

## IDENTIFICATION

**Species:** *Asparagus officinalis*

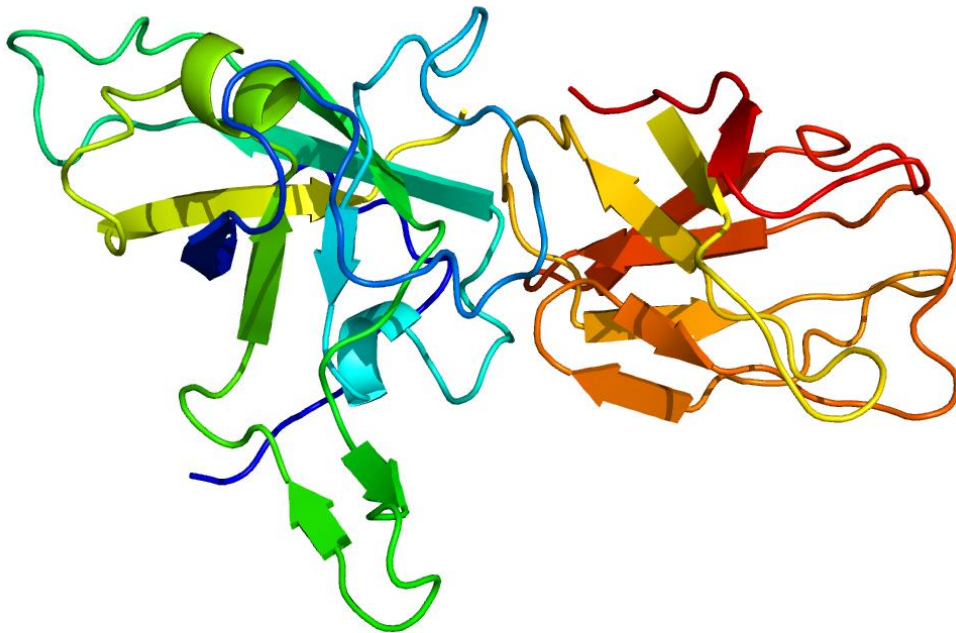
**Locus:** evm.model.AsparagusV1\_03.1682

**Gene Model:** evm.model.AsparagusV1\_03.1682

**Description:** AofEXPA-03

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

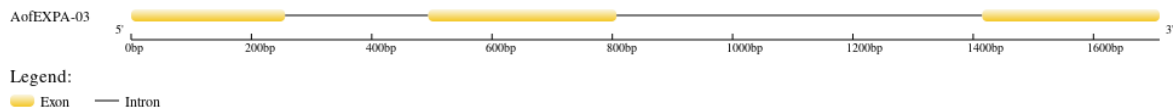
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Aofficinalis\\_V1\\_1](https://phytozome-next.jgi.doe.gov/info/Aofficinalis_V1_1)

KEGG: <https://www.genome.jp/entry/T05243>

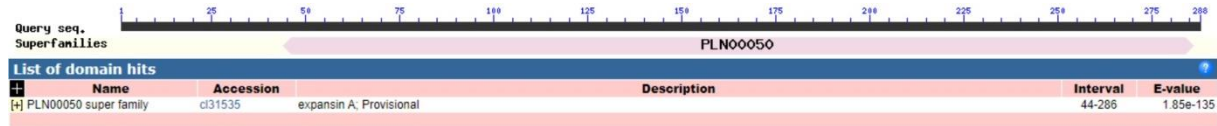
## EXTERNAL RESOURCES

-

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AofEXPA-03

MIPFTLQQTPLAPLSINPLFKPPLHSPLTHPKQAKRTFSSSLLMAFLGLFFVGSLSLLSS  
ALGNWEGWANAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNG  
LSCGSCYEIRCVDPRWCLQGSIVITATNFCPPNNALPNNAGGWCNPPQEHFDLSQPV  
FEQIAKYSAGIVPVSYRRKRGGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG  
WEQMSRNWQNWQSNLLDGQSLFSKVTISDGRITIVSYDAAPSSWSFGQTFGTGSQFL  
\*

### CDS (coding sequence)

>AofEXPA-03

ATGATACCCTTCACTCTTCAACAAACTCCCTTGGCTCCACTTTCAATAAACCTCT  
ATTTAAACCCCCCTCCACTCTCCTCTCACTACCCCAAGCAAGCAAAGAGAACA  
TTCTCCTCCTCTTTGCTAATGGCTTTTCTTGGGCTTTTCTTTGTGGGTTCTCTCAT  
TGCTCTCCTCTGCTCTTGGCAATGGAGAAGGATGGGCTAATGCTCATGCCACCTTC  
TATGGAGGTGGTGTATGCATCTGGCACAAATGGGTGGGGCTTGTGGGTATGGGAATT  
TGTACAGCCAAGGATATGGGACTAATACTGCAGCTCTGAGCACTGCTCTGTTCAA  
CAATGGTTTAAGCTGTGGGTCCTGTTATGAGATTAGGTGTGTTGATGATCCTAGGT  
GGTGCCTTCAAGGCTCCATTGTGATCACTGCCACCAATTTCTGCCACCAAACAA  
TGCTCTCCCTAATAATGCAGGGGGGTGGTGAATCCTCCACAAGAGCATTGAT  
CTCTCTCAGCCTGTCTTTGAGCAGATTGCCAAGTACAGTGCTGGAATTGTCCCTGT  
TTCTTACAGAAGGAAGAGAGGGGGTATAAGATTCACCATCAACGGCCACTCCTAC  
TTCAATCTCGTCCTCATACCAACGTAGGAGGGGCCGGAGACGTGCACTCTGTGT  
CAATCAAAGGGTCAAGGACAGGGTGGGAGCAAATGTCAAGAACTGGGGCCAA  
AACTGGCAGAGCAACTCCCTCCTCGACGGCCAATCCCTCTCTTTCAAGGTCACCA  
TTAGCGACGGCCGACCATTTGTCTCCTACGATGCTGCTCCTTCTTCATGGTCCTTT  
GGCCAGACCTTCACTGGTTCCCAATTCTCTAA

### Nucleotide

>AofEXPA-03

ATGATACCCTTCACTCTTCAACAAACTCCCTTGGCTCCACTTTCAATAAACCTCT  
ATTTAAACCCCCCTCCACTCTCCTCTCACTACCCCAAGCAAGCAAAGAGAACA  
TTCTCCTCCTCTTTGCTAATGGCTTTTCTTGGGCTTTTCTTTGTGGGTTCTCTCAT

TGCTCTCCTCTGCTCTTGGCAATGGAGAAGGATGGGCTAATGCTCATGCCACCTTC  
TATGGAGGTGGTGGTATGCATCTGGCACAATGGGTACATCTCTGCTAAAATTCTGCT  
TTAGCATAAAATTGCTGATAACCCCCTCGTCCATTCCTTCAGTAGCACTTATCATC  
CCGAGATTGGTTTCGAAAGTGCTAATAGAACAGTTGAGGGGTTATGTGTGCTGTT  
AAGGGTATGGACGAGGGGGTTATCTGCGATTTACCCTTTTTTTGTAATTATCTTTTG  
ATGATACTCGTTTCCTAAGCAGCTTTTTTTTTTTGTGTGTGTGTGTAGGTGGGGCTT  
GTGGGTATGGGAATTTGTACAGCCAAGGATATGGGACTAATACTGCAGCTCTGAG  
CACTGCTCTGTTCAACAATGGTTTAAGCTGTGGGTCCTGTTATGAGATTAGGTGTG  
TTGATGATCCTAGGTGGTGCCTTCAAGGCTCCATTGTGATCACTGCCACCAATTTT  
TGCCACCAAACAATGCTCTCCCTAATAATGCAGGGGGGTGGTGC AATCCTCCAC  
AAGAGCATTGATCTCTCTCAGCCTGTCTTTGAGCAGATTGCCAAGTACAGTGCT  
GGAATTGTCCCTGTTTCTTACAGAAGGTGACTTTTTTTTTGGGTAAC TTTCTGATA  
AATTACCATGGAATTTGATTCTTCACTTGGC NNNNNNNNNNTTATGTTAAGCTAC  
TTCTTTAAGGTGGTGGTTGTCGGCTTATTATTACAAGGGATTGTTGTTCCATTTTG  
GCTTGTGCATTTGGAGATAAAAAAAGGACTCTGGCTAGAAA ACTTTTTTTATTATT  
ATTTTAAACATCTAGGAAAGCTACTACTTTGTTGCATGCTTGTGCATGAGCTTACT  
GCTGCCTAGATTTAAAAAGGGTACTCTACATCTTACCTTTGACTAGGAACTTCTA  
TTTATAGAGAACTACTCAAAGATGGTTAAAATCTAGTTGAAATAGTAATAAGAC  
TGGTCAATCCTCCATAGGACCTAAGTGATGGTGAGAGGAGAGTAATCATAGTCAC  
ATTACTTAGAATTCACTATTTGACTTTACCTTAAAAGTTAATGGTTTAGTCTTAAT  
AAACGGACCCATAAGAAGAAATCCTAAAGCCGACCAGAGATGGACATAAGAAA  
ACTTAGTCGAAACTCGTTTAAGAATGATATGATAATATTCAACTTAACAAAGAAG  
AGAAAATAAACTCTATAACATGTAGGAAGAGAGGGGGTATAAGATTCACCATCA  
ACGGCCACTCCTACTTCAATCTCGTCCTCATCACCAACGTAGGAGGGGCCGGAGA  
CGTGC ACTCTGTGTCAATCAAAGGGTCAAGGACAGGGTGGGAGCAAATGTCAAG  
AAACTGGGGCCAAA ACTGGCAGAGCAACTCCCTCCTCGACGGCCAATCCCTCTCT  
TTCAAGGTCACCATTAGCGACGGCCGCACCATTGTCTCCTACGATGCTGCTCCTTC  
TTCATGGTCCTTTGGCCAGACCTTCACTGGTTCCCAATTCCTCTAA