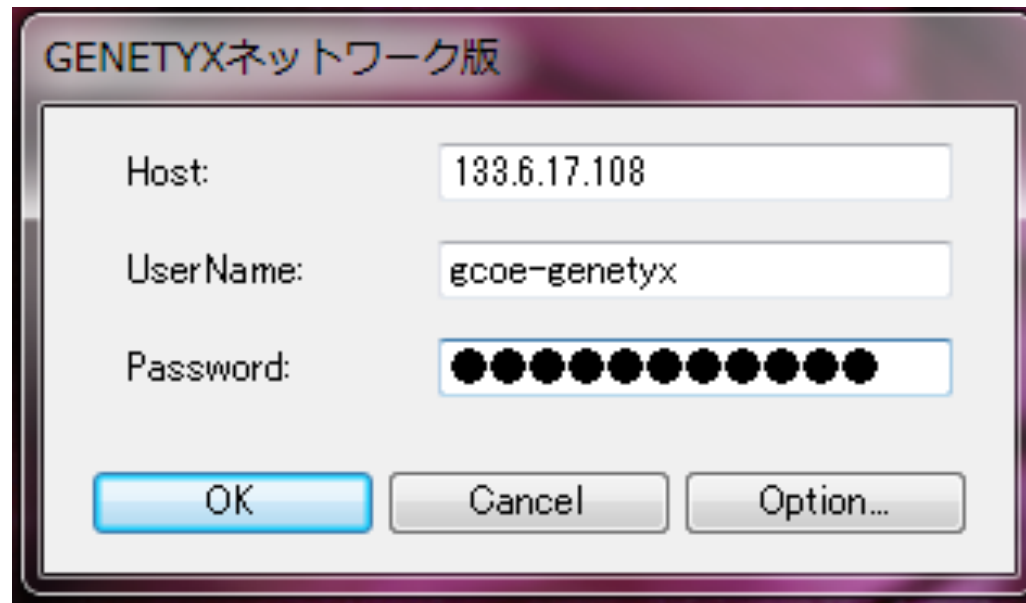


内容

配列解析ソフト”Genetyx”を試してみる

Genetyx ネットワーク版の起動



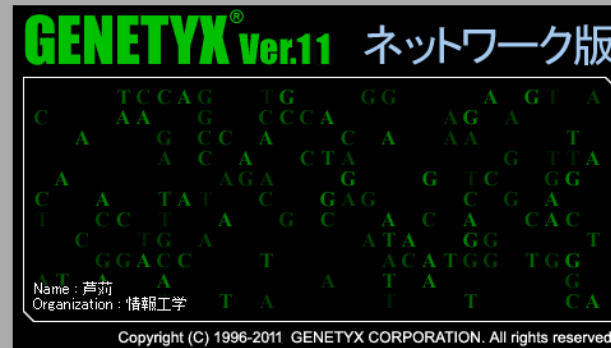
A screenshot of the GENETYXネットワーク版 (Genetyx Network Edition) login dialog box. The dialog has a title bar with the text "GENETYXネットワーク版". Inside, there are three input fields: "Host:" with the value "133.6.17.108", "UserName:" with the value "gcoe-genetyx", and "Password:" with a masked password represented by 12 black dots. At the bottom, there are three buttons: "OK" (highlighted in blue), "Cancel", and "Option...".

授業HPからHost, User Name, Passwordをコピー＆ペースト

Genetyx ネットワーク版の起動

↑②新規作成

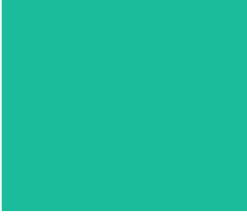
①Genetyxの起動



Ready

The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa* ssp. *japonica* cv. Nipponbare genome sequencing by the **International Rice Genome Sequencing Project** with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation.

➔ More

GBrowse Browse rice genome and genes ★★★★★	BLAST Execute NCBI BLAST against rice genome or genes ★★★★★		BLAT Align your sequence with rice genome ★★★★★
ID Converter Convert IDs between RAP and MSU ★★★★★		Keyword search Keywords Search Advanced	
Batch Retrieval ★★★★★			

What's New

NEWS

04/Aug/2017 **NEW**

- We have updated CGSNL annotation and manual curation data (see [update_2017-08-04.txt](#)).
- miRNA data from miRBase and FST data of the Taiwan Rice Insertional Mutant (TRIM) have been updated.

14/Apr/2017

- We have updated CGSNL annotation and manual curation data (see [update_2017-04-14.txt](#)).

05/Aug/2016

- We have updated CGSNL annotation and manual curation data (see [update_2016-08-05.txt](#)).

09/Mar/2016

➔ More

BLAST

Query sequence

☒ Enter query sequence in FASTA format

☐ Upload FASTA file [ファイルを選択](#) [ファイル未選択](#)

Search database

☒ DNA database

Rice genome sequence (IRGSP-1.0)

☐ Protein database

Rice genes (translated CDS)

Search program

blastn (DNA query vs DNA database)

Advanced options



Submit

Reset

BLAST

Query sequence

☒ Enter query sequence in FASTA format

```
>expansin genome  
ACCAACACATTGTTTGTGTTGTCCTAAAACACTAATAATTTCTCATATATTTTATAA  
AGTGTAACCTAATTTGACCAAAACCACAAAACATAGGGAAAGATGAGAAGGAAGAA  
GATAAGAATGATCATAGGTAATAGTTGGCTTGATTTCCATCTTGTTATTGTTTGGGA  
AAGCTGAATTTCCGTGCTAGGCTAGGATCTTAAGTTCTTAATACAAATTCCTAACT  
AGAATTTTGGACTGATCCACGGTGTCTGACTCAACTACAGTTGGGGATGCCATGT  
TGGTATTTAGATTTGTCGGGAGCTAGTGTTCCTACTTCATTATTTAAACATTTTT  
ATCCTTAAATAAATATTGGAATATTCATAATAGTGGATGACAAAGATGAACACA  
ACACAAAATTAAGTTGAAATATGCACCTTTCCATGTTTTAAACACAGTAATCCATT  
TTCCATCTGTACTTTGACTGGGTATTGTACTTATTGATTGAGGTAGCATGAAACTC
```

☐ Upload FASTA file ファイルを選択 ファイル未選択

Search database

☐ DNA database

Rice genome sequence (IRGSP-1.0)

☒ Protein database

Rice genes (translated CDS)

Search program

blastx (Translated DNA query vs Protein database)

Advanced options

Submit

Reset

BLAST result

Query: expansine (6000 letters)

Hit	Description	Length	Bit score	E-value
Os04t0228400-01 	Expansin precursor (Alpha-expansin OsEXPA1).	262 aa	446	8e-151
Os06t0718100-01 	Similar to Alpha-expansin precursor.	264 aa	333	1e-98
Os01t0823100-01 	Alpha-expansin OsEXPA2.	252 aa	331	1e-96
Os03t0155300-00 	Similar to Alpha-expansin precursor.	251 aa	330	4e-93
Os03t0155500-00 	Similar to Expansin-A25.	243 aa	319	9e-93
Os02t0267200-00 	Alpha-expansin OsEXPA13.	263 aa	319	1e-92
Os01t0248900-01 	Alpha-expansin, Mediation of the cell extension and growth, Root system architecture	252 aa	314	2e-92
Os03t0428700-01 	Similar to Expansin-A31.	257 aa	312	8e-91
Os02t0268400-00 	Similar to Expansin-A23.	262 aa	313	1e-90
Os02t0268050-00 	Similar to Expansin-A23.	262 aa	313	1e-90
Os02t0267700-00 	Similar to Expansin-A14.	252 aa	314	2e-90
Os05t0477600-01 	Alpha-expansin OsEXPA4.	247 aa	312	5e-90
Os02t0267900-00 	Similar to Expansin-A24.	279 aa	313	1e-89
Os02t0268600-00 	Similar to Expansin-A22.	275 aa	311	4e-89
Os10t0439200-00 	Similar to Expansin-A28.	245 aa	299	2e-88
Os10t0439100-00 	Similar to cDNA clone:002-180-G03, full insert sequence.	256 aa	309	6e-88
Os01t0274500-00 	Similar to Expansin-A11	235 aa	298	4e-86

Os04t0228400-01



Details

DB reference

Gene Ontology (GO)

Biological Process: plant-type cell wall

Cellular Component: extracellular region

Functional domain (InterPro)

Expansin (IPR002963)

Expansin/pollen allergen, DPBB domain

Pollen allergen/expansin, C-terminal (

Expansin/Lol pl (IPR007118)

Barwin-related endoglucanase (IPR00

Barwin-like endoglucanase (IPR01473

Full-length cDNA

J023022N21 (Online Clone Ordering

Expression Databases

TENOR (Os04t0228400-01)

RiceXPro (AK069548)

Others

Oryzabase (2964)

KEGG (Os04t0228400-01)

Os04t0228400-01



Details

DB references

Sequences

Gene Structure

Transcript

1135 bp

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1).
GCCATTAGCAGCATTCCACGGCAGCAGCGCGGCACACATGGCCGGCTCGTCAGCCG
CAACGTCGTGTGCTCGGTTCTCTGGCATTGCTGGCGACATGCCTCTCTGGAACGAGGCCG
CATCGTTCACGGCGTCCGGCTGGAACAAGGCGTTTCGCCACCTTCTACGGCGGCACTGACG
CTTCAGGAACGATGGGTGGGCGGTGGGTACGGGACCTGTACTCGACGGGTACGGGA
CGAACACGGCGGCGCTGAGCACGCTGCTGTTCAACAGCGGGCGCTGTCGGGCGAGTGCT
ACCGGATCATGTGCGACTACAGCGGCAGAGCGGTTCTGCATCTCCGGCAGCTCGGTGA
CCATCAGCGGACCAACCTCTGCCCGCGAAGTACGGCTCCCCAACGACGCGCGGGGT
GGTGCAACCCGCGCGGCGAGCACTTCGACATGGCCGAACCGCGGTGGTCAAGATCGGG
TCTACGTCGGCGGCATCGTGCCGTGATGTACAGCGGGTGCCGTGCGCAAGCAGGGCG
GGGTGAGGTTACCATTCAACGGCAGGACTACTTCGAGCTGGTGCTCGTCCAACGCTCG
GCGGCGTCCGCTCCATCCAGTCCGTGTGATCAAGGGGTCGAGGACCGGTGGATGGCCA
TGTCAGGAATTGGGCGCTCAACTGGCAGTCCAACGCCTACCTCGACGCCAGAGCCTGT
CGTTCGAAGTCAACAGCAGCAGCGGCAGACGCTACCTTCTCTGACGTGCGCCGCGGG
GCTGGACGTCGCGCCAGACCTTCTCGACCTCACAGCAGTTCCTTAAGTAATTAATATT
AATGAGTTATTACTGGTCCATTATATATGTGTTTAATTCGAGGCTATATATATCATCGG
CGTCGGCGGTAAAGACTAAAGATATATTACTAGTAGCTGTTTGGGTTGCCCAAGTTT
GGAGCATGCGCGCACAGTGTTTGGTGTGGCGAGCTATATATATGATTGCAAGCTAAGG
ACACCTGCTTTTTTCAATGCGAATTAAGGCGTATATATATGTACAGTTTGCAGAGTGCT
TGCCAATCGATGATCGGCATGCTTTACTGTAACGACCACACAAGGAGTTTTCACT

CDs

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1).
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CTCCTCTGGAACGAGGCGCATCTGTTTCAGGCGTCCGGCTGGAACAAGGCGTTTCGCCACC
TTCTACGGCGCAGTGACGCTTCAGGAACGATGGGTGGGCGCTGTGGGTACGGGACCTG
TACTCGACGGGTACGGGACGAACACGGCGCGCTGAGCACGGTGCTGTTTCAACGACGGG
GCGTCGTGCGGCGAGTGCTACCGGATCATGTGCGGACTACAGCGGCAGAGCGGTTCTGC
ATCTCCGGCAGCTCGGTGACCATCAGCGGACCAACCTCTGCCCGCCGAATACGCGGCTC
CCCAACGACGCGCGGGGTGGTGCAACCCGCGCGGCGAGCACTTCGACATGGCCGAACCG
GCGTGGCTCAAGATCGGCTGTACGTCGGCGGCATCGTGCCGCTGATGTACAGCGGGTG
CCGTGCGCAAGCAGGCGGGGTGAGGTTCAACATCAACGGCAGGGACTACTTCAGAGTGT
GTGCTCGTCTCCAACGTGCGGCGGCTCGGCTCCATCCAGTCGGTGTGATCAAGGGGTCG
AGGACCGGGTGGATGGCCATGTCCAGGAATTGGGCGCTCAACTGGCAGTCCAACGCCTAC
CTCGACGGCCAGAGCCTGTCTGTTCAAGGTACCAGCAGCAGCGGCAGACGCTACCTTC
CTCGAGCTGCCCCGCGGGCTGAGCGTTCGCGCAGACCTTCTCGACCTCACAGCAGTTC
TCTTTAA

Protein

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1).
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PNDAGWCNPNRQHFDMAEPAWLKIGVVGIVPVMYQRVPCAKGGVRFITNGRDYFEL
VLVSNVGGVGSIQSVSIKGRSRTGMWMSRNWGNWQSNAYLDGQSLFKVTSSDGQTYTF
LDVAPAGWTFQGTFSTSQQS*

Os04t0228400-01



Details

DB references

Sequences

Gene Structure

5'UTR

chr04:8599014..8599054 (+ strand) : 41 bp

CDs

chr04:8599055..8599208 (+ strand) : 154 bp

chr04:8599309..8599940 (+ strand) : 632 bp

3'UTR

chr04:8599941..8600248 (+ strand) : 308 bp

FASTA

>Os04t0228400-01 class=Sequence position= chr04:8599014..8600248 (+ strand)
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CTGGCATTCG TGCGCAGATG CCTCCTCTGG AACGAGGCC CATCGTTCAG GCGTCCGGC TGGAAACAG CGTTCGCCAC
CTTCTACGGC GGCAGTGACG CTCACGGAAC GATGGGTAAG TTCGTAGCTA GCTAGTACT GTAGCTAGGA ATGGATCCAT
CGTGCAATCG GTGACGTTGG TTCAATGTGA TCGGTGTGCT CGTGTGTGTG TGCAGGTGGG GGGTGTGGGT ACGGGGACCT
GTACTCGACG GGGTACGGGA CGAACACGGC GCGCTGAGC ACGGTGCTGT TCAACGACGG GCGTCTGTC GGGCAGTGCT
ACCGGATCAT GTGCGACTAC CAGGCGGACA GCGGTTCTG CATCTCCGGC ACGTCGGTGA CCATCAGCGC GACCAACCTC
TGCCCGCCGA ACTACGCGCT CCCCACGAC GCGCGCGGGT GGTGCAACCC GCGCGCGCAG CACTTCGACA TGGCGGAACC
GGCGTGGCTC AAGATCGGCG TCTACGTCG CGGCATCGTG CCGGTGATGT ACCAGCGGTT GCGTCCGCC AAGCAGGCGG
GGGTGAGGTT CACCATCAAC GGCAGGAGCT ACTTCGAGCT GGTGTCGCTC TCCAACGTCG GCGGCTCGCG CTCATCCAG
TCGGTGTGCA TCAAGGGGTC GAGGACCGGG TGGATGGCCA TGTCCAGGAA TTGGGGCGTC AACTGGCAGT CCAACGCTTA
CTTCGACGGC CAGAGCCTGT CGTTCAGGT CACCAGCAGC GACGCCAGA CGTCACTT CCTCGAGCTC GCCCGCGGG
GCTGGACGTT CGGCCAGACC TTCTCGACCT CACAGCAGT CTCTTAAGTA ATTAATATT AATGAGTTAT TACTGTCCA
TTATATATG TGTTTAATTC CGAGCGTATA TTATCATCG CGTCGGGCTG TAAAGACTAA AGATATATA CTAGTAGCTG
TTTGGGTTG CCACAAGTTT GGAGCATGG CGCACAAAGT TTTGGTGGG CGAGCTATAT ATATGATTG CAAGCTAAGG
ACACCTGCTT TTTTCAATGC GAATTAACG GGTATATA TGTACAGTT GCGAGTGTCT TGCCAATCA TGTGCGCAT
GCTTACTGT AACCAGCACA CAAGGAGTTT TCAGT

アミノ酸配列をコピー

イネのゲノムに存在しているEXPANSINを系統解析する

配列を並べて(Alignment)して、配列を元に遺伝子群を分類する

FASTAフォーマットで読み込む

DNA の塩基配列やタンパク質のアミノ酸配列のalignmentを行うための記述形式

(例)

>Name1

MADG....(配列).....

>Name2

MADA....(配列).....

>Name3

MADA....(配列).....

```
>OsEXPA1
MAGSSAATSCARFLALLATCLLWNEAASFTASGWNKAFATFYGGSDASGT
MGGACGYGDLYSTGYGTNTAALSTVLFNDGASCGQCYRIMCDYQADRRFC
ISGTSVTITATNLCPNYPALPNDAGWCNPPRQHFDMAEPALWKIGVYVG
GIVPVMYQVRVPCAKQGGVRFTINGRDYFELVLVSNVGGVGSIQSVSIKGS
RTGWMAMSRNWGVNWQSNAYLDGQSLSFKVTSSDGQTLTFLDVAPAGWTF
GQTFSTSQQFS
> OsEXPA2
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GYGNLYSTGYGTNTAALSTVLFNDGAACGSCYELRCDNDGQWCLPGSVTV
TATNLCPNYPALPNDGGWCNPPRPHFDMAEPALQIGVYRAGIVPVSYR
RVPCVKKGGIRFTINGHSYFNLVLTNVAGPGDVQSVSIKGSSTGWQPM
RNWQNWQSNYSYLDGQSLSFQVAVSDGRVTVTNNVVPAGWQFGQTFEGGQ
F
> OsEXPA3
MLSGMEKQPAMLLVLVTLCAFAKXSVASAFATFYGGKDGSCGTMGGAC
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TITATNLCPNWPALPSNCGWCNPPRPHFDMSQPAWENIAVYQAGIVPVN
YKRVPCQRSGGIRFAISGHDYFELVTVTVNGGSGVVAQMSIKGSNTGWMA
MSRNWGANWQSNAYLAGQSLSFIVQLDDGRKVTAWNAPSNWFFGATYST
SWVQF
> OsEXPA4
MAIAGVLFLLFLARQASAAGYGGWQSAHATFYGGGDASGTMGGACGYGNL
YSQGYGTNTAALSTALFNDGAACGSCYELRCDNAGSSCLPGSITVTATNF
CPPNYGLPSDDGGWCNPPRPHFDMAEPALHIAQYRAGIVPVSFRRVPCV
KKGGVRFTVNGHSYFNLVLTNVAGAGDVRSVSIKGSRTGWQPMNRNWGQ
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> OsEXPA5
MSSRRDVLAVVLVAALLPPALSRGLWLGHGHLGHGHRWRAPHVGGHGGQ
QGPQQHAPLGGGWSSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTA
ALSTALFNNGLSGACFEVRCDAAGGGSHSCLPGSVVVTATNFCPPNNAL
PSDDGGWCNPPRAHFDMSQPVFQRIALFKAGIVPVSYRRVACQKKGGIRF
TINGHSYFNLVLTNVGGAGDVHAVAVKSERSAAWQALSRNWQNWQSAAL
LDGQALSFRVTTGDGRSVVSNNAVPRGWSFGQTFSGAQFN
> OsEXPA6
MAPPLLLLLLASLLLVAARRALGLGLGQWQPGHATFYGGGDASGTMGGACG
YGNLYSQGYGTNTAALSTALFNRLSCGSCYRTRCAGDHRRSCLPGCATV
```

BLAST result

Query: expansine (6000 letters)



Hit	Description	Length	Bit score	E-value
Os04t0228400-01 	Expansin precursor (Alpha-expansin OsEXPA1).	262 aa	446	8e-151
Os06t0718100-01 	Similar to Alpha-expansin precursor.	264 aa	333	1e-98
Os01t0823100-01 	Alpha-expansin OsEXPA2.	252 aa	331	1e-96
Os03t0155300-00 	Similar to Alpha-expansin precursor.	251 aa	330	4e-93
Os03t0155500-00 	Similar to Expansin-A25.	243 aa	319	9e-93
Os02t0267200-00 	Alpha-expansin OsEXPA13.	263 aa	319	1e-92
Os01t0248900-01 	Alpha-expansin, Mediation of the cell extension and growth, Root system architecture	252 aa	314	2e-92
Os03t0428700-01 	Similar to Expansin-A31.	257 aa	312	8e-91
Os02t0268400-00 	Similar to Expansin-A23.	262 aa	313	1e-90
Os02t0268050-00 	Similar to Expansin-A23.	262 aa	313	1e-90
Os02t0267700-00 	Similar to Expansin-A14.	252 aa	314	2e-90
Os05t0477600-01 	Alpha-expansin OsEXPA4.	247 aa	312	5e-90
Os02t0267900-00 	Similar to Expansin-A24.	279 aa	313	1e-89
Os02t0268600-00 	Similar to Expansin-A22.	275 aa	311	4e-89
Os10t0439200-00 	Similar to Expansin-A28.	245 aa	299	2e-88
Os10t0439100-00 	Similar to cDNA clone:002-180-G03, full insert sequence.	256 aa	309	6e-88
Os01t0274500-00 	Similar to Expansin-A11	235 aa	298	4e-86

Os04t0228400-01



Details

DB reference

Gene Ontology (GO)

Biological Process: plant-type cell wall

Cellular Component: extracellular regio

Functional domain (InterPro)

Expansin (IPR002963)

Expansin/pollen allergen, DPBB domain

Pollen allergen/expansin, C-terminal (

Expansin/Lol pl (IPR007118)

Barwin-related endoglucanase (IPR00

Barwin-like endoglucanase (IPR01473

Full-length cDNA

J023022N21 (Online Clone Orderin

Expression Databases

TENOR (Os04t0228400-01)

RiceXPro (AK069548)

Others

Oryzabase (2964)

KEGG (Os04t0228400-01)

Os04t0228400-01



Details

DB references

Sequences

Gene Structure

Transcript

1135 bp

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1) .
GCCATTAGCAGCATTCCACGGCAGCAGCAGCGCGCACACATGGCCGGCTCGTCAGCCG
CAACGTCGTGTGCTCGGTTCTCTGGCATTGCTGGCGACATGCCTCTCTGGAACGAGGCCG
CATCGTTCACGGCGTCCGGCTGGAACAAGGCGTTTCGCCACCTTCTACGGCGGCACTGACG
CTTCAGGAACGATGGGTGGGCGGTGGGTACGGGACCTGTACTCGACGGGTACGGGA
CGAACACGGCGGCGCTGAGCACGCTGCTGTTCAACAGCAGGGGCGTCTGCGGGCAGTGCT
ACCGGATCATGTGCGACTACAGGCGGACAGGGGTTCTGCATCTCCGGCAGCTCGGTGA
CCATCAGCGGACCAACCTCTGCCCGCGAAGTACGGCTCCCCAACGACGCGCGGGGT
GGTGCAACCCGCGCGGCGAGCACTTCGACATGGCCGAACCGGCGTGGTCAAGATCGGG
TCTACGTCGGCGGCATCGTGCCGTGATGTACCAGCGGGTGCCGTGCGCAAGCAGGGCG
GGGTGAGGTTACCATTCAACGGCAGGACTACTTCGAGCTGGTGCTCGTCCAACGCTCG
GCGGCGTCCGCTCCATCCAGTCGGTGTGATCAAGGGGTCGAGGACCGGTGGATGGCCA
TGTCAGGAATTGGGCGCTCAACTGGCAGTCCAACGCCTACCTCGACGCCAGAGCCTGT
CGTTCGAAGTCAACAGCAGCAGCGCCAGACGCTACCTTCTCTGACGTCGCCCCGGCGG
GCTGGACGTCGCGCCAGACCTTCTCGACCTCACAGCAGTTCCTTAAGTAATTAATATT
AATGAGTTATTACTGGTCCATTATATATGTGTTTAATTCGAGCGCTATATATCATCGG
CGTCGGCGGTAAAGACTAAAGATATATTACTAGTAGCTGTTTGGGTTGCCCAAGTTT
GGAGCATGCGCGCACAAAGTGTGTTGGTGGGAGCTATATATATGATTGCAAGCTAAGG
ACACCTGCTTTTTTCAATGCGAATTAAGAGGCTATATATATGACAGTTTGCAGAGTGCT
TGCCAATCGATGATCGGCATGCTTTACTGTAACGACCACACAAGGAGTTTTCACT

CDs

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1) .
ATGGCCGGCTCGTCAGCCGCAACGTCGTGTGCTCGGTTCTCTGGCATTGCTGGCGACATGC
CTCCTCTGGAACGAGGCGCATCGTTTCAGGCGTCCGGCTGGAACAAGGCGTTTCGCCACC
TTCTACGGCGCAGTGACGCTTCAGGAACGATGGGTGGGCGCTGTGGGTACGGGACCTG
TACTCGACGGGTACGGGACGAACACGGCGCGCTGAGCACGGTGCTGTTCAACGACGGG
GCGTCGTGCGGCGAGTGTACCGGATCATGTGCGGACTACAGCGGACAGCGGTTCTGC
ATCTCCGGCAGCTCGGTGACCATCAGCGGACCAACCTCTGCCCGCCGAATACGCGGCTC
CCCAACGACGCGCGGGTGGTGCAACCCGCGCGGCGAGCACTTCGACATGGCCGAACCG
GCGTGGCTCAAGATCGGCTGTACGTCGGCGGCATCGTGCCGCTGATGTACCAGCGGGTG
CCGTGCGCAAGCAGGCGGGGTGAGGTTCAACATCAACGGCAGGGACTACTTCAGAGCTG
GTGCTCGTCTCCAACGTGCGGCGGCTCGGCTCCATCCAGTCGGTGTGATCAAGGGGTCG
AGGACCGGGTGGATGGCCATGTCCAGGAATTGGGCGCTCAACTGGCAGTCCAACGCCTAC
CTCGACGGCCAGAGCCTGTGCTTCAAGGTACCAGCAGCAGCGCCAGACGCTACCTTC
CTCGAGCTGCCCCGGCGGCTGAGCGTTCGCGCAGACCTTCTCGACCTCACAGAGTTC
TCTTTAA

Protein

>Os04t0228400-01 Expansin precursor (Alpha-expansin OsEXPA1) .
MAGSSAATSCARFLALLATCLLWNEAASFASGNWKAFAFYGGSDASGTMGGACGYGDL
YSTGYGNTAALSTVLFDNGASCCQYRIMCDYQADRRFCISGTSVTITATNLCPNPYAL
PNDAGWCNPNRQHFDMAEPAWLKIGVYVGGIVPVMYQRVPCAKGGVRFITNGRDYFEL
VLVSNVGGVGSIQSVSIKGSRTGMWMSNRNWNWQSNAYLDGQSLFKVTSSDGQTYTF
LDVAPAGWTFQGTFSTSQQS*

Os04t0228400-01



Details

DB references

Sequences

Gene Structure

5'UTR

chr04:8599014..8599054 (+ strand) : 41 bp

CDs

chr04:8599055..8599208 (+ strand) : 154 bp

chr04:8599309..8599940 (+ strand) : 632 bp

3'UTR

chr04:8599941..8600248 (+ strand) : 308 bp

FASTA

>Os04t0228400-01 class=Sequence position= chr04:8599014..8600248 (+ strand)
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CTGGCATTCG TGCGGACATG CCTCCTCTGG AAGCAGGCGG CATCGTTTAC GCGTCCGGG TGGAAACAG CGTTCGCCAC
CTTCTACGGC GGCAGTGACG CTCACAGAAC GATGGGTAAG TTCGTAGCTA GCTAGTACT GTAGCTAGGA ATGGATCCAT
CGTGCAATCG GTGACGTTGG TTCAATGTGA TCGTGTGCTG CGTGTGTGTG TGCAGGTGGG GGGTGTGGGT ACGGGGACCT
GTACTCGACG GGGTACGGGA CGAACACGGC GCGCTGAGC ACGTGTCTGT TCAACGACGG GCGTCTGTC GGGCAGTGTCT
ACCGGATCAT GTGCGACTAC CAGGCGGACA GCGGTTCTG CATCTCCGGC ACGTCGGTGA CCATCAGCGG GACCAACCTC
TGCCCGCCGA ACTACGCGCT CCCCACGAC GCGGCGGGGT GGTGCAACCC GCGCGGCGAG CACTTCGACA TGGCGGAACC
GGCGTGGCTC AAGATCGGCG TCTACGTCG CGGCATCGTG CCGGTGATGT ACCAGCGGAT GCGTCCGCC AAGCAGGCGG
GGGTGAGGTT CACCATCAAC GGCAGGAGCT ACTTCGAGCT GGTGTCGTC TCCAACGTCG GCGGCGTCGG CTCATCCAG
TCGGTGTGCA TCAAGGGGTC GAGGACCGGG TGGATGGCCA TGTCCAGGAA TTGGGGCGTC AACTGGCACT CCAACGCGTA
CTTCGACGGC CAGAGCCTGT CGTTCAGGT CACCAGCAGC GACGCCAGA CGTCACTT CCTCGAGCTC GCCCGCGGG
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TTATATATG TGTTTAATTC CGAGCGTATA TTATCATCG CGTCGGGCTG TAAAGACTAA AGATATATA CTAGTAGCTG
TTTGGGTTG CCACAAGTTT GGAGCATGG CGCACAAGT TTTGGTGGG CGAGCTATAT ATATGATTG CAAGCTAAGG
ACACCTGCTT TTTTCAATGC GAATTAACG GGTATATATA TGTACAGTT GCGAGTGTCT TGCCAATCA TGTGCGCAT
GCTTACTGT AACCAGCACA CAAGGAGTTT TCACCT

アミノ酸配列をコピー

Alignment

今回は授業用にBLAST検索の結果の中からイネのEXPANSINを集めて既にFASTAフォーマットにしてあるファイルを使用する

1. “OsEXPA”を開く
2. コピーしてwordに張り付ける
3. ファイル→保存 (Ctrl + S)
4. ファイルの種類”書式なし (*.txt)”を選択
5. デスクトップに保存

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>OsEXPA1↓
MAGSSAATSCARFLALLATCLLWNEAASFTASGWNKAFATFYGGSDASGT↓
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F↓
> OsEXPA3↓
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> OsEXPA4↓
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> OsEXPA5↓
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TINGHSYFNLVLTNVGAGDVHVA/VKSERSAAWQALSNNWQGNWQSA↓
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[18. B1遺伝子cDNA](#)

[19. B2遺伝子cDNA](#)

[20. B3遺伝子cDNA](#)

[21. B4遺伝子cDNA](#)

[22. B5遺伝子cDNA](#)

[23. B1遺伝子アミノ酸](#)

[24. B2遺伝子アミノ酸](#)

[25. B3遺伝子アミノ酸](#)

[26. B4遺伝子アミノ酸](#)

[27. B5遺伝子アミノ酸](#)

[28. C1遺伝子アミノ酸配列](#)

[29. C2遺伝子アミノ酸配列](#)

[30. C3遺伝子アミノ酸配列](#)

[31. C4遺伝子アミノ酸配列](#)

[32. Gid1-GenomicDNA](#)

[33. Gid1-cDNA](#)

[34. OsExpansin Genome seq](#)

[35. OsExpansin genes](#)



[36. OsExpansin1 アミノ酸配列](#)

[37. 他の植物のExpansin genes](#)

[38. APETALA2](#)

[39. salinity stress](#)

[Host:133.6.17.108](#)

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制限酵素マップ：

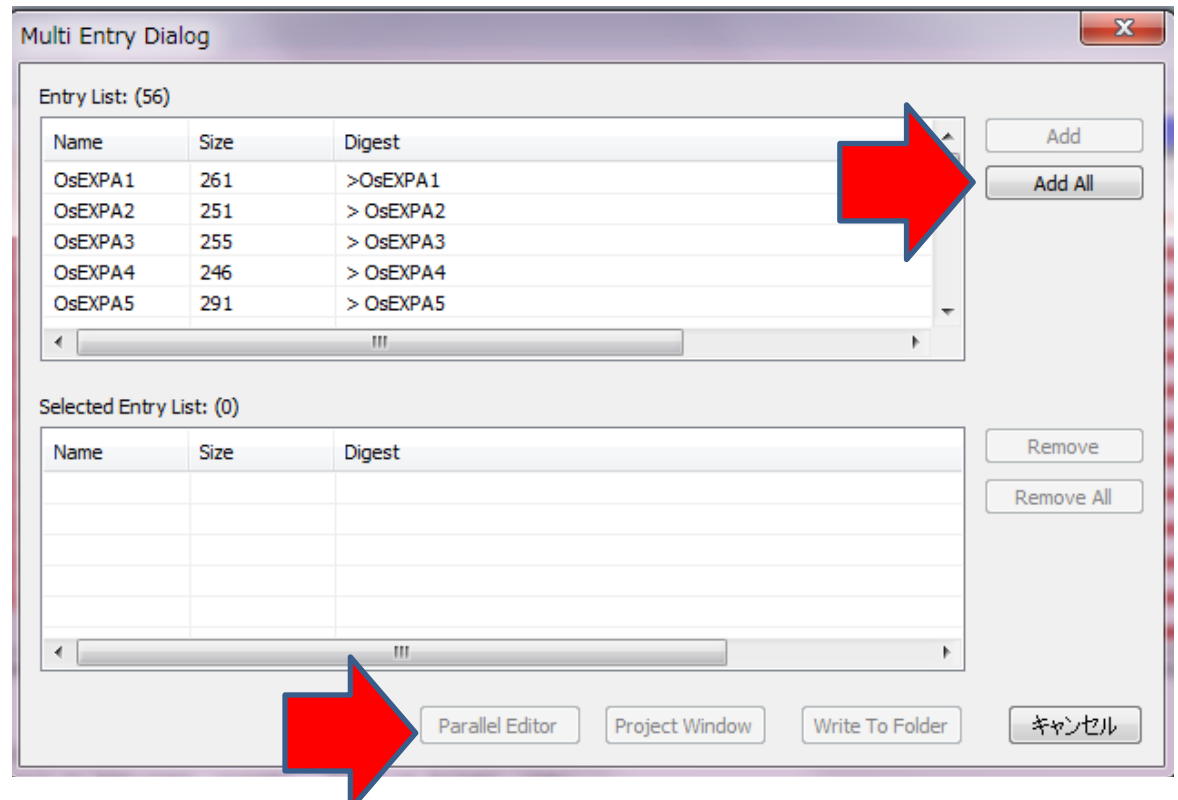
1. [WebCutter](#) ：制限酵素切断部位解析ソフト

>OsEXPA1
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Alignment

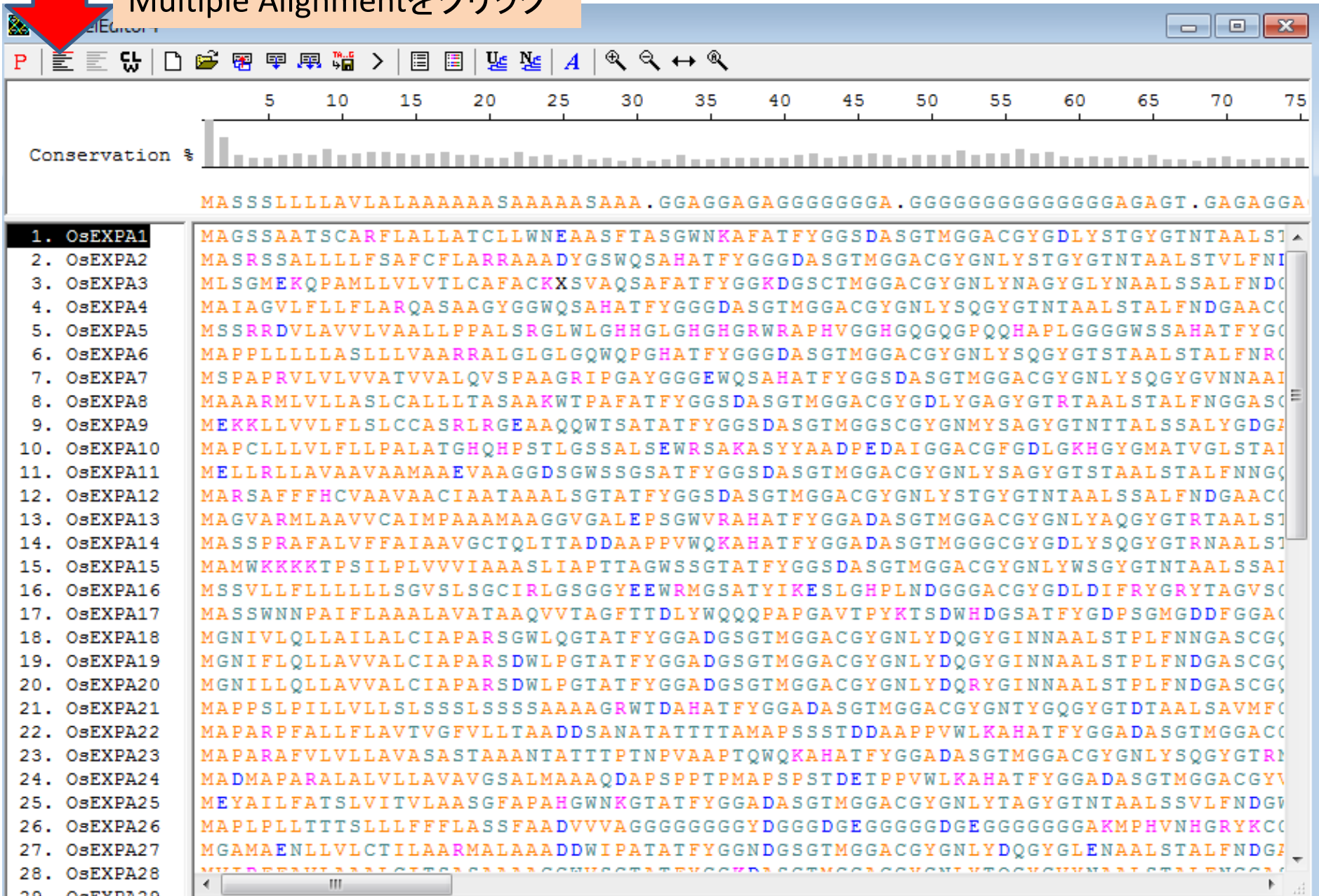
今回は授業用にBLAST検索の結果の中からイネのEXPANSINを集めて既にFASTAフォーマットにしてあるファイルを使用する

1. “OsEXPA”を開く
2. コピーしてwordに張り付ける
3. ファイル→保存 (Ctrl + S)
4. ファイルの種類”書式なし (*.txt)”を選択
5. デスクトップに保存
6. Genetyxにドラッグ & ドロップ
7. Add All
8. Parallel Editor



Alignment

Multiple Alignmentをクリック



Alignment終了後、“Create Picture”をクリック

Conservation 3

Alignment終了後、“Create Picture”をクリック

1. OsEXPA1
2. OsEXPA2
3. OsEXPA3
4. OsEXPA4
5. OsEXPA5
6. OsEXPA6
7. OsEXPA7
8. OsEXPA8
9. OsEXPA9
10. OsEXPA10

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-----MAGSSAATSCARFLALLATCLLWNEAASFTASGWNKAFATFYGGSDA:
-----MASRSSALLLFSAFCLARRA-ADYGSWQSAHATFYGGGDA:
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-----MAAARMVLVLLASLC--ALLLTASAAKWTPAFATFYGGSDA:
-----MEKKLLVVLFLSLCCASRLRGEAAQQWTSATATFYGGSDA:
-----MAPCLLLVLFLLPALATGHQHPSTLGSSALSEWRSKASYAA-DPI

GENETYX Ver.11 - Untitled1.emf

File Edit Homology Internet Search Application View Window Help

Seq1 1 emf

Frame Settings

Match %

Option

Color

Difference

Font...

Grayにすると論文のような感じになる

配列の幅

LOCUS ORIGIN

OsEXPA1 1 -----MAGSSAATSCARFLALLATCLLWNEAASFT 30

OsEXPA2 1 -----MASRSSALLLLFSAFCFLARRA-AAD 25

OsEXPA3 1 -----MLSGMEKQPAMLLVLVTLCAFAACK 24

OsEXPA4 1 -----MAIAGVLFLLFLARQASAAG 20

OsEXPA5 1 MSSRRDVLAVVLVAALLPPALSRGLWLGHGHLGHGHRWRAPHVGGHGQGGPQQHAPLG 60

OsEXPA6 1 -----MAPPLLLLLLASLLLVAARRALGLG 24

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OsEXPA8 82 CD--TRKTQWCKPGT-SITVTATNLCBPNYALSGDAGGWCNPPRRHFDMSQPAWETIAVY 138

OsEXPA9 84 CD--ASATRWCKNGT-SVTVTATNLCBPNYSESGDAGGWCNPPRRHFDMSQPAWEAIAVY 140

OsEXPA10 89 CV---DDLKYCLPGT-SIVVTATNLCBPNGFLPADAGGVCNPPNHHELLPIQSFEKIALW 144

GENETYX Ver.11 - Untitled1.emf

File Edit Homology Internet Search Application View Window Help

Seq1 1 emf

Frame Settings

Match %

Option

Color

Difference

Font...

Grayにすると論文のような感じになる

配列の幅

File: Save as: emfでデスクトップに保存: パワーポイントにペースト

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OsEXPA3 1 -----MSPAPRVLVLVVATVVALQVSPAAGRIPGAYG 32

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OsEXPA5 1 -----MEKKLLVVLFLSLCCASRLRGEA 23

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OsEXPA5 61 GGGWSSAHATFYGGGDASGTMGACGCGNLYSQGYGTNTAALSTALFNNGLSCGACFEVR 120

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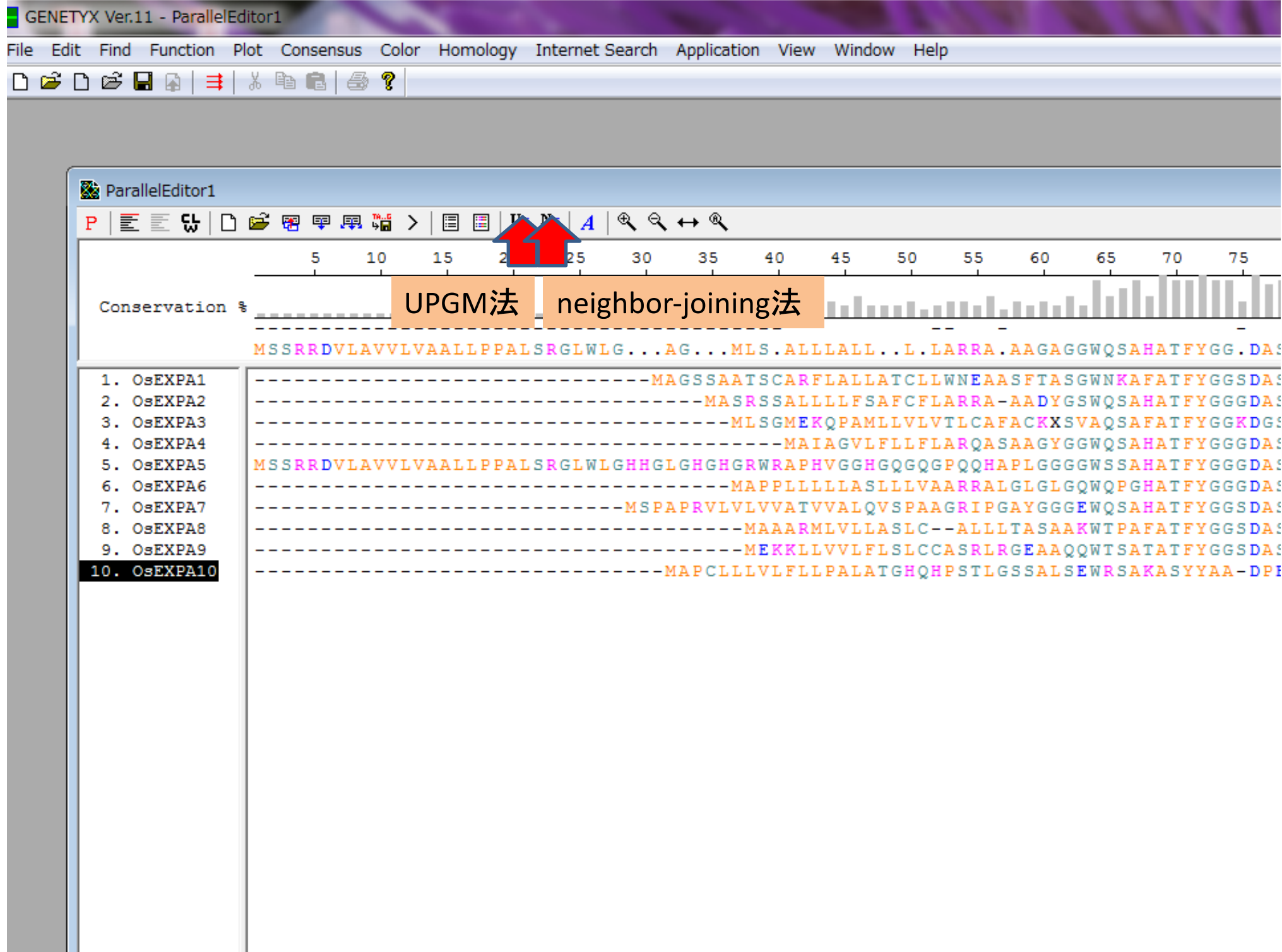
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OsEXPA3	1	-----MLSGMEKQPAMLLVLVTLCAFAACK	24
OsEXPA4	1	-----MAIAGVLFLLFLARQASAAG	20
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OsEXPA2	86	CD--NDGQW-CLFGS--VTVTATNLCPPNYALPNDGGWCNPPRPHFDMAEPALFQIGVY	140
OsEXPA3	85	CD--TSQTKWCKRGGNSITITATNLCPPNWALPSNSGGWCNPPLOHFDMSQPAWENIAVY	142
OsEXPA4	81	CD--NAGSS-CLFGS--ITVTATNLCPPNYGLPSDDGGWCNPPRPHFDMAEPALFHIAQY	135
OsEXPA5	121	CDAGGGGSHSCLFGS--VVVTATNLCPPNNALPSDDGGWCNPPRAHFDMSQPVFQRTALF	178
OsEXPA6	85	CA--GDHRRSCLPGGATVTVTATNLCPPNYALPSDGGGWCNPPRRHFDLAEPALFRTIARH	142
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OsEXPA10	89	CV---DDLKYCLEGT-SIVVTATNLCAPNFGLPADAGGVCNPPNHFFLLPIQSFEKIALW	144
OsEXPA1	149	VGGIVFVMYQRVPCAKOGGVREFTINGRDYFELVLVSNVGGVGSIQSVSIKGS-----RTG	203
OsEXPA2	141	RAGIVFVSYYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGEGDVQSVSIKGS-----STG	195
OsEXPA3	143	QAGIVFVNYYRRVPCQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGS-----NTG	197
OsEXPA4	136	RAGIVFVSFRRVPCVKKGGVRETVNGHSYFNLVLVTNVAGAGDVRSVSIKGS-----RTG	190
OsEXPA5	179	KAGIVFVSYYRRVACQKKGGIRFTINGHSYFNLVLVTNVGGAGDVHAVAVKSE-----RSA	233
OsEXPA6	143	AAGIVFVSFRRVACARKGGVRETVNGHAYFNLVLVTNVGGAGDVRS LAVXGSGSGSRVGG	202
OsEXPA7	152	RAGIVFVSYYRRVPCRKKGGVREFTINGFRYFNLVLITNVAGAGDIVRASVKGT-----STG	206
OsEXPA8	139	RAGIVFVNYYRRVPCQRSGGIRFAVNGHSYFELVLVTNVGGSGAVAQMWIKGS-----GTG	193
OsEXPA9	141	SSGIVFVRYARTPCRRVGGIRFGIAGHDYFELVLVTNVAGSGAVAAAWVKGS-----GTE	195
OsEXPA10	145	KAGVMEIQYRRVNCRLDGGVREFAVAGRSFELTVLISNVGGAGDVRSVKIKGT-----ESG	199
OsEXPA1	204	-WMAMSRNWQNNWQSNAYLDGQSLSEKVTSSDGQTLTFLDVAPAGWTFGQTFSTSQQFS-	261
OsEXPA2	196	-WQPM SRNWQNNWQSNAYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF---	251
OsEXPA3	198	-WMAMSRNWGANWQSNAYLAGQSLSEIVQLDDGRKVTAWNVAPESNWFFGATYSTSWVQF-	255
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OsEXPA6	203	RWQPM SRNWQNNWQSNAYLDGKALSFRVTAGDRSLTCADVAPAGWQFGQTFEGRQF---	259
OsEXPA7	207	-WPM SRNWQNNWQSNVVLVGOALSFRVTGSDRRTSTSWNAAPAGWHFGQTFEGKNERV-	264
OsEXPA8	194	-WMAMSRNWGANWQSNARLDGOALSFRVQADGRVVTAAADVAPAGWSFGATYTSS-AQFY	251
OsEXPA9	196	-WLSMSRNWGENWQSNAYLTGOALSFRVQADDGGVVTAADVAPANNWQFGSTYQSD-VNFS	253
OsEXPA10	200	-WLSMGRNWQINWHINSDFRGQPLSELTSSDGKTLTNYNVVPKEWDFGKTYTGKQFLL-	257
OsEXPA1	261	-	261
OsEXPA2	251	-	251
OsEXPA3	255	-	255
OsEXPA4	246	-	246
OsEXPA5	291	-	291
OsEXPA6	259	-	259
OsEXPA7	264	-	264
OsEXPA8	251	-	251



[18. B1遺伝子cDNA](#)

[19. B2遺伝子cDNA](#)

[20. B3遺伝子cDNA](#)

[21. B4遺伝子cDNA](#)

[22. B5遺伝子cDNA](#)

[23. B1遺伝子アミノ酸](#)

[24. B2遺伝子アミノ酸](#)

[25. B3遺伝子アミノ酸](#)

[26. B4遺伝子アミノ酸](#)

[27. B5遺伝子アミノ酸](#)

[28. C1遺伝子アミノ酸配列](#)

[29. C2遺伝子アミノ酸配列](#)

[30. C3遺伝子アミノ酸配列](#)

[31. C4遺伝子アミノ酸配列](#)

[32. Gid1-GenomicDNA](#)

[33. Gid1-cDNA](#)

[34. OsExpansin Genome seq](#)

[35. OsExpansin genes](#)

[36. OsExpansin1 アミノ酸配列](#)

[37. 他の植物のExpansin genes](#)

[38. APETALA2](#)

[39. salinity stress](#)

[Host:133.6.17.108](#)

[UserName:gcoe-genetyx](#)

[pass word:xytenegeocg](#)



アミノ酸配列をコピーして

制限酵素マップ：

1. [WebCutter](#) ：制限酵素切断部位解析ソフト

タンパク質配列の情報を見る

The screenshot shows the GENETYX Ver.11 interface. The 'Peptide' menu is open, displaying various analysis options. A red arrow points to the 'Peptide' menu, and another red arrow points to the 'Seq Info...' option. The main window displays a protein sequence with residue numbers 10, 70, 130, 190, 250, 260, 270, 280, 290, and 300. The sequence is: >Sequence2_1 T...
MAGSSAATSC AR...
YSTGYGTNTA AL...
PNDAGGWCNP PR...
VLVSNVGGVG SIQSVSIKGS RIGWMAMSRN WGVNWQSNAY LDGQSLSFKV TSSDGQTLTF
LDVAPAGWTF GQTFSTISQQF S*

配列情報を表示します

FASTA

Untitled1.txt

[[GENETYX : Amino Acid Composition]

Date : 2015.11.22

Filename : Sequence2_1.gpt

Sequence Size : 262

Sequence Position: 1 - 262

hydrophobic: 138 (52.67%)

neutral : 82 (31.30%)

hydrophilic: 41 (15.65%)

other : 1 (0.38%)

[hydrophobic residues]

Gly(G)	32 (12.21%)	Ala(A)	27 (10.31%)	Val(V)	16 (6.11%)	Leu(L)	17 (6.49%)
Ile(I)	8 (3.05%)	Met(M)	7 (2.67%)	Phe(F)	14 (5.34%)	Trp(W)	8 (3.05%)
Pro(P)	9 (3.44%)						

[neutral residues]

Ser(S)	26 (9.92%)	Thr(T)	21 (8.02%)	Asn(N)	13 (4.96%)	Gln(Q)	12 (4.58%)
Cys(C)	10 (3.82%)						

[hydrophilic residues]

Asp(D)	11 (4.20%)	Glu(E)	3 (1.15%)	Lys(K)	5 (1.91%)	His(H)	1 (0.38%)
Arg(R)	10 (3.82%)	Tyr(Y)	11 (4.20%)				

[other residues]

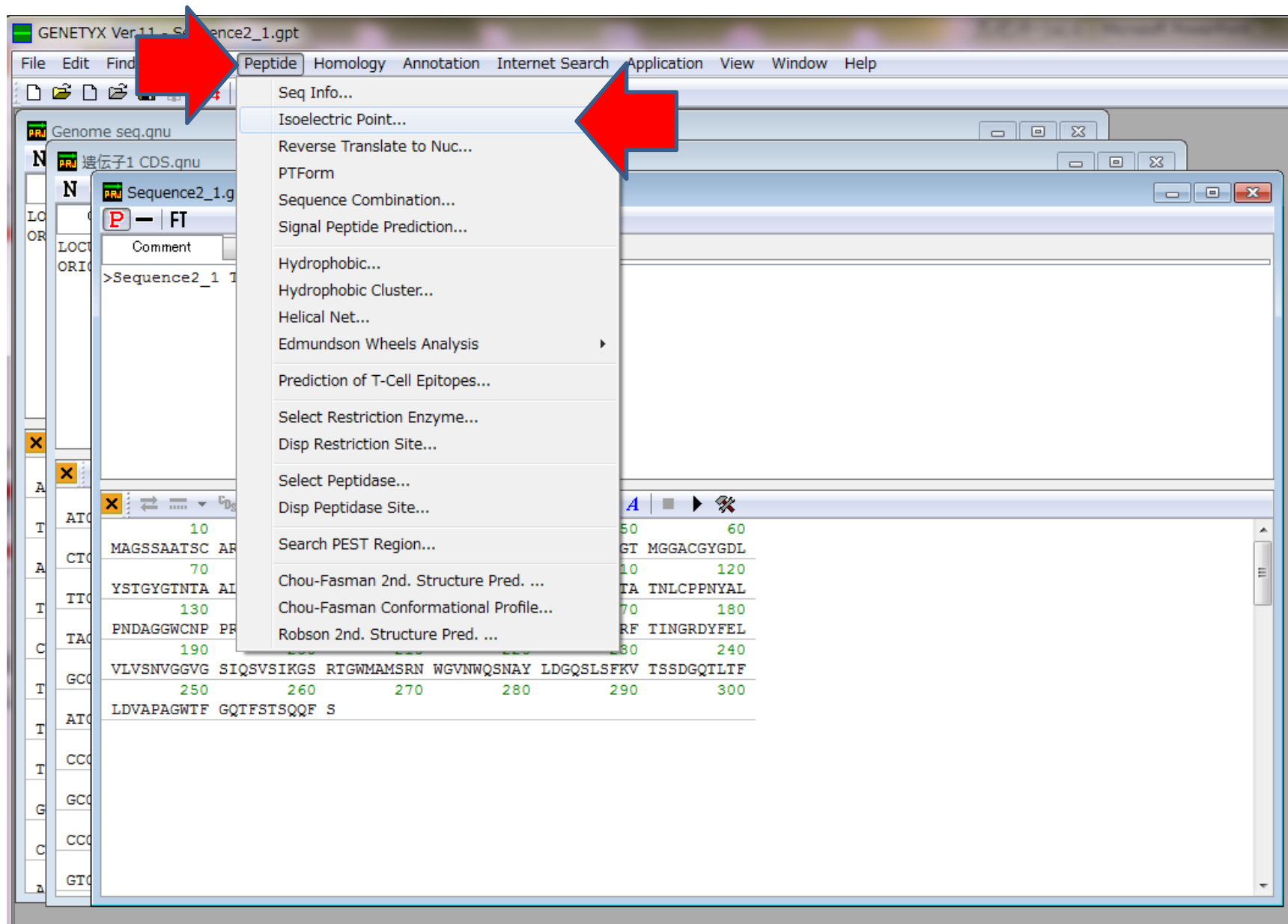
Asx(B)	0 (0.00%)	Glx(Z)	0 (0.00%)	Xaa(X)	0 (0.00%)	??? (?)	1 (0.38%)
--------	------------	--------	------------	--------	------------	---------	------------

Average Molecular Weight = 27747.75

Monoisotopic Molecular Weight = 27730.0945

分子量約27.7kDであると予想

等電点の検出



[18. B1遺伝子cDNA](#)

[19. B2遺伝子cDNA](#)

[20. B3遺伝子cDNA](#)

[21. B4遺伝子cDNA](#)

[22. B5遺伝子cDNA](#)

[23. B1遺伝子アミノ酸](#)

[24. B2遺伝子アミノ酸](#)

[25. B3遺伝子アミノ酸](#)

[26. B4遺伝子アミノ酸](#)

[27. B5遺伝子アミノ酸](#)

[28. C1遺伝子アミノ酸配列](#)

[29. C2遺伝子アミノ酸配列](#)

[30. C3遺伝子アミノ酸配列](#)

[31. C4遺伝子アミノ酸配列](#)

[32. Gid1-GenomicDNA](#)

[33. Gid1-cDNA](#)

[34. OsExpansin Genome seq](#)



OsExpansinのゲノム配列をコピーして

[35. OsExpansin genes](#)

[36. OsExpansin1 アミノ酸配列](#)

[37. 他の植物のExpansin genes](#)

[38. APETALA2](#)

[39. salinity stress](#)

[Host:133.6.17.108](#)

[UserName:gcoe-genetyx](#)

[pass word:xytenegeocg](#)

制限酵素マップ：

1. [WebCutter](#) ：制限酵素切断部位解析ソフト

N

FT

Comment

Map

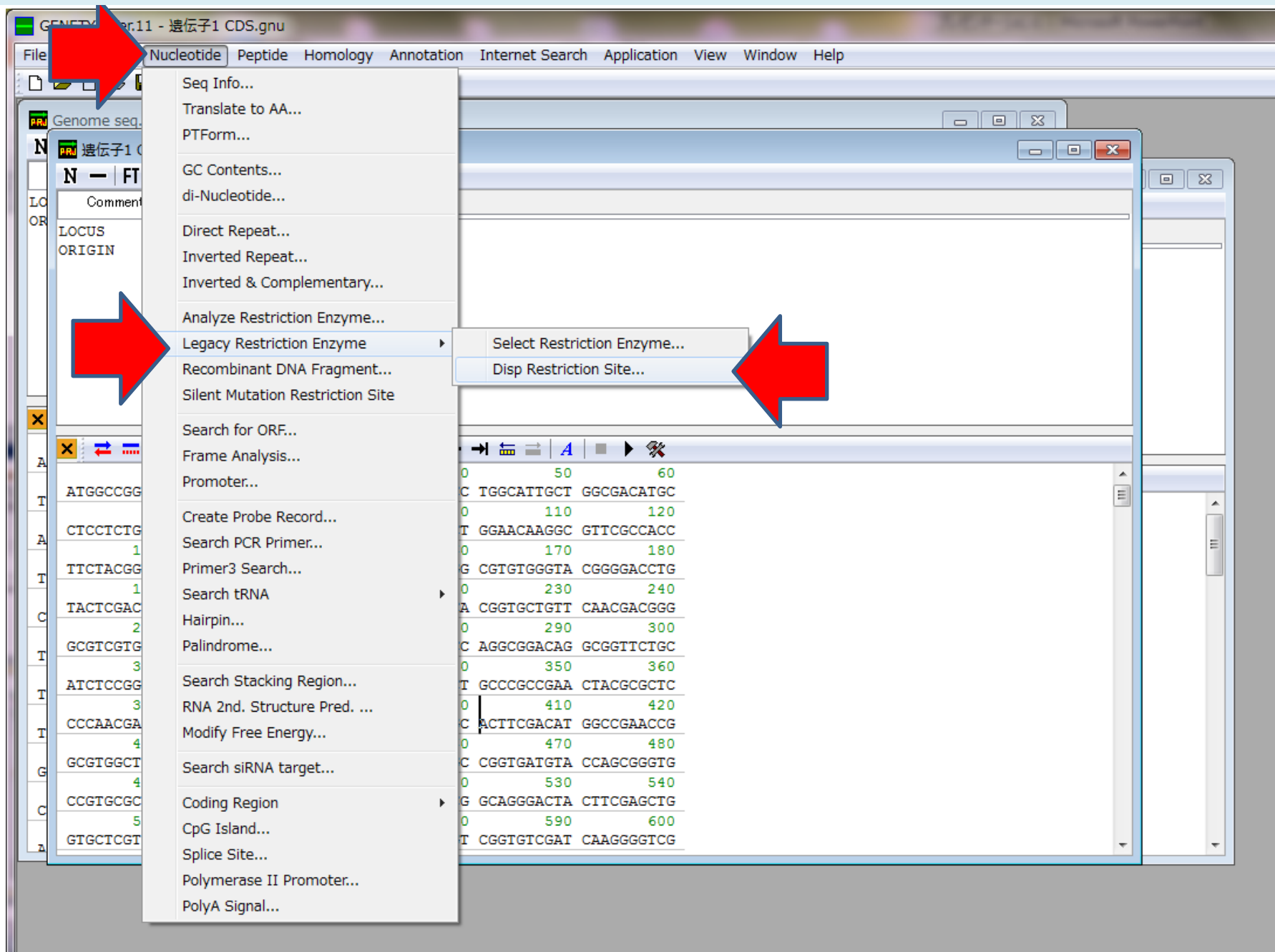
LOCUS

ORIGIN



10	20	30	40	50	60
ACCAACACAT	TGTTTGTGTT	GTGCCTAAAA	CACTAATAAT	TTCTCATATA	TTTTATAAAG
70	80	90	100	110	120
TGTAAC TTAA	TTTGACCAAA	CCACAAA A CT	ATAGGGAAAG	ATGAGAAGGA	AGAAGATAAG
130	140	150	160	170	180
AATGATCATA	GGTAATAGTT	GGCTTGATTT	TCCATCTTGG	TTATTGTTTG	GAAAGCTGAA
190	200	210	220	230	240
TTTTCCGTGC	TAGGCTAGGA	TCTTAAGTTC	TTAATACAAA	TTCCTAACTA	GAATTTTGG A
250	260	270	280	290	300
CTGATCCACG	GTGTTCTGAC	TCAACTACAG	TTGGGGATGC	CA TGTTGGTA	TTTAGATTTG
310	320	330	340	350	360
TCGGGAGCTA	GTGTTTTCTT	ACTTCATTAT	TTAAAACATT	TTTATCCTTA	AAATAAAAATA
370	380	390	400	410	420
TTGGAATATT	CAATAATTAG	TGGATGACAA	AGATGAACAC	AACACAAAAT	TAAGTTGAAA
430	440	450	460	470	480
TATGCACCTT	TTCCATGTTT	TAAACACAGT	AATCCATTTT	TCCATCTTGT	ACTTTGACTG
490	500	510	520	530	540
GGTTATTGTA	CTTATTGATT	GAGGTAGCAT	GAAACTCCTG	CGAAA A CTCC	ATGACCCAAG
550	560	570	580	590	600
CTCCCAATGA	TGGGTAAGTA	GCACAAGTAC	TAGGTAAC TA	AGAAATTTTA	ATGGTGTCTT
610	620	630	640	650	660
AAACATACAA	TTAGTCAATC	ATACCACCCA	AACTAGTCTA	TCATGCCACT	AAATTTGTCT
670	680	690	700	710	720
TTTCTGCTGC	TTTCTGCTGC	TTTCTGCTGC	TTTCTGCTGC	TTTCTGCTGC	TTTCTGCTGC

制限酵素サイトの検出





Untitled6.txt

Untitled7.txt

Untitled8.emf

Untitled9.txt

[GENETYX : Search Restriction Fragment]

Date : 2017.10.24

Filename : Sequence4

Sequence Size : 6000

Sequence Position: 1 - 6000

[Linear]

(1) AatII : GACGTC : 1 Sites

1- 3828: 3828 base

3829- 6000: 2172 base

(2) Acc65I : GGTACC : 1 Sites

1- 4705: 4705 base

4706- 6000: 1295 base

(3) AccB7I : CCANNNNTGG : 1 Sites

1- 3729: 3729 base

3730- 6000: 2271 base

(4) AcuI : CTGAAG/CTTCAG : 1 Sites

1- 3125: 3125 base

3126- 6000: 2875 base

(5) AgeI : ACCGGT : 1 Sites

1- 4376: 4376 base

4377- 6000: 1624 base

(6) AhdI : GACNNNNNGTC : 1 Sites

1- 3340: 3340 base

3341- 6000: 2660 base



Untitled6.txt

Untitled7.txt

[GENETYX : Restriction Map]

Date : 2017.10.24

Filename : Sequence4

Sequence Size : 6000

Sequence Position: 1 - 6000

[Linear]

10 20 30 40 50 60
 ACCAACACATTGTTTGTGTTGTGCCTAAACACTAATAATTTCTCATATATTTTATAAAG

/ / /
 FspEI FspEI MluCI PsiI
 Tsp509I
 TspEI

70 80 90 100 110 120
 TGTAACCTTAATTTGACCAAACCAAAACTATAGGGAAAGATGAGAAGGAAGAAGATAAG

// // // /
 MseI FspEIFspEI SfcI FspEI HpyAV MboII
 Tru9I FspEI FspEI
 MluCI MboII
 Tsp509I
 TspEI

130 140 150 160 170 180
 AATGATCATAGGTAATAGTTGGCTTGATTTCCATCTTGGTTATTGTTTGGAAAGCTGAA

/ /// / / /
 BclI FspEI CviKI-1 BccI FspEI FspEI ApoI
 FbaI FspEI FspEI AluI MluCI
 BfuCI CviKI-1
 DpnI Tsp509I
 TspEI



Untitled6.txt

[[GENETYX : Search Restriction Site]

Date : 2017.10.24

Filename : Sequence4

Sequence Size : 6000

Sequence Position: 1 - 6000

[Linear]

Res. Enz. : Recog. Seq. Count: Recog. Seq. Pos.

Res. Enz.	Recog. Seq.	Count	Recog. Seq. Pos.
AatII	: GACGTC	(1)	: 3824
Acc65I	: GGTACC	(1)	: 4705
AccB7I	: CCANNNNTGG	(1)	: 3723
AcuI	: CTGAAG/CTTCAG	(1)	: 3140
AgeI	: ACCGGT	(1)	: 4376
AhdI	: GACNNNNNGTC	(1)	: 3335
Alw44I	: GTGCAC	(1)	: 4872
AlwNI	: CAGNNNCTG	(1)	: 3770
ApaLI	: GTGCAC	(1)	: 4872
AvrII	: CCTAGG	(1)	: 1115
BamHI	: GGATCC	(1)	: 3192
BanII	: GRGCTC	(1)	: 5422
BbrPI	: CACGTG	(1)	: 4811
BbsI	: GAAGAC/GTCTTC	(1)	: 5797
BclI	: TGATCA	(1)	: 123
BglII	: AGATCT	(1)	: 2608
BlnI	: CCTAGG	(1)	: 1115
BlpI	: GCTNAGC	(1)	: 3313
BpmI	: CTGGAG/CTCCAG	(1)	: 1191
Bpu10I	: CCTNAGC/GCTNAGG	(1)	: 4073
Bpu1102I	: GCTNAGC	(1)	: 3313
BpuEI	: CTTGAG/CTCAAG	(1)	: 3527
BseYI	: CCCAGC/GCTGGG	(1)	: 1051
BsiWI	: CGTACG	(1)	: 2501
BsmBI	: CGTCTC/GAGACG	(1)	: 3646

[18. B1遺伝子cDNA](#)

[19. B2遺伝子cDNA](#)

[20. B3遺伝子cDNA](#)

[21. B4遺伝子cDNA](#)

[22. B5遺伝子cDNA](#)

[23. B1遺伝子アミノ酸](#)

[24. B2遺伝子アミノ酸](#)

[25. B3遺伝子アミノ酸](#)

[26. B4遺伝子アミノ酸](#)

[27. B5遺伝子アミノ酸](#)

[28. C1遺伝子アミノ酸配列](#)

[29. C2遺伝子アミノ酸配列](#)

[30. C3遺伝子アミノ酸配列](#)

[31. C4遺伝子アミノ酸配列](#)

[32. Gid1-GenomicDNA](#)

[33. Gid1-cDNA](#)



配列をコピー

[34. OsExpansin Genome seq](#)

[35. OsExpansin genes](#)

[36. OsExpansin1 アミノ酸配列](#)

[37. 他の植物のExpansin genes](#)

[38. APETALA2](#)

[39. salinity stress](#)

[Host:133.6.17.108](#)

[UserName:gcoe-genetyx](#)

[pass word:xytenegeocg](#)

制限酵素マップ：

1. [WebCutter](#) ：制限酵素切断部位解析ソフト

Sequence4

N — FT

Comment

Map

LOCUS
ORIGIN



10	20	30	40	50	60
ATGGCCGGCA	GCGACGAGGT	CAACCGCAAC	GAGTGCAAGA	CGGTGGTGCC	GCTCCACACA
70	80	90	100	110	120
TGGGTGCTCA	TCTCCAACCT	CAAGCTGTCG	TACAACATTC	TGCGGCGGGC	GGACGGGACG
130	140	150	160	170	180
TTCGAGCGGG	ACCTCGGGGA	GTACCTGGAC	AGGAGGGTGC	CGGCGAACGC	GCGGCCCGCTG
190	200	210	220	230	240
GAGGGGGTGT	CGTCGTTTCA	CCACATCATC	GACCAGTCGG	TGGGGCTGGA	GGTGCGCATC
250	260	270	280	290	300
TACCGGGCGG	CGGCGGAGGG	TGACGCGGAG	GAGGGGGCGG	CGGCGGTGAC	GCGGCCCCATC
310	320	330	340	350	360
CTTGAGTTCC	TGACGGACGC	GCCAGCGGCG	GAGCCGTTCC	CGGTGATCAT	ATTCTTCCAC
370	380	390	400	410	420
GGCGGCAGCT	TCGTGCACTC	GTCGGCCAGC	TCGACCATCT	ACGACAGTCT	GTGCCGCCGG
430	440	450	460	470	480
TTCGTGAAGC	TGAGCAAGGG	CGTCGTGGTG	TCCGTCAACT	ACCGGCGCGC	GCCGGAGCAC
490	500	510	520	530	540
CGCTACCCGT	GCGCGTACGA	CGACGGGTGG	ACCGCGCTCA	AGTGGGTCAT	GTCGCAGCCG
550	560	570	580	590	600
TTCAATGCGCA	GCGGCGGGCA	CGCGCAGGCC	CGCGTGTTCC	TCTCCGGCGA	CAGCTCCGGC
610	620	630	640	650	660
GGCAACATCG	CCCACCACGT	CGCCGTCCGC	GCCGCCGACG	AGGGCGTCAA	GGTCTGCGGC
670	680	690	700	710	720
AACATCCTGC	TCAACGCCAT	GTTGCGCGGC	ACCGAGCGCA	CGGAGTCGGA	GCGGCGGCTC
730	740	750	760	770	780

GENETYX Ver.11 - Sequence4

File Edit Find Nucleotide Peptide Homology Annotation Internet Search Application View Window Help

Seq Info...
Translate to AA...
PTForm...
GC Contents...
di-Nucleotide...
Direct Repeat...
Inverted Repeat...
Inverted & Complementary...
Analyze Restriction Enzyme...
Legacy Restriction Enzyme
Recombinant DNA Fragment...
Silent Mutation Restriction Site
Search for ORF...
Frame Analysis...
Promoter...
Create Probe Record...
Search PCR Primer...
Primer3 Search...
Search tRNA
Hairpin...
Palindrome...
Search Stacking Region...
RNA 2nd. Structure Pred. ...
Modify Free Energy...
Search siRNA target...
Coding Region
CpG Island...
Splice Site...

Sequence4

N — FT

Comment Map

LOCUS
ORIGIN

10 20 30 40 50 60
ATGGCCGGCA GCGACGAGGT CAACCGCAAC GAGTGCAAGA CGGTGGTGCC GCTCCACACA
70 80 90 100 110 120
TGGGTGCTCA TCTCCAACCT CAAGCTGTCTG TACAACATTC TCGGGCGGGC GGACGGGACG
130 140 150 160 170 180
TTCGAGCGGG ACCTCGGGGA GTACCTGGAC AGGAGGGTGC CGGCGAACGC GCGGCCGCTG
190 200 210 220 230 240
GAGGGGGTGT CGTCGTTTCA CCACATCATC GACCAGTCGG TGGGGCTGGA GGTGCGCATC
250 260 270 280 290 300
TACCGGGCGG CGGCGGAGGG TGACGCGGAG GAGGGGGCGG CGGCGGTGAC GCGGCCCATC
310 320 330 340 350 360
CTTGAGTTCC TGACGGACGC GCCAGCGGCG GAGCCGTTCC CGGTGATCAT ATTCTTCCAC
370 380 390 400 410 420
GGCGGCAGCT TCGTGCACTC GTCGGCCAGC TCGACCATCT ACGACAGTCT GTGCCGCCGG
430 440 450 460 470 480
TTCGTGAAGC TGAGCAAGGG CGTCGTGGTG TCCGTCAACT ACCGGCGCGC GCCGGAGCAC
490 500 510 520 530 540
CGCTACCCGT GCGCGTACGA CGACGGGTGG ACCGCGCTCA AGTGGGTCAT GTCGCAGCCG
550 560 570 580 590 600
TTCATGCGCA GCGGCGGCGA CGCGCAGGCC CGCGTGTTC TCTCGGCGA CAGCTCGGGC

GENETYX Ver.11 - Sequence4

File Edit Find Nucleotide Peptide Homology Annotation Internet Search Application View Window Help

Sequence4

N — FT

Comment Map

LOCUS
ORIGIN

10 20 30 40 50 60
ATGGCCGGCA GCGACGAGGT CAACCGCAAC GAGTGCAAGA CGGTGGTGCC GCTCCACACA
70 80 90 100 110 120
TGGGTGCTCA TCTCCAATT CAAGCTGTCTG TACAACATTC TCGGGCGGGC GGACGGGACG
130 140 150 160 170 180
TTCGAGCGGG ACCTCGGGGA GTACCTGGAC AGGAGGGTGC CGGCGAACGC GCGGCCGCTG
190 200 210 220 230 240
GAGGGGGTGT CGTCGTTCGA CCACATCATC GACCAGTCGG TGGGGCTGGA GGTGCGCATC
250 260 270 280 290 300
TACCGGGCGG CGGCGGAGGG TGACGCGGAG GAGGGGGCGG CGGCGGTGAC GCGGCCCATC
310 320 330 340 350 360
CTTGAGTTCC TGACGGACGC GCCAGCGGCG GAGCCGTTCC CGGTGATCAT ATTCTTCCAC
370 380 390 400 410 420
GGCGGCAGCT TCGTGCACTC GTCGGCCAGC TCGACCATCT ACGACAGTCT GTGCCGCCGG
430 440 450 460 470 480
TTCGTGAAGC TGAGCAAGGG CGTCGTGGTG TCCGTCAACT ACCGGCGCGC GCCGGAGCAC
490 500 510 520 530 540
CGTACCCGT GCGCGTACGA CGACGGGTGG ACCGCGCTCA AGTGGGTCAT GTCGCAGCCG
550 560 570 580 590 600
TTCATGCGCA GCGGCGGCGA CGCGCAGGCC CGCGTGTTC TCTCCGGCGA CAGCTCCGGC
610 620 630 640 650 660
GGCAACATCG CCCACCACGT CGCCGTCCGC GCCGCCGACG AGGGCGTCAA GGTCTGCGGC

Translate to AA for Thesis

Nuc. Seq. Position (1 - 1065) : 1

1 - 1065

Translation Position :
1 - 1065 Add

Genetic Code : The Standard Code

A.A. Format : ☒ 1-Left ☐ 1-Center ☐ 1-Right

Frame : ☒ 1-Frame ☐ 3-Frame ☐ Complete

Result : ☒ Project Window ☐ Text ☐ Block

Numbering : ☒ Every tenth character ☐ Line first 8
☐ Amino Acid Numbering No. of 1st Amino Acid

OK Cancel

GENETYX Ver.11 - Sequence4_1.gpt

File Edit Find Nucleotide Peptide Homology Annotation Internet Search Application View Window Help

Sequence4

N — FT

Comment Map

LOCUS
ORIGIN

Sequence4_1.gpt

P — FT

Comment Map

>Sequence4_1 Translated Sequence4 |1 frame|355 AA.

10
ATGGCCGGCA G

70
TGGGTGCTCA T

130
TTCGAGCGGG A

190
GAGGGGGTGT C

250
TACCGGGCGG C

310
CTTGAGTTCC T

370
GGCGGCAGCT T

430
TTCGTGAAGC T

490
CGCTACCCGT G

550
TTCATGCGCA G

610
GGCAACATCG C

10 20 30 40 50 60
MAGSDEVNRN ECKTVVPLHT WVLISNFKLS YNILRRADGT FERDLGEYLD RRVPANARPL

70 80 90 100 110 120
EGVSSFDHII DQSVGLEVRI YRAAAEGDAE EGAAAVTRPI LEFLTDAPAA EPFPVLIFFH

130 140 150 160 170 180
GGSFVHSSAS STIYDSLRR FVKLSKGVVV SVNYRRAPRH RYPCAYDDGW TALKWVMSQP

190 200 210 220 230 240
FMRSGGDAQA RVFLSGDSSG GNIAHHVAVR AADEGVKVCN NILLNAMFGG TERTESERRL

250 260 270 280 290 300
DGKYFVTLQD RDWYWKAYLP EDADRDHPAC NPFPGNGRRL GGLPFAKSLI IVSGLDLTCD

310 320 330 340 350 360
RQLAYADALR EDGHHVKVQ CENATVGfYL LPNTVHYHEV MEEISDFLNA NLYY*

GENETYX Ver.11 - [Sequence4]

File Edit Find Nucleotide Peptide Homology Annotation Internet Search Application View Window Help

Undo Ctrl+Z

Redo Ctrl+Y

Cut Ctrl+X

Copy Ctrl+C

Paste Ctrl+V

Paste Special... Ctrl+Shift+V

Clear

Select All Ctrl+A

Selector...

Add Color Region...

Remove Color Region

Add Underline...

Remove Underline

DNA to RNA (ATGC -> AUGC)

RNA to DNA (AUGC -> ATGC)

Reverse Complement (ATGC -> GCAT)

Reverse (ATGC -> CGTA)

Complement (ATGC -> TACG)

Upper Case(O)

Lower Case(W)

Circular

Lock Sequence

Voice

ATGGCC

TGGGTG

TTCGAG

GAGGGG

TACCGG

CTTGAG

GGCGGC

TTCGTG

CGCTAC

550 560 570 580 590 600

TTCATGCGCA GCGGCGGCGA CGCGCAGGCC CGCGTGTTCC TCTCCGGCGA CAGCTCCGGC

610 620 630 640 650 660

GGCAACATCG CCCACCACGT CGCCGTCCGC GCCGCCGACG AGGGCGTCAA GGTCTGCGGC

670 680 690 700 710 720

AACATCCTGC TCAACGCCAT GTTCGGCGGC ACCGAGCGCA CGGAGTCGGA GCGGCGGCTC

50 60

GGTGGTGCC GCTCCACACA

110 120

GCGGCGGGC GGACGGGACG

170 180

GGCGAACGC GCGGCCGCTG

230 240

GGGGCTGGA GGTGCGCATC

290 300

GGCGGTGAC GCGGCCCATC

350 360

GGTGATCAT ATTCTTCCAC

410 420

CGACAGTCT GTGCCGCCGG

470 480

CCGGCGCGC GCCGGAGCAC

530 540

GTGGGTCAT GTCGCAGCCG

GENETYX Ver.11 - [Sequence4]

File Edit Find Nucleotide Peptide Homology Annotation Internet Search Application View Window Help

Undo Ctrl+Z

Redo Ctrl+Y

Cut Ctrl+X

Copy Ctrl+C

Paste Ctrl+V

Paste Special... Ctrl+Shift+V

Clear

Select All Ctrl+A

Selector...

Add Color Region...

Remove Color Region

Add Underline...

Remove Underline

DNA to RNA (ATGC -> AUGC)

RNA to DNA (AUGC -> ATGC)

Reverse Complement (ATGC -> GCAT)

Reverse (ATGC -> CGTA)

Complement (ATGC -> TACG)

Upper Case(O)

Lower Case(W)

Circular

Lock Sequence

Voice

LOCUS ORIGIN

TACCGG

ACCCAC

AAGCTC

CTCCCC

ATGGCC

GAACTC

CCGCCG

AAGCAC

GCGATG

550 560 570 580 590 600

AAGTACGCGT CGCCGCCGCT GCGCGTCCGG GCGCACAAGG AGAGGCCGCT GTCGAGGCCG

610 620 630 640 650 660

CCGTTGTAGC GGGTGGTGCA GCGGCAGGCG CGGCCGGCTGC TCCCGCAGTT CCAGACGCCG

50 60

CCACCACGG CGAGGTGTGT

110 120

CGCCGCCCG CCTGCCCTGC

170 180

CCGCTTGCG CGCCGGCGAC

230 240

CCCCGACCT CCACGCGTAG

290 300

CGCCACTG CGCCGGGTAG

350 360

CCACTAGTA TAAGAAGGTG

410 420

GCTGTCAGA CACGGCGGCC

470 480

GGCCGCGCG CGGCCTCGTG

530 540

CACCCAGTA CAGCGTCGGC