

Neighbor joining of amino acid sequences

MEGA (Molecular Evolutionary Genetic Analysis v3.1)

Values are % of bootstrap (1000x)

BCM Search Launcher

BCM sequencing tools

translation from Nucleotides to Amino acids

CLUSTALW

EBI's site

for global alignment of aa sequences  
Save output as ALN file

Read w/ JALview  
color by ~~gen~~ % identity

MEGA

convert from CLUSTAL file

Protein sequences

Data explorer

Primer 3

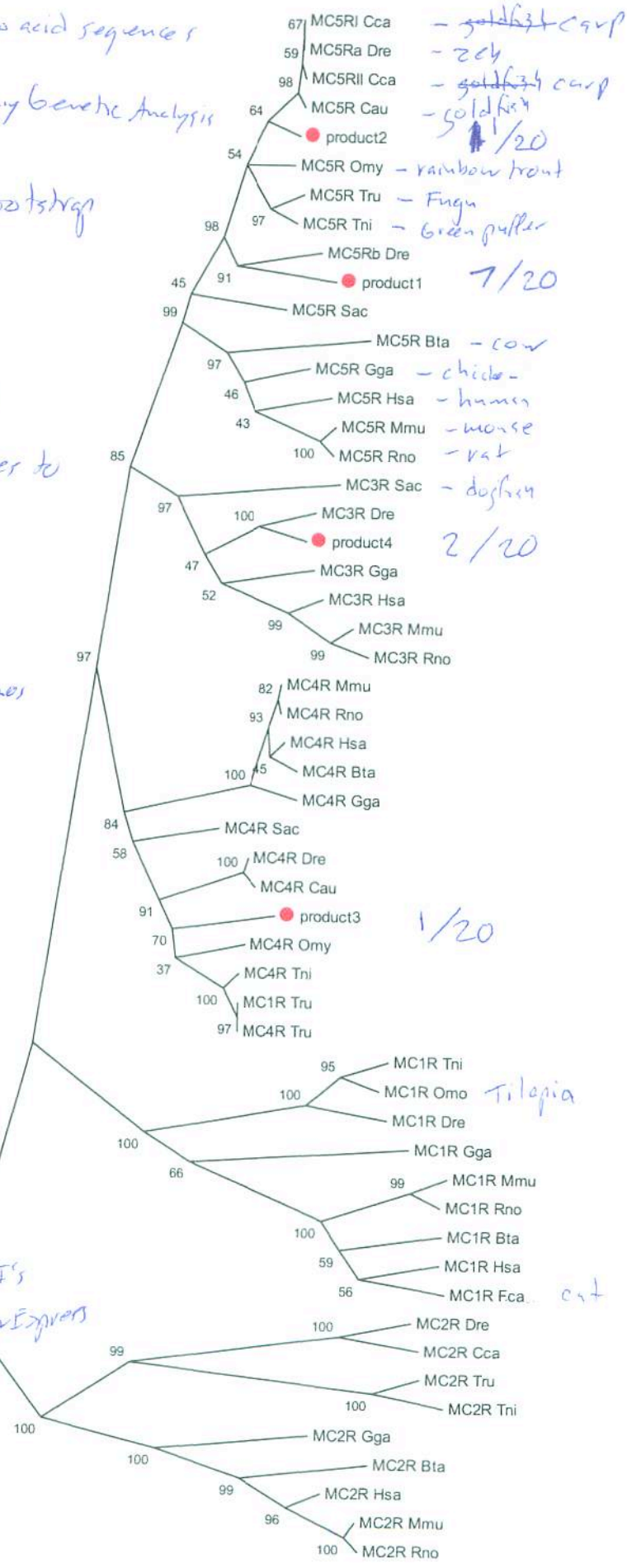
initial primer design

MFold

primer analysis

watching for self and heterodimers

ABI's  
Primer Express



0.1