

At3g22960, PK_p-α, 67% coverage

msqsiqfstpshtphllhphsqfnrplssisfrfrplttikytsira
sssspspdlldssssssqvlspngtgavksdersvavattdts
gievdtvteaekengfrstrrtklictigpatcgfeqlealavggmnvarl
nmchgtrdwhrgvirsvrrlneekgfavaimmdtegeihmgdlgg
easakaedgenvttvrafdsrptisvsydgfaedvrvgdellvd
ggmvrfeiekigpdkclctdpgllpranltfwrtdgslvrenampti
sskdwlididfgiaegvdfiavsvksaevinhksylaarsrggeigvia
kiesidsltnleeiilasdgamvargdlgaqipleqvpaqqrivqvcr
lnkpivasqllesmieypttraevadvseavrqrdsalmlsgesa
mgqfjdkaltvrtvslrierwwrekrhesvplqaignsfsdkiseeic
nsaakmannlgvdavfvyttsghmaslvsrcrpdcpifattttsvrrl
nlqwgliplrfsfddmesnlkftslksrgmiksgdlviavsdmlqsi
qvmnvp

At5g52920, PK_p-β₁, 21 % coverage

maqvatrsiqgsmispnggsvstrsekllkpasfavkvlgne
akrsgrvsvrrrvdttvrsarvetevipvspedvnpreeqlerlle
mqqfgdtsvgmwsksptvrrktkivctvgpstntremiwlkiaeagmn
varmnmshgdhashkkvidlvkeynaqtkdntiaimldtkgpevrs
gdllppimldpgqefttiergvstpscvsvnyddfndveagdmllv
dggmmsfmvksktdsvkcevvdggelksrrhlnvrgksatpsite
kdwedikfvenkvdfyavsvkdaqvhelkkylnsgadihvivki
esadsipnlhsiitadgamvargdlgaelpieevpilqeeiinlcrsm
gkavivatnmlsmivhpttraevsdiaivregadavmlsgetah
gkfpkkaagvmhtvalrteatitsgempplngqafknhmsemfayh
atmmsntlgtstvvftrtgfmailshyrpsgtiyafnekkqqrlalyqg
vcpiymeftddaeeffanalatlkkqgmvkkggeeiaivqsqtqpiwrs
qsthniqvrkv

At1g32440, PK_p-β₂, 10% coverage

maaygqissgmtvdpqvlsssrnigvslsplrtligagvrtsi
slrqcslsvrsiki sedsrpkayaengafdvglldsssyrladsrts
sndsrrktkivctigpssssremiwlkiaeagmnvarlnmshgdhas
hqitidlvkeynsfvdkaiaimldtkgpevrgdvpqpfleegqefnft
ikrgvslkdtvsvnyddfndvevgdillvdggmmslavksktsdlvk
cvvidggelqsrhlnvrgksatpsitdkdwedikfvdnqvdfyavs
fvkdakvhelknylktcsadisvivkiesadsiknlpsiisacdgamv
argdlgaelpieevpllqeeiirrcrsihkpvivatnmlsmihpttra
evsdiaivregadaimlsgetahgkfpkavnmhtvalrteaspv
rtsasrttaykghmgqmfaahasimantlssplivftrtgsmavllshyr
psatifaftnqrimqrlalyqgvmpiyemfsddaedyarsikllqden
mkegqhvtlvqsgsqpiwreesthliqvrkikigg

Supplemental Figure 2. Protein sequences, predicted transit peptides, and proteomics coverage of PK_p-α, PK_p-β₁, and PK_p-β₂. Gene Loci, encoded subunit, and percent coverage by proteomics are listed. ChloroP predicted chloroplast transit peptides are in bold. Peptide fragments identified by proteomics are highlighted in gray.