

# SBGN AF update

Huaiyu Mi

For the SBGN Team

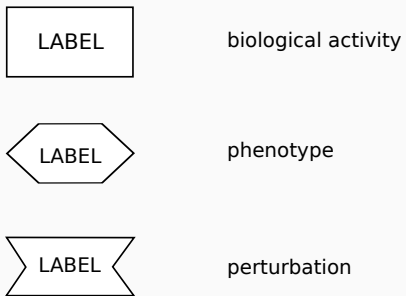
University of Southern California

School of Medicine

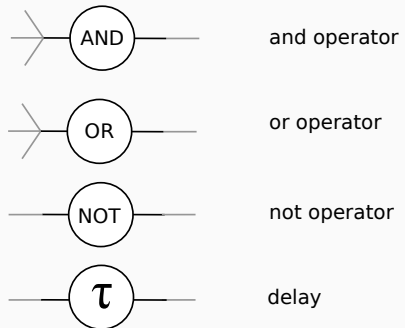
# SBGN-AF reference card

## SYSTEMS BIOLOGY GRAPHICAL NOTATION ACTIVITY FLOW DIAGRAM REFERENCE CARD

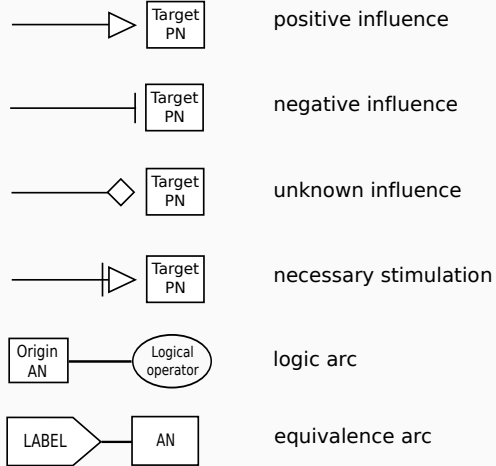
### Activity Nodes



### Logical Operators

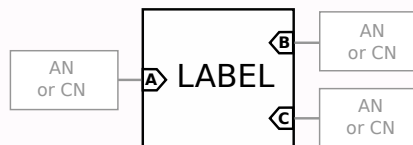


### Modulating Arcs

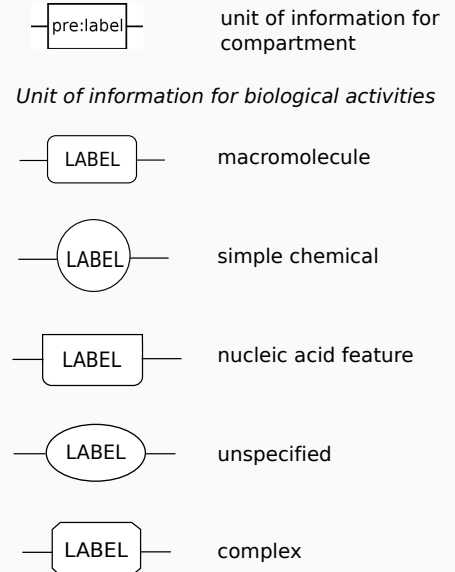


### Reference Node

#### Submap



### Auxiliary Units

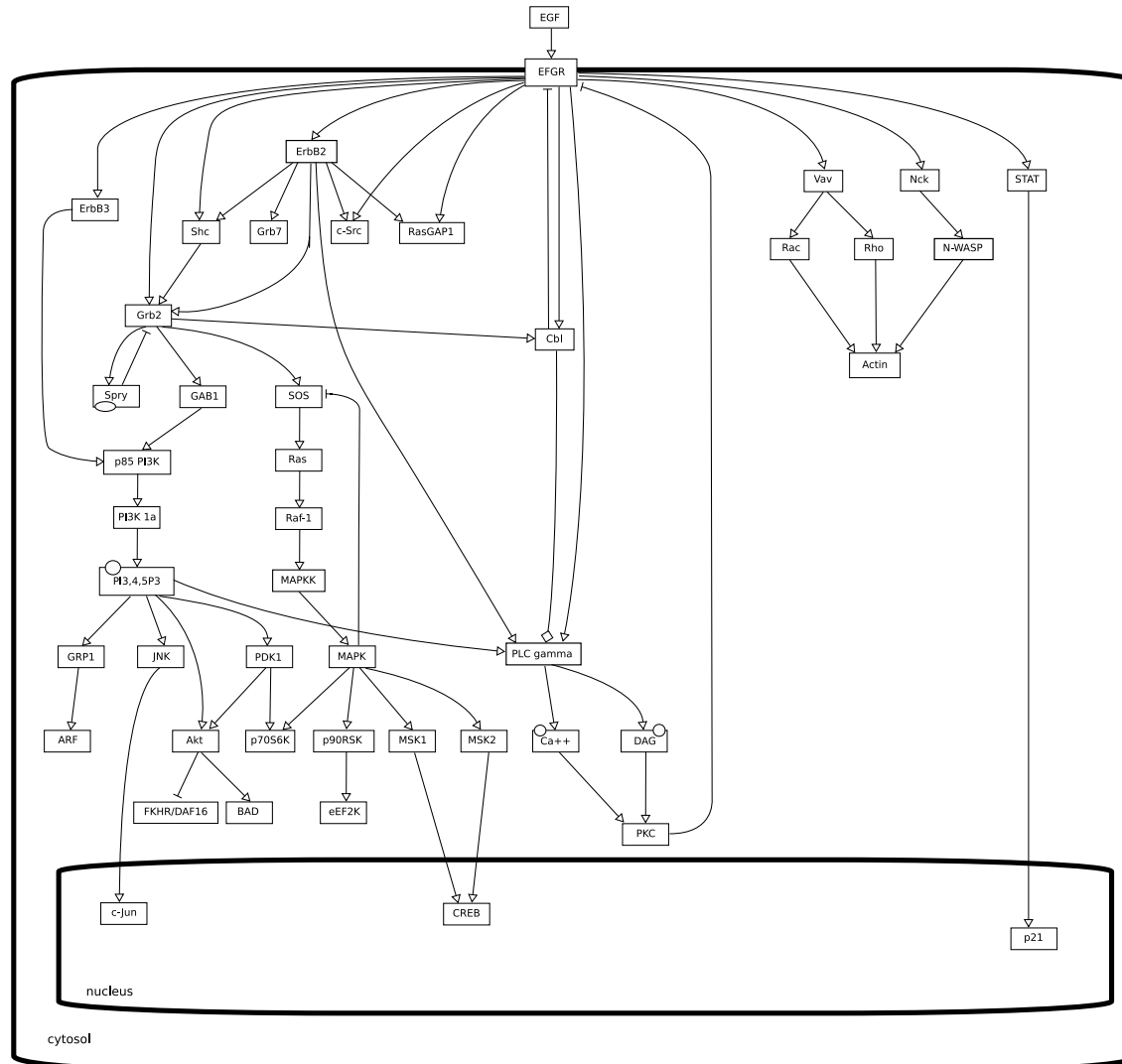


### Container Nodes



# Example

## -EGF receptor signaling pathway



# SBGN-AF specification

- Level 1 Release 1.0 was released in Sept. 2009
- Level 1 Release 1.1 was released in April 2011

# **CURRENT ISSUES**

# Perturbation and Phenotype

PD

AF



perturbing agent  
(EPN)

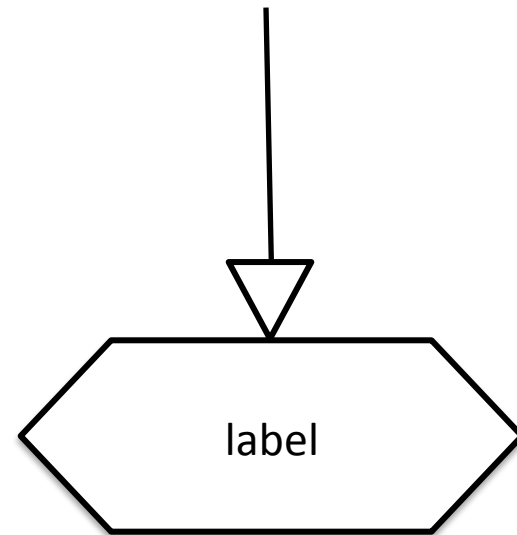
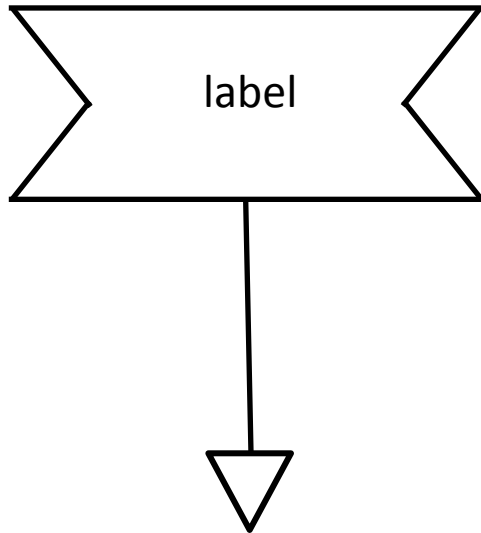
perturbation  
(AN)



phenotype  
(PN)

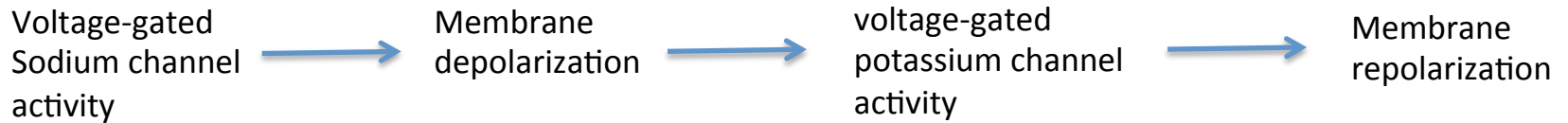
phenotype  
(AN)

# Perturbation and Phenotype



# Problem

How to represent the following sequence of events?





# Solution for *perturbation*

Remove *perturbation* as an activity node. Instead, use it as a decoration of an activity node.



Online vote results:

Agree: 5

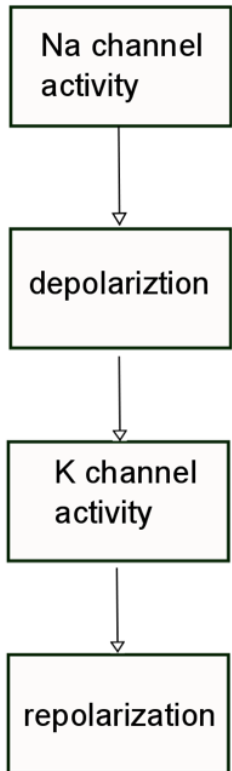
Disagree: 2

# Proposals for *phenotype*

1. Remove *phenotype* glyph, and use *activity node* to represent it.

# Proposals for *phenotype*

Prop 1

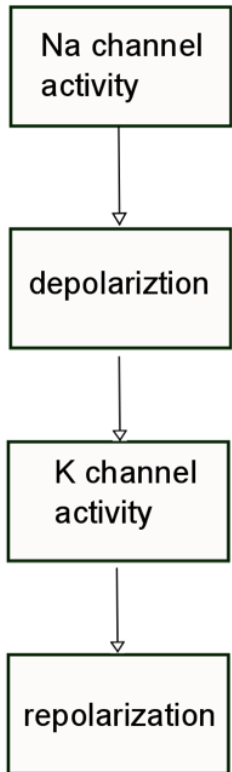


# Proposals for *phenotype*

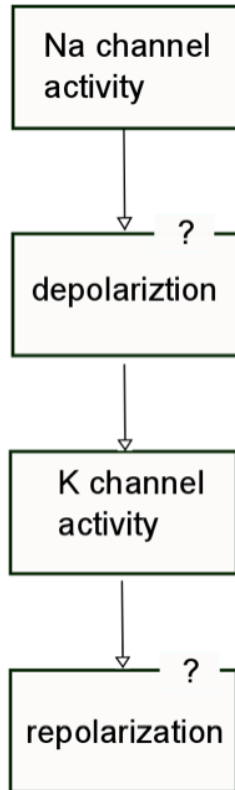
1. Remove *phenotype* glyph, and use *activity node* to represent it.
2. Remove *phenotype* glyph, use *activity node* with a specific decoration that reflects the fact that it can be observed.

# Proposals for *phenotype*

Prop 1



2

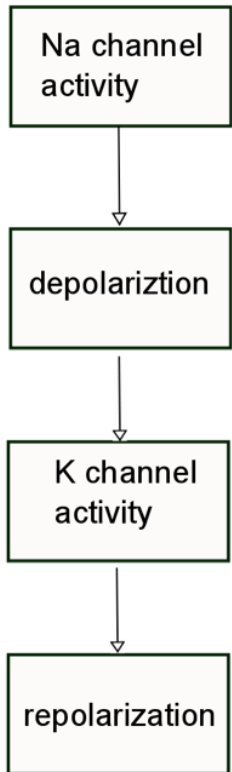


# Proposals for *phenotype*

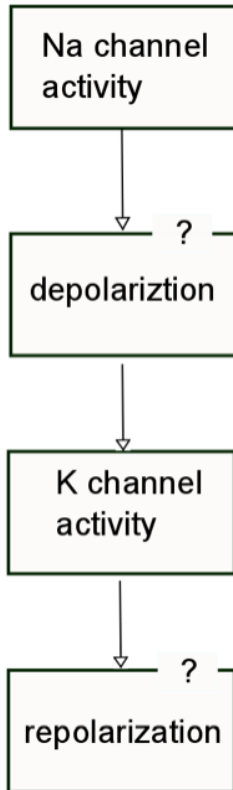
1. Remove *phenotype* glyph, and use *activity node* to represent it.
2. Remove *phenotype* glyph, use *activity node* with a specific decoration that reflects the fact that it can be observed.
3. Remove *phenotype* glyph, use *activity node* with a *phenotype* glyph as a decoration.

# Proposals for *phenotype*

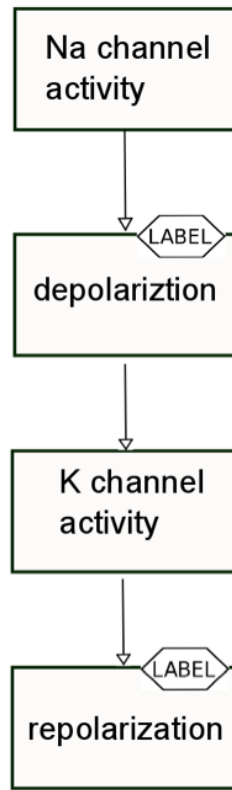
Prop 1



2



3



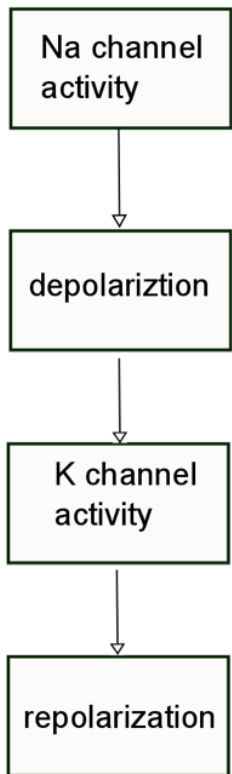
# Proposals for *phenotype*

1. Remove *phenotype* glyph, and use *activity node* to represent it.
2. Remove *phenotype* glyph, use *activity node* with a specific decoration that reflects the fact that it can be observed.
3. Remove *phenotype* glyph, use *activity node* with a *phenotype* glyph as a decoration.
4. Keep *phenotype* glyph, and it can only be the output of an influence arc, but design a new influence arc such as “causation”.

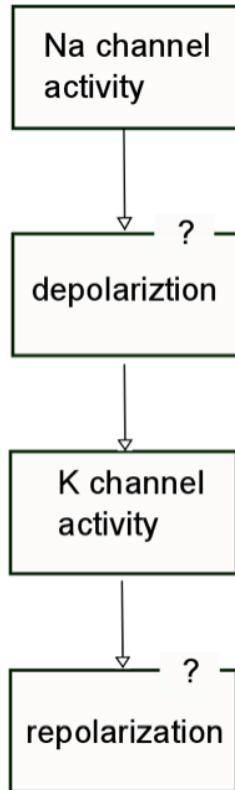


# Proposals for *phenotype*

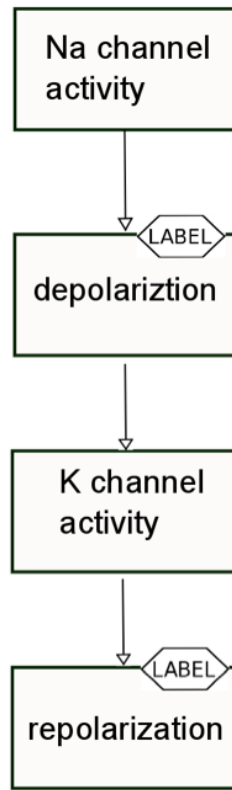
Prop 1



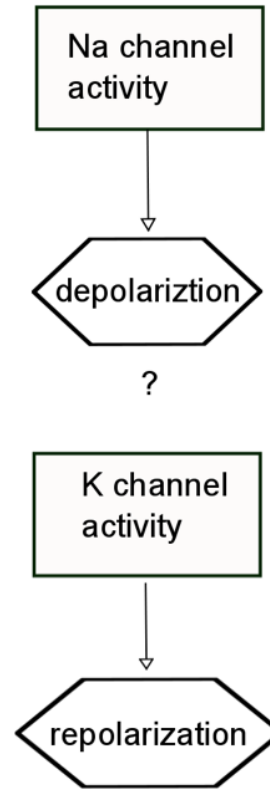
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3



4

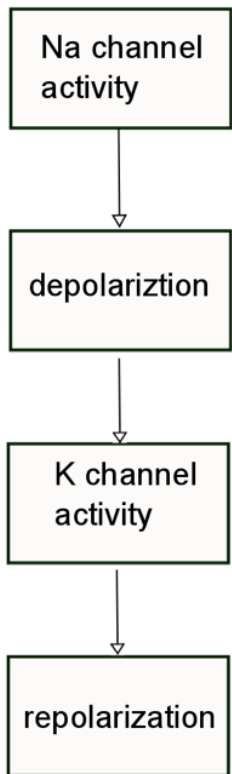


# Proposals for *phenotype*

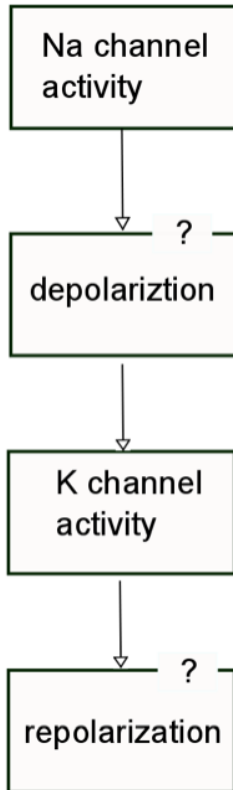
1. Remove *phenotype* glyph, and use *activity node* to represent it.
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4. Keep *phenotype* glyph, and it can only be the output of an influence arc, but design a new influence arc such as “causation”.
5. Allow *phenotype* glyph to be both input and output of influence arcs.

# Proposals for *phenotype*

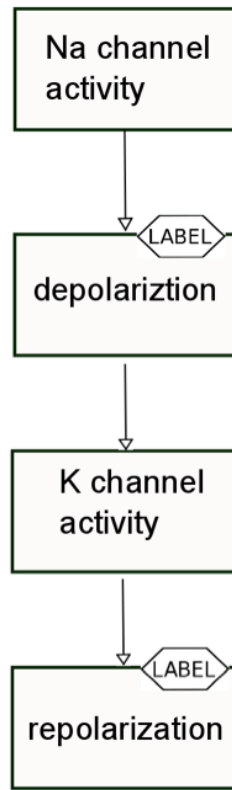
Prop 1



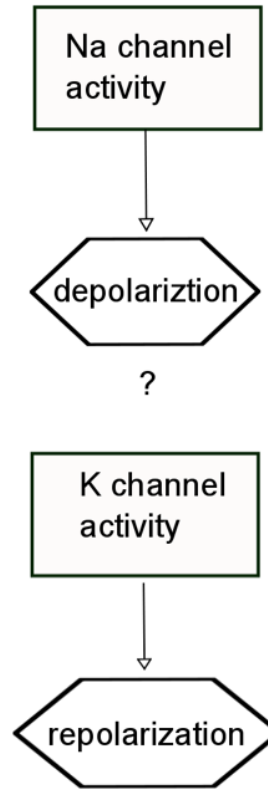
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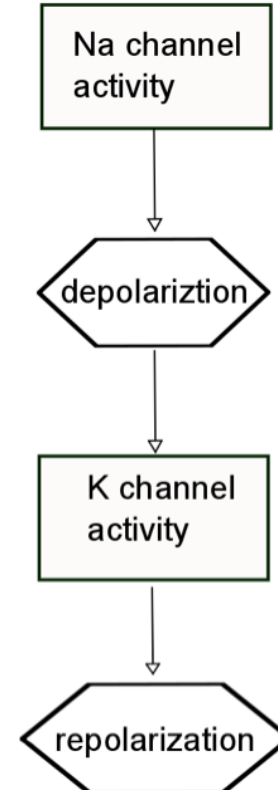
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4



5

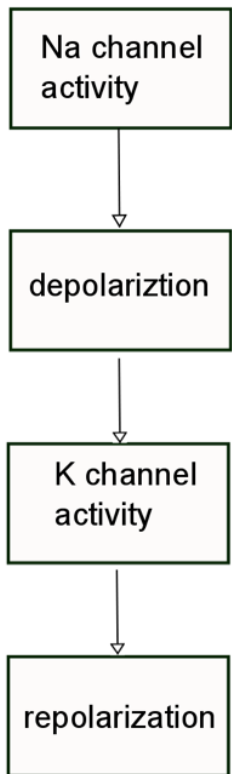


# Proposals for *phenotype*

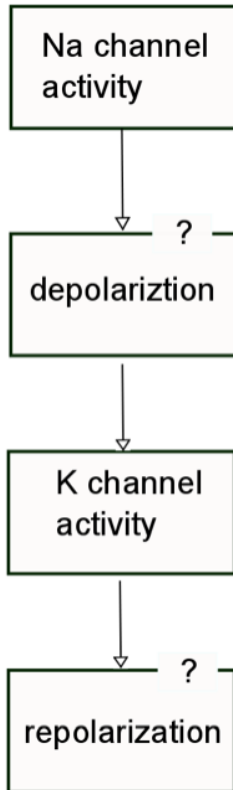
1. Remove *phenotype* glyph, and use *activity node* to represent it.
2. Remove *phenotype* glyph, use *activity node* with a specific decoration that reflects the fact that it can be observed.
3. Remove *phenotype* glyph, use *activity node* with a *phenotype* glyph as a decoration.
4. Keep *phenotype* glyph, and it can only be the output of an influence arc, but design a new influence arc such as “causation”.
5. Allow *phenotype* glyph to be both input and output of influence arcs.
6. Keep the current spec, i.e., *phenotype* glyph can only be the output of an arc.

# Proposals for *phenotype*

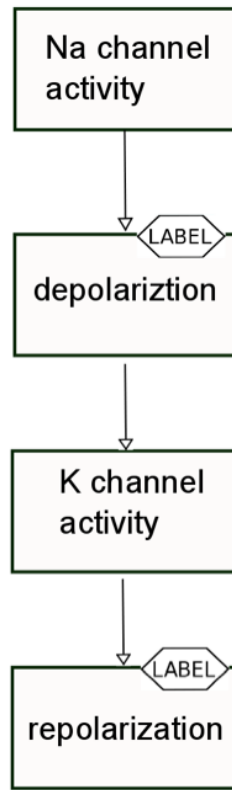
Prop 1



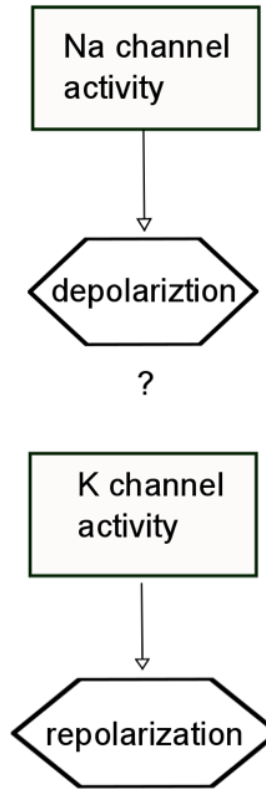
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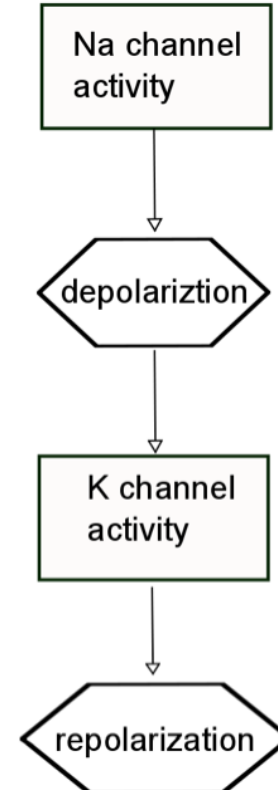
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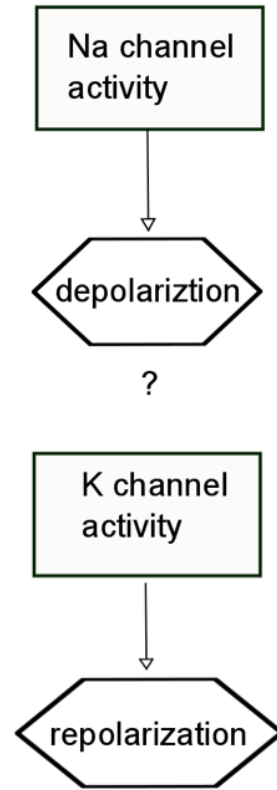
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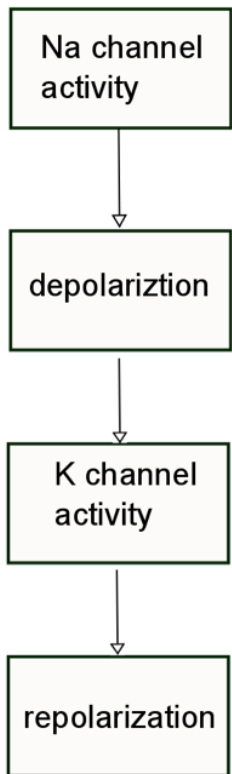


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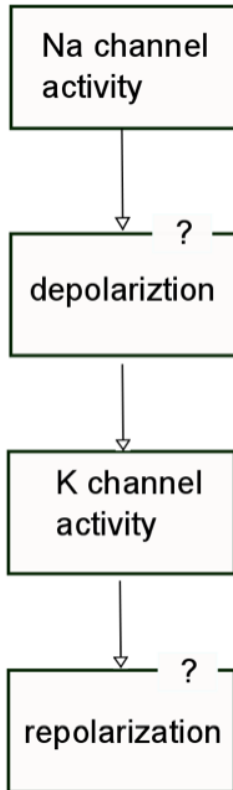


# Proposals for *phenotype*

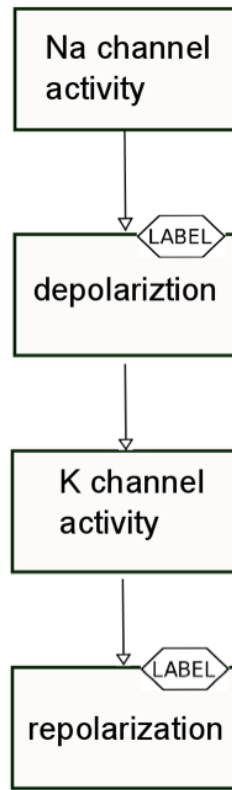
Prop 1



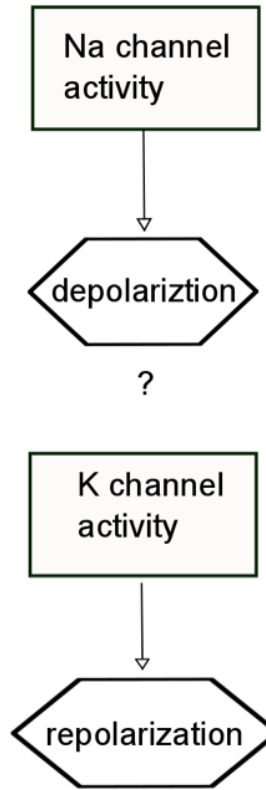
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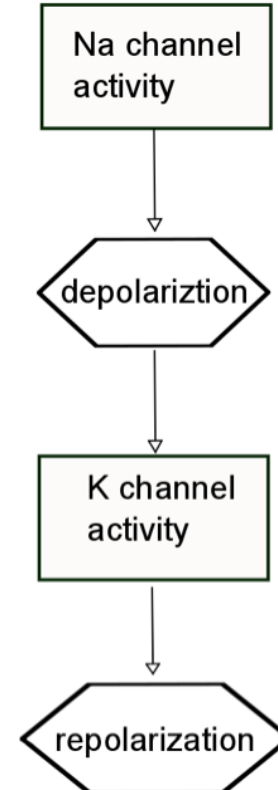
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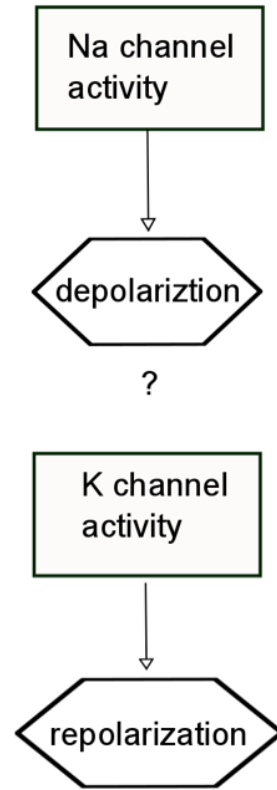
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5



6



Vote 1

1

3

2

**POSSIBLE SUPPORT TO GO  
CURATION**

# EFEMP1-EGF-containing fibulin-like extracellular matrix protein 1

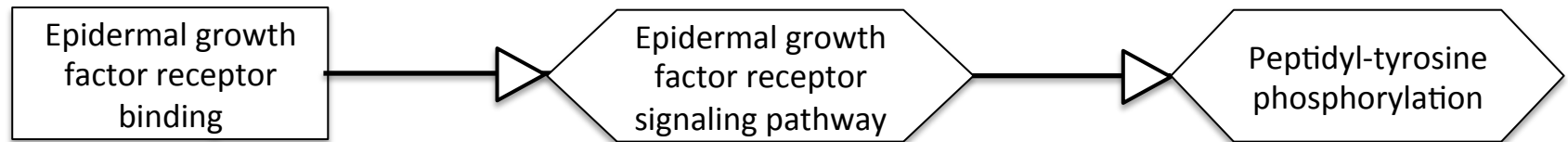
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Process				
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<a href="#">GO:0007173</a>	epidermal growth factor receptor signaling pathway	P	IDA	PMID:19804359
<a href="#">GO:0007601</a>	visual perception	P	TAS	PMID:10369267
<a href="#">GO:0018108</a>	peptidyl-tyrosine phosphorylation	P	IDA	PMID:19804359
<a href="#">GO:0032331</a>	negative regulation of chondrocyte differentiation	P	IDA	PMID:20005202
Function				
<a href="#">GO:0005006</a>	epidermal growth factor-activated receptor activity	F	IDA	PMID:19804359
<a href="#">GO:0005154</a>	epidermal growth factor receptor binding	F	IDA	PMID:19804359
<a href="#">GO:0005509</a>	calcium ion binding	F	IEA	InterPro2GO
<a href="#">GO:0005509</a>	calcium ion binding	F	IEA	InterPro2GO
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:12620389
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:16713569
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:19275936
<a href="#">GO:0008083</a>	growth factor activity	F	IEA	Swiss-Prot Keywords2GO



# EFEMP1-EGF-containing fibulin-like extracellular matrix protein 1

GO Identifier	GO Term Name	Aspect Evidence Reference		
Process				
<a href="#">GO:0006355</a>	regulation of transcription, DNA-dependent	P	IDA	PMID:20005202
<a href="#">GO:0007172</a>	epidermal growth factor receptor signaling pathway	P	IDA	PMID:19804359
<a href="#">GO:0007601</a>	visual perception	P	TAS	PMID:10369267
<a href="#">GO:0018106</a>	peptidyl-tyrosine phosphorylation	P	IDA	PMID:19804359
<a href="#">GO:0032331</a>	negative regulation of chondrocyte differentiation	P	IDA	PMID:20005202
Function				
<a href="#">GO:0005006</a>	epidermal growth factor-activated receptor activity	F	IDA	PMID:19804359
<a href="#">GO:0005154</a>	epidermal growth factor receptor binding	F	IDA	PMID:19804359
<a href="#">GO:0005509</a>	calcium ion binding	F	IEA	InterPro2GO
<a href="#">GO:0005509</a>	calcium ion binding	F	IEA	InterPro2GO
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:12620389
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:16713569
<a href="#">GO:0005515</a>	protein binding	F	IPI	PMID:19275936
<a href="#">GO:0008083</a>	growth factor activity	F	IEA	Swiss-Prot Keywords2GO

# EFEMP1-EGF-containing fibulin-like extracellular matrix protein 1



# NEDD4

Fuction	Function		
<a href="#">GO:0004842</a> ubiquitin-protein ligase activity	F	IEA	Compara
<a href="#">GO:0004842</a> ubiquitin-protein ligase activity	F	IDA	PMID:17996703
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:10642508
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:10642508
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:10642508
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:12796489
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:19345329
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<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:20562859
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<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:9305852
<a href="#">GO:0005515</a> protein binding	F	IPI	PMID:9990509
<a href="#">GO:0016874</a> ligase activity	F	IEA	Swiss-Prot Keywords2GO
<a href="#">GO:0016881</a> acid-amino acid ligase activity	F	IEA	InterPro2GO
<a href="#">GO:0019871</a> sodium channel inhibitor activity	F	IEA	Compara
<a href="#">GO:0019871</a> sodium channel inhibitor activity	F	IDA	PMID:10642508
<a href="#">GO:0019904</a> protein domain specific binding	F	IPI	PMID:12907594
<a href="#">GO:0031698</a> beta-2 adrenergic receptor binding	F	IDA	PMID:18544533
<a href="#">GO:0043130</a> ubiquitin binding	F	IDA	PMID:9990509
<a href="#">GO:0050815</a> phosphoserine binding	F	IEA	Compara
<a href="#">GO:0050815</a> phosphoserine binding	F	ISS	GO_REF:0000024
<a href="#">GO:0050816</a> phosphothreonine binding	F	IEA	Compara
<a href="#">GO:0050816</a> phosphothreonine binding	F	ISS	GO_REF:0000024
<a href="#">GO:0070063</a> RNA polymerase binding	F	IPI	PMID:17996703
<a href="#">GO:0070064</a> proline-rich region binding	F	IEA	Compara
<a href="#">GO:0070064</a> proline-rich region binding	F	IPI	PMID:11342538
<a href="#">GO:0070064</a> proline-rich region binding	F	IMP	PMID:15126635

# NEDD4

Fuction	Process
<a href="#">GO:0004842</a> ubiquitin-protein ligase activity	<a href="#">GO:0006464</a> protein modification process P IEA InterPro2GO
<a href="#">GO:0004842</a> ubiquitin-protein ligase activity	<a href="#">GO:0006622</a> protein targeting to lysosome P IDA PMID:17116753
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0007041</a> lysosomal transport P IDA PMID:18544533
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0007399</a> nervous system development P IEA Swiss-Prot Keywords2GO
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0010766</a> negative regulation of sodium ion transport P IEA Compara
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0010766</a> negative regulation of sodium ion transport P IDA PMID:10642508
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0010768</a> negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage P IMP PMID:17996703
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0014068</a> positive regulation of phosphatidylinositol 3-kinase cascade P IMP PMID:17218260
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0016567</a> protein ubiquitination P IEA Compara
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0016567</a> protein ubiquitination P IDA PMID:17996703
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0019089</a> transmission of virus P IMP PMID:15126635
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0030948</a> negative regulation of vascular endothelial growth factor receptor signaling pathway P IEA Compara
<a href="#">GO:0005515</a> protein binding	<a href="#">GO:0030948</a> negative regulation of vascular endothelial growth factor receptor signaling pathway P ISS GO_REF:0000024
<a href="#">GO:0016874</a> ligase activity	<a href="#">GO:0031175</a> neuron projection development P IEP PMID:9990509
<a href="#">GO:0016881</a> acid-amino acid ligase activity	<a href="#">GO:0031623</a> receptor internalization P IDA PMID:18544533
<a href="#">GO:0019871</a> sodium channel inhibitor activity	<a href="#">GO:0032801</a> receptor catabolic process P IDA PMID:18544533
<a href="#">GO:0019871</a> sodium channel inhibitor activity	<a href="#">GO:0034644</a> cellular response to UV P IMP PMID:17996703
<a href="#">GO:0019904</a> protein domain specific binding	<a href="#">GO:0042787</a> protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17218260
<a href="#">GO:0031698</a> beta-2 adrenergic receptor binding	<a href="#">GO:0042787</a> protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17996703
<a href="#">GO:0043130</a> ubiquitin binding	<a href="#">GO:0042921</a> glucocorticoid receptor signaling pathway P IDA PMID:8649367
<a href="#">GO:0050815</a> phosphoserine binding	<a href="#">GO:0044111</a> development involved in symbiotic interaction P IMP PMID:15126635
<a href="#">GO:0050815</a> phosphoserine binding	<a href="#">GO:0044419</a> interspecies interaction between organisms P IEA Swiss-Prot Keywords2GO
<a href="#">GO:0050816</a> phosphothreonine binding	<a href="#">GO:0045732</a> positive regulation of protein catabolic process P IEA Compara
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<a href="#">GO:0070063</a> RNA polymerase binding	<a href="#">GO:0046824</a> positive regulation of nucleocytoplasmic transport P IDA PMID:17218261
<a href="#">GO:0070064</a> proline-rich region binding	<a href="#">GO:0048814</a> regulation of dendrite morphogenesis P IEA Compara
<a href="#">GO:0070064</a> proline-rich region binding	<a href="#">GO:0048814</a> regulation of dendrite morphogenesis P ISS GO_REF:0000024
<a href="#">GO:0070064</a> proline-rich region binding	<a href="#">GO:0050847</a> progesterone receptor signaling pathway P IDA PMID:8649367
	<a href="#">GO:0051592</a> response to calcium ion P TAS PMID:9405440
	<a href="#">GO:0070534</a> protein K63-linked ubiquitination P ISS GO_REF:0000024

Function



# NEDD4

Fuction	Process
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process P IEA InterPro2GO
GO:0004842 ubiquitin-protein ligase activity	GO:0006622 protein targeting to lysosome P IDA PMID:17116753
GO:0005515 protein binding	GO:0007041 lysosomal transport P IDA PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development P IEA Swiss-Prot Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IEA Compara
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IDA PMID:10642508
GO:0005515 protein binding	GO:0010768 negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage P IMP PMID:17996703
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade P IMP PMID:17218260
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IEA Compara
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IDA PMID:17996703
GO:0005515 protein binding	GO:0019089 transmission of virus P IMP PMID:15126635
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P IEA Compara
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P ISS GO_REF:0000024
GO:0016874 ligase activity	GO:0031175 neuron projection development P IEP PMID:9990509
GO:0016881 acid-amino acid ligase activity	GO:0031623 receptor internalization P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0032801 receptor catabolic process P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0034644 cellular response to UV P IMP PMID:17996703
GO:0019904 protein domain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17218260
GO:0031698 beta-2 adrenergic receptor binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17996703
GO:0043130 ubiquitin binding	GO:0042921 glucocorticoid receptor signaling pathway P IDA PMID:8649367
GO:0050815 phosphoserine binding	GO:0044111 development involved in symbiotic interaction P IMP PMID:15126635
GO:0050815 phosphoserine binding	GO:0044419 interspecies interaction between organisms P IEA Swiss-Prot Keywords2GO
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IEA Compara
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IDA PMID:14973438
GO:0070063 RNA polymerase binding	GO:0046824 positive regulation of nucleocytoplasmic transport P IDA PMID:17218261
GO:0070064 proline-rich region binding	GO:0048814 regulation of dendrite morphogenesis P IEA Compara
GO:0070064 proline-rich region binding	GO:0048814 regulation of dendrite morphogenesis P ISS GO_REF:0000024
GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway P IDA PMID:8649367
	GO:0051592 response to calcium ion P TAS PMID:9405440
	GO:0070534 protein K63-linked ubiquitination P ISS GO_REF:0000024
	Function

# NEDD4

Fuction	Process
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process P IEA InterPro2GO
GO:0004842 ubiquitin-protein ligase activity	GO:0006622 protein targeting to lysosome P IDA PMID:17116753
GO:0005515 protein binding	GO:0007041 lysosomal transport P IDA PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development P IEA Swiss-Prot Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IEA Compara
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IDA PMID:10642508
GO:0005515 protein binding	GO:0010768 negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage P IMP PMID:17996703
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade P IMP PMID:17218260
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IEA Compara
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IDA PMID:17996703
GO:0005515 protein binding	GO:0019089 transmission of virus P IMP PMID:15126635
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P IEA Compara
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P ISS GO_REF:0000024
GO:0016874 ligase activity	GO:0031175 neuron projection development P IEP PMID:9990509
GO:0016881 acid-amino acid ligase activity	GO:0031623 receptor internalization P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0032001 receptor catabolic process P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0034644 cellular response to UV P IMP PMID:17996703
GO:0019904 protein domain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17218260
GO:0031698 beta-2 adrenergic receptor binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17996703
GO:0043130 ubiquitin binding	GO:0042921 glucocorticoid receptor signaling pathway P IDA PMID:8649367
GO:0050815 phosphoserine binding	GO:0044111 development involved in symbiotic interaction P IMP PMID:15126635
GO:0050815 phosphoserine binding	GO:0044419 interspecies interaction between organisms P IEA Swiss-Prot Keywords2GO
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IEA Compara
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IDA PMID:14973438
GO:0070063 RNA polymerase binding	GO:0046824 positive regulation of nucleocytoplasmic transport P IDA PMID:17218261
GO:0070064 proline-rich region binding	GO:0048814 regulation of dendrite morphogenesis P IEA Compara
GO:0070064 proline-rich region binding	GO:0048814 regulation of dendrite morphogenesis P ISS GO_REF:0000024
GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway P IDA PMID:8649367
	GO:0051592 response to calcium ion P TAS PMID:9405440
	GO:0070534 protein K63-linked ubiquitination P ISS GO_REF:0000024
	Function



# NEDD4

Fuction		Process			
GO:0004842	ubiquitin-protein ligase activity	GO:0006464	protein modification process	P	IEA InterPro2GO
GO:0004842	ubiquitin-protein ligase activity	GO:0006622	protein targeting to lysosome	P	IDA PMID:17116753
GO:0005515	protein binding	GO:0007041	lysosomal transport	P	IDA PMID:18544533
GO:0005515	protein binding	GO:0007399	nervous system development	P	IEA Swiss-Prot Keywords2GO
GO:0005515	protein binding	GO:0010766	negative regulation of sodium ion transport	P	IEA Compara
GO:0005515	protein binding	GO:0010766	negative regulation of sodium ion transport	P	IDA PMID:10642508
GO:0005515	protein binding	GO:0010768	negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage	P	IMP PMID:17996703
GO:0005515	protein binding	GO:0014068	positive regulation of phosphatidylinositol 3-kinase cascade	P	IMP PMID:17218260
GO:0005515	protein binding	GO:0016567	protein ubiquitination	P	IEA Compara
GO:0005515	protein binding	GO:0016567	protein ubiquitination	P	IDA PMID:17996703
GO:0005515	protein binding	GO:0019089	transmission of virus	P	IMP PMID:15126635
GO:0005515	protein binding	GO:0030948	negative regulation of vascular endothelial growth factor receptor signaling pathway	P	IEA Compara
GO:0005515	protein binding	GO:0030948	negative regulation of vascular endothelial growth factor receptor signaling pathway	P	ISS GO_REF:0000024
GO:0016874	ligase activity	GO:0031175	neuron projection development	P	IEP PMID:9990509
GO:0016881	acid-amino acid ligase activity	GO:0031623	receptor internalization	P	IDA PMID:18544533
GO:0019871	sodium channel inhibitor activity	GO:0032001	receptor catabolic process	P	IDA PMID:18544533
GO:0019871	sodium channel inhibitor activity	GO:0034644	cellular response to UV	P	IMP PMID:17996703
GO:0019904	protein domain specific binding	GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	P	IMP PMID:17218260
GO:0031698	beta-2 adrenergic receptor binding	GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	P	IMP PMID:17996703
GO:0043130	ubiquitin binding	GO:0042921	glucocorticoid receptor signaling pathway	P	IDA PMID:8649367
GO:0050815	phosphoserine binding	GO:0044111	development involved in symbiotic interaction	P	IMP PMID:15126635
GO:0050815	phosphoserine binding	GO:0044419	interspecies interaction between organisms	P	IEA Swiss-Prot Keywords2GO
GO:0050816	phosphothreonine binding	GO:0045732	positive regulation of protein catabolic process	P	IEA Compara
GO:0050816	phosphothreonine binding	GO:0045732	positive regulation of protein catabolic process	P	IDA PMID:14973438
GO:0070063	RNA polymerase binding	GO:0046824	positive regulation of nucleocytoplasmic transport	P	IDA PMID:17218261
GO:0070064	proline-rich region binding	GO:0048814	regulation of dendrite morphogenesis	P	IEA Compara
GO:0070064	proline-rich region binding	GO:0048814	regulation of dendrite morphogenesis	P	ISS GO_REF:0000024
GO:0070064	proline-rich region binding	GO:0050847	progesterone receptor signaling pathway	P	IDA PMID:8649367
		GO:0051592	response to calcium ion	P	TAS PMID:9405440
		GO:0070634	protein K63-linked ubiquitination	P	ISS GO_REF:0000024

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Fuction	Process
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process P IEA InterPro2GO
GO:0004842 ubiquitin-protein ligase activity	GO:0006622 protein targeting to lysosome P IDA PMID:17116753
GO:0005515 protein binding	GO:0007041 lysosomal transport P IDA PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development P IEA Swiss-Prot Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IEA Compara
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport P IDA PMID:10642508
GO:0005515 protein binding	GO:0010768 negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage P IMP PMID:17996703
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade P IMP PMID:17218260
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IEA Compara
GO:0005515 protein binding	GO:0016567 protein ubiquitination P IDA PMID:17996703
GO:0005515 protein binding	GO:0019089 transmission of virus P IMP PMID:15126635
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P IEA Compara
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor receptor signaling pathway P ISS GO_REF:0000024
GO:0016874 ligase activity	GO:0031175 neuron projection development P IEP PMID:9990509
GO:0016881 acid-amino acid ligase activity	GO:0031623 receptor internalization P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0032001 receptor catabolic process P IDA PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0034644 cellular response to UV P IMP PMID:17996703
GO:0019904 protein domain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17218260
GO:0031698 beta-2 adrenergic receptor binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process P IMP PMID:17996703
GO:0043130 ubiquitin binding	GO:0042921 glucocorticoid receptor signaling pathway P IDA PMID:8649367
GO:0050815 phosphoserine binding	GO:0044111 development involved in symbiotic interaction P IMP PMID:15126635
GO:0050815 phosphoserine binding	GO:0044419 interspecies interaction between organisms P IEA Swiss-Prot Keywords2GO
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IEA Compara
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process P IDA PMID:14973438
GO:0070064 RNA polymerase binding	GO:0046824 positive regulation of nucleocytoplasmic transport P IDA PMID:17218261
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GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway P IDA PMID:8649367
	GO:0051592 response to calcium ion P TAS PMID:9405440
	GO:0070634 protein K63-linked ubiquitination P ISS GO_REF:0000024



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# Acknowledgements

- The entire SBGN community