

IDENTIFICATION

Species: *Olea europaea*

Locus: Oeu013876

Gene Model: Oeu013876.1

Description: OeuEXPA-18

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Oeuropaea_v1_0

KEGG: <https://www.genome.jp/entry/T05244>

EXTERNAL RESOURCES

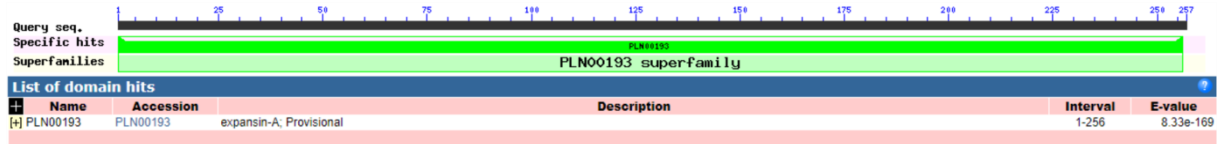
<http://olivegenome.org/>

<https://genomaolivar.dipujaen.es/db/index.php>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>OeuEXPA-18

MTKNVILPIVLIIGISCFMKASAITTSJWTQAHATFYGGSDASGTMGGACGYGNLYS
TGYGTRTAALSTALFNDGAACGQCYKIMCDYNADPKWCIKGTSVTVTATNFCPPNY
ALPSDNGGWCNPPRQHFDMAQPSWEKIGIYRGGIVPVIYQRPCKKHGGVRFTINGR
NYFELVMISNVANAGSIQSVQIKGSKTNWMAMSRNWGANWQSN SYLNGQSISFKVT
TTDQTRTFLNIVPSNWGFGQTFSSPAQF*

CDS (coding sequence)

>OeuEXPA-18

ATGACTAAAAATGTCATTTTACCAATTGTACTTATAATTGGAATCTCATGTTTTCT
CATGAAGGCTAGTGCCATTACAACCTTCTGGTTGGACTCAAGCTCATGCAACCTTC
TATGGAGGCAGTGATGCTTCCGGGACAATGGGTGGTGCTTGTGGATATGGGAATT
TGTATTCAACTGGTTATGGGACTAGAAGTGCAGCATTGAGCACTGCATTGTTCAA
TGATGGAGCAGCATGTGGGCAATGTTACAAGATTATGTGTGATTATAATGCTGAT
CCTAAATGGTGCATCAAGGGAACCTTCTGTTACCGTACTGCTACAAACTTTTGTCC
TCCAAATTATGCTCTTCCCAGTGACAATGGAGGTTGGTGCAACCCACCACGCCAA
CATTTCGACATGGCTCAACCCTCTTGGGAAAAGATAGGCATTTATAGAGGTGGAA
TCGTGCCCCTCATCTACCAAAGGGTTCCTGTGCAAGAAACATGGCGGAGTTAGATT
CACCATCAATGGAAGAACTACTTTGAGCTTGTAATGATTAGTAATGTGGCAAAT
GCTGGATCTATTCAATCAGTGCAAATCAAGGGCTCGAAAACCAACTGGATGGCTA
TGTCTAGGAATTGGGGGGCTAATTGGCAATCCAATTCTTACCTCAATGGCCAATC
TATATCCTTCAAGGTCACAACCACTGATGGTCAAACAAGAACTTTCCTAAACATT
GTCCCATCAAATTGGGGTTTCGGCCAAACATTTTCAAGCCCTGCCCAATTCTAA

Nucleotide

>OeuEXPA-18

ATGACTAAAAATGTCATTTTACCAATTGTACTTATAATTGGAATCTCATGTTTTCT
CATGAAGGCTAGTGCCATTACAACCTTCTGGTTGGACTCAAGCTCATGCAACCTTC
TATGGAGGCAGTGATGCTTCCGGGACAATGGGTATGAAACTTGGAAAGATTTTAT
TTTTCTTGTAGATCTACTAGAAGATCGTTAAAACGTGTTTTTTATAATTGTTT
TGTTTTGTAACAGGTGGTGCTTGTGGATATGGGAATTTGTATTCAACTGGTTATGG

GACTAGAACTGCAGCATTGAGCACTGCATTGTTCAATGATGGAGCAGCATGTGGG
CAATGTTACAAGATTATGTGTGATTATAATGCTGATCCTAAATGGTGCATCAAGG
GAACTTCTGTTACCGTACTGCTACAACTTTTGTCTCCAAATTATGCTCTTCCC
AGTGACAATGGAGGTTGGTGCAACCCACCACGCCAACATTCGACATGGCTCAAC
CCTCTTGGGAAAAGATAGGCATTTATAGAGGTGGAATCGTGCCCGTCATCTACCA
AAGGTCATAACTTTTCTCTCTTAATATATATTAATATCTCTATCCAATCTTTTCA
GAAAGCTGCTACAGAGATAGGACGTGTCCCCGTATATTGACCCTGTTAATAAAGT
CCCTATACATGGAGCTTTATTCTCTTTTTGAATCTCAACTTGACGACTGATATTCT
ATCTGTGATGCAGGGTCCGTGCAAGAAACATGGCGGAGTTAGATTCACCATCAA
TGGAAGAACTACTTTGAGCTTGTAATGATTAGTAATGTGGCAAATGCTGGATCT
ATTCAATCAGTGCAAATCAAGGGCTCGAAAACCAACTGGATGGCTATGTCTAGGA
ATTGGGGGGCTAATTGGCAATCCAATTCTTACCTCAATGGCCAATCTATATCCTTC
AAGGTCACAACCACTGATGGTCAAACAAGAACTTTCCTAAACATTGTCCCATCAA
ATTGGGGTTTCGGCCAAACATTTTCAAGCCCTGCCCAATTCTAA