PA\_PAO1 Code

nohup IntaRNA -t PA\_PAO1 \_1.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_1\_targets.txt &> nohuphsa-PA\_PAO1\_1.out &

nohup IntaRNA -t PA\_PAO1\_2.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_2\_targets.txt &> nohuphsa-PA\_PAO1\_2.out &

nohup IntaRNA -t PA\_PAO1\_3.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_3\_targets.txt &> nohuphsa-PA\_PAO1\_3.out &

nohup IntaRNA -t PA\_PAO1\_4.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_4\_targets.txt &> nohuphsa-PA\_PAO1\_4.out &

nohup IntaRNA -t PA\_PAO1\_5.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_5\_targets.txt &> nohuphsa-PA\_PAO1\_5.out &

nohup IntaRNA -t PA\_PAO1\_6.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_6\_targets.txt &> nohuphsa-PA\_PAO1\_6.out &

nohup IntaRNA -t PA\_PAO1\_7.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_7\_targets.txt &> nohuphsa-PA\_PAO1\_7.out &

nohup IntaRNA -t PA\_PAO1\_8.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_8\_targets.txt &> nohuphsa-PA\_PAO1\_8.out &

nohup IntaRNA -t PA\_PAO1\_9.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_9\_targets.txt &> nohuphsa-PA\_PAO1\_9.out &

nohup IntaRNA -t PA\_PAO1\_10.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_10\_targets.txt &> nohuphsa-PA\_PAO1\_10.out &

nohup IntaRNA -t PA\_PAO1\_11.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_11\_targets.txt &> nohuphsa-PA\_PAO1\_11.out &

nohup IntaRNA -t PA\_PAO1\_12.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_12\_targets.txt &> nohuphsa-PA\_PAO1\_12.out &

nohup IntaRNA -t PA\_PAO1\_13.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_13\_targets.txt &> nohuphsa-PA\_PAO1\_13.out &

nohup IntaRNA -t PA\_PAO1\_14.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_14\_targets.txt &> nohuphsa-PA\_PAO1\_14.out &

nohup IntaRNA -t PA\_PAO1\_15.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_15\_targets.txt &> nohuphsa-PA\_PAO1\_15.out &

nohup IntaRNA -t PA\_PAO1\_16.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_16\_targets.txt &> nohuphsa-PA\_PAO1\_16.out &

nohup IntaRNA -t PA\_PAO1\_17.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_17\_targets.txt &> nohuphsa-PA\_PAO1\_17.out &

nohup IntaRNA -t PA\_PAO1\_18.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_18\_targets.txt &> nohuphsa-PA\_PAO1\_18.out &

nohup IntaRNA -t PA\_PAO1\_19.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_19\_targets.txt &> nohuphsa-PA\_PAO1\_19.out &

nohup IntaRNA -t PA\_PAO1\_20.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_20\_targets.txt &> nohuphsa-PA\_PAO1\_20.out &

nohup IntaRNA -t PA\_PAO1\_21.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_21\_targets.txt &> nohuphsa-PA\_PAO1\_21.out &

nohup IntaRNA -t PA\_PAO1\_22.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_22\_targets.txt &> nohuphsa-PA\_PAO1\_22.out &

nohup IntaRNA -t PA\_PAO1\_23.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out PA\_PAO1\_23\_targets.txt &> nohuphsa-PA\_PAO1\_23.out &