

STN[®]

To PSIPS and Beyond

**Exploring the Content and Utility of
USGENE[®]**

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Agenda

- STN[®] sequence databases
- USGENE[®] database content
- The 7 basic steps of USGENE BLAST[®]
- Comparisons and conclusions

BLAST is a registered trademark of the U.S. National Library of Medicine (NLM)

STN sequence searchable databases

- CAS REGISTRYSM
 - Chemical Abstracts Service (CAS) Registry File
- DGENE
 - Thomson Scientific GENESEQTM
- PCTGEN
 - WIPO/PCT Patent Application Biosequences
- USGENE
 - The USPTO Genetic Sequence Database

See Effective patent sequence searching on STN:

http://www.stn-international.com/training_center/bioseq/epss.pdf

USGENE is the USPTO Genetic Sequence Database

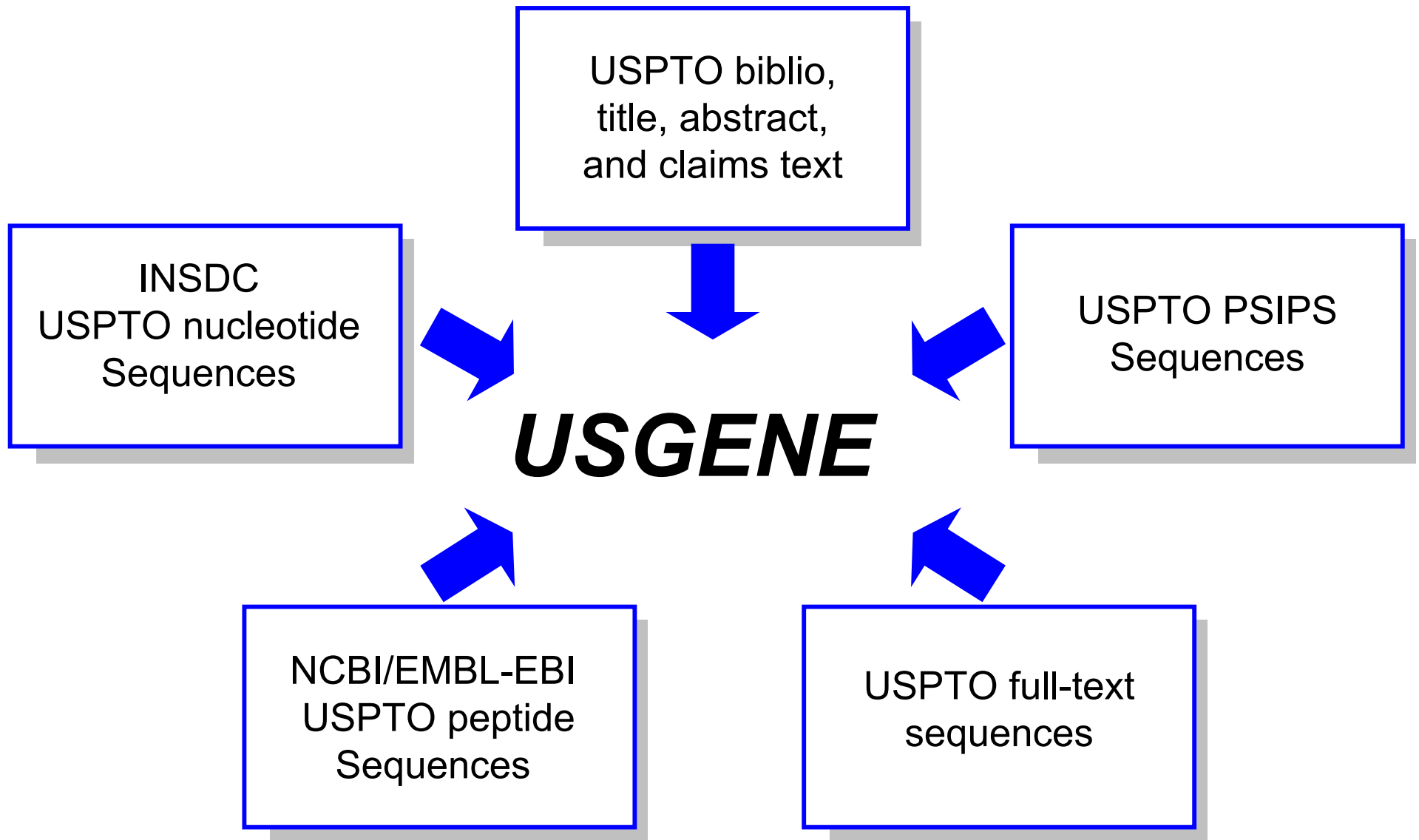
- Sequences from all relevant USPTO published patent applications and issued (granted) patents
- Assignee and full inventor names; publication, application and parent case PCT numbers and dates; original publication **title, abstract, and claims**
- Organism name, sequence length, Molecule Type, SEQ ID, and feature tables for features/annotations
- Produced by the SequenceBase Corporation
- Updated weekly – within **7 days** of publication
- 1982 – present

USGENE consolidates unique USPTO sequence data from different sources

- USPTO Publication Site for Issued and Published Sequences (PSIPS)
- International Nucleotide Sequence Database Collaboration (INSDC) (NCBI/EMBL/DDBJ)
- USPTO Protein Database (NCBI/EMBL)
- USPTO Patents and Applications Full-Text

The USGENE Sequence Source (/SSO) field indicates which source any given USGENE sequence record was derived from.

USGENE combines these sequences with bibliographic data and claims text



USGENE records include full patent bibliography, title and abstract

L1 ANSWER 1 OF 1 USGENE COPYRIGHT 2007 SEQUENCEBASE ALL display format.
AN 7255990.1 (1) DNA (2) USGENE
TI Method for screening genes expressing at desired sites (Patent) (3)
IN Higo Kenichi (Tsukuba, JP); Iwamoto Masao (Tsukuba, JP) (4)
PA National Institute of Agrobiological Sciences (Ibaraki JP) (5)
PI US 7255990 B2 20070814
US 20040086855 A1 20040506
WO 2003044227 A 20030530
AI US 2001-221596 20011121
RLI WO 2001-JP10195 20011121
ED 20070817
DT Patent
AB The present invention relates to a method for inferring a plant organ, in which a certain gene is to be expressed, using a part of a base sequence, a method for searching for a gene which is to be expressed at a desired site, and a composition, kit, system and program for carrying out these methods. The present invention also relates to a method for inferring a plant organ, in which a plant gene is to be expressed, based on information about the presence or absence of a base sequence which is highly similar to (7)

See (1) - (7) on slide 10.

USGENE records also include patent or published application claims text

CLM US7255990 B2: 1. A method for detecting a gene which is expressed in a flower and other organs in a rice plant, ALL display format (cont.)
of: (1) searching a gene population using a T₁ transposon
(8) sequence consisting of SEQ ID NO: 1 as a key sequence, (2) selecting a gene having the transposon sequence in the vicinity of a putative protein coding region, and (3) detecting expression of said gene in the flower and other organs.

2. The method according to claim 1, wherein the expression of said gene includes expression of at least one site selected from a stamen and a pistil.

3. The method according to claim 1, wherein the gene population is a library and the key sequence is a probe sequence.

4. The method according to claim 3, wherein the database is a DNA library.

5. The method according to claim 3, wherein the search

All USGENE sequences are provided in STN standardized format

SSO NUCLEIC; USPTO; GRANTED (9)

ORGN Zea mays (10)

SQL 352 (11)

SEQ

(12)

```
1 gggctctgttt agttcccaaa caaaattttt cacgctgtta cataggatgt
51 ttggacacat gcatagagta ctaaattgtag aaaaaaaca attaacatt
101 tcgccttgaa attacgagac aaatctttta agcctaattg cgccatgatt
151 tgacaatttg gtgctacaat aaatatttgc taataataga ttaattaggc
201 ttaataaatt cgtcttgcag tttccagacg gaatctgtaa tttattttat
251 gagatacagc tgcttcgatc ttccatcaca tattcagacc gtacctaatc
301 tgaaaggtta gtaatttgaa ctgcgtagta atgctacaag gtaaataaat
351 ca
```

FEATURE TABLE: (13)

Key |Location |

=====+=====+=====

misc_feature | (1) .. (352) |

ALL display format (cont.)

See (8) - (13)
on slide 11.

USGENE sample record annotations

- 1) USGENE Accession Number (AN), including the sequence identity number (SEQ ID NO)
- 2) Molecule Type (MTY)
- 3) Original publication title – a “Published Application” or “Patent” indication is given in parentheses
- 4) Full inventor names, city and state/country
- 5) Patent assignee name, city and state/country
- 6) Publication, application and related PCT parent case application details and dates
- 7) Original patent or published application abstract

USGENE sample record annotations

- 8) Published application or granted patent claims
- 9) The Sequence Source (SSO) – nucleic or protein; PSIPS/USPTO, NCBI, etc; granted or application
- 10) Organism (where given) – providing the name of the organism from which the sequence is derived
- 11) Searchable and sortable Sequence Length (SQL)
- 12) Standardized patent sequence (SEQ) – each USGENE record is based upon a sequence
- 13) Feature table including sequence modifications, features and/or annotations, as provided by the patent applicant or assignee

USGENE represents a new tool for tackling business critical searches

- DGENE and REGISTRY sequences are indexed by Thomson from the DWPISM basic and by CAS from the CAplusSM basic respectively
 - 65% of basic patents are PCT published applications
- Sequence listing variation often occurs between published application and granted patent stage
 - Especially important, e.g. for freedom-to-operate
- USGENE provides sequences from both USPTO **published applications** and **granted patents**

Example: sequence listing variation between patent family members

```
L1 ANSWER 1 OF 1 WPINDEX COPYRIGHT 2007 THE THOMSON CORP on STN
AN 1994-358278 [44] WPINDEX
TI New polynucleotide(s) specific for hepatitis C virus types 4, 5 and 6 -
and related antigenic peptide(s) and antibodies, useful in vaccines,
diagnosis, HCV typing and treatment
DC B04; D16; S03
IN PIKE I H; SIMMONDS P; YAP P L
PA (COMM-N) COMMON SERVICES AGENCY; (MURE-N) MUREX DIAGNOSTICS INT INC; . . .
PI WO 9425602 A1 19941110 (199444)* EN 70[5]
AU 9465797 A 19941121 (199508) EN
FI 9505224 A 19951220 (19960228) EN
EP 698101 A1 19960228 (19960228) EN
JP 09500009 W 19970107 (19970107) EN
AU 695259 B 19980813 (19980813) EN
EP 698101 B1 20041103 (20041103) EN
DE 69434116 E 20041209 (20041209) EN
US 20050032047 A1 20050210 (200512) EN
US 6881821 B2 20050419 (200527) EN
. . . . .
ADT WO 9425602 A1 WO 1994-GB957 19940505 . . . . .
PRAI GB 1994-263 19940107
GB 1993-9237 19930505
```

In this example the patent family has:

- 9 sequences from WO 9425602 in DGENE
- 58 sequences from US 6881821 in USGENE

Agenda

- STN[®] sequence databases
- USGENE[®] database content
- **The 7 basic steps of USGENE BLAST[®]**
- Comparisons and conclusions

USGENE offers the same sequence search options as DGENE

- NCBI BLAST similarity
 - RUN BLAST
- FASTA similarity
 - RUN GETSIM
- Sequence Code Match (SCM)
 - RUN GETSEQ
- Offline BATCH and ALERT options

The *DGENE Workshop Manual* is the complete guide:

http://www.stn-international.com/training_center/bioseq/dgene_wm.pdf

The 7 basic steps of USGENE BLAST

- 1) SAVE, UPLOAD, and VERIFY a query text file (L1)
- 2) RUN the BLAST search (/SQP or /SQN)
- 3) Decide how many answers to keep (L2)
- 4) SORT SCORE in Descending order (L3)
- 5) Review answers in a free-of-charge format
e.g. D L3 TRI ORGN ALIGN 1-
- 6) Display selected answers in bibliographic format, e.g. D L3 BIB AB CLM ALIGN 1,3,10
- 7) Ensure session transcript was captured and Logoff

The 7 basic steps of USGENE BLAST

- 1) SAVE, UPLOAD, and VERIFY the sequence query text file (L1)
 - Upload options
 - STN Express[®]: Use UPLOAD command or Upload Query Wizard (STN Express 8.01+)
 - STN[®] on the WebSM: Use Upload feature or Sequence Assistant (link below)
 - Verify the sequence with D LQUE

STN on the Web Sequence Search Assistant:

http://www.stn-international.com/training_center/bioseq/seq_se_ass.pdf

Requirements for sequences for the STN Express Upload Query Wizard

- Sequence queries must be saved individually in text (.txt) format
- Files may
 - Be 3 letter codes (amino acids) or single letter
 - Have header information as seen in, e.g. WIPO ST.25, USPTO PSIPS or EMBL formats
 - Include sequence count numbers
- Query (.txt) files must
 - Be 10,000 characters or less
 - Not have any lines longer than 300 characters
- After upload to STN verify with D LQUE

Examples of formats that work

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 4

LENGTH: 724

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; Note = synthetic construct

SEQUENCE: 4

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu

1 5

Gly Leu Arg Glu Phe Leu

20

USPATFULL/USPAT2 format

<210> SEQ ID NO 137

<211> LENGTH: 951

<212> TYPE: DNA

<213> ORGANISM: Zea mays

<400> SEQUENCE: 137

accgaggccg acttcccggt cactggccac gacgggacgt gcatctcaa actgaaaaat 60

acaagggttg tatccataga ttcgttcgag cgtgtgceca tcaactacga gagagecgtg 120

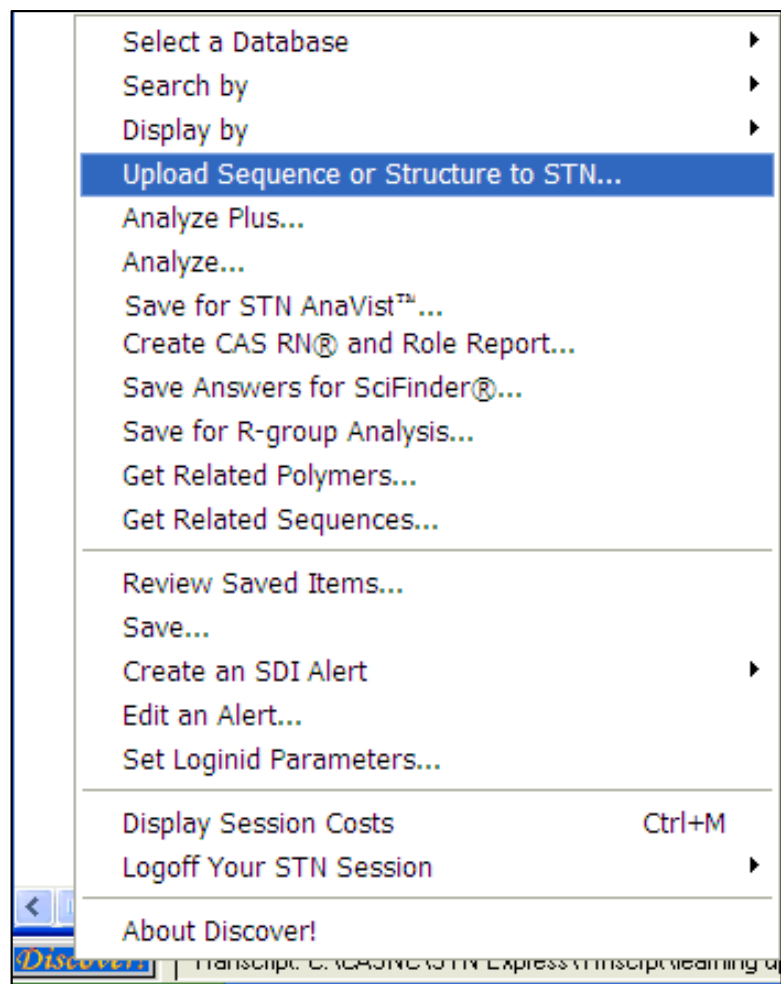
cagaaggccg tggcgcacca gcctgttagt gccagcattg aagcatctcg gcgcgcgttc 180

cagctctaca gttctggcat cttegacggg agatgcggga cgtacctgga ccacgggttg 240

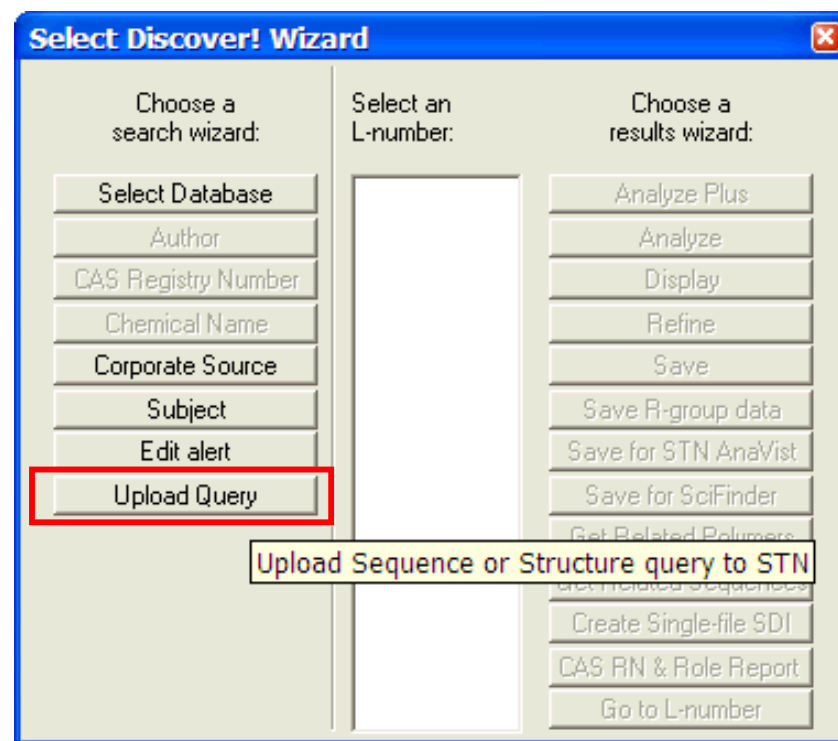
USPTO PSIPS ST.25 format

a) Choose the Upload Query Wizard

From the Discover! button menu.

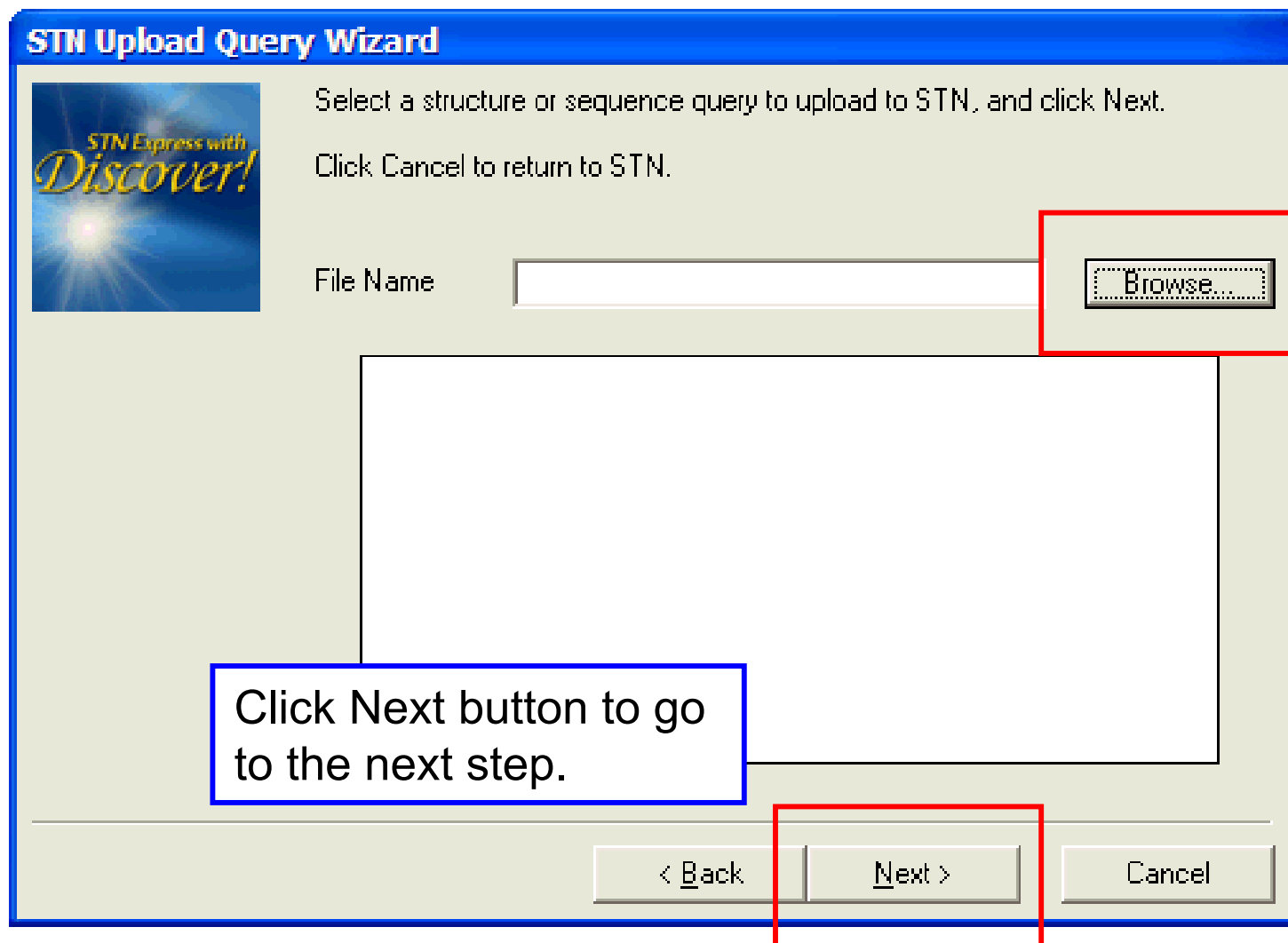


OR

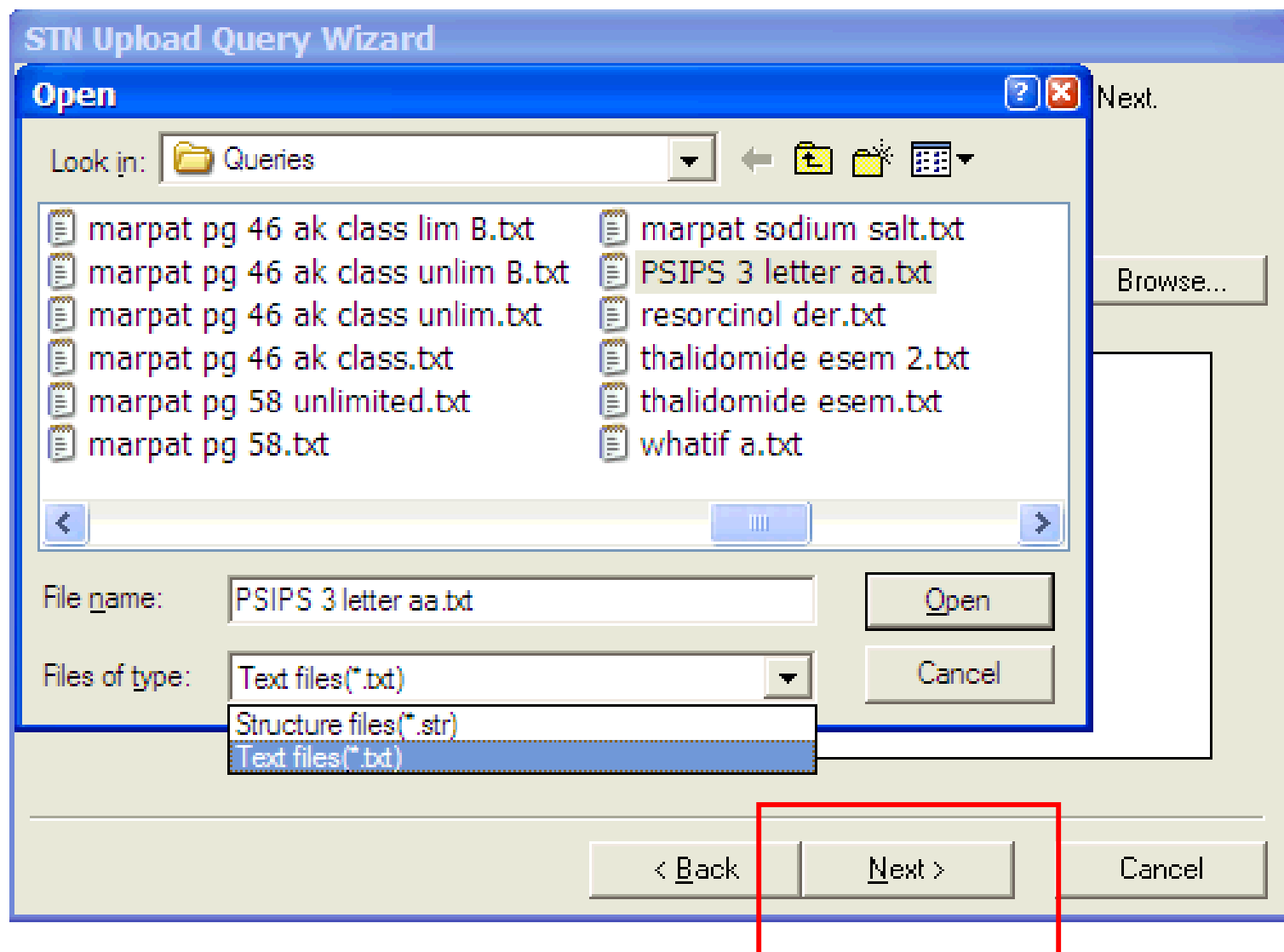


From the Select Discover!
Wizard window.

b) Browse to locate sequence file



c) Change File type to .txt



d) Verify it's the right query!

STN Upload Query Wizard

STN Express with Discover!


Select a structure or sequence query to upload to STN, and click Next.
Click Cancel to return to STN.

File Name

```
1 vqtvplsrif dhamleahra helaidtyqe feetyipkdq  
kysflhdsqt  
51 sfcfsdsipt psnmeetqgk snlellrisl llieswlepv  
rflrsmfann  
101 lvytdsdsdd yhlkdleeg iqtlmgrled gsrtgqilk  
qtyskfdtns  
151 hnhdallkny gllycfrkdm dkvetflrmv qcrsvegscg f
```

e) Select STN file to upload to

STN Upload Query Wizard



Select a database from the list below, or more than one database by holding the Ctrl key while making your selection, and click Finish

To exit the Wizard click Cancel.

Databases:

DGENE	Derwent Geneseq Database 1981 - present
PCTGEN	World Patent Application Biosequences

Use PCTGEN to upload queries and verify them (lower connect hour). The resulting L-numbers may be searched in DGENE, PCTGEN, or USGENE.

Click Finish for the file to be “scrubbed” and uploaded to STN.

[View this Database Summary Sheet on the Web](#)

< Back Finish Cancel

1) SAVE, UPLOAD, and VERIFY (cont.)

=> FILE PCTGEN

=> UPL R BLAST

These commands are automatically run by the STN Express Sequence Query Upload wizard.

UPLOAD SUCCESSFULLY COMPLETED

L1 GENERATED

=> D L1 LQUE

L1 ANSWER 1 PCTGEN COPYRIGHT 2007 WIPO on STN

LQUE vqtvplsrldhamleahrahelaidtyqefeetyipkdqkysflhdsqtsfcfsdsi
ptpsnmeetqqksnllellrislllieswlepvrflrsmfannlvdydtsdsddyhllkd
leegiqtlmgrledgsrrtgqilkqtyskfdtnshhdallknygllycfrkdmdkve
tflrmvqcrsvegscgf

=>

The sequence query is now ready for searching directly in USGENE using the L-number (L1).

The 7 basic steps of USGENE BLAST

2) RUN the BLAST search

- Protein search: RUN BLAST L1 /SQP
- Nucleotide search: RUN BLAST L1 /SQN
- Translated search: RUN BLAST L1 /TSQN

2) RUN the USGENE BLAST search

=> **FILE USGENE**

FILE 'USGENE' ENTERED AT 08:15:27 ON 22
COPYRIGHT (C) 2007 SEQUENCEBASE CORP

USGENE is updated within 7 days
of publication by the USPTO.

FILE LAST UPDATED: 17 AUG 2007 <20070817/UP>
MOST RECENT PUBLICATION DATE: 16 AUG 2007 <20070816/PD>

FILE COVERS 1982 TO DATE

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION (SLART) IS AVAILABLE
IN THE BASIC INDEX (/BI) AND FEATURE TABLE (/FEAT) FIELDS <<<

=> **RUN BLAST L1 /SQP -F F**

Turn the Low Complexity Filter off
with the syntax... /SQP -F F

BLAST Version 2.2

The BLAST software is used herein with permission of the
National Center for Biotechnology Information (NCBI) of
the National Library of Medicine (NLM). See also,

BLAST SEARCHING

RUN BLAST command syntax

Similarity Searching with BLAST (protein/polypeptides)

=> RUN BLAST L1 (sequence or L-number)

/SQP (protein) (default)

-e (*Expect-value*)

-f (*Filter*) (*on by default*)

-w (*Word size*)

-m (*Matrix*)

-g (*Gap penalty*)

-x (*Gap extension*)

BATCH (*offline*)

ALERT (*Alert/SDI*)

RUN BLAST command syntax

Similarity Searching with BLAST (Nucleic acids)

=> **RUN BLAST L1** (sequence or L-number)

/SQN (nucleotide)

SIN (single strand)

COM (complementary strand)

BOTH (both strands) (default)

-e (Expect-value)

-f (Filter)

-w (Word size)

-g (Gap penalty)

-x (Gap extension)

-q (penalty for mismatch)

-r (reward for match)

BATCH (offline)

ALERT (Alert/SDI)

RUN BLAST advanced options

Expectation Value (-E)

Expectation value (E-Value) is the statistical significance threshold for reporting matches against a sequence database. The E-value can be any positive number, and the default value is 10. This means that 10 matches may be expected to be found merely by chance. In general E-value is lowered to make the search more precise and raised to retrieve more answers.

Word Size (-W)

Word Size is the length of the character string fragments of a sequence query which are used as the basis for a BLAST search. For SQN the default is 11 and the range 7-23. For all other BLAST searches the default is 3 and the range 2-3. For short search queries, reducing the default word size can give improved search results.

RUN BLAST advanced options (cont.)

Low Complexity Filtering (on by default) (-F)

The low complexity filter can eliminate biologically uninteresting segments that have low compositional complexity and are statistically significant, as determined by specific programs for peptide or nucleotide sequences in nature. Filtering is applied to the query sequence and is indicated by a series of Xs for peptide sequences and Ns for nucleotide sequences. Low complexity filtering can be turned off (i.e. set to F - false).

Peptide similarity matrices (-M)

For peptide based searches SQP and TSQN the advanced options provide additional scoring matrices to the default BLOSUM62 (next slide)

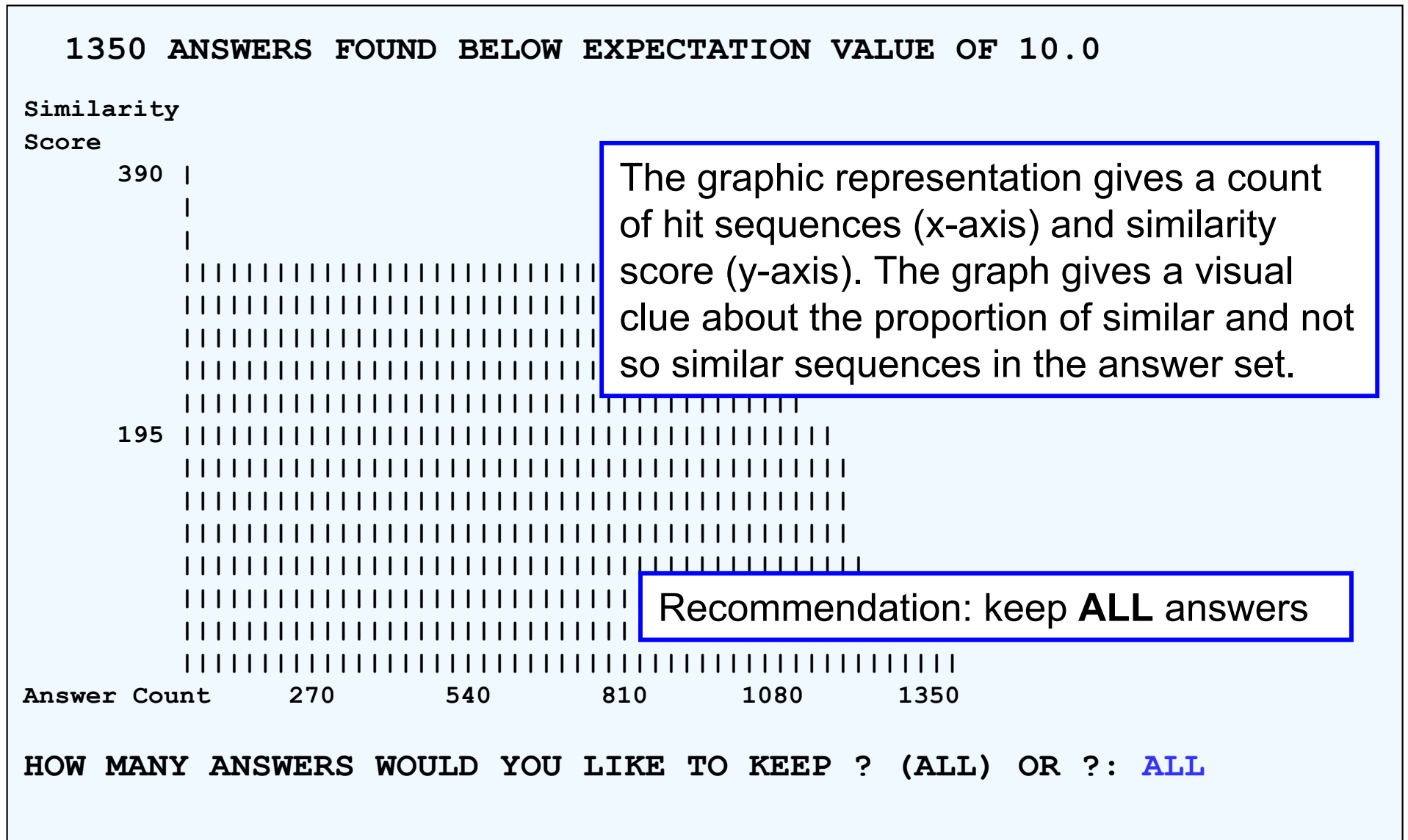
Guidelines from NCBI on the use of Advanced Settings for peptide sequence searching are as follows:

<u>Query Length</u>	<u>Matrix</u>	<u>Gap costs</u>
<35	PAM-30	(9,1)
35 – 50	PAM-70	(10,1)
50 – 85	BLOSUM-80	(10,1)
>85	BLOSUM-62	(11,1) (BLAST default)

The 7 basic steps of USGENE BLAST

- 3) Decide how many answers to keep (L2)
 - How many answers would you like to keep? (ALL) or ?:
 - Recommendation: Keep **ALL** answers

3) Decide how many answers to keep



The 7 basic steps of USGENE BLAST

- 4) SORT by SCORE descending (L3)
 - SOR L2 SCORE D
 - Option: limit using text terms and/or dates (L4)
 - Remember to SORT L4 SCORE D !! (L5)

4) SORT by SCORE descending

HOW MANY ANSWERS WOULD YOU LIKE TO KEEP ? (ALL) OR ? : **ALL**

L2 RUN STATEMENT CREATED

```
L2      1350 VQTVPLSRLFDHAMLEAHRAHEL AIDTYQEF EETYIPKDQKYSFLHDSQT
          SFCFSDSIPTPSNMEETQQKSNLELLRISLLLI ESWLEPVRF LRSMFANN
          LVYDTSDDSDDYHLLKDL EEGIQTLMGRLEDGSRRTGQILKQTYSKFDTNS
          HNHDALLKNYGLLYCFR KDMDKVETFLRMVQCRSVEGSCGF/SQP.-F F
```

Answer set arranged by accession number; to sort by descending similarity score, enter at an arrow prompt (=>) "sor score d".

=> **SOR SCORE D**

PROCESSING COMPLETED FOR L2

```
L3      1350 SOR L2 SCORE D
```

Use SORT SCORE D to sort by descending BLAST score.

The 7 basic steps of USGENE BLAST

- 5) Review answers using a *free-of-charge* format including alignment (ALIGN), while “parked” in the STNGUIDESM file
- D L5 TRI ORGN ALIGN 1-
 - FILE STNGUIDE

5) Review answers with a free-of-charge format including alignment

=> D L3 TRI ORGN ALIGN 1-30; FILE STNGUIDE

L3 ANSWER 1 OF 1350 USGENE COPYRIGHT 2007 SEQUENCEBASE CORP on STN
TI Recombinant DNA transfer vectors ([Patent](#))
MTY Protein
SQL 191
ORGN Unknown
BLASTALIGN

This top hit comes from a U.S. issued patent.

Query = 191 letters

Length = 191

Score = 390 bits (1001), Expect = e-113

Identities = 191/191 (100%), Positives = 191/191 (100%)

Query: 1 VQTVPLSRLFDHAMLEAHRAHEL AIDTYQEF EETYIPKDQKY SFLHDSQTSFCFSDSIPT
VQTVPLSRLFDHAML+AHRAH+LAIDTYQEF EETYIPKDQKY SFLHDSQTSFCFSDSIPT
Sbjct: 1 VQTVPLSRLFDHAMLQA HRAHQLAIDTYQEF EETYIPKDQKY SFLHDSQTSFCFSDSIPT
Query: 61 PSNMEETQQKSNLELLRISLLLIESWLEPVRFLRSMFANNLVYDTSDDSDDYHLLKDLEEG
PSNMEETQQKSNLELLRISLLLIESWLEPVRFLRSMFANNLVYDTSDDSDDYHLLKDLEEG
Sbjct: 61 PSNMEETQQKSNLELLRISLLLIESWLEPVRFLRSMFANNLVYDTSDDSDDYHLLKDLEEG
. . . .

5) Review answers with a free-of-charge format including alignment

```
L3      ANSWER 5 OF 1350  USGENE COPYRIGHT 2007 SEQUENCEBASE CORP on STN
TI      Genetic polymorphisms associated with myocardial infarction, methods
        of detection and uses thereof (PublishedApplication)
MTY     Protein
SQL     217
ORGN    Homo Sapiens
BLASTALIGN
        Query   = 191 letters
        Length  = 217
        Score   = 387 bits (995), Expect = e-113
        Identities = 189/191 (98%), Positives = 191/191 (99%)
Query:  1  VQTVPLSRLFDHAMLEAHRAHELAIPTYQEFEEETYIPKDQKYSFLHDSQTSFCFSDSIPT
          VQTVPLSRLFDHAML+AHRAH+LAIDTYQEFEEETYIPKDQKYSFLHDSQTSFCFSDSIPT
Sbjct:  1  VQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFEEETYIPKDQKYSFLHDSQTSFCFSDSIPT
Query:  61  PSNMEETQOKSNLELLRISLLLIESW
          PSNMEETQOKSNLELLRISLLLIESW
Sbjct:  61  PSNMEETQOKSNLELLRISLLLIESW
Query: 121  IQTLMGRLEDGSRRTGQILKQTYSKFDTNSHNHDALLKNYGLLYCFRKDMDKVETFLRMV
          IQTLMGRLEDGSRRTGQILKQTYSKFDTNSHNHDALLKNYGLLYCFRKDMDKVETFLRMV
Sbjct: 147  IQTLMGRLEDGSRRTGQILKQTYSKFDTNSHNHDALLKNYGLLYCFRKDMDKVETFLRMV
. . . .
```

The 5th from top hit comes from a U.S. published application.

BLAST alignment details are explained on the next slide. . . .

Understanding BLAST alignments

Query	the length of the query sequence
Length	the length of the answer sequence
Score	a relative score assigned by BLAST
Expect	Expectation Value – a value representing the chance that an answer is a random hit. The closer to zero, the less likely the hit is random
Identities	the number of exact letter matches between query and answer within the displayed local alignment. The amino acid letter is repeated* in the display
Positives	a combination of identities and amino acid family matches shown with + (plus) in the alignment
Gaps	shown as dashes - where BLAST must break the query or answer to maintain an alignment

(* For nucleic acid searches a vertical bar is used to indicate nucleotide identities in the alignment display.)

Option: refine USGENE BLAST results with text and/or date search terms

HOW MANY ANSWERS WOULD YOU LIKE TO KEEP ? (ALL) OR ? : **ALL**

L2 RUN STATEMENT CREATED

L2 1350 VQTVPLSRLFDHAMLEAHRAHEL AIDTYQEF EETYIPKDQKYSFLHDSQT
SFCFSDSIPTPSNMEETQQKSNLELLRISLLLI ESWLEPVRFLRSMFANN
LVYDTSDDYHLLKDL EEGIQTLMGRLEDGSRRTGQILKQTYSKFD TNS
HNHDALLKNYGLLYCFERKDM DKVETFLRMVQCRSVEGSCGF/SQP.-F F

Answer set arranged by accession number; to sort by descending similarity score, enter at an arrow

=> **SOR SCORE D**

PROCESSING COMPLETED FOR L2

L3 1350 SOR L2 SCORE D

The BLAST search (L2) is further refined to sequences from granted patents, with application year prior to 1996, and to a specific text search term (L4).

=> **S L2 AND SOMATOMAMMOTROPIN AND AY<1996 AND GRANTED/SSO**

L4 7 L2 AND SOMATOMAMMOTROPIN AND AY<1996 AND GRANTED/SSO

=> **SOR SCORE D**

PROCESSING COMPLETED FOR L4

L5 7 SOR L4 SCORE D

If you limit using text and/or date terms remember to SORT SCORE D again!

The 7 basic steps of USGENE BLAST

- 6) Display selected relevant answers in a bibliographic format including alignment
 - D L5 BIB AB CLM ALIGN 1 5 6
- 7) Ensure your STN Express session transcript was captured and then logoff

6) Display selected USGENE answers in a preferred bibliographic format

=> D BIB AB CLM ORGN SSO ALIGN 1 3 5

L5 ANSWER 1 OF 7 USGENE COPYRIGHT 2007 SEQUENCEBASE CORP on STN

AN 4363877.1 Protein USGENE

TI Recombinant DNA transfer vectors (Patent)

IN Goodman Howard M. (San Francisco, CA); Sh.
Seeburg Peter H. (San Francisco, CA)

PA The Regents of the University of California.

PI US 4363877 A 19821214

AI US 1978-897710 19780419

AB Recombinant DNA transfer vectors containing codons for human
somatammotropin and for human growth hormone.

CLM US4363877 A: What is claimed is:

1. A recombinant DNA transfer vector comprising codons for human
chorionic **somatammotropin** comprising the nucleotide

ORGN Unknown

SSO PROTEIN; EMBL; **GRANTED**

BLASTALIGN

This sequence hit comes from a U.S. granted patent, with an application date prior to 1996, and a key concept in the abstract and claims.

Note: this USGENE sequence record, sourced from EMBL, is an example of one which is not indexed in DGENE or REGISTRY.

Review: 7 steps of USGENE BLAST

- 1) SAVE, UPLOAD, and VERIFY a query text file (L1)
- 2) RUN the BLAST search (/SQP or /SQN)
- 3) Decide how many answers to keep (L2)
- 4) SORT SCORE in Descending order (L3)
- 5) Review answers in a free-of-charge format
e.g. D L3 TRI ALIGN 1-
- 6) Display selected answers in bibliographic format, e.g. D L3 BIB AB ECLM ALIGN 1,3,10
- 7) Ensure session transcript was captured and Logoff

The importance of using the correct BLAST advanced options

```
=> RUN BLAST GSSFLSPEHQR/SQP
```

```
BLAST Version 2.2 . . . . .
```

```
NO ANSWERS FOUND BELOW THRESHOLD OF 10
```

Changing BLAST options is especially important for short sequence queries!

```
=> RUN BLAST GSSFLSPEHQR/SQP -M PAM30 -W 2 -E 1000 -F F
```

```
BLAST Version 2.2 . . . . .
```

```
712 ANSWERS FOUND BELOW EXPECTATION VALUE OF 1000.0
```

```
HOW MANY ANSWERS WOULD YOU LIKE TO KEEP ? (ALL) OR ?: ALL
```

```
L1 RUN STATEMENT CREATED
```

```
L1 712 GSSFLSPEHQR/SQP.-M PAM30 -W 2 -E 1000 -F F
```

Answer set arranged by accession number; to sort by descending similarity score, enter at an arrow prompt (=>) "sor score d".

The importance of using the correct BLAST advanced options (cont.)

=> **SOR L1 SCORE D**

PROCESSING COMPLETED FOR L1

L2 712 SOR L1 SCORE D

Correct use of BLAST options
finds relevant sequence hits.

=> **D TRI ALIGN**

L2 ANSWER 1 OF 712 USGENE COPYRIGHT 2007 SEQUENCEBASE CORP on STN

TI Fluorescently labeled growth hormone secretagogue (Patent)

MTY Protein

SQL 18

BLASTALIGN

Query = 11 letters

Length = 18

Score = 37.5 bits (81), Expect = 1e-09

Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 1 GSSFLSPEHQR 11

GSSFLSPEHQR

Sbjct: 1 GSSFLSPEHQR 11

Exploring USGENE search fields

- USGENE is similar in design to DGENE, but has a number of unique additional search fields

/ECLM Exemplary (1st) claim text

/SEQC Sequence count (total number of sequences)

/SSO Sequence source (NCBI, USPTO, etc)

/SEQN Sequence Identity Number (SEQ ID NO)

- The USGENE Basic Index (/BI) comprises

- Title (/TI), abstract (/AB), organism name (/ORGN), and molecule type (/MTY) fields

- Add Exemplary Claim (/ECLM), e.g. using

=> **S VIRUS/BI,ECLM**

=> **SET SFIELDS BI ECLM**

Useful USGENE display fields/formats

TRIAL*	Title, Molecule Type, Sequence Length
SCAN*	Random Title
ALIGN*	BLAST/GETSIM Sequence Alignment
SCORE*	Similarity Score (for post-processing)
BIB	Inventors, Assignees, numbers, dates
AB	Original abstract
ECLM	Exemplary (1 st) claim text
CLM	All claims text
BRIEF	BIB + AB + ECLM, sequence, sequence source (SSO), feature table (FEAT)
ALL	BRIEF with CLM instead of ECLM

(* Free of charge display formats in USGENE.)

USGENE Original Sequence (SEQO)

=> D SEQO

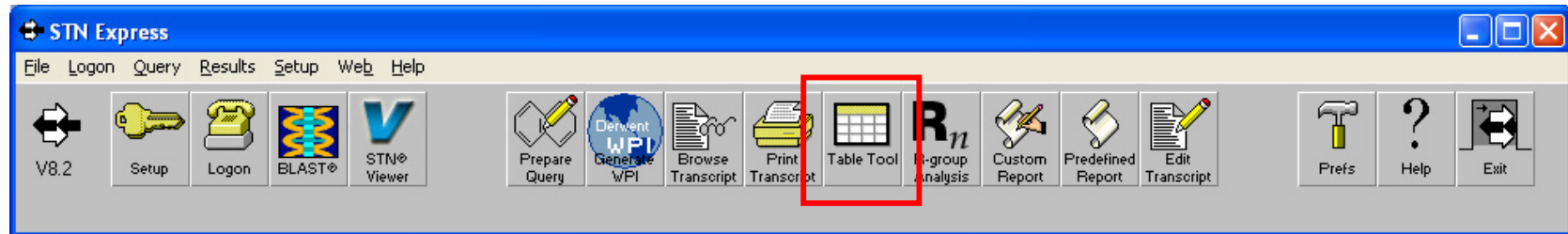
L1 ANSWER 1 OF 1 USGENE COPYRIGHT
SEQO

```
cgctcgcagt ctgtgggccc tccgggaggc ggcggaggcc accgcgggga gaggggcggg 00
cgcagc atg gca gcc tcc tta cgg ctc ctc gga gct gcc tcc ggt ctc 108
Met Ala Ala Ser Leu Arg Leu Leu Gly Ala Ala Ser Gly Leu
1 5 10
cgg tac tgg agc cgg cgg ctg cgg ccg gca gcc ggc agc ttt gca gcg 156
Arg Tyr Trp Ser Arg Arg Leu Arg Pro Ala Ala Gly Ser Phe Ala Ala
15 20 25 30
gtg tgt tct agg tca gtg gct tca aag act cca gtt gga ttc att gga 204
Val Cys Ser Arg Ser Val Ala Ser Lys Thr Pro Val Gly Phe Ile Gly
35 40 45
ctg ggc aac atg ggg aat cca atg gc
Leu Gly Asn Met Gly Asn Pro Met Al
50 5
```

The original input format of a USGENE sequence is available for display using the **SEQO** display field.

Often the original format includes the patent applicant's alignment of the nucleotide sequence coding region with the corresponding protein sequence.

USGENE results can be post-processed into tables using STN Express 8.2



STN Online and Results - [Table Output - USGENE POST PROCESS.tb1]











Accession Number	Title	Assignee	Abstract	Exemplary Claim	BLAST Alignment	BLAST Score
7141547.2216 Protein USGENE	Albumin fusion proteins comprising GLP-1 polypeptides (Patent)	Human Genome Sciences Inc (Rockville MD)	The present invention encompasses albumin fusion proteins. Nucleic acid molecules encoding the albumin fusion proteins of the invention are also encompassed by the invention, as are vectors containing these nucleic acids, host cells transformed with these nucleic acids vectors, and methods of making the albumin fusion proteins of the invention and using these nucleic acids, vectors, and/or host cells. Additionally the present invention encompasses pharmaceutical compositions comprising albumin fusion proteins and methods of treating, preventing, or ameliorating diseases, disorders or conditions using albumin fusion proteins of the invention.	US7141547 B2: What is claimed is:1. An albumin fusion protein comprising two or more tandemly oriented GLP-1 polypeptides, wherein said GLP-1 polypeptides are selected from wild-type GLP-1, GLP-1 fragments, and GLP-1 variants, fused to albumin comprising the amino acid sequence of SEQ ID NO:1038, an albumin fragment, or albumin variant thereof, wherein said albumin fragment or albumin variant increases the serum plasma half-life of the GLP-1 polypeptides, and wherein said fusion protein has GLP-1 activity.	<pre> Query = 11 letters Length = 28 Score = 26.9 bits (58), Expect = 5e-06 Identities = 11/11 (100%), Positives = 11/11 (100%) Query: 1 C S S F L S P E H Q R 11 C S S F L S P E H Q R Sbjct: 1 C S S F L S P E H Q R 11 </pre>	38
7074910.442 Protein USGENE	PRO4340 nucleic acids (Patent)	Genentech Inc (South San Francisco CA)	The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.	US7074910 B2: What is claimed is:1. An isolated nucleic acid comprising: (a) the nucleic acid sequence of SEQ ID NO: 129 or the complement thereof; (b) the full-length coding sequence of the nucleic acid of SEQ ID NO: 129 or the complement thereof; (c) the cDNA derived from the ATCC access number 203867 or the complement thereof.	<pre> Query = 11 letters Length = 117 Score = 26.9 bits (58), Expect = 2e-05 Identities = 11/11 (100%), Positives = 11/11 (100%) Query: 1 C S S F L S P E H Q R 11 C S S F L S P E H Q R Sbjct: 24 C S S F L S P E H Q R 34 </pre>	38
7160993.442 Protein USGENE	Nucleic acids encoding PRO4400 polypeptides	Genentech Inc (South San Francisco CA)	The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein	US7160993 B2: What is claimed is:1. A nucleic acid molecule comprising the nucleic acid sequence of	<pre> Identities = 11/11 (100%), Positives = 11/11 (100%) Query: 1 C S S F L S P E H Q R 11 </pre>	

STN Express 8.2 tables can be saved, e.g., as Excel® files for forwarding to other colleagues.



Agenda

- STN[®] sequence databases
- USGENE[®] database content
- The 7 basic steps of USGENE BLAST[®]
- Comparisons and conclusions

How does USGENE compare to other USPTO sequence data sources?

	USPTO PGP's	USPTO Patents	USPTO claims text	Value added
USGENE				
DGENE (DWPI basics)				
REGISTRY (CAplus basics)				
EMBL-EBI				

How does USGENE compare to other USPTO sequence data sources? (cont.)

	Update Frequency	Typical Timeliness	Value added
USGENE	Weekly	7 days	
REGISTRY	Daily	27 days	
DGENE	Biweekly	65 days	
EMBL-EBI	Daily	1-3 months	

Several factors contribute to the concept of “comprehensiveness”

- Backfile and diversity of authority coverage
- Timeliness from publication to online update
- Indexed patent family member (basic patent, published application, granted patent, etc.)
- Value-added indexing versus applicant data
- Editorial indexing rules (e.g. claimed, example, disclosure or derived sequences, etc.)

See *Effective patent sequence searching on STN (Part I)*:

http://www.stn-international.com/training_center/bioseq/epss.pdf

Comparing STN databases...

- **DGENE**
 - The most comprehensive patent sequence database
 - Implemented in-house at major patent offices
- **REGISTRY**
 - More timely than DGENE; complementary indexing
 - Unique non-patent literature coverage
- **USGENE**
 - More timely than DGENE and REGISTRY (7 days)
 - Sequences from equivalent USPTO applications and patents
- **PCTGEN**
 - The most timely database (24 hours)
 - Sequences from equivalent WIPO/PCT publications

Conclusions

- USGENE is a vital new tool for business critical patent searches, providing a complete collection of U.S. Issued Patent sequences with searchable claims text
- USGENE also provides a collection of published application sequence data, not covered by NCBI/EMBL
- USGENE provides the most timely source of USPTO patent sequence data – within 7 days of publication
- DGENE and REGISTRY provide additional value-added indexing for U.S. patents and published applications
- DGENE, REGISTRY and USGENE are all required for a comprehensive search of USPTO sequence data

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- CAS in North America
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