

IDENTIFICATION

Species: *Populus trichocarpa*

Locus: Potri.019G057500

Gene Model: Potri.019G057500.3.p

Description: PtEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Ptrichocarpa_v4_1

KEGG: <https://www.genome.jp/entry/gn:T01077>

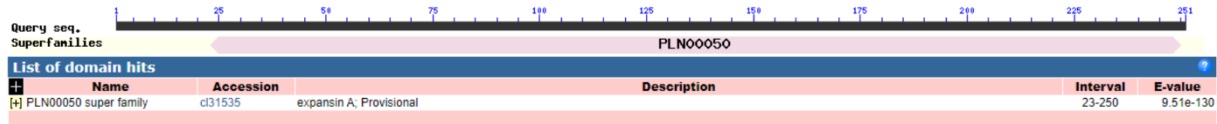
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PtEXPA-29

MTMAATISLLLFLHLCLIGTYGDSGGWQGGHATFYGGGDASGTMGGACGYGNLY
SQGYGTNTAALSTALFNGLSCGSCYEMRCDNDPKWCLPGSITVTATNFCPPNSALS
NDNGGWCNPPQLQHFDMAEPAFLQIAQYRAGIVPISFRRVPCVKKGGIRFTINGHSYFN
LVLITNVAGAGDVHSVSIKGSKTGWQAMSRNWGQNWQSNLYLNGQSLSFQVTTSD
GRTVTSYNAVPENWQFGQTFSGGQF*

CDS (coding sequence)

>PtEXPA-29

ATGACAATGGCAGCTACTATCTCTCTTCTCTTGTGTTGCGCTCCACTTGTGCCTTAT
AGGCACTTATGGGGACTCCGGAGGGTGGCAAGGTGGCCATGCCACTTTCTATGGC
GGGGGTGATGCTTCTGGGACAATGGGAGGTGCTTGTGGGTATGGCAATTTGTACA
GTCAAGGGTATGGTACTAACACTGCAGCACTTAGTACTGCCCTTTTCAACAATGG
CTTGAGCTGTGGTTCTTGTATGAGATGAGATGTGACAATGATCCCAAATGGTGC
CTCCCTGGGTCCATCACCGTCACAGCCACTAACTTCTGCCCCCTAACTCTGCCTT
GTCTAATGACAACGGTGGCTGGTGTAACTCCCTCCAGCACTTTGACATGGCT
GAGCCAGCTTTCTTGCAAATTGCTCAATACAGAGCTGGAATTGTACCAATCTCAT
TCAGAAGGGTCCCCTGTGTCAAGAAAGGAGGAATAAGGTTTACCATCAATGGAC
ACTCTTACTTTAATTTGGTGTGATCACAAACGTTGCTGGAGCAGGAGATGTTTCAT
TCAGTGTGATCAAGGGTTCTAAGACAGGGTGGCAAGCTATGTCAAGGAACTGG
GGCCAGAAGTGGCAAAGCAATTCTTACCTCAATGGCCAAAGTCTTTCTTTCCAAG
TCACCACAAGTGATGGTAGGACTGTGACTAGCTACAACGCAGTGCCAGAAAAT
GGCAATTTGGCCAAACATTTTCAGGCGGTCAATTCTAG

Nucleotide

>PtEXPA-29

AGCACCAAGCGTCGAGTCTTTCTCACACAACTCTCCCTCTCCTCGCCTGATAGAT
ACACCTTACCAGCAACAATGACAATGGCAGCTACTATCTCTCTTCTCTTGTGTTGCG
CTCCACTTGTGCCTTATAGGCACTTATGGGGACTCCGGAGGGTGGCAAGGTGGCC
ATGCCACTTTCTATGGCGGGGGTGTGCTTCTGGGACAATGGGTATGTTTCAGCA
ACTTTTCTTTCTTCATAGGGCAATAATGCTACTTCTACTGAAAGGTTTTTCCAAT
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CTGCAGCACTTAGTACTGCCCTTTCAACAATGGCTTGAGCTGTGGTTCTTGTTAT
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CAGCCACTAACTTCTGCCCCCTAACTCTGCCTTGTCTAATGACAACGGTGGCTGG
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TCAATACAGAGCTGGAATTGTACCAATCTCATTGAGAAGGTAAAAATCAACCTCT
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GATTGGCAAGTGGCTTCCGTCGGTTACAATTAATATGCTGCAAAAATTAACGAA
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GTGTGATCAAGGGTTCTAAGACAGGGTGGCAAGCTATGTCAAGGAACTGGGGC
CAGAACTGGCAAAGCAATTCTTACCTCAATGGCCAAAGTCTTTCTTTCCAAGTCA
CCACAAGTGATGGTAGGACTGTGACTAGCTACAACGCAGTGCCAGAAAACCTGGC
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