Research data:

Finding homologs between sequences for chr8 700,001..795,000

Chr8 sequence Annotations

Annotation: chr8

PASTE CODING REGION HERE:



Chr8: 49454356..49458686

Peptide Sequences being Compared:

>bf188fb9-3064-46b8-b71d-0d255aacfb81 (sequence:mRNA) 316 residues [chr8:49455025-49458016 - strand] [peptide]

MGRAPCCDKKGLKKGPWTPEEDQILVDFIKKNGGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGP

FTQEEEKLVIQLHGILGNRWATIASQLPGRTDNEIKNLWNTHLKKRLMGMGLDPQTHELISSCSTTVKAP

ASPITRHMAQWESARLEAEARLSRESSLFNPIPLGKTDSDYFLRIWNSEIGESFRKFNREDKTACQSPVS

QASSSTKCGSISAITTEISPILLGSSIAGSNQNEDNECKSCKSYPEEMMVGYDTSSSDELEDSSDSALQM

LLDFPINNDMSFLEEDIDKYSTPSAMLTENSFICPL

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**casein kinase 1-like protein HD16**

>XP\_023885896.1 casein kinase 1-like protein HD16 [Quercus suber] (Cork Oak)

MPELRSGARRSKRVDDLYPAPQPIDQGDNWLLPAQNRTRRRAAGRGRAGGNAALAKGPSPAVLTRPTAAA

RGRGIRLIDLDPEPCEVLPEAVALGAAEPLYNQVEVVADIDIGMEGGSADKVMGVEEEASTTPVPERVKV

GNSPVYKIERKLGKGGFGQVYVGRRVSGGTDADVTEVALKFEHRNSKGCNYGPPYEWQVYNTLNGCYGIP

WVHYKGRQGDFYILVMDILGPSLWDVWNSFGQSMSPNMAACIAVEAISILEKLHLKGFVHGDVKPENFLL

GQPGTPDEKKLYLIDLGLASRWKDASSGQHVEYDQRPDIFRGTIRYASVHAHLGRTGSRRDDLESLAYTL

IFLIRGRLPWQGYQGDNKSFLVCKKKMATSPELMCCFCPPPFKQFLEAVTNMKFDEEPNYSKLISFFESL

IEPCTPLRPIRIDGALKVGQKRARLLINLEEDEQPKKKVRLGSPATQWISVYNARRPMKQRYHYNVADTR

LHQHVDKGNEDGLYISCVASATNLWALIMDAGTGFSSQVYELSAVFLHKDWIMEQWEKNFYISSIAGAAN

GSSLVVMSKGTPYTQQSYKVSESFPFKWINKKWKEGFHVTSMTTAGSRWGVVMSRNAGYSDQVVELDFLY

PSEGIHRRWESGYRITSMAATADQGAFILSIPKRKTMDETQETLRTSAFPSTHVKEKWSKNLYIASICYG

RTVC

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Annotation: chr8a

chr8:9261006..9268356 (7.35 Kb)

Peptide Sequences Being Compared:

>83489d87-64ca-4c4c-86fe-97cb6c08c474 (sequence:mRNA) 145 residues [chr8:9262103-9267252 + strand] [peptide]

MGTKLKTVVATFFLCFLLFPLVFSASNGGLVRIGLKKTKLDKNNRVAAQLESKDGEVRSASIRKYYLRGN

SGDPEDIDIVSLKNYMDAQYFGEIGIGTPPQKFTVIFDTGSSNLWVPSSKCYFSVNQLISIMEPELFLGT

LVKTM

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**aspartic proteinase-like isoform X2 [Quercus suber]**

>XP\_023901186.1 aspartic proteinase-like isoform X2 [Quercus suber]

MGNKLKTVVATFFLCFLLFPLVFSASNGGLVRIGLKKTKLDKNNRVAAQLESKDGEVRSASIRKYYLRGN

SGDPEDIDIVSLKNYMDAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSSSST

YKKNGKPADIHYGTGAISGYFSQDHVKVGDLVVKNQEFIEATREPSITFLVAKFDGILGLGFKEISVGNA

VPLWYNMVKQGLVKEPVFSFWFNRNTDEEEGGEIVFGGVDPNHYKGKHTYVPVTQKGYWQFDMGDVLIDG

QTTGFCASGCSAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECKAVVAEYGETIIKMLLEKDQPMKIC

SQIGLCTFDGTRGVSMDIESVVDNTRKASNGLRDAMCSTCEMTVVWMQNQLKQNQTQDRILTYVNELCDR

LPSPMGESAVDCGSLSSLPNVSLTIGGRVFDLSPEQYVLKVGEGEAAQCISGFTALDVPPPRGPLWILGD

VFMGRYHTVFDYGNQRVGFAEAA