

Ontology	Biological role	p-value	Fold	Genes	Binding sites
GO Molecular Function	SMAD binding	1.2×10^{-5}	2.2	17	36
	protein phosphatase binding	7.5×10^{-4}	2.1	18	25
GO Biological Process	placenta development	9.0×10^{-9}	2.4	31	56
	embryonic placenta development	4.1×10^{-8}	2.6	24	44
	stem cell maintenance	1.2×10^{-7}	2.9	19	34
	stem cell differentiation	1.8×10^{-7}	2.5	22	43
	stem cell development	2.4×10^{-7}	2.6	20	37
GO Cellular Component	catenin complex	6.7×10^{-7}	4.2	6	18
Mouse Phenotypes	abnormal placenta development	1.5×10^{-13}	2.1	57	116
	abnormal trophoblast layer morphology	1.3×10^{-11}	2.5	36	71
	extramedullary hematopoiesis	3.2×10^{-10}	2.4	38	68
	abnormal placenta junctional zone morphology	7.9×10^{-10}	3.1	21	41
	abnormal spongiotrophoblast layer morphology	2.1×10^{-9}	3.0	20	40
PANTHER Pathway	Interferon-gamma signaling pathway	6.3×10^{-13}	5.3	15	30
Pathway Commons	IL2-mediated signaling events	5.5×10^{-12}	2.7	34	63
	IL6-mediated signaling events	2.6×10^{-9}	2.9	19	43
	TCR signaling in naive CD8+ T cells	4.0×10^{-8}	2.2	38	57
	FAS (CD95) signaling pathway	1.3×10^{-7}	2.1	37	61
	Arf6 downstream pathway	4.9×10^{-6}	2.1	32	46
BioCyc Pathway	-				
TreeFam	-				