

# PANTHER: A Library of Protein Families and Subfamilies Indexed by Function

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*Genome Res.* 2003 13: 2129-2141

Diemer, Anushya Muruganujan and Apurva Narechania Paul D. Thomas ,et al

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Group C

Members : 郭書麟、曾致遠、柯懿婷、陳珮欣

Speaker : 吳行展

Date: 95/12/21

# PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways

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*Nucleic Acids Research*, 2006, Vol. 00, Database issue D1–D6

Huaiyu Mi, Nan Guo, Anish Kejariwal and Paul D. Thomas\*



# Outline

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- **Introduction**
- **Method**
- **Manipulation**
- **Conclusion**



# Introduction

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- In the genomic era , one of the fundamental goals is to **characterize the function of proteins** on a large scale.

# Introduction



- PANTHER (**P**rotein **A**Nalysis **T**Hrough **E**volutionary **R**elationships)
- A freely available, comprehensive software system for relating protein sequence evolution to the evolution of specific protein functions and biological roles.



# Genes, transcripts and proteins

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- Classifies genes by their functions
- Database of genes, transcripts and proteins in the following species:
  - Human (NCBI, Celera)
  - Mouse (NCBI, Celera)
  - Rat (NCBI, Celera)
  - *Drosophila melanogaster* (FlyBase)



# Genes, transcripts and proteins

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- Classifications for these genes are based on **Hidden Markov Models (HMMs)**, statistical models that describe **families and subfamilies** of protein sequences.



# Genes, transcripts and proteins

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- Proteins are **classified by expert biologists** into families and subfamilies of shared function
- Categorized by **molecular function** and **biological process** ontology terms.



# Families and HMMs

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- A library (PANTHER/LIB) of protein families and subfamilies and associated data such as
  - Phylogenetic trees
  - Multiple sequence alignments(MSA)
  - HMMs.

# Families and HMMs

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- PANTHER version 6.1 contains 5547 protein families, divided into 24,582 functionally
- Distinct protein subfamilies by expert biologist curators.
- Each protein family is represented by a phylogenetic tree defining its subfamilies.
- Families and subfamilies are also represented by HMMs and associated with functional ontology terms.

# Families and HMMs



# Pathways

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- PANTHER Pathway consists of **over 130, primarily signaling pathways**, each with subfamilies and protein sequences mapped to **individual pathway components**.
- .
- A component is usually a single protein in a given organism, but multiple proteins can sometimes play the same role.



# Pathways

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- Pathways are drawn using **CellDesigner** software, capturing molecular level events in both **signaling** and **metabolic** pathways, and can be exported in **SBML** format.
- Pathway diagrams are interactive and include tools for visualizing gene expression data in the context of the diagrams

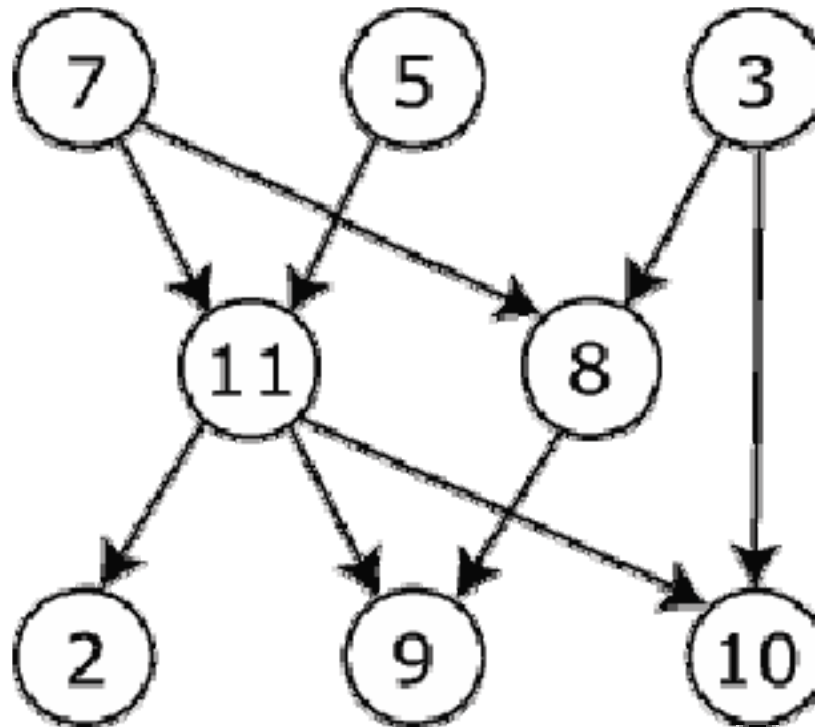
# Ontologies

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- A collection of terms (**PANTHER/X**) describing protein molecular functions and biological processes.
- The PANTHER/X ontology is a controlled vocabulary of **molecular function** and **biological process** terms, arranged as **directed acyclic graphs (DAGs)** similar to the **Gene Ontology™ (GO)**, but greatly abbreviated and simplified to facilitate high-throughput analyses.

# Ontologies

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**A simple directed acyclic graph (DAG)**

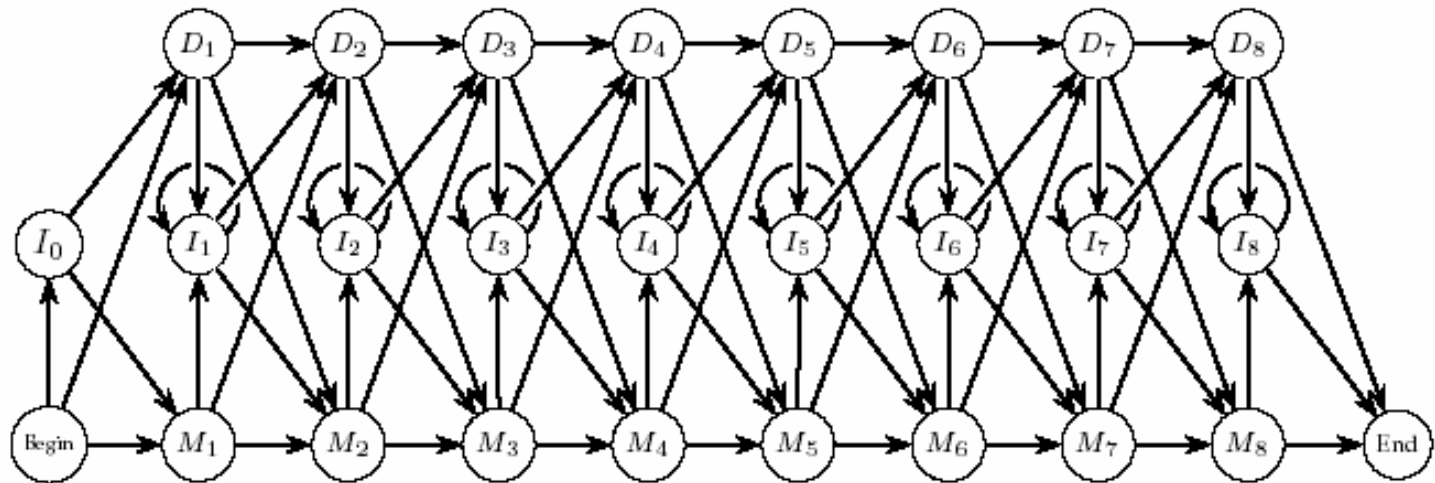
# Methods

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- Making a Collection of HMM for Protein Families
  - Use BLAST to separate a protein database into families of related proteins
  - Construct a multiple alignment for each protein family.
  - Construct a profile HMM model and optimize the parameters of the model (**transition and emission probabilities**).
  - **Align the target sequence** against each HMM to find the best fit between a target sequence and an HMM



# Methods



A profile HMM



# Methods

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1. Family clustering.
2. Multiple sequence alignment (MSA), family HMM, and family tree building.
3. Family/subfamily definition and naming.
4. Subfamily HMM building.
5. Molecular function and biological process association.

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The PANTHER (Protein **AN**alysis **TH**rough Evolutionary Relationships) Classification System is a unique resource that **classifies genes by their functions**, using published scientific experimental evidence and evolutionary relationships to predict function even in the absence of direct experimental evidence. Proteins are **classified by expert biologists** into families and subfamilies of shared function, which are then categorized by molecular function and biological process ontology terms. For an increasing number of proteins, detailed biochemical interactions in canonical pathways are captured and can be viewed interactively.

To get started, try either a [text search](#), [browsing by function](#), or take a look at interactive pie charts that summarize the functions of whole genomes for [Human](#), [Mouse](#), [Rat](#) and [Drosophila melanogaster](#).

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A library (PANTHER/LIB) of protein families and subfamilies and associated data such as phylogenetic trees, multiple sequence alignments and HMMs.

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### News

(December 8, 2006)

PANTHER 6.1 released

PANTHER Pathways version 1.31 released

Additional PANTHER HMMs have been integrated into InterPro

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### Publications

[How to cite PANTHER](#)

["Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools."](#) Thomas, et al.

["The PANTHER database of protein families, subfamilies, functions and pathways."](#) Mi,

## Prowler ?

Browse the PANTHER system using the Prowler, and retrieve results for different data associated with the ontology and pathway terms, such as individual genes or families and subfamilies of proteins. [About the PANTHER Ontologies](#)

### PANTHER Browser

#### Biological Process

Molecular Function  
Pathway  
Species





- |                                     |                          |  |
|-------------------------------------|--------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Carbohydrate metabolism                            |
| <input type="checkbox"/>            | <input type="checkbox"/> | Amino acid metabolism                              |
| <input type="checkbox"/>            | <input type="checkbox"/> | Lipid, fatty acid and steroid metabolism           |
| <input type="checkbox"/>            | <input type="checkbox"/> | Nucleoside, nucleotide and nucleic acid metabolism |
| <input type="checkbox"/>            | <input type="checkbox"/> | Protein metabolism and modification                |
| <input type="checkbox"/>            | <input type="checkbox"/> | Electron transport                                 |
| <input type="checkbox"/>            | <input type="checkbox"/> | Coenzyme and prosthetic group metabolism           |
| <input type="checkbox"/>            | <input type="checkbox"/> | Nitrogen metabolism                                |
| <input type="checkbox"/>            | <input type="checkbox"/> | Phosphate metabolism                               |
| <input type="checkbox"/>            | <input type="checkbox"/> | Sulfur metabolism                                  |
| <input type="checkbox"/>            | <input type="checkbox"/> | Other metabolism                                   |
| <input type="checkbox"/>            | <input type="checkbox"/> | Signal transduction                                |

### Result Types

 Get Results

4,195 - Gene  
6,723 - Protein & Transcript  
**11,577 - Training Sequence**  
801 - PANTHER Family  
101 - Pathway Component

### Your Selection Summary

All Training Sequence results must belong to the following Biological Process, or its subcategories:

I. Carbohydrate metabolism



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 Celera: ☐ H. sapiens ☐ M. musculus ☐ R. norvegicus

 FlyBase: ☐ D. melanogaster

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Genes

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Customize genes criteria to search on:

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☐ RefSeq Protein ID

☐ 1700 Probe ID

☐ PANTHER Biological Process

☐ InterPro

☐ Species

☐ Celera Gene ID

☒ Gene Symbol

☐ Celera Transcript ID

☐ Celera Protein ID

☐ PANTHER Molecular Function

☐ PANTHER Family/Subfamily

☐ Pathway

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<input type="button" value="clr"/> <input type="button" value="all"/>	<a href="#">Gene ID</a>	<a href="#">Gene Name</a> <a href="#">Gene Symbol</a>	<a href="#">PANTHER Best Hit</a>	<a href="#">PANTHER Score</a>	<a href="#">PANTHER Molecular Function</a>	<a href="#">PANTHER Biological Process</a>	<a href="#">Pathway</a>	<a href="#">Public Start Pos</a>	<a href="#">Public End Pos</a>	<a href="#">Public Location</a> (chromosome)	<a href="#">Species</a>
<input type="checkbox"/> 1.	<a href="#">GeneID:7157</a>	tumor protein p53 (Li-Fraumeni syndrome) <a href="#">TP53</a>	<a href="#">CELLULAR TUMOR ANTIGEN P53</a> ( <a href="#">PTHR11447:SF6</a> )	0E+00 ●●●	<a href="#">Other transcription factor</a>	<a href="#">DNA repair</a> <a href="#">mRNA transcription regulation</a> <a href="#">Induction of apoptosis</a> <a href="#">Cell cycle control</a> <a href="#">Cell proliferation and differentiation</a> <a href="#">Tumor suppressor</a>	<a href="#">P53 pathway feedback loops</a> <a href="#">1-&gt;P53</a>  <a href="#">Huntington disease-&gt;P53 tumor suppressor phosphoprotein</a>  <a href="#">Apoptosis signaling pathway-&gt;Tumor protein p53</a>  <a href="#">p53 pathway-&gt;p53</a>  <a href="#">p53 pathway-&gt;p53</a>	7512464	7531642	17	NCBI: H. sapiens

## PANTHER GENE INFORMATION

---

Gene ID:	<a href="#">GeneID:7157</a>
Gene Name:	tumor protein p53 (Li-Fraumeni syndrome)
Gene Symbol(s):	<a href="#">TP53</a> <a href="#">TRP53</a> <a href="#">p53</a> <a href="#">LFS1</a>
Public Gene Location:	Chr. 17 7512464 - 7531642 <a href="#">Map Viewer</a>
Organism:	Homo sapiens
Related sequences:	<a href="#">M13121</a> <a href="#">M22881</a> <a href="#">U94788</a> <a href="#">X02469</a>
ABI Assays:	<a href="#">TagMan® Gene Expression Assays</a> <a href="#">TagMan® SNP Genotyping Assays</a>

## PANTHER CLASSIFICATION

---

PANTHER Molecular Function:

[Transcription factor](#)

↳ [Other transcription factor](#)

PANTHER Biological Process:

[Nucleoside, nucleotide and nucleic acid metabolism](#)

↳ [DNA metabolism](#)

↳ [DNA repair](#)

↳ [mRNA transcription](#)

↳ [mRNA transcription regulation](#)

[Apoptosis](#)

↳ [Induction of apoptosis](#)

[Cell cycle](#)

↳ [Cell cycle control](#)

[Cell proliferation and differentiation](#)

[Oncogenesis](#)

↳ [Tumor suppressor](#)

Pathway Categories:

[P53 pathway feedback loops 1](#)

↳ [p53](#)

[Huntington disease](#)

↳ [P53 tumor suppressor phosphoprotein](#)

[Apoptosis signaling pathway](#)

↳ [Tumor protein p53](#)

[p53 pathway](#)

↳ [p53](#)

[p53 pathway](#)

↳ [p53](#)

[p53 pathway feedback loops 2](#)

↳ [p53](#)

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## TRANSCRIPT / PROTEIN PAIRS

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Transcript	Protein	PANTHER Score	PANTHER Links	PANTHER Best Hit
<a href="#">NM_000546</a>	<a href="#">NP_000537</a>	<a href="#">0E+00</a> ●●●	<a href="#">Tree</a> <a href="#">MSA</a> <a href="#">Additional scores</a>	<a href="#">CELLULAR TUMOR ANTIGEN P53 (PTHR11447:SF6)</a>

## PANTHER GENE INFORMATION

---

Gene ID: [GeneID:7157](#)

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<a href="#">clr</a>	<a href="#">all</a>	<a href="#">▲</a> <a href="#">Family ID</a>	<a href="#">Family Name</a>	<a href="#">Training Sequence</a>	<a href="#">PANTHER Molecular Function</a>	<a href="#">PANTHER Biological Process</a>	<a href="#">Pathway</a>	<a href="#">Interpro</a>
<input type="checkbox"/>	1.	<a href="#">PTHR11447:SF6</a>	<a href="#">CELLULAR TUMOR ANTIGEN P53</a>	29	<a href="#">Other transcription factor</a>	<a href="#">DNA repair</a> <a href="#">mRNA transcription regulation</a> <a href="#">Induction of apoptosis</a> <a href="#">Cell cycle control</a> <a href="#">Cell proliferation and differentiation</a> <a href="#">Tumor suppressor</a>	<a href="#">P53 pathway feedback loops 1-&gt;P53</a> <a href="#">Huntington disease-&gt;P53 tumor suppressor phosphoprotein</a> <a href="#">Apoptosis signaling pathway-&gt;Tumor protein p53</a> <a href="#">p53 pathway-&gt;p53</a> <a href="#">p53 pathway-&gt;p53</a> <a href="#">p53 pathway feedback loops 2-&gt;p53</a>	

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## PANTHER SUBFAMILY INFORMATION

Subfamily: [CELLULAR TUMOR ANTIGEN P53 \(PTHR11447:SF6\)](#)

Family: [CELLULAR TUMOR ANTIGEN P53-RELATED](#)

PANTHER Links:



[Tree](#) [MSA](#)

PANTHER Molecular Function: [Transcription factor](#)

↳ [Other transcription factor](#)

PANTHER Biological Process: [Nucleoside, nucleotide and nucleic acid metabolism](#)

↳ [DNA metabolism](#)

↳ [DNA repair](#)

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PANTHER TREE VIEWER [close window](#)



Family Name : CELLULAR TUMOR ANTIGEN P53-RELATED (PTHR11447)

Tree MSA

Tree	Grid	MSA									
	gi	sf_name	definition	organism	molecular f...	comments	biological p...	keywords	similarity	function	evic
SF8-TUMOR PROTEIN P73-LIKE (P73L) (P63)	SF8	TUMOR PROTEIN P73-LIKE (...)		Vertebrates,...	Other transc...		DNA repair,D...				
SF7-TUMOR PROTEIN P73	SF7	TUMOR PROTEIN P73		Vertebrates,...	Other transc...		DNA repair,D...				
SF6-P53_BRARE	P53_BRARE	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Brachydanio...	Other transc...		DNA repair,D...				
SF6-Q7ZW62_BRARE	Q7ZW62_BR...	CELLULAR TUMOR ANTIGE...	Tumor suppressor p53	Brachydanio...	Other transc...		DNA repair,D...				
SF6-Q5XHJ3_XENLA	Q5XHJ3_XE...	CELLULAR TUMOR ANTIGE...	Tp53 protein	Xenopus lae...	Other transc...		DNA repair,D...				
SF6-P53_XENLA	P53_XENLA	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Xenopus lae...	Other transc...		DNA repair,D...				
SF6-Q7T1D0_XENLA	Q7T1D0_XE...	CELLULAR TUMOR ANTIGE...	Tumor supressor protein p53	Xenopus lae...	Other transc...		DNA repair,D...				
SF6-P53_CHICK	P53_CHICK	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Gallus gallus...	Other transc...		DNA repair,D...				
SF6-Q9N252_PIG	Q9N252_PIG	CELLULAR TUMOR ANTIGE...	P53 protein	Sus scrofa (...)	Other transc...		DNA repair,D...				
SF6-P53_BOVIN	P53_BOVIN	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Bos taurus (...)	Other transc...		DNA repair,D...				
SF6-Q29446_BOVIN	Q29446_BO...	CELLULAR TUMOR ANTIGE...	P53 (Fragment)	Bos taurus (...)	Other transc...		DNA repair,D...				
SF6-Q66HM0_RAT	Q66HM0_RAT	CELLULAR TUMOR ANTIGE...	Hypothetical protein (Fragme...	Rattus norve...	Other transc...		DNA repair,D...				
SF6-Q9EQL0_RAT	Q9EQL0_RAT	CELLULAR TUMOR ANTIGE...	P53 alternative splice isofo...	Rattus norve...	Other transc...		DNA repair,D...				
SF6-Q80ZA1_MOUSE	Q80ZA1_MO...	CELLULAR TUMOR ANTIGE...	Tumor suppressor p53	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q70366_MOUSE	Q70366_MO...	CELLULAR TUMOR ANTIGE...	Tumor suppressor p53	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q925E2_MOUSE	Q925E2_MO...	CELLULAR TUMOR ANTIGE...	P53 tumor suppressor (Frag...	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q91XH8_MOUSE	Q91XH8_MO...	CELLULAR TUMOR ANTIGE...	Transformation related prote...	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q64451_MOUSE	Q64451_MO...	CELLULAR TUMOR ANTIGE...	P53 cellular tumor antigen (F...	Mus musculu...	Other transc...		DNA repair,D...				
SF6-P53_MOUSE	P53_MOUSE	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q9ER40_MOUSE	Q9ER40_MO...	CELLULAR TUMOR ANTIGE...	Transformation related prote...	Mus musculu...	Other transc...		DNA repair,D...				
SF6-Q95326_CANFA	Q95326_CA...	CELLULAR TUMOR ANTIGE...	P53 protein (Fragment)	Canis familia...	Other transc...		DNA repair,D...				
SF6-Q28299_CANFA	Q28299_CA...	CELLULAR TUMOR ANTIGE...	P53 (Fragment)	Canis familia...	Other transc...		DNA repair,D...				
SF6-Q6JAD8_MAIZE	Q6JAD8_MA...	CELLULAR TUMOR ANTIGE...	Putative tumor protein p53	Zea mays (M...	Other transc...		DNA repair,D...				
SF6-P53_HUMAN	P53_HUMAN	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Homo sapien...	Other transc...		DNA repair,D...				
SF6-Q5U0E4_HUMAN	Q5U0E4_HU...	CELLULAR TUMOR ANTIGE...	Tumor protein p53 (Li-Fraum...	Homo sapien...	Other transc...		DNA repair,D...				
SF6-P53_PIG	P53_PIG	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Sus scrofa (...)	Other transc...		DNA repair,D...				
SF6-P53_HORSE	P53_HORSE	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Equus caball...	Other transc...		DNA repair,D...				
SF6-P53_FELCA	P53_FELCA	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Felis silvestri...	Other transc...		DNA repair,D...				
SF6-Q9TUX4_CANFA	Q9TUX4_CA...	CELLULAR TUMOR ANTIGE...	P53 protein (Fragment)	Canis familia...	Other transc...		DNA repair,D...				
SF6-P53_CANFA	P53_CANFA	CELLULAR TUMOR ANTIGE...	Cellular tumor antigen p53 (T...	Canis familia...	Other transc...		DNA repair,D...				
SF6-Q28344_CANFA	Q28344_CA...	CELLULAR TUMOR ANTIGE...	P53 protein (Fragment)	Canis familia...	Other transc...		DNA repair,D...				

Family Name : CELLULAR TUMOR ANTIGEN P53-RELATED (PTHR11447)

Tree MSA

Tree	Grid	MSA
SF10-Q6I9N3_RAT		.....DNQVVCILAILPAGEDMF--NMVGIYKITEVPAEEMPCIMQLFS--NMHLCHGKYSQHMTVEVMRRCSHHERCSD..G.DD..GTPP.....
SF8-TUMOR PROTEIN P73-LIKE (P73L) (P63)		
SF7-TUMOR PROTEIN P73		
SF6-P53_BRARE		..QSGTAKLNLKFCQLAKPPG-IAIYK/AESGTAWTCSPKLDGKTC/VVDAPG-SYRAIYKSEM/VVCPHRTPD..G.DN..LAPAGHLIRVEGNQRANYR...EDNITLRHSVFVPYEAPQ
SF6-Q7ZW62_BRARE		..QSGTAKLNLKFCQLAKPPG-IAIYK/AESGTAWTCSPKLDGKTC/VVDAPG-SYRAIYKSEM/VVCPHRTPD..G.DN..LAPAGHLIRVEGNQRANYR...EDNITLRHSVFVPYEAPQ
SF6-Q5XHJ3_XENLA		..QNGTAKLNLKFCQLAKPPG-IAVYVAEONGT/AVTYLNFCAKTPN..RVEERG-LRAV/SEIVVACHESV.G.ED..AAPPShLMRVEGNLQASYM...EDVNSGRHSVCVPYEGP
SF6-P53_XENLA		..QNGTAKLNLKFCQLAKPPG-IAVYVAEONGT/AVTYLNFCAKTPN..RVEERG-LRAV/SEIVVACHESV.G.ED..AAPPShLMRVEGNLQASYM...EDVNSGRHSVCVPYEGP
SF6-Q7T1D0_XENLA		..QNGTAKLNLKFCQLAKPPG-IAVYVAEONGT/AVTYLNFCAKTPN..RVEERG-LRAV/SEIVVACHESV.G.ED..AAPPShLMRVEGNLQASYM...EDVNSGRHSVCVPYEGP
SF6-P53_CHICK		..GTAKSYLNKLVYCRLAHPPG-SAVVVAE.....TASVTYLNKYGAKPCDQVQAPISSIAVVKSEIVVRGRCG..G.DD..LAPAGHLIRVEGNLQASYM...EDVNSGRHSVCVPYEGP
SF6-Q9N252_PIG		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....HSGKTCCTSPKLFCAKTCVWAPP3-TFAMYLEHERRPSSDY..D..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_BOVIN		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....QTAVTCTYLNKHLAKIP..VDPGPGVRAAKLMT/VCFRSCG..G.DD..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q29446_BOVIN		.....QI...DS.....ECTIHYNFMCSNC...MGGMNRRLPILITILE.DSW.....
SF6-Q6HMO_RAT		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTA/MOYLNKLFCAKTCV..ASTPGTRAAIKKTEYVRRHCS..G.DD..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q9EQL0_RAT		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASYCTSLNKQLQALQ..VTPTRFAIY/SMTVIHHERSIG..L..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q80ZA1_MOUSE		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVNTYPLNLIQALACIQL..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q70366_MOUSE		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVNTYPLNLIQALACIQL..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q925E2_MOUSE		.....LNKLFQQLAKPPG-MAIYMITEV/SATPPAG-SRYRAMAIYKKSQHMTVEVRRCPHERCSD..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q91XH8_MOUSE		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVNTYPLNLIQALACIQL..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q64451_MOUSE		.....LNKLFQQLAKPPG-MAIYMITEV/SATPPAG-SRYRAMAIYKKSQHMTVEVRRCPHERCSD..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_MOUSE		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVNTYPLNLIQALACIQL..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q9ER40_MOUSE		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVNTYPLNLIQALACIQL..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q95326_CANFA		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....HSGKTCCTSPKLFCAKTCV..VSPPA/SRAIY/SQMV/VHHEDE..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q28299_CANFA		.....KSTEV--KSEFVTEVYRRCPHERCSDS..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q6JAD8_MAIZE		.....MAIYMITEV/IAIYK/SQHMTVEVRRCPHERCSD..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_HUMAN		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVTYSPKMFCL/CPVL..DS?G-RVMAQIHNEVPHHEC..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q5U0E4_HUMAN		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASVTYSPKMFCL/CPVL..DS?G-RVMAQIHNEVPHHEC..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_PIG		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....HSGKTCCTSPKLFCAKTCV..VSPPA/SRAIYKSEM/VVACHESV..G.DD..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_HORSE		..SGTAKLNLKFCQLAKPPG-MAIYMITEV/VTCTSPNINQGLTQL..VSPG-TVMAIYKSEIVVACHESV..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_FELCA		..QSGTAKLNLKFCQLAKPPG-MAIYMITEV.....GTASYCTSLNKQLQALQ..VSPPA/SRAIYKSEM/VVACHESV..G.DD..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q9TUX4_CANFA		.....AKSVLNKLFQQLAKPPG-MAIYMITEV/VVSSPPPN/TCVRAIYKSEIVVACHESV..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-P53_CANFA		..HSGTAKLNLKFCQLAKPPG-MAIYMITEV.....SGTASVTYSPKMFCL/CPVL..DS?G-RVMAQIHNEVPHHEC..G..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE
SF6-Q28344_CANFA		.....KSTEV--KSEFVTEVYRRCPHERCSDS..G.DG..LAPAGHLIRVEGNLRAEYF...DDRNTFRHSVVPYEPPE

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## TRANSCRIPT / PROTEIN INFORMATION

---

Transcript ID:	<a href="#">NM_000546</a>
Protein ID:	<a href="#">NP_000537</a>
Gene ID:	<a href="#">GeneID:7157</a>
Gene Name:	tumor protein p53 (Li-Fraumeni syndrome)
Gene Symbol:	<a href="#">TP53</a>
Organism:	Homo sapiens
Public Gene Location:	Chr.17 7512464 - 7531642 <a href="#">Map Viewer</a>
ABI Assays:	<a href="#">TaqMan® Gene Expression Assays</a> <a href="#">TaqMan® SNP Genotyping Assays</a>
Related sequences:	<a href="#">U94788</a> <a href="#">X02469</a> <a href="#">M22881</a> <a href="#">M13121</a>



## SEQUENCE DETAILS

### Transcribed Sequence - all exons

>NM\_000546

```
ACTTGTTCATGGCGACTGTCCAGCTTTGTGCCAGGAGCCTCGCAGGGGTTGATGGGATTGGGGTTTTCC
CCTCCCATGTGCTCAAGACTGGCGCTAAAAGTTTTGAGCTTCTCAAAAGTCTAGAGCCACCGTCCAGG
GAGCAGGTAGCTGCTGGGCTCCGGGGACACTTTGCGTTCGGGCTGGGAGCGTGCTTTCCACGACGGTG
ACACGCTTCCCTGGATTGGCAGCCAGACTGCCTTCCGGGTCACTGCCATGGAGGAGCCGCAGTCAGAT
CCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCAGACCTATGGAACTACTTCCCTGAAAACAA
CGTTCTGTCCCCCTTGCCGTCCCAAGCAATGGATGATTTGATGCTGTCCCCGGACGATATTGAACAAT
GGTTCACTGAAGACCCAGGTCCAGATGAAGCTCCCAAGATGCCAGAGGCTGCTCCCCGCGTGGCCCCCT
GCACCAGCAGCTCCTACACCGGGGGCCCCCTGCACCAGCCCCCTCCTGGCCCCCTGTCATCTTCTGTCCC
TTCCCAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCAATTCTGGGACAGCCAAAGT
CTGTGACTTGCACGTAATCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTG
CAGCTGTGGGTTGATTCCACACCCCCGCCCCGGCACCCGCGTCCGCGCCATGGCCATCTACAAGCAGTC
ACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAGCGCTGCTCAGATAGCGATGGTCTGG
CCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACT
TTTCGACATAGTGTGGTGGTGCCCTATGAGCCGCTGAGGTTGGCTCTGACTGTACCACCATCCACTA
```

### Protein Sequence

>NP\_000537

```
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGPDEAPRMPE
AAPRVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQ
LAKTCPVQLWVDSTPPPGRVRAMAIYKQSQHMTFVVRRCPPHHERCSDSDGLAPPQHILIRVEGNLRVE
YLDNRNTFRHSVVVPYEPPEVGSDCCTTIHYNMCMNSSCMGCMNRRPILTIITLEDSSGNLLGRNSFEV
RVCACPGDRRTTEENLRKKGEPPHELPPGSTKRALPNMTSSSPQPKKKPLDGEYFTLQIRGRERFEM
FRELNLEALELKDAQAGKEPGGSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD
```

## PANTHER CLASSIFICATION

---

PANTHER Best Hit: [CELLULAR TUMOR ANTIGEN P53\(PTHR11447:SF6\)](#)

Score: [0.00E00](#) ●●●

Links: [Tree](#) [MSA](#) [Additional scores](#)

PANTHER Molecular Function: [Transcription factor](#)  
↳ [Other transcription factor](#)

PANTHER Biological Process: [Nucleoside, nucleotide and nucleic acid metabolism](#)  
↳ [DNA metabolism](#)  
↳ [DNA repair](#)  
↳ [mRNA transcription](#)  
↳ [mRNA transcription regulation](#)  
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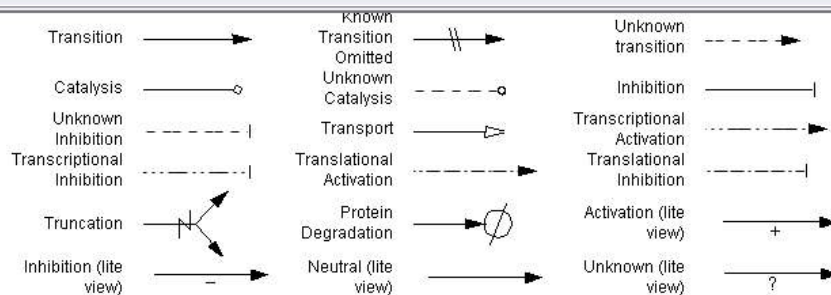
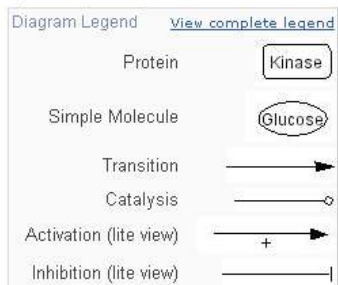
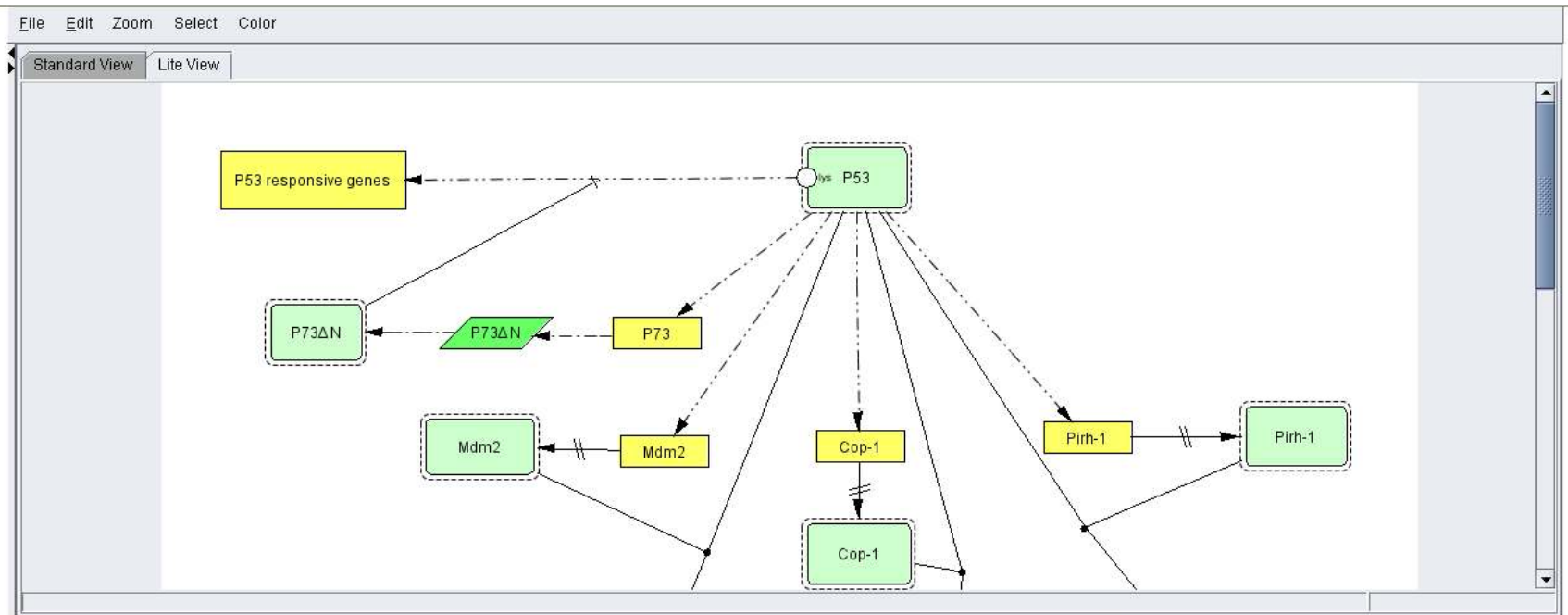
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<input type="button" value="clr"/>	<input type="button" value="all"/>	<a href="#">Δ Pathway Accession</a>	<a href="#">Pathway Name</a>	<a href="#">Components</a>	<a href="#">Subfamilies</a>	<a href="#">Training Sequence</a>
<input type="checkbox"/>	1.	<a href="#">P00006</a>	<a href="#">Apoptosis signaling pathway</a>	<a href="#">72</a>	<a href="#">102</a>	<a href="#">839</a>
<input type="checkbox"/>	2.	<a href="#">P00029</a>	<a href="#">Huntington disease</a>	<a href="#">60</a>	<a href="#">149</a>	<a href="#">1239</a>
<input type="checkbox"/>	3.	<a href="#">P00057</a>	<a href="#">Wnt signaling pathway</a>	<a href="#">49</a>	<a href="#">266</a>	<a href="#">2085</a>
<input type="checkbox"/>	4.	<a href="#">P00059</a>	<a href="#">p53 pathway</a>	<a href="#">70</a>	<a href="#">88</a>	<a href="#">548</a>
<input type="checkbox"/>	5.	<a href="#">P04392</a>	<a href="#">P53 pathway feedback loops 1</a>	<a href="#">11</a>	<a href="#">8</a>	<a href="#">73</a>
<input type="checkbox"/>	6.	<a href="#">P04398</a>	<a href="#">p53 pathway feedback loops 2</a>	<a href="#">32</a>	<a href="#">51</a>	<a href="#">393</a>

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# P53 PATHWAY FEEDBACK LOOPS 1 ?

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Click components to make selections. **Right-click** components for more options.

Pathway Diagram **Pathway Description**

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Search selections for:  
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  - Cop-1 (PROTEIN)
  - Mdm2 (PROTEIN)
  - Mdm2 (GENE)
  - P53 (PROTEIN)**
  - P53 responsive genes
  - P73 (GENE)
  - P73DeltaN (RNA)
  - P73DeltaN (PROTEIN)
  - Pirh-1 (GENE)
  - Pirh-1 (PROTEIN)
  - Ub (SIMPLE\_MOLECULE)
  - a27\_degraded (DEGRADATION\_PRODUCT)
  - a28\_degraded (DEGRADATION\_PRODUCT)
  - a29\_degraded (DEGRADATION\_PRODUCT)

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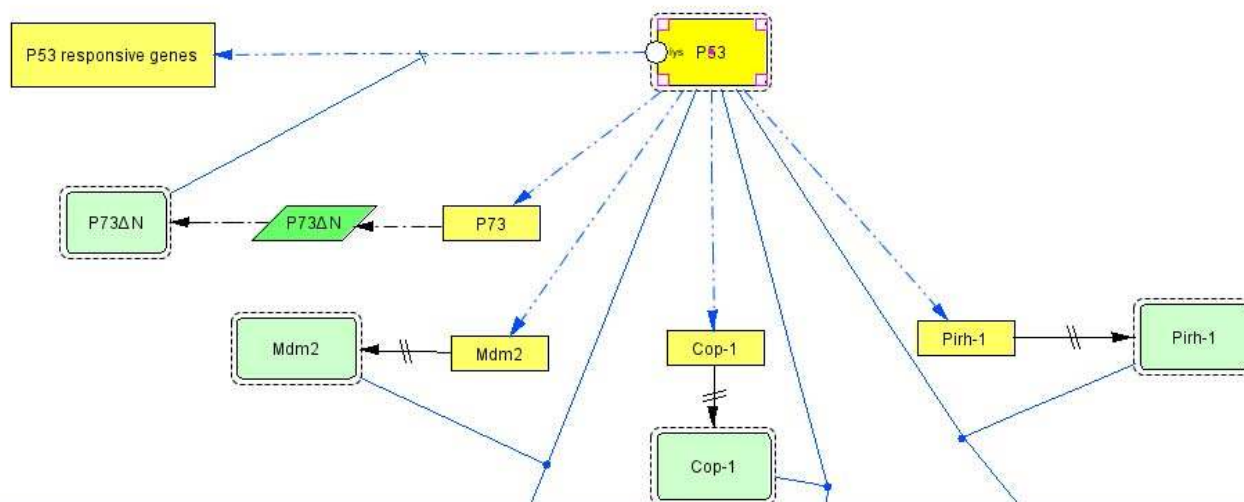


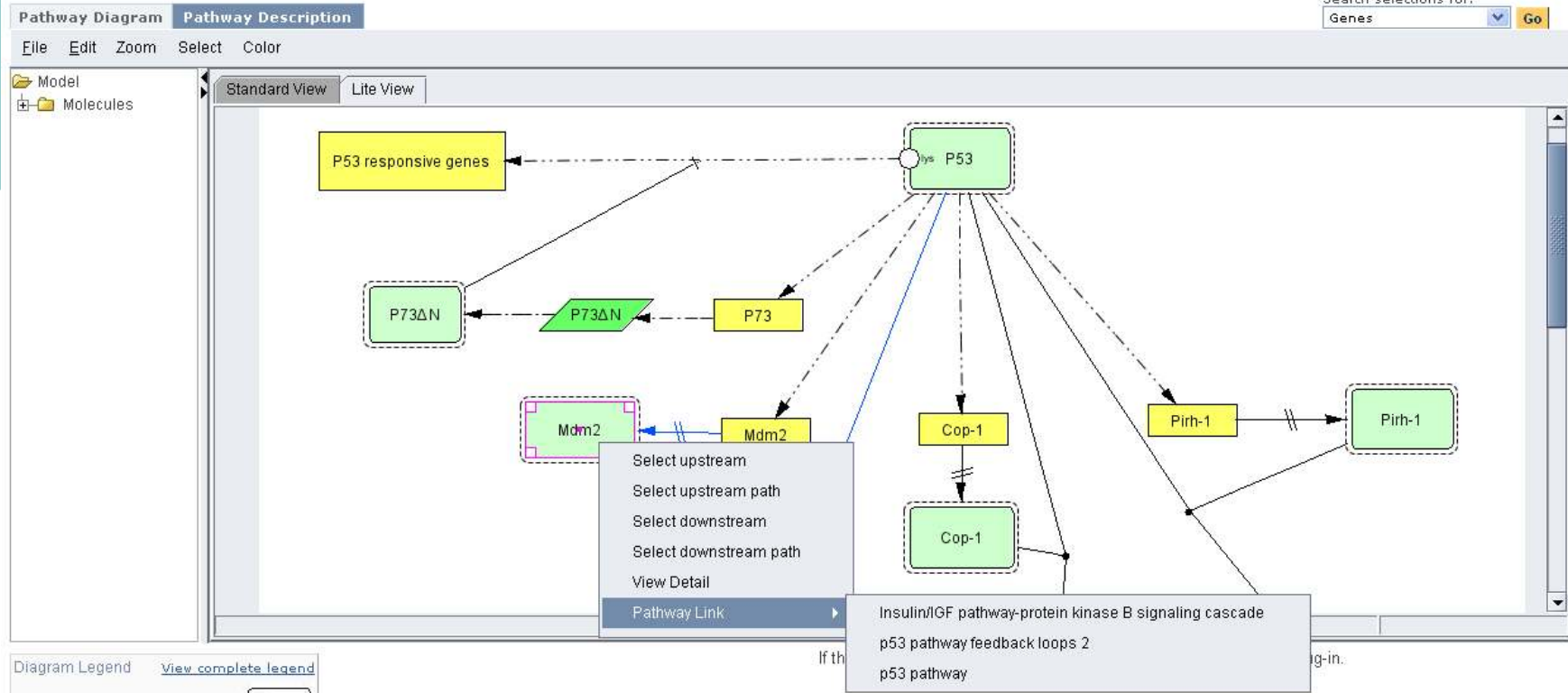
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## P53 PATHWAY FEEDBACK LOOPS 1 ?

Export:

Click components to make selections. Right-click components for more options.



**Pathway Diagram** **Pathway Description**

**Definition :** The p53 pathway responds to stresses that can disrupt the fidelity of DNA replication and cell division. A stress signal is transmitted to the p53 protein by post-translational modifications. This results in the activation of the p53 protein as a transcription factor that initiates a program of cell cycle arrest, cellular senescence or apoptosis. The transcriptional network of p53-responsive genes produces proteins that interact with a large number of other signal transduction pathways in the cell and a number of positive and negative autoregulatory feedback loops act upon the p53 response. This diagram illustrates 3 such negative feedback loops.

**Pathway Accession :** P04392

**Components :** [11](#)

**Families/Subfamilies :** [8](#)

**Training Sequences :** [73](#)

**References :** [PubMed: 15838523](#)

**Author :** Huaiyu Mi, Amie Levine

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<div> <div>clr</div> <div>all</div> </div>		<div> <div>Category ID</div> </div>	Name	Parent	Child	Families	Subfamilies
<input type="checkbox"/> 1.		<a href="#">BP00031</a>	Nucleoside, nucleotide and nucleic acid metabolism	-	<a href="#">Chromatin packaging and remodeling</a> <a href="#">DNA metabolism</a> <a href="#">Metabolism of cyclic nucleotides</a> <a href="#">Nucleoside, nucleotide and nucleic acid transport</a> <a href="#">Other nucleoside, nucleotide and nucleic acid metabolism</a> <a href="#">Pre-mRNA processing</a> <a href="#">Purine metabolism</a> <a href="#">Pyrimidine metabolism</a> <a href="#">RNA catabolism</a> <a href="#">RNA localization</a> <a href="#">Regulation of nucleoside, nucleotide metabolism</a> <a href="#">Reverse transcription</a> <a href="#">mRNA transcription</a> <a href="#">rRNA metabolism</a> <a href="#">tRNA metabolism</a>	<a href="#">594</a>	<a href="#">3179</a>
<input type="checkbox"/> 2.		<a href="#">BP00034</a>	DNA metabolism	<a href="#">Nucleoside, nucleotide and nucleic acid metabolism</a>	<a href="#">DNA degradation</a> <a href="#">DNA recombination</a> <a href="#">DNA repair</a> <a href="#">DNA replication</a>	<a href="#">107</a>	<a href="#">379</a>

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## PANTHER CATEGORY INFORMATION

Name:	Nucleoside, nucleotide and nucleic acid metabolism
Definition:	Metabolic processes of nucleotides and nucleic acids, including the breakdown and biosynthesis of nucleosides, nucleotides and nucleic acids.
Category ID:	BP00031
Child:	<a href="#">Chromatin packaging and remodeling</a> <a href="#">DNA metabolism</a> <a href="#">Metabolism of cyclic nucleotides</a> <a href="#">Nucleoside, nucleotide and nucleic acid transport</a> <a href="#">Other nucleoside, nucleotide and nucleic acid metabolism</a> <a href="#">Pre-mRNA processing</a> <a href="#">Purine metabolism</a> <a href="#">Pyrimidine metabolism</a> <a href="#">RNA catabolism</a> <a href="#">RNA localization</a> <a href="#">Regulation of nucleoside, nucleotide metabolism</a> <a href="#">Reverse transcription</a> <a href="#">mRNA transcription</a> <a href="#">rRNA metabolism</a> <a href="#">tRNA metabolism</a>
Number Subfamilies/Families:	<a href="#">3773</a>

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# Conclusion

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- To characterize the function of proteins is important.
- For this , PANTHER is a strong and powerful hunter.



# Thanks for your attention

---

Nelson