ambl

michael smith laboratories

UBC

MICB 405 Bioinformatics
Mini-Lab #2 - BLAST

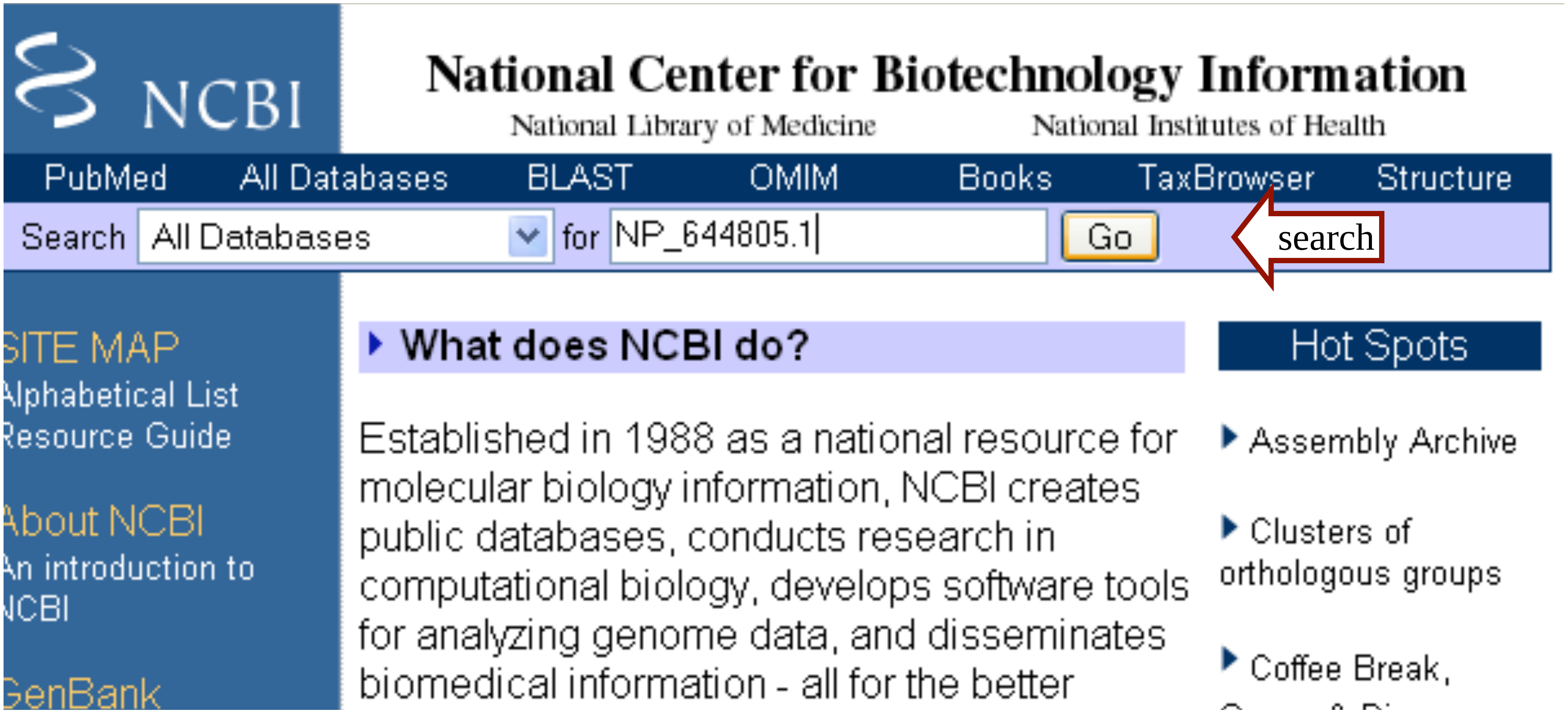
Dr. Joanne Fox
joanne@msl.ubc.ca

We gratefully acknowledge the funding for the development of these teaching materials provided by UBC students through the Teaching and Learning Enhancement Fund (TLEF) from 2005-2007.

Objectives

- By the end of today’s tutorial:
  - You will use the web interface at the NCBI to run a BLAST search.
  - You will investigate the graphical view, the BLAST “hits” list, and the pairwise alignments for the results of this BLAST search.
  - You will view the taxonomy reports for this BLAST result.

Search Entrez for NP_644805.1



National Center for Biotechnology Information

National Library of Medicine National Institutes of Health

SITE MAP
Alphabetical List
Resource Guide

About NCBI
An introduction to NCBI

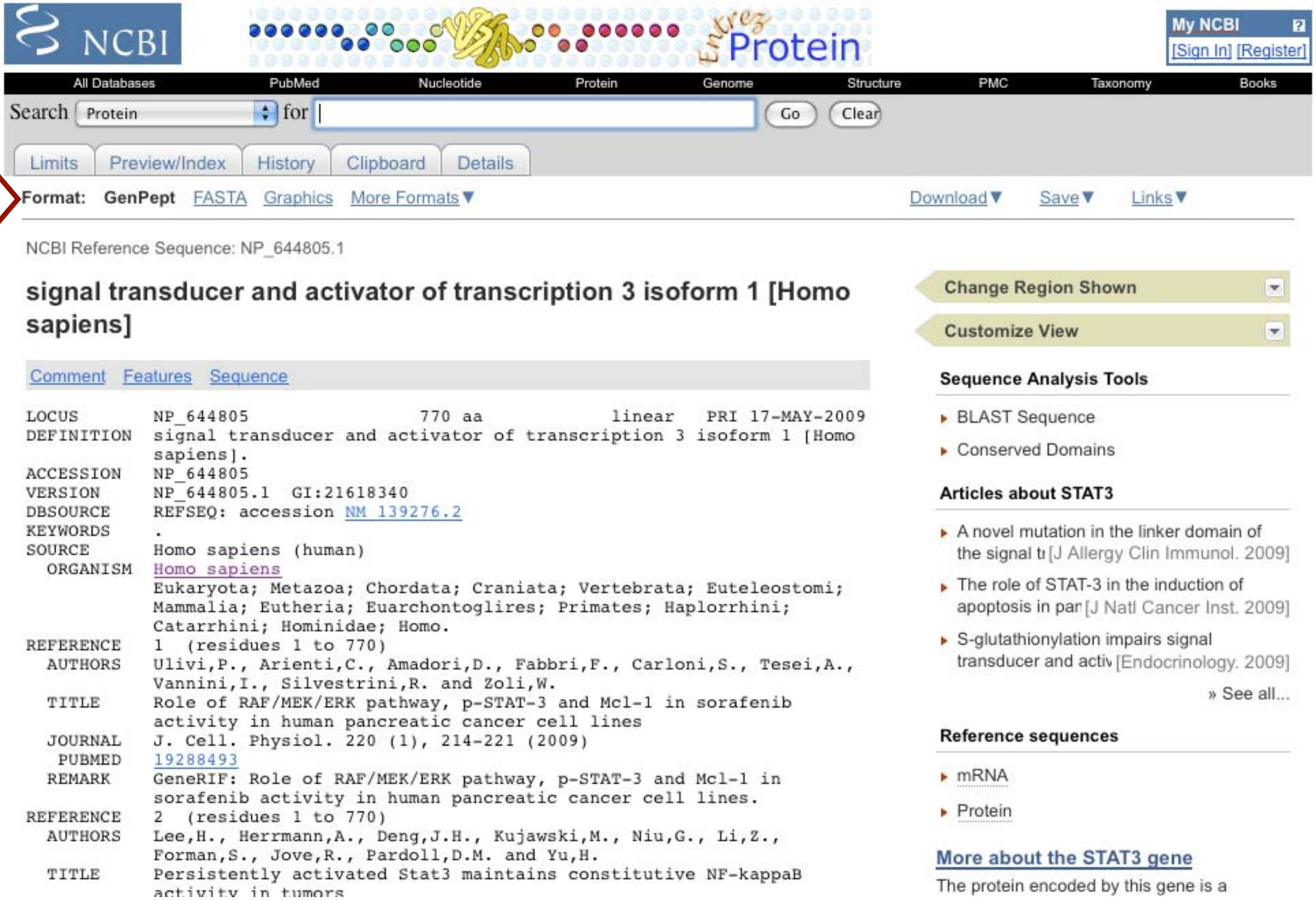
GenBank

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better

Retrieve FASTA sequence

FASTA



NCBI Reference Sequence: NP_644805.1

signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]

```
LOCUS       NP_644805                770 aa            linear   PRI 17-MAY-2009
DEFINITION  signal transducer and activator of transcription 3 isoform 1 [Homo
            sapiens].
ACCESSION   NP_644805
VERSION     NP_644805.1  GI:21618340
DBSOURCE    REFSEQ: accession NM_139276.2
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 770)
  AUTHORS   Ulivi,P., Arienti,C., Amadori,D., Fabbri,F., Carloni,S., Tesei,A.,
            Vannini,I., Silvestrini,R. and Zoli,W.
  TITLE     Role of RAF/MEK/ERK pathway, p-STAT-3 and Mcl-1 in sorafenib
            activity in human pancreatic cancer cell lines
  JOURNAL   J. Cell. Physiol. 220 (1), 214-221 (2009)
   PUBMED   19288493
  REMARK    GeneRIF: Role of RAF/MEK/ERK pathway, p-STAT-3 and Mcl-1 in
            sorafenib activity in human pancreatic cancer cell lines.
REFERENCE   2  (residues 1 to 770)
  AUTHORS   Lee,H., Herrmann,A., Deng,J.H., Kujawski,M., Niu,G., Li,Z.,
            Forman,S., Jove,R., Pardoll,D.M. and Yu,H.
  TITLE     Persistently activated Stat3 maintains constitutive NF-kappaB
            activity in tumors
```

Sequence Analysis Tools

- BLAST Sequence
- Conserved Domains

Articles about STAT3

- A novel mutation in the linker domain of the signal tı [J Allergy Clin Immunol. 2009]
- The role of STAT-3 in the induction of apoptosis in par [J Natl Cancer Inst. 2009]
- S-glutathionylation impairs signal transducer and activ [Endocrinology. 2009]

» See all...

Reference sequences

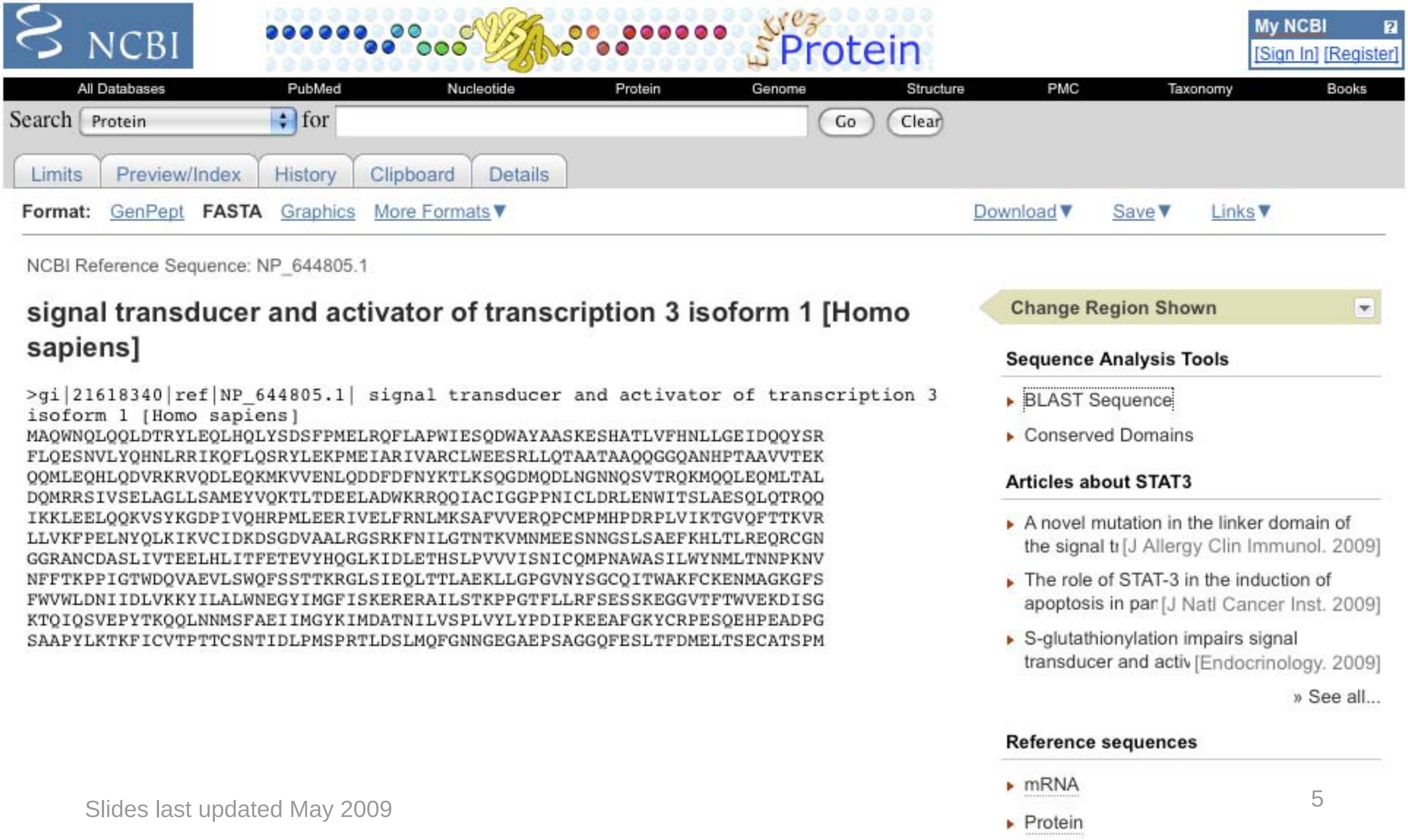
- mRNA
- Protein

More about the STAT3 gene

The protein encoded by this gene is a

Slides last updated May 2009

Copy (and Paste) Sequence



NCBI Reference Sequence: NP_644805.1

signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]

```
>gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3
isoform 1 [Homo sapiens]
MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSR
FLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEK
QQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTAL
DQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQ
IKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVR
LLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
GGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNV
NFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFS
FWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISG
KTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPG
SAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMELTSECATSPM
```

Sequence Analysis Tools

- BLAST Sequence
- Conserved Domains

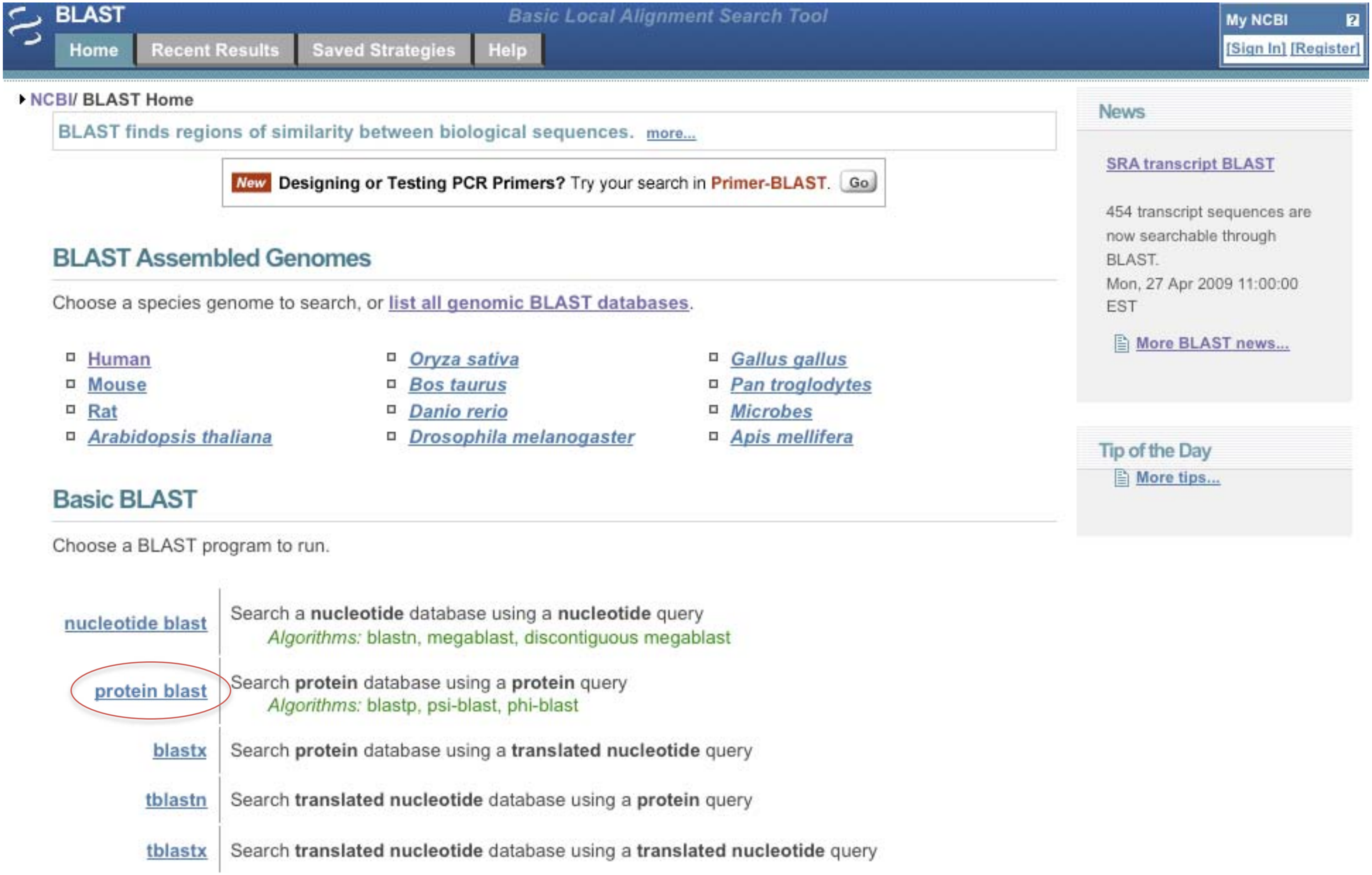
Articles about STAT3

- A novel mutation in the linker domain of the signal t [J Allergy Clin Immunol. 2009]
- The role of STAT-3 in the induction of apoptosis in par [J Natl Cancer Inst. 2009]
- S-glutathionylation impairs signal transducer and acti [Endocrinology. 2009]

» See all...

Reference sequences

- mRNA
- Protein



NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. more...

New Designing or Testing PCR Primers? Try your search in Primer-BLAST.

BLAST Assembled Genomes

Choose a species genome to search, or list all genomic BLAST databases.

- Human
- Mouse
- Rat
- *Arabidopsis thaliana*
- *Oryza sativa*
- *Bos taurus*
- *Danio rerio*
- *Drosophila melanogaster*
- *Gallus gallus*
- *Pan troglodytes*
- *Microbes*
- *Apis mellifera*

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous 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

News

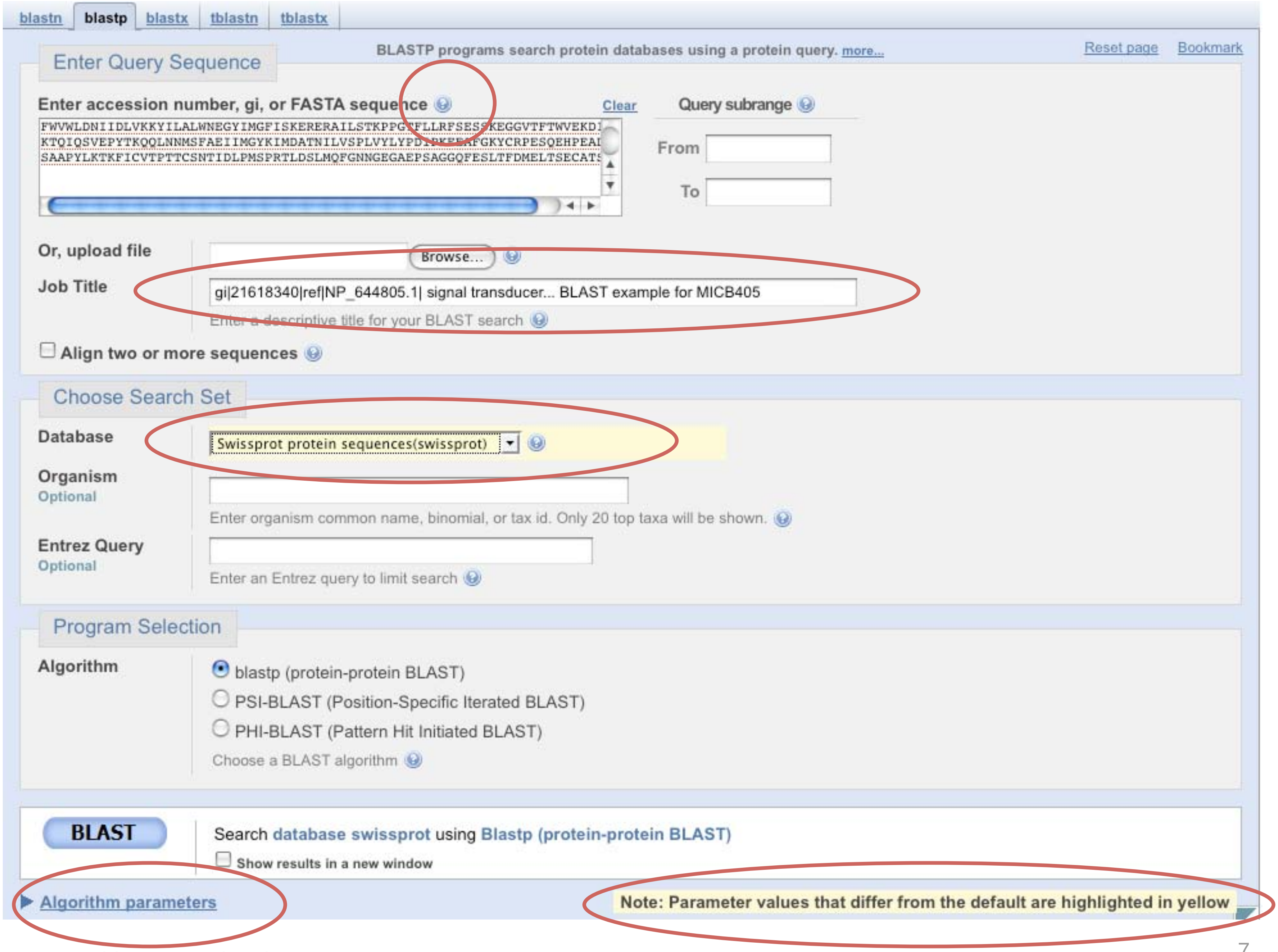
SRA transcript BLAST

454 transcript sequences are now searchable through BLAST.
Mon, 27 Apr 2009 11:00:00 EST

More BLAST news...

Tip of the Day

More tips...



BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

Enter accession number, gi, or FASTA sequence

```
FWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKD
KTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEA
SAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMELTSECAT
```

Query subrange
From
To

Or, upload file

Job Title: gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database: Swissprot protein sequences(swissprot)

Organism
Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query
Optional

Enter an Entrez query to limit search

Program Selection

Algorithm
- ● blastp (protein-protein BLAST)
- ○ PSI-BLAST (Position-Specific Iterated BLAST)
- ○ PHI-BLAST (Pattern Hit Initiated BLAST)

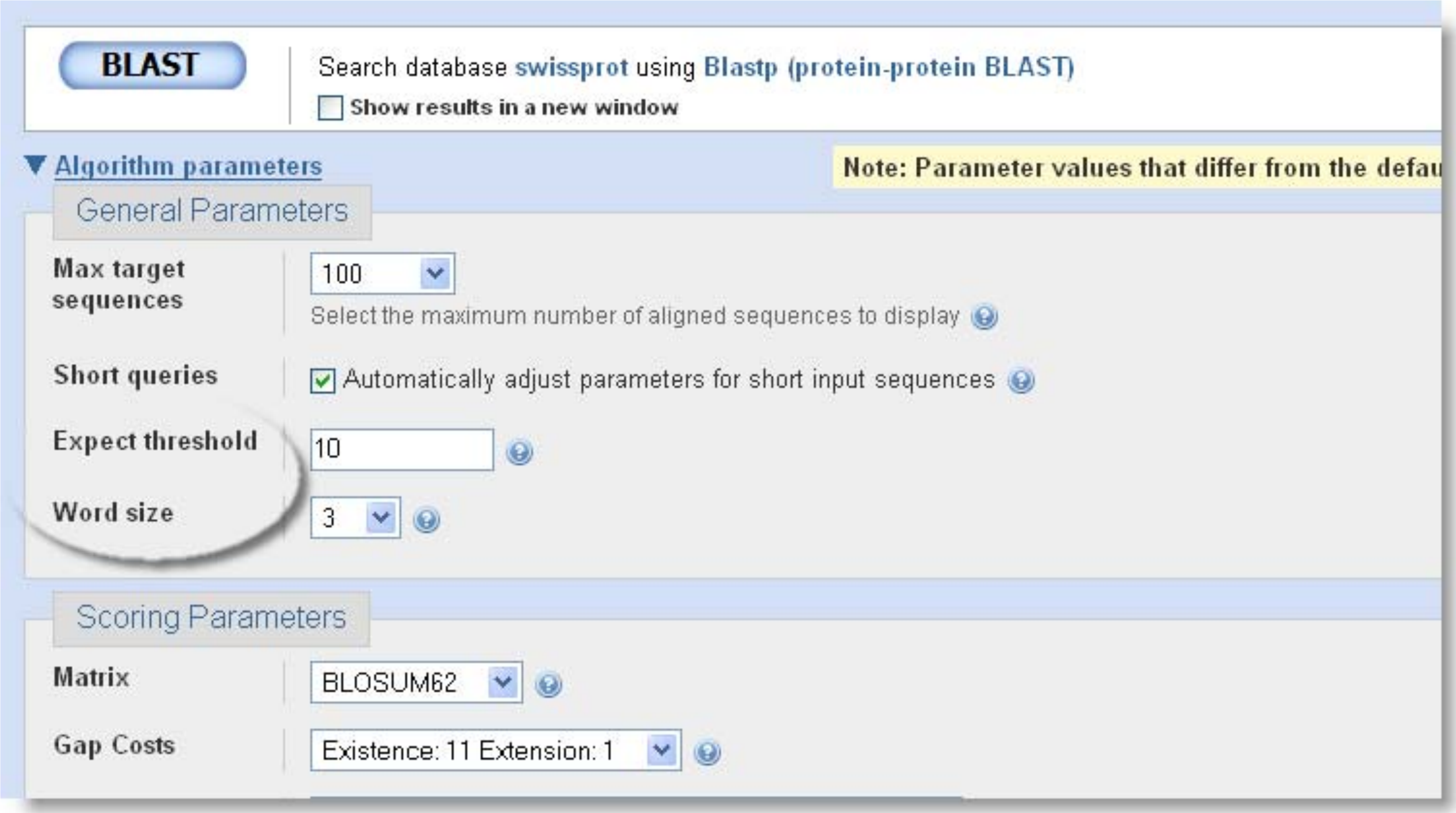
Choose a BLAST algorithm

Search database swissprot using Blastp (protein-protein BLAST)

☐ Show results in a new window

▶ Algorithm parameters

Note: Parameter values that differ from the default are highlighted in yellow



Search database swissprot using Blastp (protein-protein BLAST)

☐ Show results in a new window

▼ Algorithm parameters

Note: Parameter values that differ from the defau

General Parameters

Max target sequences 100

Select the maximum number of aligned sequences to display

Short queries ☑ Automatically adjust parameters for short input sequences

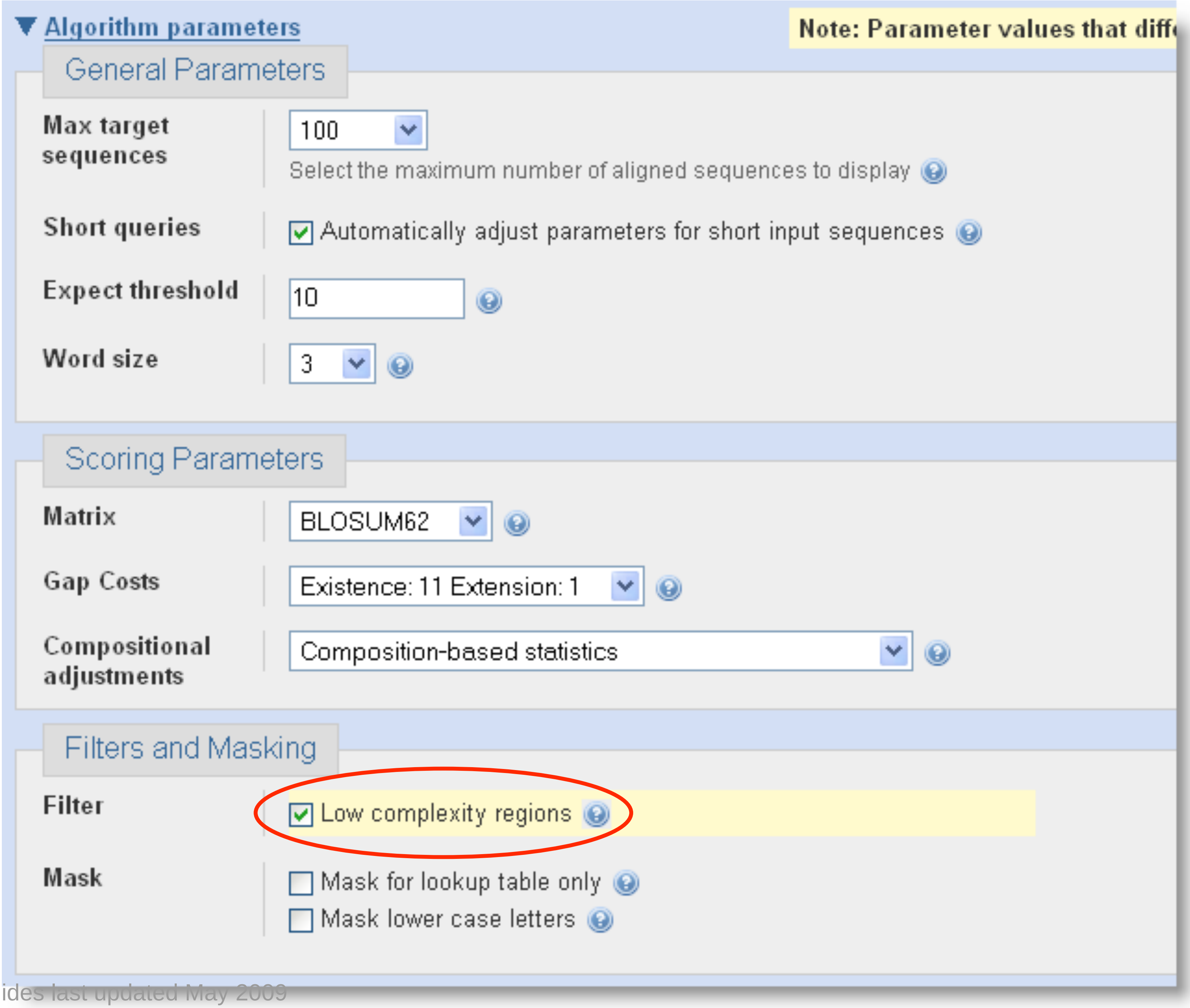
Expect threshold 10

Word size 3

Scoring Parameters

Matrix BLOSUM62

Gap Costs Existence: 11 Extension: 1



▼ Algorithm parameters

Note: Parameter values that diff

General Parameters

Max target sequences: 100
Select the maximum number of aligned sequences to display

Short queries: ☑ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

Scoring Parameters

Matrix: BLOSUM62

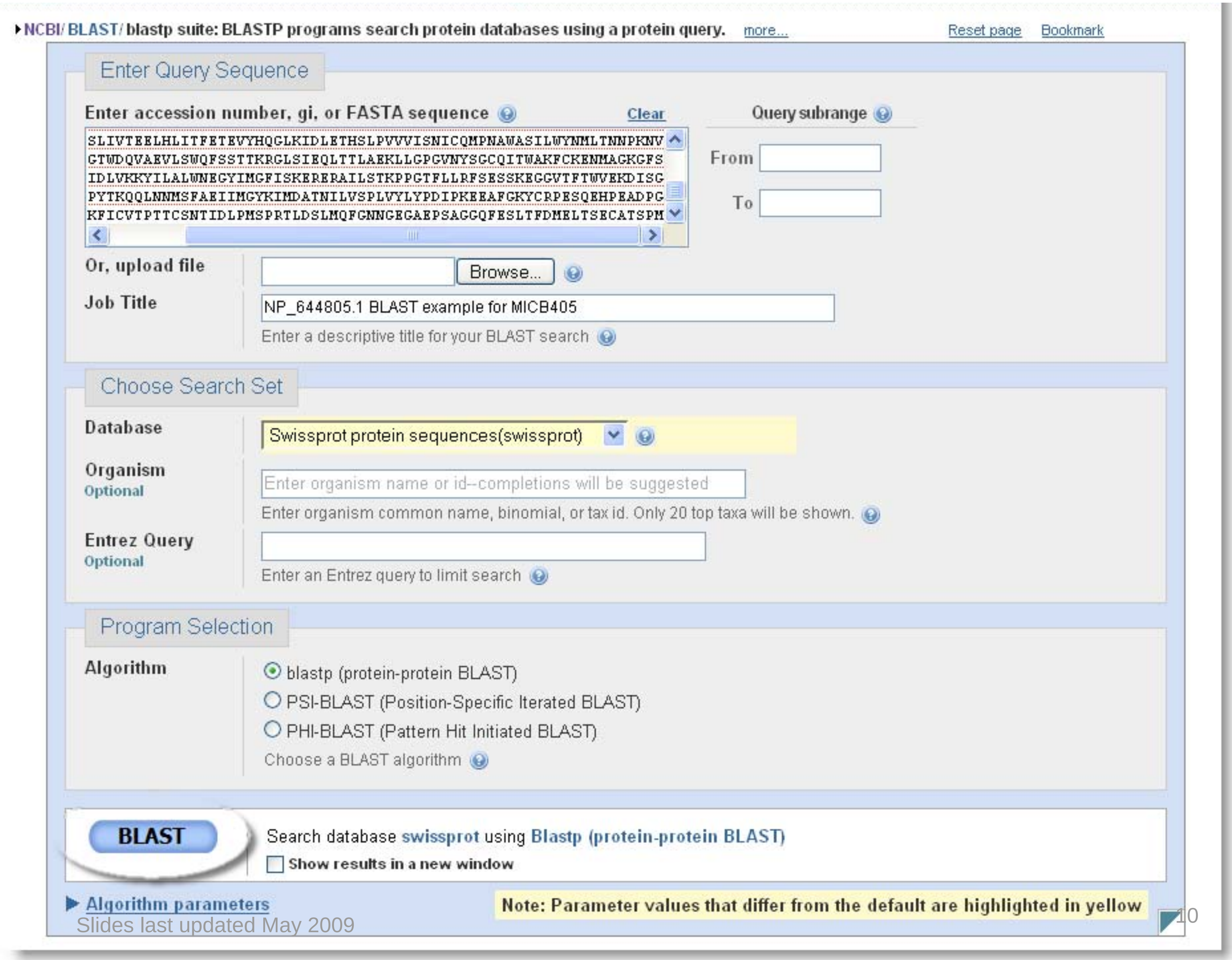
Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Composition-based statistics

Filters and Masking

Filter: ☑ Low complexity regions

Mask: ☐ Mask for lookup table only
☐ Mask lower case letters



▸ NCBI/ BLAST/ blastp suite: BLASTP programs search protein databases using a protein query. more... Reset page Bookmark

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

```
SLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNV
GTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFS
IDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISG
PYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPG
KFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMELTSECATSPM
```

Query subrange

From

To

Or, upload file Browse...

Job Title: NP_644805.1 BLAST example for MICB405

Enter a descriptive title for your BLAST search

Choose Search Set

Database: Swissprot protein sequences(swissprot)

Organism
Optional

Enter organism name or id--completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query
Optional

Enter an Entrez query to limit search

Program Selection

Algorithm

● blastp (protein-protein BLAST)

○ PSI-BLAST (Position-Specific Iterated BLAST)

○ PHI-BLAST (Pattern Hit Initiated BLAST)

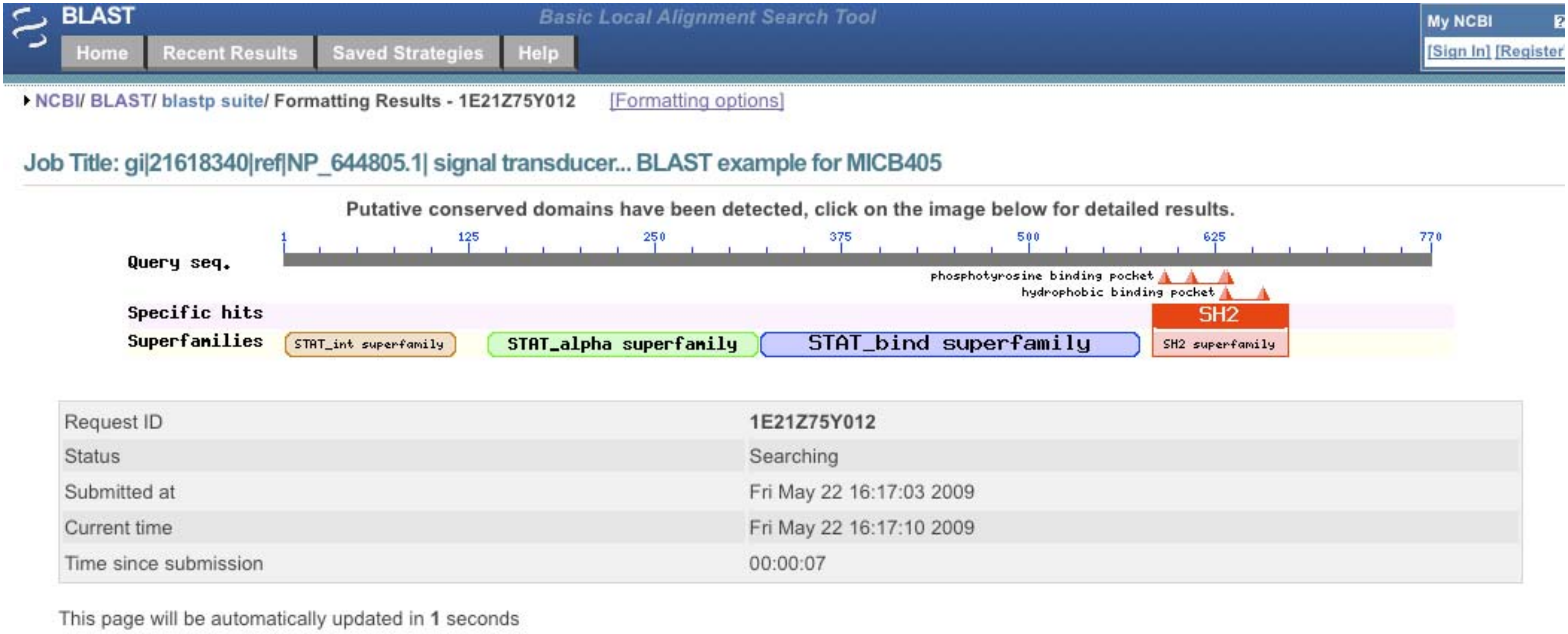
Choose a BLAST algorithm

Search database swissprot using Blastp (protein-protein BLAST)

☐ Show results in a new window

▶ Algorithm parameters

Note: Parameter values that differ from the default are highlighted in yellow



NCBI/ BLAST/ blastp suite/ Formatting Results - 1E21Z75Y012 [Formatting options]

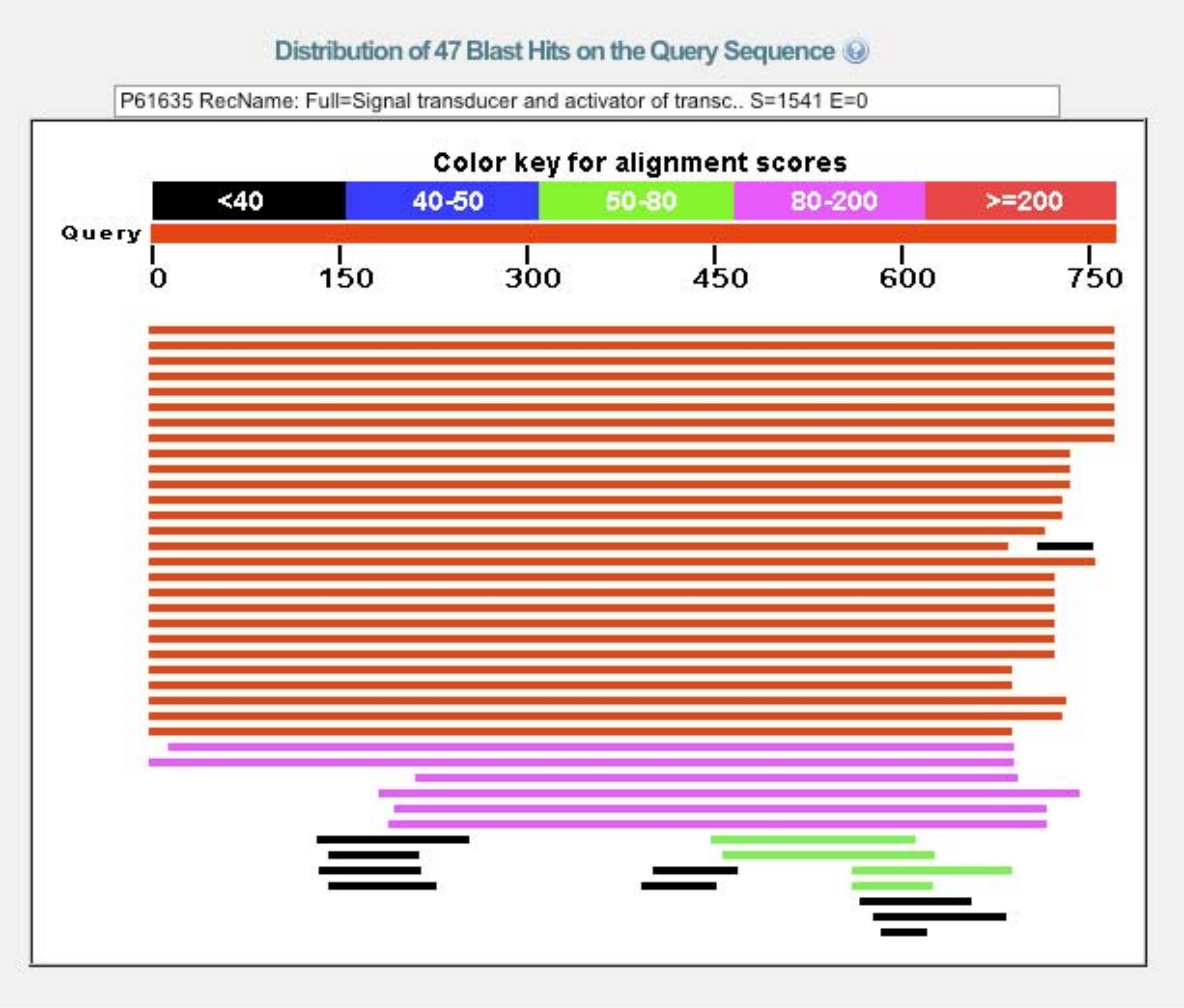
Job Title: gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Putative conserved domains have been detected, click on the image below for detailed results.

Request ID	**1E21Z75Y012**
Status	Searching
Submitted at	Fri May 22 16:17:03 2009
Current time	Fri May 22 16:17:10 2009
Time since submission	00:00:07

This page will be automatically updated in **1** seconds

A graphical view of your BLAST results:

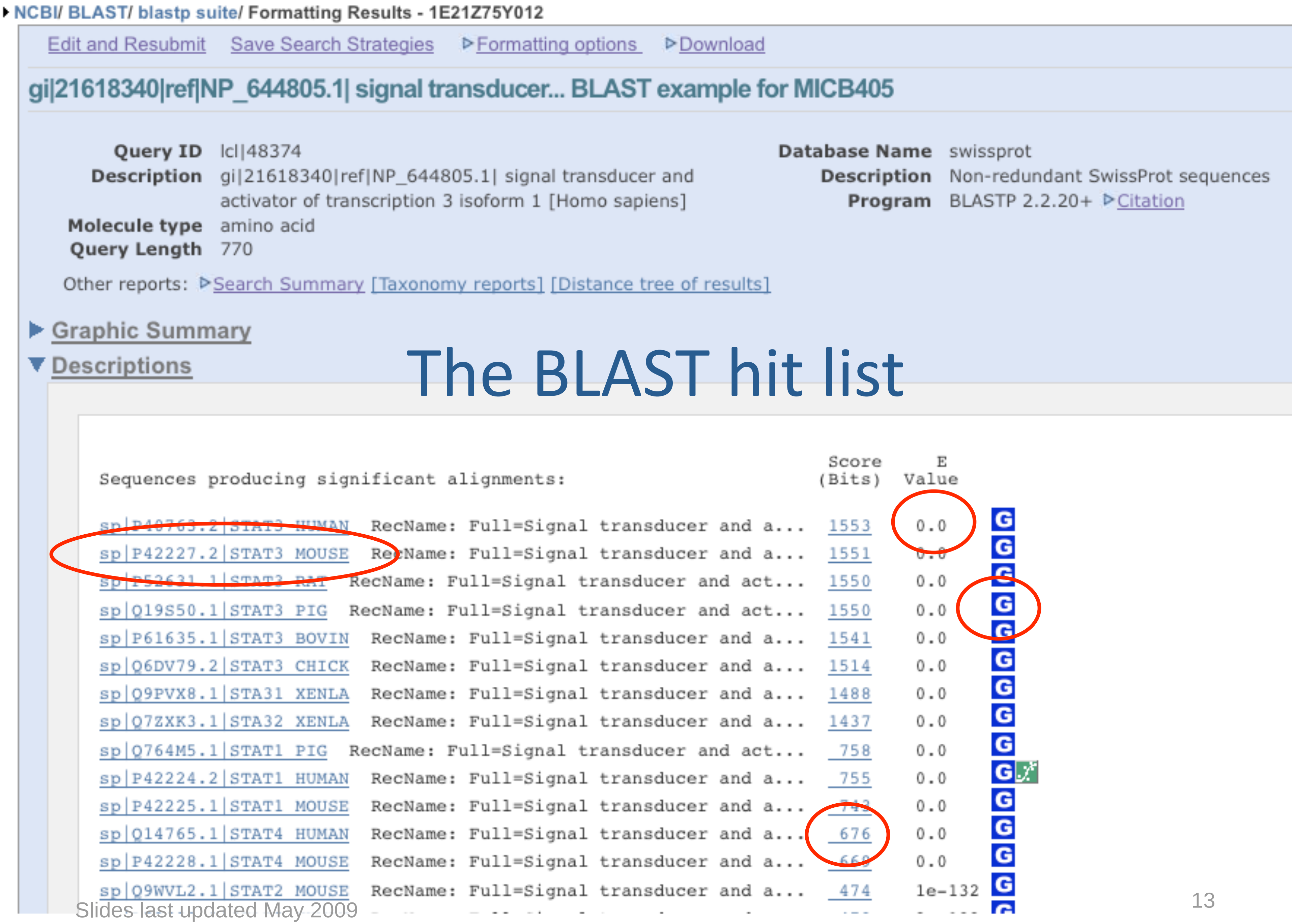


Distribution of 47 Blast Hits on the Query Sequence

P61635 RecName: Full=Signal transducer and activator of transc.. S=1541 E=0

Slides last updated May 2009

The BLAST hit list



NCBI/ BLAST/ blastp suite/ Formatting Results - 1E21Z75Y012

gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

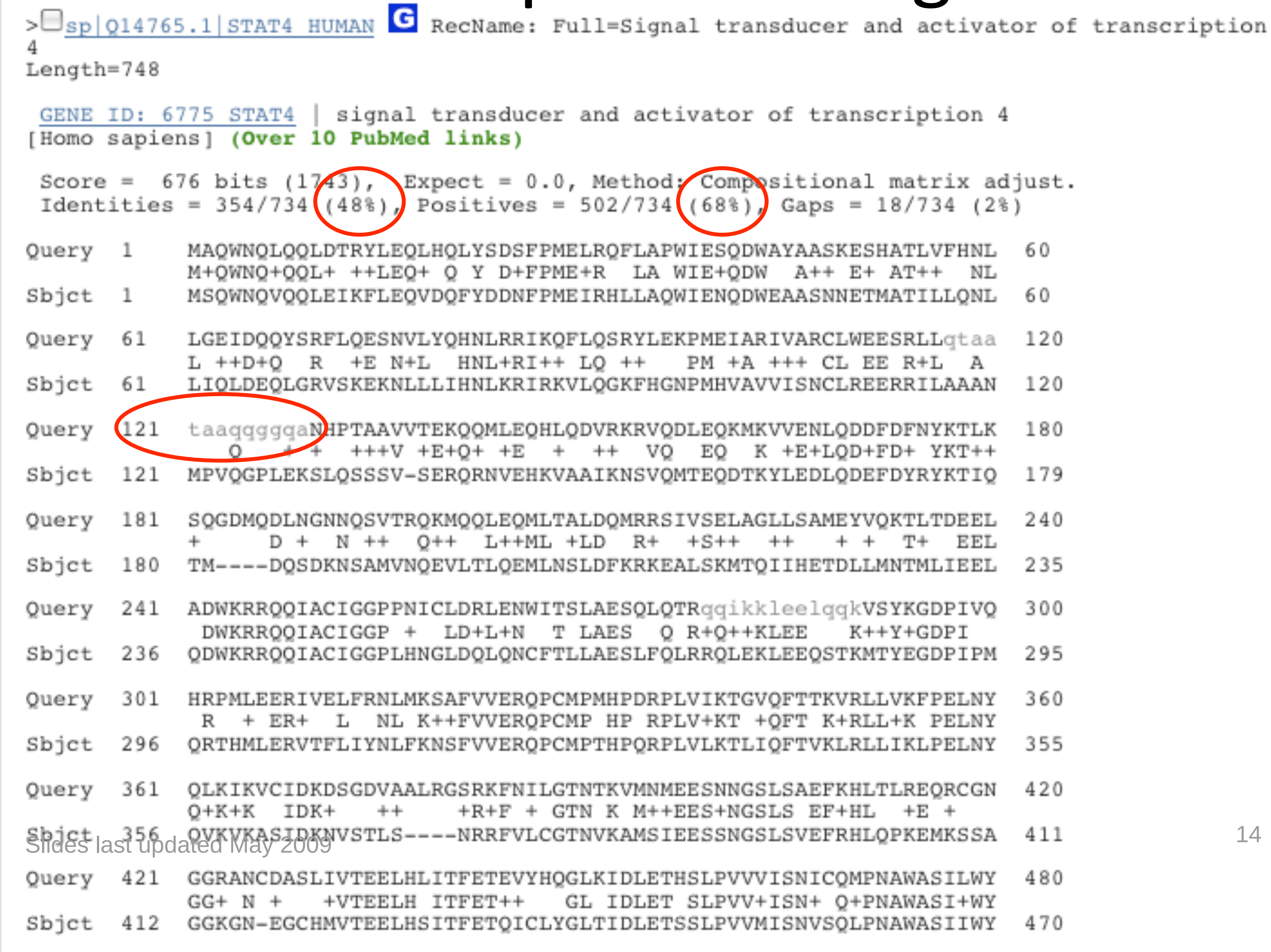
Query ID lcl|48374
Description gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]
Molecule type amino acid
Query Length 770

Database Name swissprot
Description Non-redundant SwissProt sequences
Program BLASTP 2.2.20+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

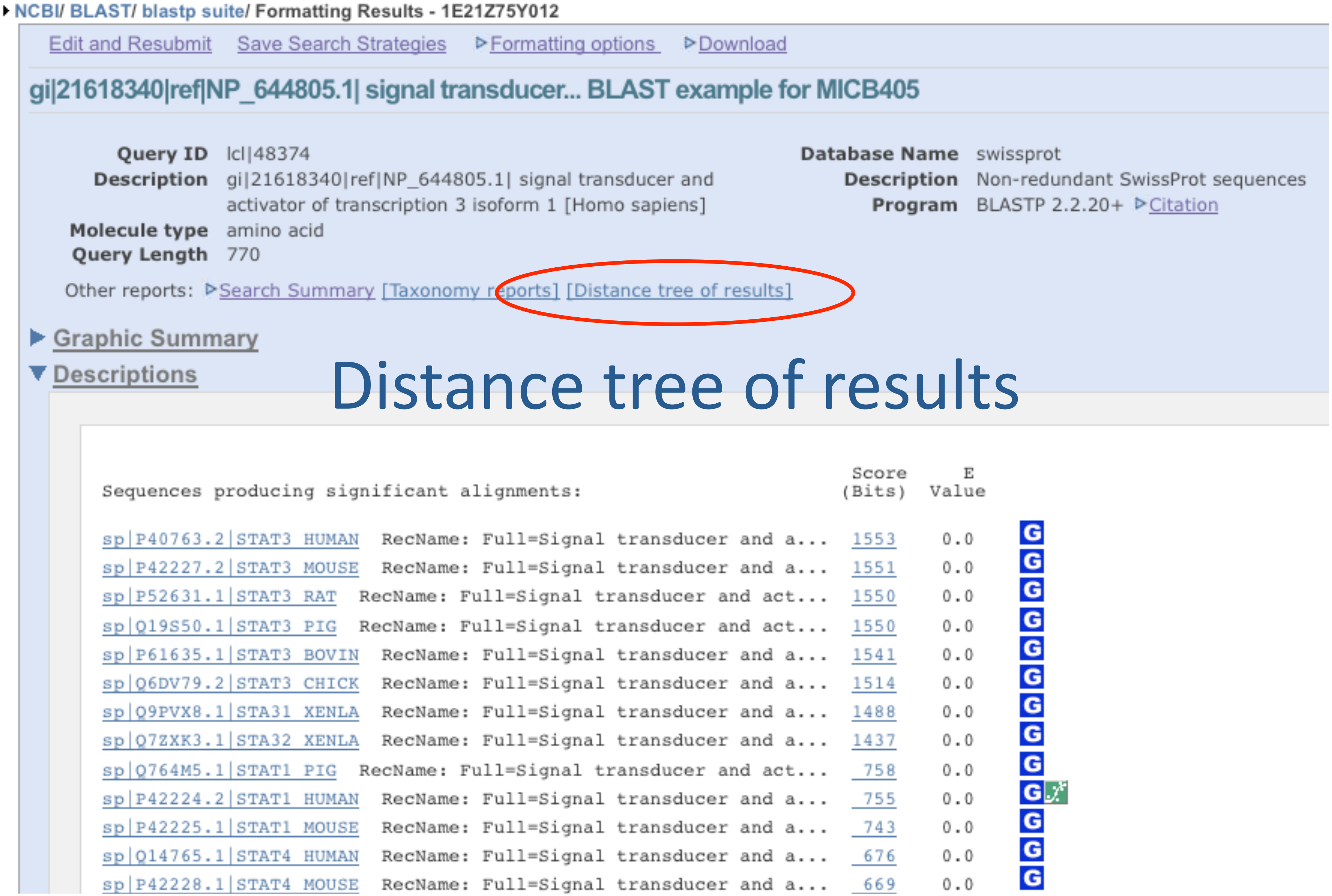
```
                                                                     Score     E
Sequences producing significant alignments:                          (Bits)  Value

sp|P40763.2|STAT3_HUMAN  RecName: Full=Signal transducer and a...    1553    0.0
sp|P42227.2|STAT3_MOUSE  RecName: Full=Signal transducer and a...    1551    0.0
sp|P52631.1|STAT3_RAT  RecName: Full=Signal transducer and act...    1550    0.0
sp|Q19S50.1|STAT3_PIG  RecName: Full=Signal transducer and act...    1550    0.0
sp|P61635.1|STAT3_BOVIN  RecName: Full=Signal transducer and a...    1541    0.0
sp|Q6DV79.2|STAT3_CHICK  RecName: Full=Signal transducer and a...    1514    0.0
sp|Q9PVX8.1|STA31_XENLA  RecName: Full=Signal transducer and a...    1488    0.0
sp|Q7ZXK3.1|STA32_XENLA  RecName: Full=Signal transducer and a...    1437    0.0
sp|Q764M5.1|STAT1_PIG  RecName: Full=Signal transducer and act...     758    0.0
sp|P42224.2|STAT1_HUMAN  RecName: Full=Signal transducer and a...     755    0.0
sp|P42225.1|STAT1_MOUSE  RecName: Full=Signal transducer and a...     743    0.0
sp|Q14765.1|STAT4_HUMAN  RecName: Full=Signal transducer and a...     676    0.0
sp|P42228.1|STAT4_MOUSE  RecName: Full=Signal transducer and a...     669    0.0
sp|Q9WVL2.1|STAT2_MOUSE  RecName: Full=Signal transducer and a...     474    1e-132
```

BLAST local pairwise alignment



```
>☐sp|Q14765.1|STAT4_HUMAN G RecName: Full=Signal transducer and activator of transcription
4
Length=748

 GENE ID: 6775 STAT4 | signal transducer and activator of transcription 4
[Homo sapiens] (Over 10 PubMed links)

 Score =  676 bits (1743),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 354/734 (48%), Positives = 502/734 (68%), Gaps = 18/734 (2%)

Query  1    MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL  60
            M+QWNQ+QQL+ ++LEQ+ Q Y D+FPME+R  LA WIE+QDW  A++ E+ AT++  NL
Sbjct  1    MSQWNQVQQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDWEAASNNETMATILLQNL  60

Query  61   LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLqtaa  120
            L ++D+Q  R  +E N+L  HNL+RI++ LQ ++   PM +A +++ CL EE R+L  A
Sbjct  61   LIQLDEQLGRVSKEKNLLLIHNLKRIRKVLQGKFHGNPMHVAVVISNCLREERRILAAAN  120

Query  121  taaqqggqaNHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK  180
               Q   + +  +++V +E+Q+ +E  +  ++  VQ  EQ  K +E+LQD+FD+ YKT++
Sbjct  121  MPVQGPLEKSLQSSSV-SERQRNVEHKVAAIKNSVQMTEQDTKYLEDLQDEFDYRYKTIQ  179

Query  181  SQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEEL  240
            +     D +  N ++  Q++  L++ML +LD  R+  +S++  ++   + +  T+  EEL
Sbjct  180  TM----DQSDKNSAMVNQEVLTLQEMLNSLDFKRKEALSKMTQIIHETDLLMNTMLIEEL  235

Query  241  ADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRqqikkleelqqkVSYKGDPIVQ  300
             DWKRRQQIACIGGP +  LD+L+N  T LAES  Q R+Q++KLEE   K++Y+GDPI
Sbjct  236  QDWKRRQQIACIGGPLHNGLDQLQNCFTLLAESLFQLRRQLEKLEEQSTKMTYEGDPIPM  295

Query  301  HRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNY  360
             R  + ER+  L  NL K++FVVERQPCMP HP RPLV+KT +QFT K+RLL+K PELNY
Sbjct  296  QRTHMLERVTFLIYNLFKNSFVVERQPCMPTHPQRPLVLKTLIQFTVKLRLLIKLPELNY  355

Query  361  QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN  420
            Q+K+K  IDK+   ++    +R+F + GTN K M++EES+NGSLS EF+HL  +E +
Sbjct  356  QVKVKASIDKNVSTLS----NRRFVLCGTNVKAMSIEESSNGSLSVEFRHLQPKEMKSSA  411

Query  421  GGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWY  480
            GG+ N +   +VTEELH ITFET++   GL IDLET SLPVV+ISN+ Q+PNAWASI+WY
Sbjct  412  GGKGN-EGCHMVTEELHSITFETQICLYGLTIDLETSSLPVVMISNVSQLPNAWASIIWY  470
```

Distance tree of results



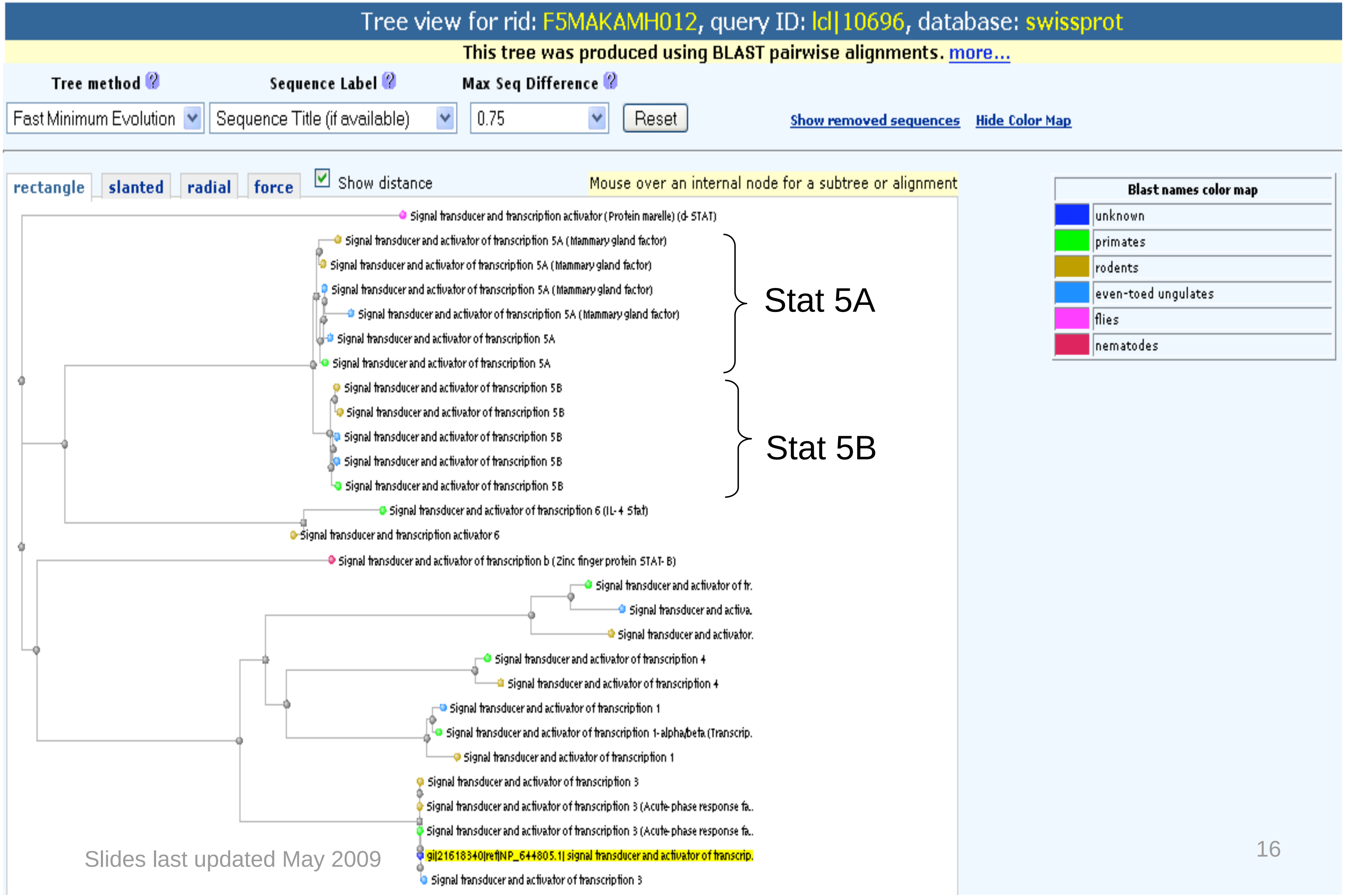
gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Query ID	lcl|48374	**Database Name**	swissprot
Description	gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]	**Description**	Non-redundant SwissProt sequences
Molecule type	amino acid	**Program**	BLASTP 2.2.20+ ▷Citation
Query Length	770		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results]

```
                                                                Score    E
Sequences producing significant alignments:                    (Bits)  Value

sp|P40763.2|STAT3_HUMAN  RecName: Full=Signal transducer and a...  1553    0.0    G
sp|P42227.2|STAT3_MOUSE  RecName: Full=Signal transducer and a...  1551    0.0    G
sp|P52631.1|STAT3_RAT  RecName: Full=Signal transducer and act...  1550    0.0    G
sp|Q19S50.1|STAT3_PIG  RecName: Full=Signal transducer and act...  1550    0.0    G
sp|P61635.1|STAT3_BOVIN  RecName: Full=Signal transducer and a...  1541    0.0    G
sp|Q6DV79.2|STAT3_CHICK  RecName: Full=Signal transducer and a...  1514    0.0    G
sp|Q9PVX8.1|STA31_XENLA  RecName: Full=Signal transducer and a...  1488    0.0    G
sp|Q7ZXK3.1|STA32_XENLA  RecName: Full=Signal transducer and a...  1437    0.0    G
sp|Q764M5.1|STAT1_PIG  RecName: Full=Signal transducer and act...   758    0.0    G
sp|P42224.2|STAT1_HUMAN  RecName: Full=Signal transducer and a...   755    0.0    G
sp|P42225.1|STAT1_MOUSE  RecName: Full=Signal transducer and a...   743    0.0    G
sp|Q14765.1|STAT4_HUMAN  RecName: Full=Signal transducer and a...   676    0.0    G
sp|P42228.1|STAT4_MOUSE  RecName: Full=Signal transducer and a...   669    0.0    G
```

BLAST Tree View Widget



Tree view for rid: F5MAKAMH012, query ID: lcl|10696, database: swissprot

This tree was produced using BLAST pairwise alignments. more...

Tree method: Fast Minimum Evolution

Sequence Label: Sequence Title (if available)

Max Seq Difference: 0.75

Blast names color map	
🟦	unknown
🟩	primates
🟫	rodents
🟦	even-toed ungulates
🟪	flies
🟥	nematodes

Slides last updated May 2009

Taxonomy reports

NCBI/ BLAST/ blastp suite/ Formatting Results - 1E21Z75Y012

gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Query ID lcl|48374
Description gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]
Molecule type amino acid
Query Length 770

Database Name swissprot
Description Non-redundant SwissProt sequences
Program BLASTP 2.2.20+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

```
                                                                  Score    E
Sequences producing significant alignments:                       (Bits)  Value

sp|P40763.2|STAT3_HUMAN  RecName: Full=Signal transducer and a...  1553    0.0     G
sp|P42227.2|STAT3_MOUSE  RecName: Full=Signal transducer and a...  1551    0.0     G
sp|P52631.1|STAT3_RAT  RecName: Full=Signal transducer and act...  1550    0.0     G
sp|Q19S50.1|STAT3_PIG  RecName: Full=Signal transducer and act...  1550    0.0     G
sp|P61635.1|STAT3_BOVIN  RecName: Full=Signal transducer and a...  1541    0.0     G
sp|Q6DV79.2|STAT3_CHICK  RecName: Full=Signal transducer and a...  1514    0.0     G
sp|Q9PVX8.1|STA31_XENLA  RecName: Full=Signal transducer and a...  1488    0.0     G
sp|Q7ZXK3.1|STA32_XENLA  RecName: Full=Signal transducer and a...  1437    0.0     G
sp|Q764M5.1|STAT1_PIG  RecName: Full=Signal transducer and act...   758    0.0     G
sp|P42224.2|STAT1_HUMAN  RecName: Full=Signal transducer and a...   755    0.0     G
sp|P42225.1|STAT1_MOUSE  RecName: Full=Signal transducer and a...   743    0.0     G
sp|Q14765.1|STAT4_HUMAN  RecName: Full=Signal transducer and a...   676    0.0     G
sp|P42228.1|STAT4_MOUSE  RecName: Full=Signal transducer and a...   669    0.0     G
```

Sorting BLAST results by Taxonomy

▸NCBI/ BLAST/ blastp/ Formatting Results - F5MAKAMH012 [Reformat these Results] [Edit and Resubmit] [Sign in above to save your search strategy]

Job Title: gi|21618340|ref|NP_644805.1| signal transducer...

▶ Sho

Tax BLAST Report

Index

- Lineage Report
- Organism Report
- Taxonomy Report
- Help

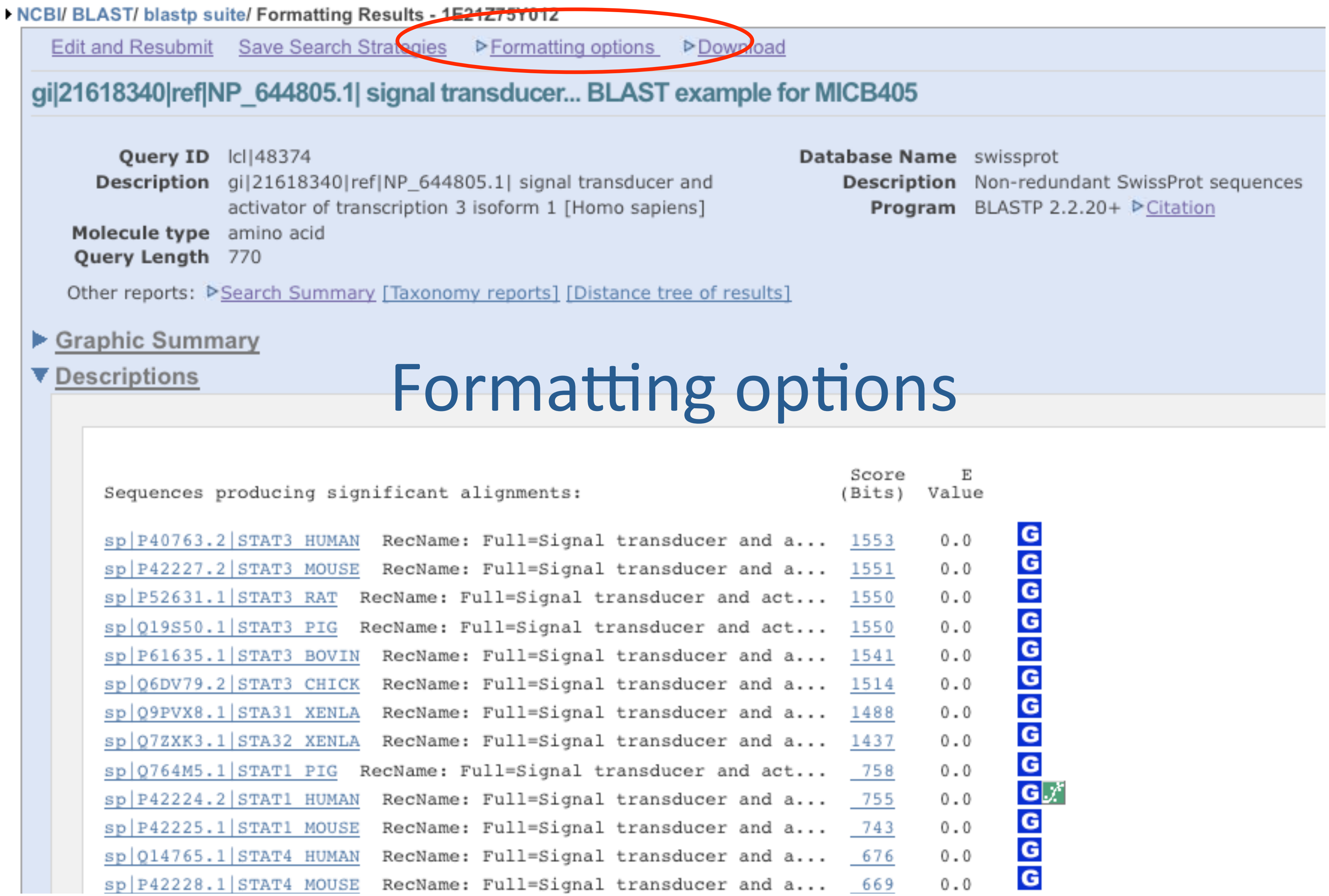
Lineage Report

```
cellular organisms
. Fungi/Metazoa group [eukaryotes]
. . Bilateria           [animals]
. . . Coelomata           [animals]
. . . . Tetrapoda           [vertebrates]
. . . . . Amniota             [vertebrates]
. . . . . . Eutheria            [placentals]
. . . . . . . Euarchontoglires    [placentals]
. . . . . . . . Hominidae           [primates]
. . . . . . . . . Homo sapiens (man) --------------------- 1510 19 hits [primates]                  Signal transducer and activator of transcription 3 (Acute-p
. . . . . . . . . Pongo pygmaeus (orang-utan) ............   31  1 hit  [primates]                  Structural maintenance of chromosomes protein 3 (Chondroiti
. . . . . . . . Mus musculus (mouse) --------------------- 1509 17 hits [rodents]                   Signal transducer and activator of transcription 3 (Acute-p
. . . . . . . . Rattus norvegicus (brown rat) ............ 1508  8 hits [rodents]                   Signal transducer and activator of transcription 3
. . . . . . . . Oryctolagus cuniculus (domestic rabbit) .    33  2 hits [rabbits & hares]           Ezrin (p81) (Cytovillin) (Villin-2)
. . . . . . . Bos taurus (cow) --------------------------- 1499  5 hits [even-toed ungulates]       Signal transducer and activator of transcription 3
. . . . . . . Sus scrofa (wild boar) .....................  737  4 hits [even-toed ungulates]       Signal transducer and activator of transcription 1
. . . . . . . Ovis aries (domestic sheep) ................  250  1 hit  [even-toed ungulates]       Signal transducer and activator of transcription 5A (Mammar
. . . . . . . Canis lupus familiaris (dogs) ..............   34  1 hit  [carnivores]                Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmus
. . . . . . Gallus gallus (bantam) -----------------------   40  2 hits [birds]                     Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, gizz
. . . . . Xenopus laevis (clawed frog) -------------------   32  1 hit  [frogs & toads]             E3 SUMO-protein ligase NSE2 (Non-structural maintenance of 
. . . . Anopheles gambiae --------------------------------  166  1 hit  [flies]                     Signal transducer and transcription activator (Ag-STAT)
. . . . Drosophila melanogaster ..........................  145  3 hits [flies]                     Signal transducer and transcription activator (Protein mare
. . . . Drosophila pseudoobscura .........................   36  1 hit  [flies]                     Protein purity of essence
. . . Caenorhabditis briggsae ----------------------------  137  1 hit  [nematodes]                 Signal transducer and activator of transcription 1
. . . Caenorhabditis elegans (nematode) ..................  135  3 hits [nematodes]                 Signal transducer and activator of transcription 1
. . Neurospora crassa ------------------------------------   31  1 hit  [ascomycetes]               Autophagy-related protein 11
. Thermoplasma volcanium ---------------------------------   36  1 hit  [euryarchaeotes]            Potassium-transporting ATPase A chain (Potassium-translocat
. Sulfolobus solfataricus ................................   33  1 hit  [crenarchaeotes]            DNA double-strand break repair rad50 ATPase
. Chlamydophila pneumoniae ...............................   32  1 hit  [chlamydias]                Putative ATP:guanido phosphotransferase CPn_0701/CP_0045/CP
. Escherichia coli .......................................   32  1 hit  [enterobacteria]            K99 fimbrial protein precursor
. Sulfolobus acidocaldarius ..............................   32  1 hit  [crenarchaeotes]            Proteasome alpha subunit (Multicatalytic endopeptidase comp
```

Organism Report

```
 Homo sapiens (man) [primates] taxid 9606
sp|P40763|STAT3_HUMAN Signal transducer and activator of t...     1510  0.0
sp|P42224|STAT1_HUMAN Signal transducer and activator of t...      732  0.0
sp|Q14765|STAT4_HUMAN Signal transducer and activator of t...      660  0.0
sp|P52630|STAT2_HUMAN Signal transducer and activator of t...      459  2e-128
sp|P51692|STA5B_HUMAN Signal transducer and activator of t...      284  1e-75
sp|P42229|STA5A_HUMAN Signal transducer and activator of t...      283  2e-75
```

Formatting options



NCBI/ BLAST/ blastp suite/ Formatting Results - 1E21Z75Y012

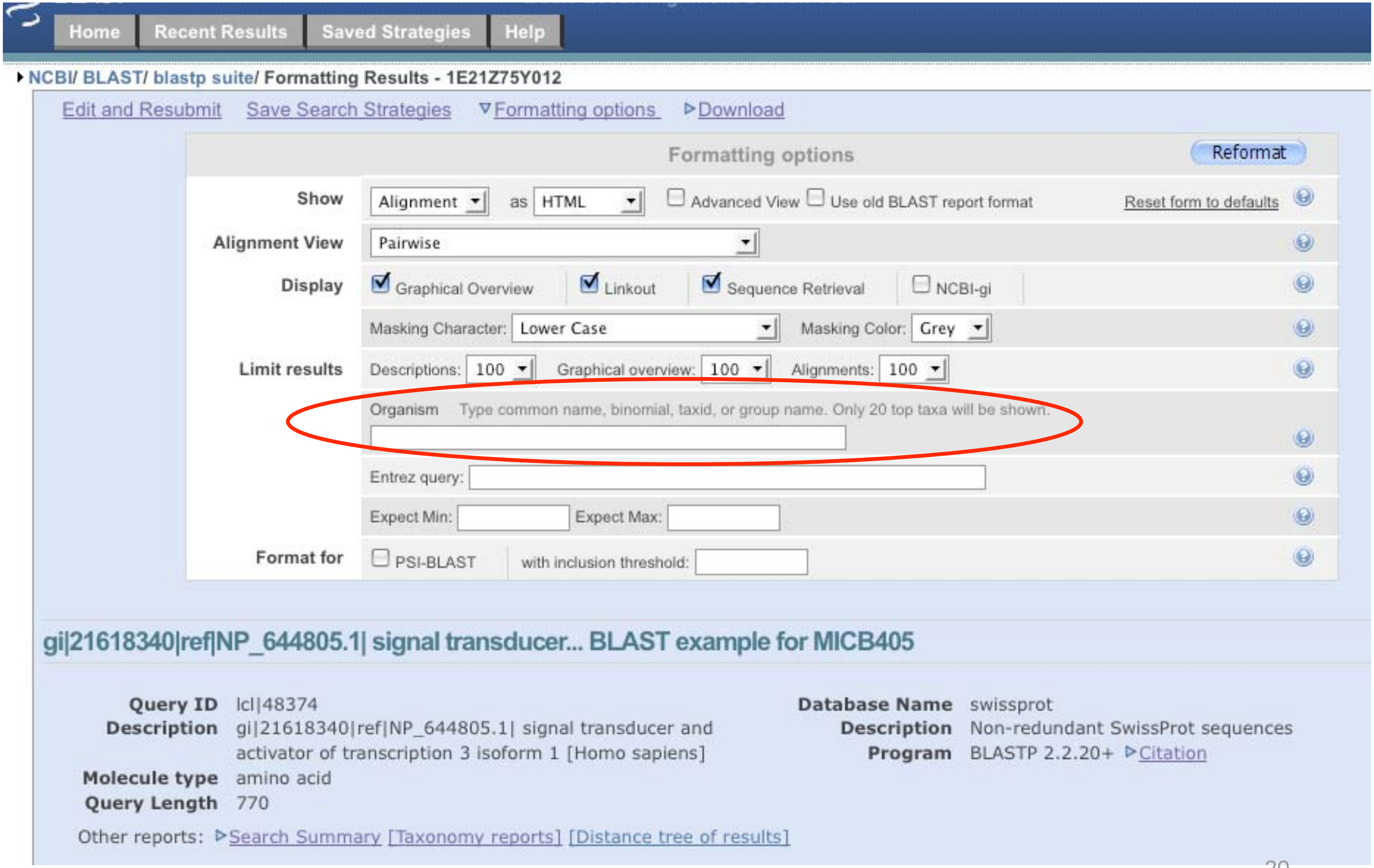
gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Query ID	lcl|48374	**Database Name**	swissprot
Description	gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]	**Description**	Non-redundant SwissProt sequences
Molecule type	amino acid	**Program**	BLASTP 2.2.20+ ▷Citation
Query Length	770		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results]

```
                                                                     Score     E
Sequences producing significant alignments:                          (Bits)  Value

sp|P40763.2|STAT3_HUMAN  RecName: Full=Signal transducer and a...    1553    0.0   G
sp|P42227.2|STAT3_MOUSE  RecName: Full=Signal transducer and a...    1551    0.0   G
sp|P52631.1|STAT3_RAT  RecName: Full=Signal transducer and act...    1550    0.0   G
sp|Q19S50.1|STAT3_PIG  RecName: Full=Signal transducer and act...    1550    0.0   G
sp|P61635.1|STAT3_BOVIN  RecName: Full=Signal transducer and a...    1541    0.0   G
sp|Q6DV79.2|STAT3_CHICK  RecName: Full=Signal transducer and a...    1514    0.0   G
sp|Q9PVX8.1|STA31_XENLA  RecName: Full=Signal transducer and a...    1488    0.0   G
sp|Q7ZXK3.1|STA32_XENLA  RecName: Full=Signal transducer and a...    1437    0.0   G
sp|Q764M5.1|STAT1_PIG  RecName: Full=Signal transducer and act...     758    0.0   G
sp|P42224.2|STAT1_HUMAN  RecName: Full=Signal transducer and a...     755    0.0   G
sp|P42225.1|STAT1_MOUSE  RecName: Full=Signal transducer and a...     743    0.0   G
sp|Q14765.1|STAT4_HUMAN  RecName: Full=Signal transducer and a...     676    0.0   G
sp|P42228.1|STAT4_MOUSE  RecName: Full=Signal transducer and a...     669    0.0   G
```

Limit Results by Organism



NCBI/ BLAST/ blastp suite/ Formatting Results - 1E21Z75Y012

Edit and Resubmit Save Search Strategies ▽Formatting options ▷Download

Formatting options

Show	Alignment as HTML ☐ Advanced View ☐ Use old BLAST report format Reset form to defaults
Alignment View	Pairwise
Display	☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☐ NCBI-gi
	Masking Character: Lower Case Masking Color: Grey
Limit results	Descriptions: 100 Graphical overview: 100 Alignments: 100
	Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.
	Entrez query:
	Expect Min: Expect Max:
Format for	☐ PSI-BLAST with inclusion threshold:

gi|21618340|ref|NP_644805.1| signal transducer... BLAST example for MICB405

Query ID lcl|48374
Description gi|21618340|ref|NP_644805.1| signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]
Molecule type amino acid
Query Length 770

Database Name swissprot
Description Non-redundant SwissProt sequences
Program BLASTP 2.2.20+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results]

Links

- NCBI BLAST page

  http://www.ncbi.nlm.nih.gov/BLAST/
- The NCBI Query Tutorial

  http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/query_tutorial.html
- The NCBI BLAST Tutorial

  http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/tut1.html
- The NCBI BLAST Program Selection Guide.

  http://www.ncbi.nlm.nih.gov/blast/producttable.shtml