

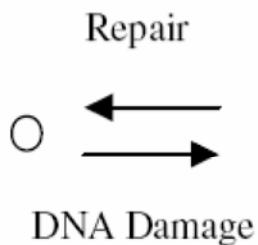


Tumor-associated gene (*TAG*): a specialized database for cancer research

利用生物資訊學的分析來找尋新穎癌症相
關基因之研究

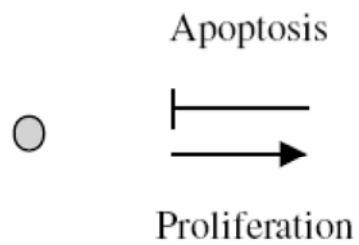
Carcinogenesis

Initiation



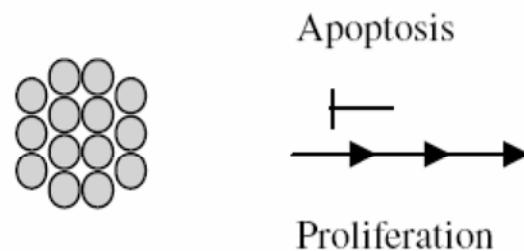
**Normal
cell**

Promotion

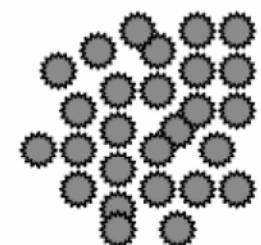


**Initiated
cell**

Progression



Focal Lesion



Cancer



Oncogene

A proto-oncogene can be activated by

- ✓ Genetic alterations (point mutation or translocation)

Translocation of the ABL proto-oncogene (chr. 9) to the BCR gene (chr. 22) produces a BCR/ABL fusion protein resulting in Chronic Myelogenous Leukemia.
(Rowley Nature 1973)

- ✓ Increasing the number of copies of the proto-oncogene (amplification)



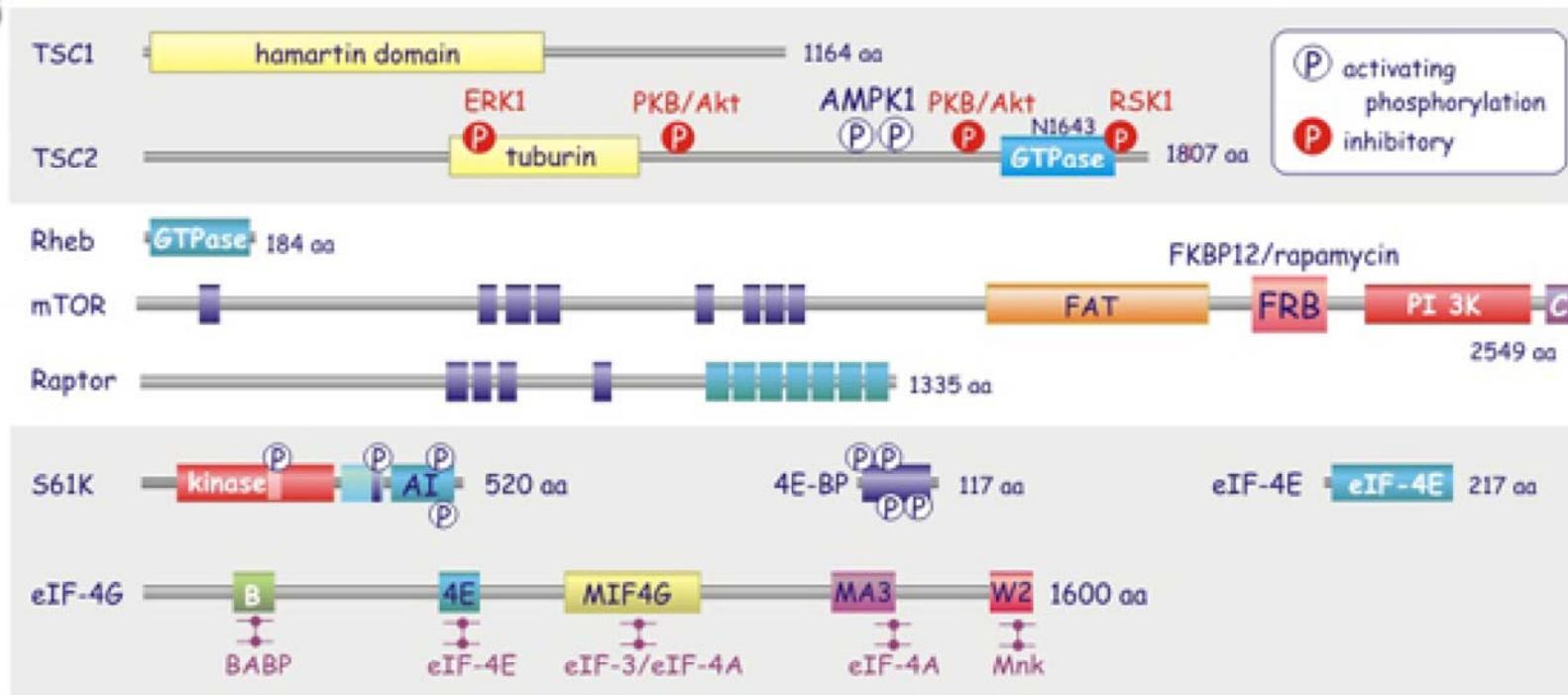
Tumor suppressor gene

A TSG can be inactivated by

- ✓ Genetic alterations (point mutation or methylation)
- ✓ Decreasing the number of copies of the tumor suppressor gene (functional haploinsufficiency)

Reduction of p53 dosage can promote cancer formation.
(Venkatachalam et al. 1998)

Domain structure of proteins



AI auto-inhibitory domain

AGC kinase C-terminal motif (HM motif included)

C FAT C-terminal (redox sensor)

FAT FRAP/ATM/TRRAP domain

HEAT: huntingtin, EF3, PP2A regulatory, TOR
(resembles armadillo)

kinase serine/threonine kinase domain

MA3 MA-3, DAP-5, eIF-4G domain (highly alpha-helical)

MIF4G middle domain of eIF-4G (rich in alpha-helices)

PI 3-K phosphatidyl inositol 3-kinase

FRB rapamycin binding region

WD, Trp-Arg domain
(β -transducin domain)

W2 domain found in eIF-4 γ ,
eIF-5 and eIF-2 α

B BABP binding region

4E 4E binding region

Hypothesis

All tumor-associated genes (*TAG*)
share common functional domains

Annotation of known oncogenes
or tumor suppressor can **help to**
identify novel *TAG* genes with
similar functions

Objective

To identify novel tumor-associated genes
based on computational strategy

- ✓ Establish a tumor-associated gene (*TAG*) database and build a user-friendly web interface for searching and analysis of *TAG* information.
- ✓ Define oncogene/TSG signature domain profiles and apply the profiles to search for novel *TAGs*.

Flow Chart

Text mining

Information retrieval

Gene-related: GeneCards, Entrez Gene,
Gene Ontology
Protein-related: SwissProt, InterPro

Collecting and Extracting System

TAG Database (662 genes)

Oncogene: 246; Tumor suppressor gene: 265; Other:151

Search by
chromosome

Text Search

Oncogenic
domain analysis

Search for Non-
TAG gene

TAG Database Homepage



About This Project - Windows Internet Explorer
http://www.binfo.ncku.edu.tw/TAG/GeneDoc.php

我的最愛 About This Project

Binfo 國立成功大學生物資訊中心
NCKU Bioinformatics Center

Tumor Associated Gene

[Oncogenic Domain Analysis](#) [Text Search](#) [List by Chromosome](#) [Non-TAG gene search](#)

The completion of human genome sequences allows one to rapidly identify and analyze genes of interest through the use of computational approach. The available annotations including physical characterization and functional domains of known tumor-related genes thus can be used to study the role of genes involved in carcinogenesis. The tumor-associated gene (TAG) database was designed to utilize information from well-characterized oncogenes and tumor suppressor genes to facilitate cancer research. All target genes were identified through text-mining approach from the PubMed database. A semi-automatic information retrieving engine was built to collect specific information of these target genes from various resources and store in the TAG database. At current stage, 662 TAGs including 246 oncogenes, 265 tumor suppressor genes, and 151 genes related to oncogenesis were collected. Information collected in TAG database can be browsed through user-friendly web interfaces that provide searching genes by chromosome or by keywords. The "consensus domain analysis" tool functions to identify conserved protein domains and GO terms among selected TAG genes. In addition, the "oncogenic domain analysis" can analyze oncogenic potential of any user-provided protein based on a weighed term frequency table calculated from the TAG proteins. This study was supported by grant from National research program for genomic medicine (NRPGM) and personnel from Bioinformatics Center of Center for Biotechnology and Biosciences in the National Cheng Kung University, Taiwan.

[Contact](#) [NCKU Bioinformatics Center](#)

TAG web site designed and supported by [Dillon Chan](#).
Last Modified: 2010/7/21
Counter : 38953

939 Visitors
20 Sep 2010 - 26 Jun 2012

如何使用 NCKU TAG database



網址：<http://www.binfo.ncku.edu.tw>

研究資源 → 應用資源 → TAG Database



首頁(Home) | 簡介(Introduction) | 本中心服務(Service) | 研究資源(Resources) | 相關連結(Links) | 意見留言(Contact)

◎應用資源

- Vector NTI
- IBM軟體下載
- NCKU BLAST
- NCKU SNP Database
- TAG Database**

成功大學-前瞻生物醫學科學研討會，邀請多位名大演講，歡迎踴躍參與！... ~ more

點選此連結

NCKU TAG Database 首頁



Oncogenic Domain 分析介面

Tumor Associated Gene

[Oncogenic Domain Analysis](#)[Text Search](#)[List by Chromosome](#)[Non-TAG gene search](#)

The completion of human genome sequencing has made it possible to use computational approaches to identify tumor related genes. The TAG database was built to facilitate cancer research. This semi-automated information retrieval engine was built to collect specific information of these target genes from various resources and store in the TAG database. At current stage, 476 TAGs including 164 oncogenes, 161 tumor suppressor genes and 51 genes related to oncogenesis were collected. Information collected in TAG database can be browsed through web interfaces that provide searching functions to identify conserved protein domain analysis. "Oncogenic potential analysis" can analyze oncogenic potential of proteins isolated from the TAG proteins. This study was conducted by the National Research Program for Genomic Medicine (NRPGM) and personnel from Bioinformatics Center of Center for Biotechnology and Biostemce National Cheng Kung University, Taiwan.

文字搜尋界面

以染色體為列表

Non-TAG Gene 搜尋界面

TAG Database 簡介

寫信給成大生物資訊中心

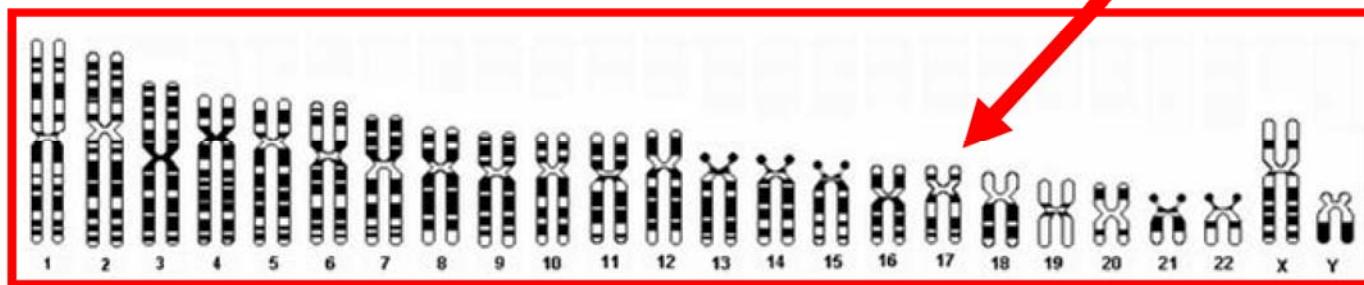
回成功大學生物資訊中心首頁

[Contact](#)[NCKU Bioinformatics Center](#)

TAG 搜尋介面: 一、利用染色體位置

1. 點選你要搜尋的染色體圖示，在此以染色體17為例

List by chromosome



TAG 搜尋介面一 (結果)

基因正式縮寫

致癌/抑癌基因分類

基因全名

Symbol	Location	Category	Name
ALOX15	17p13.3	Other	arachidonate 15-lipoxygenase
CRK	17p13.3	Oncogene	v-crk sarcoma virus CT10 oncogene homolog (avian)
MYBBP1A	17p13.3	Tumor suppressor gene	MYB binding protein (P160) 1a
TP53	17p13.1	Tumor suppressor gene	tumor protein p53 (Li-Fraumeni syndrome)
NTN1	17p13-p12	Other	netrin 1
USP6	17q11	Oncogene	ubiquitin specific peptidase 6 (Tre-2 oncogene)
NF1	17q11.2	Tumor suppressor gene	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
THRA	17q11.2	Oncogene	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)
EVI2B	17q11.2	Other	ecotropic viral integration site 2B
ERBB2	17q11.2 q12 17q21.1	Oncogene	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogen homolog (avian)
CCL2	17q11.2-q21.1		chemokine (C-C motif) ligand 2
GRB7	17q12		GTP-bound protein 7
LHX1	17q12		

染色體上的位置

點選Gene Symbol連結，在此以TP53為例，可以瀏覽該基因的詳細資訊。



基因詳細資訊

基因正式縮寫
 基因全名
 致癌/抑癌基因分類
 基因別名

 染色體的位置

 蛋白質相關訊息

Gene content	
<u>Symbol</u>	TP53 (approved by HUGO)
<u>Name</u>	tumor protein p53 (Li-Fraumeni syndrome)
<u>Category</u>	Tumor suppressor gene
<u>Alias</u>	LFS1 P53 TRP53 p53
<u>Cytogenetic band</u>	NCBI: 17p13.1 Ensembl: 17p13.1
<u>Protein information</u>	<p>P53_HUMAN Size: 393 amino acids Mass: 43653 Da</p> <ul style="list-style-type: none"> Subcellular location: Cytoplasmic and nuclear Subunit: Interacts with AXIN1. Probably part of a complex consisting of TP53, HIPK2 and AXIN1 (By similarity). Binds DNA as a homotetramer. Interacts with histone acetyltransferases EP300 and methyltransferases HRMT1L2 and CARM1, and recruits them to promoters. In vitro, the interaction of TP53 with cancer- associated/HPV (E6) viral proteins leads to ubiquitination and degradation of TP53 giving a possible model for cell growth regulation. This complex formation requires an additional factor, E6-AP, which stably associates with TP53 in the presence of E6. C- terminus interacts with TAF1, when TAF1 is part of the TFIID complex. Interacts with ING4 and this interaction may be indirect. Found in a complex with CABLES1 and TP73. Interacts with HIPK1, HIPK2, and P53DINP1. Interacts with WWOX Function: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that

Domain相關資訊

Protein Domain/Family				
Source	ID	Domain	Name	Type
InterPro	IPR002117	P53	p53 tumor antigen	Family
	IPR008967	P53_like_DNA_bnd	p53-like transcription factor, DNA-binding	Domain
	IPR010991	p53_tetrameristn	p53, tetramerisation	Domain
Blocks	IPB002117	p53	p53 tumor antigen	
	IPB010991	p53	p53, tetramerisation	

資料庫來源

選擇此圖示可以連結說明網頁

存取號碼，點選此連結可以瀏覽原始網頁內容

Domain 名稱簡寫

Domain 全名

Domain 的型態

Gene Ontology相關資訊



GO term 類別

點選此圖示可以連結說明網頁

Type	Term	Evidence	Source	Pub
Biological Process	apoptosis	IDA	GOA	PubMed
	base-excision repair	TAS	GOA	PubMed
	caspase activation via cytochrome c	IDA	GOA	PubMed
	cell aging	IMP	GOA	PubMed
	cell cycle	IEA	GOA	
	cell cycle arrest	TAS	GOA	PubMed

GO term 全名

驗證編碼

GO term 來源

參考文獻

Disease相關資訊

資料庫來源

Disease說明

Disorder & Mutation	
<u>Source</u>	<u>Disease</u>
SWISS-PROT	defects in tp53 are involved in head and neck squamous cell carcinomas (hnsc) [mim:601400] and oral squamous cell carcinoma (OSCC). Cigarette smoke is a prime mutagenic agent in cancer of the aerodigestive tract.
SWISS-PROT	Defects in TP53 are found in Barrett metaplasia; also known as Barrett esophagus. It is a condition in which the normally stratified squamous epithelium of the lower esophagus is replaced by a metaplastic columnar epithelium. The condition develops as a complication in approximately 10% of patients with chronic gastroesophageal reflux disease and predisposes to the development of esophageal adenocarcinoma.

相關資訊網站連結

TP53 cross reference

PubMed	OMIM	Entrez Gene	CGAP	NCKU SNP	Nucleotide	Swiss-Prot	Map Viewer	HomoloGene
------------------------	----------------------	-----------------------------	----------------------	--------------------------	----------------------------	----------------------------	----------------------------	----------------------------

欄位說明網頁

Gene content	
欄位	說明
<i>Symbol</i>	The official symbol approved by the UCL/HGNC Human Gene Nomenclature database
<i>State</i>	The gene approved or not approved by the UCL/HGNC Human Gene Nomenclature database
<i>Name</i>	The official name approved by the UCL/HGNC Human Gene Nomenclature database
<i>Category</i>	The gene's category ("oncogene", "tumor suppress gene", "other")
<i>Alias</i>	A list of synonyms approved by HUGO, GDB, and/or SWISSPROT
<i>Cytogenetic band</i>	The (cytogenetic) locus of the gene by NCBI (Entrez Gene) or Ensembl
<i>Size</i>	The length of the protein sequence
<i>Mass</i>	The molecular weight rounded to the nearest mass unit (Dalton)
<i>Subcellular location</i>	Description of the subcellular location of the mature protein
<i>Subunit</i>	Description of the quaternary structure of a protein
<i>Tissue specificity</i>	Description of the tissue-specific expression of mRNA or protein
<i>Function</i>	General description of the function(s) of a protein
<i>Catalytic activity</i>	Description of the reaction(s) catalyzed by an enzyme
<i>Similarity</i>	Description of the similarity(ies) (sequence or structural) of a protein with other proteins
<i>Other Resources</i>	Hyperlink to other web resources (PubMed, OMIM, Entrez Gene, Swiss-Prot, CGAP, NCKU SNP, Nucleotide, Map Viewer, HomoloGene)

TAG 搜尋介面：二、利用關鍵字

Text Search



Text Search : **myc** Run Reset

- Query can be combined with operators & (AND), | (OR) and () (Operator precedence determines the order in which the operations are applied).
- Text search is designed to search information in the following items:

Gene Content: symbol, category, state, name, alias, function, subcellular location, similarity, subunit, catalytic activity, domain, curation, post-translational modifications, swiss-prot

Protein Domains/Families: id, domain

Gene Ontology: term, evidence

Disorders & Mutations: disease

1. 輸入你要搜尋的關鍵字，在此以myc為例：
2. 你可以利用” & ”(AND)、” | ”(OR)、” () ”(Priority)布林運算符號，做更精確的搜尋。

TAG 搜尋介面二 (結果一)



There are 17 TAG genes found in the search!

1. 被搜尋的關鍵字會以紅色標示出來。

Click the hyperlink of gene symbol for detailed information!

or Mark the gene in checkbox for consensus analysis!

[FRAT1](#) : frequently rearranged in advanced T-cell lymphomas

Oncogene

Function: Positively regulates the Wnt signaling pathway by stabilizing beta-catenin through the association with GSK-3. May play a role in tumor progression and collaborate with PIM1 and **MYC** in lymphomagenesis

[MYC](#) : v-myc myelocytomatosis viral oncogene homolog (avian)

Oncogene

Symbol: MYC

Name: v-myc myelocytomatosis viral oncogene homolog (avian)

Alias: C-MYC | c-Myc

Swiss-Prot: MYC_HUMAN

Protein Domain/Family: IPR003327 Leucine zipper, **Myc**

Protein Domain/Family: IPR012682 Transcription regulator **Myc**, N-terminal

Protein Domain/Family: IPR002418 Transcription regulator **Myc**

Protein Domain/Family: IPB002418 **Myc** proto-oncogene signature

Protein Domain/Family: IPB003327 Leucine zipper, **Myc**

Disorder & Mutation: Overexpression of **MYC** is implicated in the etiology of a variety of hematopoietic tumors

Disorder & Mutation: A chromosomal aberration involving **MYC** may be a cause of a form of B-cell chronic lymphocytic leukemia. Translocation

2. 點選Gene Symbol連結，在此以MYC為例，可以瀏覽該基因的詳細資訊。

TAG 搜尋介面: 三、進階分析



⚠ Click the hyperlink of gene symbol for detailed information!

or Mark the gene in checkbox for consensus analysis!

<input checked="" type="checkbox"/> MYC : v-myc myelocytomatosis viral oncogene homolog (avian)	Oncogene
Symbol: MYC	
Name: v-myc myelocytomatosis viral oncogene homolog (avian)	
Alias: c-Myc v-myc myelocytomatosis viral oncogene homolog (avian) Myc proto-oncogene protein (c-Myc) (Transcription factor p64)	
Protein Domain/Family: IPR003327 Leucine zipper, Myc	
Protein Domain/Family: IPR002418 Transcription regulator Myc	
Protein Domain/Family: IPB002418 Myc proto-oncogene signature	
Protein Domain/Family: IPB003327 Leucine zipper, Myc	
<input checked="" type="checkbox"/> MYCL1 : v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Oncogene
Symbol: MYCL1	
Name: v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	
Alias: L-MYC MYCL v-myc myelocytomatosis viral oncogene homolog L-myc-1 proto-oncogene protein	
Swiss-Prot: MYCL1_HUMAN	
Protein Domain/Family: IPR002418 Transcription regulator Myc	
Protein Domain/Family: IPB002418 Myc proto-oncogene signature	

Do you want to analyze data according to the classification of TAGs? Yes No



1. 勾選要做進階分析(consensus analysis)的基因。
2. 選擇在進階分析時，是否要根據基因的類別來做分組，然後按”Run Consensus Analysis”按鈕進行分析。

TAG 搜尋介面三 (進階分析結果)



基因正式縮寫

Symbol	Category	Protein Domain/Family
MYC	Oncogene	InterPro Basic helix-loop-helix dimerisation region bHLH Transcription regulator Myc Leucine zipper, Myc Transcription regulator Myc, N-terminal
	Blocks	Basic helix-loop-helix dimerization domain bHLH proto-oncogene signature Leucine zipper, Myc

致癌/抑癌基因分類

GO term 全名

Gene Ontology
Biological Process
cell cycle arrest cell proliferation iron ion homeostasis positive regulation of cell proliferation regulation of transcription from RNA polymerase II promoter
Molecular Function
protein binding transcription factor activity
Cellular Component
nucleus

Symbol	Category	InterPro
MYCL1	Oncogene	Basic helix-loop-helix dimerisation region bHLH Transcription regulator Myc Transcription regulator Myc, N-terminal
	Blocks	Basic helix-loop-helix dimerization domain bHLH Myc proto-oncogene signature

這兩個基因共有的
Domain 編號及全名

InterPro	Protein Domain
IPR002418	Transcription regulator Myc
IPR012682	Transcription regulator Myc, N-terminal
IPR001092	Basic helix-loop-helix dimerisation region bHLH

Blocks	Protein Domain
IPB001092	Basic helix-loop-helix dimerization domain bHLH
IPB002418	Myc proto-oncogene signature

這兩個基因共有的
GO term 全名

GO Term
Molecular Function
transcription factor activity
Cellular Component
nucleus

TAG 搜尋介面: 四、Domain 分析

1. 在此輸入要分析的序列名稱，如未指定則由系統自行指派。

Domain analysis

2. 在此輸入要分析的FASTA格式之胺基酸序列。

Enter or paste a PROTEIN sequence in FASTA format

Please input the sequence name: **VAV1**

```
>gi|33991320|gb|AAH13361.2| VAV1 protein [Homo sapiens]
MIVLPLYSRLDKRFLCLKNIRTFLSTCCEKFGKLRSELFIAFDLFDVQDFGKVITYTLSALSWTPIAQNRC
IMPFPTEEESVGDEDIYSGLSDQIDDTEVEEDEDLYDCVENEAEGLDEIYEDLMRSEPVSMPKMTEYDKR
CCCLREIQQTEEKYTDTLSIQQHFLKPLQRFLKPQDIEIIIFINIEDLLRVHTHFLKEMKEALGTPGAM
LYQVFIFYKERFLVYGRYCSQVESASKHLDRAAAREDVQMKEECISQRANNGRTLRLDLMVPMQRW
YHLLLQELVKHTQEAMEKENRLALDAMRDLAQCVNEVKRDNETLRQITNFQLSIEFLDQSLAHYGF
DGELKITSVERRSKMDRYAFLLDKALLICKRRGDSYDLKDFVNLSFQVRDDSSGDRDNKKWSHMLTIE
DQGAQGYELFFKTRELKKKWMEQFEMAIISNIYPENATANGHDFQMFSEETTSCKACQMLLRGTQGYR
CHRCRASAHKECLGRVPPCGRHGQDFPGTMKKDKLHRRAQDKKRNELGLPKMEVFQEYYGLPFPGAIGP
FLRLNPGDIVELTKAEEQNWEGRNTSTNEIGWFPCNRVVKPYVHGPQDLSVHLWYAGPMERAGAESIL
ANRSDGTFLVRQRVKDAAEFAISIKYNVEVKHIKINTAEGLYRITEKKAFRGLTELVEFYQQNSLKDCF
SLDTTLQFPFKEPEKRTISRAVGSTKYFGTAKARYDFCARDSELSLKEGDIIKILNKKQQGWWRGEI
YGRVGMFPANYWEEDYSEYC
```

or Upload a file: 瀏覽...

3.或是在此上傳所要分析的FASTA格式之胺基酸序列檔案。

TAG 搜尋介面四 (結果一)

Query Sequence

```
>VAV1
MIVLPLYSRLDKRFLCLKNIRTFLSTCCEKFGFLKRSELFEAFDLFDVQDFGKVIVYILSAL
SWTPIAQNRCIMPFPTEEESVGDEDIYSGLSDQIDDTVEEDEDLYDCVENEAEGLDEIYE
DLMRSEPVSMPPKMTEDKRCCLREIQQTEEKYTDTLGSIQQHFLKPLQRFLKPQDIEI
IFINIEDLLRVHHTFLKEMKEALGTPGAANLYQVFIFYKERFLVYGRYCSQVESASKHLD
RVAAAREDVQMKLEECQRANNGRFTLRDLMVPMQRVLKYHLLLQELVKHTQEAMEKEN
LRLALDAQRDLAQCVCNEVKRDNETLHQITNFQLSIEENLDQSLAHYGRPKIDGELKITSVE
RRSKMDRYAFLIDKALLLCKRRGDSYDLKDFVNLLHSEOVRDDSSGDRDNKKWSHMFLIE
TQMFSFEEETTSCKACQML
KLHRRAQDKKRMEGLP
GRNTSTNEIGWFPCNRV
WKDAAEFAISIKYNVEV
TTLQFPFKEPEKRTISR
```

被分析的胺基酸序列

有哪些Oncogene具有此Domain

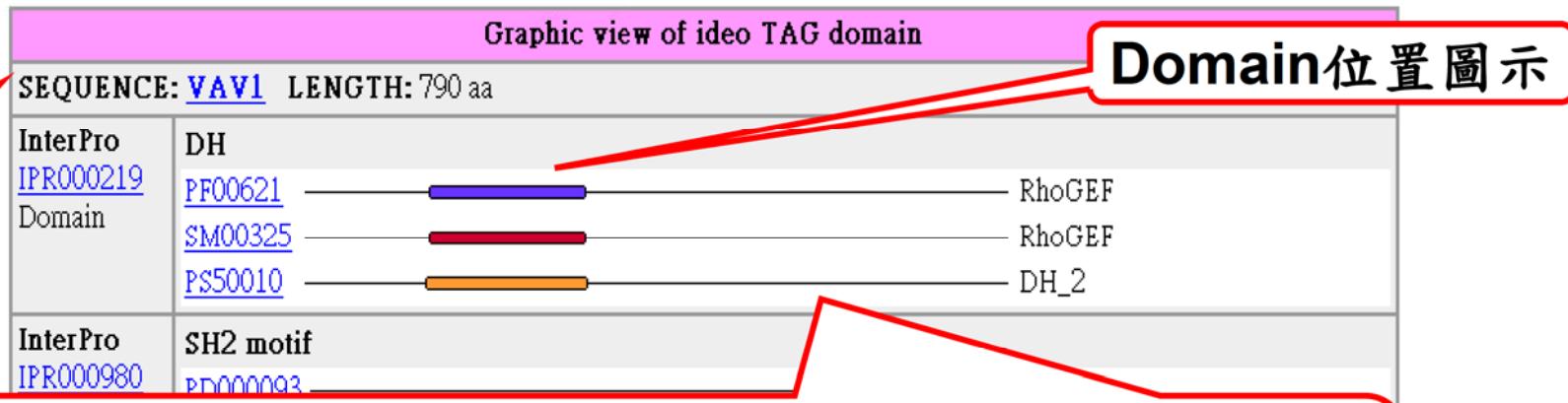
有哪些Tumor Suppressor Gene具有此Domain

Summary of domain identified		
Domain ID	Oncogene	Tumor suppressor gene
IPR000219	AKAP13 , MCF2 , MCF2L , NET1 , VAV1	--
IPR000980	ABL1 , CBL , CRK , FER , FES , FGR , FYN , LCK , SRC , STAT3 , YES1	--
IPR001331	AKAP13 , MCF2 , MCF2L , NET1	--
IPR001452	ABL1 , CRK , CTTN , FGR , FYN , LCK , SRC , VAV1 , YES1	ABI2 , BIN1 , DLG1
IPR001849	AKAP13 , AKT1 , AKT2 , MCF2 , MCF2L , NET1 , VAV1	--
IPR002219	RAF1	--
IPR011511	CRK , VAV1	DLG1
Weight Score	9.044	0.309

Potential Oncogene weight score: > 4
 Potential Tumor Suppressor Gene weight score: > 1

加權分數範圍說明

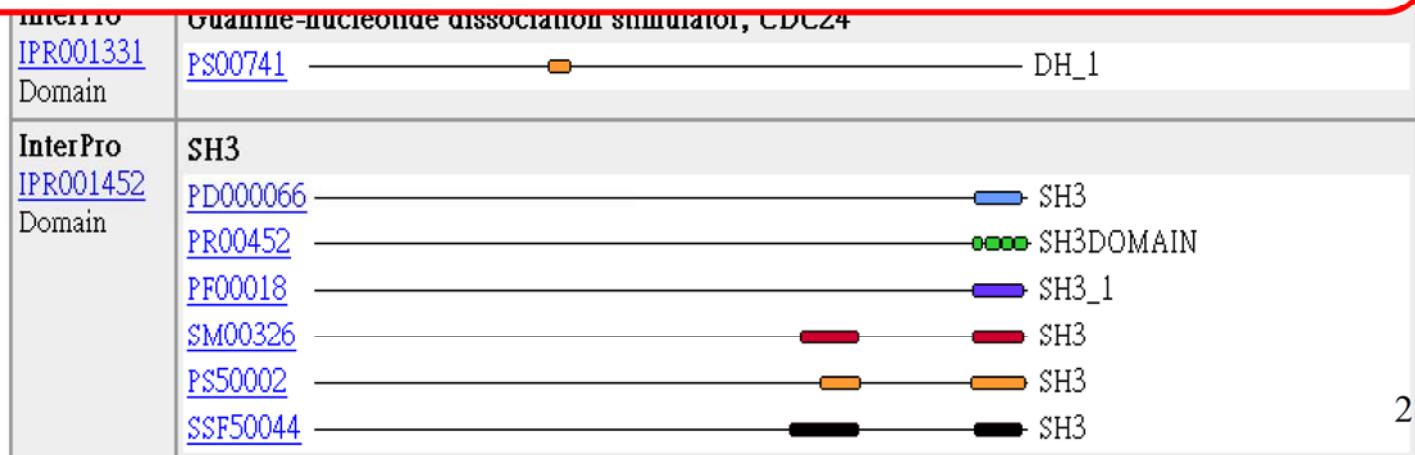
TAG 搜尋介面四 (結果二)



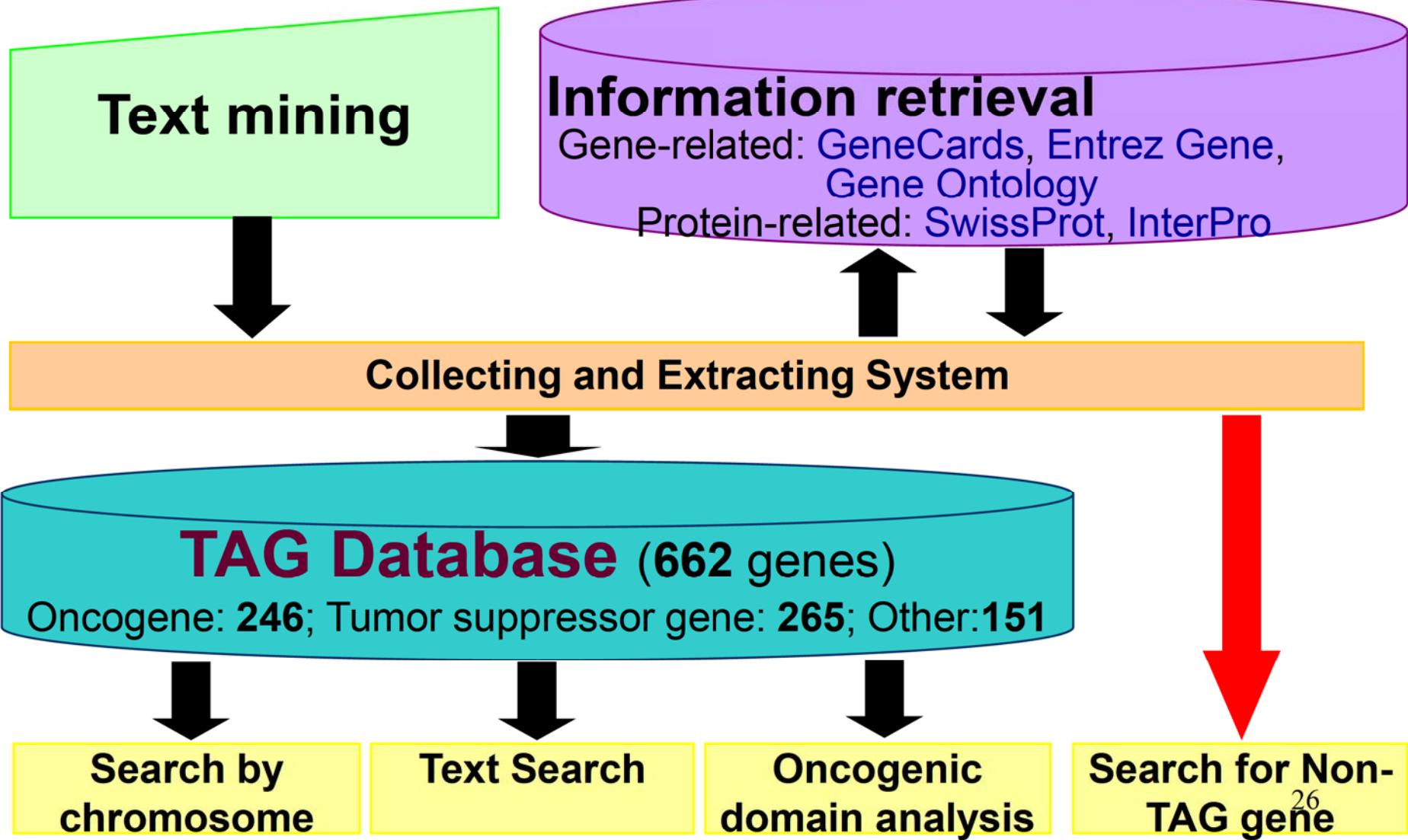
序列名稱及長度

Domain位置圖示

以此 domain為例，代表在Pfam, SMART及PROSITE domain資料庫中都有定義此domain，且經過分析後，其domain在此序列中預測的位置都相同。



Flow Chart



Tumor Associated Gene

[Oncogenic Domain Analysis](#)[Text Search](#)[List by Chromosome](#)

Non-TAG Gene Search

Please input your query:

輸入你要搜尋的關鍵字，在此以**TPH2**為例

[About](#)[Contact](#)[NCKU Bioinformatics Center](#)

TAG web site designed and supported by [Dillon Chan](#).

Last Modified: 2006/6/12

Counter : 2618

TAG 搜尋介面五 (結果一)

1. 被搜尋的關鍵字會以紅色標示出來。

There are 5 Non-TAG genes found in the search!

 Click the hyperlink of gene symbol for detailed information!

TPH2 tryptophan hydroxylase 2 (Chromosome 12:70,618,893-70,712,488)

The following lines in the GeneCard text contribute to matching your query:

- **GENE:** TPH2 | tryptophan hydroxylase 2
- **CHEM:** Tryptophan hydroxylase 2; **TPH2**, NTPH | 607478 | {Unipolar depression, susceptibility to}, 608516
- **MOUSE HOMOLOG:** Tph2 (on chromosome 10, - cM) Feb 25 2006 | gbaccs: AU043594 AY090565 | alleles:id=MGI:3521924;symbol=Tph2;category=Spontaneous;phenotypes=[ptid=MP:0003631;ptdesc="nervous system phenotype",ptid=MP:0005387;ptdesc="immune system phenotype"] && id=MGI:3521925;symbol=Tph2;category=Spontaneous;phenotypes=[ptid=MP:0003631;ptdesc="nervous system phenotype",ptid=MP:0005387;ptdesc="immune system phenotype"]
- **SWISSPROT:** GENE: TPH2
- **UNIGENE:** Hs.376337 | Tryptophan hydroxylase 2 | **TPH2** | AK094614 . . .
- **LITERATURE:** Postmortem parietal cortex **TPH2** expression is not altered in schizophrenic, unipolar-depressed, and bipolar patients vs control subjects. . . .
- **HGNC:** accs=AY098914| aliases=NTPH, FLJ37295 | dateApproved=03/04/2003 | dateModified=25/03/2004 | dateNameChangeId= | description=tryptophan hydroxylase 2 | eg_curatedId=121278 | egMappedId=121278 | enzymeIds= | gdbId= | geneFamName= | hgnc=20692 | loc=12q15 | mgdId=MGI:251811 | omimId=608516 | prevNames= | priorSymbols= | pubmedIds=12511643 | refseqId=NM_173353 | refseqMappedId=NM_173353 | status=Approved | symbol=**TPH2** | uniprotId=Q8IWU9
- **HomoloGene:** HomoloGene: Organism=Mm|Symbol=**Tph2**|Location=|Description=tryptophan hydroxylase
- **BLAST_Similarity:**=87.57|Prot_Similarity=93.24|EntrezGene=216343|GenBank=NM_173391.1|Protein=NP_775567.1|HomologeneId=27831|FormatType=new . . .
- **ACEVIEW:** aceviewSymbol=**TPH2** | acc=AY098914;quality=1,acc=NM_173353;quality=1,acc=BM466099;quality=1,acc=AK094614;quality=2,acc=BG532070;quality=2,acc=BG530287;quality=2
- **COPINFO:** geneSymbol=**TPH2** | numDocs=3
- **UCGENE:** geneSymbol=**TPH2**

TPD2 tryptophan 2,3-dioxygenase (Chromosome 4:157,182,452-157,199,155)

The following lines in the GeneCard text contribute to matching your query:

- **ALIASES:** tryptophan 2,3-dioxygenase (GDB)| **TPH2** (OMIM)| **TPH2** (EG)| TRPO (OMIM)| TRPO (SP)| TRPO (EG)| Tryptamin 2,3-dioxygenase (SP)| Tryptophan 2,3-

2. 點選 Gene Symbol 連結，可以瀏覽該基因的詳細資訊。

TAG 搜尋介面五 (結果二)



基因詳細資訊

Gene content

Symbol	TPH2 (approved by HUGO)
Name	tryptophan hydroxylase 2
Category	--
Alias	FLJ37295 NTPH tryptophan hydroxylase 2 Tryptophan 5-hydroxylase 2 (EC 1.14.16.4) (Tryptophan 5-mono-oxygenase 2) (Neuronal tryptophan hydroxylase)
Cytogenetic band	NCBI: 12q21.1 Ensembl: --
Protein information	<p>TPH2 HUMAN Size: 490 amino acids Mass: 56057 Da</p> <ul style="list-style-type: none"> Tissue specificity: Brain specific. Catalytic activity: L-tryptophan + tetrahydrobiopterin + O₂) = 5- hydroxy-L-tryptophan + 4a-hydroxytetrahydrobiopterin. 2 MGI mutant phenotypes (inferred from 2 alleles [IMAGE]) for Tph2; immune system nervous system Similarity: Belongs to the biopterin-dependent aromatic amino acid hydroxylase family.

Protein Domain/Family

Source	ID	Domain	Name	Type
InterPro	IPR001273	Aaa_hydroxylase	Aromatic amino acid hydroxylase	Family
	IPR002912	ACT_bd	Amino acid-binding ACT	Domain
	IPR005963	Tyr_5_mOase	Tyrosine 5-monoxygenase	Family
Blocks	IPB001273	Aromatic	Aromatic amino acid hydroxylase	

Gene Ontology (from LouieLink)

Type	Term	Evidence	Source	Pub
Biological Process	aromatic amino acid family metabolism	IEA	GOA	
	metabolism	IEA	GOA	
	serotonin biosynthesis from tryptophan	IEA	GOA	
Molecular Function	amino acid binding	IEA	GOA	
	iron ion binding	IEA	GOA	
	metal ion binding	IEA	GOA	
	monoxygenase activity	IEA	GOA	
	tryptophan 5-monoxygenase activity	IEA	GOA	

TPH2 cross reference

[PubMed](#) [OMIM](#) [Entrez Gene](#) [CGAP](#) [NCKU SNP](#) [Nucleotide](#) [Swiss-Prot](#) [Map Viewer](#) [HomoloGene](#)

Summary



Nucleic Acids Research

ABOUT THIS JOURNAL CONTACT THIS JOURNAL SUBSCRIPTIONS CURRENT ISSUE ARCHIVE SEARCH

Oxford Journals > Life Sciences > Nucleic Acids Research > Database Summary Paper 922

< PREVIOUS NEXT >

TAG

• Compilation Paper
• Category List
• AlphaNumeric List
• Category/Paper List
• Search Summary Papers

NAR Molecular Biology Database Collection entry number 922

<http://www.binfo.ncku.edu.tw/OG/>

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³Bioinformatics Center, Center for Biotechnology and Biosciences, National Cheng Kung University, Tainan 701, Taiwan

Contact hssun@mail.ncku.edu.tw

Database Description

The compilation of human genome sequence has advanced a gigantic step toward a new era of biomedical research. Though the sequence itself is not the key for many currently unanswered questions related to human diseases, it sheds light on potential genetic solution of these diseases. We believe that the available annotations including physical characterization and functional protein domains of known tumor-related genes can be used to study the mechanisms underlying tumorigenesis. The tumor-associated gene (TAG; <http://www.binfo.ncku.edu.tw/TAG>) database was designed to utilize information from well-characterized oncogenes and tumor suppressor genes to facilitate cancer research. All target genes were identified through text-mining approach from the PubMed database. A semi-automatic information retrieving module was built to extract cancer information of these target genes from various resources and store in the TAG database.

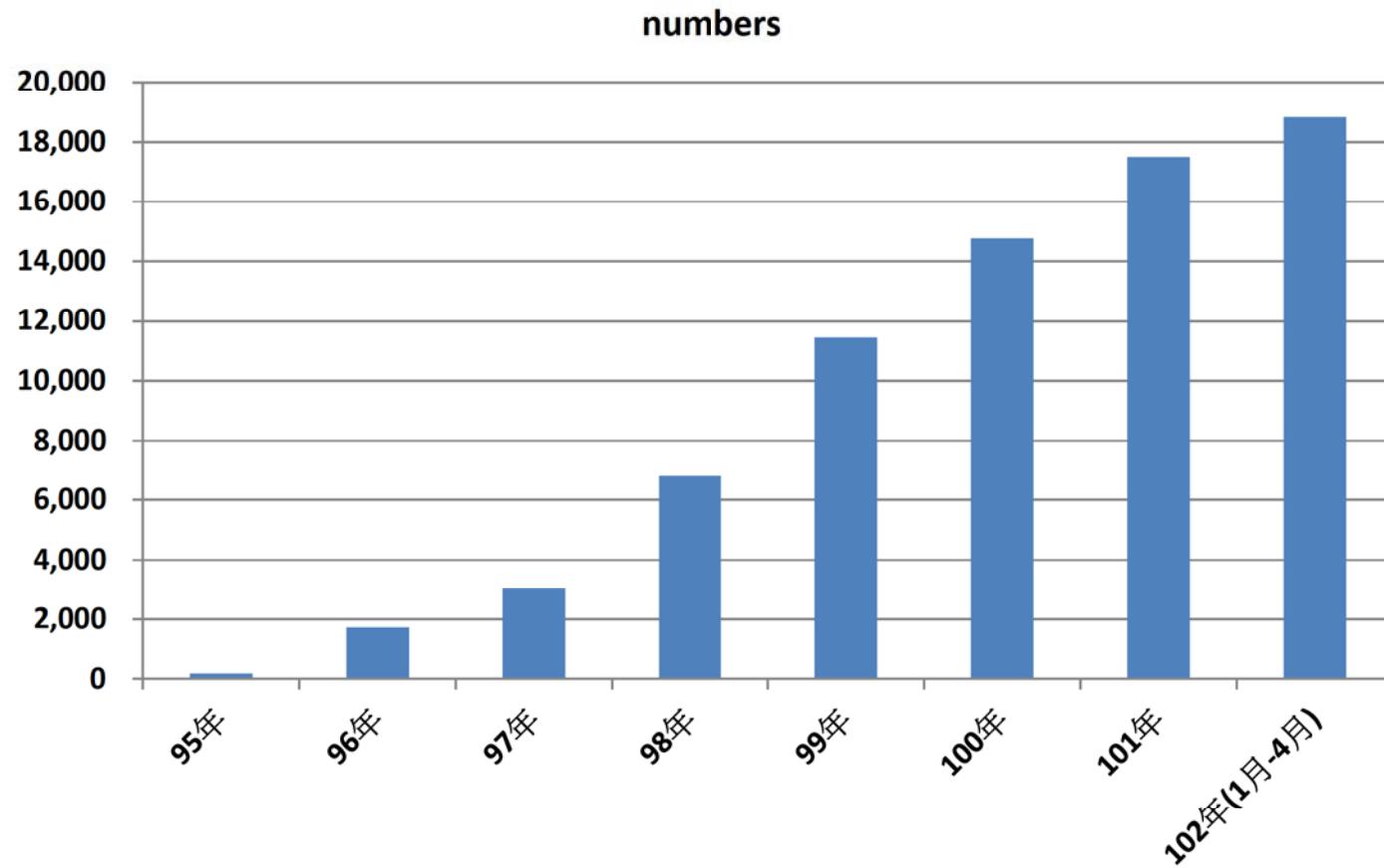
NAR Molecular Database Online #922, 2007

- ✓ **TAG database contains 662 genes including 246 oncogenes and 265 tumor suppressor genes.**
- ✓ **A online web interface** is provided for a user-friendly environment to search information in the **TAG database**.
- ✓ **Non-TAG gene searching** provides user additional advantage to collect gene information in the **TAG database**.

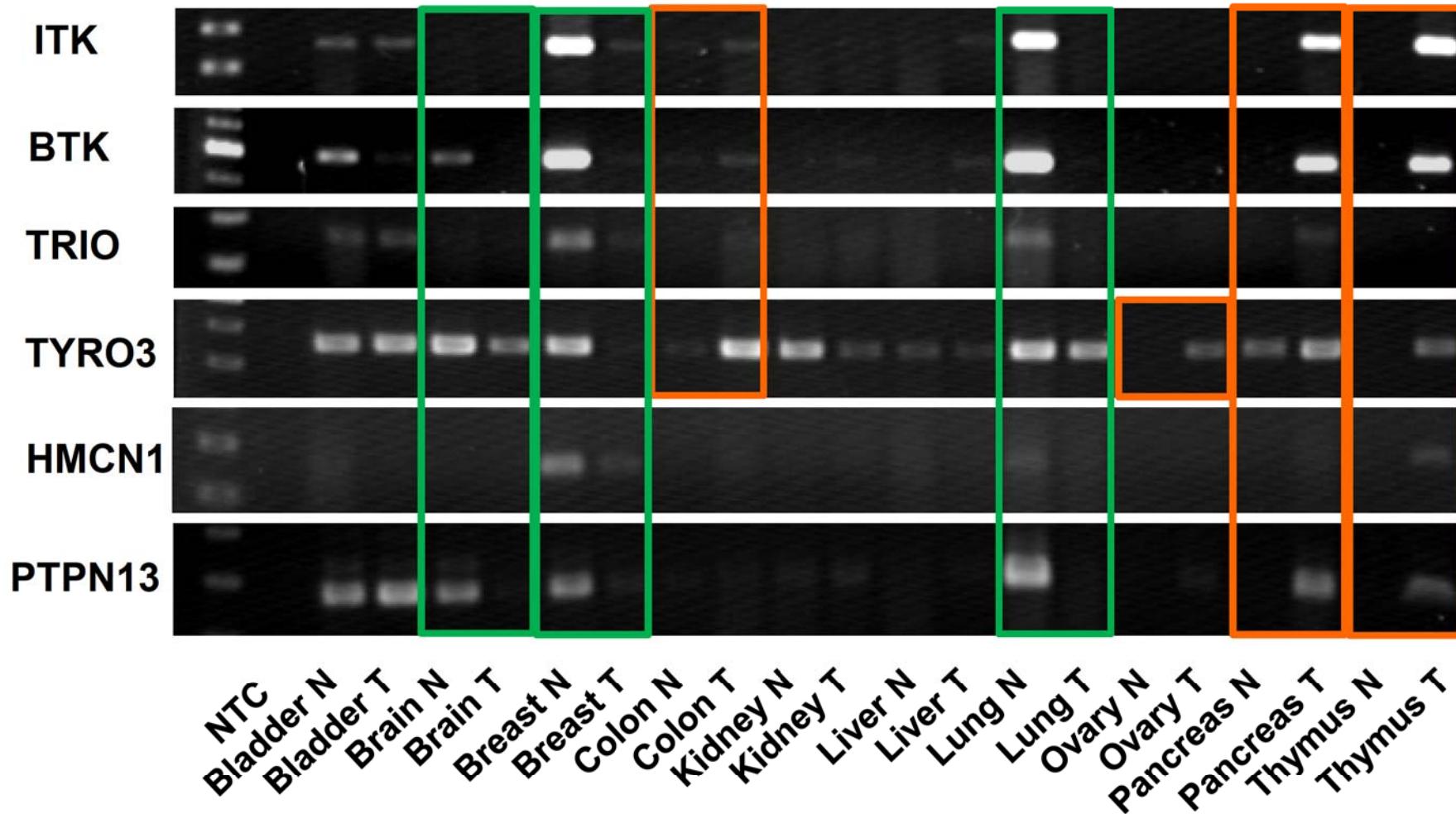
Visitors around the world



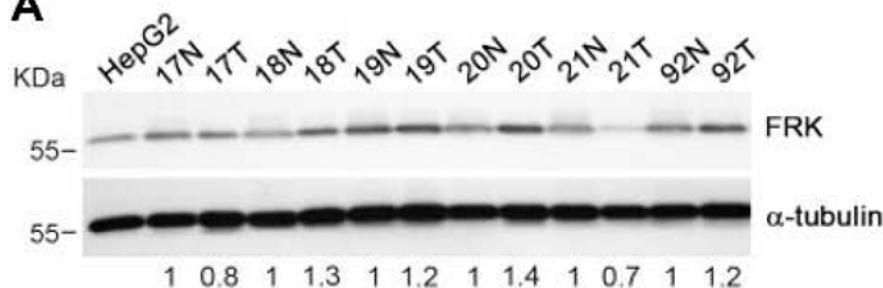
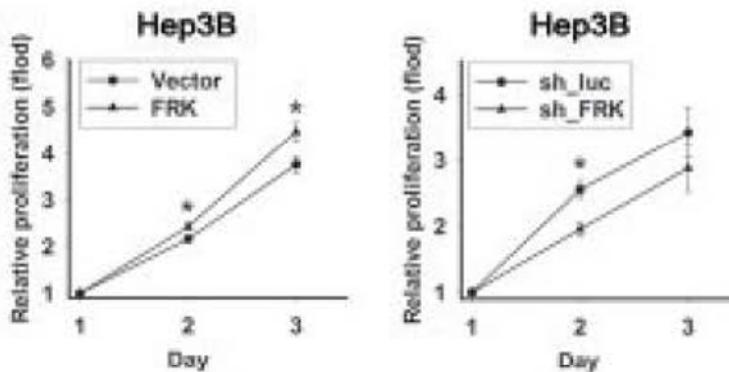
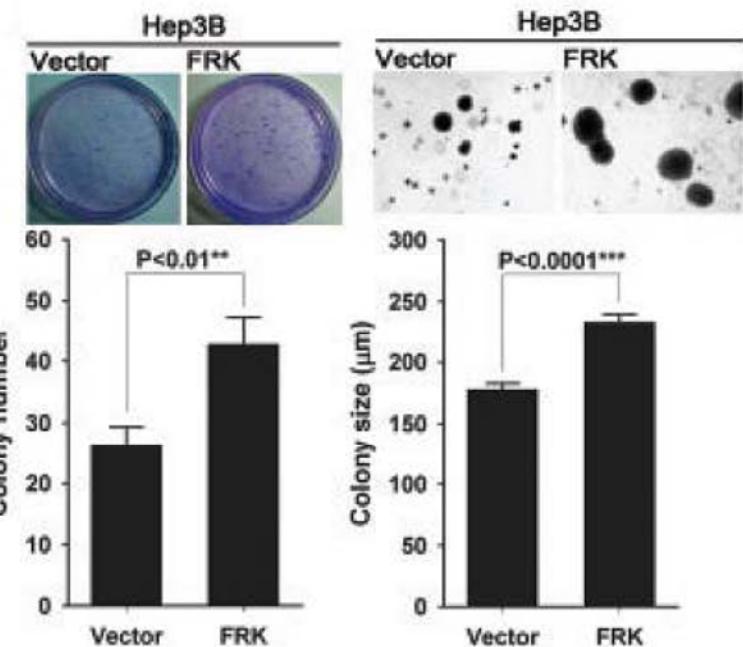
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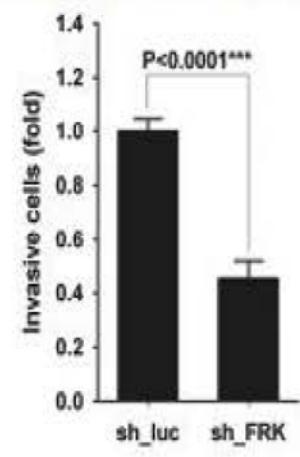
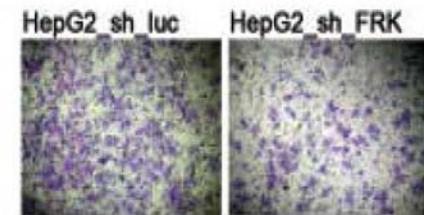
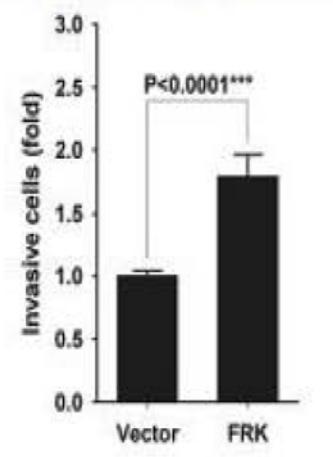
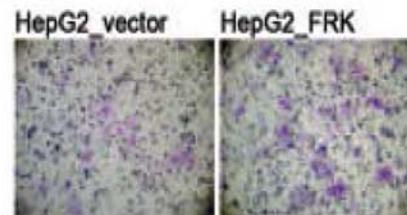
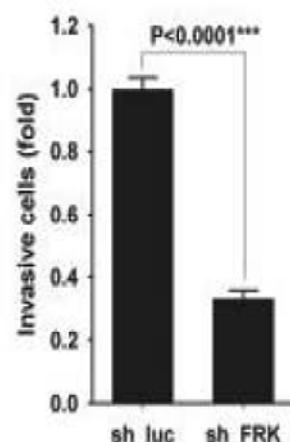
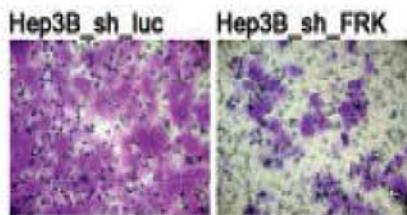
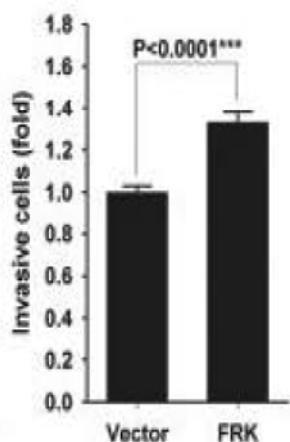
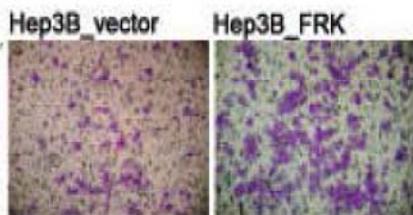
Screen potential TAGs



FRK plays roles in HCC tumorigenesis

**A****B****Overexpression****Knockdown****C**

FRK plays roles in HCC tumorigenesis



Genome analysis

Advance Access publication December 24, 2012

***In silico* identification of oncogenic potential of fyn-related kinase in hepatocellular carcinoma**

Jia-Shing Chen^{1,†}, Wei-Shiang Hung^{1,†}, Hsiang-Han Chan¹, Shaw-Jenq Tsai^{2,3} and H. Sunny Sun^{1,3,*}

¹Institute of Molecular Medicine, College of Medicine, ²Department of Physiology, College of Medicine and

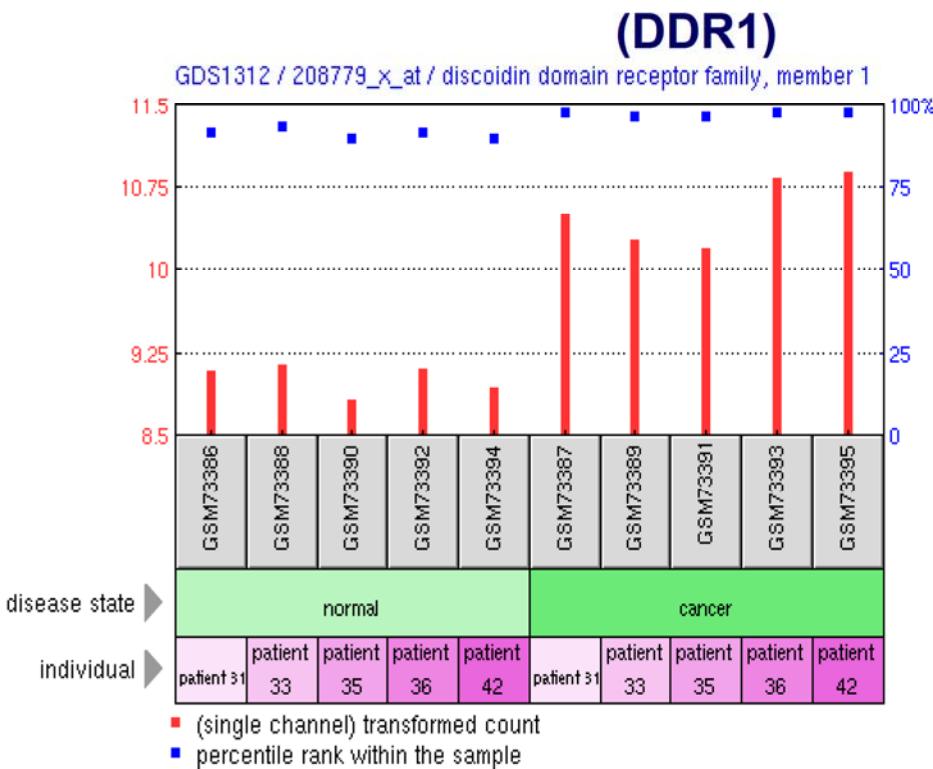
³Bioinformatics Center, Center for Biotechnology and Biosciences, National Cheng Kung University, Tainan 70101, Taiwan, Republic of China

Associate Editor: Alfonso Valencia

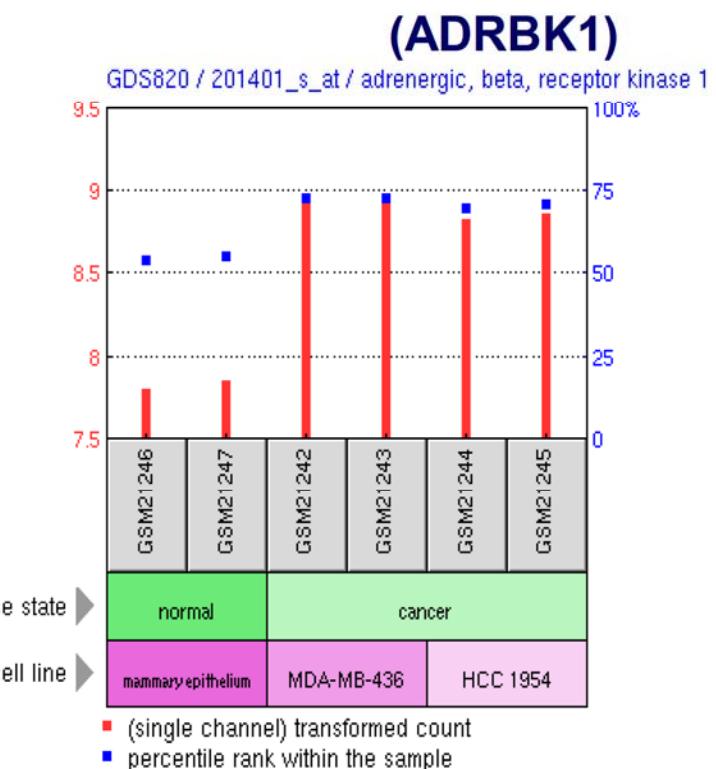
Potential Oncogenes



Gastric cancers



Breast cancer

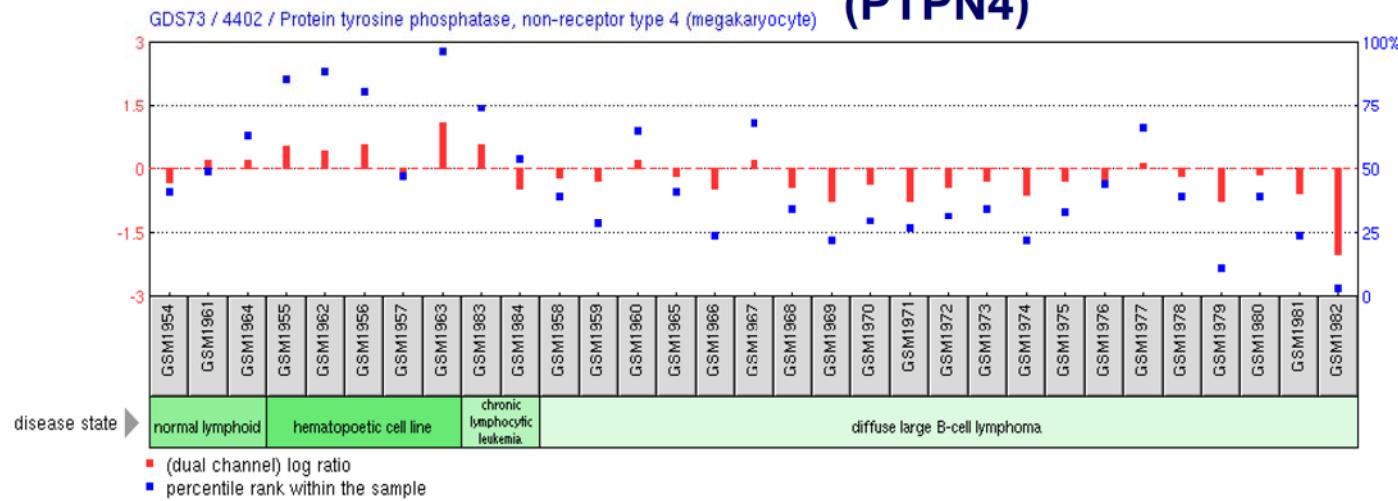


Potential TSGs



Diffuse large B-cell lymphoma

(PTPN4)



Glial brain tumors

(PTPRS)

