

IDENTIFICATION

Species: *Daucus carota*

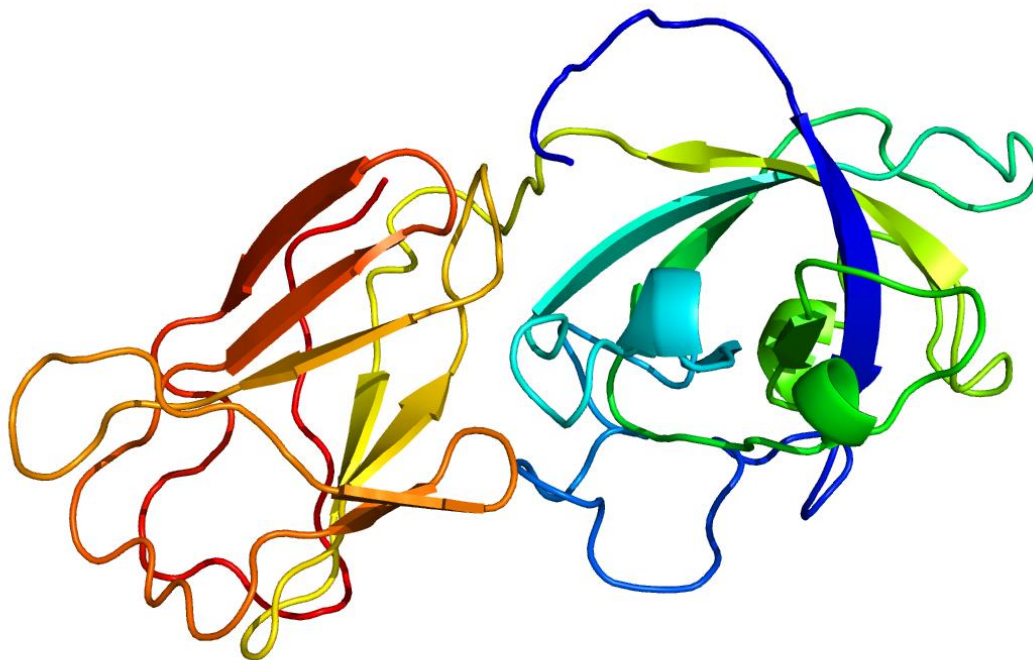
Locus: DCAR_025379

Gene Model: DCAR_025379

Description: DcEXPA-18

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>

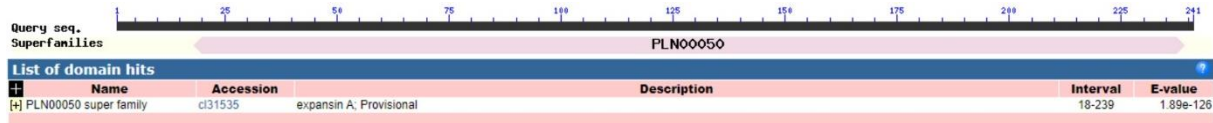
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>DcEXPA-18

MTVIFVIGILSIISSAEGYSGGGWINAHATFYGGGDASGTMGGACGYGNLMSQGYGT
DTTALSTALFNGLSCGACFQITCVNDPQWCLRGITITVTATNFCPPGGWCDPPNHFF
DLSEPVFLRIAQYRAGIVPVVYRRVPCMRSSGGIRFTINGHSYFNLVLITNVGGAGDVN
SVAIKGSNSQWQQMSRNWQNWQSNLYLNGQSLFRVTTSDGSTVVSYNVAPSGW
SFGQTYTGAQFR*

CDS (coding sequence)

>DcEXPA-18

ATGACTGTAATTTTCGTTATCGGAATTTTGTCGATTATAATCTCGTCTGCTGAAGG
GTATAGTGGAGGGGGCTGGATAAATGCTCATGCTACCTTTTATGGAGGTGGTGAT
GCTTCCGGGACAATGGGTGGGGCATGTGGTTATGGGAACCTGATGAGCCAGGGA
TATGGGACAGATACAACTGCACTGAGCACAGCCTTGTTAACAATGGCTTAAGCT
GTGGAGCATGCTTTCAAATCACTTGTGTGAATGATCCACAGTGGTGCCTCCGTGG
ACAATCACCGTCACCGCCACAACTTCTGCCACCAGGCGGCTGGTGTGATCCA
CAAACCACCACTTTGATCTCTCTGAGCCTGTCTTTCTTCGCATTGCTCAATACAG
AGCTGGAATTGTCCCTGTTGTTTACAGAAGGGTACCCTGCATGAGAAGTGGAGGA
ATTAGGTTACCATAAACGGTCACTCCTACTTCAACCTGGTCCTCATAACAAATGT
TGGAGGAGCCGGAGACGTAATTCAGTGGCTATAAAGGGTTCCAACCTCTCAATG
GCAACAAATGTCAAGGAATTGGGGACAGAACTGGCAGAGCAACAGCTACCTCAA
TGGGCAGAGCCTCTCTTTTAGGGTCACCACAAGTGATGGCAGCACCGTAGTGTCC
TATAATGTCGCACCTTCAGGCTGGTCTTTTGGACAGACCTATACTGGTGCCCAATT
CCGGTAG

Nucleotide

>DcEXPA-18

ATGACTGTAATTTTCGTTATCGGAATTTTGTCGATTATAATCTCGTCTGCTGAAGG
GTATAGTGGAGGGGGCTGGATAAATGCTCATGCTACCTTTTATGGAGGTGGTGAT
GCTTCCGGGACAATGGGTATGAATACATGCACCTCCTTACTAATACCAATTTATG
TTTTTACGAATGATAAACGATAATTAAGGCCTCTTGCTCTGACGGTATCTCCATT
GCTGTAAATAATGTAAAAAACGAGGTGGAGTGCTGAGCGTTTTTTAATTATTAGA
AAAATGAAAACTTGAACCTGATATATTTTATTGTACAGGTGGGGCATGTGGTTAT

GGGAACCTGATGAGCCAGGGATATGGGACAGATACAACCTGCACTGAGCACAGCC
TTGTTTAAACAATGGCTTAAGCTGTGGAGCATGCTTTCAAATCACTTGTGTGAATGA
TCCACAGTGGTGCCTCCGTGGAACAATCACCGTCACCGCCACAACTTCTGCCCA
CCAGGCGGCTGGTGTGATCCACCAAACCACCCTTTGATCTCTCTGAGCCTGTCTT
TCTTCGCATTGCTCAATACAGAGCTGGAATTGTCCCTGTTGTTTACAGAAGGTGA
GTAGTATTACATGATTTTTGGATATGTAACATAACAACCTATGTGATCAAGACTAA
ATTTGTTACATAATTAACCTGCTGATTAAATTTAATGCATTCATAGGGTACCCTGC
ATGAGAAGTGGAGGAATTAGGTTCCACCATAAACGGTCACTCCTACTTCAACCTGG
TCCTCATAACAAATGTTGGAGGAGCCGGAGACGTAAATTCAGTGGCTATAAAGG
GTTCCAACCTCTCAATGGCAACAAATGTCAAGGAATTGGGGACAGAACTGGCAGA
GCAACAGCTACCTCAATGGGCAGAGCCTCTCTTTTAGGGTCACCACAAGTGATGG
CAGCACCGTAGTGTCCATAATGTCGCACCTTCAGGCTGGTCTTTTGGACAGACCT
ATACTGGTGCCCAATTCCGGTAG