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PENGANTAR BIOINFORMATIKA

IBT 431

By Seprianto S.Pi, M.Si



Pertemuan 8

Analisis Hasil Sekuens

Sasaran Perkuliahan

- Mahasiswa mampu menjelaskan tentang apa itu primer
- Mahasiswa Mampu menganalisis karakter primer yang baik
- Mahasiswa mampu mendesain urutan DNA primer sesuai dengan urutan gen yang diinginkan
- Mahasiswa mampu menghitung nilai T_m dan T_a primer

Analisis DNA Sequence:

1. DNA Sequence database searching
2. DNA Sequence Alignment : pairwise
3. DNA Sequence Alignment : Multiple

1.Sequence database searching:

Nucleotida Search

(Tujuan: Mendapatkan & Memahami format sekuen nukleotida GenBank)

Masuk ke web NCBI

Pilih : nucleotide

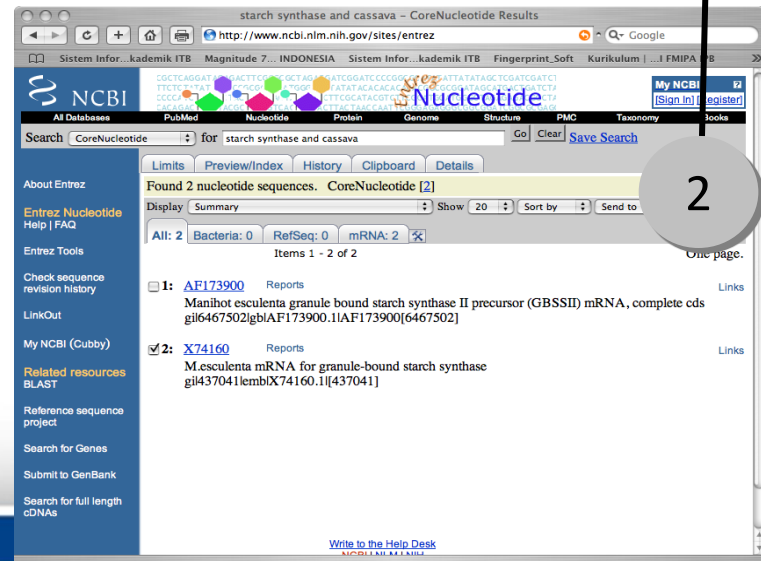
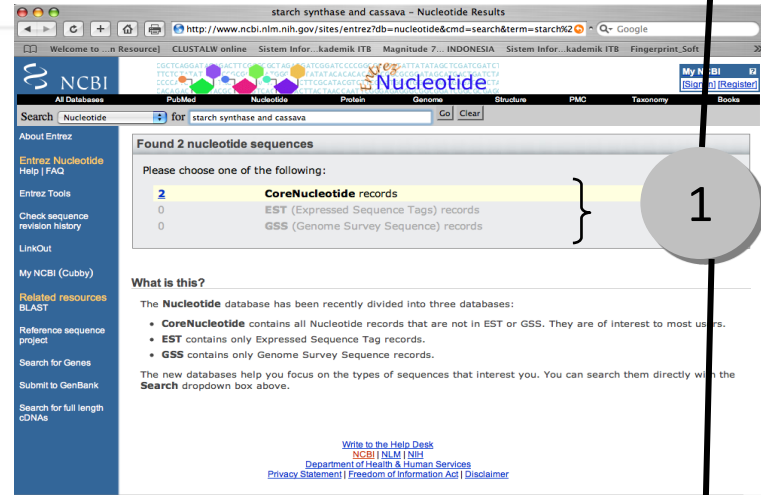
Ketik : Starch synthase and cassava

Tekan : Go

AAA



Output



NCBI Sequence Viewer v2.0

Search: CoreNucleotide for [X74160] [Go] [Clear]

Display: GenBank [Show] [Send to] [Hide] [sequence] [all but gene, CDS and mRNA features]

Range: from **begin** to **end** [Reverse complemented strand] [Features] [Refresh]

1: X74160. Reports M.esculenta mRNA ...[gi:437041]

Features Sequence

LOCUS X74160 2168 bp mRNA linear PLN 30-DEC-1993

DEFINITION M.esculenta mRNA for granule-bound starch synthase.

ACCESSION X74160

VERSION X74160.1 GI:437041

KEYWORDS granule-bound starch synthase.

SOURCE Manihot esculenta (cassava)

ORGANISM Manihot esculenta

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Malpighiales; Euphorbiaceae; Cronoideae; Manihoteae; Manihot.

REFERENCE 1

AUTHORS Salehuzzaman, S.N., Jacobsen, E. and Visser, R.G.

TITLE Isolation and characterization of a cDNA encoding granule-bound starch synthase in cassava (Manihot esculenta Crantz) and its antisense expression in potato

JOURNAL Plant Mol. Biol. 23 (5), 947-962 (1993)

PUBMED 8265633

REFERENCE 2 (bases 1 to 2168)

AUTHORS Visser, R.G.F.

TITLE Direct Submission

JOURNAL Submitted (13-JUL-1993) R.G.F. Visser, Department of Plant Breeding, P O Box 386, 6700 AJ Wageningen, NETHERLANDS

FEATURES source

1..2168

/organism="Manihot esculenta"

/mol_type="mRNA"

/cultivar="M.col 22"

/db_xref="taxon:3983"

/issue_type="laborous roots"

/clone_lib="cDNA library"

1

Keyword

Features Table : mendeskripsikan daerah gen dan properties secara biologi dari urutan nukleotida yg telah diidentifikasi :

CDS (coDing Segment) - mendeskripsikan ORF gen

Poly A_signal

Repeat Region & etc

NCBI Sequence Viewer v2.0

1..2168

/organism="Manihot esculenta"

/mol_type="mRNA"

/cultivar="M.col 22"

/db_xref="taxon:3983"

/issue_type="laborous roots"

/clone_lib="cDNA library"

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1..2168

/gene="GBSS"

CDS

75..1901

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/codon_start=1

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transit peptide

75..308

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/note="amyloplast"

niasc feature

308..309

/gene="GBSS"

/note="epilase site"

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/note="Imperfect"

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/gene="GBSS"

/spk_type="INVERTED"

polyA_signal

2136..2141

/note="putative"

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2

Urutan Protein

NCBI Sequence Viewer v2.0

ORIGIN

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1621 acacagatg ccaaatggy gottcctg ttgaattg caaattat tcaagatg

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1921 tttgaggt tagaataat tgactatt ggaatagt taacggag ataataatc

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2041 atgattct tggagag gattgtct ggaactgt ttaagaga ttacaata

2101 agtatata cgtttgct gggttatg ggaataaa agtttact tctgaaaa

2161 aaaaaa

3

Urutan DNA

Save Hasil Pencarian : Format FASTA

NCBI Sequence Viewer v2.0

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&id=437041

Search: CoreNucleotide for [X74160] for

Display: FASTA Show 5 Send to [Send to] Hide: [] sequence [] all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand [] Features: [+] Refresh

FASTA

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JOURNAL Submitted (13-JUL-1993) R.G.F. Visser, Department of Plant Breeding, P O Box 386, 6700 AJ Wageningen, NETHERLANDS

FEATURES
source
1..2168
/organism="Manihot esculenta"

NCBI Sequence Viewer v2.0

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&id=437041

Search: CoreNucleotide for [X74160] for

Display: FASTA Show 5 Send to [Send to] Hide: [] sequence [] all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand [] Features: [+] Refresh

FASTA

X74160. Reports M.esculenta mRNA ...[gi:437041]

>gi [437041] [emb] [X74160.1] M.esculenta mRNA for granule-bound starch synthase
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1
Pilihan : send to
Text, File dll

NCBI Sequence Viewer v2.0

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nucleotide&id=437041

Search: CoreNucleotide for [X74160] for

Display: FASTA Show 5 Send to [Send to] Hide: [] sequence [] all but gene, CDS and mRNA features

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FASTA

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>gi [437041] [emb] [X74160.1] M.esculenta mRNA for granule-bound starch synthase
ATCAAACTCCACCTCCACCAACCAACACAGCCAGCAATTTTCGGCTAGCTCTACACCGAGGAG
CACCATGGCACTGTAAATAGCTGCACATTTCTTCAGGAGCTCACACTGGAGATCCATAGAG
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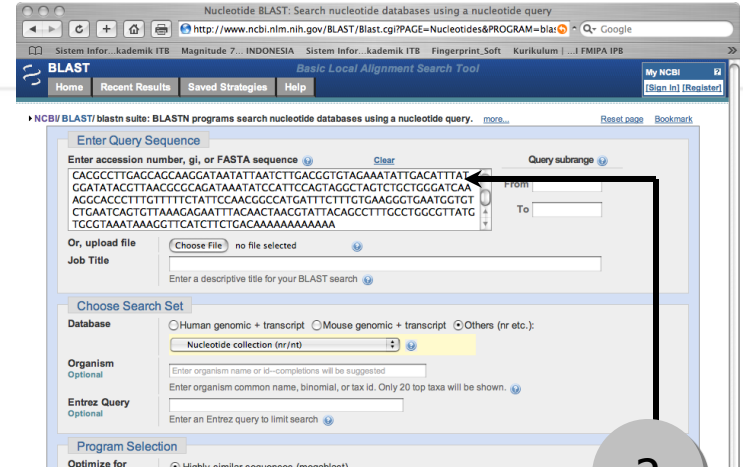
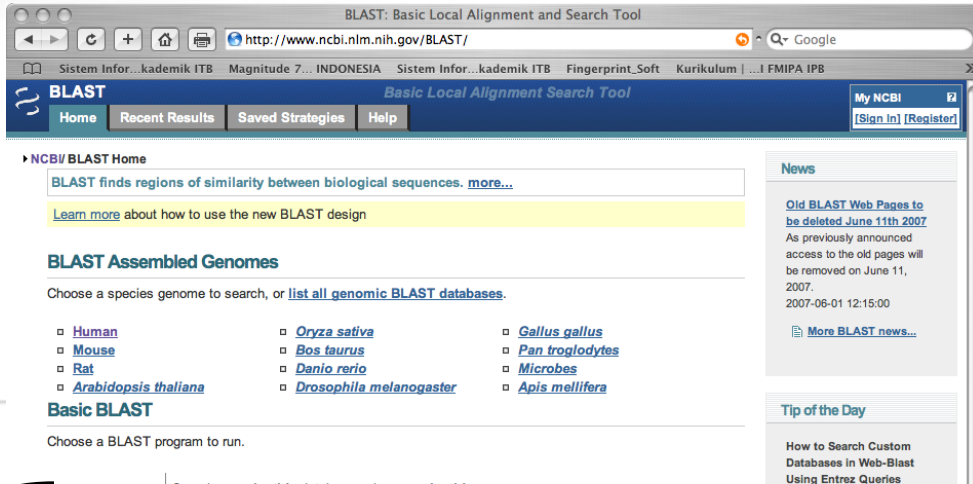
Disclaimer | Write to the Help Desk

2
Outfile dalam
format FASTA

Smart, Creative and Entrepreneurial

2. Sequence Alignment : BLAST (Basic Local Alignment Search) - Pairwise Alignment

(Tujuan: Mencari sekuen yang homolog/ serupa, mencari fungsi gen)



- nucleotide blast** Search a **nucleotide** database using a **nucleotide** query
Algorithms: blastn, megablast, discontinuous megablast
- protein blast** Search **protein** database using a **protein** query
Algorithms: blastp, psi-blast, phi-blast
- blastx** Search **protein** database using a **translated nucleotide** query
- tblastn** Search **translated nucleotide** database using a **protein** query
- tblastx** Search **translated nucleotide** database using a **translated nucleotide** query

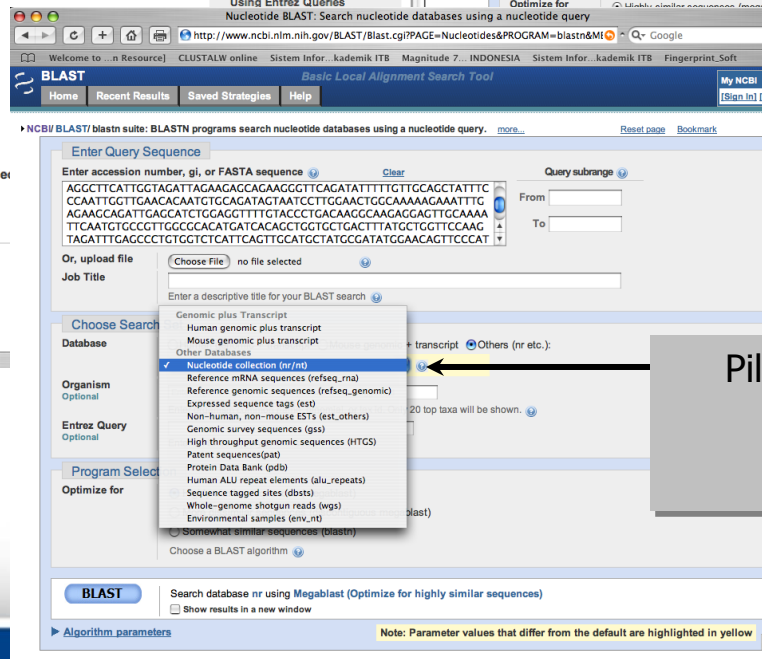
Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Search [trace archives](#)
- Find [conserved domains](#) in your sequence (cds)
- Find sequences with similar [conserved domain architecture](#) (cdart)
- Search sequences that have [gene expression profiles](#) (GEP)

Pilihan program BLAST :
nucleotide blast

1



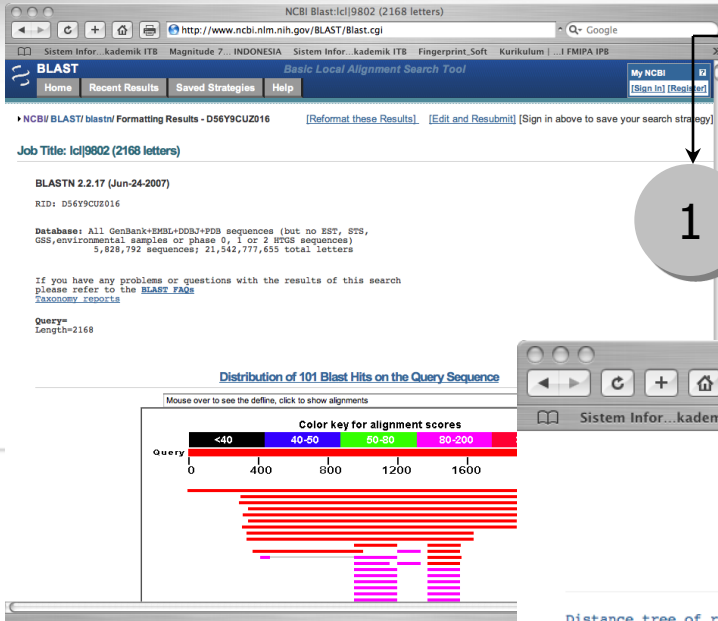
Input copy/paste
urutan nukleotida-
format FASTA

2

Pilihan : *nucleotide
collection*
Tekan : *BLAST*

3

Hasil/ OUTPUT BLAST (1)



The Bit score : ukuran statistical significance dari alignment (Score tinggi menunjukkan more similar pada dua sequence)

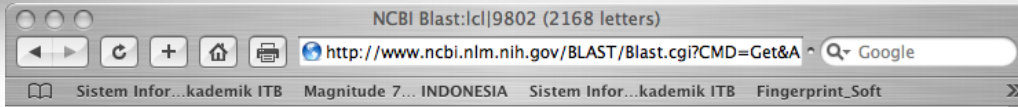
The E-value (expectation value) : nilai E-value rendah menunjukkan more similar pada dua sequence

Output

1 = The Graphic display

2 = The Hit list

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
X74160.1	M.esculenta mRNA for granule-bound starch synthase	4004	4004	100%	0.0	100%	
AF097922.1	Astragalus membranaceus granule-bound glycogen (starch)	976	976	73%	0.0	78%	
AJ006293.1	Antirrhinum majus mRNA for granule-bound starch synthase	889	889	74%	0.0	77%	
AF210699.1	Perilla frutescens granule-bound starch synthase (GBSSI)	848	848	71%	0.0	77%	
AB071604.1	Ipomoea batatas GBSSI mRNA for granule-bound starch synthase	848	848	73%	0.0	76%	
U44126.1	Ipomoea batatas starch synthase (SPSS67) mRNA, complete	824	824	71%	0.0	76%	
EF472254.1	Sorghum bicolor granule-bound starch synthase II precursor	411	411	72%	8e-111	72%	
AF109395.1	Triticum aestivum granule-bound starch synthase GBSSII	281	281	59%	7e-72	71%	U UG
AF486521.1	Hordeum vulgare granule bound starch synthase Ib precursor	259	259	59%	3e-65	71%	
AF285991.1	Prunus virginiana granule-bound starch synthase gene, partial	230	230	11%	2e-56	83%	
AY665923.1	Capsicum eximium granule bound starch synthase (GBSSI)	204	204	8%	1e-48	86%	
AF309144.1	Ipomoea cairica granule-bound starch synthase (waxy) gene	204	204	8%	1e-48	86%	
AB071976.1	Ipomoea batatas GBSSI gene for granule-bound starch synthase	204	204	8%	1e-48	85%	
EF221764.1	Triticum aestivum granule bunch starch synthase II mRNA	202	202	29%	5e-48	73%	
AF111128.1	Ipomoea carnea granule-bound starch synthase (waxy) gene	200	200	8%	2e-47	86%	
AF309140.1	Ipomoea arachnosperma granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111143.1	Ipomoea setosa granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111142.1	Ipomoea argillicola granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111140.1	Ipomoea asarifolia granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111139.1	Ipomoea asarifolia granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111136.1	Ipomoea amnicola granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111122.1	Ipomoea obscura granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	
AF111121.1	Ipomoea ochracea granule-bound starch synthase (waxy) gene	198	198	8%	7e-47	85%	



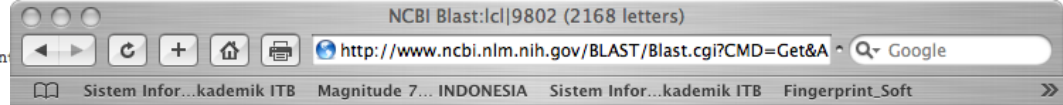
Alignments

Get selected sequences Select all Deselect all Distance tree of results

emb|X74160.1|MEGBSS M. esculenta mRNA for granule-bound starch synthase 1
Length=2168

Score = 4004 bits (2168), Expect = 0.0
Identities = 2168/2168 (100%), Gaps = 0/2168 (0%)
Strand=Plus/Plus

```
Query 1 ATCAAATCTCCACTCCACCACAACCACCAGCGGAACCTATTTGCGCCTAAGCTTC
Sbjct 1 ATCAAATCTCCACTCCACCACAACCACCAGCGGAACCTATTTGCGCCTAAGCTTC
Query 61 CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTTCGTTCCAGGAGCTCA
Sbjct 61 CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTTCGTTCCAGGAGCTCA
Query 121 TGAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGG
Sbjct 121 TGAGCATCCATGCATTAGAGACTAAGGCTAATAATTTGTCTCACACTGGACCCTGG
Query 181 AAACATCACTCCCAATGGTTAAGGTCCTCAACACTATGGATAAACTCCAAATG
Sbjct 181 AAACATCACTCCCAATGGTTAAGGTCCTCAACACTATGGATAAACTCCAAATG
Query 241 CACAATCAAAAAGCTGTGAAAAAGGTCCTGCCACCGGCAATGGTAGGCTGCTGCC
Sbjct 241 CACAATCAAAAAGCTGTGAAAAAGGTCCTGCCACCGGCAATGGTAGGCTGCTGCC
Query 301 TTATTTGGTTCATGGAATGAATTTAATCTTTGTTGGAGCTGAAGTTGGTCCCTGG
Sbjct 301 TTATTTGGTTCATGGAATGAATTTAATCTTTGTTGGAGCTGAAGTTGGTCCCTGG
Query 361 AAACATGGTGGACTTGGTATGTTCTTTGGAGGACTCCCCCTGCCATGGCCGCAAGA
Sbjct 361 AAACATGGTGGACTTGGTATGTTCTTTGGAGGACTCCCCCTGCCATGGCCGCAAGA
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NCBI Blast:lc|9802 (2168 letters)

gb|AF097922.1|AF097922 Astragalus membranaceus granule-bound glycogen (starch) synthase mRNA, complete cds
Length=2107

Score = 976 bits (528), Expect = 0.0
Identities = 1271/1627 (78%), Gaps = 62/1627 (3%)
Strand=Plus/Plus

```
Query 306 TGTGGTCAATGGAATGATTTAATCTTTGTTGGAGCTGAAGTTGGTCCCTGGGACAAAAC 365
Sbjct 324 TGTGGGAATGGGATGATTTGTTGTTTGTGGAGCTGAGGTGGGACCATTGGAGTAAAC 383
Query 366 GGTGGACTTGGTATGATCTTTGGAGGACTCCCCCTGCCATGGCCGCAAGA-GGGCACCG 424
Sbjct 384 GGAGGACTTGGTATGATCTTTGGAGGACTTCCACCAGCTTTGGCTGGAA-ATGGGCACCG 442
Query 425 CGTCATGACAGTGTCTCCCGCTATGACCAGTACAAGGATGCTTTGGGATACCT-CTGTAT 483
Sbjct 443 TGTATGACTGTGTCACCGCTTACGATCAATACAAGGATGCATGGGACA-CTGGTGTGT 501
Query 484 CGGTGGAGATTAAAAATGGAGATAGGAGATAGGAGATAGGAGATAGGAGATAGGAGATAG 502
Sbjct 502 CTGTGGAGATCAAAATGGAGATAGGAGATAGGAGATAGGAGATAGGAGATAGGAGATAG 502
Query 543 AGAGGAGTTGATCGGGTGGAGGAGTTGAGGAGTTGAGGAGTTGAGGAGTTGAGGAGTTGAG 561
Sbjct 561 CGAGGAGTTGATCGGTGGAGGAGTTGAGGAGTTGAGGAGTTGAGGAGTTGAGGAGTTGAG 561
Query 603 -ACTGGATCTAAAATAATGGCCC- 603
Sbjct 620 GACCGAATCTAAACTCATGGCCCTAA-AACTGGTGGATTATAAAGATAACCAACTTA 678
Query 661 GATTTAGCTTGTATGCTTTGCTGCTCTGGAGGCACCGAGAGTTTGAACCTGAACAGCA 720
Sbjct 679 GATTCAGCTTGTATGCTTTGCTGCTCTGGAGGCACCGAGAGTTTGAACCTGAACAGCA 720
Query 721 GCAAAAATTTCTCAGGATCCCTACGG 721
Sbjct 739 ACAAAATTTCTCAGGATCCCTACGG 739
Query 781 CTGCTCTGCTTCCATGATCTTAA 781
Sbjct 781 CTGCTCTGCTTCCATGATCTTAA 781
```

Length : panjang alignment, berapa panjang dua segmen dari sequences yang BLAST meng-alignmen (penjajaran)

Identities : persentase kesamaan dari nukleotida sama antara dua sequence yang di jajarkan

Gaps: nukleotida yang tidak di jajarkan.

NCBI Blast:cl|9802 (2168 letters)

http://www.ncbi.nlm.nih.gov/BLAST/blast.cgi

Distance tree of results **NEW**

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
X74160.1	M.esculenta mRNA for granule-bound starch synthase	4004	4004	100%	0.0	100%	
AF097922.1	Astragalus membranaceus granule-bound glycogen (starch)	976	976	73%	0.0	78%	
AJ006293.1	Antirrhinum majus mRNA for granule-bound starch synthase	889	889	74%	0.0	77%	
AF210699.1	Perilla frutescens granule-bound starch synthase (GBSSI)	848	848	71%	0.0	77%	
AB071606.1	Ipomoea batatas GBSSI mRNA for granule-bound starch synthase	848	848	73%	0.0	76%	
U44126.1	Ipomoea batatas starch synthase (SPS17) mRNA, compl	824	824	71%	0.0	76%	
EF472254.1	Sorghum bicolor granule-bound starch synthase II precursor	411	411	72%	8e-111	72%	
AF109395.1	Triticum aestivum granule-bound starch synthase GBSSII	281	281	59%	7e-72	71%	
AF486521.1	Hordeum vulgare granule bound starch synthase 1b precursor	259	259	59%	3e-65	71%	
AF285991.1	Prunus virginiana granule-bound starch synthase gene, pa	230	230	11%	2e-56	83%	
AY665923.1	Capisicum eximium granule bound starch synthase (GBSSI)	204	204	8%	1e-48	86%	
AF309144.1	Ipomoea cairica granule-bound starch synthase (waxy) ge	204	204	8%	1e-48	86%	
AB071976.1	Ipomoea batatas GBSSI gene for granule-bound starch sy	204	204	8%	1e-48	85%	
EF221764.1	Triticum aestivum granule bunch starch synthase II						
AF111126.1	Ipomoea carnea granule-bound starch synthase (waxy)						
AF309140.1	Ipomoea arachnosperma granule-bound starch synthase						
AF111143.1	Ipomoea setosa granule-bound starch synthase (waxy)						
AF111142.1	Ipomoea argillicola granule-bound starch synthase (wa						
AF111140.1	Ipomoea asarifolia granule-bound starch synthase (wa						
AF111138.1	Ipomoea asarifolia granule-bound starch synthase (wa						

Slanted

Blast Tree View Widget

http://www.ncbi.nlm.nih.gov/blast/treeview/blast_tree_view.cgi?reqes

Tree view for rid: **D56Y9CUZ016**, query ID: **cl|9802**, database: **nr**

This tree was produced using BLAST pairwise alignments. [more...](#)

Tree method: Evolution, Sequence Label, Max Seq Difference

slanted radial force Show distance

Rectangle

Blast Tree View Widget

http://www.ncbi.nlm.nih.gov/blast/treeview/blast_tree_vir

Tree view for rid: **D56Y9CUZ016**, query ID: **cl|9802**, database: **nr**

This tree was produced using BLAST pairwise alignments. [more...](#)

method: Evolution, Sequence Label, Max Seq Difference

rectangle slanted radial force Show distance

3. Sequence Alignment : CLUSTAL - Multiple Alignment : Koleksi

Data (1)

(Tujuan: Mencari kesamaan sekuen, fungsi, evolusi/kekerabatan)

Pilih : All Databases

Ketik : Starch synthase and wheat

Tekan : Go

Output : pilih asesion number/DNA target dgn memberikan Tick pd kotak yg telah ada. Display : summary

1

http://www.ncbi.nlm.nih.gov/sites/gquery?term=starch%20synthase%20and%20wheat

NCBI Entrez, The Life Sciences Search Engine

Search across databases starch synthase and wheat

Result counts displayed in gray indicate one or more terms not found

54	PubMed: biomedical literature citations and abstracts	none	Books: online books
104	PubMed Central: free, full text journal articles	none	OMIM: online Mendelian Inheritance in Man
none	Site Search: NCBI web and FTP sites	none	OMIA: online Mendelian Inheritance in Animals
56	CoreNucleotide: Core subset of nucleotide sequence records	none	dbGaP: genotype and phenotype
4	EST: Expressed Sequence Tag records	10	UniGene: gene-oriented clusters of transcript sequences
none	GSS: Genome Survey Sequence records	none	CDD: conserved protein domain database
83	Protein: sequence database	none	3D Domains: domains from Entrez Structure
2	Genome: whole genome sequences	none	UniSTS: markers and mapping data
none	Structure: three-dimensional macromolecular structures	none	PopSet: population study data sets
1	Taxonomy: organisms in GenBank	none	GEO Profiles: expression and molecular abundance profiles
none	SNP: single nucleotide polymorphism	none	GEO DataSets: experimental sets of GEO data
10	Gene: gene-centered information	none	Cancer Chromosomes: cytogenetic data
			PubChem BioAssay: bioactivity screens of small molecules

2

starch synthase and wheat - CoreNucleotide Results

http://www.ncbi.nlm.nih.gov/sites/entrez?db=nucleotide&cmd=search&term=starch synthase and wheat

NCBI Nucleotide

Search CoreNucleotide for starch synthase and wheat

Found 60 nucleotide sequences. CoreNucleotide [56] EST [4]

Display Summary Show 20 Sort by Send to

All: 56 Bacteria: 1 RefSeq: 2 mRNA: 26

Items 1 - 20 of 56 Page 1 of 3 Next

- 1: [AY954026](#) Reports
Triticum aestivum granule-bound starch synthase GBSS (waxy) gene, waxy-B1e allele, partial cds gi63054376|gb|AY954026.1|[63054376]
- 2: [NC_003070](#) Reports
Arabidopsis thaliana chromosome 1, complete sequence gi42592260|ref|NC_003070.5|[42592260]
- 3: [NC_003075](#) Reports
Arabidopsis thaliana chromosome 4, complete sequence gi30698542|ref|NC_003075.3|[30698542]
- 4: [CS501455](#) Reports
Sequence 1 from Patent WO2007009823 gi138979795|emb|CS501455.1|pat|WO2007009823|1|[138979795]
- 5: [EF466009](#) Reports
Triticum aestivum starch synthase III mRNA, partial cds gi134142363|gb|EF466009.1|[134142363]
- 6: [EF221764](#) Reports
Triticum aestivum granule bunch starch synthase II mRNA, partial cds gi125657170|gb|EF221764.1|[125657170]
- 7: [EF221762](#) Reports

Koleksi Data (2)

Pilih Display : FASTA

1

starch synthase and wheat - CoreNucleotide Results

http://www.ncbi.nlm.nih.gov/sites/entrez?db=nucleotide&cmd=search&term=starch synthase and wheat

NCBI Nucleotide

Search CoreNucleotide for starch synthase and wheat

Display: FASTA

Found 56 EST [4]

1: [AY954026](#) Reports Triticum aestivum...[gi:63054376]

2: [EF466009](#) Reports Triticum aestivum starch synthase III mRNA, partial cds

3: [EF221764](#) Reports Triticum aestivum granule-bound starch synthase II mRNA, partial cds

4: [EF221764](#) Reports Triticum aestivum granule-bound starch synthase II mRNA, partial cds

5: [EF221764](#) Reports Triticum aestivum granule-bound starch synthase II mRNA, partial cds

6: [EF221764](#) Reports Triticum aestivum granule-bound starch synthase II mRNA, partial cds

7: [EF221764](#) Reports Triticum aestivum granule-bound starch synthase II mRNA, partial cds

Output : format FASTA

2

NCBI Sequence Viewer v2.0

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?view=fasta&query_key=1

NCBI Nucleotide

Search CoreNucleotide for

Display: FASTA

Item 1 - 5 of 6

1: [AY954026](#). Reports Triticum aestivum...[gi:63054376]

```
>gi|63054376|gb|AY954026.1| Triticum aestivum granule-bound starch synthase
GGGCCCTCTGGCCCTGCTACCTCAAGAGCACTACCAGTCCAAATGGCCATATATGACGGCCAAAGGTTTGG
CAACTTCTGAACTTCATATCTCTCCGATATCAATCTTTGGCGTTCAATCATCTGGCTGGATTT
TACATTCGAACCTCCATTTGATGGATAGTGGCGCTTCTGCATCCCAACATCTCGTACCAGGGCCGCTTCT
CCTCGACGACTTCGGCGAGCTCAACTGCCGACAGTTCGAATCGCTCTGACTCATCGACGGCTA
CGAACAGCCGTTGGAGGGGGCCCAAGTCACTGATGAAGCCCGGATCTCGACGGCCCAAGGTCCTG
ACGGTGAAGCCCTACTACGGTGAAGGCTCATCTCCGGCAAGCCAGGGGCTGCGAGCTCGAACATCA
TGGCCCTCACGGCCATCACCG
```

2: [EF466009](#). Reports Triticum aestivum...[gi:134142363]

```
>gi|134142363|gb|EF466009.1| Triticum aestivum starch synthase III mRNA, pa
TTGGCGTGGATGTATATGGAAGGAATGACCCGACATTTGGGTTCTCTGTCATCTGCTCTAGA
GTTTATCTCCAGCAATGAATTTCTCCACATATAATACATTTGCCATGATTTGGTCAAGTCTCCGGTCCGG
TGGCTATAAAGGAACACTATTCCCAATCCAGAAATGGCAAGCACTCGGTTGTATTTACCATCCACAATC
TTGAATTTGGAGCACATATATTTGTAAGCAATGACATCTGTGATAAAGCCACAACTTTCTCTCAT
ATATTCAGGGGACGTGGCAGGCCATGGCCCATTTGCTCTCATCTGAGAAATTCACGGCATTTCTCAAT
GAAATGATCCAGATATCTGGGATCCCTACACTGACAAATTTATCCCGTCCCTTATCTTTGAGAGTG
TTGTCGAAGGCAAGAGCGCTGCAAAAGGGCCCTTGACAGCAAGATTTGGATTACAGCAAACTGATGTCCC
TATTGTCGGAATCATCACC
```

3: [EF221764](#). Reports Triticum aestivum...[gi:125657170]

```
>gi|125657170|gb|EF221764.1| Triticum aestivum granule-bound starch synthas
TTGGCGTGGATGTATATGGAAGGAATGACCCGACATTTGGGTTCTCTGTCATCTGCTCTAGA
TCGCTATGATCAGTACAGGATACATGGGATACAAATTTCTGTTGAGGTAATTTGGTGCACAGAA
GAAACAGTCCGCTTTTTTCACTGCTACAAAAGGGGAGTTGATCGTGTTTTGTGATCACTATGTTTC
TTGAGAAGGATGGGGCAAACTGGATCAAAATTTGACGGCCCTACCCTGGAACAGACTCCCGAGATAA
CAAGTACGGTTCTGCTTTTGTGCTTGTGCTATGGAGGCTCCGAGGGTCTTAACTCAATAATTTCT
GAATCTTCTCTGGACATATGGAAGAAATGTTGCTTTGTTGCAAAATGACTGGCACACTGCAATTTG
CATGCTATTTGAAGACATGTATAAGCAAAATGGAATTTAGAGAAATGCAAGGTTGCTTTCATCAATC
CAATATCCGCTACAGGGCAGATTTCCCAAGCGGACTTCGAACTTCTTAAATTTACCTGAAAGTTTCTG
CCTCTATTTGATTTGTTGATGGGCATGTTAAGCCAGTAGTTGGGAGAAAGATTAACTGATGAAGGAC
GGATCAGTGAAGTGTGATGTTGCTTACACTAGTCCACATATGCTCAAAAGAACTCACTTTCGGCCGAGA
GAAAGGTTGAGTGGGCTCTCTGCAAGCCCTTGAACTGGAATTTGAAATGGAATGGAT
GTTTGTGATTTGGAATCCAGCAACAGATTAATACATCAGTGTCAAAATACAAATGCAACACCGGTGGCAGAA
CAAGAGCTCTCAATAAAGAAAATCTGCAAGCTGAAGTTGGATTGCTGTGGACTCTAGCATACCTGTTAT
```

Koleksi Data (3)

Pilih Display : FASTA dan Send to TEXT or FILE

Output : format FASTA - File TEXT

1

2

The screenshot shows the NCBI Sequence Viewer interface. In the top left, a search bar contains the query 'AY954026.1'. Below the search bar, the 'Display' dropdown is set to 'FASTA' and the 'Send to' dropdown is set to 'Text'. The main content area displays the FASTA sequence for the selected entry: `>gi|63054376|gb|AY954026.1| Triticum aestivum granule-bound starch synthase GBSS (waxy) gene, waxy-Ble allele, partial cds`. The sequence is shown in a monospaced font with line wrapping. The interface also includes navigation buttons like 'Previous sequence' and 'Next sequence'.

PROGRAM CLUSTAL W -Global Alignment

Format Data DNA sequence untuk input PROGRAM CLUSTAL W

Buka : //srs6.ebi.ac.uk

Pilih : Tools - Similarity & Homology - Clustal W

1

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?query_key=5&db=...

Welcome to ...n Resource] CLUSTALW online Sistem Infor...kademik ITB Magnitude 7... INDONESIA

>gi|63054376|gb|AY954026.1| Triticum aestivum granule-bound starch synthase GBSS (waxy) gene, partial cds

```
GGGCGCTCTGGCGCTGCTACCTCAAGAGCAACTACCAGTCCAATGGCATCTATATGACGGCCCAAGGTTTTC
CAACTTCTGAAACTCATATCTCTCCGCATATCAATCTTTGGCGTTCATTCATCTGGCGCTGGATTT
TACATTCGAACCTCCATTTCCATGGATAGTGGCGTTCGCATCCACAACATCTCGTACCAGGCGCGTCTC
CTTCCGACACTTCGGCCAGCTCAACTGCCCGCAGCTTCAAGTCTCCTCCGATTCATCGACGGCTCA
CGACAAGCCGCTGGAGGGGCGCAAGTCAACTGGATGAAGCCGGGATCTCGAGGCGCAGAGGTCGTG
ACGGTGAAGCCCTACTACGCTGAGGAGCTCATCTCCGGCGAAGCCAGGGGCTCGAGCTCGACAACATCA
TGGCGCTCACGGGCATCACC
```

>gi|134142363|gb|EF466009.1| Triticum aestivum starch synthase III mRNA, partial cds

```
TTGGCGTGGATGCGTATATGGAAGGAATGATGACCCGAGATTTGGGTTCTCTGTCTATCTGGCTTAGA
GTTTATCCTCCAGAAATGAATTTTCTCCACATATAATACATTTGCCATGATGGCTCAAGTCTCCGGTCCG
TGGCTATATAAGGAACACTATTTCCCAATCCAGAAATGGCAAGCACTCGGGTGTATTTACCATCCACAATC
TTGAATTTGGAGCACATATATTTGGTAAAGCAATGACATAGTGTGAAGGCCACAACGTTTCTCCATAC
ATATTCGAAGGACCTGGCAGGCCATGGCGCCATGCTCCCTCACTCGTAGAATAATCTACCGCATTCCTCAAT
GGAAATGATCCAGATATCTGGGATCCGTACACTGACAATTTATCCCGGTCCCTTATCTGTGAGAGATG
TTGTCGAAGCCAAAGAGCGCTGCAAAAAGGCCCTTGACGACAGAGTTGGATACAGCAAACTGATGTCCC
TATTGTCGGAATCATCACC
```

>gi|125657170|gb|EF221764.1| Triticum aestivum granule bunch starch synthase II mRNA, partial cds

```
TTGGTATGTCGATAGGAGGATGGCCCGAGCTCTGGCTGCAATGGGACACCGGGTATGACGATAGCTCC
TCGCTATGATCAGTACAAGGATACATGGGATACAAATGTTCTCTGAGGTAATTTGGTGGACAGAAACA
GAAACAGTCCGCTTTTTCACCTGCTACAAAAGGGAGTTGATCGTGTGTTTGTGATCATCTATGTTTC
TTGGAAGGTATGGGGCAAAACTGGATCAAAAATGTCAGCGGCTACCCTGGAACAGACTCCGAGATAA
CCAGTACCGTCTCGCTCTTTGGCTTGGCTGCAATGGAGGCTCGAGGGTCTTAAATCTCAATAATCTC
GAATACTCTCTGGACCATATGGAGAAAATGTTGCTTTGTCGAAATGACTGGCACACTGCAGCTTTTGC
CATGCTATTTGAAGAGCATGTATAAGCAAAAATGGAATTTATGAGAAATGCCAAGTTCCTTCTGCATTCA
CAATATCCGCTATCAGGGCAGATTTCCAGAGCGGACTTCGAACCTCTTAAATTTACCTGAAAGTTTCGTG
CCTTCATTTGATTTGTTGATGGGCATGTTAAGCCAGTAGTTGGGAGAAAGATTAACCTGGATGAAGCCAG
GGATCACTGAGTGTGATGTTGCTTACAGTTAGTCCACATTAATGTCAAAAGCACTCACTTCCGGCCAGA
GAAAGGTGTTGAGTTGGATGGCTCCTCTCGTCAAAAAGCCCTTGAACCTGGAATTTGAAATGGAAATGGAT
GTTGTTGATTTGGAATCCAGCAACAGATAAGTACATCAGTCTCAATAACAAATGCAACACCGTGGCAGAA
CAAGAGCTCTCAATAAAGAAAATCTGCAAGCTGAAGTTGGATTTGCTGTTGAGCTTACATACCTGTTAT
AGTTTTCAATTTGACGCTCTTGAAGAAACAGAAAAGGTCAGACATACTAATTCAGCCATACCCGAGTTTTC
GAGGAGAAATGTTTCAGATAATGTTCTCCGACAGGGAAGAGAAAATGGAGGAGAACTGATGCTGCTAG
AAGCGAAGTACCCACAGAA
```

>gi|125657167|gb|EF221762.1| Triticum aestivum starch synthase I-1-like mRNA, partial sequence

```
GGGAGGACGTCAGTTTTCATGCTTGGATCTGGGATCCAAATTTTGAAGCGTGGATGAGATCTACCGA
CTCGAGTTACAAGGATAAATCCGCTGGATGGGTTGGATTTAGTGTCCAGTTTCCACAGAAATAACTGTGA
GTTTCCGATATATGTTAATGCCATCCAGGTTTGAACCTGTGCTTAAATCAGCTATATGCTATGCCAAT
ATGGTACAGTTCCTGTAGTTTCAAGGAACTGGGGCCCTCCGAGACACAGTCCGAGCTTCAACCTTTTGG
TCCAAAAGGAGAGGAGGTTACAGGCTGGGGCTTCTCACCCCTAACCTGGACAAGATGTTTGGGCAATFG
CGAACCCGATGTCGACATTCAGGGAGCAACACCGCTCCTGGGAGGGGCTCATGAACGAGGCATGACAAA
AAGACCATACCTGGGACCATCCCGCCGAGCAGTACGACGAGATCTTCCGAATGGCCCTCTGTTGACAGCC
ATACGCTATGATAGACGGGACTGGGGAGGTCGAAGCCGAGCTCTCTTGGGCTCAGAAACATGTTCTCTC
ATCCTTCCCGGGCCCGAAGGATACCCCTGTACATTTGCTGGAAACCGGGTCTCTCTACAAATAGTGCAAT
CGCGCTGCTGCTTGGTTCCCGGCTTCGAGAGTAAATGATGCTGTGCTGCTGGCGGCTGACAGCTTCG
GGTGGATGACAGTTTTCGGGGAATAAGGAAGGGGCTCGAGAAATGGTTAAACGACCAAGTTCG
```

2

SRS@EBI (srs.ebi.ac.uk)

http://srs6.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSession

CLUSTALW online Sistem Infor...kademik ITB Magnitude 7... INDONESIA

EBI Search

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Protein Functional Analysis

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Sequence Analysis

Similarity & Homology

Structural Analysis

Tools - Miscellaneous

Web Services

Downloads

online searchable help.

look in our [SRS@EBI](#)

FAQ for answers to commonly asked questions

Want to know how to use SRS? go to the Help page

Linking to SRS? Please read our Linking to SRS guide for important information regarding linking to our SRS server.

Public SRS servers worldwide

Check Text Search

Search Tips

Matching: Enter Text Here

Nucleotides

Search

Results

MAFFT

MUSCLE

Pepstats/ Pepwindow/ Pepinfo

PromoterWise

SAPS

T-Coffee

Transeq

Feedback/comments please send them to us using the support form.

27.07.07 Due to resource limitations we have removed a number of databanks from SRS@EBI. For details and links to alternative services please see the [SRS@EBI](#) wiki.

biowisdom SRS

List Search

Search Tips

Paste in a list of sequence ID's. The list must be of the format DATABASE:ID. e.g. EMBL:AB046566 or UNIPROT:104K_THEAN. For more details see the [wiki](#).

Ensure each entry is on a single line and that the database(s) exists on this server. Multiple databases can be searched simultaneously. There is a maximum limit of 500 ID's.

List file Choose File no file selected

Search

Open 'http://www.ebi.ac.uk/Tools/clustalw/index.html' in a new tab

Tampilan program CLUSTAL W

1

Parameter-parameter yang dapat dirubah sesuai dengan kepentingan (input, output dll)

1. Copy & Paste : file FASTA - DNA sequence yang akan di alignment.
2. Pilih : Run

OUTPUT (1)

The screenshot shows the ClustalW web interface. At the top, there is a navigation bar with 'EMBL-EBI' and 'EB-eye Search' logos, a search input field, and a 'Go' button. Below this is a menu with 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. The main content area is titled 'ClustalW Results' and contains a table of search results. Below the table is a 'Scores Table' section with a 'Sort by' dropdown menu and a 'View Output File' button. The browser's address bar shows the URL: 'http://www.ebi.ac.uk/cgi-bin/clustalw/result?tool=clustalw&jobid=clu...'. The browser's title bar says 'ClustalW'.

1

Output file yang dapat di save di komputer

2

Results of search

Number of sequences	5
Alignment score	24606
Sequence format	Pearson
Sequence type	nt
ClustalW version	1.83
JalView	Start Jalview
Output file	clustalw-20070828-10483861.output
Alignment file	clustalw-20070828-10483861.aln
Guide tree file	clustalw-20070828-10483861.dnd
Your input file	clustalw-20070828-10483861.input

To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the JalView button, reload the page and check your browser settings to enable Java Applets.

Scores Table

Sort by:

SeqA	Name	Len (nt)	SeqB	Name	Len (nt)	Score
1	Nolanaperuviana	880	2	Lyciumdeserti	889	94
1	Nolanaperuviana	880	3	glaucavoucher	889	94
1	Nolanaperuviana	880	4	Oryzasativa	442	8
1	Nolanaperuviana	880	5	Oryzarufipogon	437	3
2	Lyciumdeserti	889	3	glaucavoucher	889	97
2	Lyciumdeserti	889	4	Oryzasativa	442	3
2	Lyciumdeserti	889	5	Oryzarufipogon	437	5
3	glaucavoucher	889	4	Oryzasativa	442	7
3	glaucavoucher	889	5	Oryzarufipogon	437	5
4	Oryzasativa	442	5	Oryzarufipogon	437	99

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

Sort by:

Tugas Praktikum

Lakukan Analisis DNA sequence yang meliputi : (Hasil disimpan pada Folder masing -masing)

1. DNA Sequence database searching (website NCBI)
2. DNA Sequence Alignment : pairwise alignment (BLAST)
3. DNA Sequence Alignment : Multiple alignment (Program Clustal W) - 8 sampel DNA sequence yang di alignment.

Pada gen-gen dibawah ini :

No	Nama Gen	Tugas Kelompok
1	Acc Synthase	I
2	Amylase	II
3	Luciferase	III
4	Catalase	IV
5	Endochitinase	V
6	Alcohol dehydrogenase	VI
7	Chalcone synthase	VII

THANK
YOU



607132.wordpress.com

Noviani's Blog

