AF Code

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

nohup IntaRNA -t AF\_18.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_18\_targets.txt &> nohuphsa-AF\_18.out &

nohup IntaRNA -t AF\_19.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_19\_targets.txt &> nohuphsa-AF\_19.out &

**nohup IntaRNA -t AF\_20.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_20\_targets.txt &> nohuphsa-AF\_20.out &**

**nohup IntaRNA -t AF\_21.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_21\_targets.txt &> nohuphsa-AF\_21.out &**

**nohup IntaRNA -t AF\_22.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_22\_targets.txt &> nohuphsa-AF\_22.out &**

nohup IntaRNA -t AF\_23.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_23\_targets.txt &> nohuphsa-AF\_23.out &

nohup IntaRNA -t AF\_24.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_24\_targets.txt &> nohuphsa-AF\_24.out &

nohup IntaRNA -t AF\_25.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_25\_targets.txt &> nohuphsa-AF\_25.out &

nohup IntaRNA -t AF\_26.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_26\_targets.txt &> nohuphsa-AF\_26.out &

nohup IntaRNA -t AF\_27.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_27\_targets.txt &> nohuphsa-AF\_27.out &

nohup IntaRNA -t AF\_28.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_28\_targets.txt &> nohuphsa-AF\_28.out &

nohup IntaRNA -t AF\_29.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_29\_targets.txt &> nohuphsa-AF\_29.out &

nohup IntaRNA -t AF\_30.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_30\_targets.txt &> nohuphsa-AF\_30.out &

nohup IntaRNA -t AF\_31.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_31\_targets.txt &> nohuphsa-AF\_31.out &

nohup IntaRNA -t AF\_32.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_32\_targets.txt &> nohuphsa-AF\_32.out &

nohup IntaRNA -t AF\_33.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_33\_targets.txt &> nohuphsa-AF\_33.out &

nohup IntaRNA -t AF\_34.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_34\_targets.txt &> nohuphsa-AF\_34.out &

nohup IntaRNA -t AF\_35.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_35\_targets.txt &> nohuphsa-AF\_35.out &

nohup IntaRNA -t AF\_36.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_36\_targets.txt &> nohuphsa-AF\_36.out &

nohup IntaRNA -t AF\_37.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_37\_targets.txt &> nohuphsa-AF\_37.out &

nohup IntaRNA -t AF\_38.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_38\_targets.txt &> nohuphsa-AF\_38.out &

nohup IntaRNA -t AF\_39.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out AF\_39\_targets.txt &> nohuphsa-AF\_39.out &