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# For monomer structure prediction (e2e)
${RUN_ROSETTAFOLD} $ROSETTAFOLD_APPDIR/run_e2e_ver.sh $ROSETTAFOLD_APPDIR/example/input.fasta
output/

# For monomer structure prediction (pyrosetta)
${RUN_ROSETTAFOLD} $ROSETTAFOLD_APPDIR/run_pyrosetta_ver.sh $ROSETTAFOLD_APPDIR/example/input.fasta
output/

# For complex modeling
${RUN_ROSETTAFOLD} python $ROSETTAFOLD_APPDIR/network/predict_complex.py \
    -i $ROSETTAFOLD_APPDIR/example/complex_modeling/paired.a3m \
    -o output/ -Ls 218 310

# For PPI screening using faster 2-track version (example input and output are at example/complex_2track)
${RUN_ROSETTAFOLD} python $ROSETTAFOLD_APPDIR/network_2track/predict_msa.py \
    -msa $ROSETTAFOLD_APPDIR/example/complex_2track/input.a3m \
    -npz output/complex.npz -L1 218
```

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