

## IDENTIFICATION

**Species:** *Sesamum indicum*

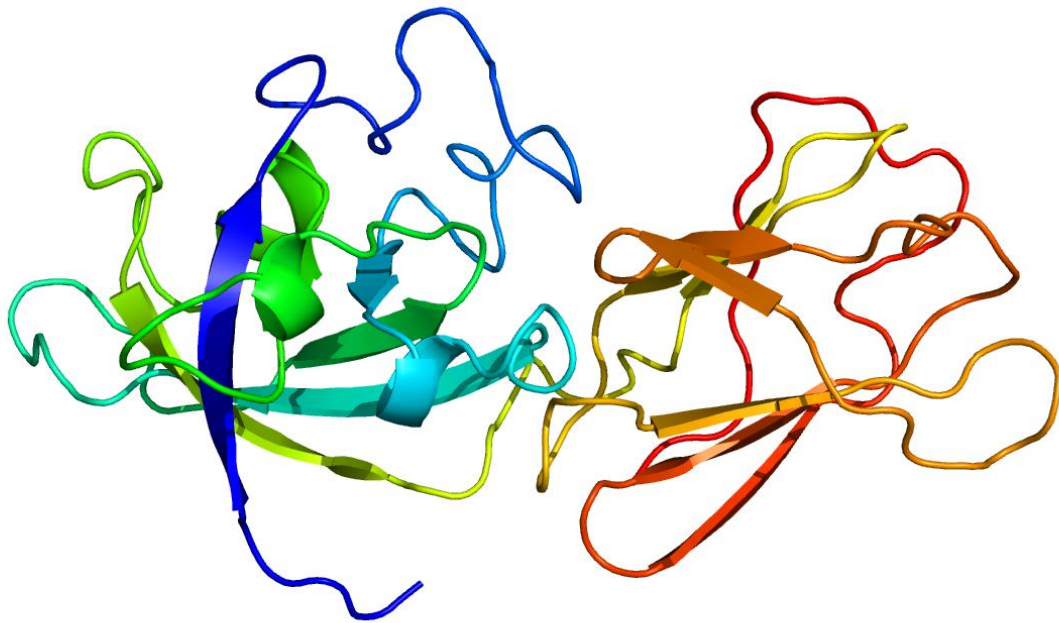
**Locus:** XP\_011098644

**Gene Model:** XP\_011098644.1

**Description:** SinEXPA-22

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

NCBI: <https://www.ncbi.nlm.nih.gov/genome/?term=Sesamum+indicum%5Borgn%5D>

KEGG: <https://www.genome.jp/entry/gn:T04135>

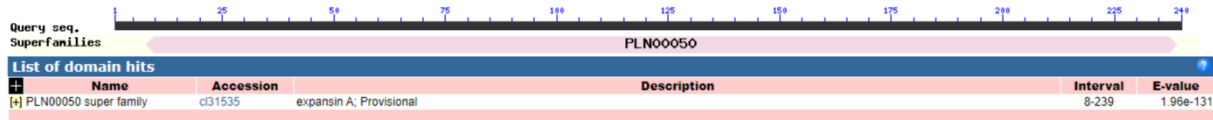
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SinEXPA-22

MTSFAVFLVGGFFSFVTSAYGYYGGWINAHATFYGGGDASGTMGGACGYGNLYSQG  
YGTNTAALSTALFNGLSCGACFQLVCVNDPQWCLRGSIIVTATNFCPPGGWCDPPN  
HHFDLSQPVFLRIAQYRAGIVPVLVYRRVPCRRSGGIRFTINGHSYFNLVLTNVGGAG  
DVQAVYIKGSRTAWQPMSRNWQNWQSN SYLNGQSLSFKVTTS DGRSVVSYNVAP  
PNWSFGQTFSGGQFR

### CDS (coding sequence)

>SinEXPA-22

CTCCCTCCACCCCTATTTATTCCCATCAAACACTTTATTCACCTTCCTCACAACCTCCT  
CCTCCTTCTGCACATGCTCAAACCTTTTAGCCTCTCTAGAGTGGAAATATGACTAG  
TTTTGCAGTTTTCTTAGTGGGTTTTTCTCGTTTGTGACATCTGCATATGGCTATTA  
TGGAGGTTGGATTAATGCTCATGCCACCTTCTATGGAGGAGGTGATGCATCTGGA  
ACAATGGGCGGGGCTTGTGGGTATGGAAACCTGTACAGCCAGGGATATGGAACCT  
AATACAGCAGCACTCAGCACAGCTCTGTTTAAACAATGGTTTGAGCTGTGGAGCAT  
GTTTTCAGTTGGTGTGCGTGAATGATCCACAATGGTGTCTACGGGGATCCATAAT  
CGTCACAGCCACCAATTTCTGCCCTCCAGGCGGGTGGTGTGATCCCCCAACCAC  
CACTTTGATCTCTCTCAGCCTGTTTTCTACGTATCGCACAGTATAGAGCCGGCAT  
CGTGCCCGTCTCTACAGAAGAGTGCCGTGCAGAAGAAGTGGGGGAATCAGGTT  
CACCATCAACGGCCACTCATATTTCAATCTAGTCCTCGTAACTAATGTCTGGGGGT  
GCTGGAGATGTACAGGCAGTGTACATCAAGGGATCAAGAACTGCATGGCAGCCA  
ATGTCAAGAACTGGGGCCAAAACCTGGCAGAGCAATTCATACCTCAATGGACAA  
AGCCTGTCTTTCAAGGTTACCACAAGCGATGGCCGAAGCGTCGTCTCGTACAACG  
TTGCTCCGCCCAACTGGTCTTTTGGCCAGACGTTCTCCGGAGGTCAATTCCGCTAG  
GCCAGTACTGCAACCAGCGATCAACGGGAGTATGGTGTATAAACTGAACTGTT  
TAACTAATTATAATCTAGTTTAGTGCGAGAAAAGACACTATAAGAATCCAATATA  
TACTTAAAAGGGCTTATTTTGAAGGAGCCCTAGCTACTCCTTAATTTGCAGTGAGT  
AGTATATATCTACTTCACA

### Nucleotide

>SinEXPA-22

TGGTACAACATCACATGAGTTTTGATCTTAATAATGTAAGGGCTGGACCGCAGTT  
TAATGTTGAAATATCGTTTTTTGATTTCTGGAAGTCGCAAGTTTGGCTGAGAAA  
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TGGCCGTTGATGGTGAACCTGATTCCCCACTTCTTCTGCACGGCACTCTGTACGA  
CAAACATGATCAAGCAAATCTCCTTAATTAGTTATTATTACAATAGGTAAAAGT  
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