

## IDENTIFICATION

**Species:** *Phalaenopsis equestris*

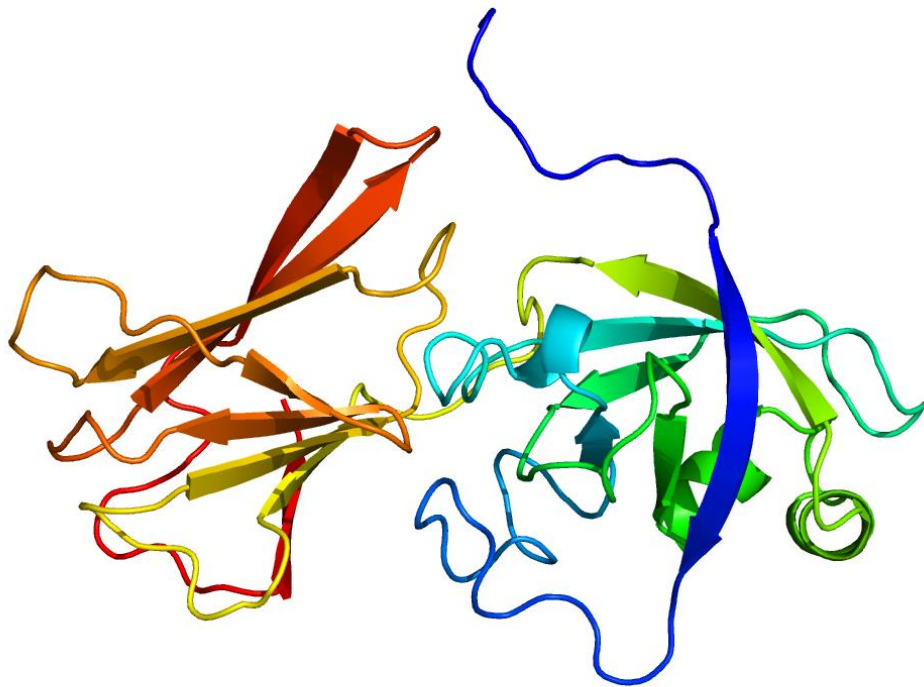
**Locus:** XP\_020574186

**Gene Model:** XP\_020574186.1

**Description:** PeqEXLA-03

**Family:** Expansin Like Alpha

**3D structure:**



## GENOME DATABASES

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

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

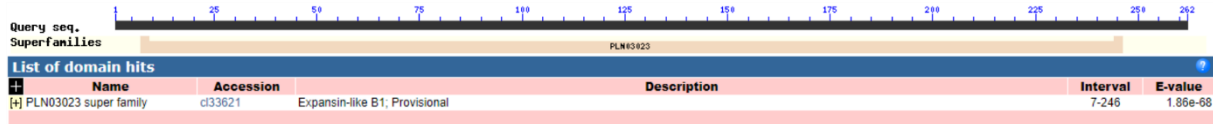
## EXTERNAL RESOURCES

[http://orchidbase.itps.ncku.edu.tw/est/Phalaenopsis\\_2019.aspx](http://orchidbase.itps.ncku.edu.tw/est/Phalaenopsis_2019.aspx)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PeqEXLA-03

MKLSTFFLLFPIFLSLATACDRCVHKSVA VFSPPSSLPAGACGYGSLALNFSHGLIAA  
ASSKIYRDGVGCGGCFQIRCRNTELCNGAGVKVVVTDLDKSNRTDFRLSSRAFAAM  
ARPGMVAGLQTVGVVDAEHKRIPCDYSNKNLSIRVEESSRRPSLLTVKLIYQGGQTD  
VVAVDVARFGSPA WQFMTRLNGPVWTTTRQAPGGPLQFRFVVTGGYDGKWWVAQQ  
EVLPAEWRSGEVYDTGVQITDIAQEGCSPCDTEEWR

### CDS (coding sequence)

>PeqEXLA-03

TTTCCTCATAATATCACCGCTGATTCATCCTCATCCAGTGGCCCTGCCCTCGCCGA  
CCATTTCTATCGCGGCTCCAGCAAAGTCGACCCGCCGCCATTAGCATTTCGAGA  
AATCCACTTTACAGAATTCTACAGTCGTAGAACAGCCAAAAGACATTACTTCCTC  
TCTCACTCAATCCGCGTCCCTTTTCCCCTCCACTATAAACTCCTGTCCAGA  
TCGATTCCCTCCAACCCACCAGCGCCACCATCCCCACACTCCACCACCAATCCAC  
CATGAAGCTTTCAACTTTCTTCCCTCCTTCCCAATCTTCCCTCCTCCCTCGCCACAGC  
TTGCGATAGATGCGTTCACAAATCCAAAGTCGCCGTTTTTTCTCCCCCTCCTCTC  
TTCCAGCCGGAGCTTGTGGCTATGGCTCCTGGCTCTCAACTTCAGTCATGGACTT  
ATCGCCGCCGCAAGTTCTAAAATTTATCGCGATGGCGTTGGCTGCGGTGGCTGTT  
TCCAGATTCGGTGCAGGAATACAGAGCTCTGTAATGGAGCAGGGGTGAAGGTTG  
TGGTGACCGATCTTGATAAGAGCAATAGAACTGATTTTAGGCTCAGTTCTCGGGC  
CTTCGCTGCTATGGCGCGGCCGGGATGGTCGCCGACTGCAGACAGTTGGGGTG  
GTCGATGCAGAACACAAAAGGATTCGGTGC GACTATTCAAACAAGAACCTATCC  
ATAAGAGTGGAGGAGAGCAGCCGGAGGCCAGTTTATTAACGGTCAAACCTATC  
TACCAAGGTGGACAAACTGACGTCGTGGCAGTCGACGTGGCGCGGTTTCGGTTCGC  
CAGCATGGCAGTTCATGACCCGGCTCAACGGCCCGGTCTGGACCACCAGGCAAG  
CACCGGGCGGCCCGCTTCAGTTCGGTTCGTGGTGACGGGTGGGTACGACGGCAA  
GTGGGTGTGGGCCCAACAGGAGGTGTTGCCGGCTGAGTGGCGGTCCGGCGAGGT  
GTACGATACGGGAGTTCAGATCACCGATATAGCGCAGGAGGGCTGTTCTCCTTGT  
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GCCTAAATAAGAAAGGAAACCATATAATGTAAAAGATCAGAAGGTTATAATTGT  
AAGTATATGG



TTTTTTAATGTTTTAATGAAATATATGACTAAAGGACTATAACAAATAAATCTTC  
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CGAAGAGAAAACCTTAGCCATAAAATCATATCAATTCTTCTGAGAAGTCGCTACT  
GCACCCACCGATCCAACCTGTTGTCATTACAGCAGAGAATTATATATGTTATAGTT  
CAGTTATAATTATTATTCCTGAATTATTCTCTTAGGTTTCTAATCATTAATTTAATA  
ATTTATTTTCTAAAATTCCAACCTTACCTCTCAAATTCAGATTTTATTTATATTG  
TCACTTTGCATTTTGTTGCTCCGATCCCTCCCACTTTGAGTTTAGAGAGATAACTT  
TCCCCTC