A:923:A:H8	1.84	0.41
1:A:1515:G:H1	1:A:1565:U:H3	1.67	0.41
1:A:1772:G:C2	1:A:1773:A:H1'	2.55	0.41
1:A:2826:U:C2	1:A:2827:A:H1'	2.55	0.41
13:M:92:ILE:HG13	13:M:119:PHE:HB3	2.03	0.41
31:a:118:A:N7	31:a:295:U:C2	2.88	0.41
31:a:814:C:H2'	31:a:815:A:H8	1.85	0.41
31:a:1330:C:OP1	49:s:70:LYS:NZ	2.52	0.41
32:b:57:LEU:O	32:b:61:SER:OG	2.31	0.41
34:d:13:ARG:HE	34:d:25:GLU:HA	1.85	0.41
35:e:58:GLU:HA	35:e:61:LYS:HB3	2.02	0.41
39:i:79:GLN:HA	39:i:82:ARG:HG2	2.02	0.41
42:l:129:LEU:H	42:l:129:LEU:HG	1.47	0.41
1:A:68:A:H3'	1:A:69:C:H4'	2.01	0.41
1:A:223:G:N2	1:A:474:A:H8	2.18	0.41
1:A:227:G:H2'	1:A:228:A:C8	2.55	0.41
1:A:353:A:N6	1:A:1249:U:OP1	2.54	0.41
1:A:410:G:H5'	1:A:411:A:H8	1.86	0.41
1:A:597:U:H2'	1:A:598:G:C8	2.56	0.41
1:A:995:U:O5'	1:A:995:U:H6	2.02	0.41
1:A:1016:G:OP1	1:A:1018:A:H3'	2.21	0.41
1:A:1286:G:H5''	15:O:2:PRO:N	2.35	0.41
1:A:1306:A:H2'	1:A:1307:G:O4'	2.21	0.41
1:A:1499:U:O4	1:A:2731:C:C4	2.72	0.41
1:A:1759:G:C4	1:A:1772:G:H8	2.38	0.41
5:E:20:SER:N	5:E:203:GLU:OE2	2.52	0.41
7:G:30:LYS:NZ	7:G:80:SER:O	2.45	0.41
10:J:19:VAL:HG22	10:J:27:ASN:HB3	2.03	0.41
12:L:20:LEU:HB3	12:L:40:VAL:HG21	2.02	0.41
14:N:31:HIS:HB2	14:N:85:LYS:HG2	2.02	0.41
15:O:58:ARG:HA	15:O:61:TRP:CE3	2.55	0.41
31:a:249:G:H2'	31:a:250:C:C6	2.55	0.41
31:a:628:C:O2	34:d:130:SER:OG	2.29	0.41
31:a:708:G:H4'	31:a:712:A:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1166:G:N2	31:a:1189:A:C6	2.89	0.41
31:a:1326:G:C4	49:s:4:SER:HB3	2.56	0.41
31:a:1423:A:H2	31:a:1498:G:H22	1.69	0.41
32:b:114:ILE:HD12	32:b:114:ILE:HA	1.83	0.41
32:b:166:PRO:HG3	32:b:196:ILE:HD11	2.02	0.41
40:j:71:LYS:O	40:j:72:ARG:NH1	2.51	0.41
1:A:923:A:H2	1:A:944:G:H22	1.68	0.41
1:A:1071:A:N1	1:A:1072:A:N6	2.68	0.41
1:A:2668:A:C5	1:A:2669:G:H1'	2.55	0.41
1:A:2886:G:N2	1:A:2888:A:O5'	2.52	0.41
5:E:205:VAL:HG23	5:E:206:LEU:HD22	2.01	0.41
7:G:63:THR:OG1	7:G:64:ASN:OD1	2.33	0.41
20:T:25:GLY:O	20:T:45:GLU:N	2.47	0.41
24:X:22:THR:HG23	24:X:46:GLN:HG2	2.03	0.41
31:a:69:G:C6	31:a:100:A:N1	2.89	0.41
31:a:73:G:H2'	31:a:74:G:O4'	2.21	0.41
31:a:251:A:N6	31:a:289:G:O2'	2.47	0.41
31:a:1233:C:H5''	31:a:1234:U:H5''	2.02	0.41
31:a:1404:A:N6	31:a:1511:A:O2'	2.51	0.41
31:a:1408:A:H5''	31:a:1409:C:H5'	2.03	0.41
32:b:87:ALA:HB1	32:b:218:ALA:HB3	2.03	0.41
35:e:42:LYS:HB2	35:e:42:LYS:HE3	1.81	0.41
49:s:52:TYR:HA	49:s:57:HIS:HA	2.02	0.41
50:t:34:ASN:O	50:t:38:ALA:N	2.53	0.41
1:A:462:U:N3	1:A:2434:A:C2	2.88	0.41
1:A:613:G:N1	1:A:2525:C:H5'	2.36	0.41
1:A:883:C:H2'	1:A:884:U:C5	2.56	0.41
1:A:940:U:H2'	1:A:941:A:C8	2.55	0.41
1:A:1247:G:H4'	1:A:1251:A:O5'	2.21	0.41
1:A:1512:U:H2'	1:A:1513:A:H8	1.83	0.41
1:A:1888:U:H2'	1:A:1889:G:C8	2.55	0.41
1:A:2238:U:O4	1:A:2239:A:N6	2.52	0.41
7:G:163:ARG:NH2	7:G:167:GLU:O	2.54	0.41
10:J:105:GLU:H	10:J:105:GLU:HG3	1.50	0.41
14:N:41:ARG:NE	31:a:354:G:H5''	2.36	0.41
20:T:52:ILE:HD13	20:T:52:ILE:HA	1.91	0.41
31:a:212:A:H2'	31:a:213:G:H8	1.86	0.41
31:a:271:A:OP2	50:t:73:ARG:NH1	2.54	0.41
31:a:600:U:O4	31:a:656:A:N6	2.53	0.41
31:a:1130:G:OP1	39:i:87:ARG:NE	2.54	0.41
31:a:1250:U:O2'	37:g:38:THR:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1322:G:H8	49:s:6:LYS:HE3	1.86	0.41
32:b:70:VAL:HA	32:b:92:ILE:HB	2.02	0.41
52:v:30:ARG:HD2	52:v:30:ARG:HA	1.88	0.41
1:A:351:G:H21	1:A:372:A:HO2'	1.58	0.41
1:A:422:G:C2	1:A:444:C:N3	2.89	0.41
1:A:790:G:O2'	1:A:793:G:O2'	2.25	0.41
1:A:902:A:C5	1:A:903:G:O6	2.73	0.41
1:A:1462:G:H1'	1:A:1626:A:H62	1.86	0.41
1:A:1485:G:H1	1:A:1598:U:H3	1.67	0.41
1:A:2163:A:H62	1:A:2183:G:H21	1.69	0.41
1:A:2220:U:H2'	1:A:2221:U:H6	1.85	0.41
1:A:2479:C:C4	1:A:2480:A:H1'	2.56	0.41
1:A:2867:U:H2'	1:A:2868:G:C8	2.55	0.41
31:a:182:A:C6	31:a:231:U:H4'	2.56	0.41
31:a:504:G:N2	31:a:506:A:N7	2.67	0.41
31:a:514:G:H2'	31:a:515:C:C6	2.55	0.41
31:a:560:U:H2'	31:a:561:A:C8	2.55	0.41
31:a:765:U:O2'	31:a:888:C:O2	2.34	0.41
33:c:10:LEU:HA	33:c:10:LEU:HD13	1.84	0.41
33:c:86:LEU:HD23	33:c:100:ILE:HG12	2.03	0.41
34:d:85:ASN:HA	34:d:88:ILE:HG12	2.02	0.41
48:r:69:HIS:ND1	48:r:70:MET:HE2	2.36	0.41
1:A:45:G:C5	1:A:218:G:C4	3.09	0.41
1:A:267:G:O3'	1:A:474:A:N6	2.54	0.41
1:A:319:G:H4'	1:A:325:A:H61	1.86	0.41
1:A:509:G:N2	1:A:512:A:OP2	2.46	0.41
1:A:577:A:H4'	1:A:578:G:C8	2.55	0.41
1:A:611:U:H3	16:P:79:ARG:HH11	1.69	0.41
1:A:901:G:H2'	1:A:902:A:C8	2.55	0.41
1:A:1004:A:H2'	1:A:1006:G:C8	2.54	0.41
1:A:1230:G:H2'	1:A:1231:A:C8	2.56	0.41
1:A:1365:G:N1	1:A:1367:C:O4'	2.53	0.41
1:A:1466:G:O3'	1:A:1535:G:O2'	2.31	0.41
1:A:1632:A:N7	1:A:1633:A:N6	2.68	0.41
1:A:2319:U:H1'	1:A:2402:G:C4'	2.50	0.41
1:A:2436:G:H2'	1:A:2437:G:C8	2.56	0.41
1:A:2690:G:H3'	1:A:2691:G:C8	2.56	0.41
1:A:2701:G:O6	1:A:2759:G:N1	2.52	0.41
1:A:2702:A:C3'	1:A:2703:C:H4'	2.51	0.41
1:A:2869:G:O6	1:A:2887:G:H1'	2.21	0.41
2:B:47:C:H2'	2:B:48:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:62:GLY:H	6:F:95:ARG:NH1	2.18	0.41
7:G:86:VAL:HG22	7:G:132:LYS:HG2	2.01	0.41
11:K:40:SER:OG	11:K:41:TRP:N	2.54	0.41
12:L:66:LEU:HD23	12:L:66:LEU:HA	1.89	0.41
13:M:24:GLY:H	13:M:47:ASP:HB2	1.85	0.41
16:P:90:GLN:HA	16:P:91:PRO:HD3	1.96	0.41
20:T:68:LYS:HE3	20:T:68:LYS:HB2	1.90	0.41
31:a:51:A:O2'	31:a:368:G:N2	2.53	0.41
31:a:122:C:O2'	31:a:298:C:O2	2.35	0.41
31:a:238:G:OP1	46:p:32:ARG:NH2	2.54	0.41
31:a:398:C:H2'	31:a:399:G:C8	2.56	0.41
31:a:583:G:H4'	31:a:584:C:H5'	2.02	0.41
31:a:666:G:O6	31:a:755:U:C4	2.74	0.41
31:a:1301:U:H5''	37:g:41:ARG:HE	1.86	0.41
31:a:1357:G:H1	31:a:1383:G:H3'	1.85	0.41
31:a:1481:G:H2'	31:a:1482:G:C8	2.56	0.41
34:d:94:LEU:HD21	34:d:121:VAL:HG11	2.03	0.41
37:g:22:LEU:HD22	37:g:25:LYS:HB3	2.03	0.41
39:i:31:THR:HG22	39:i:34:ASN:HA	2.03	0.41
41:k:23:ILE:HG22	41:k:32:VAL:HA	2.03	0.41
41:k:35:THR:HG1	41:k:40:ASN:H	1.67	0.41
41:k:94:GLU:H	41:k:94:GLU:HG2	1.52	0.41
42:l:94:LEU:HD22	42:l:115:LEU:HD23	2.02	0.41
44:n:24:CYS:HB3	44:n:39:LEU:HA	2.03	0.41
52:v:55:GLU:HA	52:v:68:GLU:HB3	2.03	0.41
52:v:82:ASN:HA	52:v:85:LEU:HB2	2.02	0.41
1:A:178:A:H2'	1:A:179:A:C8	2.55	0.41
1:A:191:A:H2	1:A:210:A:H61	1.68	0.41
1:A:409:G:N2	1:A:411:A:H62	2.19	0.41
1:A:417:A:C8	1:A:419:U:C2	3.09	0.41
1:A:418:G:H4'	1:A:419:U:H5'	2.03	0.41
1:A:627:C:H1'	1:A:628:G:C8	2.56	0.41
1:A:1015:C:O2'	1:A:1027:A:H2'	2.21	0.41
1:A:1249:U:H5''	1:A:1249:U:H6	1.86	0.41
1:A:2396:A:H3'	1:A:2397:G:H5'	2.03	0.41
1:A:2480:A:N6	1:A:2527:U:N3	2.62	0.41
1:A:2822:C:H4'	1:A:2823:G:C8	2.56	0.41
1:A:2822:C:H4'	1:A:2823:G:H8	1.86	0.41
2:B:5:G:H21	13:M:43:GLN:HE22	1.67	0.41
4:D:59:TYR:CZ	4:D:71:LYS:HD3	2.56	0.41
5:E:162:ASN:O	5:E:166:SER:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:300:G:N2	31:a:617:A:C6	2.86	0.41
31:a:1358:U:H2'	31:a:1359:A:H8	1.85	0.41
31:a:1381:G:H2'	31:a:1382:U:C6	2.56	0.41
31:a:1450:U:O2	31:a:1472:G:C2	2.73	0.41
31:a:1506:U:H2'	31:a:1507:C:C6	2.56	0.41
33:c:51:VAL:HG22	33:c:69:THR:HA	2.02	0.41
34:d:77:LYS:HE2	34:d:77:LYS:HB2	1.86	0.41
34:d:93:ARG:HD3	34:d:95:ASP:HB2	2.03	0.41
38:h:18:ASN:HD21	38:h:72:ARG:HD3	1.86	0.41
40:j:46:LYS:HE3	40:j:46:LYS:HB2	1.81	0.41
46:p:19:ARG:NH2	46:p:36:GLN:OE1	2.53	0.41
50:t:12:LYS:HA	50:t:15:GLU:HB2	2.03	0.41
50:t:69:ASN:O	50:t:73:ARG:NH2	2.54	0.41
1:A:471:G:H2'	1:A:472:C:O4'	2.21	0.40
1:A:1469:G:H2'	1:A:1470:G:C8	2.56	0.40
1:A:1947:C:H2'	1:A:1948:G:C8	2.50	0.40
1:A:2725:U:H2'	1:A:2726:C:C6	2.56	0.40
31:a:143:A:H62	31:a:224:U:H5''	1.86	0.40
31:a:331:U:H5''	50:t:21:ASN:ND2	2.36	0.40
31:a:481:C:H4'	46:p:85:ASP:HB2	2.03	0.40
31:a:511:A:H62	31:a:551:G:N2	2.19	0.40
31:a:611:U:H2'	31:a:612:G:C8	2.56	0.40
31:a:1261:A:H2'	31:a:1262:A:C8	2.57	0.40
32:b:187:VAL:O	32:b:202:ALA:N	2.52	0.40
35:e:35:ALA:O	35:e:50:THR:OG1	2.33	0.40
39:i:41:LEU:HA	39:i:42:PRO:HD3	1.89	0.40
40:j:65:PHE:HD1	40:j:65:PHE:HA	1.73	0.40
1:A:446:G:O2'	1:A:447:A:H5''	2.20	0.40
1:A:1043:U:H3'	1:A:1198:G:C6	2.57	0.40
1:A:1874:A:C4	1:A:1875:A:H1'	2.56	0.40
1:A:1880:A:H2'	1:A:1881:A:C8	2.56	0.40
1:A:2094:G:N1	1:A:2471:G:C6	2.89	0.40
1:A:2544:C:N3	1:A:2594:G:N1	2.42	0.40
1:A:2557:U:OP1	1:A:2562:G:N2	2.55	0.40
1:A:2824:G:H2'	1:A:2825:U:C6	2.57	0.40
7:G:73:ASN:O	7:G:77:GLN:HB2	2.21	0.40
8:H:93:LEU:HD13	8:H:101:LEU:HB2	2.03	0.40
32:b:50:VAL:HG22	32:b:217:MET:HE3	2.03	0.40
38:h:69:ASN:HB3	38:h:71:GLU:HG3	2.03	0.40
39:i:59:THR:HB	39:i:63:TYR:HB2	2.03	0.40
49:s:36:ARG:HD3	49:s:72:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:t:33:LYS:HB3	50:t:33:LYS:HE3	1.87	0.40
52:v:93:LYS:O	52:v:97:ASN:N	2.51	0.40
1:A:864:A:H5'	1:A:1226:G:C6	2.56	0.40
1:A:872:U:H2'	1:A:2457:A:O4'	2.21	0.40
1:A:893:G:N7	1:A:977:A:H2	2.19	0.40
1:A:1359:A:OP1	17:Q:11:ARG:NH2	2.32	0.40
1:A:2053:U:H2'	1:A:2054:G:N9	2.35	0.40
1:A:2095:U:O2'	1:A:2271:U:OP1	2.27	0.40
1:A:2378:G:C2	1:A:2392:G:O6	2.75	0.40
1:A:2516:G:H2'	1:A:2517:G:C8	2.56	0.40
1:A:2643:C:C4	26:Z:5:LYS:HB3	2.56	0.40
2:B:85:U:H1'	2:B:86:A:N6	2.37	0.40
15:O:14:ARG:HH11	15:O:14:ARG:HD2	1.72	0.40
31:a:193:C:H1'	31:a:194:G:H3'	2.03	0.40
31:a:859:U:H2'	31:a:860:U:C6	2.56	0.40
31:a:957:C:OP2	43:m:107:ARG:N	2.55	0.40
31:a:1085:G:O2'	32:b:103:ASN:HB2	2.21	0.40
31:a:1234:U:O2'	31:a:1332:C:OP2	2.27	0.40
31:a:1440:C:H2'	31:a:1441:C:C6	2.56	0.40
37:g:146:GLU:HA	37:g:149:LYS:HG2	2.02	0.40
38:h:38:GLU:O	38:h:42:SER:N	2.54	0.40
45:o:7:ARG:HD2	45:o:7:ARG:HA	1.90	0.40
46:p:75:LEU:HD22	46:p:80:ILE:HD13	2.02	0.40
1:A:33:U:O4	1:A:492:G:O2'	2.21	0.40
1:A:96:G:H2'	1:A:97:C:O4'	2.22	0.40
1:A:615:A:OP2	16:P:79:ARG:HD2	2.21	0.40
1:A:1634:A:N7	1:A:1635:A:N6	2.69	0.40
1:A:2777:A:O2'	1:A:2779:C:N4	2.39	0.40
1:A:2902:A:C4	1:A:2903:A:N1	2.90	0.40
5:E:110:LEU:HD23	5:E:110:LEU:HA	1.94	0.40
7:G:54:ARG:HD3	7:G:65:HIS:HB2	2.02	0.40
13:M:87:LYS:HB3	13:M:87:LYS:HE3	1.85	0.40
15:O:105:ALA:HB1	16:P:40:PHE:HZ	1.86	0.40
31:a:77:G:H3'	31:a:78:A:C8	2.55	0.40
31:a:250:C:O2'	31:a:253:U:OP1	2.32	0.40
31:a:564:C:H2'	31:a:565:G:C8	2.56	0.40
31:a:585:G:H4'	31:a:824:A:H3'	2.03	0.40
31:a:660:U:C2	31:a:761:A:N7	2.89	0.40
31:a:1395:G:H2'	31:a:1396:G:H8	1.87	0.40
31:a:1524:A:H2'	31:a:1525:U:C6	2.56	0.40
31:a:1527:G:N2	31:a:1530:A:OP2	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:171:THR:HG22	33:c:173:PRO:HD3	2.02	0.40
35:e:62:LYS:NZ	35:e:65:GLU:OE2	2.49	0.40
37:g:31:MET:HB3	37:g:34:GLY:HA2	2.04	0.40
39:i:18:VAL:HG23	39:i:70:HIS:HB3	2.03	0.40
1:A:45:G:C2	1:A:218:G:C2	3.09	0.40
1:A:150:A:N6	1:A:179:A:H61	2.20	0.40
1:A:223:G:H4'	1:A:225:A:H2	1.86	0.40
1:A:1054:A:H8	1:A:1054:A:O5'	2.05	0.40
1:A:1324:A:N1	1:A:1692:C:H5	2.20	0.40
1:A:2147:G:N2	1:A:2205:C:O2	2.55	0.40
1:A:2268:A:H2'	1:A:2269:G:C8	2.56	0.40
1:A:2806:U:H1'	1:A:2808:A:C6	2.57	0.40
2:B:60:C:H2'	2:B:61:C:H6	1.87	0.40
4:D:26:THR:OG1	4:D:199:GLY:O	2.40	0.40
7:G:152:ARG:H	7:G:162:ILE:HD12	1.87	0.40
13:M:33:VAL:HG11	13:M:105:VAL:HG13	2.04	0.40
13:M:83:LYS:HE3	13:M:83:LYS:HB2	1.73	0.40
15:O:90:ILE:HG21	15:O:90:ILE:HD13	1.87	0.40
27:1:9:CYS:HB3	27:1:12:CYS:HB2	1.90	0.40
31:a:571:A:H2'	31:a:575:G:C8	2.57	0.40
31:a:1095:G:H1'	31:a:1114:C:H41	1.86	0.40
41:k:31:ILE:H	41:k:31:ILE:HG13	1.76	0.40
43:m:75:LEU:O	43:m:79:ARG:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	272/274 (99%)	260 (96%)	11 (4%)	1 (0%)	30	42
4	D	213/215 (99%)	194 (91%)	19 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	204/206 (99%)	187 (92%)	17 (8%)	0	100	100
6	F	171/173 (99%)	142 (83%)	29 (17%)	0	100	100
7	G	171/173 (99%)	154 (90%)	17 (10%)	0	100	100
8	H	143/145 (99%)	130 (91%)	13 (9%)	0	100	100
9	I	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
10	J	144/146 (99%)	134 (93%)	10 (7%)	0	100	100
11	K	135/137 (98%)	128 (95%)	7 (5%)	0	100	100
12	L	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
13	M	116/118 (98%)	103 (89%)	13 (11%)	0	100	100
14	N	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
15	O	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
16	P	100/102 (98%)	92 (92%)	7 (7%)	1 (1%)	12	18
17	Q	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
18	R	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
19	S	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	12	18
20	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
21	U	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
22	V	47/49 (96%)	39 (83%)	8 (17%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
25	Y	57/59 (97%)	44 (77%)	13 (23%)	0	100	100
26	Z	46/48 (96%)	39 (85%)	7 (15%)	0	100	100
27	1	45/47 (96%)	45 (100%)	0	0	100	100
28	2	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
29	3	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	10
30	4	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
32	b	224/226 (99%)	206 (92%)	18 (8%)	0	100	100
33	c	200/202 (99%)	174 (87%)	26 (13%)	0	100	100
34	d	196/198 (99%)	166 (85%)	30 (15%)	0	100	100
35	e	154/156 (99%)	133 (86%)	21 (14%)	0	100	100
36	f	93/95 (98%)	86 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	150/152 (99%)	142 (95%)	8 (5%)	0	100	100
38	h	129/131 (98%)	110 (85%)	19 (15%)	0	100	100
39	i	125/127 (98%)	99 (79%)	26 (21%)	0	100	100
40	j	95/97 (98%)	79 (83%)	16 (17%)	0	100	100
41	k	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
42	l	133/135 (98%)	116 (87%)	17 (13%)	0	100	100
43	m	100/104 (96%)	84 (84%)	16 (16%)	0	100	100
44	n	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
45	o	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
46	p	87/89 (98%)	80 (92%)	7 (8%)	0	100	100
47	q	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
48	r	52/54 (96%)	47 (90%)	5 (10%)	0	100	100
49	s	78/80 (98%)	63 (81%)	15 (19%)	0	100	100
50	t	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
51	u	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
52	v	158/162 (98%)	144 (91%)	14 (9%)	0	100	100
All	All	5487/5589 (98%)	4951 (90%)	532 (10%)	4 (0%)	49	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	41	ALA
16	P	51	PRO
19	S	52	PRO
29	3	20	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	220/221 (100%)	184 (84%)	36 (16%)	2	2
4	D	173/173 (100%)	146 (84%)	27 (16%)	2	3
5	E	168/168 (100%)	139 (83%)	29 (17%)	2	2
6	F	141/152 (93%)	112 (79%)	29 (21%)	1	1
7	G	122/151 (81%)	102 (84%)	20 (16%)	2	2
8	H	123/123 (100%)	103 (84%)	20 (16%)	2	2
9	I	100/100 (100%)	83 (83%)	17 (17%)	2	2
10	J	109/112 (97%)	85 (78%)	24 (22%)	1	1
11	K	110/114 (96%)	94 (86%)	16 (14%)	3	3
12	L	96/101 (95%)	76 (79%)	20 (21%)	1	1
13	M	85/94 (90%)	68 (80%)	17 (20%)	1	1
14	N	93/100 (93%)	80 (86%)	13 (14%)	3	4
15	O	96/96 (100%)	86 (90%)	10 (10%)	7	10
16	P	84/86 (98%)	65 (77%)	19 (23%)	1	1
17	Q	88/90 (98%)	80 (91%)	8 (9%)	9	13
18	R	78/80 (98%)	63 (81%)	15 (19%)	1	2
19	S	81/88 (92%)	63 (78%)	18 (22%)	1	1
20	T	78/82 (95%)	66 (85%)	12 (15%)	2	3
21	U	59/60 (98%)	47 (80%)	12 (20%)	1	1
22	V	39/41 (95%)	36 (92%)	3 (8%)	12	19
23	W	58/60 (97%)	46 (79%)	12 (21%)	1	1
24	X	52/52 (100%)	39 (75%)	13 (25%)	0	1
25	Y	23/56 (41%)	20 (87%)	3 (13%)	4	5
26	Z	35/44 (80%)	26 (74%)	9 (26%)	0	0
27	1	44/45 (98%)	39 (89%)	5 (11%)	5	8
28	2	39/39 (100%)	36 (92%)	3 (8%)	12	19
29	3	55/55 (100%)	45 (82%)	10 (18%)	2	2
30	4	35/35 (100%)	29 (83%)	6 (17%)	2	2
32	b	196/196 (100%)	157 (80%)	39 (20%)	1	1
33	c	138/164 (84%)	101 (73%)	37 (27%)	0	0
34	d	147/174 (84%)	117 (80%)	30 (20%)	1	1
35	e	118/122 (97%)	93 (79%)	25 (21%)	1	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	f	80/83 (96%)	63 (79%)	17 (21%)	1	1
37	g	118/128 (92%)	96 (81%)	22 (19%)	1	2
38	h	111/112 (99%)	86 (78%)	25 (22%)	1	1
39	i	86/105 (82%)	67 (78%)	19 (22%)	1	1
40	j	81/87 (93%)	64 (79%)	17 (21%)	1	1
41	k	82/90 (91%)	65 (79%)	17 (21%)	1	1
42	l	111/117 (95%)	88 (79%)	23 (21%)	1	1
43	m	62/92 (67%)	41 (66%)	21 (34%)	0	0
44	n	48/52 (92%)	33 (69%)	15 (31%)	0	0
45	o	77/80 (96%)	55 (71%)	22 (29%)	0	0
46	p	73/75 (97%)	57 (78%)	16 (22%)	1	1
47	q	65/75 (87%)	49 (75%)	16 (25%)	1	1
48	r	48/49 (98%)	38 (79%)	10 (21%)	1	1
49	s	67/70 (96%)	52 (78%)	15 (22%)	1	1
50	t	61/67 (91%)	52 (85%)	9 (15%)	3	3
51	u	40/48 (83%)	32 (80%)	8 (20%)	1	1
52	v	147/147 (100%)	103 (70%)	44 (30%)	0	0
All	All	4440/4751 (94%)	3567 (80%)	873 (20%)	3	1

All (873) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	3	ILE
3	C	5	LYS
3	C	9	ILE
3	C	10	THR
3	C	13	ARG
3	C	23	GLU
3	C	25	THR
3	C	27	THR
3	C	34	LEU
3	C	37	LEU
3	C	40	LYS
3	C	60	ARG
3	C	64	VAL
3	C	71	LYS

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Mol	Chain	Res	Type
3	C	75	ASN
3	C	93	LEU
3	C	116	VAL
3	C	137	VAL
3	C	139	THR
3	C	146	LEU
3	C	168	GLU
3	C	176	LEU
3	C	180	GLU
3	C	181	VAL
3	C	198	LEU
3	C	203	VAL
3	C	207	LYS
3	C	219	THR
3	C	220	VAL
3	C	241	ILE
3	C	254	THR
3	C	255	LEU
3	C	257	LYS
3	C	261	ARG
3	C	271	VAL
3	C	274	ARG
4	D	2	THR
4	D	3	LYS
4	D	12	MET
4	D	13	THR
4	D	15	VAL
4	D	18	GLU
4	D	21	GLU
4	D	23	ILE
4	D	25	VAL
4	D	26	THR
4	D	27	VAL
4	D	36	LEU
4	D	40	THR
4	D	74	GLU
4	D	85	LYS
4	D	100	GLU
4	D	101	VAL
4	D	107	VAL
4	D	138	ARG
4	D	145	SER

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Mol	Chain	Res	Type
4	D	156	MET
4	D	176	ASN
4	D	177	THR
4	D	178	VAL
4	D	179	THR
4	D	200	ASN
4	D	215	ILE
5	E	9	LEU
5	E	13	LYS
5	E	16	SER
5	E	17	ILE
5	E	33	LEU
5	E	62	ARG
5	E	82	GLN
5	E	84	ARG
5	E	93	THR
5	E	108	LEU
5	E	115	SER
5	E	119	GLN
5	E	120	GLU
5	E	125	VAL
5	E	144	SER
5	E	146	LEU
5	E	150	LYS
5	E	152	VAL
5	E	154	VAL
5	E	163	VAL
5	E	165	LEU
5	E	166	SER
5	E	176	THR
5	E	192	LEU
5	E	193	VAL
5	E	194	ILE
5	E	202	VAL
5	E	204	GLU
5	E	206	LEU
6	F	4	LEU
6	F	24	SER
6	F	31	ILE
6	F	35	VAL
6	F	44	VAL
6	F	48	LYS

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Mol	Chain	Res	Type
6	F	50	LEU
6	F	57	LEU
6	F	61	THR
6	F	67	VAL
6	F	74	ILE
6	F	76	THR
6	F	85	ILE
6	F	100	LEU
6	F	102	LYS
6	F	104	ILE
6	F	109	PRO
6	F	110	ARG
6	F	117	VAL
6	F	120	LYS
6	F	136	LEU
6	F	137	ILE
6	F	142	ASP
6	F	145	LYS
6	F	149	VAL
6	F	150	ARG
6	F	153	ASP
6	F	161	ASN
6	F	172	ASN
7	G	3	ARG
7	G	15	VAL
7	G	25	THR
7	G	34	SER
7	G	36	THR
7	G	39	GLU
7	G	43	PHE
7	G	44	LYS
7	G	49	THR
7	G	52	VAL
7	G	77	GLN
7	G	79	VAL
7	G	87	LEU
7	G	102	ASP
7	G	103	LEU
7	G	120	ASN
7	G	121	ILE
7	G	137	SER
7	G	144	LEU

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Mol	Chain	Res	Type
7	G	155	GLU
8	H	1	MET
8	H	3	GLN
8	H	12	ILE
8	H	25	THR
8	H	29	LEU
8	H	37	LEU
8	H	40	LYS
8	H	46	THR
8	H	49	VAL
8	H	51	THR
8	H	66	THR
8	H	74	VAL
8	H	87	SER
8	H	93	LEU
8	H	100	ARG
8	H	112	SER
8	H	114	ARG
8	H	125	VAL
8	H	136	GLN
8	H	144	ARG
9	I	2	ILE
9	I	6	THR
9	I	9	LYS
9	I	19	VAL
9	I	21	THR
9	I	40	VAL
9	I	42	THR
9	I	43	VAL
9	I	66	LYS
9	I	81	GLU
9	I	98	ILE
9	I	102	VAL
9	I	105	GLU
9	I	106	LEU
9	I	110	ASN
9	I	116	SER
9	I	120	GLU
10	J	3	LEU
10	J	6	LEU
10	J	12	SER
10	J	18	ARG

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Mol	Chain	Res	Type
10	J	19	VAL
10	J	46	VAL
10	J	51	GLU
10	J	57	LEU
10	J	61	LEU
10	J	64	ARG
10	J	69	ILE
10	J	71	ARG
10	J	77	VAL
10	J	79	LEU
10	J	83	ASN
10	J	91	VAL
10	J	95	LEU
10	J	96	LEU
10	J	99	SER
10	J	103	LYS
10	J	105	GLU
10	J	107	SER
10	J	110	LYS
10	J	121	LEU
11	K	5	LYS
11	K	11	ARG
11	K	17	THR
11	K	37	THR
11	K	39	THR
11	K	45	ARG
11	K	64	VAL
11	K	76	LYS
11	K	77	LYS
11	K	90	VAL
11	K	96	VAL
11	K	97	VAL
11	K	110	SER
11	K	122	SER
11	K	125	LEU
11	K	129	THR
12	L	8	ARG
12	L	9	THR
12	L	11	ASP
12	L	17	LEU
12	L	20	LEU
12	L	24	LEU

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Mol	Chain	Res	Type
12	L	29	ARG
12	L	33	THR
12	L	45	GLU
12	L	47	LEU
12	L	53	LYS
12	L	58	SER
12	L	72	LEU
12	L	77	THR
12	L	95	GLU
12	L	104	LEU
12	L	112	ASP
12	L	117	VAL
12	L	121	LEU
12	L	122	VAL
13	M	5	ILE
13	M	6	ASP
13	M	19	ARG
13	M	20	THR
13	M	21	ASN
13	M	22	LEU
13	M	30	ARG
13	M	35	ARG
13	M	52	THR
13	M	66	THR
13	M	68	THR
13	M	80	ILE
13	M	86	ASP
13	M	87	LYS
13	M	92	ILE
13	M	108	LEU
13	M	115	SER
14	N	14	GLN
14	N	17	THR
14	N	19	LEU
14	N	42	ILE
14	N	44	VAL
14	N	50	ILE
14	N	52	ARG
14	N	57	VAL
14	N	60	THR
14	N	73	GLU
14	N	90	ARG

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Mol	Chain	Res	Type
14	N	98	LYS
14	N	102	LEU
15	O	4	VAL
15	O	20	LEU
15	O	51	ARG
15	O	74	MET
15	O	83	LEU
15	O	84	LYS
15	O	90	ILE
15	O	96	SER
15	O	103	GLU
15	O	109	LEU
16	P	10	LYS
16	P	16	GLU
16	P	22	VAL
16	P	25	LEU
16	P	26	ASP
16	P	27	VAL
16	P	34	THR
16	P	36	ASP
16	P	61	THR
16	P	63	ASN
16	P	65	GLN
16	P	67	ARG
16	P	77	LYS
16	P	79	ARG
16	P	80	LYS
16	P	86	LYS
16	P	97	ILE
16	P	98	ASP
16	P	100	ILE
17	Q	1	MET
17	Q	6	VAL
17	Q	19	LEU
17	Q	20	VAL
17	Q	81	THR
17	Q	95	ASN
17	Q	104	VAL
17	Q	105	VAL
18	R	5	ASP
18	R	6	ILE
18	R	13	THR

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Mol	Chain	Res	Type
18	R	14	GLU
18	R	16	SER
18	R	28	ASP
18	R	42	VAL
18	R	47	ASN
18	R	53	VAL
18	R	56	MET
18	R	69	GLN
18	R	72	THR
18	R	76	ARG
18	R	80	VAL
18	R	89	LEU
19	S	15	LYS
19	S	19	LYS
19	S	20	GLU
19	S	23	VAL
19	S	24	ILE
19	S	26	THR
19	S	34	VAL
19	S	45	GLN
19	S	56	ILE
19	S	57	LEU
19	S	60	GLU
19	S	65	VAL
19	S	66	SER
19	S	68	VAL
19	S	75	THR
19	S	79	THR
19	S	93	ILE
19	S	97	SER
20	T	15	ARG
20	T	17	ASP
20	T	21	LEU
20	T	26	LYS
20	T	30	VAL
20	T	36	THR
20	T	52	ILE
20	T	55	VAL
20	T	72	VAL
20	T	82	LEU
20	T	89	ILE
20	T	92	LEU

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Mol	Chain	Res	Type
21	U	19	LYS
21	U	24	SER
21	U	28	ARG
21	U	29	LEU
21	U	67	LEU
21	U	72	ASP
21	U	74	VAL
21	U	75	VAL
21	U	85	LYS
21	U	87	VAL
21	U	88	SER
21	U	92	VAL
22	V	27	ARG
22	V	33	LEU
22	V	41	ASP
23	W	2	LYS
23	W	4	LYS
23	W	11	THR
23	W	14	ILE
23	W	24	GLU
23	W	25	LEU
23	W	39	GLU
23	W	47	ARG
23	W	52	ARG
23	W	54	LYS
23	W	61	GLU
23	W	63	GLU
24	X	5	GLN
24	X	12	VAL
24	X	15	ARG
24	X	17	GLU
24	X	18	THR
24	X	20	ARG
24	X	23	VAL
24	X	35	VAL
24	X	38	GLU
24	X	43	ILE
24	X	46	GLN
24	X	50	VAL
24	X	56	VAL
25	Y	1	MET
25	Y	5	ILE

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Mol	Chain	Res	Type
25	Y	38	GLU
26	Z	5	LYS
26	Z	7	ARG
26	Z	8	THR
26	Z	11	THR
26	Z	18	THR
26	Z	24	VAL
26	Z	30	CYS
26	Z	37	LYS
26	Z	42	VAL
27	1	15	ARG
27	1	19	THR
27	1	36	CYS
27	1	43	THR
27	1	44	LEU
28	2	26	LYS
28	2	31	VAL
28	2	40	ARG
29	3	14	VAL
29	3	15	LYS
29	3	30	SER
29	3	31	HIS
29	3	32	LEU
29	3	38	THR
29	3	45	ARG
29	3	59	LYS
29	3	62	LEU
29	3	65	LYS
30	4	2	LYS
30	4	11	CYS
30	4	15	LYS
30	4	25	VAL
30	4	27	CYS
30	4	33	LYS
32	b	3	VAL
32	b	7	LYS
32	b	9	LEU
32	b	11	GLU
32	b	14	VAL
32	b	20	THR
32	b	21	ARG
32	b	26	LYS

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Mol	Chain	Res	Type
32	b	28	LYS
32	b	43	LEU
32	b	50	VAL
32	b	51	ASP
32	b	58	LYS
32	b	60	VAL
32	b	62	GLU
32	b	75	GLN
32	b	81	LYS
32	b	83	GLU
32	b	89	GLN
32	b	92	ILE
32	b	101	LEU
32	b	116	GLU
32	b	126	PHE
32	b	127	GLU
32	b	128	VAL
32	b	134	VAL
32	b	144	LEU
32	b	145	ILE
32	b	161	LEU
32	b	164	VAL
32	b	170	ARG
32	b	173	ILE
32	b	184	VAL
32	b	186	ILE
32	b	187	VAL
32	b	205	ASP
32	b	213	LEU
32	b	221	ILE
32	b	223	GLU
33	c	5	ILE
33	c	10	LEU
33	c	31	LEU
33	c	32	LEU
33	c	36	LEU
33	c	40	LYS
33	c	42	ILE
33	c	45	GLU
33	c	57	GLU
33	c	63	ILE
33	c	78	LYS

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Mol	Chain	Res	Type
33	c	94	THR
33	c	95	ASP
33	c	105	ILE
33	c	108	VAL
33	c	109	ASP
33	c	111	ASP
33	c	113	ARG
33	c	114	LEU
33	c	115	VAL
33	c	118	ASN
33	c	121	ARG
33	c	128	SER
33	c	143	LEU
33	c	148	ILE
33	c	150	THR
33	c	160	ASP
33	c	165	GLU
33	c	166	GLN
33	c	167	TYR
33	c	172	VAL
33	c	174	LEU
33	c	177	LEU
33	c	178	ARG
33	c	191	THR
33	c	197	VAL
33	c	201	ILE
34	d	10	LYS
34	d	11	LYS
34	d	22	THR
34	d	26	LEU
34	d	35	GLN
34	d	51	LEU
34	d	52	ARG
34	d	55	GLN
34	d	58	ARG
34	d	61	TYR
34	d	63	MET
34	d	65	GLU
34	d	71	THR
34	d	74	ILE
34	d	84	GLU
34	d	85	ASN

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Mol	Chain	Res	Type
34	d	89	LEU
34	d	93	ARG
34	d	103	LEU
34	d	111	ARG
34	d	114	VAL
34	d	115	ASN
34	d	128	ILE
34	d	139	ILE
34	d	141	VAL
34	d	152	VAL
34	d	156	GLU
34	d	163	GLU
34	d	165	LEU
34	d	193	LEU
35	e	10	GLU
35	e	13	GLU
35	e	15	VAL
35	e	24	VAL
35	e	31	PHE
35	e	32	ARG
35	e	56	VAL
35	e	65	GLU
35	e	69	LYS
35	e	72	VAL
35	e	81	THR
35	e	88	ARG
35	e	93	SER
35	e	105	VAL
35	e	106	ILE
35	e	114	VAL
35	e	123	ILE
35	e	124	LEU
35	e	132	THR
35	e	134	ILE
35	e	137	VAL
35	e	141	ILE
35	e	156	LEU
35	e	157	ARG
35	e	163	GLU
36	f	6	VAL
36	f	10	VAL
36	f	14	ILE

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Mol	Chain	Res	Type
36	f	20	LYS
36	f	22	LEU
36	f	39	GLU
36	f	52	ILE
36	f	56	LYS
36	f	57	ASP
36	f	65	VAL
36	f	73	THR
36	f	76	PHE
36	f	84	ASP
36	f	86	ILE
36	f	87	ILE
36	f	91	VAL
36	f	93	ARG
37	g	7	VAL
37	g	9	LYS
37	g	11	ASP
37	g	12	VAL
37	g	22	LEU
37	g	24	THR
37	g	29	LYS
37	g	32	LEU
37	g	38	THR
37	g	41	ARG
37	g	48	ASP
37	g	91	VAL
37	g	94	GLU
37	g	99	LEU
37	g	105	VAL
37	g	109	ARG
37	g	115	THR
37	g	120	LEU
37	g	125	LEU
37	g	131	THR
37	g	135	VAL
37	g	137	LYS
38	h	7	ILE
38	h	10	MET
38	h	20	VAL
38	h	24	LYS
38	h	26	GLU
38	h	32	ILE

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Mol	Chain	Res	Type
38	h	39	ILE
38	h	46	ILE
38	h	53	GLU
38	h	59	VAL
38	h	61	ARG
38	h	62	LEU
38	h	70	ASP
38	h	82	LYS
38	h	94	MET
38	h	96	LYS
38	h	98	LEU
38	h	101	LEU
38	h	103	ILE
38	h	105	LEU
38	h	112	VAL
38	h	113	ILE
38	h	114	THR
38	h	115	ASP
38	h	120	LYS
39	i	17	SER
39	i	20	ARG
39	i	24	VAL
39	i	31	THR
39	i	32	VAL
39	i	37	VAL
39	i	40	TYR
39	i	46	LEU
39	i	54	PHE
39	i	56	VAL
39	i	57	THR
39	i	60	LYS
39	i	65	VAL
39	i	66	LEU
39	i	67	VAL
39	i	81	ILE
39	i	101	LYS
39	i	116	LYS
39	i	129	PHE
40	j	10	LEU
40	j	11	LYS
40	j	18	ILE
40	j	27	GLU

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Mol	Chain	Res	Type
40	j	31	ARG
40	j	35	ASP
40	j	40	ILE
40	j	45	GLU
40	j	50	THR
40	j	51	ILE
40	j	52	ILE
40	j	55	VAL
40	j	59	LYS
40	j	65	PHE
40	j	77	VAL
40	j	80	THR
40	j	88	MET
41	k	22	HIS
41	k	31	ILE
41	k	32	VAL
41	k	36	ASP
41	k	37	GLU
41	k	40	ASN
41	k	42	LEU
41	k	53	LYS
41	k	59	THR
41	k	64	GLN
41	k	69	THR
41	k	82	VAL
41	k	94	GLU
41	k	97	ILE
41	k	101	GLN
41	k	105	LEU
41	k	108	THR
42	l	3	THR
42	l	31	LYS
42	l	36	THR
42	l	39	ASN
42	l	42	GLN
42	l	44	ARG
42	l	47	CYS
42	l	54	THR
42	l	62	LEU
42	l	63	ARG
42	l	67	ARG
42	l	80	ILE

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Mol	Chain	Res	Type
42	l	88	GLN
42	l	89	GLU
42	l	99	ARG
42	l	100	VAL
42	l	106	VAL
42	l	112	ARG
42	l	115	LEU
42	l	120	VAL
42	l	128	SER
42	l	129	LEU
42	l	134	LYS
43	m	9	ILE
43	m	13	LYS
43	m	20	THR
43	m	22	ILE
43	m	31	GLN
43	m	35	GLU
43	m	57	ARG
43	m	59	VAL
43	m	60	VAL
43	m	63	TYR
43	m	64	LYS
43	m	68	ASP
43	m	75	LEU
43	m	80	LEU
43	m	89	ILE
43	m	95	LEU
43	m	100	GLN
43	m	102	THR
43	m	107	ARG
43	m	108	THR
43	m	110	LYS
44	n	3	LYS
44	n	4	THR
44	n	14	GLN
44	n	22	THR
44	n	24	CYS
44	n	27	CYS
44	n	31	HIS
44	n	33	VAL
44	n	35	ARG
44	n	38	LYS

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Mol	Chain	Res	Type
44	n	44	PHE
44	n	45	ARG
44	n	52	GLN
44	n	53	ILE
44	n	56	VAL
45	o	3	ILE
45	o	8	LYS
45	o	11	ILE
45	o	14	GLU
45	o	15	TYR
45	o	17	VAL
45	o	27	VAL
45	o	28	GLN
45	o	32	LEU
45	o	40	ASN
45	o	42	HIS
45	o	43	LEU
45	o	46	HIS
45	o	47	LYS
45	o	48	LYS
45	o	50	HIS
45	o	56	LEU
45	o	74	ASP
45	o	75	ILE
45	o	80	GLU
45	o	81	LEU
45	o	85	LEU
46	p	4	LYS
46	p	7	LEU
46	p	10	LEU
46	p	21	VAL
46	p	22	VAL
46	p	32	ARG
46	p	39	THR
46	p	53	ASP
46	p	54	GLU
46	p	58	LEU
46	p	59	LYS
46	p	68	THR
46	p	74	ILE
46	p	75	LEU
46	p	78	GLU

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Mol	Chain	Res	Type
46	p	81	MET
47	q	14	VAL
47	q	26	LEU
47	q	29	THR
47	q	34	LYS
47	q	39	ARG
47	q	48	THR
47	q	51	GLU
47	q	52	ASN
47	q	67	ARG
47	q	70	SER
47	q	76	ARG
47	q	77	LEU
47	q	78	VAL
47	q	80	ILE
47	q	81	VAL
47	q	83	GLU
48	r	24	THR
48	r	33	LEU
48	r	45	LEU
48	r	50	THR
48	r	55	LYS
48	r	60	LEU
48	r	72	LEU
48	r	73	LEU
48	r	75	TYR
48	r	76	VAL
49	s	5	ILE
49	s	15	LEU
49	s	19	VAL
49	s	28	LYS
49	s	29	GLN
49	s	30	VAL
49	s	31	ILE
49	s	32	LYS
49	s	48	THR
49	s	58	VAL
49	s	60	VAL
49	s	61	TYR
49	s	64	GLU
49	s	67	VAL
49	s	69	HIS

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Mol	Chain	Res	Type
50	t	8	ILE
50	t	12	LYS
50	t	14	THR
50	t	15	GLU
50	t	22	ILE
50	t	49	LEU
50	t	65	LEU
50	t	70	LYS
50	t	73	ARG
51	u	5	VAL
51	u	12	LEU
51	u	17	ARG
51	u	18	ARG
51	u	21	ARG
51	u	33	ARG
51	u	43	VAL
51	u	44	LYS
52	v	2	ILE
52	v	3	ARG
52	v	4	PHE
52	v	6	ILE
52	v	14	THR
52	v	17	ILE
52	v	27	LYS
52	v	28	LEU
52	v	30	ARG
52	v	34	ASP
52	v	35	VAL
52	v	39	VAL
52	v	44	VAL
52	v	45	LYS
52	v	46	THR
52	v	57	THR
52	v	58	ILE
52	v	60	LEU
52	v	63	VAL
52	v	68	GLU
52	v	73	ASP
52	v	74	LEU
52	v	78	ILE
52	v	83	ASN
52	v	84	LYS

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Mol	Chain	Res	Type
52	v	85	LEU
52	v	88	GLN
52	v	89	VAL
52	v	90	ARG
52	v	93	LYS
52	v	102	ASP
52	v	137	LYS
52	v	144	MET
52	v	147	GLU
52	v	150	VAL
52	v	151	LEU
52	v	155	LEU
52	v	162	VAL
52	v	164	THR
52	v	165	ASP
52	v	168	THR
52	v	173	ILE
52	v	176	ARG
52	v	184	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	86	ASN
3	C	143	ASN
3	C	153	GLN
3	C	226	ASN
3	C	230	HIS
3	C	232	HIS
4	D	47	ASN
4	D	50	GLN
4	D	176	ASN
4	D	200	ASN
5	E	75	GLN
5	E	82	GLN
5	E	119	GLN
7	G	74	ASN
7	G	106	ASN
8	H	24	GLN
8	H	48	HIS
8	H	81	HIS
10	J	54	GLN

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Mol	Chain	Res	Type
11	K	35	GLN
11	K	46	GLN
11	K	71	HIS
13	M	39	HIS
13	M	43	GLN
13	M	48	ASN
15	O	37	GLN
15	O	52	GLN
15	O	81	ASN
16	P	18	GLN
16	P	65	GLN
16	P	81	ASN
17	Q	61	ASN
17	Q	95	ASN
18	R	37	GLN
19	S	8	ASN
19	S	67	ASN
20	T	88	HIS
21	U	37	GLN
22	V	23	ASN
24	X	19	GLN
25	Y	3	GLN
27	1	26	ASN
28	2	7	GLN
32	b	55	ASN
32	b	94	GLN
32	b	103	ASN
32	b	203	ASN
32	b	225	GLN
33	c	64	ASN
33	c	118	ASN
33	c	135	GLN
33	c	151	GLN
33	c	166	GLN
34	d	35	GLN
34	d	55	GLN
34	d	67	GLN
34	d	70	ASN
34	d	118	HIS
34	d	137	GLN
34	d	166	ASN
35	e	135	ASN

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Mol	Chain	Res	Type
35	e	146	ASN
36	f	69	ASN
36	f	70	ASN
36	f	77	GLN
37	g	18	HIS
37	g	67	ASN
37	g	148	ASN
38	h	22	HIS
39	i	16	ASN
39	i	29	ASN
39	i	62	ASN
39	i	68	ASN
39	i	128	GLN
40	j	15	HIS
41	k	40	ASN
41	k	64	GLN
42	l	42	GLN
42	l	85	HIS
44	n	11	GLN
44	n	52	GLN
45	o	9	ASN
45	o	28	GLN
45	o	40	ASN
45	o	68	ASN
49	s	29	GLN
49	s	43	ASN
49	s	69	HIS
50	t	21	ASN
50	t	34	ASN
50	t	62	GLN
50	t	64	ASN
50	t	69	ASN
52	v	7	HIS
52	v	83	ASN
52	v	88	GLN
52	v	152	GLN
52	v	158	HIS
52	v	186	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2899/2905 (99%)	1357 (46%)	256 (8%)
2	B	114/115 (99%)	33 (28%)	2 (1%)
31	a	1537/1539 (99%)	710 (46%)	0
All	All	4550/4559 (99%)	2100 (46%)	258 (5%)

All (2100) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	A
1	A	12	U
1	A	13	A
1	A	14	A
1	A	22	C
1	A	24	G
1	A	26	G
1	A	27	G
1	A	28	A
1	A	32	C
1	A	33	U
1	A	34	U
1	A	35	G
1	A	36	G
1	A	37	C
1	A	39	C
1	A	43	A
1	A	44	A
1	A	45	G
1	A	46	C
1	A	47	C
1	A	48	G
1	A	49	A
1	A	50	U
1	A	51	G
1	A	53	A
1	A	54	G
1	A	58	G
1	A	63	U
1	A	64	A
1	A	65	A
1	A	67	G
1	A	69	C
1	A	71	A

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Mol	Chain	Res	Type
1	A	74	U
1	A	75	G
1	A	82	G
1	A	84	A
1	A	88	G
1	A	90	A
1	A	91	A
1	A	92	G
1	A	94	A
1	A	95	A
1	A	96	G
1	A	97	C
1	A	98	U
1	A	99	U
1	A	100	U
1	A	101	G
1	A	102	A
1	A	103	U
1	A	105	C
1	A	109	G
1	A	117	A
1	A	118	A
1	A	119	U
1	A	125	A
1	A	130	A
1	A	140	A
1	A	141	U
1	A	150	A
1	A	151	U
1	A	156	A
1	A	157	U
1	A	158	G
1	A	161	A
1	A	167	U
1	A	168	A
1	A	170	C
1	A	172	U
1	A	174	U
1	A	176	A
1	A	177	G
1	A	178	A
1	A	179	A

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Mol	Chain	Res	Type
1	A	180	G
1	A	181	G
1	A	182	C
1	A	183	A
1	A	184	C
1	A	186	C
1	A	194	A
1	A	199	A
1	A	200	A
1	A	201	C
1	A	202	A
1	A	203	U
1	A	210	A
1	A	216	A
1	A	218	G
1	A	219	A
1	A	224	A
1	A	225	A
1	A	227	G
1	A	229	A
1	A	230	A
1	A	232	U
1	A	233	U
1	A	235	G
1	A	236	A
1	A	237	U
1	A	240	C
1	A	241	C
1	A	242	U
1	A	243	U
1	A	248	G
1	A	251	G
1	A	253	G
1	A	255	G
1	A	262	G
1	A	263	G
1	A	264	G
1	A	267	G
1	A	269	G
1	A	270	C
1	A	271	C
1	A	272	C

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Mol	Chain	Res	Type
1	A	275	A
1	A	283	G
1	A	286	U
1	A	287	G
1	A	289	U
1	A	292	U
1	A	295	G
1	A	297	G
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	303	G
1	A	305	A
1	A	306	C
1	A	307	A
1	A	308	C
1	A	310	C
1	A	311	U
1	A	315	C
1	A	317	G
1	A	318	A
1	A	320	U
1	A	324	A
1	A	325	A
1	A	326	A
1	A	327	G
1	A	328	G
1	A	329	A
1	A	330	C
1	A	331	G
1	A	332	A
1	A	333	C
1	A	334	A
1	A	335	U
1	A	336	U
1	A	337	A
1	A	338	G
1	A	340	C
1	A	341	G
1	A	342	A

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Mol	Chain	Res	Type
1	A	344	U
1	A	345	C
1	A	346	A
1	A	348	C
1	A	349	U
1	A	350	G
1	A	351	G
1	A	352	A
1	A	353	A
1	A	354	A
1	A	355	G
1	A	356	A
1	A	357	U
1	A	359	A
1	A	362	C
1	A	363	A
1	A	364	A
1	A	365	A
1	A	366	G
1	A	367	A
1	A	368	A
1	A	371	U
1	A	372	A
1	A	373	A
1	A	374	U
1	A	375	A
1	A	376	A
1	A	377	U
1	A	378	C
1	A	379	C
1	A	380	U
1	A	381	G
1	A	382	U
1	A	383	A
1	A	388	A
1	A	389	A
1	A	391	A
1	A	392	U
1	A	393	G
1	A	394	U
1	A	395	U
1	A	398	C

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Mol	Chain	Res	Type
1	A	400	C
1	A	401	U
1	A	402	C
1	A	403	U
1	A	404	U
1	A	405	G
1	A	406	A
1	A	407	G
1	A	408	U
1	A	409	G
1	A	410	G
1	A	411	A
1	A	412	U
1	A	413	C
1	A	416	G
1	A	417	A
1	A	420	A
1	A	422	G
1	A	423	A
1	A	425	G
1	A	429	C
1	A	432	G
1	A	433	U
1	A	434	G
1	A	435	A
1	A	437	A
1	A	438	U
1	A	439	U
1	A	444	C
1	A	445	G
1	A	447	A
1	A	449	U
1	A	451	U
1	A	452	G
1	A	457	G
1	A	458	A
1	A	459	C
1	A	460	C
1	A	461	A
1	A	462	U
1	A	463	C
1	A	464	U

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Mol	Chain	Res	Type
1	A	467	U
1	A	468	A
1	A	470	G
1	A	472	C
1	A	474	A
1	A	476	A
1	A	477	U
1	A	479	C
1	A	480	U
1	A	481	C
1	A	484	U
1	A	488	G
1	A	489	A
1	A	490	C
1	A	491	C
1	A	492	G
1	A	493	A
1	A	494	U
1	A	495	A
1	A	496	G
1	A	497	U
1	A	500	A
1	A	501	C
1	A	506	A
1	A	510	U
1	A	512	A
1	A	513	G
1	A	514	G
1	A	519	G
1	A	520	G
1	A	521	U
1	A	522	G
1	A	523	A
1	A	524	A
1	A	525	A
1	A	526	A
1	A	527	G
1	A	529	A
1	A	531	C
1	A	532	C
1	A	533	C
1	A	534	G

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Mol	Chain	Res	Type
1	A	535	G
1	A	536	A
1	A	541	G
1	A	544	U
1	A	545	G
1	A	546	A
1	A	547	A
1	A	548	A
1	A	550	A
1	A	551	G
1	A	553	A
1	A	554	C
1	A	555	C
1	A	556	U
1	A	557	G
1	A	558	A
1	A	562	C
1	A	563	G
1	A	564	U
1	A	567	G
1	A	568	C
1	A	571	A
1	A	572	C
1	A	573	A
1	A	575	G
1	A	576	U
1	A	577	A
1	A	578	G
1	A	581	A
1	A	582	G
1	A	583	A
1	A	587	C
1	A	588	G
1	A	589	U
1	A	591	A
1	A	592	A
1	A	593	U
1	A	594	G
1	A	595	G
1	A	596	G
1	A	599	A
1	A	600	U

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Mol	Chain	Res	Type
1	A	601	G
1	A	604	G
1	A	605	U
1	A	606	G
1	A	608	C
1	A	614	U
1	A	615	A
1	A	616	G
1	A	617	A
1	A	618	A
1	A	621	A
1	A	622	A
1	A	623	C
1	A	624	C
1	A	626	G
1	A	627	C
1	A	628	G
1	A	629	A
1	A	630	G
1	A	631	U
1	A	633	A
1	A	634	C
1	A	635	G
1	A	638	U
1	A	639	U
1	A	640	G
1	A	641	A
1	A	644	C
1	A	645	A
1	A	646	A
1	A	647	G
1	A	648	G
1	A	649	U
1	A	650	U
1	A	651	A
1	A	657	U
1	A	658	A
1	A	659	A
1	A	660	A
1	A	665	G
1	A	667	G
1	A	668	C

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Mol	Chain	Res	Type
1	A	669	C
1	A	672	A
1	A	675	G
1	A	679	G
1	A	682	A
1	A	689	A
1	A	690	U
1	A	691	A
1	A	694	G
1	A	699	U
1	A	700	A
1	A	702	U
1	A	703	A
1	A	704	U
1	A	707	G
1	A	708	G
1	A	709	U
1	A	710	C
1	A	713	A
1	A	714	G
1	A	715	A
1	A	720	A
1	A	722	A
1	A	729	G
1	A	731	U
1	A	746	G
1	A	753	U
1	A	754	U
1	A	756	A
1	A	758	G
1	A	759	U
1	A	760	A
1	A	761	A
1	A	762	C
1	A	763	A
1	A	766	G
1	A	768	A
1	A	775	A
1	A	781	C
1	A	783	G
1	A	785	C
1	A	792	U

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Mol	Chain	Res	Type
1	A	793	G
1	A	797	A
1	A	802	G
1	A	809	A
1	A	810	A
1	A	820	G
1	A	822	G
1	A	827	A
1	A	829	U
1	A	834	A
1	A	835	U
1	A	836	C
1	A	837	G
1	A	839	A
1	A	842	U
1	A	850	G
1	A	856	U
1	A	857	C
1	A	858	U
1	A	859	C
1	A	860	U
1	A	861	C
1	A	863	G
1	A	864	A
1	A	865	A
1	A	866	A
1	A	867	U
1	A	868	A
1	A	872	U
1	A	873	U
1	A	874	A
1	A	875	G
1	A	876	G
1	A	883	C
1	A	884	U
1	A	891	A
1	A	892	U
1	A	893	G
1	A	894	A
1	A	895	U
1	A	896	U
1	A	897	A

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Mol	Chain	Res	Type
1	A	899	U
1	A	901	G
1	A	904	G
1	A	905	U
1	A	909	G
1	A	910	C
1	A	911	A
1	A	912	C
1	A	918	G
1	A	919	G
1	A	920	A
1	A	921	C
1	A	922	G
1	A	923	A
1	A	924	G
1	A	925	G
1	A	927	G
1	A	938	G
1	A	939	U
1	A	940	U
1	A	944	G
1	A	947	U
1	A	948	U
1	A	949	C
1	A	954	A
1	A	955	A
1	A	957	C
1	A	959	C
1	A	961	G
1	A	962	A
1	A	967	C
1	A	969	A
1	A	970	U
1	A	971	U
1	A	972	A
1	A	973	A
1	A	974	U
1	A	976	U
1	A	977	A
1	A	978	A
1	A	985	A
1	A	986	G

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Mol	Chain	Res	Type
1	A	987	U
1	A	988	C
1	A	989	A
1	A	990	G
1	A	991	A
1	A	993	C
1	A	994	A
1	A	995	U
1	A	996	G
1	A	997	G
1	A	998	G
1	A	1001	A
1	A	1002	U
1	A	1004	A
1	A	1005	G
1	A	1006	G
1	A	1007	U
1	A	1009	C
1	A	1011	U
1	A	1012	G
1	A	1013	U
1	A	1014	U
1	A	1015	C
1	A	1018	A
1	A	1019	A
1	A	1020	G
1	A	1022	G
1	A	1023	A
1	A	1024	A
1	A	1025	A
1	A	1026	C
1	A	1027	A
1	A	1028	G
1	A	1029	C
1	A	1030	C
1	A	1031	C
1	A	1032	A
1	A	1033	G
1	A	1034	A
1	A	1035	C
1	A	1037	A
1	A	1038	C

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Mol	Chain	Res	Type
1	A	1039	C
1	A	1040	A
1	A	1041	G
1	A	1044	A
1	A	1045	A
1	A	1046	G
1	A	1047	G
1	A	1049	C
1	A	1050	C
1	A	1051	C
1	A	1052	A
1	A	1053	A
1	A	1055	A
1	A	1056	U
1	A	1057	A
1	A	1058	U
1	A	1063	U
1	A	1064	A
1	A	1065	A
1	A	1066	G
1	A	1067	U
1	A	1069	G
1	A	1070	A
1	A	1071	A
1	A	1073	A
1	A	1074	G
1	A	1077	U
1	A	1078	G
1	A	1080	G
1	A	1083	G
1	A	1084	U
1	A	1085	U
1	A	1087	C
1	A	1088	C
1	A	1089	C
1	A	1090	A
1	A	1091	G
1	A	1092	A
1	A	1093	C
1	A	1094	A
1	A	1095	A
1	A	1100	G

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Mol	Chain	Res	Type
1	A	1103	G
1	A	1104	U
1	A	1105	U
1	A	1106	G
1	A	1109	U
1	A	1110	U
1	A	1111	A
1	A	1113	A
1	A	1114	A
1	A	1115	G
1	A	1117	A
1	A	1118	G
1	A	1119	C
1	A	1120	C
1	A	1122	U
1	A	1125	U
1	A	1127	U
1	A	1128	A
1	A	1132	A
1	A	1133	G
1	A	1138	U
1	A	1139	A
1	A	1141	U
1	A	1143	G
1	A	1145	U
1	A	1149	U
1	A	1150	A
1	A	1151	G
1	A	1152	U
1	A	1153	C
1	A	1154	G
1	A	1155	A
1	A	1156	G
1	A	1158	G
1	A	1160	C
1	A	1161	A
1	A	1162	C
1	A	1163	U
1	A	1164	G
1	A	1165	C
1	A	1168	C
1	A	1169	G

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Mol	Chain	Res	Type
1	A	1170	A
1	A	1172	A
1	A	1174	U
1	A	1175	G
1	A	1176	U
1	A	1177	A
1	A	1178	C
1	A	1180	G
1	A	1181	G
1	A	1183	G
1	A	1184	C
1	A	1185	U
1	A	1186	A
1	A	1187	A
1	A	1188	A
1	A	1189	C
1	A	1191	U
1	A	1192	A
1	A	1193	U
1	A	1194	U
1	A	1195	A
1	A	1196	C
1	A	1197	C
1	A	1198	G
1	A	1199	A
1	A	1200	A
1	A	1201	G
1	A	1202	C
1	A	1203	U
1	A	1204	G
1	A	1208	A
1	A	1209	U
1	A	1214	C
1	A	1215	U
1	A	1216	U
1	A	1217	U
1	A	1219	G
1	A	1220	A
1	A	1222	A
1	A	1224	U
1	A	1225	G
1	A	1226	G

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Mol	Chain	Res	Type
1	A	1227	U
1	A	1228	A
1	A	1231	A
1	A	1232	G
1	A	1233	A
1	A	1234	G
1	A	1236	G
1	A	1237	U
1	A	1240	U
1	A	1241	A
1	A	1242	A
1	A	1247	G
1	A	1248	U
1	A	1249	U
1	A	1250	G
1	A	1251	A
1	A	1252	A
1	A	1256	U
1	A	1257	G
1	A	1258	A
1	A	1259	U
1	A	1261	G
1	A	1263	A
1	A	1264	A
1	A	1265	G
1	A	1266	G
1	A	1267	A
1	A	1268	C
1	A	1269	A
1	A	1270	U
1	A	1273	G
1	A	1274	G
1	A	1275	A
1	A	1276	G
1	A	1278	G
1	A	1286	G
1	A	1287	U
1	A	1289	A
1	A	1290	G
1	A	1291	A
1	A	1294	G
1	A	1295	C

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Mol	Chain	Res	Type
1	A	1298	G
1	A	1299	U
1	A	1301	U
1	A	1303	A
1	A	1304	G
1	A	1305	U
1	A	1309	G
1	A	1310	A
1	A	1311	A
1	A	1312	A
1	A	1321	A
1	A	1324	A
1	A	1325	U
1	A	1333	A
1	A	1337	A
1	A	1338	U
1	A	1351	C
1	A	1354	G
1	A	1357	G
1	A	1359	A
1	A	1361	G
1	A	1363	U
1	A	1364	C
1	A	1365	G
1	A	1366	U
1	A	1367	C
1	A	1368	C
1	A	1369	G
1	A	1370	C
1	A	1373	U
1	A	1374	G
1	A	1375	G
1	A	1387	C
1	A	1389	U
1	A	1402	A
1	A	1405	G
1	A	1409	U
1	A	1416	U
1	A	1422	A
1	A	1425	G
1	A	1432	A
1	A	1433	U

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Mol	Chain	Res	Type
1	A	1449	A
1	A	1450	A
1	A	1451	U
1	A	1452	C
1	A	1453	G
1	A	1454	U
1	A	1455	U
1	A	1456	U
1	A	1459	A
1	A	1460	U
1	A	1462	G
1	A	1463	A
1	A	1464	U
1	A	1467	G
1	A	1471	A
1	A	1472	C
1	A	1479	G
1	A	1480	G
1	A	1488	A
1	A	1489	A
1	A	1490	G
1	A	1491	C
1	A	1494	G
1	A	1495	C
1	A	1496	G
1	A	1497	A
1	A	1498	U
1	A	1503	U
1	A	1504	U
1	A	1506	C
1	A	1509	G
1	A	1510	U
1	A	1514	A
1	A	1516	C
1	A	1519	U
1	A	1520	A
1	A	1525	U
1	A	1526	G
1	A	1527	A
1	A	1528	G
1	A	1533	A
1	A	1534	G

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Mol	Chain	Res	Type
1	A	1537	A
1	A	1540	U
1	A	1541	C
1	A	1545	U
1	A	1550	G
1	A	1552	U
1	A	1553	A
1	A	1554	A
1	A	1555	G
1	A	1556	G
1	A	1561	G
1	A	1562	C
1	A	1566	G
1	A	1567	A
1	A	1569	G
1	A	1570	G
1	A	1574	G
1	A	1575	A
1	A	1576	A
1	A	1577	G
1	A	1581	U
1	A	1582	U
1	A	1583	G
1	A	1584	U
1	A	1586	U
1	A	1587	C
1	A	1588	U
1	A	1591	G
1	A	1592	A
1	A	1594	U
1	A	1597	U
1	A	1601	U
1	A	1602	U
1	A	1603	U
1	A	1605	A
1	A	1606	C
1	A	1613	G
1	A	1616	A
1	A	1628	A
1	A	1629	U
1	A	1630	A
1	A	1631	G

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Mol	Chain	Res	Type
1	A	1632	A
1	A	1633	A
1	A	1634	A
1	A	1635	A
1	A	1636	U
1	A	1639	G
1	A	1651	C
1	A	1652	A
1	A	1653	A
1	A	1654	A
1	A	1658	A
1	A	1661	C
1	A	1663	G
1	A	1666	A
1	A	1676	A
1	A	1678	A
1	A	1690	A
1	A	1692	C
1	A	1693	G
1	A	1694	A
1	A	1695	G
1	A	1697	G
1	A	1698	A
1	A	1699	A
1	A	1713	A
1	A	1718	G
1	A	1719	C
1	A	1726	A
1	A	1732	U
1	A	1736	U
1	A	1737	U
1	A	1738	C
1	A	1740	G
1	A	1744	A
1	A	1757	U
1	A	1758	A
1	A	1759	G
1	A	1760	G
1	A	1761	G
1	A	1762	U
1	A	1763	U
1	A	1764	A

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Mol	Chain	Res	Type
1	A	1765	A
1	A	1766	C
1	A	1767	G
1	A	1768	C
1	A	1771	A
1	A	1772	G
1	A	1789	A
1	A	1790	G
1	A	1791	G
1	A	1797	G
1	A	1800	A
1	A	1803	G
1	A	1811	A
1	A	1815	C
1	A	1820	G
1	A	1826	G
1	A	1827	C
1	A	1828	U
1	A	1829	A
1	A	1843	U
1	A	1847	U
1	A	1856	A
1	A	1857	C
1	A	1860	C
1	A	1866	G
1	A	1875	A
1	A	1877	G
1	A	1884	G
1	A	1885	G
1	A	1886	A
1	A	1890	G
1	A	1893	A
1	A	1895	C
1	A	1897	U
1	A	1898	C
1	A	1899	U
1	A	1900	G
1	A	1901	C
1	A	1902	G
1	A	1903	A
1	A	1904	A
1	A	1909	C

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Mol	Chain	Res	Type
1	A	1910	G
1	A	1911	A
1	A	1912	A
1	A	1913	U
1	A	1914	C
1	A	1933	G
1	A	1937	G
1	A	1938	U
1	A	1939	A
1	A	1945	A
1	A	1946	A
1	A	1949	G
1	A	1950	U
1	A	1951	C
1	A	1952	C
1	A	1954	A
1	A	1956	G
1	A	1957	G
1	A	1964	A
1	A	1965	A
1	A	1972	G
1	A	1982	U
1	A	1993	A
1	A	1994	C
1	A	1996	A
1	A	1997	A
1	A	1998	A
1	A	1999	G
1	A	2009	U
1	A	2018	U
1	A	2019	G
1	A	2020	U
1	A	2023	C
1	A	2024	A
1	A	2037	G
1	A	2038	U
1	A	2043	U
1	A	2044	C
1	A	2045	A
1	A	2046	U
1	A	2047	A
1	A	2048	G

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Mol	Chain	Res	Type
1	A	2049	U
1	A	2050	A
1	A	2052	C
1	A	2053	U
1	A	2054	G
1	A	2057	A
1	A	2058	A
1	A	2059	G
1	A	2060	A
1	A	2061	U
1	A	2062	G
1	A	2063	C
1	A	2064	A
1	A	2065	G
1	A	2067	U
1	A	2070	C
1	A	2073	G
1	A	2077	C
1	A	2078	A
1	A	2079	G
1	A	2081	A
1	A	2082	C
1	A	2083	G
1	A	2084	G
1	A	2085	A
1	A	2086	A
1	A	2087	A
1	A	2088	G
1	A	2089	A
1	A	2090	C
1	A	2091	C
1	A	2094	G
1	A	2095	U
1	A	2096	G
1	A	2097	G
1	A	2104	A
1	A	2107	G
1	A	2119	U
1	A	2120	G
1	A	2126	C
1	A	2127	G
1	A	2129	C

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Mol	Chain	Res	Type
1	A	2130	A
1	A	2132	A
1	A	2133	G
1	A	2136	U
1	A	2139	A
1	A	2140	C
1	A	2142	G
1	A	2143	G
1	A	2144	A
1	A	2146	A
1	A	2147	G
1	A	2153	A
1	A	2155	C
1	A	2158	U
1	A	2160	G
1	A	2161	A
1	A	2162	A
1	A	2164	C
1	A	2165	G
1	A	2173	U
1	A	2175	G
1	A	2179	A
1	A	2180	C
1	A	2181	G
1	A	2185	A
1	A	2186	G
1	A	2188	C
1	A	2190	C
1	A	2193	G
1	A	2194	U
1	A	2195	G
1	A	2198	A
1	A	2199	U
1	A	2200	A
1	A	2203	A
1	A	2204	C
1	A	2206	C
1	A	2210	C
1	A	2211	U
1	A	2215	U
1	A	2224	U
1	A	2225	A

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Mol	Chain	Res	Type
1	A	2231	C
1	A	2232	A
1	A	2235	A
1	A	2238	U
1	A	2239	A
1	A	2240	U
1	A	2241	C
1	A	2252	A
1	A	2262	G
1	A	2265	G
1	A	2266	G
1	A	2273	G
1	A	2274	A
1	A	2275	C
1	A	2276	U
1	A	2277	G
1	A	2284	U
1	A	2285	C
1	A	2295	A
1	A	2305	A
1	A	2309	G
1	A	2310	C
1	A	2316	G
1	A	2320	C
1	A	2321	C
1	A	2322	C
1	A	2324	C
1	A	2326	G
1	A	2328	A
1	A	2330	G
1	A	2331	G
1	A	2332	U
1	A	2333	U
1	A	2334	G
1	A	2335	G
1	A	2336	A
1	A	2337	A
1	A	2338	A
1	A	2339	U
1	A	2345	A
1	A	2346	U
1	A	2347	A

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Mol	Chain	Res	Type
1	A	2348	G
1	A	2349	A
1	A	2352	G
1	A	2354	A
1	A	2358	G
1	A	2359	C
1	A	2360	A
1	A	2362	A
1	A	2363	A
1	A	2364	G
1	A	2365	G
1	A	2366	G
1	A	2369	C
1	A	2370	U
1	A	2371	U
1	A	2372	G
1	A	2373	A
1	A	2374	C
1	A	2377	C
1	A	2378	G
1	A	2379	A
1	A	2380	G
1	A	2381	A
1	A	2382	C
1	A	2388	A
1	A	2391	C
1	A	2392	G
1	A	2393	A
1	A	2396	A
1	A	2397	G
1	A	2410	G
1	A	2412	C
1	A	2417	U
1	A	2418	G
1	A	2419	A
1	A	2420	U
1	A	2427	G
1	A	2428	U
1	A	2429	U
1	A	2430	C
1	A	2432	G
1	A	2434	A

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Mol	Chain	Res	Type
1	A	2435	U
1	A	2441	G
1	A	2442	G
1	A	2443	C
1	A	2445	A
1	A	2446	U
1	A	2447	C
1	A	2448	G
1	A	2449	C
1	A	2450	U
1	A	2451	C
1	A	2452	A
1	A	2453	A
1	A	2454	C
1	A	2455	G
1	A	2456	G
1	A	2457	A
1	A	2458	U
1	A	2459	A
1	A	2460	A
1	A	2461	A
1	A	2462	A
1	A	2465	U
1	A	2467	C
1	A	2468	C
1	A	2473	G
1	A	2474	G
1	A	2475	A
1	A	2476	U
1	A	2477	A
1	A	2478	A
1	A	2479	C
1	A	2480	A
1	A	2481	G
1	A	2482	G
1	A	2483	C
1	A	2495	A
1	A	2497	G
1	A	2498	A
1	A	2499	G
1	A	2500	U
1	A	2502	C

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Mol	Chain	Res	Type
1	A	2503	A
1	A	2504	C
1	A	2505	A
1	A	2506	U
1	A	2508	G
1	A	2509	A
1	A	2510	C
1	A	2513	G
1	A	2516	G
1	A	2517	G
1	A	2518	U
1	A	2519	U
1	A	2520	U
1	A	2523	C
1	A	2524	A
1	A	2525	C
1	A	2526	C
1	A	2527	U
1	A	2528	C
1	A	2529	G
1	A	2530	A
1	A	2532	G
1	A	2543	G
1	A	2544	C
1	A	2545	A
1	A	2546	U
1	A	2547	C
1	A	2550	G
1	A	2551	G
1	A	2560	U
1	A	2561	C
1	A	2562	G
1	A	2568	A
1	A	2569	A
1	A	2570	G
1	A	2578	C
1	A	2579	U
1	A	2581	U
1	A	2582	U
1	A	2586	C
1	A	2593	A
1	A	2594	G

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Mol	Chain	Res	Type
1	A	2595	C
1	A	2596	G
1	A	2597	G
1	A	2598	U
1	A	2599	A
1	A	2600	C
1	A	2605	G
1	A	2611	U
1	A	2613	C
1	A	2626	G
1	A	2629	A
1	A	2630	G
1	A	2636	U
1	A	2638	C
1	A	2640	U
1	A	2643	C
1	A	2644	C
1	A	2645	G
1	A	2646	U
1	A	2647	C
1	A	2651	G
1	A	2652	G
1	A	2653	C
1	A	2654	G
1	A	2655	U
1	A	2656	A
1	A	2657	G
1	A	2659	A
1	A	2661	A
1	A	2662	U
1	A	2663	U
1	A	2664	U
1	A	2665	G
1	A	2666	A
1	A	2667	G
1	A	2668	A
1	A	2669	G
1	A	2672	G
1	A	2673	C
1	A	2677	C
1	A	2678	C
1	A	2679	U

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Mol	Chain	Res	Type
1	A	2680	U
1	A	2681	A
1	A	2683	U
1	A	2684	A
1	A	2686	G
1	A	2690	G
1	A	2691	G
1	A	2692	A
1	A	2697	G
1	A	2703	C
1	A	2704	A
1	A	2705	U
1	A	2716	U
1	A	2741	G
1	A	2753	U
1	A	2756	G
1	A	2757	U
1	A	2759	G
1	A	2760	A
1	A	2761	C
1	A	2771	G
1	A	2775	A
1	A	2777	A
1	A	2778	G
1	A	2779	C
1	A	2782	C
1	A	2788	A
1	A	2792	A
1	A	2793	G
1	A	2796	C
1	A	2797	C
1	A	2798	C
1	A	2802	A
1	A	2803	A
1	A	2804	G
1	A	2805	A
1	A	2806	U
1	A	2807	G
1	A	2808	A
1	A	2809	G
1	A	2811	U
1	A	2812	U

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Mol	Chain	Res	Type
1	A	2813	U
1	A	2816	C
1	A	2817	A
1	A	2818	A
1	A	2819	C
1	A	2820	U
1	A	2821	U
1	A	2822	C
1	A	2823	G
1	A	2824	G
1	A	2825	U
1	A	2827	A
1	A	2828	U
1	A	2829	A
1	A	2830	A
1	A	2831	G
1	A	2833	U
1	A	2840	A
1	A	2841	A
1	A	2844	U
1	A	2850	G
1	A	2851	G
1	A	2852	U
1	A	2853	U
1	A	2854	A
1	A	2855	A
1	A	2856	U
1	A	2857	A
1	A	2863	G
1	A	2864	A
1	A	2868	G
1	A	2869	G
1	A	2870	A
1	A	2878	U
1	A	2879	G
1	A	2886	G
1	A	2887	G
1	A	2888	A
1	A	2889	G
1	A	2891	U
1	A	2892	G
1	A	2893	A

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Mol	Chain	Res	Type
1	A	2894	C
1	A	2895	G
1	A	2896	A
1	A	2897	A
1	A	2898	U
1	A	2899	A
1	A	2900	C
1	A	2901	U
1	A	2902	A
1	A	2903	A
1	A	2904	U
1	A	2905	C
1	A	2906	G
1	A	2911	A
1	A	2913	G
1	A	2914	A
1	A	2915	C
1	A	2917	U
1	A	2919	A
1	A	2920	U
2	B	2	C
2	B	3	U
2	B	5	G
2	B	6	U
2	B	7	G
2	B	10	U
2	B	11	A
2	B	13	A
2	B	15	C
2	B	22	G
2	B	23	U
2	B	24	C
2	B	25	A
2	B	26	C
2	B	27	A
2	B	28	C
2	B	30	U
2	B	31	G
2	B	33	U
2	B	38	U
2	B	39	G
2	B	42	G

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Mol	Chain	Res	Type
2	B	50	A
2	B	51	A
2	B	55	A
2	B	84	U
2	B	85	U
2	B	86	A
2	B	87	C
2	B	88	G
2	B	95	U
2	B	106	G
2	B	115	C
31	a	7	G
31	a	8	G
31	a	9	A
31	a	10	G
31	a	11	A
31	a	14	U
31	a	15	U
31	a	16	G
31	a	24	C
31	a	27	A
31	a	30	A
31	a	31	U
31	a	33	A
31	a	40	G
31	a	42	G
31	a	43	G
31	a	45	G
31	a	47	G
31	a	48	C
31	a	49	C
31	a	50	U
31	a	51	A
31	a	52	A
31	a	59	C
31	a	60	A
31	a	62	G
31	a	63	U
31	a	66	A
31	a	67	G
31	a	68	C
31	a	69	G

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Mol	Chain	Res	Type
31	a	70	A
31	a	71	A
31	a	76	C
31	a	77	G
31	a	81	A
31	a	82	G
31	a	83	C
31	a	84	U
31	a	87	C
31	a	88	U
31	a	92	C
31	a	93	U
31	a	94	G
31	a	99	U
31	a	100	A
31	a	106	G
31	a	107	G
31	a	115	A
31	a	120	C
31	a	121	A
31	a	122	C
31	a	129	A
31	a	130	A
31	a	131	C
31	a	132	C
31	a	133	U
31	a	140	A
31	a	142	G
31	a	146	G
31	a	149	A
31	a	151	A
31	a	153	C
31	a	158	G
31	a	159	G
31	a	161	A
31	a	162	A
31	a	163	C
31	a	165	G
31	a	170	U
31	a	171	A
31	a	173	U
31	a	177	G

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Mol	Chain	Res	Type
31	a	183	U
31	a	184	A
31	a	186	U
31	a	187	U
31	a	189	G
31	a	190	A
31	a	191	A
31	a	194	G
31	a	195	C
31	a	197	U
31	a	198	G
31	a	199	G
31	a	200	U
31	a	201	U
31	a	202	C
31	a	203	A
31	a	204	A
31	a	206	A
31	a	207	G
31	a	208	U
31	a	209	G
31	a	210	A
31	a	211	A
31	a	218	U
31	a	219	C
31	a	220	U
31	a	221	U
31	a	222	G
31	a	224	U
31	a	227	C
31	a	228	A
31	a	230	U
31	a	231	U
31	a	232	A
31	a	233	U
31	a	234	A
31	a	243	C
31	a	244	G
31	a	245	C
31	a	247	C
31	a	250	C
31	a	252	U

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Mol	Chain	Res	Type
31	a	253	U
31	a	255	G
31	a	256	C
31	a	259	G
31	a	261	U
31	a	262	G
31	a	264	U
31	a	265	A
31	a	267	G
31	a	268	G
31	a	269	U
31	a	271	A
31	a	272	C
31	a	274	G
31	a	275	C
31	a	278	A
31	a	282	A
31	a	283	G
31	a	286	A
31	a	289	G
31	a	297	G
31	a	305	G
31	a	306	A
31	a	307	G
31	a	309	G
31	a	311	G
31	a	312	U
31	a	314	A
31	a	315	U
31	a	316	C
31	a	324	C
31	a	329	A
31	a	336	C
31	a	337	A
31	a	338	C
31	a	339	G
31	a	352	A
31	a	354	G
31	a	355	G
31	a	356	G
31	a	358	G
31	a	360	C

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Mol	Chain	Res	Type
31	a	363	C
31	a	371	A
31	a	372	A
31	a	375	U
31	a	376	U
31	a	377	C
31	a	380	C
31	a	381	A
31	a	384	G
31	a	392	G
31	a	395	U
31	a	396	G
31	a	397	A
31	a	398	C
31	a	403	C
31	a	405	A
31	a	406	C
31	a	412	G
31	a	413	U
31	a	414	G
31	a	416	G
31	a	417	U
31	a	419	A
31	a	420	U
31	a	421	G
31	a	422	A
31	a	423	A
31	a	425	G
31	a	426	U
31	a	427	C
31	a	429	U
31	a	430	C
31	a	431	G
31	a	432	G
31	a	433	A
31	a	434	U
31	a	435	C
31	a	436	G
31	a	437	U
31	a	438	A
31	a	440	A
31	a	441	A

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Mol	Chain	Res	Type
31	a	442	C
31	a	444	C
31	a	446	G
31	a	447	U
31	a	448	U
31	a	450	U
31	a	451	U
31	a	452	A
31	a	454	G
31	a	455	G
31	a	456	A
31	a	459	A
31	a	460	A
31	a	461	C
31	a	463	U
31	a	467	U
31	a	468	G
31	a	472	G
31	a	480	G
31	a	482	A
31	a	483	C
31	a	484	A
31	a	485	U
31	a	486	C
31	a	487	U
31	a	488	U
31	a	492	G
31	a	499	A
31	a	500	A
31	a	503	A
31	a	504	G
31	a	505	A
31	a	506	A
31	a	507	A
31	a	508	G
31	a	513	G
31	a	514	G
31	a	516	U
31	a	517	A
31	a	519	C
31	a	522	C
31	a	525	G

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Mol	Chain	Res	Type
31	a	526	C
31	a	529	G
31	a	532	G
31	a	539	U
31	a	541	A
31	a	542	U
31	a	543	A
31	a	544	C
31	a	548	G
31	a	549	G
31	a	551	G
31	a	552	G
31	a	554	A
31	a	555	A
31	a	557	C
31	a	563	C
31	a	569	U
31	a	570	U
31	a	571	A
31	a	576	G
31	a	581	A
31	a	583	G
31	a	584	C
31	a	585	G
31	a	587	G
31	a	590	U
31	a	596	G
31	a	603	A
31	a	604	A
31	a	605	G
31	a	607	C
31	a	608	U
31	a	610	A
31	a	611	U
31	a	615	A
31	a	616	A
31	a	617	A
31	a	619	C
31	a	626	C
31	a	627	U
31	a	632	C
31	a	635	G

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Mol	Chain	Res	Type
31	a	636	G
31	a	638	G
31	a	639	G
31	a	640	G
31	a	641	U
31	a	642	C
31	a	645	U
31	a	647	G
31	a	648	A
31	a	649	A
31	a	661	U
31	a	662	G
31	a	666	G
31	a	673	A
31	a	675	G
31	a	678	A
31	a	679	G
31	a	680	U
31	a	681	G
31	a	691	G
31	a	692	U
31	a	694	U
31	a	695	A
31	a	696	G
31	a	697	C
31	a	698	G
31	a	702	A
31	a	703	A
31	a	708	G
31	a	709	C
31	a	710	A
31	a	711	G
31	a	712	A
31	a	713	G
31	a	715	U
31	a	718	G
31	a	719	G
31	a	724	A
31	a	726	A
31	a	727	C
31	a	728	C
31	a	731	U

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Mol	Chain	Res	Type
31	a	732	G
31	a	736	A
31	a	739	G
31	a	742	A
31	a	743	C
31	a	744	U
31	a	747	C
31	a	749	G
31	a	750	G
31	a	753	U
31	a	756	A
31	a	760	G
31	a	761	A
31	a	762	C
31	a	763	G
31	a	766	G
31	a	767	A
31	a	771	G
31	a	774	A
31	a	775	A
31	a	779	G
31	a	781	G
31	a	782	G
31	a	783	G
31	a	784	G
31	a	785	A
31	a	794	G
31	a	795	A
31	a	796	U
31	a	799	G
31	a	800	A
31	a	801	U
31	a	812	U
31	a	813	C
31	a	814	C
31	a	817	G
31	a	818	C
31	a	820	G
31	a	821	U
31	a	823	A
31	a	824	A
31	a	825	C

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Mol	Chain	Res	Type
31	a	826	G
31	a	827	A
31	a	828	U
31	a	829	G
31	a	833	G
31	a	834	C
31	a	835	U
31	a	836	A
31	a	840	G
31	a	842	U
31	a	845	G
31	a	847	G
31	a	849	U
31	a	850	U
31	a	852	C
31	a	853	C
31	a	854	G
31	a	855	C
31	a	860	U
31	a	862	G
31	a	867	G
31	a	875	C
31	a	876	G
31	a	877	C
31	a	878	A
31	a	879	U
31	a	880	U
31	a	881	A
31	a	882	A
31	a	894	G
31	a	898	A
31	a	900	U
31	a	908	C
31	a	911	G
31	a	921	C
31	a	923	A
31	a	927	A
31	a	935	G
31	a	943	C
31	a	944	A
31	a	945	C
31	a	947	A

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Mol	Chain	Res	Type
31	a	949	C
31	a	953	G
31	a	954	G
31	a	955	A
31	a	956	G
31	a	959	U
31	a	961	U
31	a	967	A
31	a	969	U
31	a	970	U
31	a	971	C
31	a	973	A
31	a	975	G
31	a	978	A
31	a	980	G
31	a	981	C
31	a	985	G
31	a	986	A
31	a	987	A
31	a	991	U
31	a	992	A
31	a	996	A
31	a	998	U
31	a	1001	U
31	a	1002	G
31	a	1005	A
31	a	1006	U
31	a	1007	C
31	a	1011	U
31	a	1012	G
31	a	1013	A
31	a	1015	A
31	a	1016	A
31	a	1017	C
31	a	1019	C
31	a	1023	A
31	a	1024	G
31	a	1025	A
31	a	1026	U
31	a	1027	A
31	a	1029	A
31	a	1031	C

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Mol	Chain	Res	Type
31	a	1035	C
31	a	1036	C
31	a	1038	C
31	a	1040	U
31	a	1042	G
31	a	1043	G
31	a	1044	G
31	a	1046	G
31	a	1048	C
31	a	1051	A
31	a	1052	G
31	a	1055	A
31	a	1056	C
31	a	1059	G
31	a	1062	G
31	a	1064	G
31	a	1065	C
31	a	1066	A
31	a	1069	G
31	a	1071	U
31	a	1075	G
31	a	1076	U
31	a	1077	C
31	a	1081	U
31	a	1086	U
31	a	1094	U
31	a	1095	G
31	a	1096	U
31	a	1097	U
31	a	1098	G
31	a	1101	U
31	a	1103	A
31	a	1104	A
31	a	1105	G
31	a	1109	C
31	a	1111	C
31	a	1112	A
31	a	1120	C
31	a	1121	A
31	a	1122	A
31	a	1123	C
31	a	1124	C

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Mol	Chain	Res	Type
31	a	1126	U
31	a	1129	A
31	a	1130	G
31	a	1131	C
31	a	1135	G
31	a	1136	U
31	a	1137	U
31	a	1138	G
31	a	1139	C
31	a	1141	A
31	a	1142	U
31	a	1143	C
31	a	1144	A
31	a	1145	U
31	a	1146	U
31	a	1147	A
31	a	1148	A
31	a	1149	G
31	a	1150	U
31	a	1151	U
31	a	1154	G
31	a	1156	A
31	a	1157	C
31	a	1159	C
31	a	1161	A
31	a	1162	A
31	a	1163	G
31	a	1165	U
31	a	1167	A
31	a	1168	C
31	a	1169	U
31	a	1170	G
31	a	1171	C
31	a	1173	G
31	a	1174	G
31	a	1175	U
31	a	1177	A
31	a	1178	C
31	a	1179	A
31	a	1180	A
31	a	1181	A
31	a	1182	C

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Mol	Chain	Res	Type
31	a	1185	G
31	a	1189	A
31	a	1190	A
31	a	1191	G
31	a	1193	U
31	a	1198	A
31	a	1200	G
31	a	1202	C
31	a	1203	G
31	a	1206	A
31	a	1207	A
31	a	1208	A
31	a	1209	U
31	a	1210	C
31	a	1211	A
31	a	1215	U
31	a	1216	G
31	a	1219	C
31	a	1221	U
31	a	1222	U
31	a	1223	A
31	a	1224	U
31	a	1226	A
31	a	1228	U
31	a	1230	G
31	a	1231	G
31	a	1234	U
31	a	1235	A
31	a	1236	C
31	a	1237	A
31	a	1238	C
31	a	1243	G
31	a	1246	A
31	a	1247	C
31	a	1248	A
31	a	1249	A
31	a	1250	U
31	a	1251	G
31	a	1252	G
31	a	1253	A
31	a	1255	A
31	a	1256	A

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Mol	Chain	Res	Type
31	a	1257	U
31	a	1260	A
31	a	1261	A
31	a	1266	C
31	a	1267	A
31	a	1268	G
31	a	1270	G
31	a	1273	A
31	a	1274	C
31	a	1275	C
31	a	1278	G
31	a	1279	A
31	a	1282	U
31	a	1283	C
31	a	1285	A
31	a	1286	G
31	a	1287	C
31	a	1288	A
31	a	1289	A
31	a	1290	A
31	a	1291	U
31	a	1292	C
31	a	1294	C
31	a	1295	A
31	a	1296	U
31	a	1297	A
31	a	1298	A
31	a	1305	U
31	a	1306	C
31	a	1307	U
31	a	1308	C
31	a	1309	A
31	a	1310	G
31	a	1311	U
31	a	1313	C
31	a	1315	G
31	a	1318	U
31	a	1319	G
31	a	1322	G
31	a	1323	U
31	a	1324	C
31	a	1327	C

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Mol	Chain	Res	Type
31	a	1328	A
31	a	1329	A
31	a	1330	C
31	a	1332	C
31	a	1333	G
31	a	1335	C
31	a	1336	U
31	a	1337	A
31	a	1338	C
31	a	1339	A
31	a	1341	G
31	a	1344	G
31	a	1345	C
31	a	1347	G
31	a	1348	G
31	a	1356	A
31	a	1357	G
31	a	1363	G
31	a	1365	A
31	a	1367	A
31	a	1368	U
31	a	1369	C
31	a	1371	G
31	a	1373	A
31	a	1374	U
31	a	1378	A
31	a	1382	U
31	a	1383	G
31	a	1387	A
31	a	1389	G
31	a	1391	U
31	a	1392	C
31	a	1397	G
31	a	1406	A
31	a	1407	C
31	a	1408	A
31	a	1409	C
31	a	1410	C
31	a	1411	G
31	a	1421	C
31	a	1426	A
31	a	1428	A

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Mol	Chain	Res	Type
31	a	1429	G
31	a	1435	A
31	a	1439	C
31	a	1443	A
31	a	1445	G
31	a	1446	C
31	a	1448	G
31	a	1449	G
31	a	1450	U
31	a	1451	G
31	a	1454	G
31	a	1456	A
31	a	1458	C
31	a	1462	U
31	a	1463	U
31	a	1464	A
31	a	1465	G
31	a	1466	G
31	a	1467	A
31	a	1468	G
31	a	1469	C
31	a	1472	G
31	a	1473	C
31	a	1474	C
31	a	1475	G
31	a	1476	U
31	a	1482	G
31	a	1483	U
31	a	1484	G
31	a	1486	G
31	a	1487	A
31	a	1495	U
31	a	1496	U
31	a	1497	G
31	a	1504	A
31	a	1505	G
31	a	1510	A
31	a	1514	A
31	a	1515	G
31	a	1516	G
31	a	1518	A
31	a	1519	G

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Mol	Chain	Res	Type
31	a	1520	C
31	a	1524	A
31	a	1534	G
31	a	1536	G
31	a	1540	G
31	a	1541	G
31	a	1543	U

All (258) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	33	U
1	A	45	G
1	A	63	U
1	A	69	C
1	A	90	A
1	A	99	U
1	A	162	A
1	A	179	A
1	A	181	G
1	A	201	C
1	A	202	A
1	A	218	G
1	A	227	G
1	A	228	A
1	A	234	C
1	A	235	G
1	A	237	U
1	A	282	A
1	A	291	G
1	A	299	U
1	A	325	A
1	A	327	G
1	A	333	C
1	A	338	G
1	A	345	C
1	A	350	G
1	A	354	A
1	A	361	U
1	A	363	A
1	A	364	A
1	A	365	A

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Mol	Chain	Res	Type
1	A	374	U
1	A	375	A
1	A	394	U
1	A	403	U
1	A	409	G
1	A	419	U
1	A	420	A
1	A	422	G
1	A	451	U
1	A	467	U
1	A	469	A
1	A	470	G
1	A	472	C
1	A	474	A
1	A	479	C
1	A	480	U
1	A	483	C
1	A	484	U
1	A	487	U
1	A	489	A
1	A	490	C
1	A	493	A
1	A	494	U
1	A	496	G
1	A	500	A
1	A	513	G
1	A	519	G
1	A	520	G
1	A	522	G
1	A	523	A
1	A	530	C
1	A	531	C
1	A	544	U
1	A	547	A
1	A	553	A
1	A	555	C
1	A	557	G
1	A	558	A
1	A	572	C
1	A	576	U
1	A	582	G
1	A	588	G

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Mol	Chain	Res	Type
1	A	592	A
1	A	593	U
1	A	595	G
1	A	599	A
1	A	600	U
1	A	604	G
1	A	614	U
1	A	615	A
1	A	616	G
1	A	617	A
1	A	621	A
1	A	627	C
1	A	634	C
1	A	640	G
1	A	644	C
1	A	648	G
1	A	649	U
1	A	650	U
1	A	667	G
1	A	711	G
1	A	713	A
1	A	809	A
1	A	835	U
1	A	857	C
1	A	858	U
1	A	860	U
1	A	863	G
1	A	865	A
1	A	867	U
1	A	872	U
1	A	875	G
1	A	893	G
1	A	896	U
1	A	904	G
1	A	958	U
1	A	987	U
1	A	988	C
1	A	990	G
1	A	995	U
1	A	1001	A
1	A	1004	A
1	A	1005	G

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Mol	Chain	Res	Type
1	A	1013	U
1	A	1018	A
1	A	1019	A
1	A	1023	A
1	A	1025	A
1	A	1027	A
1	A	1028	G
1	A	1032	A
1	A	1033	G
1	A	1034	A
1	A	1035	C
1	A	1039	C
1	A	1040	A
1	A	1043	U
1	A	1044	A
1	A	1050	C
1	A	1056	U
1	A	1057	A
1	A	1064	A
1	A	1075	G
1	A	1082	C
1	A	1162	C
1	A	1175	G
1	A	1181	G
1	A	1184	C
1	A	1185	U
1	A	1187	A
1	A	1188	A
1	A	1190	A
1	A	1193	U
1	A	1199	A
1	A	1224	U
1	A	1236	G
1	A	1240	U
1	A	1241	A
1	A	1247	G
1	A	1248	U
1	A	1249	U
1	A	1251	A
1	A	1263	A
1	A	1267	A
1	A	1273	G

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Mol	Chain	Res	Type
1	A	1274	G
1	A	1276	G
1	A	1286	G
1	A	1288	G
1	A	1289	A
1	A	1290	G
1	A	1291	A
1	A	1298	G
1	A	1299	U
1	A	1302	G
1	A	1303	A
1	A	1357	G
1	A	1364	C
1	A	1365	G
1	A	1366	U
1	A	1369	G
1	A	1372	C
1	A	1374	G
1	A	1651	C
1	A	1692	C
1	A	1731	G
1	A	1756	U
1	A	1761	G
1	A	1789	A
1	A	2023	C
1	A	2038	U
1	A	2043	U
1	A	2044	C
1	A	2045	A
1	A	2052	C
1	A	2053	U
1	A	2057	A
1	A	2061	U
1	A	2064	A
1	A	2082	C
1	A	2084	G
1	A	2085	A
1	A	2090	C
1	A	2093	C
1	A	2094	G
1	A	2239	A
1	A	2261	G

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Mol	Chain	Res	Type
1	A	2275	C
1	A	2276	U
1	A	2295	A
1	A	2309	G
1	A	2313	A
1	A	2378	G
1	A	2392	G
1	A	2397	G
1	A	2419	A
1	A	2442	G
1	A	2452	A
1	A	2453	A
1	A	2455	G
1	A	2459	A
1	A	2461	A
1	A	2477	A
1	A	2478	A
1	A	2480	A
1	A	2481	G
1	A	2486	A
1	A	2516	G
1	A	2517	G
1	A	2518	U
1	A	2523	C
1	A	2525	C
1	A	2527	U
1	A	2543	G
1	A	2544	C
1	A	2546	U
1	A	2550	G
1	A	2556	G
1	A	2569	A
1	A	2578	C
1	A	2581	U
1	A	2595	C
1	A	2644	C
1	A	2652	G
1	A	2655	U
1	A	2664	U
1	A	2665	G
1	A	2667	G
1	A	2668	A

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Mol	Chain	Res	Type
1	A	2672	G
1	A	2703	C
1	A	2760	A
1	A	2797	C
1	A	2803	A
1	A	2805	A
1	A	2806	U
1	A	2808	A
1	A	2830	A
1	A	2840	A
1	A	2854	A
1	A	2856	U
1	A	2869	G
1	A	2878	U
1	A	2901	U
2	B	6	U
2	B	85	U

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 ⓘ

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	ERY	A	3001	-	53,53,53	2.25	12 (22%)	82,82,82	5.03	38 (46%)

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
53	ERY	A	3001	-	3/3/21/21	30/72/107/107	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	A	3001	ERY	O2-C1	10.24	1.57	1.34
53	A	3001	ERY	O10-C6	-5.14	1.36	1.44
53	A	3001	ERY	O2-C13	-4.44	1.39	1.46
53	A	3001	ERY	C19-C16	3.94	1.60	1.52
53	A	3001	ERY	C10-C11	-3.77	1.49	1.54
53	A	3001	ERY	O4-C14	3.39	1.51	1.42
53	A	3001	ERY	C23-C24	-3.02	1.47	1.53
53	A	3001	ERY	C4-C5	2.72	1.61	1.54
53	A	3001	ERY	O13-C12	-2.48	1.40	1.44
53	A	3001	ERY	O9-C22	2.36	1.47	1.41
53	A	3001	ERY	C15-C16	-2.28	1.48	1.52
53	A	3001	ERY	C7-C6	2.01	1.57	1.54

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	A	3001	ERY	O5-C16-C15	-19.27	83.30	112.95
53	A	3001	ERY	O13-C12-C13	-15.29	83.86	107.24
53	A	3001	ERY	O10-C6-C32	-14.33	75.32	108.48
53	A	3001	ERY	O13-C12-C11	-12.96	83.82	108.88
53	A	3001	ERY	O13-C12-C35	-12.83	81.67	107.84
53	A	3001	ERY	O10-C6-C7	-10.70	81.63	108.34
53	A	3001	ERY	O5-C16-C17	-9.59	89.94	103.86
53	A	3001	ERY	C15-C16-C17	9.39	123.72	107.64
53	A	3001	ERY	C20-O5-C16	6.64	131.02	117.51
53	A	3001	ERY	C31-C4-C3	-6.44	100.06	111.40
53	A	3001	ERY	C13-O2-C1	-6.36	107.09	118.20
53	A	3001	ERY	O10-C6-C5	-6.23	96.10	107.60
53	A	3001	ERY	C19-C16-C15	6.14	121.35	110.64
53	A	3001	ERY	O5-C16-C19	-5.85	95.65	110.77
53	A	3001	ERY	C32-C6-C7	5.82	120.52	111.09
53	A	3001	ERY	O3-C3-C4	5.74	115.00	108.23
53	A	3001	ERY	C32-C6-C5	5.11	118.87	110.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	A	3001	ERY	C35-C12-C11	5.09	121.96	113.14
53	A	3001	ERY	C14-O3-C3	-4.94	104.88	114.72
53	A	3001	ERY	C3-C4-C5	4.78	121.12	111.17
53	A	3001	ERY	C13-C12-C11	4.71	117.23	108.21
53	A	3001	ERY	C27-C26-C25	-4.22	106.88	113.27
53	A	3001	ERY	C35-C12-C13	3.90	116.54	111.26
53	A	3001	ERY	C34-C10-C11	-3.88	109.38	114.30
53	A	3001	ERY	C7-C6-C5	3.77	117.54	110.38
53	A	3001	ERY	C6-C5-C4	3.72	119.27	113.89
53	A	3001	ERY	C22-C23-C24	-3.56	103.44	109.15
53	A	3001	ERY	C3-C2-C1	-3.52	102.81	109.93
53	A	3001	ERY	C16-C15-C14	-2.77	110.31	114.99
53	A	3001	ERY	O12-C11-C10	-2.67	106.99	110.77
53	A	3001	ERY	O4-C18-C17	2.64	114.59	110.04
53	A	3001	ERY	C22-O7-C5	2.53	120.58	116.26
53	A	3001	ERY	O12-C11-C12	2.39	110.96	106.57
53	A	3001	ERY	C6-C7-C8	-2.36	110.89	115.61
53	A	3001	ERY	C11-C10-C9	-2.33	105.76	109.48
53	A	3001	ERY	O6-C17-C16	2.22	115.11	111.08
53	A	3001	ERY	C21-C18-C17	-2.08	109.13	112.58
53	A	3001	ERY	C22-O9-C26	2.08	116.11	112.91

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
53	A	3001	ERY	C6
53	A	3001	ERY	C12
53	A	3001	ERY	C14

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	A	3001	ERY	C10-C11-C12-C13
53	A	3001	ERY	C10-C11-C12-C35
53	A	3001	ERY	C10-C11-C12-O13
53	A	3001	ERY	O12-C11-C12-C13
53	A	3001	ERY	O12-C11-C12-C35
53	A	3001	ERY	C35-C12-C13-O2
53	A	3001	ERY	C35-C12-C13-C36
53	A	3001	ERY	O13-C12-C13-O2
53	A	3001	ERY	O13-C12-C13-C36
53	A	3001	ERY	C4-C5-C6-C7

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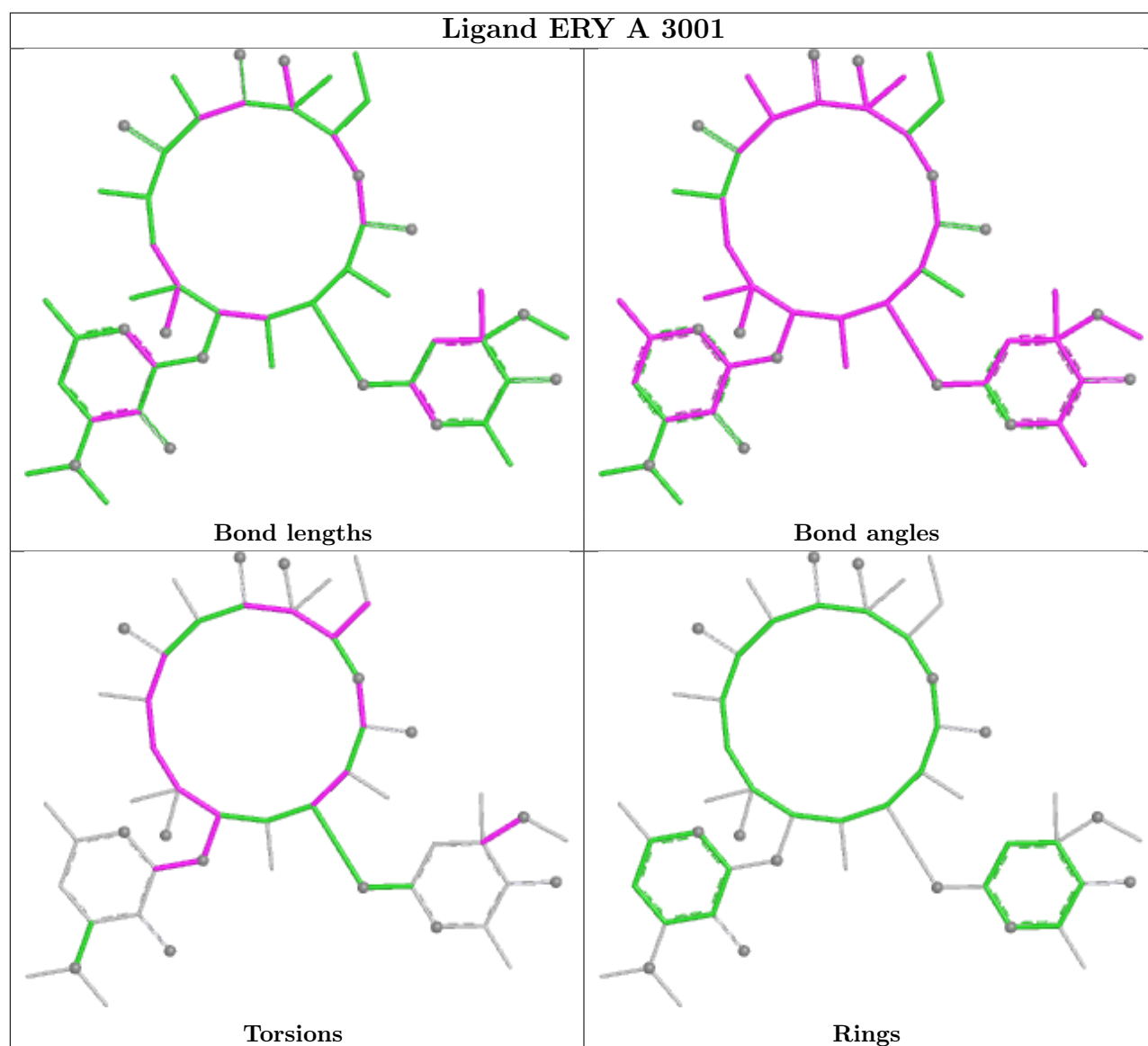
Mol	Chain	Res	Type	Atoms
53	A	3001	ERY	C4-C5-C6-C32
53	A	3001	ERY	O7-C5-C6-C7
53	A	3001	ERY	O7-C5-C6-C32
53	A	3001	ERY	C32-C6-C7-C8
53	A	3001	ERY	O10-C6-C7-C8
53	A	3001	ERY	C6-C7-C8-C9
53	A	3001	ERY	C6-C7-C8-C33
53	A	3001	ERY	O9-C22-O7-C5
53	A	3001	ERY	C2-C1-O2-C13
53	A	3001	ERY	C7-C8-C9-C10
53	A	3001	ERY	C15-C16-O5-C20
53	A	3001	ERY	C19-C16-O5-C20
53	A	3001	ERY	O1-C1-O2-C13
53	A	3001	ERY	O2-C13-C36-C37
53	A	3001	ERY	C17-C16-O5-C20
53	A	3001	ERY	C12-C13-C36-C37
53	A	3001	ERY	C11-C12-C13-O2
53	A	3001	ERY	C6-C5-O7-C22
53	A	3001	ERY	C30-C2-C3-C4
53	A	3001	ERY	C7-C8-C9-O11

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
53	A	3001	ERY	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	7
52	v	1
31	a	1
43	m	1

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Mol	Chain	Number of breaks
8	H	1
24	X	1
11	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	106:GLN	C	131:ILE	N	27.31
1	A	2207:U	O3'	2208:A	P	12.57
1	A	1939:A	O3'	1944:U	P	12.49
1	A	929:C	O3'	937:G	P	11.52
1	a	465:U	O3'	466:G	P	9.63
1	A	1096:C	O3'	1097:U	P	6.53
1	A	2217:G	O3'	2218:G	P	3.73
1	A	1153:C	O3'	1154:G	P	3.41
1	A	1448:U	O3'	1449:A	P	3.35
1	m	93:ARG	C	94:GLY	N	3.23
1	H	109:MET	C	110:LEU	N	1.18
1	X	14:GLY	C	15:ARG	N	1.15
1	K	13:HIS	C	14:ARG	N	1.10

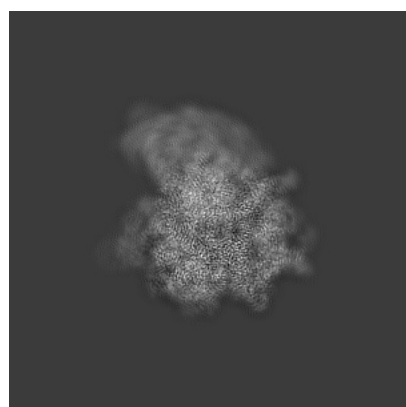
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10076. These allow visual inspection of the internal detail of the map and identification of artifacts.

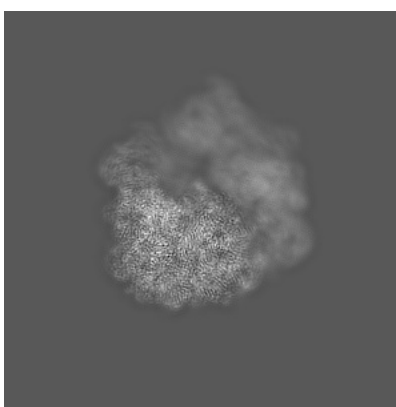
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

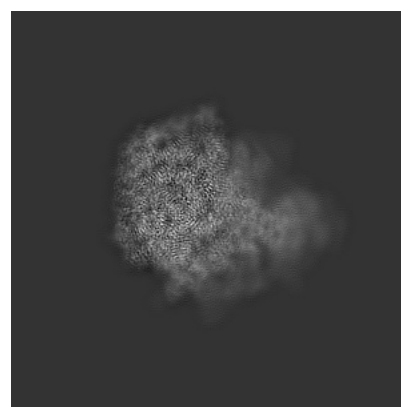
6.1.1 Primary map



X



Y

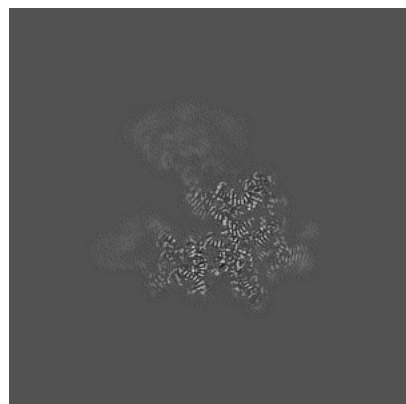


Z

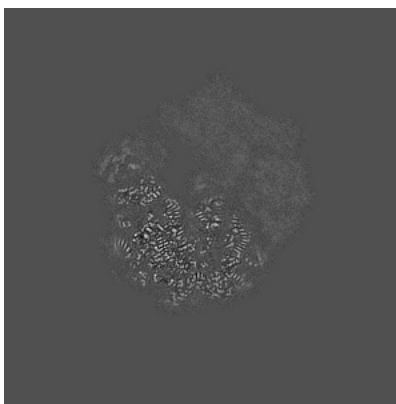
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

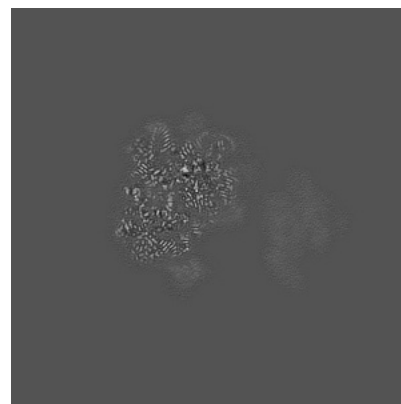
6.2.1 Primary map



X Index: 200



Y Index: 200

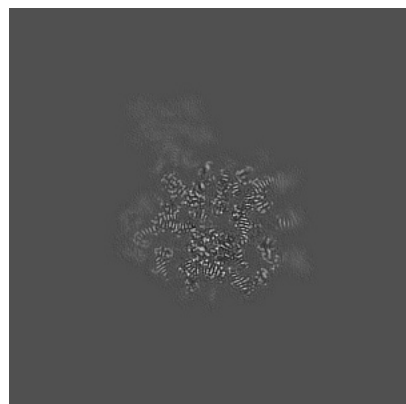


Z Index: 200

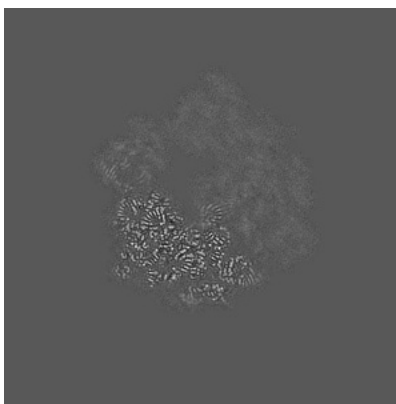
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

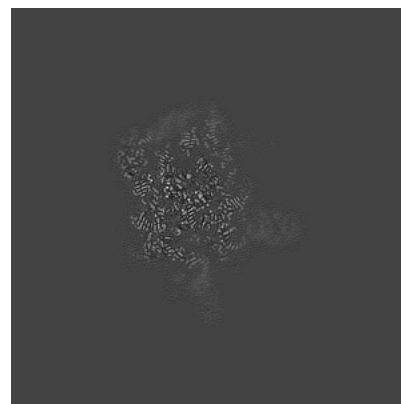
6.3.1 Primary map



X Index: 171



Y Index: 185

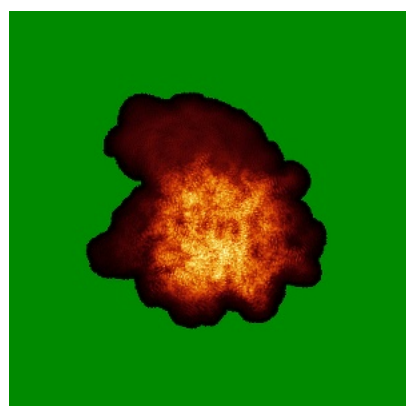


Z Index: 147

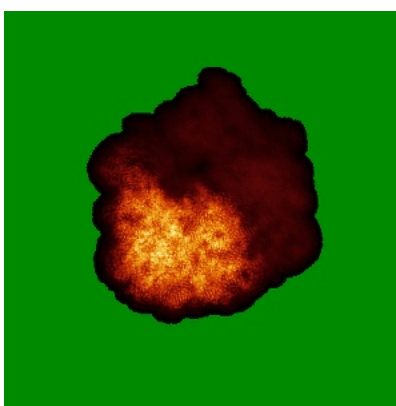
The images above show the largest variance slices of the map in three orthogonal directions.

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

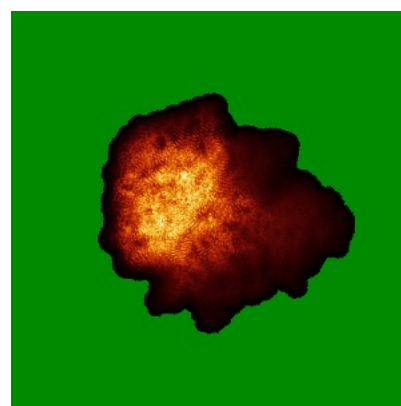
6.4.1 Primary map



X



Y

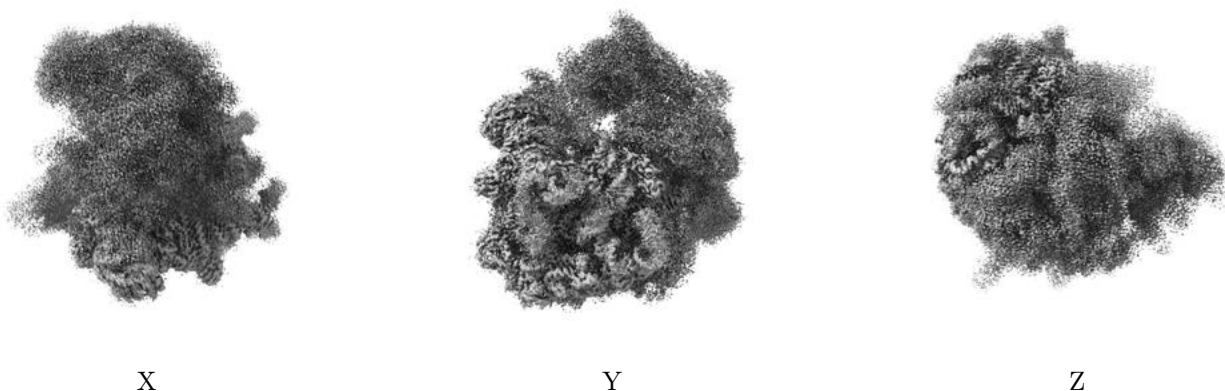


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

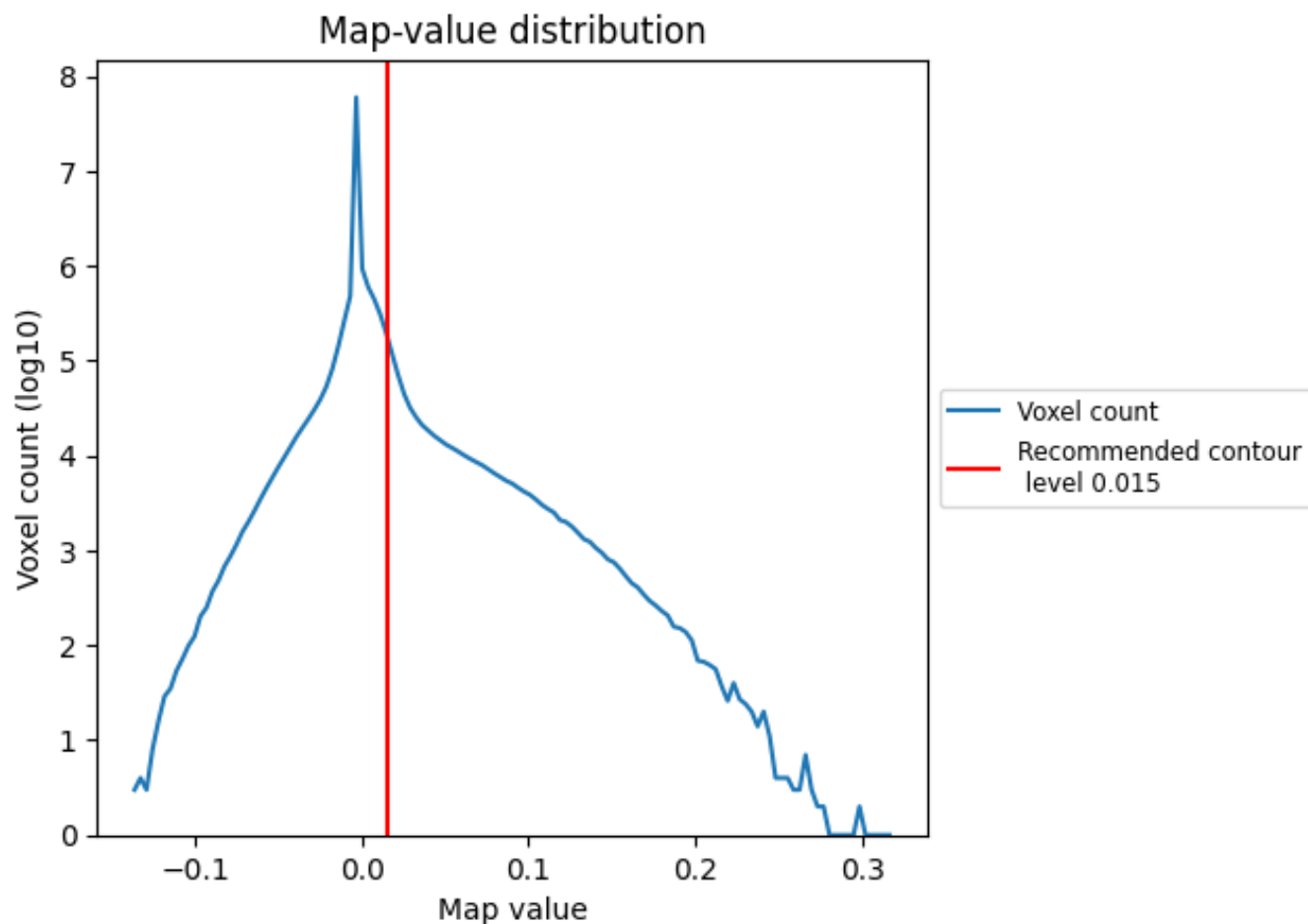
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

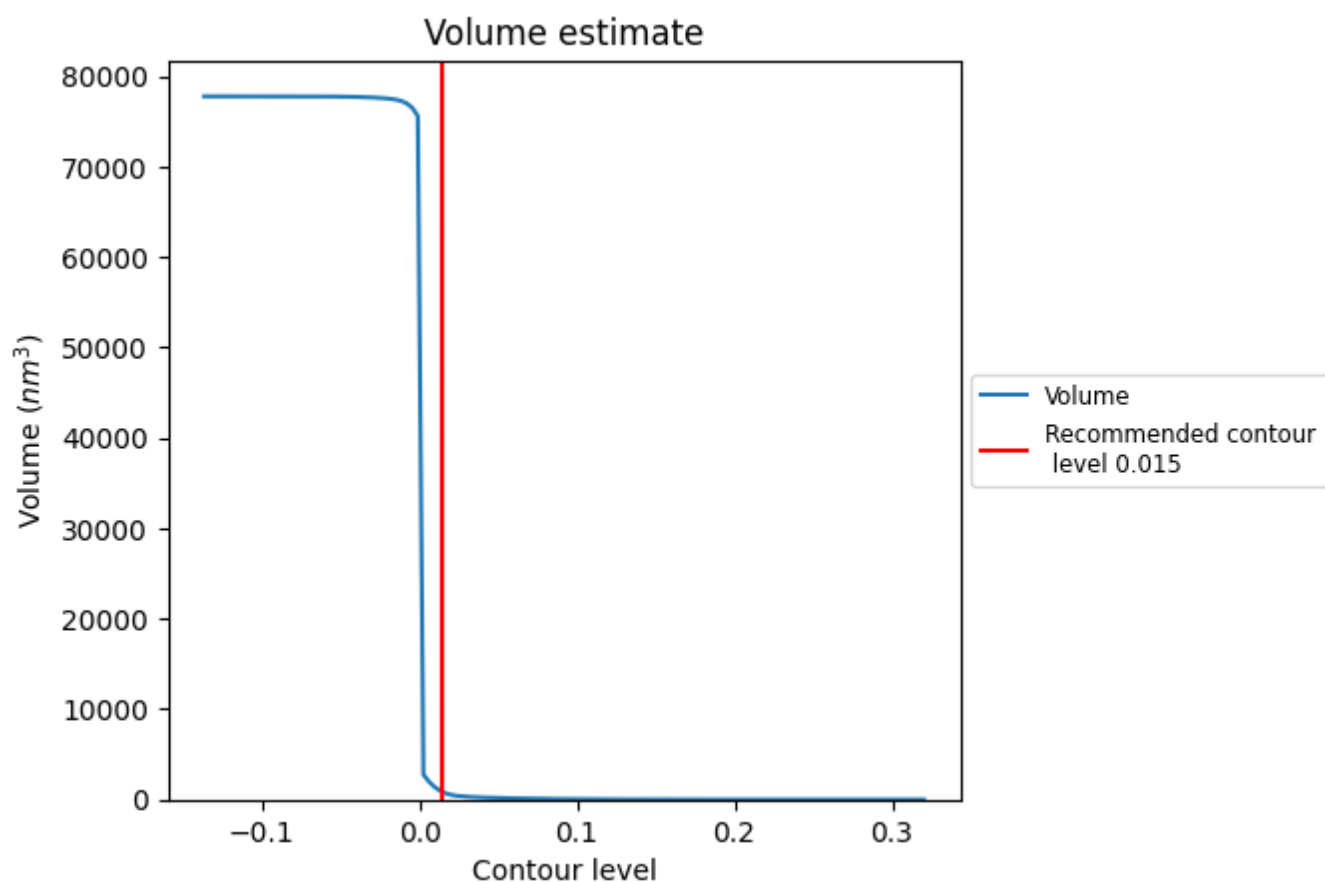
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

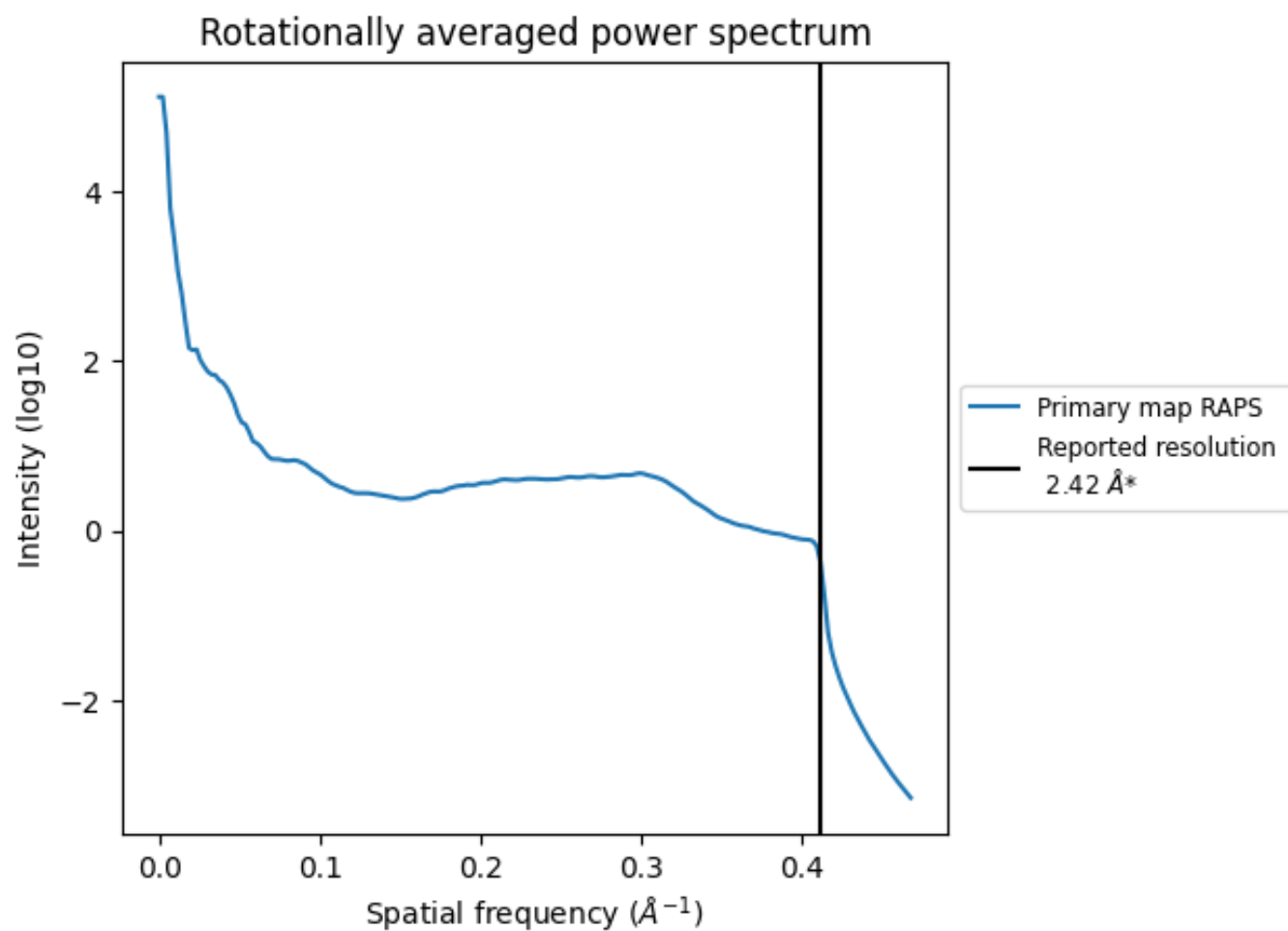
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 827 nm^3 ; this corresponds to an approximate mass of 747 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 0.412 Å⁻¹

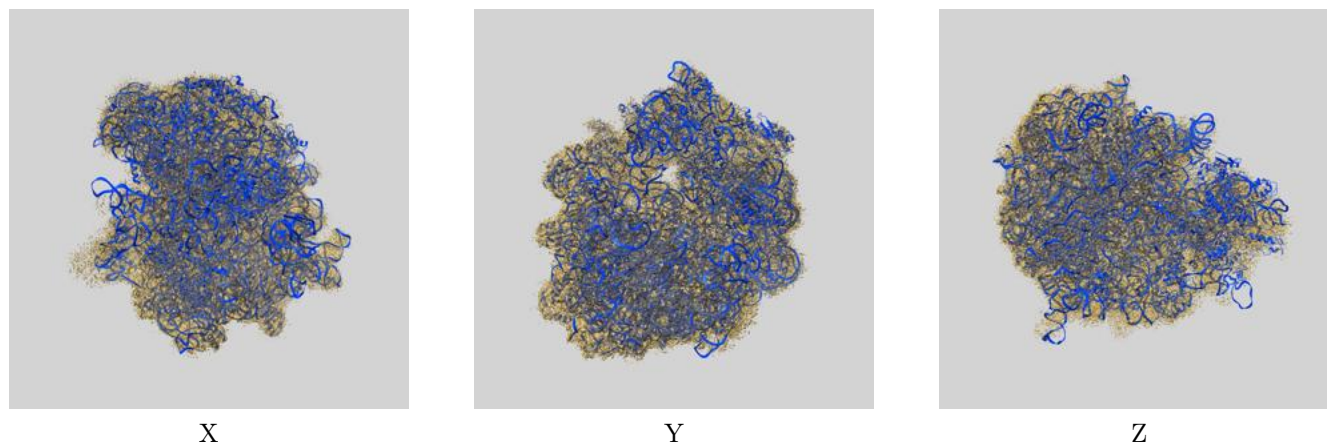
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

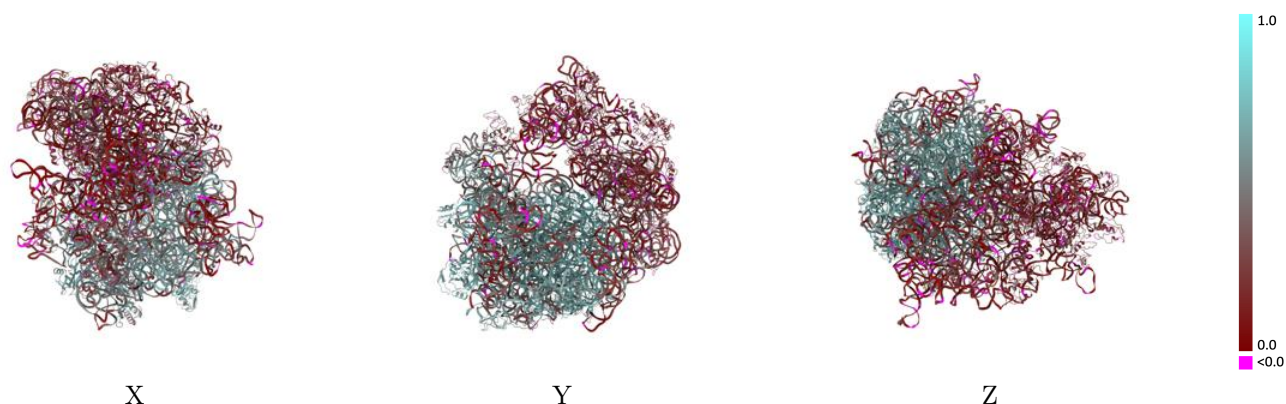
This section contains information regarding the fit between EMDB map EMD-10076 and PDB model 6S0X. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



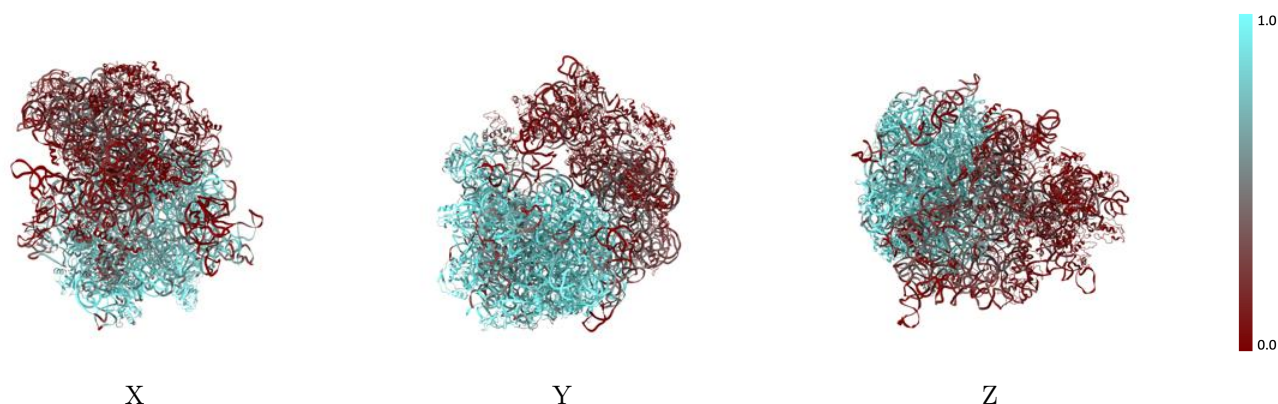
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



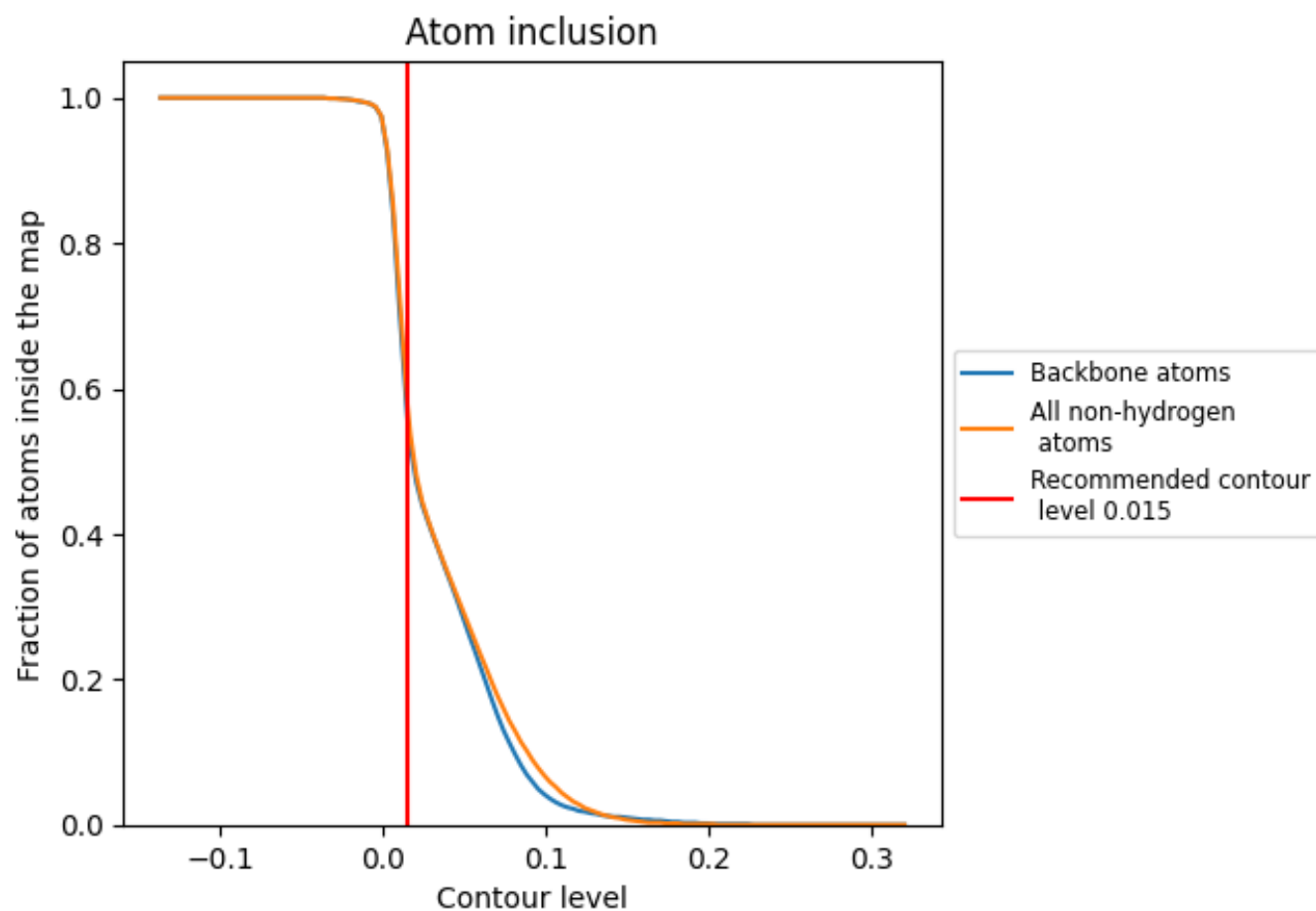
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 58% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5780	 0.3950
1	 0.6110	 0.5660
2	 0.9770	 0.7030
3	 0.9480	 0.6780
4	 0.8860	 0.6120
A	 0.7700	 0.4870
B	 0.8920	 0.5200
C	 0.9590	 0.6800
D	 0.9600	 0.6750
E	 0.9360	 0.6600
F	 0.3570	 0.2880
G	 0.5070	 0.4070
H	 0.9540	 0.6750
I	 0.9510	 0.6720
J	 0.9400	 0.6480
K	 0.9530	 0.6590
L	 0.9500	 0.6770
M	 0.7990	 0.5230
N	 0.9410	 0.6600
O	 0.9730	 0.6950
P	 0.9550	 0.6720
Q	 0.9110	 0.6470
R	 0.9100	 0.6290
S	 0.8170	 0.5610
T	 0.8420	 0.5900
U	 0.9530	 0.6660
V	 0.8880	 0.6150
W	 0.8340	 0.5500
X	 0.9460	 0.6750
Y	 0.1550	 0.2060
Z	 0.7230	 0.5340
a	 0.2680	 0.1630
b	 0.0630	 0.2110
c	 0.0760	 0.2020
d	 0.1300	 0.2350



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Chain	Atom inclusion	Q-score
e	 0.0970	 0.2040
f	 0.0780	 0.2010
g	 0.0390	 0.1850
h	 0.1500	 0.2220
i	 0.0530	 0.1810
j	 0.0980	 0.2040
k	 0.1200	 0.2060
l	 0.1700	 0.2810
m	 0.0920	 0.1990
n	 0.1240	 0.2100
o	 0.1210	 0.2160
p	 0.1990	 0.2480
q	 0.1880	 0.2290
r	 0.1380	 0.2430
s	 0.1150	 0.1900
t	 0.1290	 0.2400
u	 0.0540	 0.2300
v	 0.0240	 0.1830