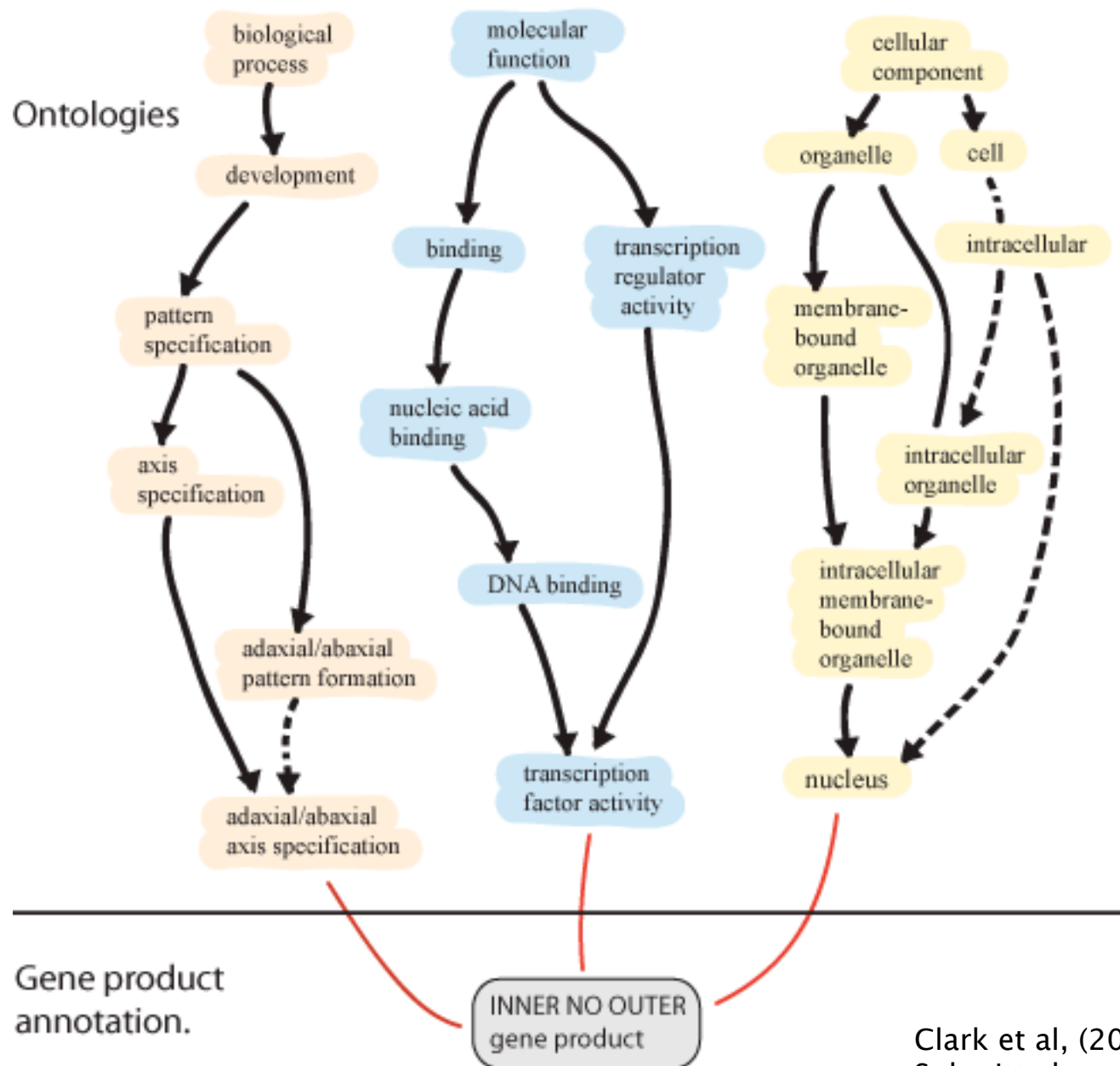




# Gene Ontology Consortium

<http://www.geneontology.org/>



Clark et al, (2005) Plant Phys Submitted.

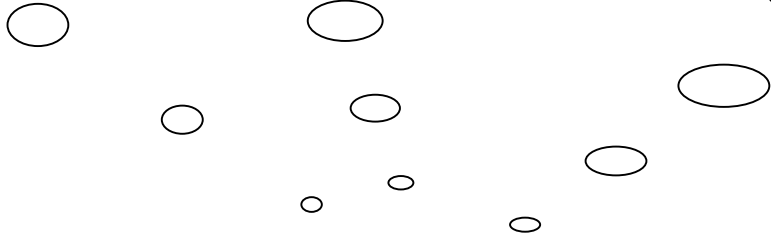
# Ontology (for our purposes)

- “an explicit specification of some topic” –  
Stanford Knowledge Systems Lab
- Includes:
  - a vocabulary of terms (names for concepts)
  - defined logical relationships to each
  - definitions

Tactition

Taction

Tactile sense



?



Tactition

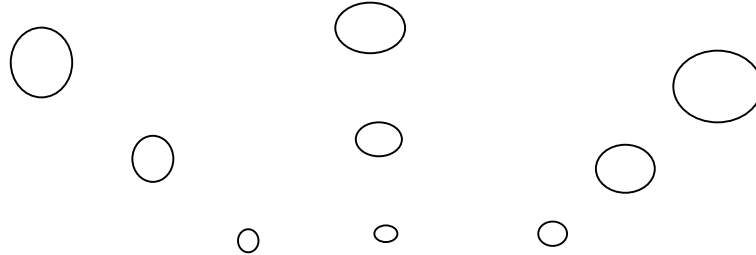
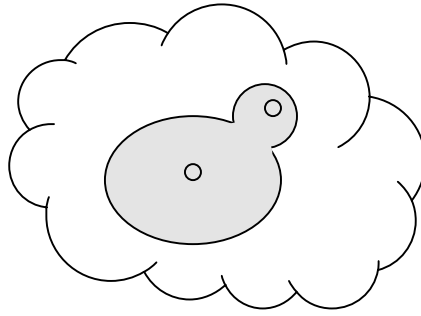
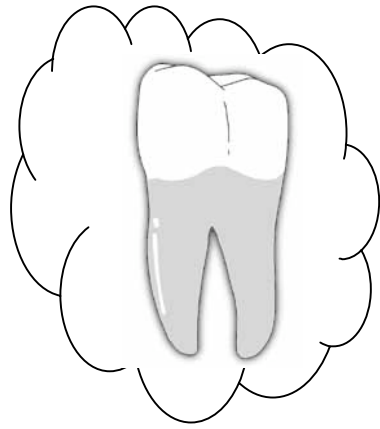
Taction

Tactile sense



perception of touch ; GO:0050975





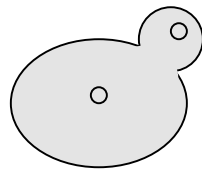
Bud initiation?





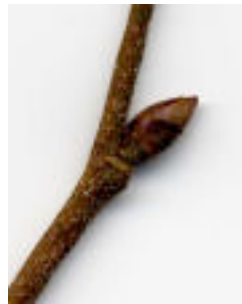
= bud initiation

**sensu Metazoa**



= bud initiation

**sensu Saccharomyces**



= bud initiation

**sensu Viridiplantae**

## mechanosensory behavior

**Accession:** GO:0007638

**Synonyms:** None

**Definition:**

Behavior that is dependent upon the sensation of movement.

**Term Lineage**   [Graphical View](#)

- GO:0003673 : Gene\_Ontology ( 146200 )
  - Ⓢ GO:0008150 : biological\_process ( 96312 )
    - Ⓢ GO:0007610 : behavior ( 2293 )
      - Ⓢ **GO:0007638 : mechanosensory behavior ( 26 )**

**External References**

- Ⓢ SP\_KW ( 1 )

**Direct Gene Product Associations**

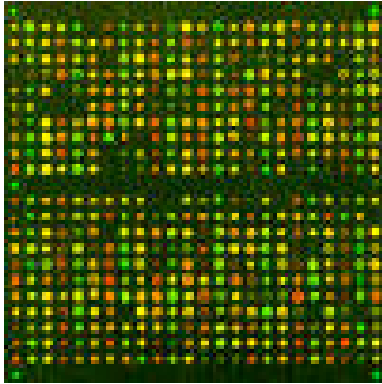
Direct Associations

**Filter Associations**

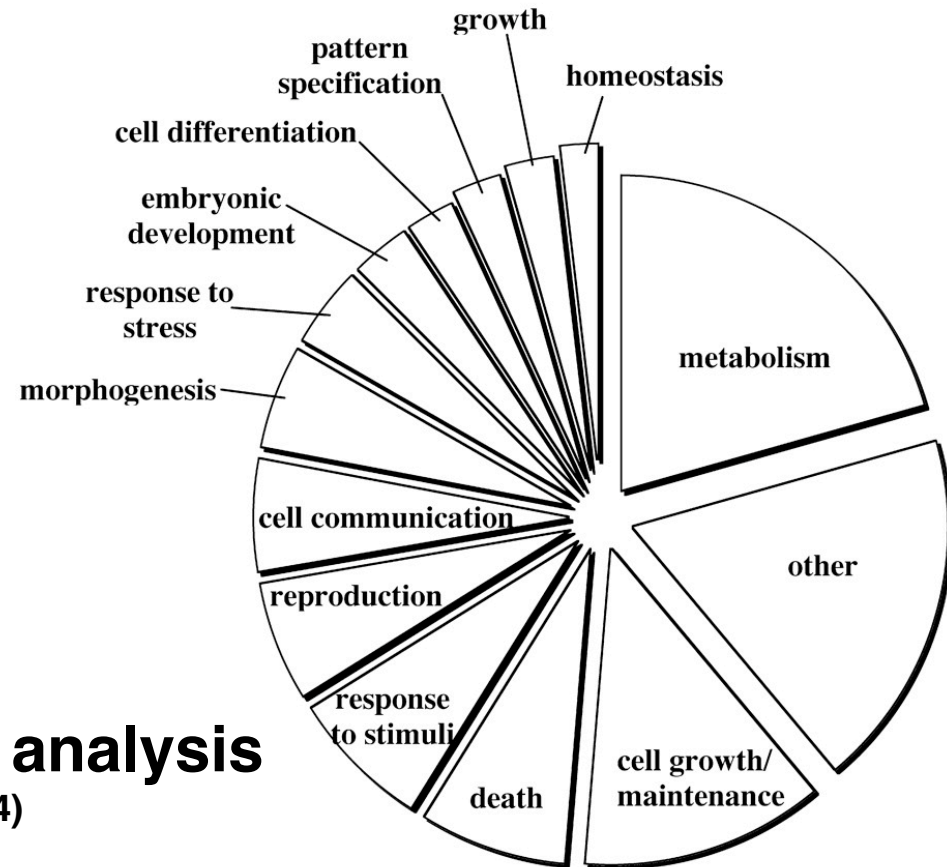
Datasource	Evidence Code	Species
All	All Curator Approved	All
FlyBase	IMP	A. aeolicus
SGD	IGI	A. fulgidus
MGI	IPI	A. pernix

Gene Symbol	Datasource	Evidence	Full Name
<input type="checkbox"/> <a href="#">bas</a>	<a href="#">FlyBase</a>	<a href="#">IMP</a>	bas
<input type="checkbox"/> <a href="#">bss</a>	<a href="#">FlyBase</a>	<a href="#">IMP</a>	bss
<input type="checkbox"/> <a href="#">C50H2.3</a>	<a href="#">Wormbase</a>	<a href="#">IMP</a>	None
<input type="checkbox"/> <a href="#">C53C9.3</a>	<a href="#">Wormbase</a>	<a href="#">IMP</a>	None
<input type="checkbox"/> <a href="#">eas</a>	<a href="#">FlyBase</a>	<a href="#">IMP</a>	eas
<input type="checkbox"/> <a href="#">EAS_DROME</a> <a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">IMP</a>	Ethanolamine kinase





## Microarray analysis



## Whole genome analysis

(J. D. Munkvold *et al.*, 2004)

# What GO is not:

- Not a way of unifying databases!
- Not a dictated standard
- Additional ontologies needed to model biology and experimentation.  
<http://obo.sourceforge.net/>



# The Three Ontologies

- *Molecular Function*: elemental activity or task
- *Biological Process*: broad objective or goal
- *Cellular Component*: location or complex



# The Three Ontologies

- *Molecular Function*: elemental activity or task  
DNA binding, catalysis of a reaction
- *Biological Process*: broad objective or goal
- *Cellular Component*: location or complex



# The Three Ontologies

- *Molecular Function*: elemental activity or task  
DNA binding, catalysis of a reaction
- *Biological Process*: broad objective or goal  
mitosis, signal transduction, metabolism
- *Cellular Component*: location or complex



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- *Molecular Function*: elemental activity or task  
DNA binding, catalysis of a reaction
- *Biological Process*: broad objective or goal  
mitosis, signal transduction, metabolism
- *Cellular Component*: location or complex  
nucleus, ribosome



# The Three Ontologies

- *Molecular Function*: elemental activity or task  
DNA binding, catalysis of a reaction
- *Biological Process*: broad objective or goal  
mitosis, signal transduction, metabolism
- *Cellular Component*: location or complex  
nucleus, ribosome

6 January 2005:

Total terms = 18244

93% have definitions

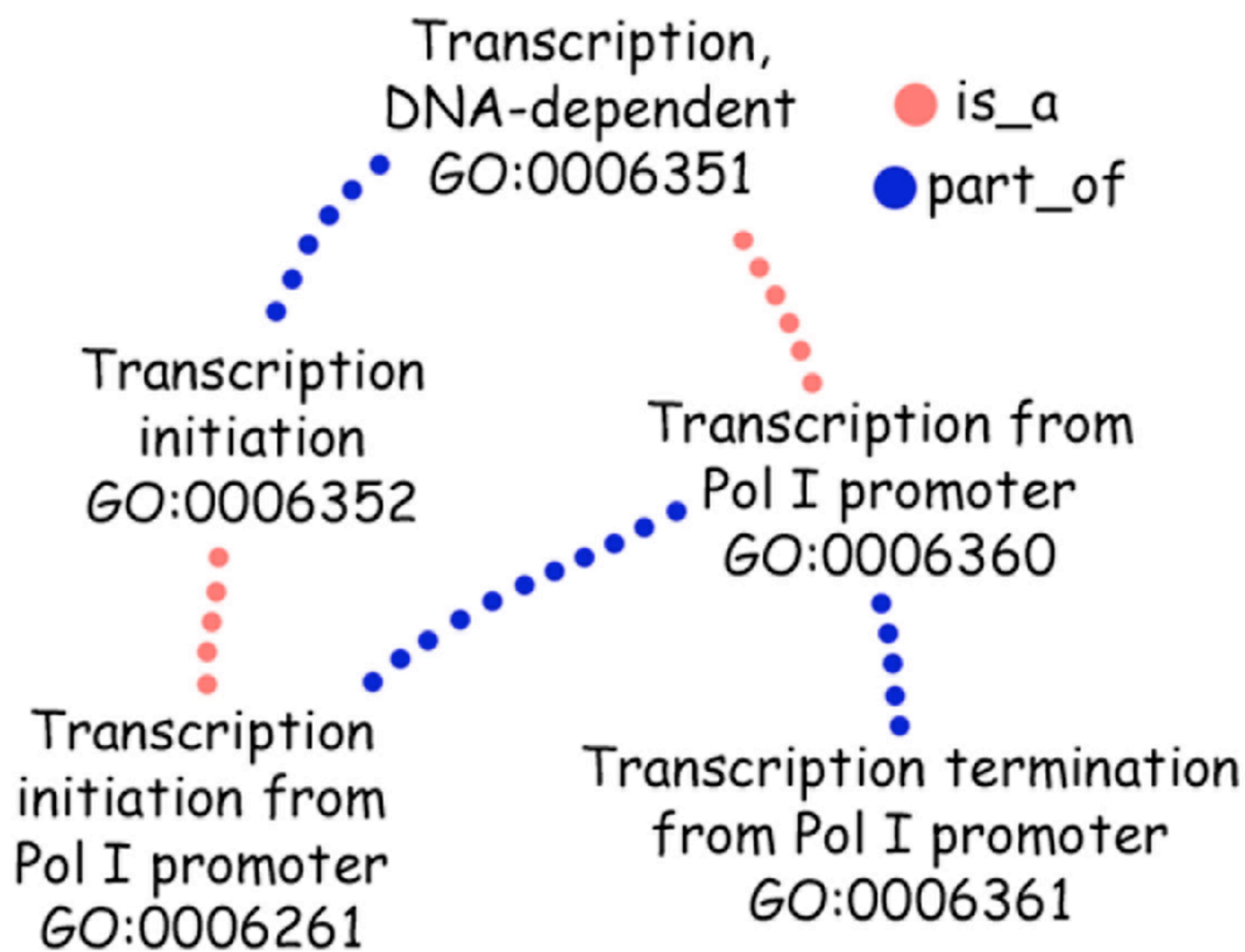
# What's in a GO term?

**term:** transcription initiation

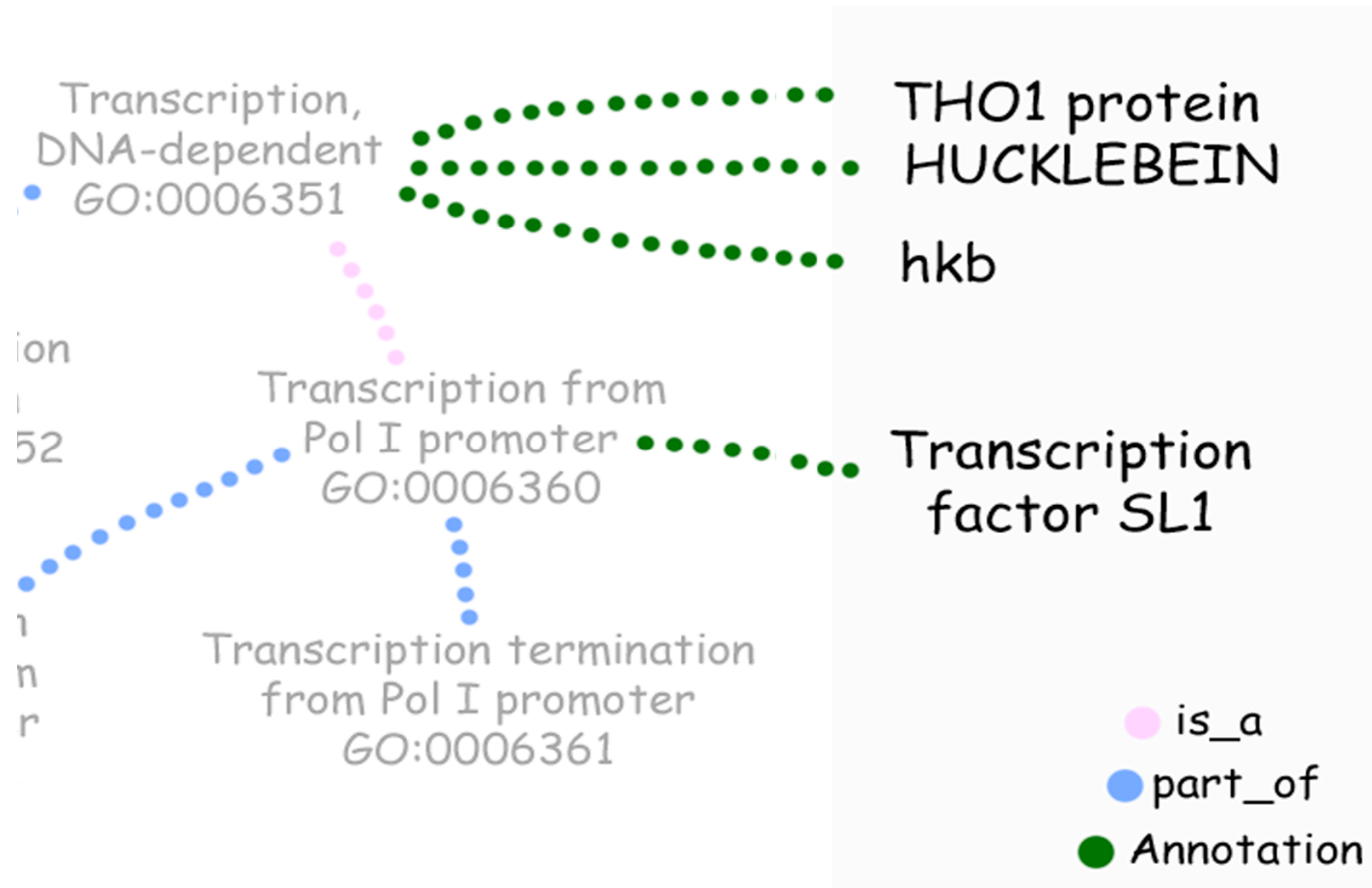
**id:** GO:0006352

**definition:** Processes involved in starting transcription, where transcription is the synthesis of RNA by RNA polymerases using a DNA template.

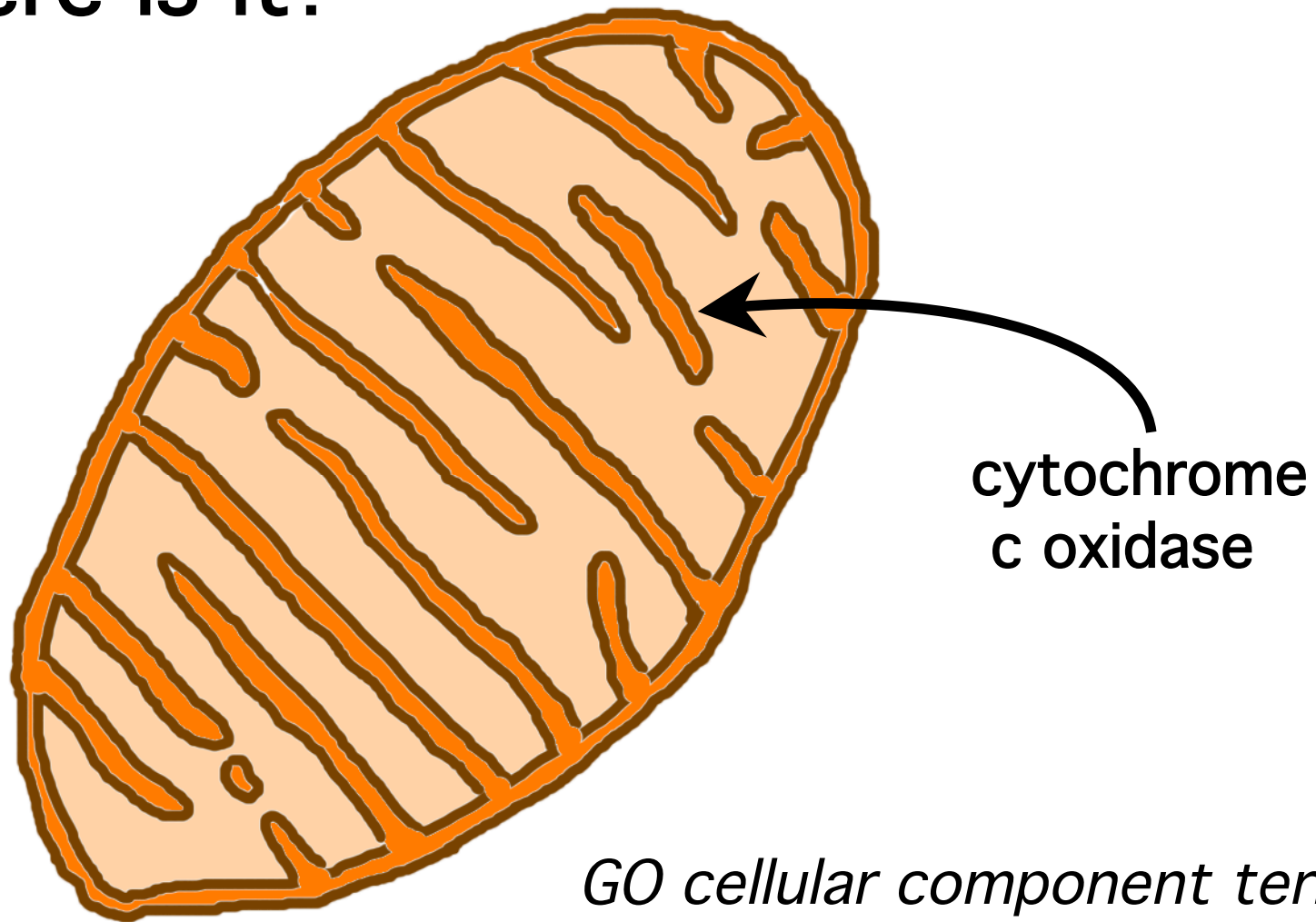




# Annotation



# Where is it?



cytochrome  
c oxidase

*GO cellular component term:*  
mitochondrial inner  
membrane ; GO:0005743

# What does it do?

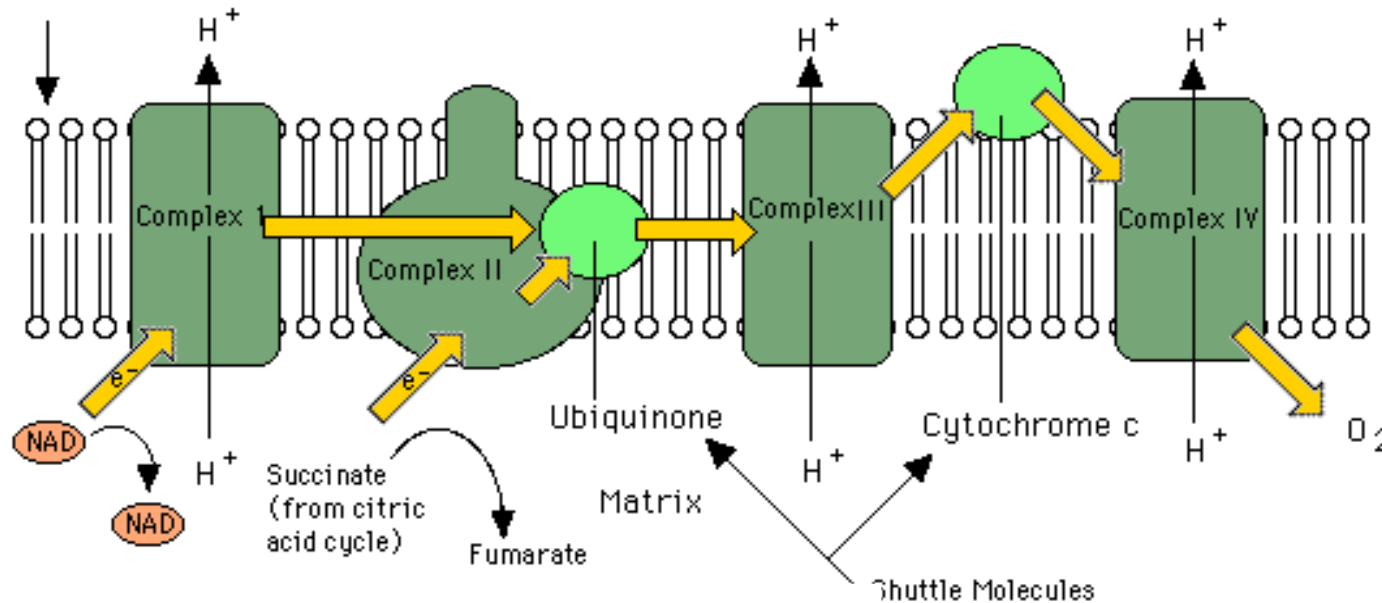
4 ferrocyanochrome c + O<sub>2</sub>

=

4 ferricyanochrome c + 2 H<sub>2</sub>O

*GO molecular function term:*  
cytochrome-c oxidase activity; GO:0004497

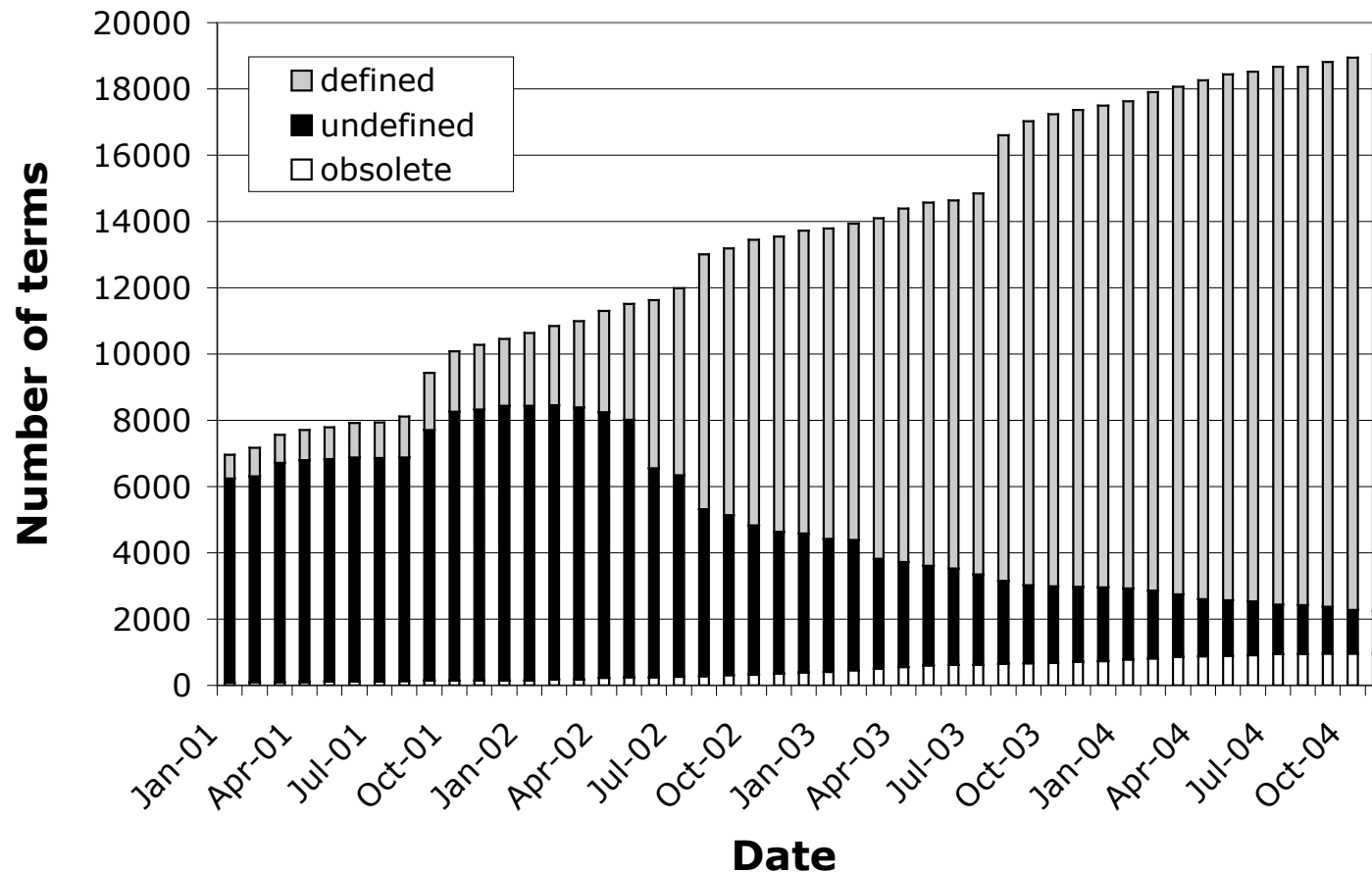
# Which process is this?



*GO biological process term:*  
electron transport ; GO:0006118

<http://ntri.tamuk.edu/cell/mitochondrion/krebpic.html>

# Request new terms



[go@geneontology.org](mailto:go@geneontology.org)

<http://sourceforge.net/projects/geneontology>

Clark et al, (2005) Plant Phys  
Submitted

**Accession:** GO:0004129

**Synonyms:** None

**Definition:**

Catalysis of the reaction: 4 ferrocytochrome c + O<sub>2</sub> = 4 ferricytochrome c + 2 H<sub>2</sub>O.

**Term Lineage**      [Graphical View](#)

[GO:0003673](#) : [Gene\\_Ontology](#) ( 146200 )

    Ⓢ [GO:0003674](#) : [molecular\\_function](#) ( 97507 )

        Ⓢ [GO:0003824](#) : [catalytic activity](#) ( 32256 )

            Ⓢ [GO:0016491](#) : [oxidoreductase activity](#) ( 4721 )

                Ⓢ [GO:0015002](#) : [heme-copper terminal oxidase activity](#) ( 123 )

                    Ⓢ **[GO:0004129](#) : [cytochrome-c oxidase activity](#) ( 118 )**

<input type="checkbox"/>	<a href="#">COX2_CAERE</a>		<a href="#">UniProt</a>	<a href="#">ISS</a>	Cytochrome c oxidase polypeptide II (Fragment)
<input type="checkbox"/>	<a href="#">COX2_HUMAN</a>	<a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">NAS</a>	Cytochrome c oxidase polypeptide II
<input type="checkbox"/>	<a href="#">COX2_YEAST</a>	<a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">IDA</a>	Cytochrome c oxidase polypeptide II precursor
<input type="checkbox"/>	<a href="#">COX3</a>		<a href="#">TAIR</a>	<a href="#">TAS</a>	None
<input type="checkbox"/>	<a href="#">COX3_CAEEL</a>	<a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">ISS</a>	Cytochrome c oxidase polypeptide III
<input type="checkbox"/>	<a href="#">COX3_HUMAN</a>	<a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">NAS</a>	Cytochrome c oxidase polypeptide III
<input type="checkbox"/>	<a href="#">COX3_YEAST</a>	<a href="#">GOst</a>	<a href="#">UniProt</a>	<a href="#">IDA</a>	Cytochrome c oxidase polypeptide III
<input type="checkbox"/>	<a href="#">COX4</a>	<a href="#">GOst</a>	<a href="#">SGD</a>	<a href="#">IDA</a>	cytochrome c oxidase subunit IV
<input type="checkbox"/>	<a href="#">Cox4b</a>		<a href="#">RGD</a>	<a href="#">IPI</a>	cytochromecoxidase,subunit4b
<input type="checkbox"/>	<a href="#">Cox4i2</a>	<a href="#">GOst</a>	<a href="#">MGI</a>	<a href="#">ISS</a>	cytochrome c oxidase subunit IV isoform 2
<input type="checkbox"/>	<a href="#">COX5A</a>	<a href="#">GOst</a>	<a href="#">SGD</a>	<a href="#">IDA</a>	cytochrome c oxidase chain Va
<input type="checkbox"/>	<a href="#">Cox5a</a>		<a href="#">RGD</a>	<a href="#">IDA</a>	cytochromecoxidase,subunitVa
<input type="checkbox"/>	<a href="#">Cox5b</a>		<a href="#">RGD</a>	<a href="#">TAS</a>	cytochromecoxidasesubunitVb
<input type="checkbox"/>	<a href="#">COX5B</a>	<a href="#">GOst</a>	<a href="#">SGD</a>	<a href="#">IDA</a>	cytochrome c oxidase chain Vb
<input type="checkbox"/>	<a href="#">COX6</a>	<a href="#">GOst</a>	<a href="#">SGD</a>	<a href="#">IDA</a>	cytochrome c oxidase subunit

# GO Slim

- [-] ⓘ **GO:0008152 : metabolism (34935)** 🌐
  - [-] ⓘ GO:0006066 : alcohol metabolism (1043)
  - [-] ⓘ GO:0006081 : aldehyde metabolism (67)
  - [-] ⓘ GO:0009308 : amine metabolism (2232)
  - [-] ⓘ **GO:0006519 : amino acid and derivative metabolism (2320)** 🌐
    - [-] ⓘ **GO:0006575 : amino acid derivative metabolism (659)** 🌐
      - [-] ⓘ GO:0018902 : 1,3-dichloro-2-propanol metabolism (0)
      - [-] ⓘ GO:0018871 : 1-aminocyclopropane-1-carboxylate metabolism (1)
      - [-] ⓘ GO:0019471 : 4-hydroxyproline metabolism (35)
      - [-] ⓘ GO:0046442 : aerobactin metabolism (0)
      - [-] ⓘ GO:0042398 : amino acid derivative biosynthesis (351)
      - [-] ⓘ GO:0042219 : amino acid derivative catabolism (70)
      - [-] ⓘ GO:0009448 : aminobutyrate metabolism (14)
      - [-] ⓘ GO:0006576 : biogenic amine metabolism (278)
      - [-] ⓘ GO:0009692 : ethylene metabolism (38)
      - [-] ⓘ GO:0046516 : hypusine metabolism (7)
      - [-] ⓘ GO:0046418 : nopaline metabolism (0)
      - [-] ⓘ GO:0046419 : octopine metabolism (1)





- biological\_process
  - behavior
  - biological\_process unknown
  - cellular process
    - cell communication
    - cell differentiation
    - cellular physiological process
      - cell activation
      - cell death
      - cell growth and/or maintenance
      - cell motility**
      - cellular defense response
      - cellular response to starvation
        - cellular response to water deprivation
      - conjugation
      - extracellular matrix organization and bionogenesis
      - host cell immortalization
      - nutrient uptake
      - photosynthesis
      - pilus retraction
      - sporulation
      - stomatal movement
    - membrane fusion
    - regulation of cellular process
  - development
  - physiological process
  - regulation of biological process
  - viral life cycle
- cellular\_component
- molecular\_function
- Types
- Obsolete

GO Obsolescence Plugin v1.003

Cannot obsolete nodes with children

Find terms

AND

Term has self with te

Term name that equals

<new filter>

NOT  Case sensitive

Advanced mode  Search all terms  Search selected terms  Search children of selection  Search obsoletes

ID: **GO:0006928**

Namespace: **process**

Term name: **cell motility**

Definition:

Text	Dbxrefs	Edit
Any process involved in the controlled movement of a cell.	GO:jl	

Synonyms

Select a synonym from the list to edit it, or press add to create a new synonym

Add Del

General DbXrefs

Select a dbxref from the list to edit it, or press add to create a new dbxref

Add Del

Comment

Commit Commit As New Term

DAG Viewer

- biological\_process
  - physiological process
    - cellular physiological process
      - cell motility**
  - cellular process
    - cellular physiological process
      - cell motility**

Dbxref Library v1.002

(GO:jic)  
(http://cancerweb.ncl.ac.uk)  
(TAIR:curators)  
(ZFIN:dh)

Use dbxref Use as def dbxref  
Import dbxrefs Export dbxrefs  
Configure dbxrefs



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Terms/Annotations

# GENE ONTOLOGY CONSORTIUM

[What is the Gene Ontology?](#)

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The goal of the Gene Ontology™ (GO) Consortium is to produce a controlled vocabulary that can be applied to all organisms even as knowledge of gene and protein roles in cells is accumulating and changing. GO provides three structured [networks](#) of defined terms to describe gene product attributes. GO is one of the controlled vocabularies of the [Open Biological Ontologies](#).

- Submit new GO term suggestions via the [Curator Requests Tracker](#) at [SourceForge](#). [Help with new term submission](#) is available.
- Send comments and questions to [go@geneontology.org](mailto:go@geneontology.org).



## Search Terms and Annotations

This search uses the [AmiGO](#) browser. You can also use one of the many other [GO Browsers](#)

<http://www.geneontology.org/>

## Contributors

FlyBase

DictyBase

GeneDB *S. pombe*

Mouse Genome Database

Genome Knowledge Base

TIGR Gramene

The Arabidopsis Information Resource

The Zebrafish Information Network

Berkeley Drosophila Genome Project

Saccharomyces Genome Database

The Institute for Genomic Research

The GO Editorial Office

Rat Genome Database

WormBase

Compugen

GeneDB for protozoa

EBI GOA project