

# Operational Text and Data Mining

- Perspective from a Research Scientist-

Dr. ADG de Roos

Brussels, 26 March 2015

WG Intellectual Property Rights and Copyright Reform

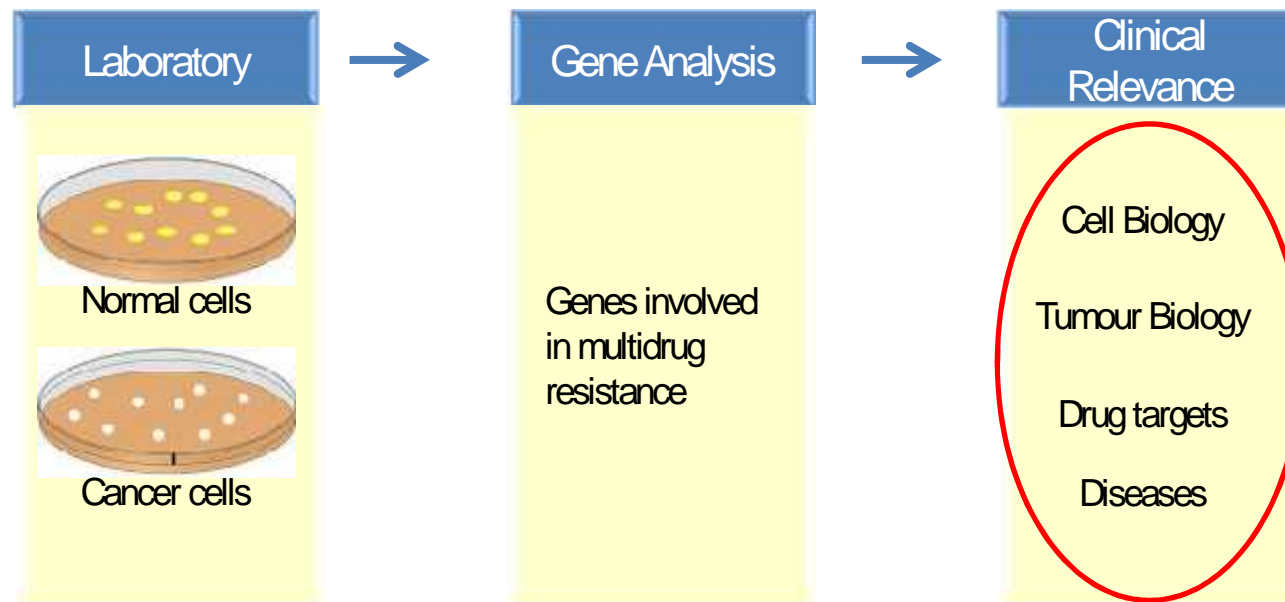
# The scientist's perspective

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- Albert de Roos
  - PhD in Life Sciences (Nijmegen, 1997)
  - Laboratory, Computer Research, Text and data mining
  - Roles in TDM pipeline as contributor and end user
- Goal is to show TDM from a scientist's perspective
  - Using state-of-the-art genomics tool (DAVID)
  - How it is built by the scientific community
  - How it used by research scientists

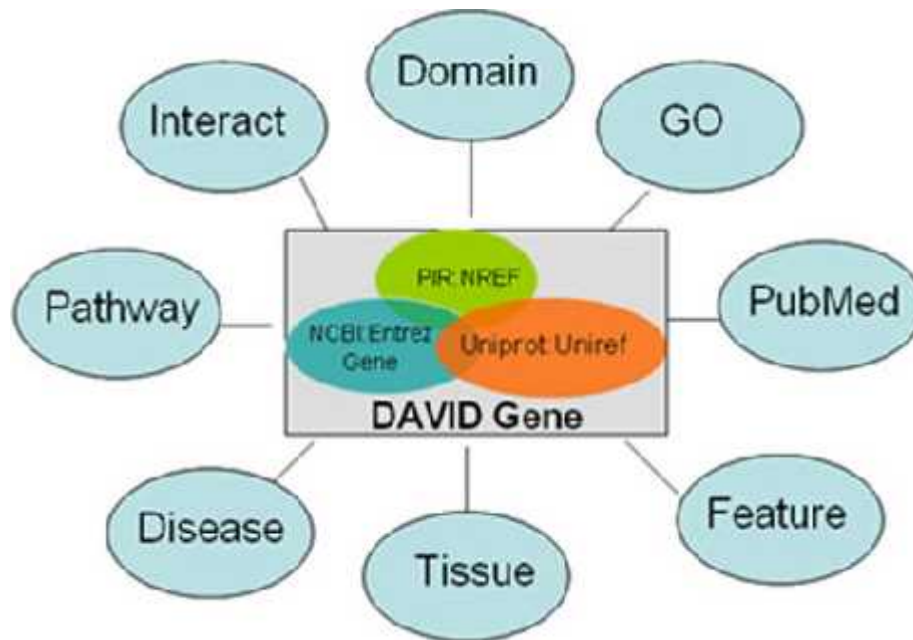
# A typical research question in cancer research

Why are some cells resistant to chemotherapy?



Protein p150 as a new target for multidrug-resistant cells

# DAVID\*: From Gene to Disease



- There is too much information to be analyzed by the individual researcher
- Set of tools for investigators to understand biological meaning behind large list of genes.
- How can I relate the difference in gene patterns to multidrug cancer resistance

\*The Database for Annotation, Visualization and Integrated Discovery ([DAVID](#))

# Cell Biology and Bioinformatics

Cell Biologist



Diseases  
Cancer Genes  
Drug Therapies  
Bioinformatics  
Advances Search

Genes  
Proteins  
Chemicals  
Raw Data  
Raw Text

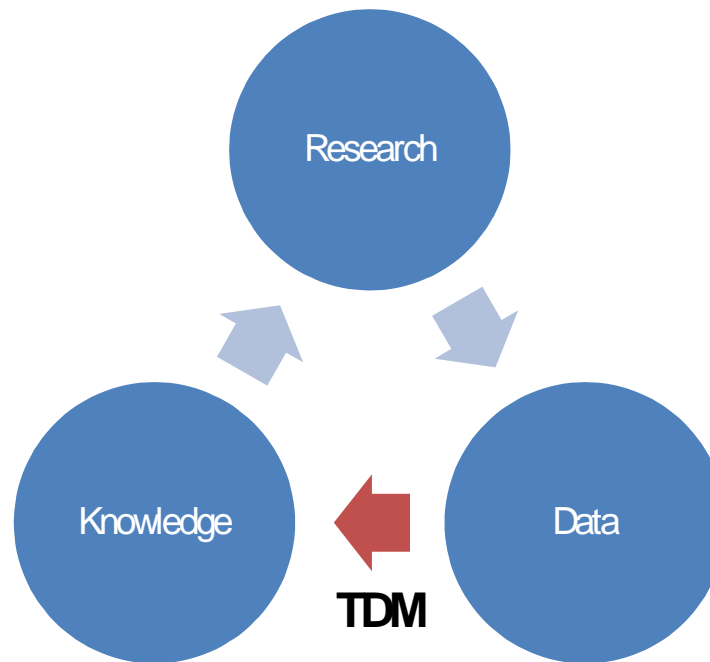


Bioinformatician

# Next research steps

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- Design new experiments based on results using additional tools and applications
- Write an article or create data sets that becomes part of the primary source of the used tools



Demo: Use of DAVID to support cancer research question

# Demo of DAVID as an Open Source Genomic Tool Set

Scientist's view on operational aspects of Text and Data Mining



BIOINFORMATICS  
DATABASE

## Analysis Wizard

DAVID Bioinformatics Resources 6.7, NIAID/NIH

[Home](#)[Start Analysis](#)[Shortcut to DAVID Tools](#)[Technical Center](#)[Downloads & APIs](#)[Term of Service](#)[Why DAVID?](#)[About Us](#)[Upload](#) [List](#) [Background](#)

### Upload Gene List

[Demolist 1](#) [Demolist 2](#)[Upload Help](#)

#### Step 1: Enter Gene List

A: Paste a list

CP1IE9  
TUBA8  
CCDC122  
RAD54

Or

B: Choose From a File

 [Geen bestand gekozen](#)☐ Multi-List File ?

#### Step 2: Select Identifier

OFFICIAL\_GENE\_SYMBOL ▼

#### Step 3: List Type

Gene List ☒

Background ☐

#### Step 4: Submit List

## Analysis Wizard

Tell us how you like the tool  
[Contact us for questions](#)



Step 1. Submit your gene list through left panel.

An example:

Copy/paste IDs to "box A" -> Select Identifier as "Affy\_ID" -> List Type as "Gene List" -> Click "Submit" button

1007\_s\_at  
1053\_at  
117\_at  
121\_at  
1255\_g\_at  
1294\_at  
1316\_at  
1320\_at  
1405\_i\_at  
1431\_at  
1438\_at  
1487\_at  
1494\_f\_at  
1598\_g\_at



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## Gene List Manager

Select to limit annotations by one or more species: [Help](#)

- Use All Species -  
Homo sapiens(855)  
Mus musculus(593)  
Bos taurus(510)

Select Species

List Manager [Help](#)

List\_1

Select List to:

Use

Rename

Remove

Combine

Show Gene List

[View Unmapped Ids](#)

## Analysis Wizard

[Tell us how you like the tool](#)  
[Contact us for questions](#)

☒ Step 1. Successfully submitted gene list

Current Gene List: List\_1

Current Background: Homo sapiens

Step 2. Analyze above gene list with one of DAVID tools

[Which DAVID tools to use?](#)



[Functional Annotation Tool](#)

- [Functional Annotation Clustering](#)
- [Functional Annotation Chart](#)
- [Functional Annotation Table](#)

[Gene Functional Classification Tool](#)

[Gene ID Conversion Tool](#)

[Gene Name Batch Viewer](#)

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## Gene List Manager

Select to limit annotations by one or more species [Help](#)

## List Manager [Help](#)

Select List to:

[View Unmapped Ids](#)

## Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: List\_1

829 DAVID IDs

Current Background: Homo sapiens

Check Defaults ☒

- ☒ Disease (1 selected)
- ☒ Functional\_Categories (3 selected)
- ☒ Gene\_Ontology (3 selected)
- ☒ General\_Annotations (0 selected)
- ☒ Literature (0 selected)
- ☒ Main\_Accessions (0 selected)
- ☒ Pathways (3 selected)
- ☒ Protein\_Domains (3 selected)
- ☒ Protein\_Interactions (0 selected)
- ☒ Tissue\_Expression (0 selected)

\*\*\*Red annotation categories denote DAVID defined defaults\*\*\*

## Combined View for Selected Annotation



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## Functional Annotation Tool

DAVID Bioinformatics Resources 6.7, NIAID/NIH

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[Upload](#) [List](#) [Background](#)

### Gene List Manager

Select to limit annotations by one or more species. [Help](#)

- Use All Species -  
Homo sapiens(855)  
Mus musculus(533)  
Bos taurus(510)  
Select Species

List Manager [Help](#)

List\_1  
[Empty field]  
[Dropdown arrow]

Select List to:

Use Rename  
Remove Combine  
Show Gene List

[View Unmapped Ids](#)

### Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: List\_1

829 DAVID IDs

Current Background: Homo sapiens

Check Defaults ☐

Clear All

- ☐ Disease (0 selected)
- ☐ Functional\_Categories (0 selected)
- ☐ Gene\_Ontology (0 selected)
- ☐ General Annotations (0 selected)
- ☐ Literature (0 selected)
- ☐ Main\_Accessions (0 selected)
- ☒ Pathways (1 selected)

<input type="checkbox"/> BBID	2.3%	19	Chart	
<input type="checkbox"/> BIOCARTE	6.6%	55	Chart	
<input type="checkbox"/> EC_NUMBER	14.4%	119	Chart	
<input checked="" type="checkbox"/> KEGG_PATHWAY	20.5%	170	Chart	
<input type="checkbox"/> PANTHER_PATHWAY	11.9%	99	Chart	
<input type="checkbox"/> REACTOME_PATHWAY	15.3%	127	Chart	

- ☐ Protein\_Domains (0 selected)
- ☐ Protein Interactions (0 selected)
- ☐ Tissue Expression (0 selected)

\*\*\*Rec annotation categories denote DAVID defined defaults\*\*\*

#### Combined View for Selected Annotation

Functional Annotation Clustering  
Functional Annotation Chart  
Functional Annotation Table



## Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List\_1

Current Background: Homo sapiens

829 DAVID IDs

 Options

Rerun Using Options

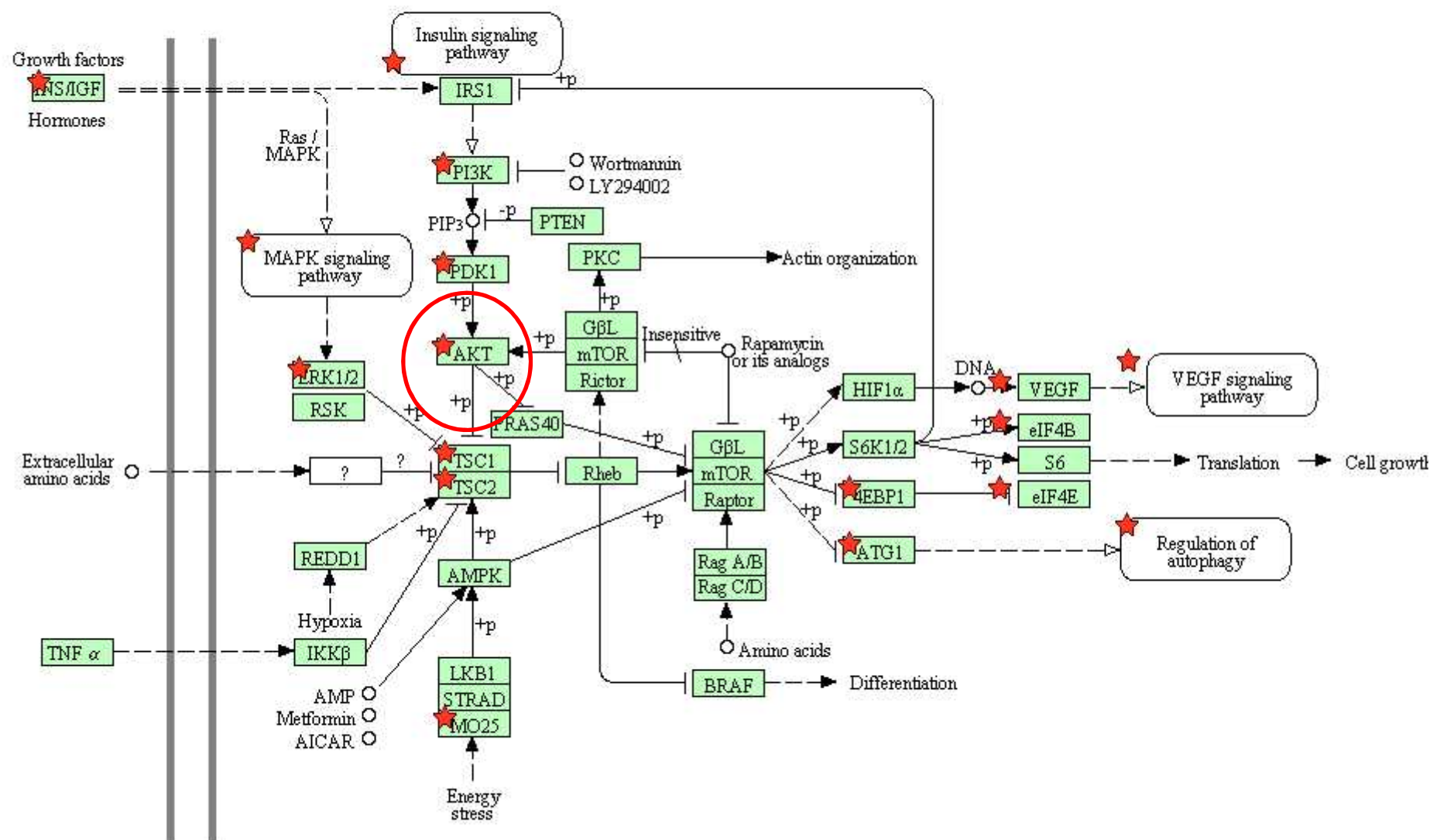
Create Sublist

44 chart records

 [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	mTCR signaling pathway	RT		24	2,9	3,3E-21	4,7E-19
<input type="checkbox"/>	KEGG_PATHWAY	Progesterone-mediated oocyte maturation	RT		18	2,2	1,8E-9	1,3E-7
<input type="checkbox"/>	KEGG_PATHWAY	Insulin signaling pathway	RT		21	2,5	1,2E-8	5,8E-7
<input type="checkbox"/>	KEGG_PATHWAY	Aldosterone-regulated sodium reabsorption	KI		12	1,4	5,3E-8	1,9E-6
<input type="checkbox"/>	KEGG_PATHWAY	Type II diabetes mellitus	RT		12	1,4	2,4E-7	6,9E-6
<input type="checkbox"/>	KEGG_PATHWAY	Colorectal cancer	RT		15	1,8	4,9E-7	1,2E-5
<input type="checkbox"/>	KEGG_PATHWAY	Renal cell carcinoma	RT		13	1,6	2,4E-6	5,0E-5
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic cancer	RT		13	1,6	3,3E-6	5,9E-5
<input type="checkbox"/>	KEGG_PATHWAY	Systemic lupus erythematosus	RT		15	1,8	3,8E-6	6,0E-5
<input type="checkbox"/>	KEGG_PATHWAY	Glioma	RT		12	1,4	5,4E-6	7,7E-5
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer	RT		11	1,3	6,0E-6	7,7E-5
<input type="checkbox"/>	KEGG_PATHWAY	Non-small cell lung cancer	KI		11	1,3	8,5E-6	1,0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Melanoma	RT		12	1,4	1,8E-5	2,0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer	RT		13	1,6	3,1E-5	3,2E-4
<input type="checkbox"/>	KEGG_PATHWAY	Acute myeloid leukemia	RT		10	1,2	1,0E-4	9,9E-4
<input type="checkbox"/>	KEGG_PATHWAY	ErbB signaling pathway	RT		12	1,4	1,2E-4	1,1E-3

## mTOR SIGNALING PATHWAY





## Gene Report

[Help and Manual](#)

 [Download File](#)

List Id: v-akt murine thymoma viral oncogene homolog 1	v-akt murine thymoma viral oncogene homolog 1	Related Genes	Homo sapiens
CHROMOSOME	14,		
CYTOBAND	14q32.32, 14q32.32 14q32.32,		
ENSEMBL_GENE_ID	ENSG00000142208,		
ENTREZ_GENE_ID	207,		
GENERIF_SUMMARY	<p>Binding of CTMP to PKBalpha reduces its activity by inhibiting phosphorylation on serine 473 and threonine 308., regulated in platelets by collagen receptor glycoprotein VI, Absence of mutations in the pleckstrin homology (PH) domain of protein kinase B (PKB/Akt) in malignant melanoma., Immunohistochemical localization of phosphorylated AKT/PKB in multiple myeloma cells., Akt enhances Mdm2-mediated ubiquitination and degradation of p53., Identification of 14-3-3zeta as a protein kinase B/Akt substrate., Phosphorylation of HDM2 by Akt, and protein binding, IGF-1 protects the cells from apoptosis by blocking the activation of caspases, which may be responsible for the loss of FAK and Akt., Akt promotes cell-cycle progression through the mechanisms of phosphorylation-dependent 14-3-3 binding to p27(Kip1) and cytoplasmic localization., AKT activation delays radiation-induced apoptosis, allowing the DNA repair mechanism more time to remove cyclobutane thymine dimers, Different cellular localization, translocation, and insulin-induced phosphorylation of PKBalpha in HepG2 cells and hepatocytes, This study shows that activation of Akt by pervanadate or serum is associated with tyrosine phosphorylation of Akt., 3' phosphoinositide lipid-dependent translocation of PKB to the plasma membrane promotes serine 473 phosphorylation, which is, in turn, necessary for PDK1-mediated phosphorylation of threonine 308 and, consequentially, full PKB activation., determination of high resolution structure of the pleckstrin homology domain of bound to phosphatidylinositol (3,4,5)-trisphosphate, connective tissue growth factor induced fibronectin production, cell migration, and cytoskeletal rearrangement are associated with recruitment of Src and phosphorylation of p42/44 MAPK and protein kinase B, These data indicate that Akt may contribute to tumor-cell proliferation by phosphorylation and cytosolic retention of p27(kip1), thus relieving CDK2 from p27-induced inhibition., Data show that activation of protein kinase B (PKB)/Akt, contributes to resistance to antiproliferative signal and breast cancer progression in part by impairing the nuclear import and action of p27., Data show that cytoplasmic relocalization of p27(kip1), secondary to Akt-mediated phosphorylation, inactivates the growth inhibitory properties of p27(kip1) and sustains the proliferation of breast cancer cells., PECAM-1 involvement through Akt/PKB activation in starvation-induced transendothelial migration of CD34+CD14+ circulating precursors, data demonstrate that Rho/ROCK pathway negatively regulates eNOS phosphorylation through inhibition of protein kinase B (PKB), whereas it downregulates eNOS expression independent of PKB, chemotherapeutic drugs exhibited their cytotoxic effects in part by down-regulating Akt signaling following TRADD expression, We conclude that normal HERG function in HEK293 cells requires basal activity of PKB. Our data represent the first evidence that PKB phosphorylation regulates K(+) channels., Decreased phosphorylation of protein kinase B and erk1/erk2 in neutrophils from patients with myelodysplastic syndrome, This protein protects HL60 leukemia cells from TRAIL-induced apoptosis through a mechanism involving NF-kappaB activation and cFLIP(L) up-regulation., our data suggest that HRG-beta1, bound to the ErbB2 ErbB3 heterodimer, in the presence of membrane ER-alpha, interacts with and activates PI 3-K/Akt., Increased phosphorylation of this protein was observed in A431 clonal variants., The protein kinase Akt induces epithelial mesenchymal transition and promotes enhanced motility and invasiveness of squamous cell carcinoma lines., activation of Notch1 signaling mediates p53 function in HPV16 E6 and E7 cell transformation via phosphatidylinositol(PI3K)-PKB/Akt pathway, Akt is activated by adrenomedullin, AKT1 is regulated by JIP1, results suggest that TRB3 promotes glucose output from liver under fasting conditions by binding to and interfering with Akt phosphorylation in response to residual insulin signaling, Akt regulates basic helix-loop helix transcription factor-coactivator complex formation and activity during neuronal differentiation, phosphorylation by Akt regulates the</p>		



Abstract Send to: [J Biol Chem. 2002 Oct 11;277\(41\):38021-8. Epub 2002 Jul 30.](#)**Direct Identification of tyrosine 474 as a regulatory phosphorylation site for the Akt protein kinase.**[Conus NM<sup>1</sup>](#), [Hannan KM](#), [Cristiano BE](#), [Hemmings BA](#), [Pearson RB](#).**Author information****Abstract**

Understanding the regulation of Akt has been of major interest for elucidating the control of normal cellular physiology as well as malignant transformation. The paradigm for activation of Akt involves phosphatidylinositol 3-kinase-dependent membrane localization followed by activating phosphorylation of Thr-308 and Ser-473. Many of the activating signals for Akt involve the stimulation of receptor and non-receptor tyrosine kinases, and the most potent activator known is the tyrosine phosphatase inhibitor pervanadate, highlighting a possible role for tyrosine phosphorylation in the regulation of the enzyme. **In this study we show that activation of Akt by pervanadate or serum is associated with tyrosine phosphorylation of Akt.** In addition, in SKOV3 ovarian carcinoma cells that exhibit high basal levels of Akt activity, Akt was tyrosine-phosphorylated in the basal state, and this phosphorylation was further enhanced by both pervanadate and insulin-like growth factor-1. We have used NH(2)-terminal sequencing and phosphate release analysis to directly identify Tyr-474 as the site of tyrosine phosphorylation. Substitution of Tyr-474 with phenylalanine abolished tyrosine phosphorylation of Akt and resulted in up to 55% inhibition of Akt activation, indicating phosphorylation at Tyr-474 is required for full activation of the kinase. Our data identifies a novel regulatory mechanism for this pleiotropic enzyme that may be applicable to the AGC family of protein kinases given the conserved nature of the COOH-terminal hydrophobic motif containing Tyr-474.

PMID: 12149249 [PubMed - indexed for MEDLINE] [Free full text](#)

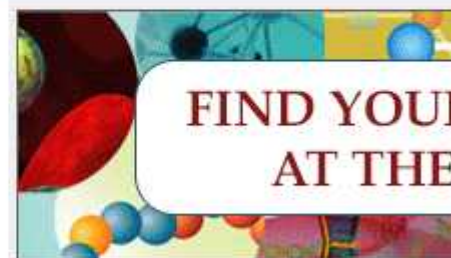
## Direct Identification of Tyrosine 474 as a Regulatory Phosphorylation Site for the Akt Protein Kinase<sup>\*</sup>,<sup>210</sup>

Nelly Marmy Conus, Katherine M. Hannan, Briony E. Cristiano,  
Brian A. Hemmings<sup>‡</sup> and Richard B. Pearson<sup>§</sup>

[+](#) Author Affiliations

### Abstract

Understanding the regulation of Akt has been of major interest for elucidating the control of normal cellular physiology as well as malignant transformation. The paradigm for activation of Akt involves phosphatidylinositol 3-kinase-dependent membrane localization followed by activating phosphorylation of Thr-308 and Ser-473. Many of the activating signals for Akt involve the stimulation of receptor and non-receptor tyrosine kinases, and the most potent activator known is the tyrosine phosphatase inhibitor pervanadate, highlighting a possible role for tyrosine phosphorylation in the regulation of the enzyme. In this study we show that activation of Akt by pervanadate or serum is associated with tyrosine phosphorylation of Akt. In addition, in SKOV3 ovarian carcinoma cells that exhibit high basal levels of Akt activity, Akt was tyrosine-phosphorylated in the basal state, and this phosphorylation was further enhanced by both pervanadate and insulin-like growth factor-1. We have used NH<sub>2</sub>-terminal sequencing and



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### This Article

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# End of Presentation

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