Manual GO annotation

Evidence: Source	Annotations	Proteins
IEA:Total	3 196 719	707 582
Manual: Total	80 280	22 957

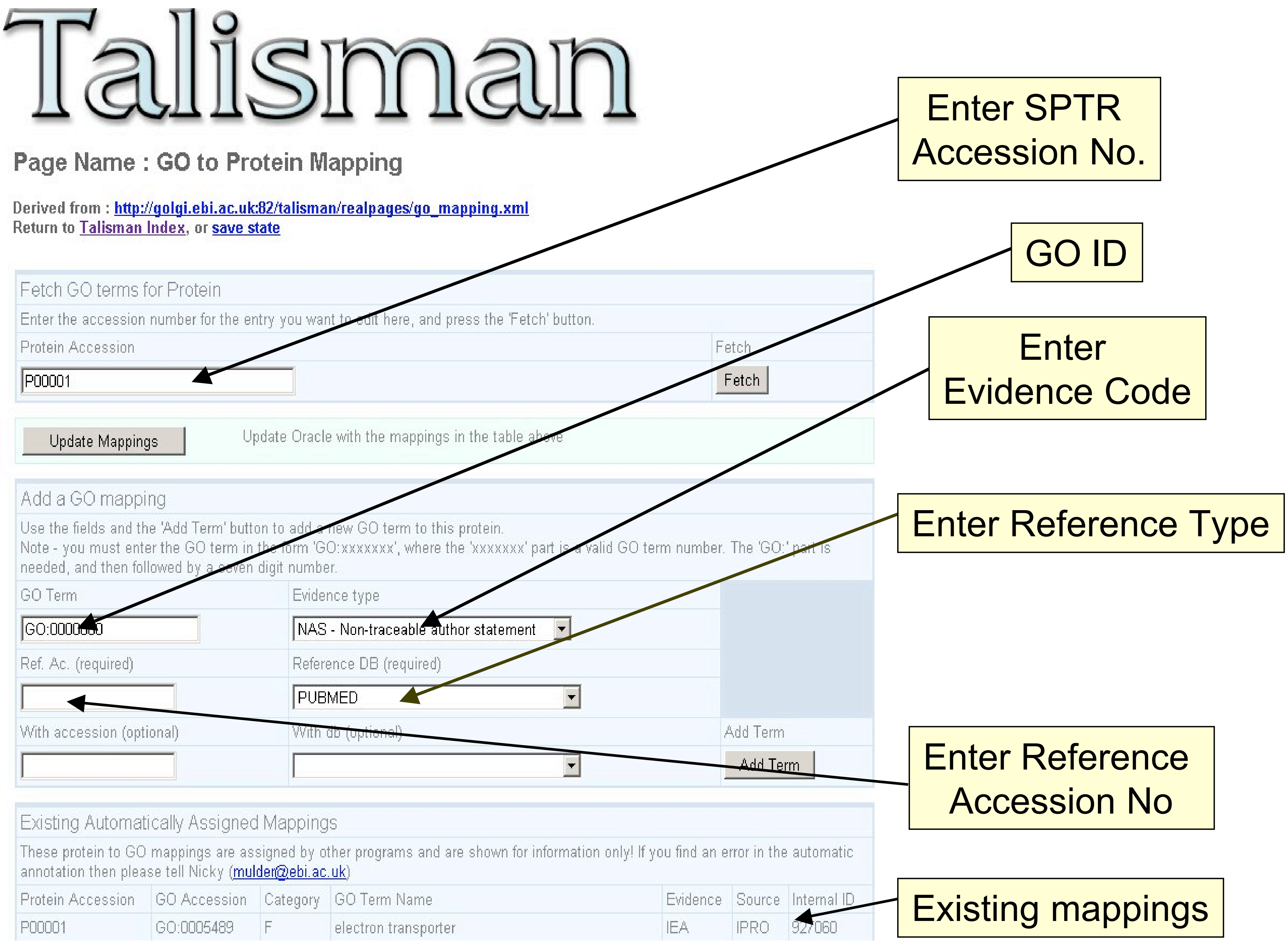
Annotation Features

- Database object: gene or gene product
- GO term ID - GO:0003677
- Reference
- Evidence code (another vocabulary)

Finding GO terms

In this study, we report the isolation and molecular characterization of the B. napus PERK1 cDNA, that is predicted to encode a novel receptor-like kinase. We have shown that like other plant RLKs, the kinase domain of PERK1 has serine/threonine kinase activity, In addition, the location of a PERK1-GTP fusion protein to the plasma membrane supports the prediction that PERK1 is an integral membrane protein…these kinases have been implicated in early stages of wound response…

Function:	protein serine/threonine kinase activity	GO:0004674 (IDA)
Component:	integral to plasma membrane	GO:0005887 (IDA)
Process:	response to wounding	GO:0009611 (NAS)



Talisman

Page Name : GO to Protein Mapping

Derived from : http://golgi.ebi.ac.uk:82/talisman/realpages/go_mapping.xml
Return to Talisman Index, or save state

Fetch GO terms for Protein

Enter the accession number for the entry you want to edit here, and press the 'Fetch' button.

Protein Accession	Fetch
P00001	Fetch

Update Mappings — Update Oracle with the mappings in the table above

Add a GO mapping

Use the fields and the 'Add Term' button to add a new GO term to this protein.
Note - you must enter the GO term in the form 'GO:xxxxxxx', where the 'xxxxxxx' part is a valid GO term number. The 'GO:' part is needed, and then followed by a seven digit number.

GO Term	Evidence type	
GO:0000000	NAS - Non-traceable author statement	
Ref. Ac. (required)	Reference DB (required)	
	PUBMED	
With accession (optional)	With db (optional)	Add Term
		Add Term

Existing Automatically Assigned Mappings

These protein to GO mappings are assigned by other programs and are shown for information only! If you find an error in the automatic annotation then please tell Nicky (mulder@ebi.ac.uk)

Protein Accession	GO Accession	Category	GO Term Name	Evidence	Source	Internal ID
P00001	GO:0005489	F	electron transporter	IEA	IPRO	927060

Enter SPTR Accession No.

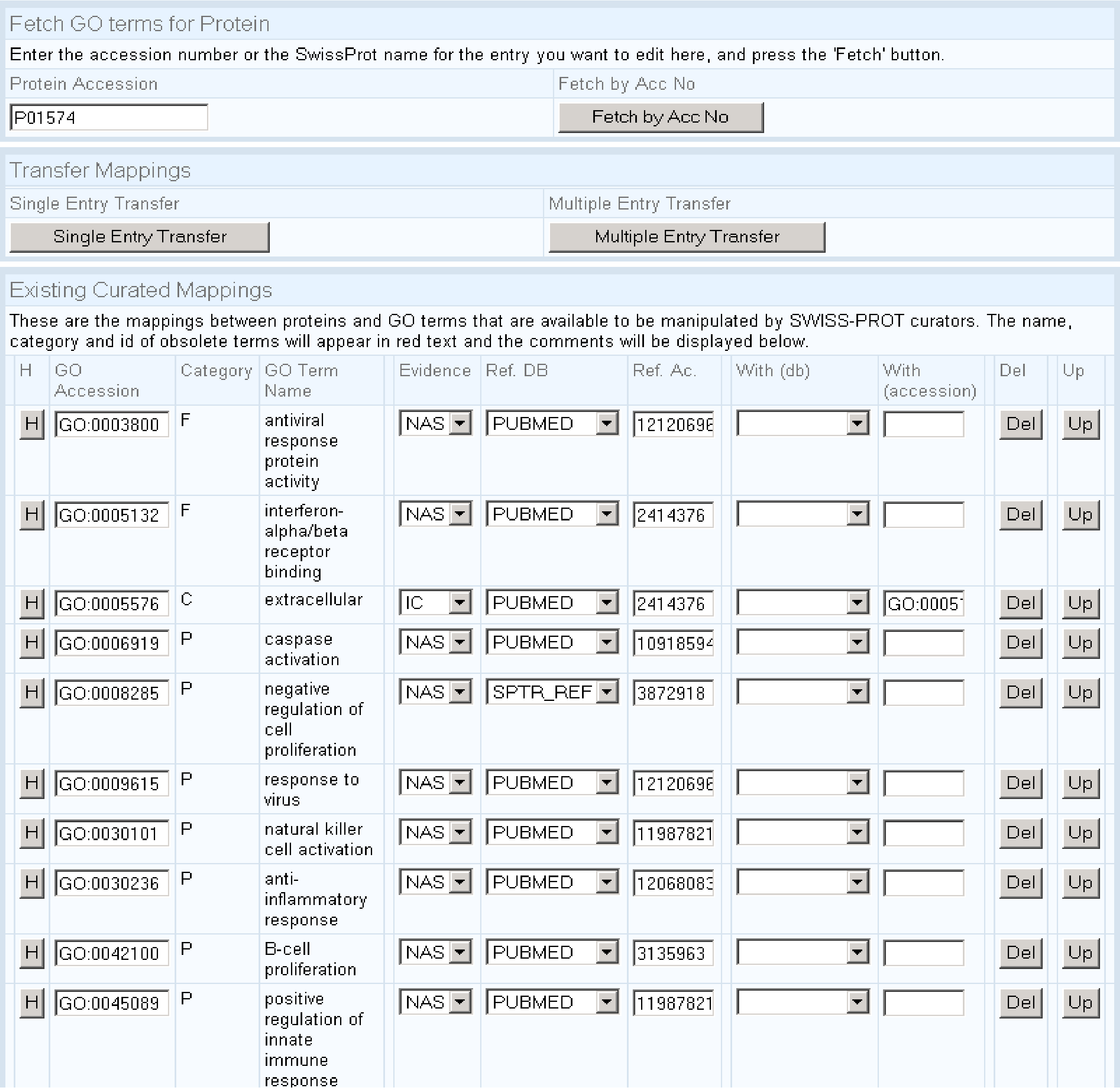
GO ID

Enter Evidence Code

Enter Reference Type

Enter Reference Accession No

Existing mappings



Fetch GO terms for Protein

Enter the accession number or the SwissProt name for the entry you want to edit here, and press the 'Fetch' button.

Protein Accession	Fetch by Acc No
P01574	Fetch by Acc No

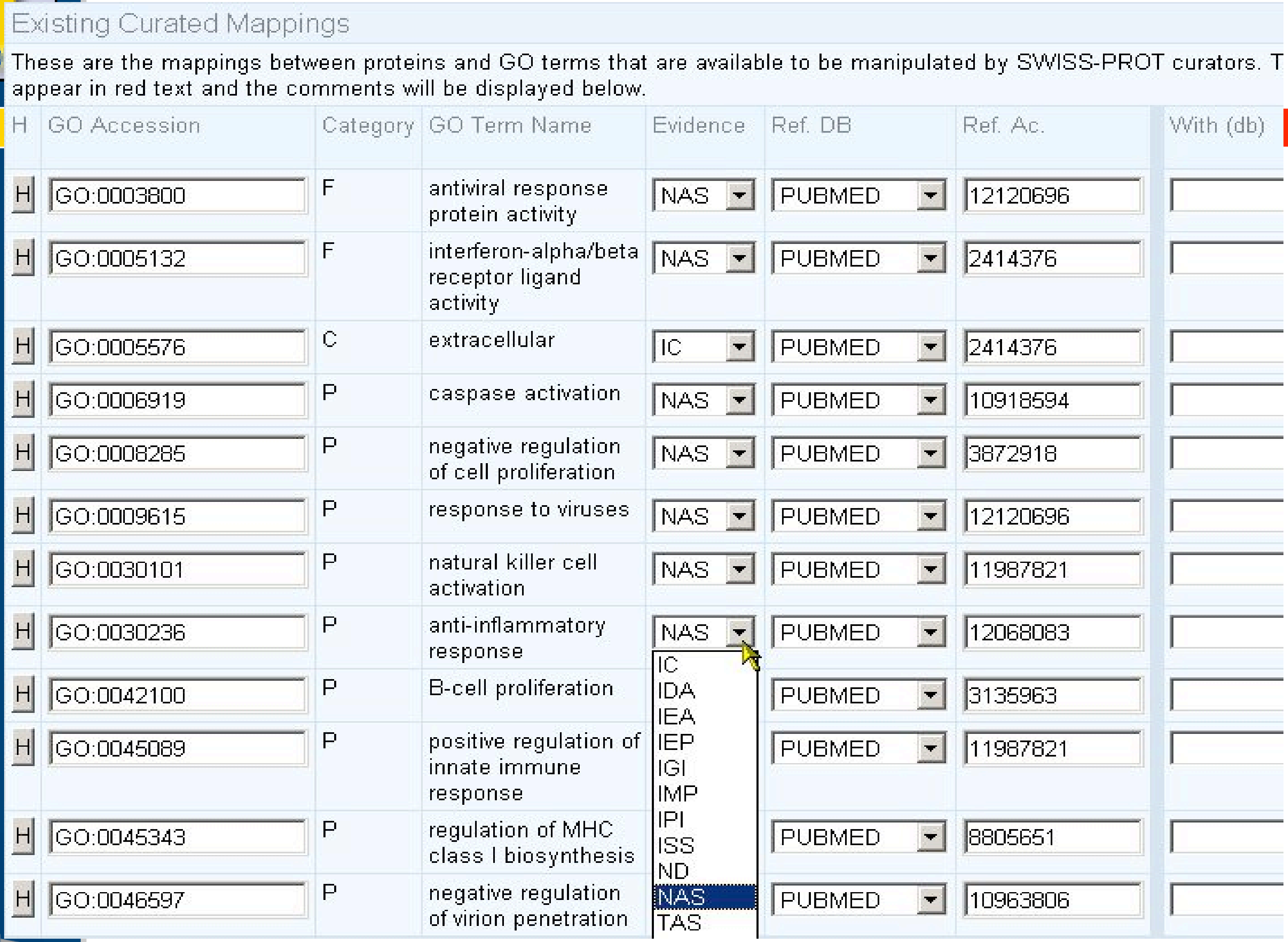
Transfer Mappings

Single Entry Transfer	Multiple Entry Transfer
Single Entry Transfer	Multiple Entry Transfer

Existing Curated Mappings

These are the mappings between proteins and GO terms that are available to be manipulated by SWISS-PROT curators. The name, category and id of obsolete terms will appear in red text and the comments will be displayed below.

H	GO Accession	Category	GO Term Name	Evidence	Ref. DB	Ref. Ac.	With (db)	With (accession)	Del	Up
H	GO:0003800	F	antiviral response protein activity	NAS	PUBMED	1212069			Del	Up
H	GO:0005132	F	interferon-alpha/beta receptor binding	NAS	PUBMED	2414376			Del	Up
H	GO:0005576	C	extracellular	IC	PUBMED	2414376		GO:0005	Del	Up
H	GO:0006919	P	caspase activation	NAS	PUBMED	1091859			Del	Up
H	GO:0008285	P	negative regulation of cell proliferation	NAS	SPTR_REF	3872918			Del	Up
H	GO:0009615	P	response to virus	NAS	PUBMED	1212069			Del	Up
H	GO:0030101	P	natural killer cell activation	NAS	PUBMED	11987821			Del	Up
H	GO:0030236	P	anti-inflammatory response	NAS	PUBMED	1206808			Del	Up
H	GO:0042100	P	B-cell proliferation	NAS	PUBMED	3135963			Del	Up
H	GO:0045089	P	positive regulation of innate immune response	NAS	PUBMED	11987821			Del	Up



Existing Curated Mappings

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appear in red text and the comments will be displayed below.

H	GO Accession	Category	GO Term Name	Evidence	Ref. DB	Ref. Ac.	With (db)
H	GO:0003800	F	antiviral response protein activity	NAS	PUBMED	12120696	
H	GO:0005132	F	interferon-alpha/beta receptor ligand activity	NAS	PUBMED	2414376	
H	GO:0005576	C	extracellular	IC	PUBMED	2414376	
H	GO:0006919	P	caspase activation	NAS	PUBMED	10918594	
H	GO:0008285	P	negative regulation of cell proliferation	NAS	PUBMED	3872918	
H	GO:0009615	P	response to viruses	NAS	PUBMED	12120696	
H	GO:0030101	P	natural killer cell activation	NAS	PUBMED	11987821	
H	GO:0030236	P	anti-inflammatory response	NAS	PUBMED	12068083	
H	GO:0042100	P	B-cell proliferation		PUBMED	3135963	
H	GO:0045089	P	positive regulation of innate immune response		PUBMED	11987821	
H	GO:0045343	P	regulation of MHC class I biosynthesis		PUBMED	8805651	
H	GO:0046597	P	negative regulation of virion penetration		PUBMED	10963806	

GO Evidence Codes

- **ISS:** Infer
- **IDA:** In
- **IPI:** Inferre
- **TAS:** Traceable
- **NAS:** Non-traceable Author Statement
- **IMP:** Inferred from Mutant Phenotype
- **IGI:** Inferred f
- **IEP:** Inf
- **IC:** Inf
- **ND:** No Da

•Enzyme assays

•*In vitro* reconstitution (transcription)

•Immunofluorescence

•Cell fractionation

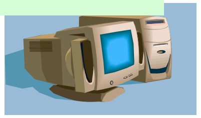
• Transcript levels

(Northern blotting, MicroArray data)

• Protein levels

(Western blotting)

- **IEA** Inferred from electronic annotation



QuickGO

http://www.ebi.ac.uk/ego

QuickGO GO Browser

NEW! Some of the search features of QuickGO have been modified- see the 'Search' page for more details.

A fast Gene Ontology browser.

Query Example: **dimerization**

- Get help with searching
- More information about this browser
- Get more information about the GOA project at the EBI
- Read the user manual
- InterPro

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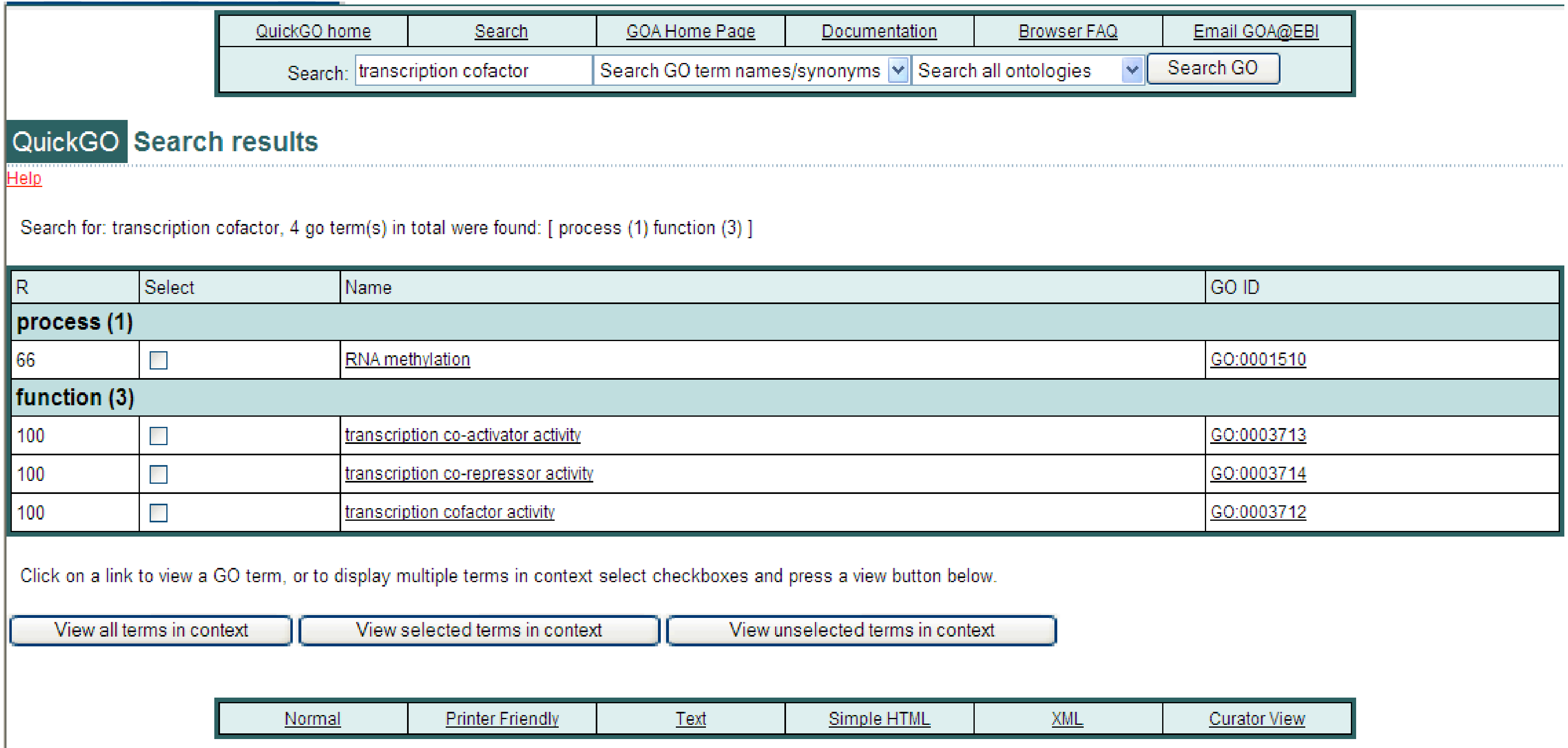


Search: transcription cofactor | Search GO term names/synonyms | Search all ontologies

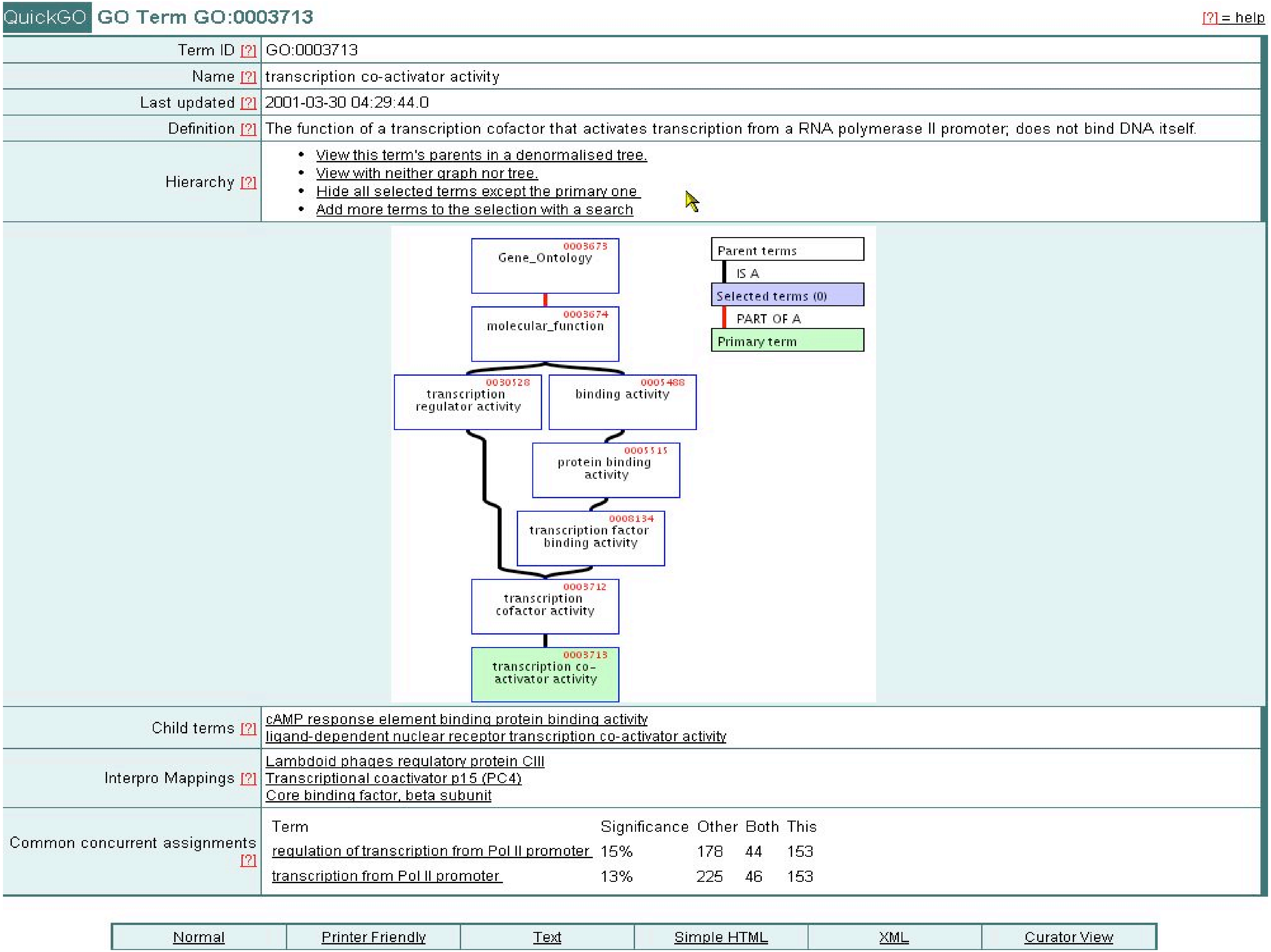
QuickGO Search results

Help

Search for: transcription cofactor, 4 go term(s) in total were found: [process (1) function (3)]

R	Select	Name	GO ID
process (1)			
66	☐	RNA methylation	GO:0001510
function (3)			
100	☐	transcription co-activator activity	GO:0003713
100	☐	transcription co-repressor activity	GO:0003714
100	☐	transcription cofactor activity	GO:0003712

Click on a link to view a GO term, or to display multiple terms in context select checkboxes and press a view button below.



QuickGO **GO Term GO:0003713**

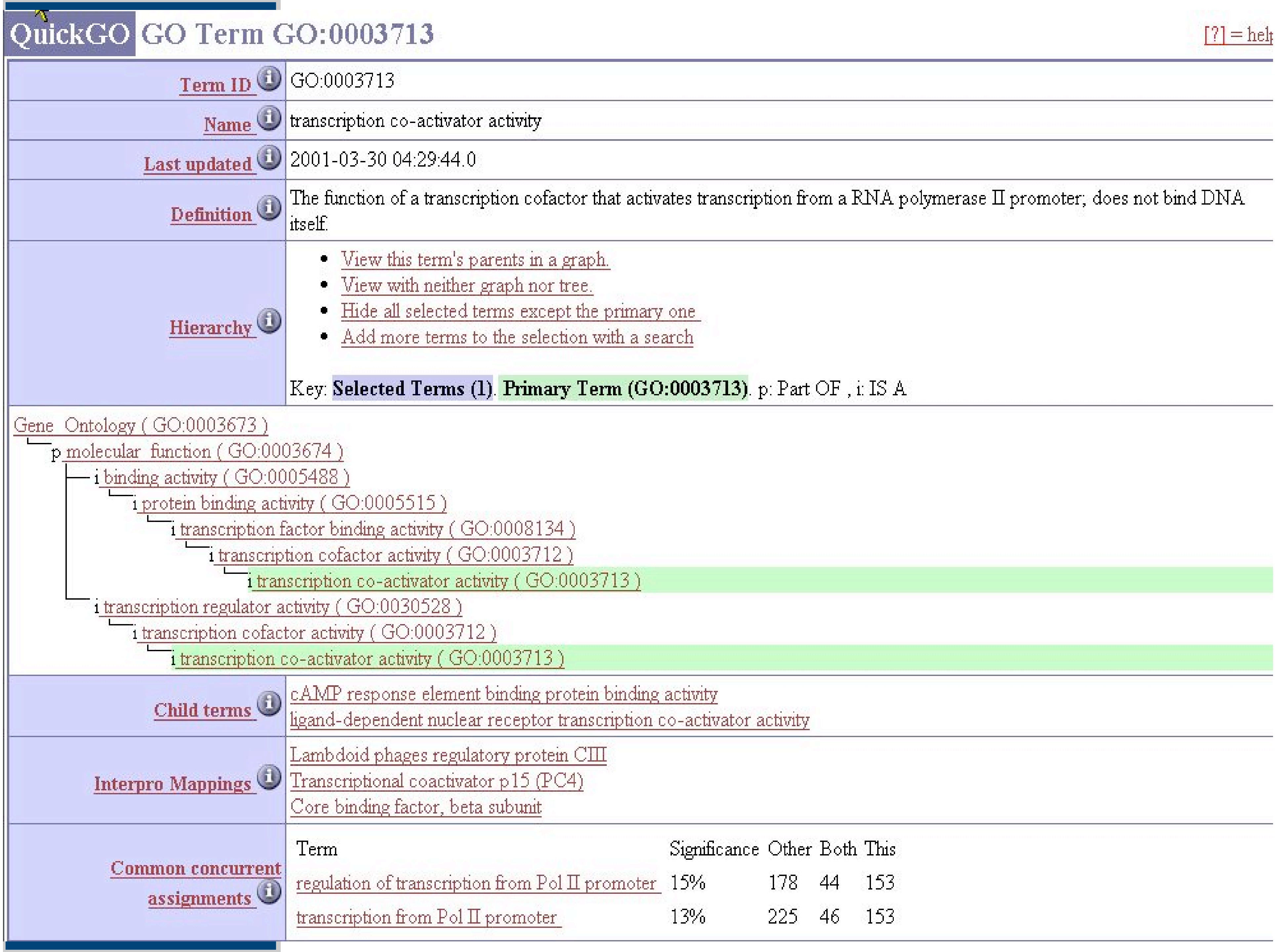
[?] = help

Term ID [?]	GO:0003713
Name [?]	transcription co-activator activity
Last updated [?]	2001-03-30 04:29:44.0
Definition [?]	The function of a transcription cofactor that activates transcription from a RNA polymerase II promoter; does not bind DNA itself.
Hierarchy [?]	• View this term's parents in a denormalised tree. • View with neither graph nor tree. • Hide all selected terms except the primary one • Add more terms to the selection with a search

Child terms [?]	cAMP response element binding protein binding activity ligand-dependent nuclear receptor transcription co-activator activity
Interpro Mappings [?]	Lambdoid phages regulatory protein CIII Transcriptional coactivator p15 (PC4) Core binding factor, beta subunit

Common concurrent assignments [?]

Term	Significance	Other	Both	This
regulation of transcription from Pol II promoter	15%	178	44	153
transcription from Pol II promoter	13%	225	46	153



QuickGO GO Term GO:0003713

[?] = hel

Term ID	GO:0003713
Name	transcription co-activator activity
Last updated	2001-03-30 04:29:44.0
Definition	The function of a transcription cofactor that activates transcription from a RNA polymerase II promoter; does not bind DNA itself.
Hierarchy	• View this term's parents in a graph. • View with neither graph nor tree. • Hide all selected terms except the primary one • Add more terms to the selection with a search Key: **Selected Terms (1)**. **Primary Term (GO:0003713)**. p: Part OF , i: IS A

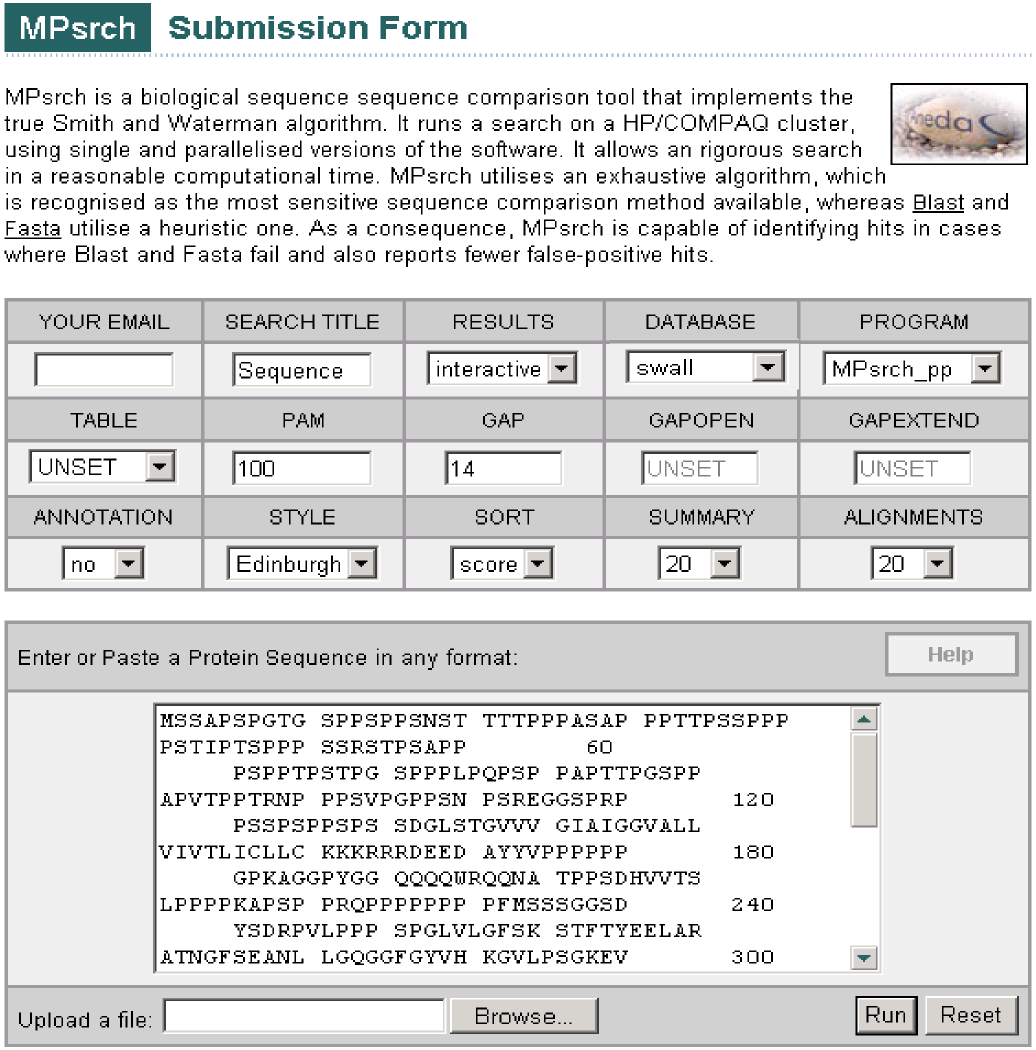
```
Gene  Ontology ( GO:0003673 )
 └─p molecular  function ( GO:0003674 )
    ├─i binding activity ( GO:0005488 )
    │  └─i protein binding activity ( GO:0005515 )
    │     └─i transcription factor binding activity ( GO:0008134 )
    │        └─i transcription cofactor activity ( GO:0003712 )
    │           └─i transcription co-activator activity ( GO:0003713 )
    └─i transcription regulator activity ( GO:0030528 )
       └─i transcription cofactor activity ( GO:0003712 )
          └─i transcription co-activator activity ( GO:0003713 )
```

Child terms	cAMP response element binding protein binding activity ligand-dependent nuclear receptor transcription co-activator activity
Interpro Mappings	Lambdoid phages regulatory protein CIII Transcriptional coactivator p15 (PC4) Core binding factor, beta subunit

Common concurrent assignments

Term	Significance	Other	Both	This
regulation of transcription from Pol II promoter	15%	178	44	153
transcription from Pol II promoter	13%	225	46	153

Mapping GO terms to orthologs using Blast and Evidence Code ISS



MPsrch Submission Form

MPsrch is a biological sequence sequence comparison tool that implements the true Smith and Waterman algorithm. It runs a search on a HP/COMPAQ cluster, using single and parallelised versions of the software. It allows an rigorous search in a reasonable computational time. MPsrch utilises an exhaustive algorithm, which is recognised as the most sensitive sequence comparison method available, whereas Blast and Fasta utilise a heuristic one. As a consequence, MPsrch is capable of identifying hits in cases where Blast and Fasta fail and also reports fewer false-positive hits.

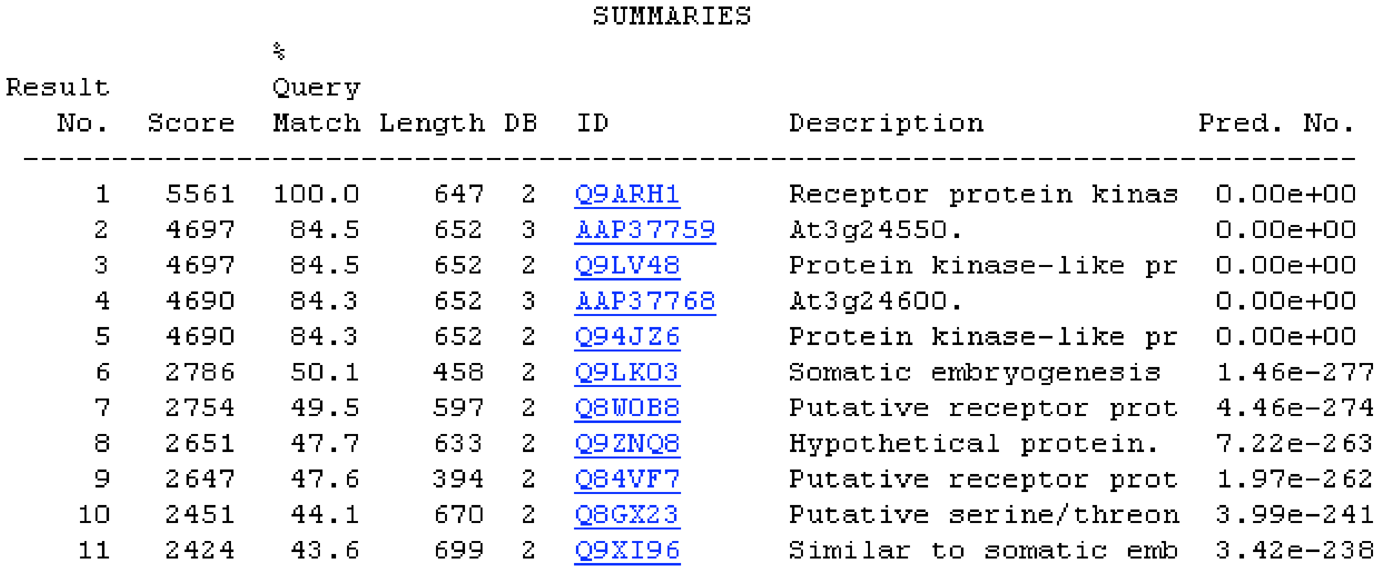
YOUR EMAIL	SEARCH TITLE	RESULTS	DATABASE	PROGRAM
	Sequence	interactive	swall	MPsrch_pp
TABLE	PAM	GAP	GAPOPEN	GAPEXTEND
UNSET	100	14	UNSET	UNSET
ANNOTATION	STYLE	SORT	SUMMARY	ALIGNMENTS
no	Edinburgh	score	20	20

Enter or Paste a Protein Sequence in any format:

```
MSSAPSPGTG SPPSPPSNST TTTPPPASAP PPTTPSSPPP
PSTIPTSPPP SSRSTPSAPP          60
      PSPPTPSTPG SPPPLPQPSP PAPTTPGSPP
APVTPPTRNP PPSVPGPPSN PSREGGSPRP          120
      PSSPSPPSPS SDGLSTGVVV GIAIGGVALL
VIVTLICLLC KKKRRRDEED AYYVPPPPPP          180
      GPKAGGPYGG QQQQWRQQNA TPPSDHVVTS
LPPPPKAPSP PRQPPPPPPP PFMSSSGGSD          240
      YSDRPVLPPP SPGLVLGFSK STFTYEELAR
ATNGFSEANL LGQGGFGYVH KGVLPSGKEV          300
```

Upload a file:

Mapping GO terms to orthologs using Blast and Evidence Code ISS



```
                                   SUMMARIES
                    %
Result            Query
  No.   Score   Match Length DB  ID          Description             Pred. No.
 -----------------------------------------------------------------------------
    1    5561   100.0    647  2  Q9ARH1      Receptor protein kinas   0.00e+00
    2    4697    84.5    652  3  AAP37759    At3g24550.               0.00e+00
    3    4697    84.5    652  2  Q9LV48      Protein kinase-like pr   0.00e+00
    4    4690    84.3    652  3  AAP37768    At3g24600.               0.00e+00
    5    4690    84.3    652  2  Q94JZ6      Protein kinase-like pr   0.00e+00
    6    2786    50.1    458  2  Q9LK03      Somatic embryogenesis    1.46e-277
    7    2754    49.5    597  2  Q8W0B8      Putative receptor prot   4.46e-274
    8    2651    47.7    633  2  Q9ZNQ8      Hypothetical protein.    7.22e-263
    9    2647    47.6    394  2  Q84VF7      Putative receptor prot   1.97e-262
   10    2451    44.1    670  2  Q8GX23      Putative serine/threon   3.99e-241
   11    2424    43.6    699  2  Q9XI96      Similar to somatic emb   3.42e-238
```

Gene Association File

DB	DB_Object_ID	DB_Object_Symbol	[NOT]	GOid	DB:Reference(|DB:Reference)	Evidence	With	Aspect
SPTR	O00505	IMA3_HUMAN		GO:0006886	GOA:interpro	IEA		P
SPTR	O00505	IMA3_HUMAN		GO:0005634	GOA:spkw	IEA		C
SPTR	O00505	IMA3_HUMAN		GO:0005643	PUBMED:9154134	TAS		C

DB_Object_Name(|Name)	DB_Object_Synonym(|Synonym)	DB_Object_Type	taxon(|taxon)	Date	Assigned by
Importin alpha-3 subunit	IPI00012092	protein	taxon:9606	20020920	SPTR
Importin alpha-3 subunit	IPI00012092	protein	taxon:9606	20011011	SPTR
Importin alpha-3 subunit	IPI00012092	protein	taxon:9606	20020630	SPTR

ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/SPTR/

General GOA Status

Electronic	Manual
77% SPTR	2.5% SPTR
58579 species	768 species (313 in house)
>3 mill assoc.	730 539 proteins

Future of GOA

- GOA needs regular updating
- Regular GOA releases
- Continue cross referencing to GOA in EBI databases
- Develop new GO mappings and collaborations
- Develop web interface to allow complicated GO queries:

Which cytokines have been implicated in inhibition apoptosis?

Which G-protein coupled receptors have been implicated in depression?

Acknowledgements

Evelyn Camon - GOA Coordinator
Daniel Barrell – GOA File updates
Emily Dimmer & Vivian Lee – GOA Curators
David Binns & John Maslen – QuickGO, Talisman
Midori Harris, Jane Lomax, Amelia Ireland,
Jennifer Clarke – GO Curators & GO Consortium
Rodrigo Lopez team – SRS & GOA web pages

Rolf Apweiler – Head of Sequence Database Group

Many Thanks

OBO Home Page:	http://obo.sourceforge.net/
GOA Home Page:	http://www.ebi.ac.uk/GOA
GO Home Page:	http://www.geneontology.org
AmiGO:	http://www.godatabase.org/cgi-bin/go.cgi
QuickGO:	http://www.ebi.ac.uk/ego
Sourceforge:	http://sourceforge.net/projects/geneontology/

Tutorials:

http://www.ebi.ac.uk/~camon/GOATutorial.htm (open in Explorer)

http://www.ebi.ac.uk/~dbarrell/goa/GOAflatfileTutorial.html

Email GOA: goa@ebi.ac.uk
Email GO: go@genome.stanford.edu