scp <uname>@crane.unl.edu:'$RNAMAKE/\*.pdb’ .

scp hsandunid@crane.unl.edu:'$WORK/RNASeq/runs/\*.tar.gz’ .

extract\_pdbs.mpi.linuxgccrelease -in:file:silent default.out

mkdir pdb

mv S\_\* pdb/

tar -zcvf pdb-file.tar.gz pdb

scp 1ehz.pdb hsandunid@rhino.unl.edu:'$WORK/RNASeq/RMSD/‘

python3 ../../../../temp/Rosetta/tools/rna\_tools/bin/easy\_cat.py runs

cat clustered.out.1.pdb|awk '/ATOM/ && $3 == "C2" {print $4}' | tr '\n' ‘  '

$WORK/main/source/cmake/build\_release/rna\_denovo -fasta ../../test.fasta -secstruct\_file ../../test.secstruct -minimize\_rna false -nstruct 25 -cst\_file test.cst -native ../../1ehz.pdb

rna\_denovo.mpi.linuxgccrelease -fasta ../../test.fasta -secstruct\_file ../../test.secstruct -minimize\_rna false -nstruct 25 -cst\_file test.cst -native ../../1ehz.pdb

-out:file:silent chunk002\_1lnt.out

tar -xvzf pdb.tar.gz pdb

novobarocde -b barcodes.txt -f \*fastq

Barcode.txt -> Distance 4 - always

Format 5 - always

dreem -fa C005P.fasta -fq1 pdb\_S1\_L001\_R1\_001.fastq -fq2 pdb\_S1\_L001\_R2\_001.fastq --dot\_bracket C005P.csv