SP\_R6 Code

nohup IntaRNA -t SP\_R6\_1.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_1\_targets.txt &> nohuphsa-SP\_R6\_1.out &

nohup IntaRNA -t SP\_R6\_2.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_2\_targets.txt &> nohuphsa-SP\_R6\_2.out &

nohup IntaRNA -t SP\_R6\_3.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_3\_targets.txt &> nohuphsa-SP\_R6\_3.out &

nohup IntaRNA -t SP\_R6\_4.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_4\_targets.txt &> nohuphsa-SP\_R6\_4.out &

nohup IntaRNA -t SP\_R6\_5.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_5\_targets.txt &> nohuphsa-SP\_R6\_5.out &

nohup IntaRNA -t SP\_R6\_6.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_6\_targets.txt &> nohuphsa-SP\_R6\_6.out &

nohup IntaRNA -t SP\_R6\_7.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_7\_targets.txt &> nohuphsa-SP\_R6\_7.out &

nohup IntaRNA -t SP\_R6\_8.txt -q human\_mature\_miRNA.fasta --outMode=C --threads=2 --out SP\_R6\_8\_targets.txt &> nohuphsa-SP\_R6\_8.out &