

# Programy:

## MC-Annotate:

Residue conformations -----  
A1 : G C2p\_endo anti  
A2 : U C2p\_endo anti  
A3 : G C3p\_endo anti  
C4 : THR  
C5 : MET  
C6 : ALA  
C7 : ILE  
C8 : LEU  
Adjacent stackings -----  
A3-A4 : adjacent\_5p upward  
A6-A7 : adjacent\_5p upward  
A7-A8 : adjacent\_5p upward  
Non-Adjacent stackings -----  
A1-A470 : outward  
A3-A105 : downward  
A5-A2420 : upward pairing  
Number of stackings = 367  
Number of adjacent stackings = 337  
Number of non adjacent stackings = 30  
Base-pairs -----  
A1-A469 : G-C Bs/O2P pairing  
A4-A5 : C-G O2P/Hh adjacent\_5p pairing  
A5-A386 : G-A Ss/C8 pairing parallel cis one\_hbond  
A5-A469 : G-C O2P/Ww O2P/Bh pairing  
A17-A382 : U-A Ww/Ww pairing antiparallel cis XX  
A18-A381 : G-C Ww/Ww pairing antiparallel cis XIX  
A20-A379 : U-A Ww/Ww pairing antiparallel cis XX

## RNA-View:

### 1. NMR

2n0j.pdb\_nmr.pdb.out

BEGIN\_base-pair

1_27, A:	1 G-C	27 A: +/+ cis	XIX
2_26, A:	2 G-U	26 A: W/W cis	XXVIII
3_25, A:	3 C-G	25 A: +/+ cis	XIX
4_24, A:	4 U-A	24 A: -/- cis	XX
13_18, A:	13 U-U	18 A: W/W cis	XVI
10_21, A:	10 U-U	21 A: W/W cis	!1H(b_b)
14_16, A:	14 U-A	16 A: S/S tran	!(s_s)

END\_base-pair

The total base pairs = 9 (from 27 bases)

-----  
Standard WW--cis WW-tran HH--cis HH-tran SS--cis SS-tran  
7 2 0 0 0 0 0  
WH--cis WH-tran WS--cis WS-tran HS--cis HS-tran

0 0 0 0 0 0

## 2. Pozostałe

BEGIN\_base-pair

6\_391, A: 6 C-G 391 A: W/W cis n/a  
7\_390, A: 7 C-G 390 A: +/- cis XIX  
685\_687, A: 2485 U-C 2487 A: S/H cis !(b\_s)  
1\_690, A: 1 G-C 2490 A: ?/H cis !(s\_s)  
24\_36, A: 24 U-A 36 A: S/H tran syn !(s\_s)

Summary of triplets and higher multiplets

BEGIN\_multiplets

23\_373\_376\_| [1 3] A: 23 G + A: 373 A + A: 376 C  
172\_358\_362\_| [2 3] A: 172 A + A: 358 A + A: 362 U  
401\_403\_455\_| [3 3] A: 401 A + A: 403 C + A: 460 G

END\_multiplets

The total base pairs = 128 (from 704 bases)

Standard	WW--cis	WW-tran	HH--cis	HH-tran	SS--cis	SS-tran
55	54	0	0	0	1	1
WH--cis	WH-tran	WS--cis	WS-tran	HS--cis	HS-tran	
2	3	5	3	2	2	

## ClaRNA:

"residue1","residue2","n\_type","weight","description","full description"  
"A1","A468","GA",0.159591577575,"?W\_345BR","?W\_345BR (O3'-1)"  
"A1","A469","GC",0.480961521063,"?W\_345BPh","?W\_345BPh (OP2-5)"  
"A1","A470","GG",1.0,"<>","<> (mo)"