SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks Supplementary material

April 5, 2021

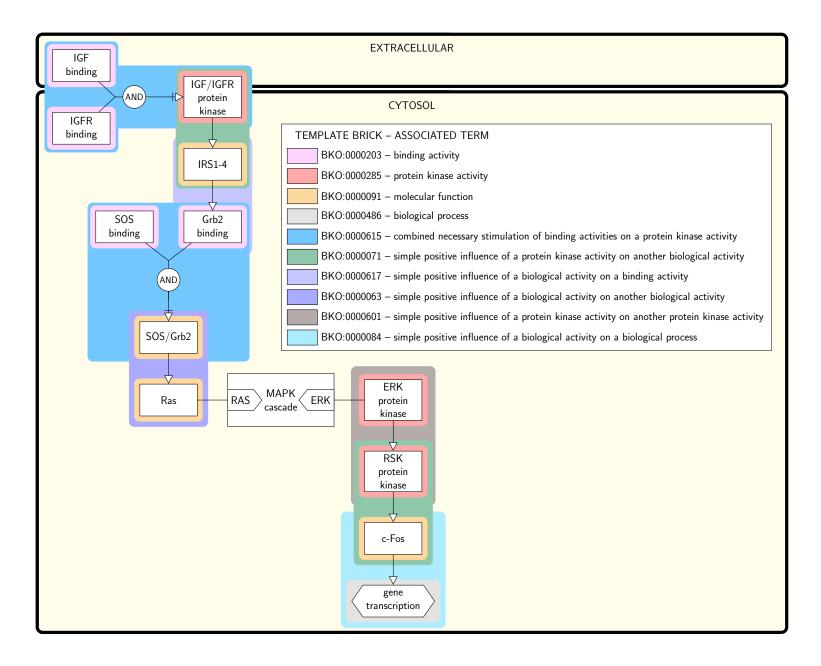


Figure S1: SBGN AF map of the Insulin/IGF pathway-mitogen activated protein kinase/MAP kinase cascade annotated with terms using template bricks. This map matches the PD map of Figure 1. Colored boxes surround individual instance bricks matched by the template bricks given in the legend. The color of the surrounding box identifies the template brick the instance is matched by. Template bricks associated with the same terms as those associated with the PD template bricks of Figure 1 share the same color (e.g. the template brick BKO:0000285 associated with the term "protein kinase activity" is in pink, as is template brick BKO:0000287 in Figure 1 which is associated with the same term). This map is annotated with some terms that do not appear in the annotation of the PD map of Figure 1, indicating that those terms do not have any PD representation (e.g. the "simple positive influence of a protein kinase on another protein kinase").

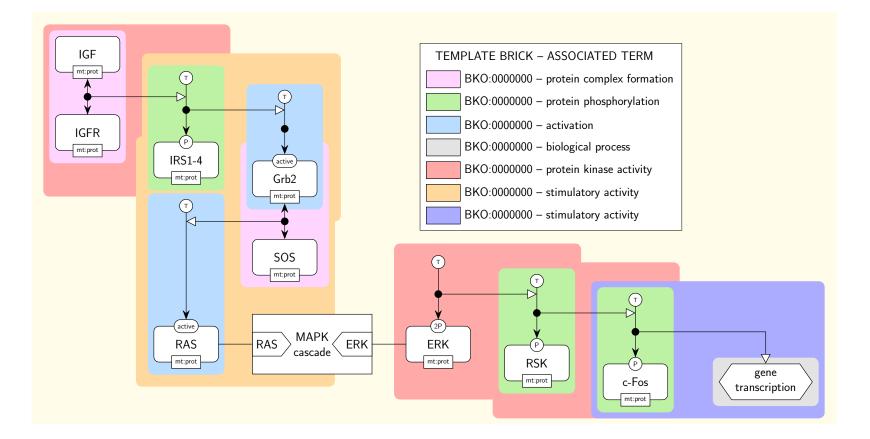


Figure S2: SBGN ER map of the Insulin/IGF pathway-mitogen activated protein kinase/MAP kinase cascade annotated with terms using template bricks. This map matches the PD map of Figure 1. Colored boxes surround individual instance bricks matched by the template bricks given in the legend. The color of the surrounding box identifies the template brick the instance is matched by. Template bricks associated with the same terms as those associated with the PD template bricks of Figure 1 share the same color (e.g. the template brick BKO:0000285 associated with the term "protein kinase activity" is in pink, as is template brick BKO:0000287 in Figure 1 which is associated with the same term).

Table S1: Alignment of PD, AF and ER template bricks associated with the terms describing common concepts encountered in molecular networks.

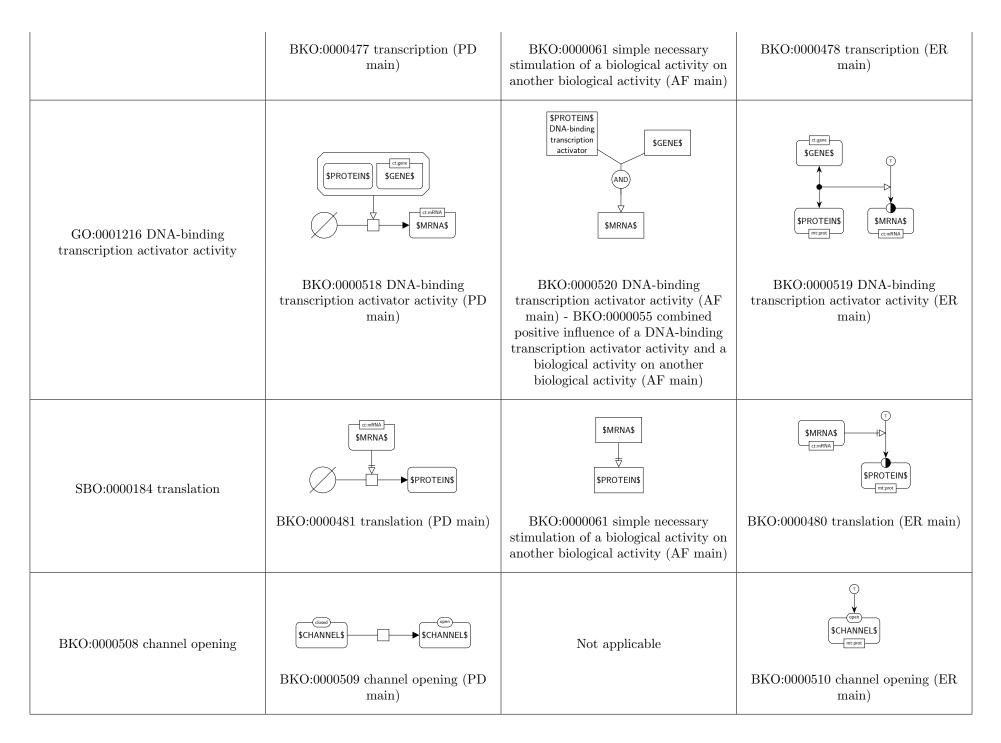
Term	PD	AF	ER	
SBO:0000177 non-covalent binding - GO:0005488 binding	\$UNSPEC_1\$ (\$UNSPEC_2\$ (\$UNSPEC_2\$) (\$UNSPEC_2\$) (\$UNSPEC_2\$) (\$UNSPEC_1\$)	\$UNSPEC_1\$ \$UNSPEC_2\$ {\$UNSPEC_N\$ binding {\$UNSPEC_1\$ binding} AND \$ \$COMPLEX\$ \$	\$UNSPEC_1\$ \$UNSPEC_2\$ {\$UNSPEC_N\$}	
	BKO:0000204 non-covalent binding (PD narrow 1)	BKO:0000203 binding (AF main) - BKO:0000042 combined necessary stimulation of binding activities on another biological activity (AF main)	BKO:0000207 non-covalent binding (ER main)	
BKO:0000221 protein multimerisation	SPROTEINS [5X3] SPROTEINS	SPROTEINS binding \$ SCOMPLEXS	\$PROTEIN\$	
	BKO:0000223 protein multimerisation (PD main)	BKO:0000203 binding (AF main) - BKO:0000059 simple necessary stimulation of a binding activity on another biological activity (AF main)	BKO:0000222 protein multimerisation (ER main)	
SBO:0000180 dissociation	\$UNSPEC_1\$) \$UNSPEC_1\$) \$UNSPEC_2\$) \$UNSPEC_2\$) \$UNSPEC_2\$) \$UNSPEC_M\$})	Not applicable	Not applicable	

	BKO:0000170 dissociation (PD narrow 1)		
BKO:0000438 protein phosphorylation	\$PROTEIN\$	Not applicable	(P(@SRESS) \$PROTEIN\$
	BKO:0000440 protein phosphorylation (PD narrow 1)		BKO:0000439 protein phosphorylation (ER main)
GO:0004672 protein kinase activity	SPROTEINS BKO:0000287 protein kinase activity (PD narrow 1)	SCATALYST\$ protein kinase \$PROTEIN\$ BKO:0000285 protein kinase activity (AF main) - BKO:0000071 simple	SCATALYSTS SPROTEINS BKO:0000282 protein kinase activity (ER broad 1)
		positive influence of a protein kinase activity on another biological activity (AF main)	
BKO:0000375 protein dephosphorylation	\$PROTEIN\$	Not applicable	
	BKO:0000370 protein dephosphorylation (PD narrow 1)		BKO:0000369 protein dephosphorylation (ER main)

GO:0004721 phosphoprotein phosphatase activity	SPROTEINS	\$CATALYST\$ phosphoprotein phosphatase \$PROTEIN\$	\$CATALYST\$
	BKO:0000233 phosphoprotein phosphatase activity (PD narrow 1)	BKO:0000068 simple negative influence of a phosphoprotein phosphatase activity on another biological activity (AF main)	BKO:0000228 phosphoprotein phosphatase activity (ER broad 1)
SBO:0000656 activation	SPROTEINS BKO:0000498 activation (PD narrow 1)	Not applicable	SPROTEINS mt.got BKO:0000495 activation (ER main)
SBO:0000208 deactivation	SPROTEINS BKO:0000211 deactivation (PD narrow 1)	Not applicable	(increase SPROTEINS (mt.pot) BKO:0000210 deactivation (ER main)
BKO:0000511 irreversible metabolic reaction	(\$\$UBSTRATE_1\$) (\$\$UBSTRATE_N\$) (\$\$PRODUCT_1\$) (\$\$PRODUCT_M\$) BKO:0000513 irreversible metabolic reaction (PD main)	Not applicable	Not applicable

BKO:0000514 reversible metabolic reaction	(\$PRODUCT_1\$) (\$SUBSTRATE_N\$) (\$PRODUCT_M\$) BKO:0000515 reversible metabolic reaction (PD main)	Not applicable	Not applicable
BKO:0000196 metabolic catalytic activity	(\$\$SUBSTRATE_1\$) (\$SUBSTRATE_1\$) (\$SUBSTRATE_N\$) (\$PRODUCT_M\$) BKO:0000197 metabolic catalytic activity (PD narrow 1)	Not applicable	Not applicable
BKO:0000196 metabolic catalytic activity	(\$\$UBSTRATE_1\$) (\$\$SUBSTRATE_1\$) (\$\$SUBSTRATE_N\$) (\$\$PRODUCT_M\$) BKO:0000198 metabolic catalytic activity (PD narrow 2)	Not applicable	Not applicable
SBO:0000183 transcription	SGENES SMRNAS	\$GENE\$ ↓ ↓ \$MRNA\$	SGENES (tigene) SMRNAS (timRNA)

-1



BKO:0000505 channel closing	SCHANNELS BKO:0000506 channel closing (PD main)	Not applicable BKO:0000507 channel closing (ER main)	SCHANNELS (mt.prot)
SBO:0000185 translocation reaction	SUNSPECS SUNSPECS BKO:0000484 translocation reaction (PD narrow 2)	Not applicable	SUNSPECS BKO:0000482 translocation reaction (ER main)
SBO:0000655 transport reaction - GO:0005215 transporter activity	\$UNSPECS	\$TRANSPORTER\$ transporter \$UNSPEC\$	\$TRANSPORTER\$
	BKO:0000090 transport reaction (PD narrow 2)	BKO:0000088 transporter activity (AF main) - BKO:0000073 simple positive influence of a transporter activity on another biological activity (AF main)	BKO:0000087 transport reaction (ER main)

Table S2: Number of instances matched by each term of the ontology in the ACSN and PANTHER databases. The number in parantheses is the number of proper instances matched by the term, i.e. the number of instances that are matched by the term and by none of its descendants. Terms matching no instances in both databases are not shown.

Term	ACSN	PANTHER	Overall
BKO:0000041 term	15708(0)	6339~(0)	22047~(0)
BKO:0000078 molecular function	7865~(0)	3165~(0)	11030(0)
BKO:0000008 modulatory activity	6275~(66)	2638(0)	8913~(66)
BKO:0000005 stimulatory activity	5207 (515)	2470 (54)	7677 (569)
BKO:0000004 catalytic activity	4692 (2547)	2416 (517)	7108 (3064)
BKO:0000003 oxidoreductase activity	2 (0)	0 (0)	2 (0)
BKO:0000002 hydroxylase activity	2 (0)	0 (0)	2 (0)
BKO:0000018 protein hydroxylase activ- ity	2 (2)	0 (0)	2 (2)
BKO:0000198 catalytic activity, acting on a	1870 (9)	1097(0)	2967 (9)
BKO:0000028 catalytic activity, adding a	1414 (34)	515 (1)	1929 (35)
· · · · ·	1414(34)	515(1)	1929(35)
chemical group on a protein	20 (20)	1 (1)	01 (01)
BKO:0000265 protein acetyltransferase activity	20(20)	1 (1)	21 (21)
BKO:0000289 protein glycosyltransferase activity	3 (3)	0 (0)	3(3)
BKO:0000314 protein kinase activity	1258 (1258)	484 (484)	1742 (1742)
BKO:0000327 protein methyltransferase	1 (1)	$\frac{101(101)}{0(0)}$	1 (1)
activity		- (-)	
BKO:0000339 protein palmitoyltrans-	1 (1)	0 (0)	1 (1)
ferase activity	- (-)	0 (0)	- (-)
BKO:0000350 protein prenyltransferase	1 (1)	0 (0)	1 (1)
activity	1 (1)	0 (0)	1 (1)
BKO:0000374 ubiquitin-like protein trans-	126 (0)	30(0)	156 (0)
ferase activity	120 (0)	30 (0)	100 (0)
BKO:0000375 ubiquitin-protein trans-	126 (126)	30 (30)	156 (156)
ferase activity BKO:0000188 catalytic activity, removing	155 (4)	TO (0)	014 (4)
· · · ·	155 (4)	59(0)	214 (4)
a chemical group from a protein	101 (101)		170 (170)
BKO:0000250 phosphoprotein phos-	121 (121)	57(57)	178(178)
phatase activity	0 (0)	0 (0)	0 (0)
BKO:0000278 protein demethylase activ-	6(6)	0 (0)	6(6)
ity			
BKO:0000303 protein deacetylase activity	11 (11)	1 (1)	12 (12)
BKO:0000362 ubiquitinyl hydrolase activ-	14 (0)	2(0)	16(0)
ity			
BKO:0000361 protein ubiquitinyl hydro-	14(14)	2(2)	16(16)
lase activity			
BKO:0000206 catalytic activity, activating	604 (604)	833 (833)	1437 (1437)
a protein			
BKO:0000636 catalytic activity, deactivat-	75(75)	115 (115)	190 (190)
ing a protein			
BKO:0000185 hydrolase activity	145(0)	59(0)	204 (0)
BKO:0000264 hydrolase activity, acting on	121(0)	$\frac{53}{57}(0)$	$\frac{1000}{178(0)}$
ester bonds	(~)	- · (-)	- (*)
BKO:0000262 phosphoric ester hydrolase	121 (0)	57 (0)	178 (0)
activity	(0)	()	
BKO:0000251 phosphatase activity	121 (0)	57 (0)	178 (0)
BKO:0000250 phosphoprotein phos-	121(0) 121(121)	57 (57)	$\frac{178(0)}{178(178)}$
	121 (121)	51 (51)	110 (110)
PKO.0000204 depectulars activity	11 (0)	1 (0)	12 (0)
BKO:0000304 deacetylase activity	11 (0)	1 (0)	12 (0)

BKO:0000303 protein deacetylase activity	11 (11)	1 (1)	12 (12)
BKO:0000362 ubiquitinyl hydrolase activ-	11(11) 14(0)	$\frac{1\ (1)}{2\ (0)}$	$\frac{12(12)}{16(0)}$
ity	14 (0)	2 (0)	10 (0)
BKO:0000361 protein ubiquitinyl hydro-	14 (14)	2 (2)	16 (16)
lase activity			
BKO:0000211 transferase activity	1380(0)	514(0)	1894 (0)
BKO:0000277 transferase activity, trans-	21 (0)	1 (0)	22(0)
ferring acyl groups			
BKO:0000275 transferase activity, trans-	21 (0)	1 (0)	22(0)
ferring acyl groups other than amino-acyl groups	00 (0)	1 (0)	01 (0)
BKO:0000266 acetyltransferase activity	20(0)	$\frac{1(0)}{1(1)}$	$\frac{21\ (0)}{21\ (21)}$
BKO:0000265 protein acetyltransferase activity	20 (20)	1(1)	21 (21)
BKO:0000340 palmitoyltransferase ac-	1 (0)	0 (0)	1 (0)
tivity	1 (0)	0 (0)	1 (0)
BKO:0000339 protein palmitoyltrans-	1 (1)	0 (0)	1 (1)
ferase activity			
BKO:0000290 transferase activity, trans-	3 (0)	0 (0)	3 (0)
ferring glycosyl groups			
BKO:0000289 protein glycosyltransferase	3(3)	0 (0)	3 (3)
activity	1070 (0)		1710(0)
BKO:0000324 transferase activity, trans-	1258~(0)	484(0)	1742 (0)
ferring phosphorus-containing groups	1959 (0)	494 (0)	1749 (0)
BKO:0000315 kinase activity	$\frac{1258 (0)}{1258 (1258)}$	$\frac{484\ (0)}{484\ (484)}$	$\frac{1742(0)}{1742(1742)}$
BKO:0000314 protein kinase activity BKO:0000337 transferase activity, trans-	(/	$\frac{484(484)}{0(0)}$	$\frac{1742 (1742)}{1 (0)}$
ferring one-carbon groups	1 (0)	0 (0)	1(0)
BKO:0000328 methyltransferase activity	1 (0)	0 (0)	1 (0)
BKO:0000327 protein methyltransferase	$\frac{1}{1}(0)$	0 (0)	$\frac{1}{1}(1)$
activity	1 (1)	0 (0)	1 (1)
BKO:0000351 transferase activity, trans-	1 (0)	0 (0)	1 (0)
ferring prenyl groups			
BKO:0000350 protein prenyltransferase	1 (1)	0 (0)	1 (1)
activity			
BKO:0000374 ubiquitin-like protein trans-	126 (0)	30(0)	156(0)
ferase activity			
BKO:0000375 ubiquitin-protein trans-	126 (126)	30(30)	$156\ (156)$
ferase activity		000 (000)	
BKO:0000212 metabolic catalytic activity BKO:0000279 demethylase activity	275(275)	802 (802)	$\frac{1077 (1077)}{6 (0)}$
BKO:0000279 demethylase activity BKO:0000278 protein demethylase activity	6 (0) 6 (6)	$ \begin{array}{c} 0 \ (0) \\ 0 \ (0) \end{array} $	
BKO:0000399 inhibitory activity	1002 (1002)	$\frac{0}{168}(168)$	$\frac{0}{1170}(1170)$
BKO:0000077 transporter activity	430 (430)	151 (151)	581 (581)
BKO:0000220 binding	150(100) 1590(113)	$\frac{101(101)}{527(25)}$	2117 (138)
BKO:0000232 protein binding	1477 (1477)	502(502)	1979 (1979)
BKO:0000088 process	9863 (0)	3852 (0)	$\frac{1010(1010)}{13715(0)}$
BKO:0000086 biochemical or transport reac-	5117 (0)	2978 (0)	8095 (0)
tion			
BKO:0000085 transport reaction	430 (0)	151(0)	581 (0)
BKO:0000563 co-transport reaction	4 (0)	4 (0)	8 (0)
BKO:0000577 symporter-mediated trans-	0 (0)	4 (4)	4 (4)
port		- (-)	
BKO:0000580 antiporter-mediated trans-	4(4)	0 (0)	4(4)
port	49C (40C)	181 (181)	F77 (F77)
BKO:0000565 passive transport	426 (426)	151 (151)	$\frac{577(577)}{1(1)}$
BKO:0000574 active transport BKO:0000103 biochemical reaction	$\frac{1 (1)}{3719 (0)}$	$\frac{0 \ (0)}{2630 \ (0)}$	$\frac{1 (1)}{6349 (0)}$
DRO.0000103 DIOCHEIIIICAI TEACHOII	0119 (0)	2030 (0)	0949 (0)

BKO:0000101 conversion	1409 (0)	1015 (0)	2424 (0)
BKO:0000099 removal of a chemical group	$\frac{1100(0)}{179(0)}$	57 (0)	$\frac{236}{236}(0)$
BKO:0000098 deacetylation	13 (0)	1 (0)	14 (0)
BKO:0000118 protein deacetylation	13 (13)	1 (1)	14 (14)
BKO:0000112 deprenylation	3 (0)	0 (0)	3 (0)
BKO:0000156 protein deprenylation	3 (3)	0 (0)	3 (3)
BKO:0000116 deubiquitination	20 (0)	3 (0)	23 (0)
BKO:0000168 protein deubiquitination	20 (20)	3 (3)	23 (23)
BKO:0000119 removal of a chemical group	179 (12)	57 (0)	236 (12)
from a protein			
BKO:0000118 protein deacetylation	13 (13)	1 (1)	14 (14)
BKO:0000156 protein deprenylation	3(3)	0 (0)	3(3)
BKO:0000168 protein deubiquitination	20 (20)	3(3)	23 (23)
BKO:0000409 protein demethylation	6(6)	0 (0)	6(6)
BKO:0000414 protein dephosphorylation	127(127)	54(54)	181 (181)
BKO:0000394 demethylation	6(0)	0 (0)	6(0)
BKO:0000409 protein demethylation	6(6)	0 (0)	6(6)
BKO:0000415 dephosphorylation	127(0)	54(0)	181 (0)
BKO:0000414 protein dephosphorylation	127(127)	54(54)	181 (181)
BKO:0000227 deactivation	66~(66)	108 (108)	174(174)
BKO:0000385 addition of a chemical group	1039(0)	440(0)	1479(0)
BKO:0000384 addition of a chemical group	1039(61)	440(1)	1479(62)
on a protein			
BKO:0000423 protein prenylation	3 (3)	0 (0)	3 (3)
BKO:0000430 protein acetylation	19 (19)	1 (1)	20 (20)
BKO:0000443 protein glycosylation	5 (5)	0 (0)	5 (5)
BKO:0000450 protein hydroxylation	2 (2)	0 (0)	2 (2)
BKO:0000460 protein methylation	1 (1)	0 (0)	1 (1)
BKO:0000470 protein myristoylation	1 (1)	0 (0)	1 (1)
BKO:0000480 protein palmitoylation	2 (2)	0 (0)	2 (2)
BKO:0000490 protein phosphorylation	835 (835)	406 (406)	1241 (1241)
BKO:0000520 protein ubiquitination	122 (122)	33 (33)	155 (155)
BKO:0000396 prenylation	$\frac{3}{2}(0)$	0(0)	3 (0)
BKO:0000423 protein prenylation	3(3)	0 (0)	3 (3)
BKO:0000431 acetylation	19 (0)	1 (0)	20 (0)
BKO:0000430 protein acetylation	19 (19)	1 (1)	20 (20)
BKO:0000441 glycosylation	5(0)	0 (0)	5 (0)
BKO:0000443 protein glycosylation	5 (5)	0(0)	5 (5)
BKO:0000451 hydroxylation	2(0)	0 (0)	$\frac{2(0)}{2(2)}$
BKO:0000450 protein hydroxylation	2 (2)	0 (0)	2 (2)
BKO:0000461 methylation	$\frac{1(0)}{1(1)}$	0 (0)	$\frac{1(0)}{1(1)}$
BKO:0000460 protein methylation	1 (1)	0 (0)	$\frac{1(1)}{1(0)}$
BKO:0000471 myristoylation	$\frac{1(0)}{1(1)}$	0 (0)	$\frac{1(0)}{1(1)}$
BKO:0000470 protein myristoylation	1 (1)	0 (0)	$\frac{1(1)}{2(0)}$
BKO:0000481 palmitoylation	2(0)	0(0)	$\frac{2(0)}{2(2)}$
BKO:0000480 protein palmitoylation	2(2)	0(0)	2(2)
BKO:0000491 phosphorylation	835 (0)	406(0)	$\frac{1241(0)}{1241(1241)}$
BKO:0000490 protein phosphorylation BKO:0000521 ubiquitination	835 (835) 122 (0)	$\frac{406 (406)}{33 (0)}$	$\frac{1241 (1241)}{155 (0)}$
BKO:0000521 ubiquitination BKO:0000520 protein ubiquitination	122(0) 122(122)	33 (0)	155(0) 155(155)
	. ,		$\frac{155(155)}{1101(1101)}$
BKO:0000567 patiention	340(340)		
BKO:0000567 activation BKO:0000175 dissociation	340(340) 226(50)	761 (761) 100 (56)	· · · ·
BKO:0000175 dissociation	226 (50)	190 (56)	416 (106)
BKO:0000175 dissociation BKO:0000174 protein complex dissociation	226 (50) 176 (166)	190 (56) 134 (123)	416 (106) 310 (289)
BKO:0000175 dissociationBKO:0000174 protein complex dissociationBKO:0000182 protein multimer dissocia-	226 (50)	190 (56)	416 (106)
BKO:0000175 dissociation BKO:0000174 protein complex dissociation	226 (50) 176 (166)	190 (56) 134 (123)	416 (106) 310 (289)

BKO:0000241 protein complex formation	1366 (1315)	399(355)	1765 (1670)
BKO:0000240 protein multimerisation	51 (51)	44 (44)	95 (95)
BKO:0000530 degradation	230 (230)	63 (63)	293 (293)
BKO:0000535 conformational transition	6 (0)	50 (0)	56 (0)
BKO:0000582 channel closing	0 (0)	6 (6)	6 (6)
BKO:0000585 channel opening	6 (6)	44 (44)	50 (50)
BKO:0000589 metabolic reaction	334 (0)	869 (0)	1203 (0)
BKO:0000588 irreversible metabolic reac-	325 (325)	868 (868)	1193 (1193)
tion			
BKO:0000591 reversible metabolic reaction	9 (9)	1 (1)	10 (10)
BKO:0000545 translocation reaction	1085 (1085)	337(337)	1422(1422)
BKO:0000131 irreversible process	8911 (8091)	3548(2257)	12459(10348)
BKO:0000530 degradation	230 (230)	63~(63)	293 (293)
BKO:0000588 irreversible metabolic reaction	325 (325)	868 (868)	1193(1193)
BKO:0000615 omitted irreversible process	295 (295)	377 (377)	672(672)
BKO:0000216 uncertain process	518(0)	48 (0)	566(0)
BKO:0000215 uncertain irreversible process	518 (518)	47 (47)	565 (565)
BKO:0000219 uncertain reversible process	518 (518)	48 (48)	566 (566)
BKO:0000249 molecular or genetic interaction	1366(0)	399(0)	1765(0)
BKO:0000244 molecular interaction	1366(0)	399(0)	1765(0)
BKO:0000241 protein complex formation	$1366\ (1315)$	399~(355)	1765 (1670)
BKO:0000240 protein multimerisation	51(51)	44 (44)	95 (95)
BKO:0000537 composite biochemical process	1900(0)	188(0)	2088(0)
BKO:0000536 transcription	970 (970)	138(138)	1108 (1108)
BKO:0000541 translation	930 (930)	50(50)	980 (980)
BKO:0000551 biological process	504(504)	148(148)	652~(652)
BKO:0000556 omitted process	295~(0)	379~(0)	674(0)
BKO:0000615 omitted irreversible process	295~(295)	377 (377)	672~(672)
BKO:0000617 omitted reversible process	0 (0)	2(2)	2(2)
BKO:0000561 reversible process	18 (9)	5(2)	23(11)
BKO:0000591 reversible metabolic reaction	9(9)	1 (1)	10 (10)
BKO:0000617 omitted reversible process	0 (0)	2 (2)	2 (2)
Total	$109681 \ (31087)$	$49986 \ (13198)$	$159667\ (44285)$

Table S3: List of the 30 template bricks representing generic concepts. For each template brick, we also give the number of instances they match in the ACSN and PANTHER databases. The number in parantheses is the number of proper instances matched by the template brick, i.e. the number of instances that are matched by the template brick and by none of its descendants.

Template brick	ACSN	PANTHER	Overall
BKO:0000130 irreversible process (PD main)	8911 (2605)	3548(251)	12459(2856)
BKO:0000387 addition of a chemical group on a	791(54)	364(1)	1155 (55)
protein (PD narrow 1)			
BKO:0000389 addition of a chemical group on a	230(6)	67(0)	297(6)
protein (PD narrow 2)			
BKO:0000391 addition of a chemical group on a	10 (0)	2(0)	12 (0)
protein (PD narrow 3)			
BKO:0000390 addition of a chemical group on a	9 (1)	8(0)	17(1)
protein (PD narrow 4)			
BKO:0000126 removal of a chemical group from	122 (11)	51(0)	173(11)
a protein (PD narrow 1)			
BKO:0000127 removal of a chemical group from	56(1)	5(0)	61(1)
a protein (PD narrow 2)			
BKO:0000129 removal of a chemical group from	0 (0)	1(0)	1 (0)
a protein (PD narrow 3)			
BKO:0000128 removal of a chemical group from	1 (0)	0 (0)	1 (0)
a protein (PD narrow 4)			
BKO:0000087 modulatory activity (PD narrow	5928(60)	2584(0)	8512 (60)
1)			
BKO:0000009 stimulatory activity (PD narrow	4965(267)	2429(18)	7394(285)
1)			
BKO:0000006 catalytic activity (PD narrow 1)	4681 (2544)	2410 (512)	7091 (3056)
BKO:0000027 catalytic activity, acting on a pro-	1495 (5)	999 (0)	2494 (5)
tein (PD narrow 1)			
BKO:0000023 catalytic activity, adding a chemi-	1138 (29)	438 (1)	1576(30)
cal group on a protein (PD narrow 1)			
BKO:0000199 catalytic activity, removing a	110 (4)	50(0)	160(4)
chemical group from a protein (PD narrow 1)			
BKO:0000029 catalytic activity, acting on a pro-	315(4)	82 (0)	397(4)
tein (PD narrow 2)			
BKO:0000024 catalytic activity, adding a chemi-	256(1)	68(0)	324(1)
cal group on a protein (PD narrow 2)			
BKO:0000200 catalytic activity, removing a	45 (0)	8 (0)	53(0)
chemical group from a protein (PD narrow 2)			
BKO:0000205 catalytic activity, acting on a pro-	10 (0)	3(0)	13 (0)
tein (PD narrow 3)			
BKO:0000026 catalytic activity, adding a chemi-	10 (0)	2(0)	12 (0)
cal group on a protein (PD narrow 3)			
BKO:0000202 catalytic activity, removing a	0 (0)	1 (0)	1 (0)
chemical group from a protein (PD narrow 3)			
BKO:0000204 catalytic activity, acting on a pro-	11 (0)	9 (0)	20 (0)
tein (PD narrow 4)			
BKO:0000025 catalytic activity, adding a chemi-	11 (2)	8 (0)	19 (2)
cal group on a protein (PD narrow 4)	. /	. /	. /
BKO:0000201 catalytic activity, removing a	0 (0)	0 (0)	0 (0)
chemical group from a protein (PD narrow 4)	~ /	. /	× /
BKO:0000081 transport reaction (PD narrow 1)	420 (0)	109 (0)	529(0)
BKO:0000082 transport reaction (PD narrow 2)	330 (0)	95 (0)	425 (0)
BKO:0000097 modulatory activity (PD narrow	11 (0)	6 (0)	17 (0)
2)	× /	× /	× /
BKO:0000017 stimulatory activity (PD narrow	11 (0)	6(0)	17(0)
2)	× /	x - /	\-/
/			

BKO:0000007 catalytic activity (PD narrow 2)	11 (3)	6(5)	17 (8)
BKO:0000562 reversible process (PD main)	18(9)	5(2)	23(11)
Total	$29906 \ (5606)$	$13364 \ (790)$	$43270 \ (6396)$

Table S4: Classification of all instances of the ACSN and PANTHER databases that were only matched by template bricks representing generic concepts (for each such template brick). All bricks that were matched by one of the 30 template bricks listed below and representing generic concepts (e.g. an irreversible process, a catalytic activity) without being matched by template bricks representing more specific concepts (e.g. a protein phosphorylation, a protein kinase activity) were classified in one of the following categories and subcategories. **Misrepresentation**: the process or activity is badly represented; Same reactant and product: a process consumes a reactant and produces a product that are exactly the same entity pools; *Phenotype as modulator*: a phenotype modulates a process (invalid SBGN); *Phenotype as reactant or product*: a phenotype is a reactant or a product of a process (invalid SBGN); *Incomplete process*: the process is missing some reactant or product; Association: the process is an incomplete association; Dissociation: the process is an incomplete dissociation; False multimer: a multimer is represented using two subunits on top of each other and not a multimer glyph; Transcription no gene ui: a transcription is represented without using a proper unit of information for the gene; Translation no ui: a translation is represented without using a proper unit of information for the mRNA; Other: none of the above. Nature of process implicit in label: the nature of the process can solely be identified by analyzing the labels of the participants of the process (e.g. the truncation of a protein, where a protein is consumed to give two or more proteins with new names); Truncation: the process is a truncation; Translocation: the process is a translocation. Other: none of the above. **Process in the ontology**: this category implies only modulatory activities whose modulated process is an instance of a template brick that belongs to the ontology (e.g. stimulation of dissociation) Activation: the process is an activation; Translocation: the process is a translocation; Complexation: the process is a complexation; *Degradation*: the process is a degradation; *Dissociation*: the process is a dissociation; *Phosphorylation*: the process is a phosphorylation; *Transcription*: the process is a transcription; *Translation*: the process is a translation; Ubiquitination: the process is an ubiquitination; Association: the process is an association; Multimer dissociation: the process is a multimer dissociation; *Multimerisation*: the process is a multimerisation; *Transporter activity*: the process is a translocation; *Channel opening*: the process is a channel opening. *Other*: none of the above. Mix of two processes of unknown nature: two processes are represented using only one SBGN process (e.g. a dissociation and a dephosphorylation); Association and deactivation: the process is an association and a deactivation; Association and multimerisation: the process is an association and a multimerisation; *Dissociation and activation*: the process is a dissociation and an activation; Dissociation and deubiquitination: the process is a dissociation and a deubiquitination; Dissociation and multimer dissociation: the process is a dissociation and a multimer dissociation; Dissociation and phosphorylation: the process is a dissociation and a phosphorylation; Dissociation and ubiquitination: the process is a dissociation and an ubiquitination; Association and phosphorylation: the process is an association and a phosphorylation: Association and activation: the process is an association and a activation; *Dissociation and acetylation*: the process is a dissociation and an acetylation; Dissociation and dephosphorylation: the process is a dissociation and a dephosphorylation; Multimer dissociation and deactivation: the process is a multimer dissociation and a deactivation; Multimerisation and activation: the process is a multimerisation and an activation; *Multimerisation and ubiquitination*: the process is a multimerisation and an ubiquitination. Multimerisation and deacetylation: the process is a multimerisation and a deacetylation; Multimerisation and phosphorylation: the process is a multimerisation and a phosphorylation; **Process of unknown nature**: we could not identify the nature of the represented process or the activity. Process not in the ontology: the process represented in the brick is not an instance of any template brick of the ontology; Non standard value in state variable: the process sets a value to a state variable that is not defined by the controlled vocabulary of the SBGN standard; Asterisk: the value is an asterisk ("*"). This value is used in CellDesigner to mean "don't care". It does not belong to the controlled vocabulary of SBGN, but its use in state variables is valid SBGN. However processes using this value cannot be linked to any specific concept of SBO or GO. Question mark: the value is a question mark ("?"). Same as for "*", but with meaning "unknown". Other: none of the above; Process involving an asRNA: the process consumes or produces an asRNA; Methylation of a naf of unspecified nature: the process is a methylation of a nuclear acid feature with no conceptual type defined (e.g. gene or mRNA); Gtp exchange: the process is a GTP/GDP exchange process; Production: the process consumes an empty set.

Template brick	Category	Subcatego	ries	ACSN	PANTHER	Overall
catalytic activity,	misrepresentation	other		1	0	1
removing a chemical	process not in the	non standard value in	asterisk	2	0	2
group from a protein (PD narrow 1)	ontology	state variable	question mark	1	0	1
catalytic activity,	misrepresentation	other		1	0	1
adding a chemical group on a protein	nature of process im- plicit in label	truncation		3	0	3
(PD narrow 1)	process not in the	non standard value in	asterisk	3	0	3
	ontology	state variable	question mark	22	1	23
addition of a chemical group on a protein	nature of process im- plicit in label	truncation		2	0	2
(PD narrow 1)	process not in the	non standard value in	asterisk	6	0	6
(I D Hallow I)	ontology	state variable	other	4	0	4
	ontology	state variable	question mark	42	1	43
	. ,,.	phenotype as modula- tor		4	0	4
	misrepresentation	phenotype as reactant or product		7	0	7
		other		0	1	1
		same reactant and product		30	0	30
	nature of process	other		14	0	14
stimulatory activity	implicit in label	truncation		1	0	1
(PD narrow 1)	-	activation		0	12	12
	process in the ontology	complexation		36	0	36
		degradation		2	0	2
		dissociation		10	0	10
		phosphorylation		23	1	24
		transcription		125	4	129
		translation		6	0	6
		ubiquitination		3	0	3
	process not in the	non standard value in	other	1	0	1
	ontology	state variable	question mark	4	0	4
		process involving an as- rna		1	0	1
addition of a chemical	process not in the	non standard value in	asterisk	3	0	3
group on a protein	ontology	state variable	question mark	3	0	3
(PD narrow 2)		in complete	association	27	8	35
,		incomplete process	dissociation	24	2	26
	misrepresentation	phenotype as reactant or product		1120	7	1127
	-	false multimer		7	0	7

		other		12	15	27
		same reactant and		141	19	160
		product				
		transcription no gene		3	0	3
		ui				
		translation no ui		2	0	2
		association and deacti-		0	1	1
		vation				
	mix of two processes	association and multi-		16	2	18
	of different nature	merisation				
		dissociation and acti-		0	2	2
		vation				
		dissociation and deu-		0	1	1
		biquitination				
		dissociation and multi-		0	2	2
		mer dissociation		0	1	1
		dissociation and phos-		0	1	1
		phorylation		0	1	1
		dissociation and ubiq-		0	1	1
		uitination		1001	110	1111
	nature of process	other translocation		1001 0	110 2	1111 2
	implicit in label	translocation		122	62	184
	nature of process im- plicit in label					184
		methylation of a naf of		2	0	2
		unspecified nature				
	process not in the	gtp exchange		25	10	35
	ontology	production		0	1	1
		non standard value in	asterisk	1	0	1
		state variable	other	19	0	19
			question mark	20	0	20
		process involving an as- rna		56	0	56
	process of unknown na- ture			7	5	12
modulatory activity (PD narrow 1)	misrepresentation	phenotype as modula- tor		4	0	4
		phenotype as reactant		2	0	2
		or product		-		
	mix of two processes of	association and phos-		1	0	1
X /	different nature	phorylation		00		
	nature of process	other		28	0	28
	implicit in label	truncation		1	0	1

		complexation		3	0	3
		degradation		2	0	2
	process in the ontology	other		14	0	14
		transcription		5	0	5
		incomplete process	association	11	0	11
		r r r r	dissociation	11	0	11
		phenotype as modula-		8	0	8
	misrepresentation	tor				
	Ĩ	phenotype as reactant		74	0	74
		or product				
		false multimer		10	0	10
		other		4	4	8
		same reactant and		74	6	80
		product				
		association and activa-		5	4	9
		tion				Ŭ
		association and deacti-		5	0	5
		vation				
	mix of two processes of different nature	association and multi-		4	0	4
		merisation		-		
		association and phos-		4	0	4
		phorylation			-	
atalytic activity (PD		dissociation and acety-		1	0	1
narrow 1)		lation			-	
		dissociation and acti-		0	1	1
		vation				
		dissociation and de-		2	0	2
		phosphorylation			-	
		multimer dissociation		0	4	4
		and deactivation				
		multimerisation and		8	2	10
		activation				
		multimerisation and		1	0	1
		ubiquitination				
		multimersation and		1	0	1
		deacetylation				
		multimerisation and		0	4	4
		phosphorylation				
	nature of process implicit in label	other		280	42	322
		translocation		0	5	5
		truncation		151	70	221
	<u> </u>	association		171	50	221
		degradation		62	23	85

process in the ontology

		dissociation		28	71	99
		multimer dissociation		2	0	2
		multimerisation		14	9	23
		transcription		1100	173	1273
		translation		75	0	75
		transporter activity		324	16	340
		methylation of a naf of		2	0	2
		unspecified nature				
	process not in the	gtp exchange		55	25	80
	ontology	non standard value in	other	7	0	7
		state variable	question mark	1	0	1
		process involving an as-	1	45	0	45
		rna				
		production		2	2	4
	process of unknown na-	-		2	1	3
	ture					
catalytic activity,	process not in the on-	non standard value in	question mark	1	0	1
adding a chemical	tology	state variable				
group on a protein						
(PD narrow 2)						
catalytic activity,	misrepresentation	other		1	0	1
acting on a protein	process in the ontology	channel opening		2	0	2
(PD narrow 1)	process not in the on-	non standard value in	other	2	0	2
	tology	state variable			-	
		phenotype as modula-		2	0	2
catalytic activity (PD	misrepresentation	tor			-	
narrow 2)		other		0	4	4
	nature of process im-	other		1	1	2
	plicit in label					
removal of a chemical	process not in the on-	non standard value in	question mark	1	0	1
group from a protein	tology	state variable				
(PD narrow 2)						
removal of a chemical			asterisk	3	0	3
group from a protein	process not in the	non standard value in	other	2	0	2
(PD narrow 1)	ontology	state variable	question mark	6	0	6
catalytic activity, act-	misrepresentation	same reactant and	1	4	0	4
ing on a protein (PD		product		-		-
narrow 2)		r				
addition of a chemical	process not in the on-	non standard value in	question mark	1	0	1
group on a protein (PD	tology	state variable		1		1
narrow 4)	101063					
narrow 4)						

catalytic activity,	process not in the on-	non standard value in	question mark	2	0	2
adding a chemical	tology	state variable				
group on a protein						
(PD narrow 4)						
Total				5606	790	6396

Table S5: Classification of all instances of the ACSN and PANTHER databases that were only matched by template bricks representing generic concepts. All bricks that were matched by one of 30 template bricks representing generic concepts (e.g. an irreversible process, a catalytic activity) without being matched by template bricks representing more specific concepts (e.g. a protein phosphorylation, a protein kinase activity) were classified in one of the following categories and subcategories. Misrepresentation: the process or activity is badly represented; Same reactant and product: a process consumes a reactant and produces a product that are exactly the same entity pools; *Phenotype* as modulator: a phenotype modulates a process (invalid SBGN); Phenotype as reactant or product: a phenotype is a reactant or a product of a process (invalid SBGN); *Incomplete process*: the process is missing some reactant or product; Association: the process is an incomplete association; Dissociation: the process is an incomplete dissociation; False multimer: a multimer is represented using two subunits on top of each other and not a multimer glyph; Transcription no gene ui: a transcription is represented without using a proper unit of information for the gene: Translation no ui: a translation is represented without using a proper unit of information for the mRNA; Other: none of the above. Nature of process implicit in label: the nature of the process can solely be identified by analyzing the labels of the participants of the process (e.g. the truncation of a protein, where a protein is consumed to give two or more proteins with new names); Truncation: the process is a truncation; Translocation: the process is a translocation. Other: none of the above. Process of unknown nature: we could not identify the nature of the represented process or the activity. Process in the ontology: this category implies only modulatory activities whose modulated process is an instance of a template brick that belongs to the ontology (e.g. stimulation of dissociation). Activation: the process is an activation; Translocation: the process is a translocation; *Complexation*: the process is a complexation; *Degradation*: the process is a degradation; Dissociation: the process is a dissociation; *Phosphorylation*: the process is a phosphorylation; *Transcription*: the process is a transcription; Translation: the process is a translation; Ubiquitination: the process is an ubiquitination; Association: the process is an association; *Multimer dissociation*: the process is a multimer dissociation; *Multimerisation*: the process is a multimerisation; Transporter activity: the process is a translocation; Channel opening: the process is a channel opening. Other: none of the above. Mix of two processes of unknown nature: two processes are represented using only one SBGN process (e.g. a dissociation and a dephosphorylation); Association and deactivation: the process is an association and a deactivation; Association and multimerisation: the process is an association and a multimerisation; Dissociation and activation: the process is a dissociation and an activation; Dissociation and deubiquitination: the process is a dissociation and a deubiquitination; Dissociation and multimer dissociation: the process is a dissociation and a multimer dissociation; Dissociation and phosphorylation: the process is a dissociation and a phosphorylation; Dissociation and ubiquitination: the process is a dissociation and an ubiquitination; Association and phosphorylation: the process is an association and a phosphorylation; Association and activation: the process is an association and a activation; Dissociation and acetylation: the process is a dissociation and an acetylation; Dissociation and dephosphorylation: the process is a dissociation and a dephosphorylation; *Multimer dissociation and deactivation*: the process is a multimer dissociation and a deactivation; Multimerisation and activation: the process is a multimerisation and an activation; Multimerisation and ubiquitination: the process is a multimerisation and an ubiquitination. Multimerisation and deacetylation: the process is a multimerisation and a deacetylation; Multimerisation and phosphorylation: the process is a multimerisation and a phosphorylation; **Process not in the ontology**: the process represented in the brick is not an instance of any template brick of the ontology; Non standard value in state variable: the process sets a value to a state variable that is not defined by the controlled vocabulary of the SBGN standard; Asterisk: the value is an asterisk ("*"). This value is used in CellDesigner to mean "don't care". It does not belong to the controlled vocabulary of SBGN, but its use in state variables is valid SBGN. However processes using this value cannot be linked to any specific concept of SBO or GO. Question mark: the value is a question mark ("?"). Same as for "*", but with meaning "unknown". Other: none of the above; Process involving an asRNA: the process consumes or produces an asRNA: Methylation of a naf of unspecified nature: the process is a methylation of a nuclear acid feature with no conceptual type defined (e.g. gene or mRNA); Gtp exchange: the process is a GTP/GDP exchange process; *Production*: the process consumes an empty set.

Category	Subcategories		ACSN	PANTHER	Overall
	same reactant and product		252	25	277
	phenotype as modulator		18	0	18
	phenotype as reactant or product		1203	7	1210
misrepresentation	1	association	38	8	46
-	incomplete process	dissociation	35	2	37
	false multimer		17	0	17
	transcription no gene ui		3	0	3
	translation no ui		2	0	2
	other		19	24	43
nature of process implicit in label	truncation		280	132	412
	translocation		0	7	7

	other		1328	154	1482
process of unknown nature			9	6	15
	activation		0	13	13
	translocation		2	0	2
	complexation		39	0	39
	degradation		66	23	89
	dissociation		38	71	109
	phosphorylation		23	1	24
	transcription		1230	177	1407
process in the ontology	translation		81	0	81
	ubiquitination		3	0	3
	association		171	50	221
	multimer dissociation		2	0	2
	multimerisation		14	9	23
	transporter activity		324	16	340
	channel opening		2	0	2
	other		14	0	14
	association and deactivation		5	1	6
	association and multimeri-		20	2	22
	sation				
	dissociation and activation		0	3	3
	dissociation and deubiquiti-		0	1	1
	nation				
	dissociation and multimer		0	2	2
mix of two processes of	dissociation				
different nature	dissociation and phosphory-		0	1	1
	lation				
	dissociation and ubiquitina-		0	1	1
	tion				
	association and phosphory-		5	0	5
	lation				
	association and activation		5	4	9
	dissociation and acetylation		1	0	1
	dissociation and dephospho-		2	0	2
	rylation				
	multimer dissociation and		0	4	4
	deactivation				
	multimerisation and activa-		8	2	10
	tion				
	multimerisation and ubiqui-		1	0	1
	tination				
	multimersation and		1	0	1
	deacetylation				
	multimerisation and phos-		0	4	4
	phorylation				
	non standard value in state	asterisk	18	0	18
	variable	question mark	104	2	106
process not in the ontology		other	35	0	35
	process involving an asrna		102	0	102
	methylation of a naf of un-		4	0	4
	specified nature				
	gtp exchange		80	35	115
	production		2	3	5
Total			5606	790	6396

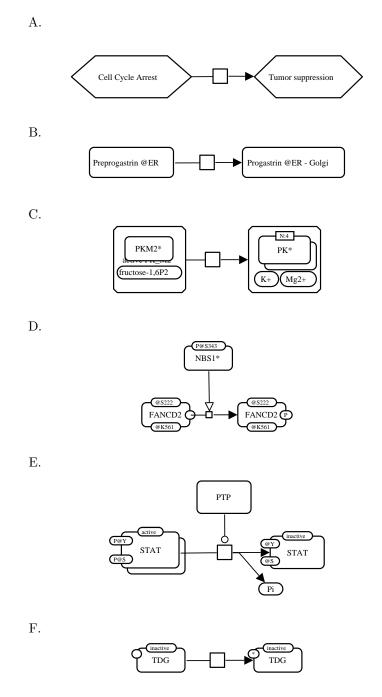


Figure S3: Example of instance bricks for each main category. A. Misrepresentation: the instance represents the consumption and production of phenotypes, which is invalid SBGN. It was retrieved from the "p53 pathway" map of the PANTHER database. B. Nature of process implicit in labels: the instance potentially represents the translocation of preprogastrin from the endoplasmic reticulum to the Golgi apparatus. It was retrieved from the "CCKR signaling map" of the PANTHER database. C. Process of unknown nature. The instance was retrieved from the "RCD master" map of the ACSN. D. Process in the ontology: the instance represents the stimulation of the phophorylation of FANCD2 bu NBS1. It was retrieved from the "Cell Cycle DNA repair master" map of the ACSN. E. Mix of two process of different nature: the instance represents the dephosphorylation and deactivation of STAT, catalyzed bu PTP. It was retrieved from the "JAK STAT signaling pathway" map of the ACSN. F. Process not in the ontology: the instance represents the modification of TDG to a state that is not indicated ("*" state variable value). It was retrieved from the "Cell Cycle DNA repair master" map of the ACSN.