CD\_630 Code

nohup IntaRNA -t CD\_630\_1.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_1\_targets.txt &> nohuphsa-CD\_630\_1.out &

nohup IntaRNA -t CD\_630\_2.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_2\_targets.txt &> nohuphsa-CD\_630\_2.out &

nohup IntaRNA -t CD\_630\_3.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_3\_targets.txt &> nohuphsa-CD\_630\_3.out &

nohup IntaRNA -t CD\_630\_4.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_4\_targets.txt &> nohuphsa-CD\_630\_4.out &

nohup IntaRNA -t CD\_630\_5.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_5\_targets.txt &> nohuphsa-CD\_630\_5.out &

nohup IntaRNA -t CD\_630\_6.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_6\_targets.txt &> nohuphsa-CD\_630\_6.out &

nohup IntaRNA -t CD\_630\_7.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_7\_targets.txt &> nohuphsa-CD\_630\_7.out &

nohup IntaRNA -t CD\_630\_8.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_8\_targets.txt &> nohuphsa-CD\_630\_8.out &

nohup IntaRNA -t CD\_630\_9.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_9\_targets.txt &> nohuphsa-CD\_630\_9.out &

nohup IntaRNA -t CD\_630\_10.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_10\_targets.txt &> nohuphsa-CD\_630\_10.out &

nohup IntaRNA -t CD\_630\_11.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_11\_targets.txt &> nohuphsa-CD\_630\_11.out &

nohup IntaRNA -t CD\_630\_12.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_12\_targets.txt &> nohuphsa-CD\_630\_12.out &

nohup IntaRNA -t CD\_630\_13.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_13\_targets.txt &> nohuphsa-CD\_630\_13.out &

nohup IntaRNA -t CD\_630\_14.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_14\_targets.txt &> nohuphsa-CD\_630\_14.out &

nohup IntaRNA -t CD\_630\_15.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_15\_targets.txt &> nohuphsa-CD\_630\_15.out &

nohup IntaRNA -t CD\_630\_16.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out CD\_630\_16\_targets.txt &> nohuphsa-CD\_630\_16.out &