

IDENTIFICATION

Species: *Phalaenopsis equestris*

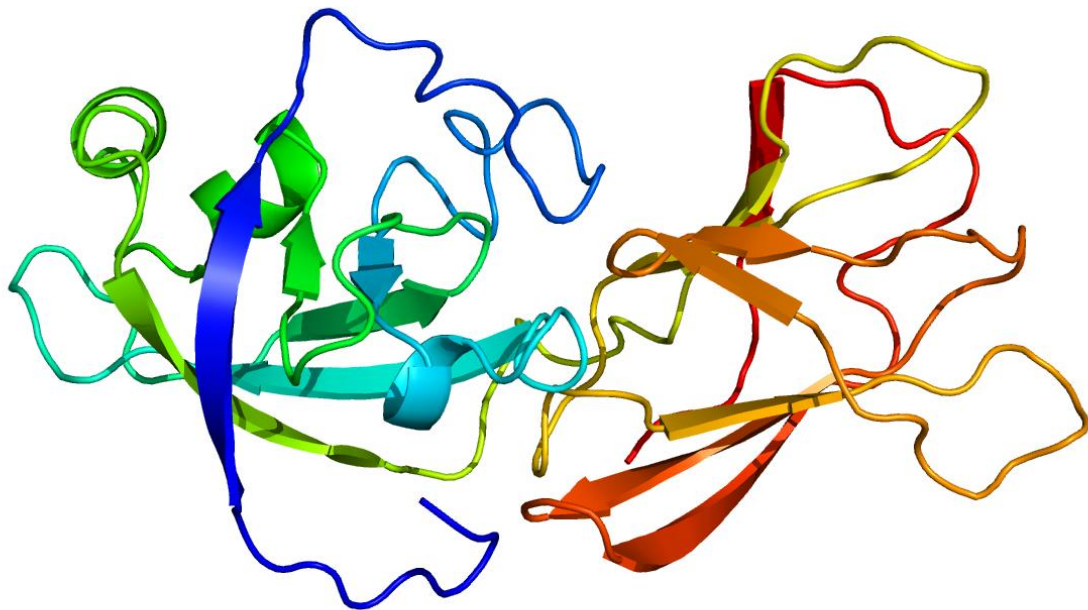
Locus: XP_020597913

Gene Model: XP_020597913.1

Description: PeqEXLA-01

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>

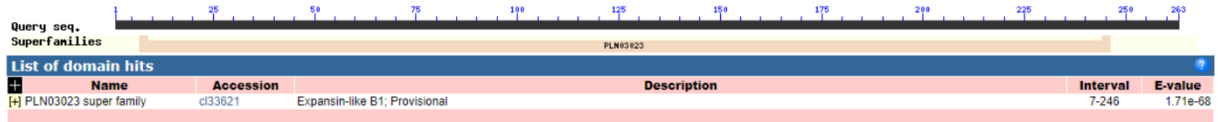
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PeqEXLA-01

MKLSTFFLLFPIFLSLATACDRCVHKSVA VFSPPSSLPAGACGYGSLALNFSHGLIAA
ASSKIYRDGVGCGGCFQIRCRNTELCNGAGVKVVVTDLDKSNRTDFRLSSRAFAAM
ARPGMVAGLQTVGVVDAEHKRIPCDYSNKNLSIRVESSRRPSLLTVKLIYQGGQTD
VVAVDVARFGSAAWQFMTRLNGPVWTRQAPGGPLQFRFVVTGGYDGKWWWAQ
QEVLPAEWRSGEVYDTGVQITEIAQEGCSPCDTEEWRG

CDS (coding sequence)

>PeqEXLA-01

AGAAGCTTTCCTCATAATATCACCGCTGATTCATCCTCATCCAGTGGCCCTGCCCT
CGCCGACCATTCTATCGCGGCTCCAGCAAAGTCGACCCGCCGCCATTAGCATT
TCGAGAAATCCACTTTACAGAATTCTACAGTCGTAGAACAGCCAAAAGACATTAC
TTCCTCTCTCACTCAATCCGCGTCCTTTTCCCACTCCTCCCACTATAAACTCCTGT
CCAGATCGATTCCCTCCAACCCACCAGCGCCACCATCCCCACACTCCACCACCAA
TCCACCATGAAGCTTTCAACTTTCTTCCTCCTCTTCCCAATCTTCCTCTCCCTCGCC
ACAGCTTGCGATAGATGCGTTCACAAATCCAAAGTCGCCGTTTTTTCTCCCCCTC
CTCTCTTCCAGCCGGAGCTTGTGGCTATGGCTCCTTGGCTCTCAACTTCAGTCATG
GACTTATCGCCGCCGCAAGTTCTAAAATTTATCGCGATGGCGTTGGCTGCGGTGG
CTGTTTCCAGATTTCGGTGCAGGAATACAGAGCTCTGTAATGGAGCAGGGGTGAAG
GTTGTGGTGACCGATCTTGATAAGAGCAATAGAAGTGAATTTAGGCTCAGTTCTC
GGGCCTTCGCTGCTATGGCGCGGCCGGGGATGGTCGCCGACTGCAGACAGTTGG
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TCGGCAGCATGGCAGTTCATGACCCGGCTCAACGGCCCGGTCTGGACCACCAGGC
AAGCACCGGGCGGCCCGCTTCAGTTCGGGTTTCGTGGTGACGGGTGGGTACGACGG
CAAGTGGGTGTGGGCCCAACAGGAGGTGTTGCCGGCTGAGTGGCGGTCCGGCGA
GGTGTACGATACGGGAGTTCAGATCACCGAAATAGCGCAGGAGGGCTGTTCTCCT
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Nucleotide

>PeqEXLA-01

TTAATGATTAGAAACCTAAGAGAATAATTCAGGAATAATAATTATAACTGAACTA
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CGACCATTTCTATCGCGGCTCCAGCAAAGTCGACCCGCCGCCATTAGCATTTCG
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CTCTCTCACTCAATCCGCGTCCTTTTCCCACTCCTCCCACTATAAACTCCTGTCC
AGATCGATTCCCTCCAACCCACCAGCGCCACCATCCCCACACTCCACCACCAATC
CACCATGAAGCTTTCAACTTTCTTCTCTCTTCCCAATCTTCTCTCCCTCGCCAC
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CTCTTCCAGGTAATCCCGCTGGCTTCTATTATCTCCATCTACTCTTCTACATCTCT
AATCACTAACCTCGCACTTGCAGCCGGAGCTTGTGGCTATGGCTCCTTGGCTCTCA
ACTTCAGTCATGGACTTATCGCCGCCGCAAGTTCTAAAATTTATCGCGATGGCGTT
GGCTGCGGTGGCTGTTTCCAGGTGAGAAATTTATCTATCGATTATTGCGATTTTG
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GTGTACGATACGGGAGTTCAGATCACCGAAATAGCGCAGGAGGGCTGTTCTCCTT
GTGACACGGAGGAATGGCGGGGGCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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