

IDENTIFICATION

Species: *Daucus carota*

Locus: DCAR_028915

Gene Model: DCAR_028915

Description: DcEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Dcarota_v2_0

KEGG: <https://www.genome.jp/entry/T05350>

EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MGGACGYGNLYSQGYGTNTAALSTALFNHGERCGACYELKCNDDPKWCLHNTITV TATNFCPPNNALSNDNGGWCNPPLRHFDLAQPAFLRIAQYRAGIVPLLYRRVPCVKK GGIRFTINGHSYFNLVLITNVGGAGDVHAVSIKGSKTGWEAMSRNWGQNWQSNAYL NGQSLFRVTSGDGKTIAANNVPPGWQFGQTFEGTQF*

Superfamilies PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A, Provisional	1-206	2.81e-117

SEQUENCES

Peptide

>DcEXPA-20

MGGACGYGNLYSQGYGTNTAALSTALFNHGERCGACYELKCNDDPKWCLHNTITV
TATNFCPPNNALSNDNGGWCNPPLRHFDLAQPAFLRIAQYRAGIVPLLYRRVPCVKK
GGIRFTINGHSYFNLVLITNVGGAGDVHAVSIKGSKTGWEAMSRNWGQNWQSNAYL
NGQSLFRVTSGDGKTIAANNVPPGWQFGQTFEGTQF*

CDS (coding sequence)

>DcEXPA-20

ATGGGAGGAGCATGTGGGTACGGGAATTTGTACAGCCAGGGCTACGGTACAAAC
ACGGCGGCTCTCAGCACAGCTCTCTCAACCACGGAGAGAGGTGCGGAGCTTGTT
ATGAGTTGAAGTGCAATGACGACCCCAAATGGTGCCTGCATAACACCATCACCGT
CACGGCAACCAACTTTTGTCCACCCAACAACGCCCTCTCCAATGACAATGGCGGA
TGGTGCAATCCTCCCCTCCGTCATTTTCGATCTCGCACAGCCTGCTTTCCTTCGTATT
GCACAATATCGCGCTGGAATTGTACCGTTACTCTACAGAAGGGTGCCTTGTGTAA
AGAAAGGGGGCATAAGGTTTACTATAAATGGCCATTCCTACTTCAATCTGGTGTT
GATAACAAACGTTGGGGGTGCAGGAGATGTCCACGCCGTATCCATAAAAGGTTTC
CAAGACAGGGTGGGAAGCCATGTCCAGAACTGGGGGCAGAACTGGCAGAGCA
ATGCCTATCTCAACGGCCAAAGCCTCTCCTTCCGGGTCACGTCGGGCGATGGCAA
GACCATTGCAGCCAACAATGTGGTTCCGCCTGGCTGGCAGTTCGGACAACTTTT
GAAGGAACTCAGTTTTAG

Nucleotide

>DcEXPA-20

ATGGGTACGTATGTAGTAGTATGTTGATATCAATGTTGATACACAAATCACACTA
TTTTCTCAGTTGTTTACGTAGGTATTTTGAGACTCGTATAAAGTATAGTTTTATA
ATGTTTTTTATCTTTTGAATAAAAATTTAAACGTCAAACTTTTATTCAGGAAAAAA
AACTATACTTTACAAGAGTCTCGTGCCAAAAGCTAACATAAATAATCTGCTTACC
ACGTTTACTTGAAATATATTTGGATTTGGTTGCAGGAGGAGCATGTGGGTACGGG
AATTTGTACAGCCAGGGCTACGGTACAAACACGGCGGCTCTCAGCACAGCTCTCT
TCAACCACGGAGAGAGGTGCGGAGCTTGTTATGAGTTGAAGTGCAATGACGACC
CCAAATGGTGCCTGCATAACACCATCACCGTCACGGCAACCAACTTTTGTCCACC
CAACAACGCCCTCTCCAATGACAATGGCGGATGGTGCAATCCTCCCCTCCGTCAT

TTCGATCTCGCACAGCCTGCTTTCCTTCGTATTGCACAATATCGCGCTGGAATTGT
ACCGTTACTCTACAGAAGGTACCTACCTGCTAATCACTCTGTAAATTACCTCCAAT
CCTCTGTATAGATTAATTAATCATCTTTAACTGCAGGGTGCCTTGTGTAAAGAAA
GGGGGCATAAGGTTTACTATAAATGGCCATTCCTACTTCAATCTGGTGTGATAA
CAAACGTTGGGGGTGCAGGAGATGTCCACGCCGTATCCATAAAAGGTTCCAAGA
CAGGGTGGGAAGCCATGTCCAGAACTGGGGGCAGAACTGGCAGAGCAATGCCT
ATCTCAACGGCCAAAGCCTCTCCTTCCGGGTCACGTCCGGGCGATGGCAAGACCAT
TGCAGCCAACAATGTGGTTCCGCCTGGCTGGCAGTTCGGACAACTTTTGAAGGA
ACTCAGTTTTAG