Model

intrinsic formalism	qualifier	entity	qualifier	reference type	reference
ODE system	represents	**interaction between cdc2 and cyclin when forming MPF**	is_version_of	GO	regulation of cell cycle

Species

intrinsic element	qualifier	entity	qualifier	reference type	reference
		EmptySet	compartment	THIS	cell
[C2]	concentration_of	**cdc2k**	compartment is_version_of	THIS UNIPROT	cell CDC2_SCHPO
[CP]	concentration_of	**cdc2k-P**	compartment is_version_of	THIS UNIPROT	cell CDC2_SCHPO
[M]	concentration_of	**p-cyclin_cdc2**	compartment has_part has_part	THIS INTERPRO UNIPROT	cell IPR006670 CDC2_SCHPO
[pM]	concentration_of	**p-cyclin_cdc2-p**	compartment has_part has_part	THIS INTERPRO UNIPROT	cell IPR006670 CDC2_SCHPO
[Y]	concentration_of	**cyclin**	compartment is_version_of	THIS INTERPRO	cell IPR006670
[YP]	concentration_of	**p-cyclin**	compartment is_version_of	THIS INTERPRO	cell IPR006670

Reactions

intrinsic element	qualifier	entity	qualifier	type	reference
k_6[M]	kinetic_law_of	**cyclin_cdc2k dissociation**	is_version_of has_reactant has_product has_product has_rate	GO THIS THIS THIS THIS	regulation of cyclin dependent protein kinase activity p-cyclin_cdc2 cdc2k p-cyclin k_6
k_8[~P][C2]	kinetic_law_of	**cdc2k phosphorylation**	is_version_of is_version_of has_reactant has_reactant has_product has_rate	GO EC THIS THIS THIS THIS	protein amino acid phosphorylation EC 2.7.1.37 cdc2k adenosine triphosphate cdc2k-P k_8
k_9[CP]	kinetic_law_of	**cdc2k dephosphorylation**	is_version_of is_version_of has_reactant has_product has_product has_rate	GO EC THIS THIS THIS THIS	protein amino acid dephosphorylation EC 3.1.3.16 cdc2k-P cdc2k Empty set (inorganic phosphate) k_9
k_3[CP][Y]	kinetic_law_of	**cyclin cdc2k-p association**	is_version_of is_version_of has_reactant has_reactant has_reactant has_product has_rate	REACTOME REACTOME THIS THIS THIS THIS THIS	68910 69282 cdc2k-P cyclin adenosine triphosphate p-cyclin_cdc2-p k_3
k_5[~P][M]	kinetic_law_of	**deactivation of cdc2 kinase**	is_version_of is_version_of is_version_of is_version_of has_reactant has_reactant has_product has_rate	GO GO EC REACTOME THIS THIS THIS THIS	negative regulation of cyclin dependent protein kinase activity protein amino acid phosphorylation EC 2.7.1.37 69260 adenosine triphosphate p-cyclin_cdc2 p-cyclin_cdc2-p k_5
k_1[aa]	kinetic_law_of	**cyclin biosynthesis**	is_version_of has_reactant has_product has_rate	GO THIS THIS THIS	translation Empty set (amino acids) cyclin k_1
k_2[Y]	kinetic_law_of	**default degradation of cyclin**	is_version_of has_reactant has_product has_rate	GO THIS THIS THIS	cyclin catabolism cyclin Empty set (amino acids) k_2
k_7[YP]	kinetic_law_of	**cdc2 kinase triggered degration of cyclin**	is_version_of has_version has_version has_reactant has_product has_product has_rate	GO REACTOME REACTOME THIS THIS THIS THIS	cyclin catabolism 69271 69766 p-cyclin Empty set (amino acids) Empty set (inorganic phosphate) k_7
[pM]× $(k'_4 + k_4([M]/[CT])^2)$	kinetic_law_of	**activation of cdc2 kinase**	is_version_of is_version_of is_version_of is has_reactant has_product catalyst_by has_rate has_rate	GO GO EC REACTOME THIS THIS THIS THIS THIS	positive regulation of cyclin dependent protein kinase activity protein amino acid dephosphorylation EC 3.1.3.16 69263 p-cyclin_cdc2-p p-cyclin_cdc2 p-cyclin_cdc2 k'_4 k_4

Behaviour

intrinsic behaviour	qualifier	entity	qualifier	reference type	reference
steady state with high values of [M]	represents results_from	**metaphase arrest** **parameter setting 1**	is_part is_version_of is_in	GO GO THIS	metaphase cell cycle arrest parameter region A, C
spontaneous oscillation	represents results_from	**rapid division cycles in early embryos** **parameter setting 2**	is_version_of is_in	GO THIS	embryonic cleavage parameter region C'
excitable switch	represents results_from	**growth-controlled division cycles in non-embryonic cells** **parameter setting 3**	is_part is_in	GO THIS	cell division parameter region B