

IDENTIFICATION

Species: *Phalaenopsis equestris*

Locus: XP_020593812

Gene Model: XP_020593812.1

Description: PeqEXPA-10

Family: Alpha Expansin

3D structure:



GENOME DATABASES

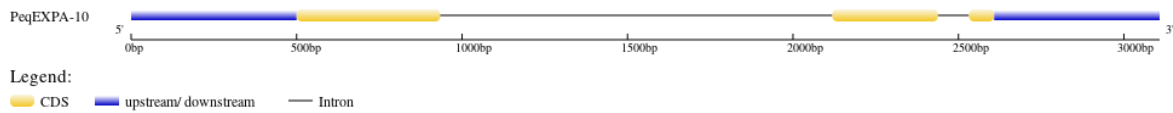
NCBI: <https://www.ncbi.nlm.nih.gov/genome/?term=Phalaenopsis+equestris>

KEGG: <https://www.genome.jp/entry/T05601>

EXTERNAL RESOURCES

http://orchidbase.itps.ncku.edu.tw/est/Phalaenopsis_2019.aspx

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MGGACGYGNLYSQGYGVETAALSTALFNAGLSCGACFELKCTEDPQWCVTGNPSIFI
 TATNFCPPNFAQPSDNGGWCNPPRPHFDLAMPFLKIAHYRAGIVPVS YRRVPCKKS
 GGIRFTINGFRYFNLVLISNVAGAGDIVKVS VKGSRTGWMTMSRNWGWQSNADL
 VGQSLFRVTGSDHRTSTSWNVVPAHWQFGQTFSGKNFRV

Superfamilies: **PLN00050**

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A, Provisional	1-208	6.34e-108

SEQUENCES

Peptide

>PeqEXPA-10

MGGACGYGNLYSQGYGVETAALSTALFNAGLSCGACFELKCTEDPQWCVTGNPSIFI
 TATNFCPPNFAQPSDNGGWCNPPRPHFDLAMPFLKIAHYRAGIVPVS YRRVPCKKS
 GGIRFTINGFRYFNLVLISNVAGAGDIVKVS VKGSRTGWMTMSRNWGWQSNADL
 VGQSLFRVTGSDHRTSTSWNVVPAHWQFGQTFSGKNFRV

CDS (coding sequence)

>PeqEXPA-10

GGGGTCTACACTGGCGGTTTCATGGCAAAGCGCGCACGCCACTTTCTACGGCGGAA
 GCGACGCCTCCGGCACAATGGGTGGGGCTTGCGGATACGGGAATCTATATAGCC
 AGGGATACGGCGTGAGACGGCGGGCTGAGCACGGCGCTATTCAACGGGGGT
 TGAGCTGCGGTGCGTGCTTTGAGTTAAAGTGTACCGAAGATCCCCAGTGGTGCGT
 AACTGGGAACCTTCGATCTTCATCACCGCGACTAATTTCTGCCCTCCGAACCTCG
 CTCAACCGTCTGATAATGGTGGATGGTGCAATCCACCTCGCCCTCATTTTCGATCTT
 GCGATGCCGATGTTTCTGAAAATAGCGCATTACCGTGCCGGCATCGTTCCAGTCT
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 CTTCGTTACTTCAACCTGGTTCTGATCTCCAATGTCGCCGGCGCCGGCGATATTG
 TGAAGGTGAGCGTAAAGGGATCTCGCACAGGGTGGATGACGATGTTCGCGAAACT
 GGGACAGAACTGGCAGTCTAATGCCGATCTGGTGGGCCAATCTCTCTCTTTCCG
 CGTACCGGCAGCGATCACCGGACCTCCACCTCCTGGAACGTTGTTCCGGCGCAC
 TGGCAGTTTGGTCAGACCTTCTCCGGCAAAAATTTTCGCGTTTGATTAAATGGTAA
 TGCTTGGTAGATTTTAGGGGCCGATTTTATAGGCCTTGTTTGGTGGTGGGTGCGCG
 CTTTTGTGTGGTATTGAGCAAGCATTATGGAAAAGTGTGAAACAGCTTCTTAGT
 GC

Nucleotide

>PeqEXPA-10

CTCTGATTATTGAATGTCTGGTAAATAGTTTTATGTGCGATGGCAGTTTTAGCTAT
 GTAGTAGAAGAGCTGGCACGGCCATTTAAAAAACCTGTTTAACTATGCTTCGAA
 AGCTGTTACGCAATAAACAAGCCCAATGGCTGCGGGCAACAACCTGTAATTGTCGG
 TAAAAAGAGTTGCCAAAGTTGTCATGAGAGTATAATGATTTTCGACTGTTTTTTGC
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CGGTGGCGGTGTATGAGGAGGCAATAAATAACG