BF\_NCTC Code

nohup IntaRNA -t BF\_NCTC\_1.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_1\_targets.txt &> nohuphsa-BF\_NCTC\_1.out &

nohup IntaRNA -t BF\_NCTC\_2.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_2\_targets.txt &> nohuphsa-BF\_NCTC\_2.out &

nohup IntaRNA -t BF\_NCTC\_3.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_3\_targets.txt &> nohuphsa-BF\_NCTC\_3.out &

nohup IntaRNA -t BF\_NCTC\_4.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_4\_targets.txt &> nohuphsa-BF\_NCTC\_4.out &

nohup IntaRNA -t BF\_NCTC\_5.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_5\_targets.txt &> nohuphsa-BF\_NCTC\_5.out &

nohup IntaRNA -t BF\_NCTC\_6.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_6\_targets.txt &> nohuphsa-BF\_NCTC\_6.out &

nohup IntaRNA -t BF\_NCTC\_7.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_7\_targets.txt &> nohuphsa-BF\_NCTC\_7.out &

nohup IntaRNA -t BF\_NCTC\_8.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_8\_targets.txt &> nohuphsa-BF\_NCTC\_8.out &

nohup IntaRNA -t BF\_NCTC\_9.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_9\_targets.txt &> nohuphsa-BF\_NCTC\_9.out &

nohup IntaRNA -t BF\_NCTC\_10.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_10\_targets.txt &> nohuphsa-BF\_NCTC\_10.out &

nohup IntaRNA -t BF\_NCTC\_11.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_11\_targets.txt &> nohuphsa-BF\_NCTC\_11.out &

nohup IntaRNA -t BF\_NCTC\_12.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_12\_targets.txt &> nohuphsa-BF\_NCTC\_12.out &

nohup IntaRNA -t BF\_NCTC\_13.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_13\_targets.txt &> nohuphsa-BF\_NCTC\_13.out &

nohup IntaRNA -t BF\_NCTC\_14.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_14\_targets.txt &> nohuphsa-BF\_NCTC\_14.out &

nohup IntaRNA -t BF\_NCTC\_15.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_15\_targets.txt &> nohuphsa-BF\_NCTC\_15.out &

nohup IntaRNA -t BF\_NCTC\_16.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_16\_targets.txt &> nohuphsa-BF\_NCTC\_16.out &

nohup IntaRNA -t BF\_NCTC\_17.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out BF\_NCTC\_17\_targets.txt &> nohuphsa-BF\_NCTC\_17.out &