

IDENTIFICATION

Species: *Daucus carota*

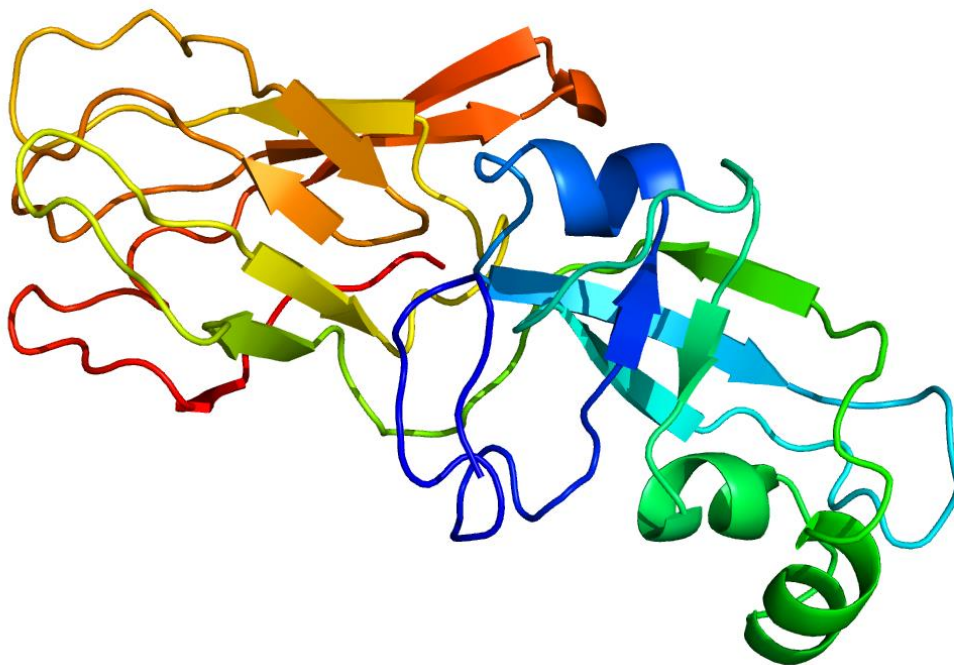
Locus: DCAR_024980

Gene Model: DCAR_024980

Description: DcEXLB-03

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

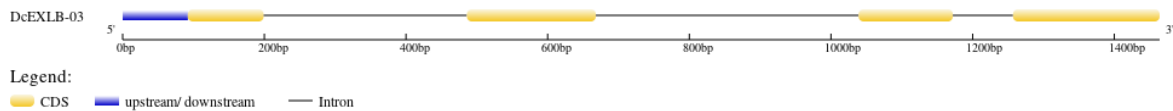
Phytozome: https://phytozome-next.jgi.doe.gov/info/Dcarota_v2_0

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

EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MSCGACGYGTFGATINGGDVSAASDLYRDGVGCGACYQVRCSDSTYCSEKGVNVVITDQGGSPSTDFILSRRAFGRMAQTDDAAASLLNLGVVDIEYRRVSCSYPSKNITVKID
Superfamilies PLN03023

Name	Accession	Description	Interval	E-value
PLN03023 super family	cl33621	Expansin-like B1; Provisional	4-209	5.63e-77

SEQUENCES

Peptide

>DcEXLB-03

MSCGACGYGTFGATINGGDVSAASDLYRDGVGCGACYQVRCSDSTYCSEKGVNVVITDQGGSPSTDFILSRRAFGRMAQTDDAAASLLNLGVVDIEYRRVSCSYPSKNITVKID
ENSNYPHYLAFSLWYQQGNSDITAVQLCETKNLSCKLLSRSYGAVWTTTSAPSGSLS
LRMLFSNDVTGDETWVVPVNNIPENWKAGDTYDTGVQVNN*

CDS (coding sequence)

>DcEXLB-03

ATGTCATGTGGGGCGTGTGGGTATGGCACATTTGGAGCAACCATTAACGGCGGGG
ATGTATCAGCTGCATCTGATCTCTACCGAGATGGTGTAGGTTGTGGTGCTTGCTAT
CAGGTGAGGTGTTCCGACAGCACGTATTGCTCAGAAAAAGGAGTAAATGTGGTT
ATAACTGACCAAGGATCTGGCCCCAGCACGGATTTTATTCTGAGCAGGCGAGCCT
TTGGACGGATGGCTCAGACTACTGATGCAGCTGCCTCTTTACTAAACCTTGGTGT
AGTTGATATTGAATACAGAAGGGTGTGCATGCAGCTATCCATCCAAAAACATAACA
GTCAAGATTGATGAGAACAGCAACTATCCTCACTACTTGGCATTCTTTATGGTA
TCAACAAGGAAACAGTGATATTACTGCTGTGCAGTTATGCGAGACAAAGAATCTT
AGCTGCAAGCTTCTGAGTCGTAGTTATGGAGCAGTATGGACGACAACTTCAGCCC
CTAGCGGATCATTGTCTCTGAGGATGCTGTTAGTAATGATGTTACTGGAGACGA
GACTTGGGTTGTTCCAGTTAACAACATTCCAGAAAACCTGGAAGGCTGGAGATACT
TATGACACTGGTGTGCAAGTGAACAATTAA

Nucleotide

>DcEXLB-03

ATGTCATGTATACAAACGCGTGCATTAACAAGTACACGTATTAAGAATAATTGC
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GCACATTTGGAGCAACCATTAACGGCGGGGATGTATCAGCTGCATCTGATCTCTA
CCGAGATGGTGTAGGTTGTGGTGCTTGCTATCAGGTGATTACACACATGCATATA
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ACACAATATAAATCTCTGCTCTACTTAATTTTCATTTCTTAAACAGGGTGTGCATGCA
GCTATCCATCCAAAAACATAACAGTCAAGATTGATGAGAACAGCAACTATCCTCA
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AATTCTCTTTATACTCTAATCACCATGTTCCATGTTTCAGACAAAGAATCTTAGCT
GCAAGCTTCTGAGTCGTAGTTATGGAGCAGTATGGACGACAACCTTCAGCCCCTAG
CGGATCATTGTCTCTGAGGATGCTGTTTAGTAATGATGTTACTGGAGACGAGACT
TGGGTTGTTCCAGTTAACAAACATTCCAGAAAACCTGGAAGGCTGGAGATACTTATG
ACACTGGTGTGCAAGTGAACAATTAA