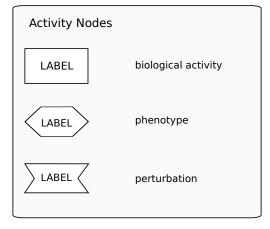
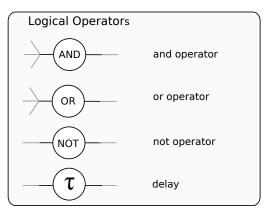
#### SBGN AF update

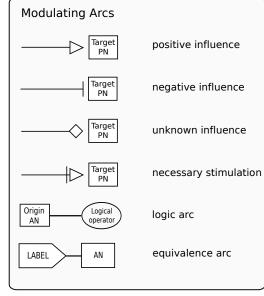
Huaiyu Mi
For the SBGN Team
University of Southern California
School of Medicine

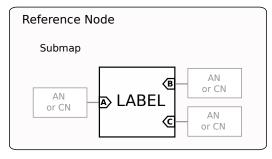
#### SBGN-AF reference card

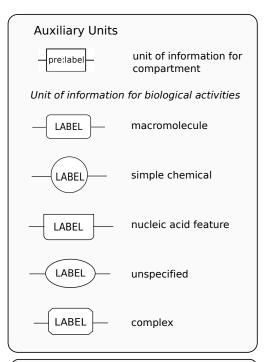
#### SYSTEMS BIOLOGY GRAPHICAL NOTATION ACTIVITY FLOW DIAGRAM REFERENCE CARD

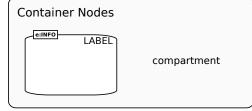






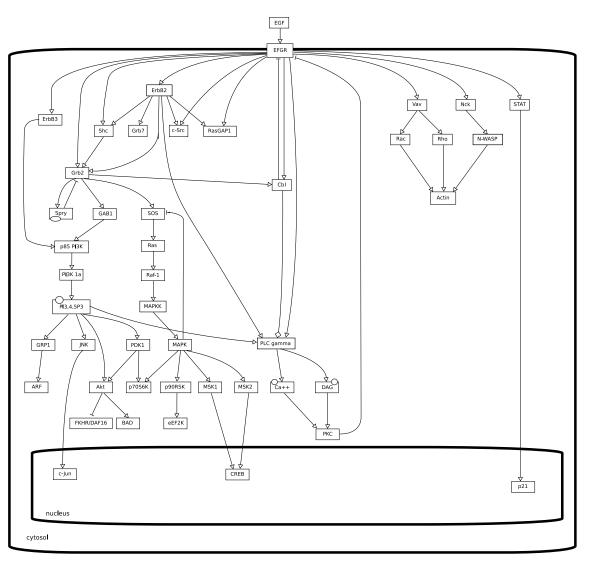






#### Example

#### -EGF receptor signaling pathway



#### SBGN-AF specification

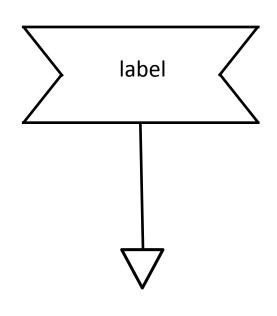
- Level 1 Release 1.0 was released in Sept. 2009
- Level 1 Release 1.1 was released in April 2011

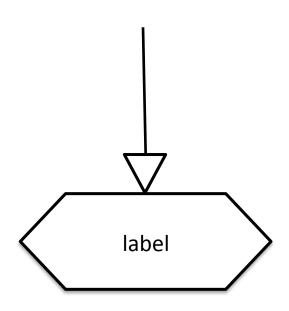
#### **CURRENT ISSUES**

#### Perturbation and Phenotype

PD AF perturbing agent perturbation (EPN) (AN) phenotype phenotype (PN) (AN)

### Perturbation and Phenotype





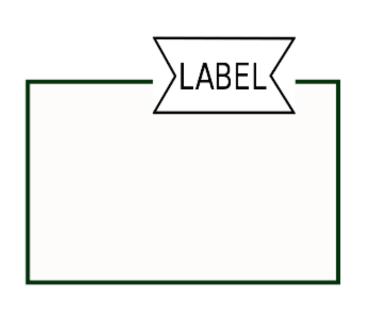
#### Problem

How to represent the following sequence of events?

Voltage-gated Membrane voltage-gated potassium channel activity Amembrane voltage-gated potassium channel repolarization

#### Solution for *perturbation*

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

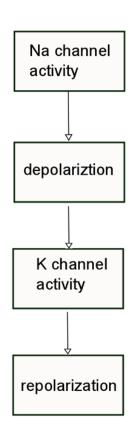


Online vote results:

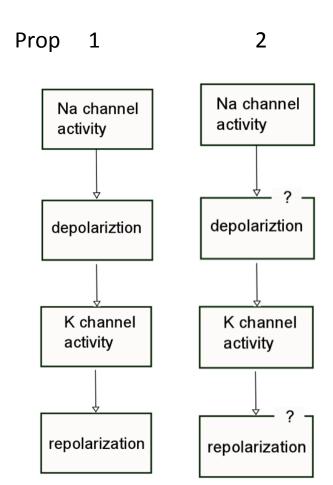
Agree: 5 Disagre: 2

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

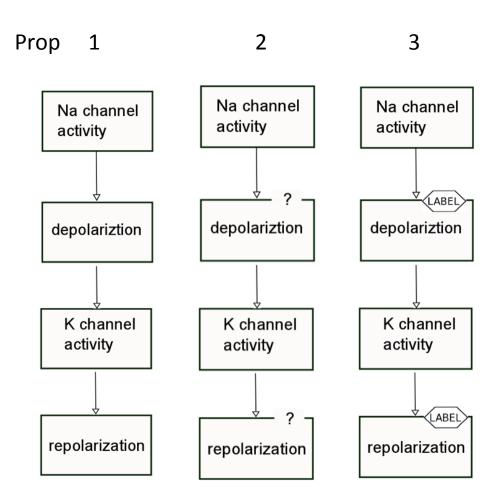
#### Prop 1



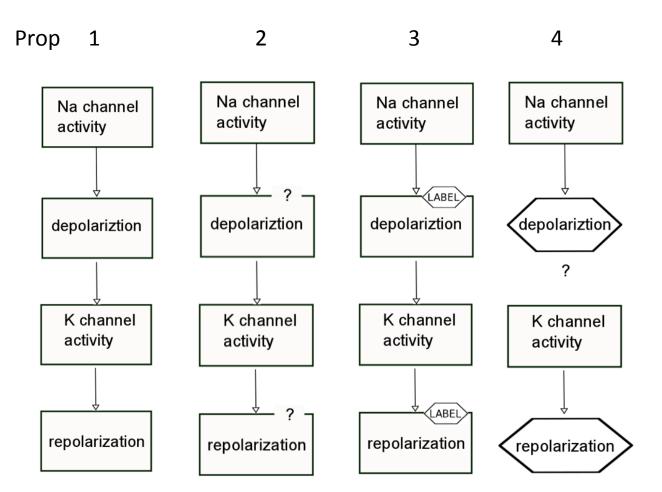
- 1. Remove *phenotype* glyph, and use *activity node* to represent it.
- 2. Remove *phenotype* glyph, use *activity node* with a specific decoration that reflects the fact that it can be observed.



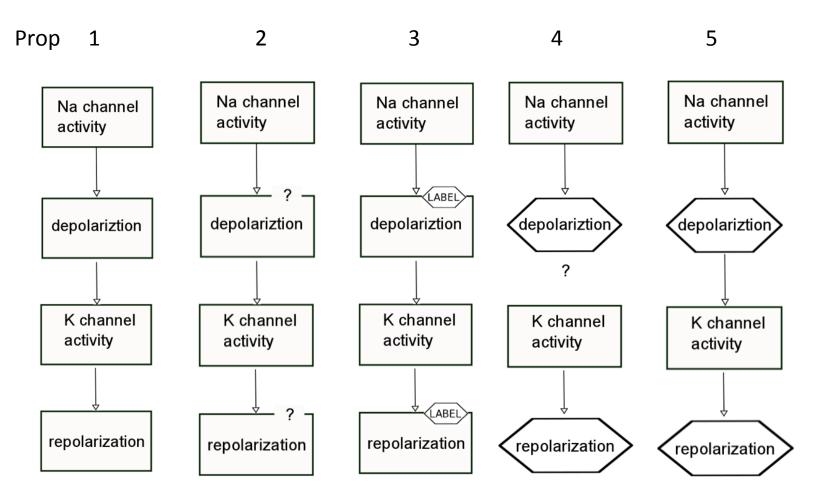
- Remove phenotype glyph, and use activity node to represent it.
- Remove phenotype glyph, use activity node with a specific decoration that reflects the fact that it can be observed.
- Remove phenotype glyph, use activity node with a phenotype glyph as a decoration.



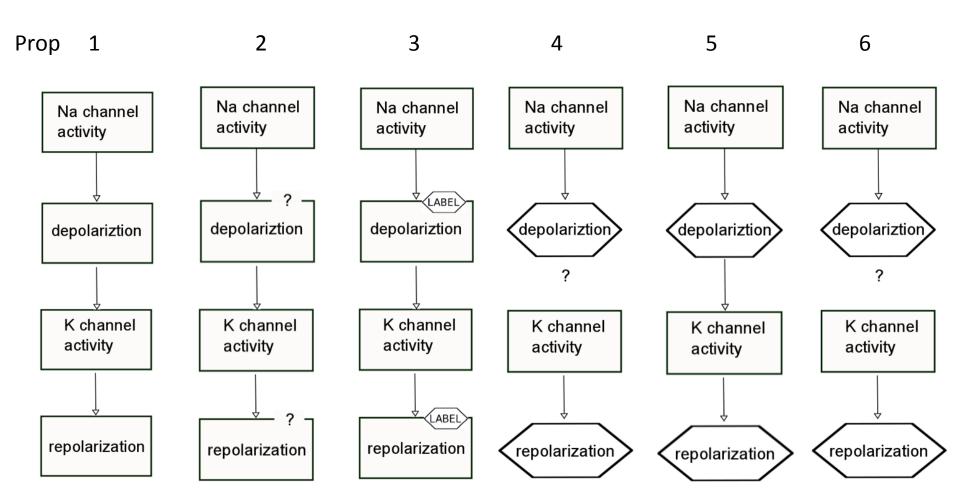
- Remove phenotype glyph, and use activity node to represent it.
- Remove phenotype glyph, use activity node with a specific decoration that reflects the fact that it can be observed.
- Remove phenotype glyph, use activity node with a phenotype glyph as a decoration.
- 4. Keep *phenotype* glyph, and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

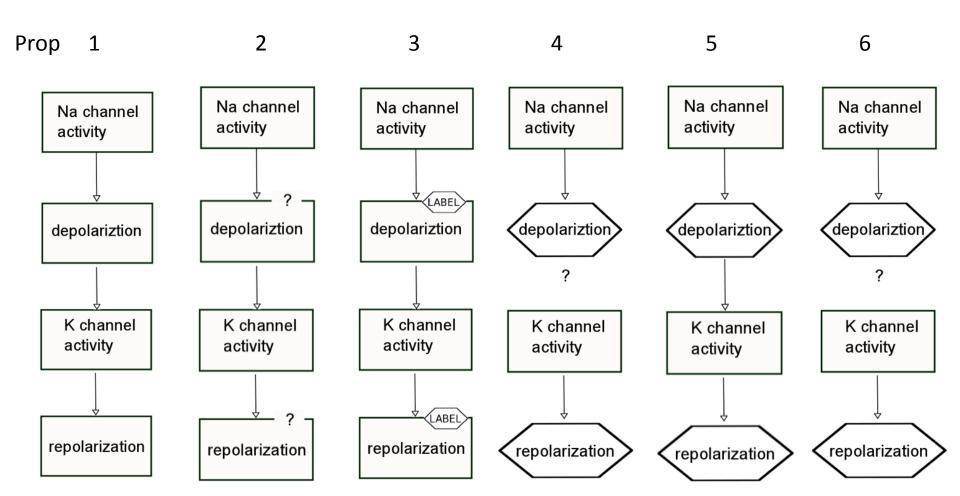


- 1. Remove *phenotype* glyph, and use *activity node* to represent it.
- Remove phenotype glyph, use activity node with a specific decoration that reflects the fact that it can be observed.
- Remove phenotype glyph, use activity node with a phenotype glyph as a decoration.
- 4. Keep phenotype glyph,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



- 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".
- Allow phenotype glyph to be both input and output of influence arcs.
- Keep the current spec, i.e., phenotype glyph can only be the output of an arc.





Vote

1

3

2

# POSSIBLE SUPPORT TO GO CURATION

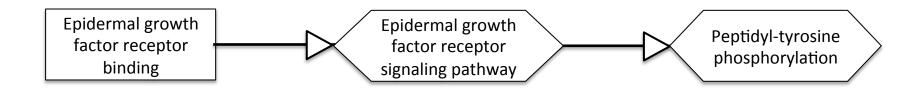
# EFEMP1-EGF-containing fibulin-like extracellular matrix protein 1

GO Identifier	GO Term Name	Aspect	Evidence	Reference
		Process	3	
GO:0006355	regulation of transcription, DNA-dependent	Р	IDA	PMID:20005202
GO:0007173	epidermal growth factor receptor signaling pathway	Р	IDA	PMID:19804359
GO:0007601	visual perception	Р	TAS	PMID:10369267
GO:0018108	peptidyl-tyrosine phosphorylation	Р	IDA	PMID:19804359
GO:0032331	negative regulation of chondrocyte differentiation	Р	IDA	PMID:20005202
		Function	1	
GO:0005006	epidermal growth factor-activated receptor activity	/F	IDA	PMID:19804359
GO:0005154	epidermal growth factor receptor binding	F	IDA	PMID:19804359
GO:0005509	calcium ion binding	F	IEA	InterPro2GO
GO:0005509	calcium ion binding	F	IEA	InterPro2GO
GO:0005515	protein binding	F	IPI	PMID:12620389
GO:0005515	protein binding	F	IPI	PMID:16713569
GO:0005515	protein binding	F	IPI	PMID:19275936
GO:0008083	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	3	
GO:0006355	regulation of transcription, DNA-dependent	Р	IDA	PMID:20005202
GO:0007172	epidermal growth factor receptor signaling pathway	Р	IDA	PMID:19804359
GO:0007601	visual perception	Р	TAS	PMID:10369267
GO:0018108	peptidyl-tyrosine phosphorylation	Р	IDA	PMID:19804359
GO:0032331	negative regulation of chondrocyte differentiation	Р	IDA	PMID:20005202
		Function	n	
GO:0005006	epidermal growth factor-activated receptor activity	y F	IDA	PMID:19804359
GO:0005154	epidermal growth factor receptor binding	F	IDA	PMID:19804359
GO:0005509	calcium ion binding	F	IEA	InterPro2GO
GO:0005509	calcium ion binding	F	IEA	InterPro2GO
GO:0005515	protein binding	F	IPI	PMID:12620389
GO:0005515	protein binding	F	IPI	PMID:16713569
GO:0005515	protein binding	F	IPI	PMID:19275936
GO:0008083	growth factor activity	F	IEA	Swiss-Prot Keywords2GO

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



Fuction	Fund	Function		
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GO:0005515 protein binding	F	IPI	PMID:9305852	
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GO:0016881 acid-amino acid ligase activity	F	IEA	InterPro2GO	
GO:0019871 sodium channel inhibitor activity	F	IEA	Compara	
GO:0019871 sodium channel inhibitor activity	F	IDA	PMID:10642508	
GO:0019904 protein domain specific binding	F	IPI	PMID:12907594	
GO:0031698 beta-2 adrenergic receptor binding	F	IDA	PMID:18544533	
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		_		
Fuction			cess	
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process	Р	IEA	InterPro2GO
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GO:0005515 protein binding	GO:0007041 lysosomal transport	Р	IDA	PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development	Р	IEA	Swiss-Prot Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport	Р	IEA	Compara
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport	Р	IDA	PMID:10642508
GO:0005515 protein binding	GO:0010768 negative regulation of transcription from RNA polymerase II	Р	IMP	PMID:17996703
GO:0005515 protein binding	promoter in response to UV-induced DNA damage			
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade	Р	IMP	PMID:17218260
GO:0005515 protein binding	GO:0016567 protein ubiquitination	Р	IEA	Compara
GO:0005515 protein binding	GO:0016567 protein ubiquitination	Р	IDA	PMID:17996703
GO:0005515 protein binding	GO:0019089 transmission of virus	Р	IMP	PMID:15126635
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	IEA	Compara
	receptor signaling pathway	_	100	00 055 00000
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	ISS	GO_REF:0000024
GO:0005515 protein binding	receptor signaling pathway GO:0031175 neuron projection development	Р	IEP	PMID:9990509
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	GO:0032801 receptor catabolic process	P	IDA	PMID:18544533
GO:0016881 acid-amino acid ligase activity	GO:0034644 cellular response to UV	P	IMP	PMID:16544533
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GO:0019904 protein domain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein	Р	IMP	PMID:17996703
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	GO:0051592 response to calcium ion	Р	TAS	PMID:9405440
	GO:0070534 protein K63-linked ubiquitination	Р	ISS	GO_REF:0000024
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Fuction		Proc		
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GO:0019871 sodium channel inhibitor activity	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein		IMP	PMID:17930703
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GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway	P	IDA	PMID:8649367
GO.0070004 proline-non-region billiamy	GO:0051592 response to calcium ion	Р	TAS	PMID:9405440
	GO:0070534 protein K63-linked ubiquitination	P	ISS	GO_REF:0000024
	do.0070004 protein Noo-iinked abiquitination	Func		GO_NET .0000024
		- WIIV	uvii.	

Fuction		Proc		
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GO:0019871 sodium channel inhibitor activity GO:0019904 protein demain specific binding	catabolic process		livir	FINID.17210200
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GO:0050815 phosphoserine binding	GO:0044419 interspecies interaction between organisms	Р	IEA	Swiss-Prot Keywords2GO
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GO:0070063 RNA polymerase binding	GO:0046824 positive regulation of nucleocytoplasmic transport	Р	IDA	PMID:17218261
GO:0070064 proline-rich region binding	GO:0048814 regulation of dendrite morphogenesis	Р	IEA	Compara
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GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway	Р	IDA	PMID:8649367
	GO:0051592 response to calcium ion	Р	TAS	PMID:9405440
	GO:0070534 protein K63-linked ubiquitination	Р	ISS	GO_REF:0000024
		Func	tion	_

Fuction		Proc	ess	
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GO:0005515 protein binding	promoter in response to UV-induced DNA damage	Г.	IIVIF	FIVIID.17990703
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade	Р	IMP	PMID:17218260
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GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	IEA	Compara
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GO:0019871 sodium channel inhibitor activity	GO:0034644 cellular response to UV	Р	IMP	PMID:17996703
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GO:0050816 shosphothreonine binding	GO:0045732 positive regulation of protein catabolic process	Р	IEA	Compara
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	GO:0070 634 protein K63-linked ubiquitination	P	ISS	GO_REF:0000024
		Func	:uon	

		_		
Fuction		Proce		
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process	Р	IEA	InterPro2GO
GO:0004842 ubiquitin-protein ligase activity	GO:0006622 protein targeting to lysosome	Р	IDA	PMID:17116753
GO:0005515 protein binding	GO:0007041 lysosomal transport	Р	IDA	PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development	Р	IEA	Swiss-Prot Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transport	Р	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	Р	IMP	PMID:17996703
GO:0005515 protein binding	promoter in response to UV-induced DNA damage			
GO:0005515 protein binding		Р	IMP	PMID:17218260
GO:0005515 protein binding	GO:0016567 protein ubiquitination	Р	IEA	Compara
GO:0005515 protein binding	GO:0016567 protein ubiquitination	Р	IDA	PMID:17996703
GO:0005515 protein binding	GO:0019089 transmission of virus	Р	IMP	PMID:15126635
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	IEA	Compara
GO:0005515 protein binding	receptor signaling pathway	_	100	00 055 000000
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	ISS	GO_REF:0000024
GO:0016874 ligase activity	GO:0031175 neuron projection development	Р	IEP	PMID:9990509
GO.0010674 ligase activity	GO:003162G receptor internalization	Р.	IDA	PMID:18544533
GO:0016881 acid-amino acid ligase activity	GO:0032801 receptor catabolic process	Р	IDA	PMID:18544533
	GO:0034644 cellular response to UV	P	IMP	PMID:17996703
GO:0019871 sodium channel inhibitor activity	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein	•	IMP	PMID:17218260
GO:0019871 sodium channel inhibitor activity	catabolic process			1 11110:17210200
GO:0019904 protein demain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein	Р	IMP	PMID:17996703
GO:0031698 beta-2 adrenergic receptor binding	catabolic process	_		
GO:0043130 ubiquitic binding	GO:0042921 glucocorticoid receptor signaling pathway	Р	IDA	PMID:8649367
GO:0050816 phosphoserine binding	GO:0044111 development involved in symbiotic interaction	Р	IMP	PMID:15126635
GO:005/815 phosphoserine binding	GO:0044419 interspecies interaction between organisms	Р	IEA	Swiss-Prot Keywords2GO
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process	Р	IEA	Compara
GO:0050816 phosphothreonine binding	GO:0045732 positive regulation of protein catabolic process	P	IDA	PMID:14973438
G(RNA polymerase binding	GO:0046824 positive regulation of protein catabolic process  GO:0046824 positive regulation of protein catabolic process	Р	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:0048844 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.0070004 profile-flori region billuling	GO:0051592 response to calcium ion	P	TAS	PMID:8649367
	GO:0070634 protein K63-linked ubiquitination	P	ISS	GO_REF:0000024
	GO.0070034 protein Ros-linked doiquitination	Funct		GO_REF.0000024

Fuction		Proce	SS	
GO:0004842 ubiquitin-protein ligase activity	GO:0006464 protein modification process	Р	IEA	InterPro2GO
GO:0004842 ubiquitin-protein ligase activity	GO:0006622 protein targeting to lysosome	Р	IDA	PMID:17116753
GO:0005515 protein binding	GO:0007041 lysosomal transport	Р	IDA	PMID:18544533
GO:0005515 protein binding	GO:0007399 nervous system development	Р	IEA	Swiss-Prot
GO:0005515 protein binding		_		Keywords2GO
GO:0005515 protein binding	GO:0010766 negative regulation of sodium ion transpor	Р	IEA	Compara
	GO:0010766 negative regulation of sodium ion transport	Р	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	Р	IMP	PMID:17996703
GO:0005515 protein binding	GO:0014068 positive regulation of phosphatidylinositol 3-kinase cascade	Р	IMP	PMID:17218260
GO:0005515 protein binding	567 protein ubiquitinatio	P	IIVII	FIVIID.17210200
Phoenica ding Protein	vEGF signaling	P /	/ 	Dendrite
Phosphoserine link	ed VEGI SIGNATING	><	_	>
G binding ding ubiquiti	nathway	P	mor	phogenesis
GO:0005515 protein binding	receptor signaling paulway			
GO:0005515 protein binding	GO:0030948 negative regulation of vascular endothelial growth factor	Р	ISS	GO_REF:0000024
GO:0005515 protein binding	receptor signaling pathway			
GO:0016874 ligase activity	GO:0031175 neuron projection development	Р	IEP	PMID:9990509
	GO:0031623 receptor internalization	Р	IDA	PMID:18544533
GO:0016881 acid-amino acid ligase activity	GO:0032801 receptor catabolic process	Р	IDA	PMID:18544533
GO:0019871 sodium channel inhibitor activity	GO:0034644 cellular response to UV	Р	IMP	PMID:17996703
GO:0019871 sodium channel inhibitor activity	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein catabolic process	Р	IMP	PMID:17218260
GO:0019904 protein domain specific binding	GO:0042787 protein ubiquitination involved in ubiquitin-dependent protein	D	IMP	PMID:17996703
GO:0031698 beta-2 adrenergic receptor binding	catabolic process	Г	IIVII	FIVIID.17990703
GO:0043130 ubiquities binding	GO:0042921 glucocorticoid receptor signaling pathway	Р	IDA	PMID:8649367
GO:0050816 phosphoserine binding	GO:0044111 development involved in symbiotic interaction	P	IMP	PMID:15126635
GO:005/815 phosphoserine binding	GO:0044419 interspecies interaction between organisms	Р	IEA	Swiss-Prot
GO:0050816 phosphothreonine binding				Keywords2GO
GO:0050816 shosphothreonine binding	GO:0045732 positive regulation of protein catabolic process	Р	IEA	Compara
	GO:0045732 positive regulation of protein catabolic process	Р	IDA	PMID:14973438
	GO:0046824 positive regulation of nucleocytoplasmic transport	Р	IDA	PMID:17218261
GO:0070064 proline-rich region binding	GO:0048214 regulation of dendrite morphogenesis	Р	IEA	Compara
GO:0070064 proline-rich region binding	GO:0048844 regulation of dendrite morphogenesis	Р	ISS	GO_REF:0000024
GO:0070064 proline-rich region binding	GO:0050847 progesterone receptor signaling pathway	Р	IDA	PMID:8649367
	GO:0051592 response to calcium ion	Р	TAS	PMID:9405440
	GO:0070534 protein K63-linked ubiquitination	Р	ISS	GO_REF:0000024
		Functi	ion	

#### Acknowledgements

The entire SBGN community