

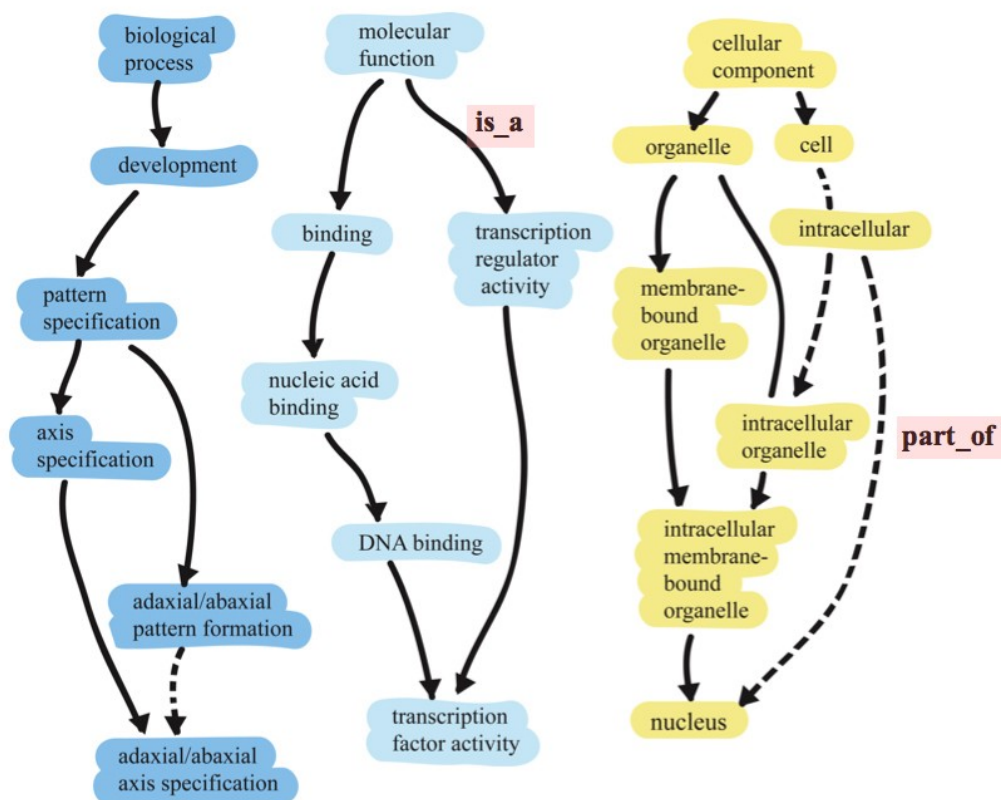
Gene Ontology: tool for the unification of biology

link: <http://www.geneontology.org>

What is Gene Ontology?

The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products in different databases. The GO collaborators are developing three structured, controlled vocabularies (ontologies) that describe gene products in terms of their associated *biological processes*, *cellular components* and *molecular functions* in a species-independent manner.

How is Gene Ontology structured?



GO-Analysis-System for SuperSAGE-Data

link: <http://genxpro.ath.cx/>

Login: GO_tool_test / STDGE2GO

GO-TERM-ID

GO-TERM-DESCRIPTION

PART-OF-RELATIONSHIP

NUMBER OF TRANSCRIPTS CONTAINING GO-TERM

CLICK: TABLE WITH ALL COUNTED TRANSCRIPTS ACCORDING TO GO-TERM

GO:0003674 : molecular_function (Transcripts found: 4980) - (TAGS found: 6024) - SCATTERPLOT

GO:0005198 : structural_molecule_activity (Transcripts found: 622) - (TAGS found: 773) - p-Value=1.23472905213E-27 - SCATTERPLOT

GO:0005488 : binding (Transcripts found: 3631) - (TAGS found: 4400) - p-Value=3.17689000143E-23 - SCATTERPLOT

GO:0003824 : catalytic_activity (Transcripts found: 2232) - (TAGS found: 2673) - p-Value=1.86567305332E-6 - SCATTERPLOT

GO:0016209 : antioxidant_activity (Transcripts found: 36) - (TAGS found: 43) - p-Value=0.00013479433451 - SCATTERPLOT

GO:0060699 : molecular_transducer_activity (Transcripts found: 522) - (TAGS found: 640) - p-Value=0.0009028099129797 - SCATTERPLOT

GO:0005215 : transporter_activity (Transcripts found: 462) - (TAGS found: 574) - p-Value=0.00132711452029 - SCATTERPLOT

GO:00030528 : transcription_regulator_activity (Transcripts found: 622) - (TAGS found: 750) - p-Value=0.026251995487 - SCATTERPLOT

GO:0015457 : auxiliary_transport_protein_activity (Transcripts found: 14) - (TAGS found: 16) - p-Value=0.272164860091 - SCATTERPLOT

GO:00030234 : enzyme_regulator_activity (Transcripts found: 336) - (TAGS found: 418) - p-Value=0.276584427489 - SCATTERPLOT

GO:0009095 : electron_carrier_activity (Transcripts found: 22) - (TAGS found: 29) - p-Value=0.31642808342 - SCATTERPLOT

GO:0045499 : chemorepellent_activity (Transcripts found: 3) - (TAGS found: 4) - p-Value=0.4221800896341 - SCATTERPLOT

GO:0045182 : translation_regulator_activity (Transcripts found: 120) - (TAGS found: 141) - p-Value=0.917435891581 - SCATTERPLOT

GO:0010860 : proteasome_regulator_activity (Transcripts found: 3) - (TAGS found: 4) - p-Value=1 - SCATTERPLOT

GO:0016530 : metalloprotease_activity (Transcripts found: 1) - (TAGS found: 1) - p-Value=1 - SCATTERPLOT

GO:0005575 : cellular_component (Transcripts found: 4689) - (TAGS found: 5894) - SCATTERPLOT

GO:0044464 : cell_part (Transcripts found: 4703) - (TAGS found: 5697) - p-Value=3.62529658923E-35 - SCATTERPLOT

GO:0005623 : cell (Transcripts found: 4703) - (TAGS found: 5697) - p-Value=3.62529658923E-35 - SCATTERPLOT

GO:0005576 : extracellular_region (Transcripts found: 603) - (TAGS found: 740) - p-Value=3.11245539826E-20 - SCATTERPLOT

GO:0044421 : extracellular_region_part (Transcripts found: 521) - (TAGS found: 644) - p-Value=1.04136022002E-15 - SCATTERPLOT

GO:0043226 : organelle (Transcripts found: 3500) - (TAGS found: 4244) - p-Value=4.0688695515E-15 - SCATTERPLOT

GO:00032991 : macromolecular_complex (Transcripts found: 1688) - (TAGS found: 1990) - p-Value=1.41976129425E-11 - SCATTERPLOT

GO:00030529 : ribonucleoprotein_complex (Transcripts found: 498) - (TAGS found: 595) - p-Value=2.23213151212E-10 - SCATTERPLOT

GO:0043234 : protein_complex (Transcripts found: 1224) - (TAGS found: 1463) - p-Value=0.000463273505668 - SCATTERPLOT

GO:0032993 : protein-DNA_complex (Transcripts found: 31) - (TAGS found: 35) - p-Value=0.853108077611 - SCATTERPLOT

GO:0044422 : organelle_part (Transcripts found: 1664) - (TAGS found: 2015) - p-Value=7.09592174685E-7 - SCATTERPLOT

GO:00031974 : membrane-enclosed_lumen (Transcripts found: 827) - (TAGS found: 739) - p-Value=0.0078867492969 - SCATTERPLOT

GO:0019012 : vitron (Transcripts found: 19) - (TAGS found: 20) - p-Value=0.107520994694 - SCATTERPLOT

GO:0044423 : vitron_part (Transcripts found: 19) - (TAGS found: 20) - p-Value=0.212722048635 - SCATTERPLOT

GO:0045202 : synapse (Transcripts found: 76) - (TAGS found: 89) - p-Value=0.455500222664 - SCATTERPLOT

GO:0044456 : synapse_part (Transcripts found: 52) - (TAGS found: 61) - p-Value=0.72273970514 - SCATTERPLOT

GO:0008150 : biological_process (Transcripts found: 5047) - (TAGS found: 6088) - SCATTERPLOT

MINIMAL P-VALUE FOR GO-TERM IN ACTUAL BRANCH / GO-LEVEL

P-VALUE FOR GO-TERM

SHOW SCATTERPLOT FOR GO-TERM IN RELATION TO ALL TRANSCRIPTS

NUMBER OF TAGS CONTAINING GO-TERM

CLICK: TABLE WITH ALL COUNTED TAGS ACCORDING TO GO-TERM

different_tag	L1_mml_Male_gonads_Gallus_tf_sum_1000000	L2_mml_Female_gonads_Gallus_tf_sum_1000000	prvalue	fold_change	description
1	44.1822	519.232	0	-3.55484	CFP50854 or TC14631
2	22.7658	132.076	0	-2.5345	BU207838 or TC14871
3	56.6867	936.603	0	-2.43629	TC150929 UPMYHB
4	392.079	1594.47	0	-2.14889	NP1061044 Chicken 6
5	98.0801	354.836	0	-1.86497	CFP23113 or TC14286
6	76.4158	247.728	0	-1.89661	TC150603 similar to U
7	1308.63	4013.68	0	-1.61577	BU4564530 or BU45393
8	98.9237	234.141	0	-1.24289	CO604439 or CO5037
9	217.577	497.493	0	-1.19315	TC150000 UPLUUN_C
10	1831.76	3478.83	0	-0.926376	TC142946 homologue

TAG	L1_mml_Male_gonads_Gallus_tf_sum_1000000	L2_mml_Female_gonads_Gallus_tf_sum_1000000	score	identity	prvalue	fold_change	description	
1	CATGGATTCTCACTGTGTAAATA	44.1822	519.232	92.0341	26	0	-3.55484	CFP50854 or TC14631
2	CATGCTTGGCGTCTACAGAGGAT	22.7658	132.076	92.0341	26	0	-2.5345	BU207838 or TC14871
3	CATGATGGTCTTACACATTAATA	33.6228	192.912	92.0341	26	0	-2.44048	TC150929 UPMYHB
4	CATGTTACTCACTTGAATVACCTGG	382.079	1094.47	92.0341	26	0	-2.14889	NP1061044 Chicken 6
5	CATGTGTGGTGGGGGAGTACCTTC	98.0801	354.836	92.0341	26	0	-1.85487	CFP23113 or TC14286
6	CATGACAGTGGCATVAAATTAAT	76.3943	244.331	92.0341	26	0	-1.89803	TC150603 similar to U
7	CATGCTAAGCTTCTCCCTTCACTC	1308.63	4013.68	92.0341	26	0	-1.61577	BU4564530 or BU45393
8	CATGTGACAGTGGTATGAAAGTGT	98.9237	234.141	92.0341	26	0	-1.24289	CO604439 or CO5037
9	CATGCTACTTAAACCACTGATGACA	217.577	497.493	92.0341	26	0	-1.19315	TC150000 UPLUUN_C
10	CATGGCGCAAAAACATGATGATGATAC	1817.50	3436.03	92.0341	26	0	-0.918722	TC142946 homologue