

IDENTIFICATION

Species: *Phalaenopsis equestris*

Locus: XP_020581041

Gene Model: XP_020581041.1

Description: PeqEXPA-09

Family: Alpha Expansin

3D structure:



GENOME DATABASES

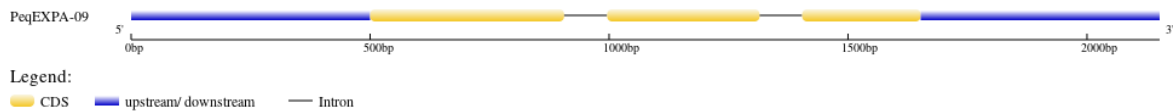
NCBI: <https://www.ncbi.nlm.nih.gov/genome/?term=Phalaenopsis+equestris>

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

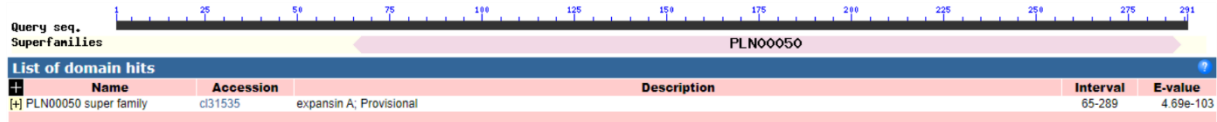
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PeqEXPA-09

MMHSFRAFHIPFSSFLLFSLLLTTNISGEVAGQHHCHPGSLRRTLPNPHRQRRYHG
KFVPGPWSRAHATFYGSRDGS DTRGGACGYSDTVAQGYGLQTAALSTALFNDGLSC
GACFEIKCVDDPKWCNPGRPSIFITATNYCPPNYNLPSNNGGWCNTPRPHFDLTLPAF
LHIAQYKAGIVPVSYRRVPCKKRGGMRFTMTGNPYFNMILVWNVGGAGDVRHVEV
KAQRRPWRTLRLHNWGQYWETNANLVGQFLSFRVTAGDGRRSTSWHVPSNWQFG
QTFEGKNFRF

CDS (coding sequence)

>PeqEXPA-09

CATGATGCATTCCCTTCCGAGCTTTCCACATTCCTTTCTCCTCCTTTCTTTTGTTC
GTTGCTTCTGACAACAAACATCTCCGGCGAAGTTGCAGGCCAGCACCACCATCAC
TGCGGTCCCGGCTCCCTCCGGAGA ACTTTGCCGAACCCCCACCGACAGCGCCGCT
ACCATGGCAAGTTTGTGCCCGGCCCGTGGTCCCGAGCACACGCCACATTCTACGG
AAGCAGGGATGGTTCTGATACAAGAGGGGGCGCATGCGGGTATTCCGACACCGT
AGCGCAAGGCTACGGCTTACAGACGGCGGCATTGAGCACCGCACTGTTCAACGA
TGGGCTGTTCGTGCGGCGCTTGT TTTGAGATAAAAATGCGTGGATGATCCCAAGTGG
TGCAACCCGGGCAGGCCTTCCATCTTCATCACCGCCACCAATTACTGCCCGCAA
ACTACAACCTCCCCAGCAACAACGGCGGTTGGTGCAACACACCCCGCCCCACTT
TGATCTCACCTGCCGGCTTTTCTCCATATTGCACAATACAAAGCGGGCATTGTTC
CTGTGTCTTACCGAAGGGTTCCATGCAAGAAGCGAGGAGGAATGAGGTTCACCAT
GACGGGAAACCCATACTTCAACATGATACTGGTGTGGAATGTGGGCGGAGCAGG
TGATGTCCGGCATGTTGAGGTGAAAGCGCAACGGCGTCCGTGGAGGACATTGAG
GCATAACTGGGGGCAATACTGGGAGACCAATGCTAATCTCGTCGGCCAATTTCTG
TCTTTCAGAGTCACCGCCGGT GATGGTCGCCGCTCCACCTCGTGGCATGTTGTTCC
TTCAA ACTGGCAGTTCGGACAAACCTTTGAGGGCAAGAACTTTAGGTTCTGAAAC
TGAAAAAAGATTAAGTAGCATGAAATTTATGGGAGCAATATATAGAATTAGATT
AAAAAAAAGTTGCATTATGGATGGTTTTTTTCTCCTTG

Nucleotide

>PeqEXPA-09

CACGAATTTATTTGTTTCACATTTTATTTTCAAATAGAAAGTCAATCATAGCACT
AAGCATACTCTTCATCGCAAACCCCATACGTTATCGACTACACACCTGAAAATAT
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ACCAAAGGAGAAAAAAACCATCCATAATGCAACTTTTTTTTAAATCTAATTCTATA
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GGACGCCGTTGCGCTTTCACCTCAACATGCCGGACATCACCTGCTCCGCCACAT
TCCACACCAGTATCATGTTGAAGTATGGGTTTCCCGTCATGGTGAACCTCATTCT
CCTCGCTTCTTGATGGAACCTAAACATACACATATCCCTAAATGAATCATGTA
CATCTAACTCACTCGACAGTTATAATGACACCAAACCTTTGGCGAAAGAAGAGTCA
CCTTCGGTAAGACACAGGAACAATGCCCGCTTTGTATTGTGCAATATGGAGAAAA
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