Protein Ontology (PRO)

for integration of knowledge on proteins, complexes and PTMs

Using Ontologies for Organizing Plant and Animal Genomics Data
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PRO in OBO Foundry

OBO Foundry

The Open Biological and Biomedical Ontologies

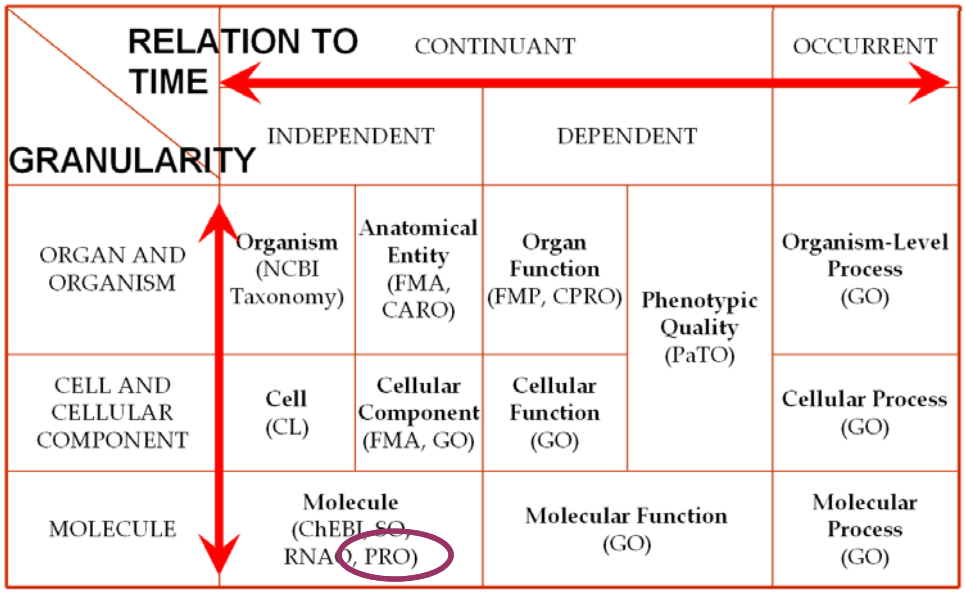
- Establishing a set of principles to create a suite of orthogonal interoperable reference ontologies

Protein Ontology (PRO)

- One of the first set of six OBO Foundry ontologies
- Reference Ontology for Proteins

OBO Foundry ontologies

Title	Domain	Prefix	File
Biological process	biological process	GO	gene_ontology_edit.obo
Cellular component	anatomy	GO	gene_ontology_edit.obo
Chemical entities of biological interest	biochemistry	CHEBI	chebi.obo
Molecular function	biological function	GO	gene_ontology_edit.obo
Phenotypic quality	phenotype	PATO	quality.obo
PRotein Ontology (PRO)	proteins	PR	pro.obo
Xenopus anatomy and development	anatomy	XAO	xenopus_anatomy.obo
Zebrafish anatomy and development	anatomy	ZFA	zebrafish_anatomy.obo



The Protein Ontology: a structured representation of protein forms and complexes
Natale DA, Arighi CN, Barker WC, Blake JA, Bult CJ, Caudy M, Drabkin HJ, D'Eustachio P, Evsikov AV, Huang H, Nchoutmboube J, Roberts NV, Smith B, Zhang J, Wu CH. (2011)
Nucleic Acids Res. 39, D539-545 [PMID:20935045]

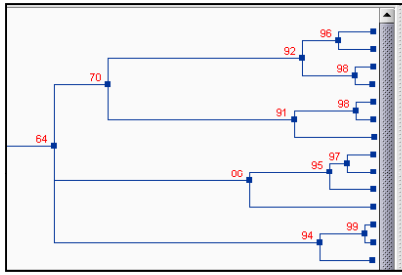
NIGMS

PRO Overview

PRO in OBO Foundry to represent protein entities

Three sub-ontologies to connect protein types necessary to model biology

- Ontology for Protein Evolution (ProEvo): Captures protein classes reflecting evolutionary relatedness of whole proteins



Node ID	Accession	PIRSF	Pfam
HCN1_RABIT	Q9MZS1	PIRSF038514:PIRSF500960	PF08412:PF00520:PF00027
HCN1_HUMAN	O60741	PIRSF038514:PIRSF500960	PF08412:PF00520:PF00027
HCN1_RAT	Q9JKB0	PIRSF038514:PIRSF500960	PF08412:PF00520:PF00027
HCN1_MOUSE	O88704	PIRSF038514:PIRSF500960	PF08412:PF00520:PF00027
HCN2_RAT	Q9JKA9	PIRSF038514:PIRSF500961	PF08412:PF00520:PF00027
HCN2_MOUSE	O88703	PIRSF038514:PIRSF500961	PF08412:PF00520:PF00027
HCN2_HUMAN	Q9UL51	PIRSF038514:PIRSF500961	PF08412:PF00520:PF00027
HCN4_RAT	Q9JKA7	PIRSF038514:PIRSF500963	PF08412:PF00520:PF00027
HCN4_MOUSE	Q70507	PIRSF038514:PIRSF500963	PF08412:PF00520:PF00027
HCN4_HUMAN	Q9Y3Q4	PIRSF038514:PIRSF500963	PF08412:PF00520:PF00027
HCN4_RABIT	Q9TV66	PIRSF038514:PIRSF500963	PF08412:PF00520:PF00027
HCN3_RAT	Q9JKA8	PIRSF038514:PIRSF500962	PF08412:PF00520:PF00027
HCN3_MOUSE	O88705	PIRSF038514:PIRSF500962	PF08412:PF00520:PF00027
HCN3_HUMAN	Q9P1Z3	PIRSF038514:PIRSF500962	PF08412:PF00520:PF00027

PR:000000676 *potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel protein*	*family*
PR:000000705 *potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1*	*gene*
PR:000000706 *potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2*	*gene*
PR:000000707 *potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3*	*gene*
PR:000000708 *potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4*	*gene*

- Ontology for Protein Forms (ProForm): Captures different protein forms of a given gene locus from genetic variations, alternative splicing, proteolytic cleavage, PTMs

PR:000002184 *Bcl2 antagonist of cell death*	*gene*	
PR:000002280 *Bcl2 antagonist of cell death isoform 1*	*sequence*	
PR:000003084 *Bcl2 antagonist of cell death isoform 1 phosphorylated form*	*modification*	*O35147; Q61337; Q92934*
PR:000003085 *Bcl2 antagonist of cell death isoform 1 phosphorylated 1*	*modification*	*O35147-1; Q61337-1*
PR:000003086 *Bcl2 antagonist of cell death isoform 1 phosphorylated 2*	*modification*	
PR:000003087 *Bcl2 antagonist of cell death isoform 1 phosphorylated 3*	*modification*	*Q61337-1:pS112/pS136*
PR:000003233 *Bcl2 antagonist of cell death isoform 1 phosphorylated 4*	*modification*	*Q61337-1:pS112/pS136/pS155*
PR:000003238 *Bcl2 antagonist of cell death isoform 1 phosphorylated 5*	*modification*	*O35147-1:pS112*
PR:000003269 *Bcl2 antagonist of cell death isoform 1 phosphorylated 6*	*modification*	*Q61337-1:pT201*
PR:000025849 *Bcl2 antagonist of cell death isoform 1 phosphorylated 7*	*modification*	*Q61337-1:pS136*
PR:000025850 *Bcl2 antagonist of cell death isoform 1 phosphorylated 8*	*modification*	*Q61337-1:pS128/pS136*

Need for Representing Proteins Forms

Alternative Splicing/Genetic Variation/PTM/Cleavage

Gene	Protein Form	Distinctive Attributes
SMAD2	Long isoform phosphorylated (PR:000000468)	***NOT has_function*** GO:00036677 DNA binding
	Short isoform phosphorylated (PR:000000469)	***has_function*** GO:00036677 DNA binding
CUL1	Unmodified form (PR:000002507)	***NOT part_of*** GO:0019005 SCF ubiquitin ligase complex
	Needylated form (PR:000000542)	***part_of*** GO:0019005 SCF ubiquitin ligase complex
CD14	Membrane form (PR:000002149)	***located_in*** GO:0005886 plasma membrane
	Soluble form (PR:000002147)	***located_in*** GO:0005615 extracellular space
ROCK1	Full length (PR:000002529)	***has_function*** GO:0004674 protein serine/threonine kinase activity
	Cleaved form (PR:000000563)	***Increased has_function*** GO:0004674 protein serine/threonine kinase activity
CREBBP	Variant R -> P(1378) (PR:000000266)	**agent_in MIM:180849**, RUBINSTEIN-TAYBI SYNDROME SO:1000118, loss_of_function_of_polypeptide

Function

Association

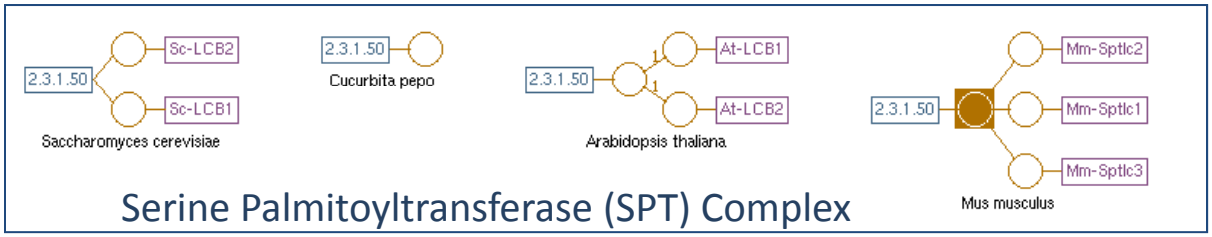
Localization

Modification

Disease

PRO Overview

- Ontology for Protein Complexes (ProComp): Captures distinct complexes as they exist in different species and defines complexes through component proteins

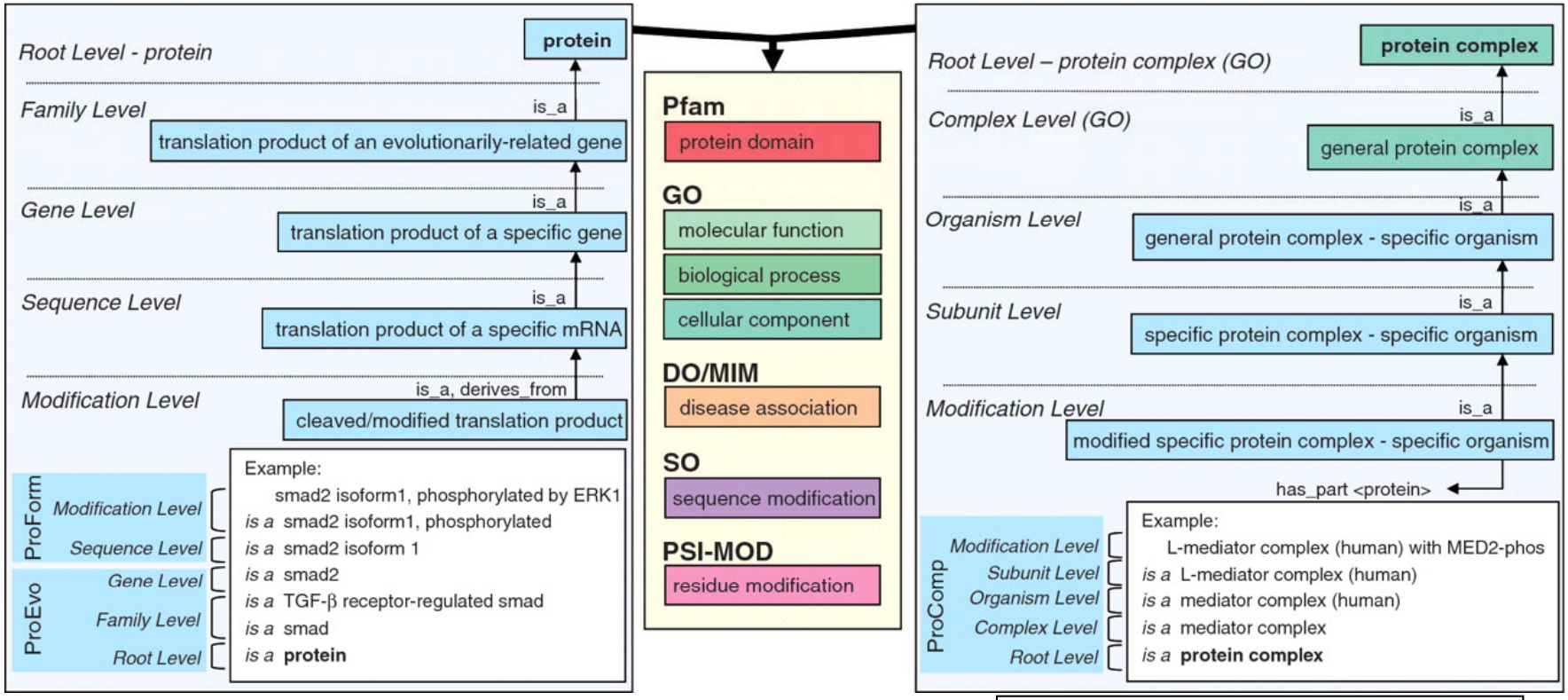


GO:0002178 *palmitoyltransferase complex*	
GO:0002179 *homodimeric serine palmitoyltransferase complex*	
PR:000026130 *bacterial serine palmitoyltransferase complex (Sphingomonas paucimobilis)*	*organism-complex*
PR:000026132 *bacterial serine palmitoyltransferase complex (Sphingomonas wittichii)*	*organism-complex*
PR:000026169 *bacterial serine palmitoyltransferase complex (Sphingobacterium multivorum)*	*organism-complex*
GO:0031211 *endoplasmic reticulum palmitoyltransferase complex*	
GO:0017059 *serine C-palmitoyltransferase complex*	
PR:000026146 *serine palmitoyltransferase complex 3 (human)*	*organism-complex*
PR:000026153 *serine palmitoyltransferase complex 5 (human)*	*organism-complex*
PR:000026145 *serine palmitoyltransferase complex core 2 (human)*	*organism-complex*

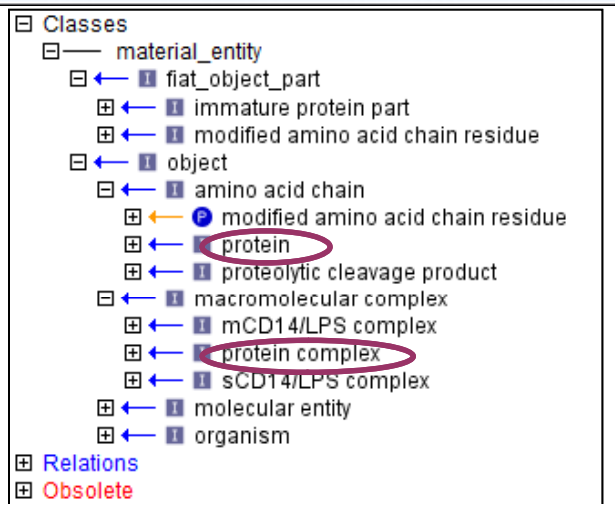
Why PRO?

- Provides formalization to support precise annotation of specific protein classes/forms/ complexes, allowing accurate and consistent data mapping, integration and analysis
- Allows specification of relationships between PRO and other ontologies, such as GO, SO (Sequence Ontology), PSI-MOD, ChEBI, MIM/Disease Ontology, PO (Plant Ontology)
- Provides stable unique identifiers to distinct protein types
- Provides a formal structure to support computer-based reasoning based on homology and shared protein attributes, including “ortho-isoform,” “ortho-modified form”

PRO Framework



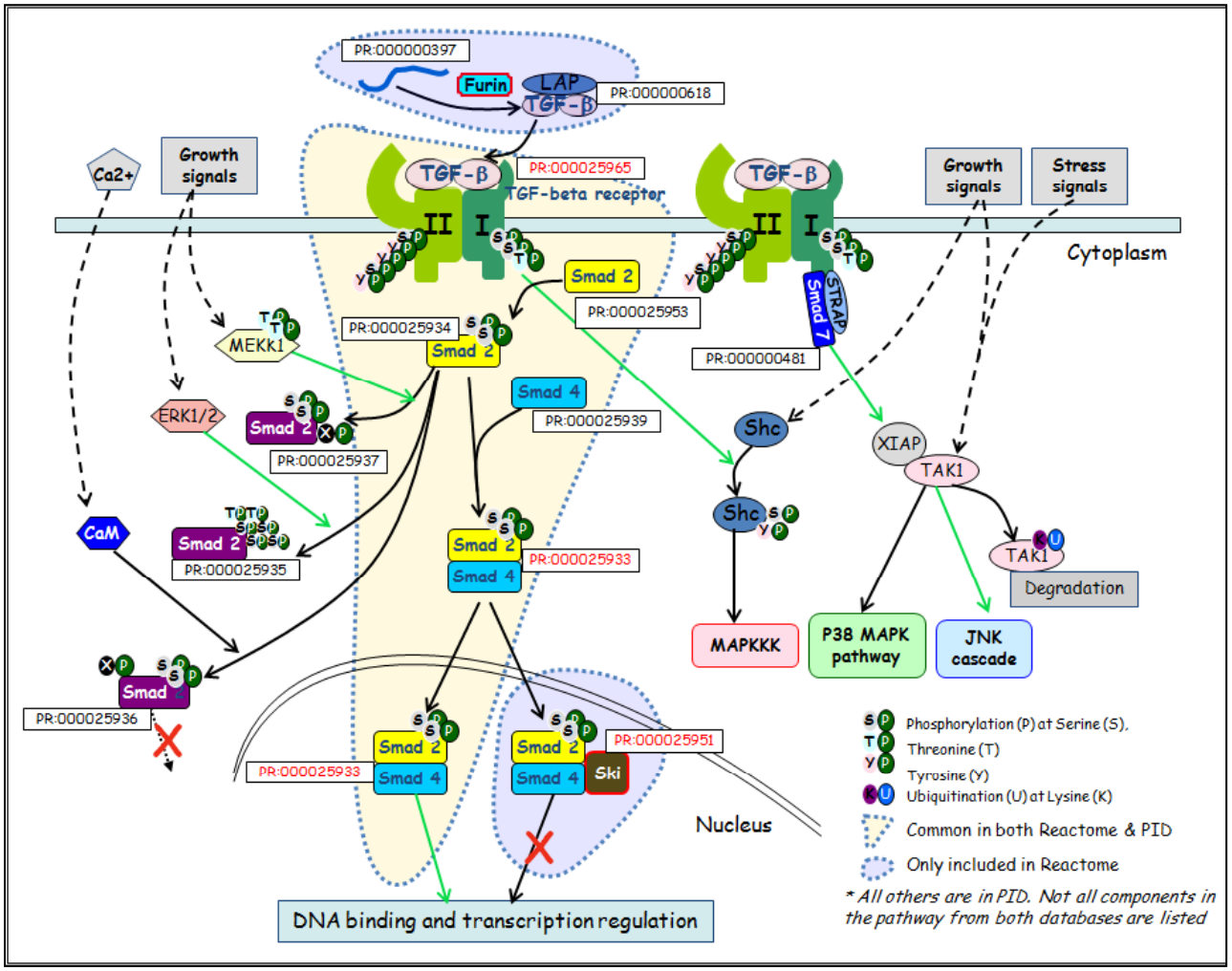
- PRO (ProForm, ProEvo, ProComp) is aligned with other OBO Foundry ontologies under the umbrella of the Basic Formal Ontology (BFO)
- PRO terms are defined/annotated using other ontologies and resources via definition of relations or mappings when appropriate



PRO in Pathway Context

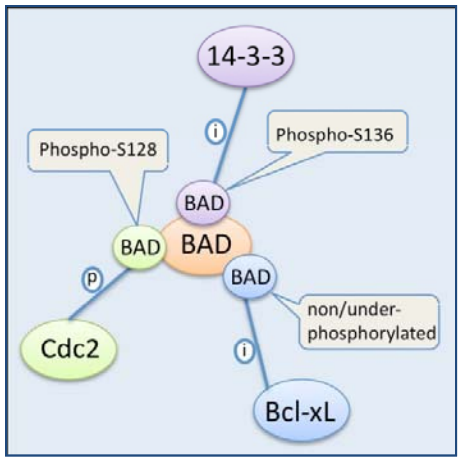
- Representation of protein forms & complexes in biological/pathway/network context
- Connecting multiple pathway/network resources

TGF-β Signaling Pathway: *Reactome, PID, coupled with literature curation*

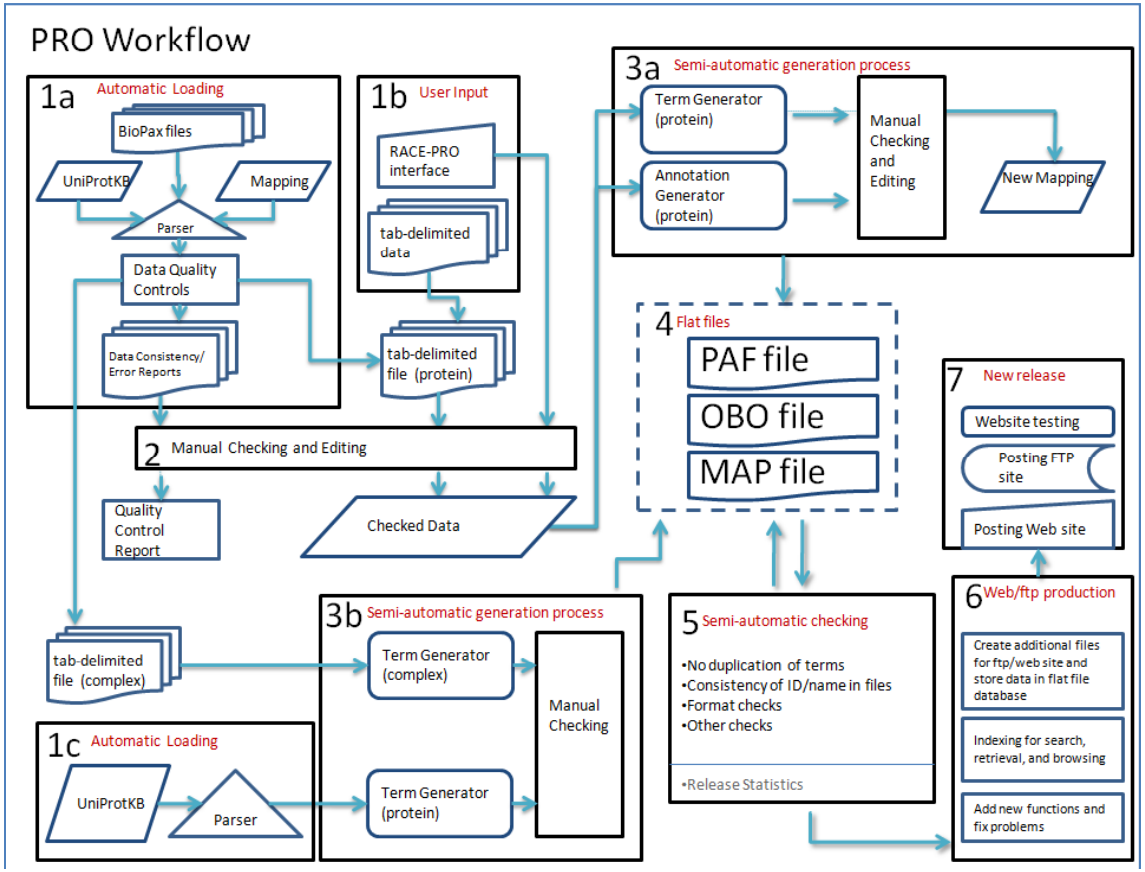


PRO Workflow

- Data Sources
  - Manual annotation (curator, collaborator, user): sourceforge tracker; Race-PRO
  - Semi-automated processing of external databases (e.g., UniProtKB, Reactome, MouseCyc, EcoCyc); coverage of 12 reference genomes forthcoming
- Integration with text mining tool: eFIP (*Functional Impact of Phosphorylation)*
- Distribution Files
  - Ontology (OBO)
  - Annotation (PAF)
  - Mappings (exact; is_a)



eFIP text mining



Plant PRO Terms

- *Arabidopsis thaliana*: 3842 gene-level terms to be added soon based on the PANTHER mapping of 12 reference genomes
- 59 terms for *Arabidopsis thaliana* and wheat on protein forms and complexes

PRO Home search | Any field | cullin | AND | Any field | + add input box | – del input box

Display Options

42 entries | 1 page | 50 / page |

Cullin-Related PRO Terms

42 selected show **click to show:** selected Hierarchy | selected OBO / PAF | OR related OBO / PAF / Cytoscape view

PRO ID	PRO Name	PRO Term Definition	Category	Parent
GO:0019005	SCF ubiquitin ligase complex	A ubiquitin ligase complex in which a cullin from the Cul1 subfamily and a RING domain protein form the catalytic core; substrate specificity is conferred by a Skp1 adaptor and an F-box protein. SCF complexes are involved in targeting proteins for degradation by the proteasome. The best characterized complexes are those from yeast and mammals (with core subunits named Cdc53/Cul1, Rbx1/Hrt1/Roc1). [PMID:15571813, PMID:15688063]		GO:0031461
GO:0031461	cullin-RING ubiquitin ligase complex	Any ubiquitin ligase complex in which the catalytic core consists of a member of the cullin family and a RING domain protein; the core is associated with one or more additional proteins that confer substrate specificity. [PMID:15571813, PMID:15688063]		GO:0043234
PR:000000013	cullin	A protein with a core domain composition consisting of a cullin domain that functions as a molecular scaffold responsible for assembling the ROC1/Rbx1 RING-based E3 ubiquitin ligases. [PIRSF:PIRSF017874]	family	PR:000000001
PR:000000043	RING-box protein 1	A RING-box protein 1 related protein that is a translation product of the RBX1 gene or a 1:1 ortholog thereof. [PRO:CNA]	gene	PR:000027961
PR:000000044	RING-box protein 2	A protein that is a translation product of the RNF7 gene or a 1:1 ortholog thereof. [PRO:CNA]	gene	PR:000000004
PR:000000092	fungal/metazoan cullin-1	A cullin that is a translation product of the CUL1 gene or a 1:1 ortholog thereof. [PRO:CNA]	gene	PR:000000013
PR:000000267	cullin-1 isoform 1	A cullin-1 that is a translation product of some mRNA giving rise to a protein with the amino acid sequence represented by UniProtKB:Q13616-1 or a 1:1 ortholog thereof. [PRO:CNA]	sequence	PR:000000092

Hierarchical View: Cullin-Related Terms

66 shown of 28321 records

PMID | Taxon | PANTHER | EcoCyc | Definition | Synonym | Gene | MGI | HGNC | Pfam | PIRSF | Reactome | UniProtKB

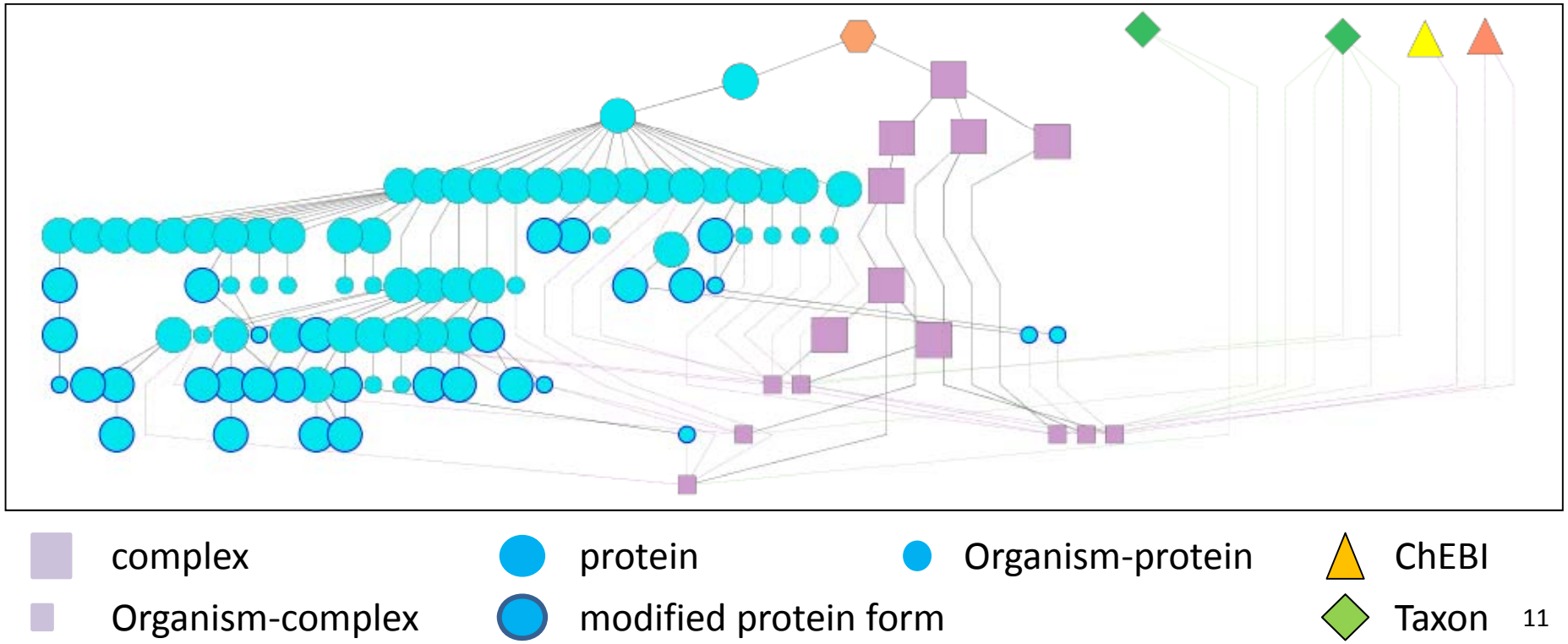
expand | sort (ID) | sort (STR) | find

	Category
GO:0032991 ***macromolecular complex***	
GO:0043234 ***protein complex***	
GO:0031461 *cullin-RING ubiquitin ligase complex*	
GO:0019005 *SCF ubiquitin ligase complex*	
PR:000026771 *SCF beta-TrCP complex (human)*	*organism-complex*
PR:000028464 *SCF(COI1) complex*	*complex*
PR:000028465 *SCF(COI1) complex (Arabidopsis thaliana)*	*organism-complex*
PR:000028457 *SCF(TIR1) complex*	*complex*
PR:000028458 *SCF(TIR1) complex (Arabidopsis thaliana)*	*organism-complex*
PR:000026772 *SCF(Skp2) complex (human)*	*organism-complex*
PR:000018263 ***amino acid chain***	
PR:000000001 ***protein***	
PR:000000013 *cullin*	*family*
PR:000006047 *cullin-2*	*gene*
PR:000006048 *cullin-3*	*gene*
PR:000006049 *cullin-4A*	*gene*
PR:000006050 *cullin-4B*	*gene*
PR:000006051 *cullin-5*	*gene*
PR:000000092 *fungal/metazoan cullin-1*	*gene*
PR:000026757 *cullin-1 (human)*	*organism-gene*
PR:000000267 *cullin-1 isoform 1*	*sequence*
PR:000000427 *cullin-1 isoform 1 neddylated form*	*modification*
PR:000000542 *cullin-1 isoform 1 neddylated 1*	*modification*
PR:000002507 *cullin-1 isoform 1 unmodified form*	*modification*
PR:000027962 *plant cullin-1*	*gene*
PR:000027963 *cullin-1 (Arabidopsis thaliana)*	*organism-gene*
PR:000027976 *plant cullin-1 rubylated form*	*modification*
PR:000027977 *cullin-1 rubylated (Arabidopsis thaliana)*	*organism-modification*
PR:000028501 *plant cullin-2*	*gene*
PR:000028494 *cullin-2 (Arabidopsis thaliana)*	*organism-gene*
PR:000028495 *plant cullin-3A*	*gene*
PR:000028496 *cullin-3A (Arabidopsis thaliana)*	*organism-gene*
PR:000028497 *plant cullin-3B*	*gene*
PR:000028498 *cullin-3B (Arabidopsis thaliana)*	*organism-gene*

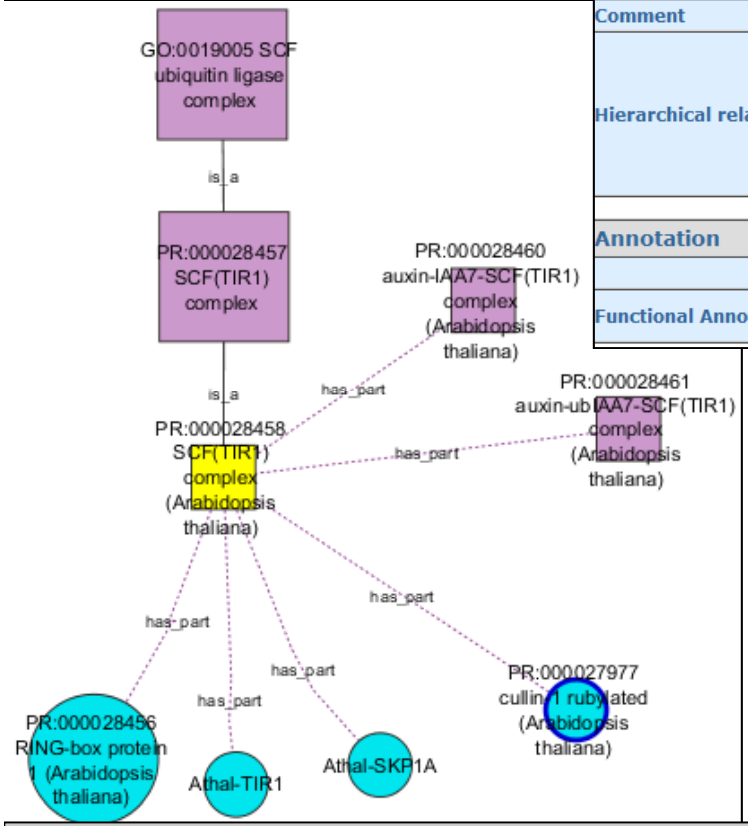
Cytoscape Network View: Cullin-Related Terms

Connecting protein forms and complexes with annotation => Modeling biology

- Show full set of relationships between terms, including those from other ontologies
- Traverse hierarchical (parent-child) relationships
- Find all components of a complex, including modified forms
- Find all complexes that a protein is constituent of = first (complex) neighbors of a protein
- Find all complexes that bind small molecules = those that have relationship to ChEBI



Cytoscape & Entry Views



Protein Ontology report for entry - PR:000028458 Show OBO stanza Retrieve related PR

Ontology Information	
PRO ID	PR:000028458
PRO name	SCF(TIR1) complex (Arabidopsis thaliana)
Synonyms	
Definition	An SCF(TIR1) complex consisting of TIR1, SKP1A(ASK1), rubylated CUL1, and one of RBX1 proteins, whose compon thaliana. [PRO:CNA, PMID:21370976]
Comment	Category=organism-complex.
Hierarchical relationship	Parent: PR:000028457 SCF(TIR1) complex Children: none has_part PR:000027956 {cardinality="1"} protein TRANSPORT INHIBITOR RESPONSE 1 (Arabidopsis thaliana) has_part PR:000027960 {cardinality="1"} SKP1-like protein 1A (Arabidopsis thaliana) has_part PR:000028456 {cardinality="1"} RING-box protein 1 (Arabidopsis thaliana) has_part PR:000027977 {cardinality="1"} cullin-1 rubylated (Arabidopsis thaliana) only_in_taxon NCBITaxon:3702 Arabidopsis thaliana

Annotation

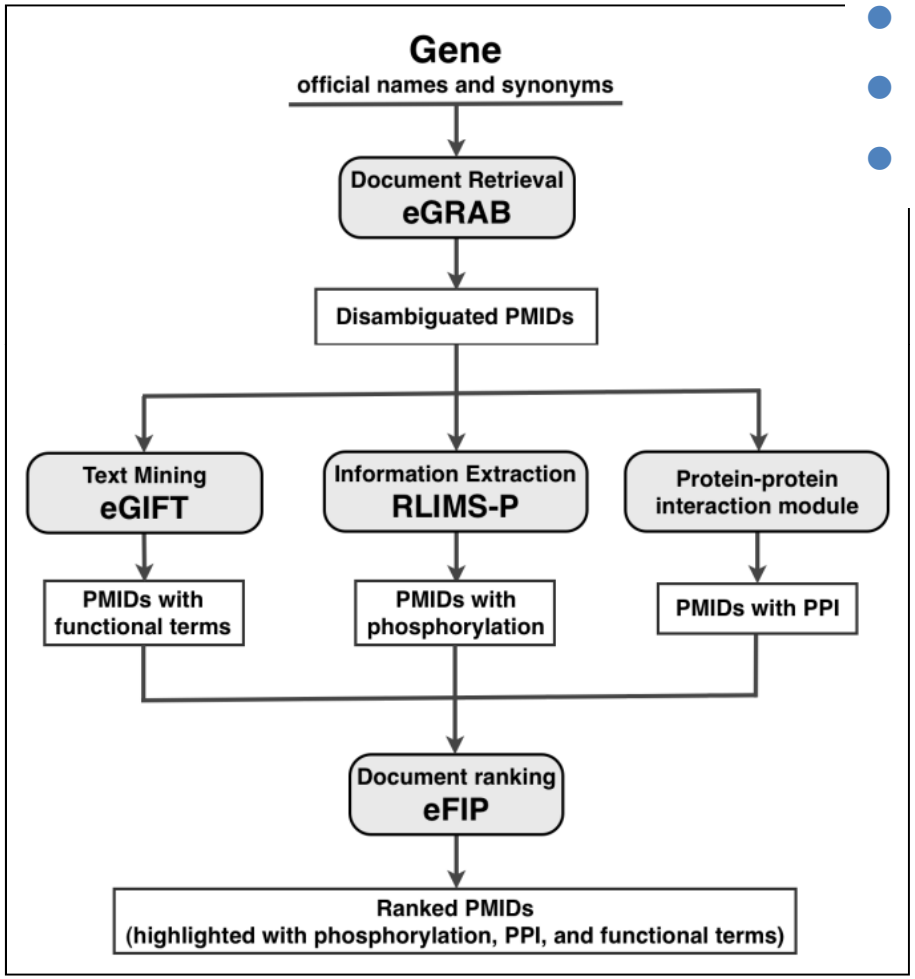
	Modifier	Relation	Ontology ID	Ontology Term	Relative_to	Interaction With	Evidence
Functional Annotation		participates_in	GO:0009734	auxin mediated signaling pathway			PMID:2137

Connecting protein forms and complexes with annotation

Data Panel

ID	ontology.name	Relation	Ontology_ID	Ontology_term	Evidence_source
PR:000028458	SCF(TIR1) complex (Arabidopsis thaliana)	participates_in	GO:0009734	auxin mediated signaling pathway	PMID:21370976

eFIP: an integrated system for mining Functional Impact of Phosphorylation from literature



- Entity recognition and document retrieval
- Information extraction
- Document ranking and evidence tagging

PMID 10837486 for gene BAD - Bcl2-associated agonist of cell death

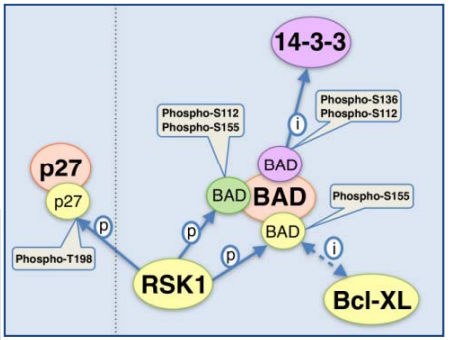
Predicted impact of phosphorylation:

Sentence #	Phosphorylation			Impact
	Substrate	Site	Kinase	
1	BAD	Ser-155	RSK1	regulates BAD/Bcl-XL interaction regulates cell survival
3,4	BAD	Ser-112 and Ser-136	N/A	promotes binding of BAD to 14-3-3 proteins
6	BAD	Ser-155	RSK1	blocking the binding of BAD to Bcl-XL
7	BAD	both Ser-112 and Ser-155	RSK1	rescues BAD -mediated cell death

Tag substrate
Tag kinase
Tag phosphorylation site
Tag protein-protein interaction
Tag functional term

Text of title and abstract:

Sentence #	Sentence
1	TI - BAD Ser-155 PHOSphorylation regulates BAD/Bcl-XL interaction and cell survival .
2	AB - The BH3 domain of BAD mediates its death-promoting activities via heterodimerization to the Bcl-XL family of death regulators .
3	Growth and survival factors inhibit the death-promoting activity of BAD by stimulating PHOSphorylation at multiple sites including Ser-112 and Ser-136 .
4	PHOSphorylation at these sites promotes binding of BAD to 14-3-3 proteins , sequestering BAD away from the mitochondrial membrane where it dimerizes with Bcl-XL to exert its killing effects .
5	We report here that the phosphorylaTION of BAD at Ser-155 within the BH3 domain is a second PHOSphorylation -dependent mechanism that inhibits the death-promoting activity of BAD .
6	Protein kinase A , RSK1 and survival factor signaling stimulate PHOSphorylation of BAD at Ser-155 , blocking the binding of BAD to Bcl-XL .
7	RSK1 phosphorylaTEs BAD at both Ser-112 and Ser-155 and rescues BAD -mediated cell death in a manner dependent upon PHOSphorylation at both sites .

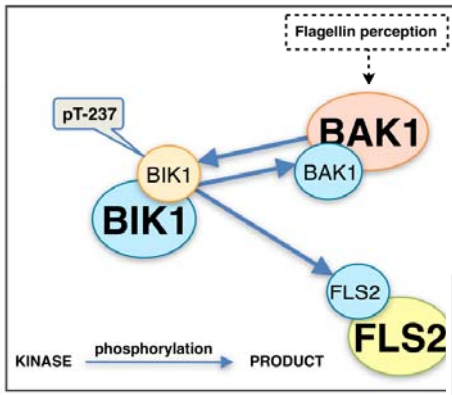


eFIP: a tool for mining functional impact of phosphorylation from literature
Arighi CN, Siu AY, Tudor CO, Nchoutmboube JA, Wu CH, Shanker VK. (2011)
Methods in Molecular Biology 694, 63-75 [PMID:21082428]

Discovery from Literature Mining

- iPTMnet: PTM network of enzyme-substrate relationships and protein-protein interactions mined from the scientific literature
- Distinct phosphorylated forms of a protein may have different interacting proteins, leading to different subcellular locations, functions and pathways

=> Knowledge captured in PRO



Sentence	Phosphorylation			Impact to protein-protein interactions	
	Substrate	Site	Kinase	How	What
5,6	cytoplasmic kinase BIK1	---	---	---	BIK1 associates with FLS2 and BAK1

Sentence	Phosphorylation			iTerms	
	Substrate	Site	Kinase	How	What
8	BIK1	The flagellin phosphorylaTION site Thr(237)	---	---	flagellin perception

Toggle highlights: Substrate Kinase Phosphorylation site Protein-protein interaction iTerm

ase , BIK1 , associates with a flagellin receptor complex to initiate

e immunity to prevent infections by detection of microbe-associated rough pattern-recognition receptors (PRRs) .

e-rich repeat receptor kinase , recognizes bacterial flagellin and ssociation with another leucine-rich repeat-receptor -like kinase ,

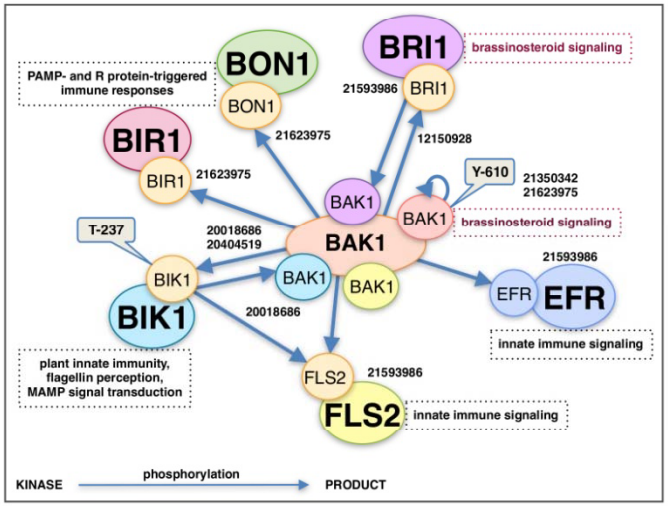
S2/BAK1 receptor complex activates intracellular signaling cascades

-like cytoplasmic kinase BIK1 that is rapidly PHOSphorylated upon n both FLS2 and BAK1 .

BAK1 in vivo and in vitro .

1 and BIK1 also directly PHOSphorylates BAK1 and FLS2 in vitro .

e Thr(237) of BIK1 is required for its phosphorylaTION on BAK1 and ely first phosphorylaTED upon flagellin perception and subsequently 1 to propagate flagellin signaling .



ABI Development: Integrative Bioinformatics for Knowledge Discovery of PTM Networks (http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=1062520)

User Annotation: RACE-PRO

Capture knowledge of protein forms/complexes of interest to support integrated analysis and computer-based reasoning

- Obtain a PRO ID for the protein objects of interest
- Define a protein object (based on literature, experimental data)
- Add annotation to that protein object
- How does it work?
  - Input your personal information (only for internal use)
  - Complete form with sequence information and annotation
  - Submit when ready (otherwise you can save for later)
  - PRO curation team will take the data, revise it, and create the corresponding PRO node in the ontology
  - User will be informed via email about the new PRO IDs and when they will be public

RACE-PRO Annotation Tool

PMID:18708362

Definition of the Protein Object

1. Enter a UniProtKB identifier (?) O75475-2 Retrieve
   OR, click here to insert a different sequence:

```
MTRDFKPGDL IFAKMKGYPH WPARVDEVPD GAVKPPTNKL PIFFFGTHET AFLGPKDIFP 60
YSENKEKYGK PNKRKGFNEG LWEIDNNPKV KFSSQQAATK QSNASSDVEV EEKETSVSKE 120
DTDHEEKASN EDVTKAVDIT TPKAARRGRK RKAEKQVETE EAGVVTTATA SVNLKVSPKR 180
GRPAATEVKI PKPRGRPKMV KQPCPSESDI ITEEDKSKKK GQEEKQPKKQ PKKDEEGQKE 240
EDKPRKEPDK KEGKKEVESK RKNLAKTGVT STSDSEEEGD DQEGEKKRKG GRNFQTAHRR 300
NMLKGQHEKE AADRKRKQEE QMETEHQTTC NLQ
```

Organism: HOMO SAPIENS

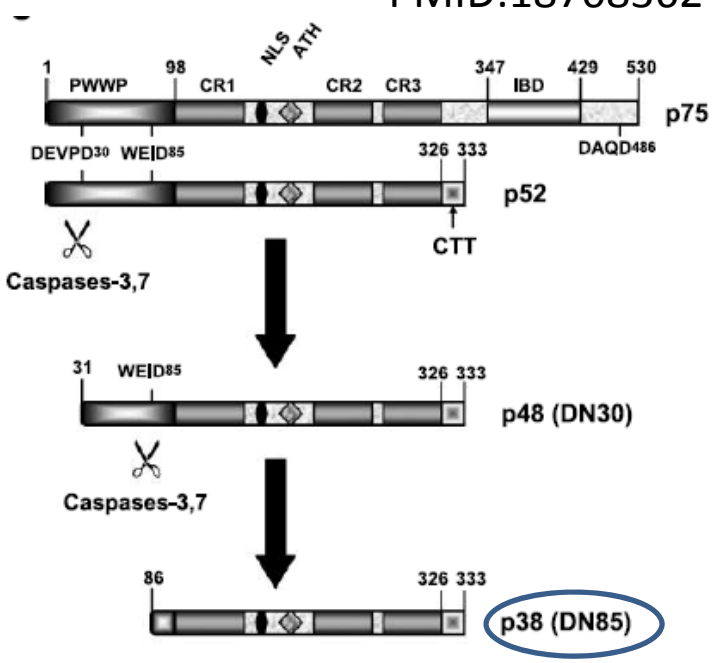
2. Specify sequence region
   ○ Full-length ◉ Region: from 86 to 333
3. Indicate post-translational modifications (add amino acid number re
   Amino acid number: --choose PTM--
4. Protein Object name (separate multiple names using ";")
   LEDGF/p38; DN85
5. Evidence Source (separate multiple IDs using
   Db name: PubMed IDs: 18708362

A-Enter accession or paste sequence

B-Define protein region and/or PTMs

C-Enter protein form name

D- Data source



Annotation of the Protein Object

Domain [more] [less] Link to PFAM

Modifier	Relation	Pfam ID	Pfam name	PMIDs
NOT	has_part	PF00855	PWWP domain	18708362

Functional Annotation [more] [less] Link to GO

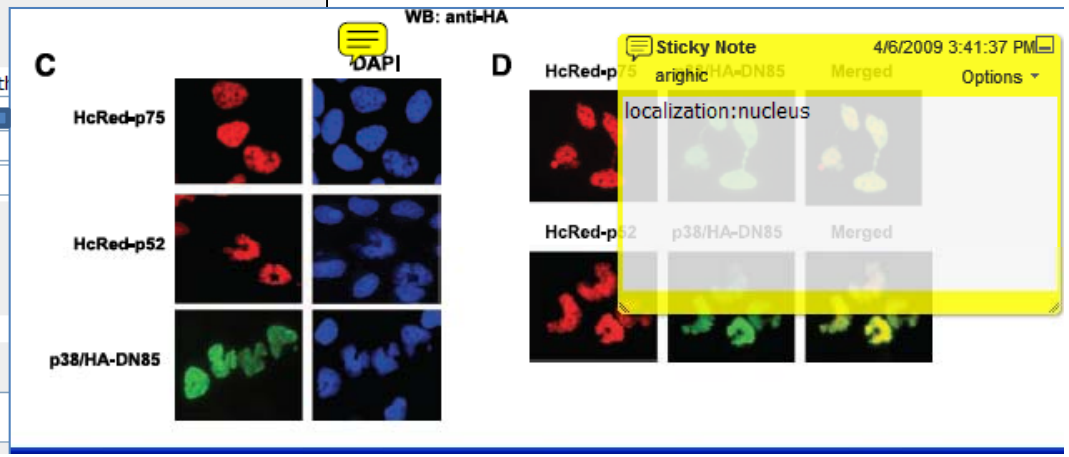
Modifier	Relation	GO ID	GO term	Interaction wit
	located_in	GO:00056	nucleus	
	participates_in	GO:00164	negative regulation of tra	

Sequence Ontology [add] Link to SO

Disease [add] Link to MIM

E- Annotation

Comments:



PRO Dissemination

- PRO Website (http://www.proconsortium.org)
  - Searching, browsing, downloading
- PRO Views
  - Entry view
  - Table summary
  - OBO stanza, OWL
  - Ontology hierarchy
  - Cytoscape network
- PRO Link: Persistent URL: http://purl.obolibrary.org/obo/PR_xxxxxxxxx
- OBO Foundry (http://www.obofoundry.org/)
- NCBO Bioportal (http://bioportal.bioontology.org/)

PRO Communities

- Ontology Developers
  - GO ontology: Interfaces of GO/PRO complexes; GO definition (e.g., GO:0005109)
  - GO annotation: precise annotation of protein forms in PomBase
  - Dendritic Cell Ontology: Define cell types based on +/- protein types [PMID:19243617]
  - Annotation Ontology for annotating scientific documents on the web [PMID:21624159]
  - Brucellosis Ontology (IDOBRU), extension of the Infectious Disease Ontology (IDO) [PMID:22041276]
- Semantic Resources
  - Royal Society of Chemistry (RSC); Science Collaboration Framework; Semantic Web Applications in Neuromedicine (SWAN); Neuroscience Information Framework (NIF)
- Pathway/Process-Modeling Resources:
  - Reactome, MouseCyc, EcoCyc/BioCyc, Center for Molecular Immunology (Duke)
- Molecule-Modeling Resources: Int'l Union of Basic and Clinical Pharmacology (IUPhar)
- Pharma/Clinical Communities: Drug Discovery & Disease Biomarker
  - Alzforum
  - Salivaomics KB/SALO (Saliva Ontology): Saliva Biomarkers
  - Pistoia

PRO Consortium Team *(current)*

Protein Information Resource (PIR) [Georgetown U & U Delaware]

Cathy Wu, Cecilia Arighi, Darren Natale, Natalia Roberts
Hongzhan Huang, Jian Zhang

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NYU School of Medicine – Reactome

Peter D'Eustachio, Michael Caudy

AlzForum

Elizabeth Wu

New Consortium Member Welcome!

National Institute of General Medical Sciences

1R01GM080646-01
3R01GM080646-04S2
2R01GM080646-06

PRO: A Protein Ontology in OBO Foundry for Integration of Biomedical Knowledge
(http://projectreporter.nih.gov/project_info_description.cfm?aid=8187900&icde=10696318)