

Table S1. Gene ontology for *Leishmania* species.

Organism	DEG	Ontology	ID	Name	Conteo Bgd	Result Count	Pct of bgd	Fold Enrichment	Odds Ratio	Valor P	Benjamini	Bonferroni
		BIOLOGICAL PROCESS	GO:0008152	metabolic process	1486	38	26	176	2.59	4509367,194	3,66049E+11	1,26713E+11
			GO:0009987	cellular process	1524	32	21	145	1.8	9,69154E+11	2,3079E+11	10
			GO:0006807	nitrogen compound metabolic process	1077	27	25	173	2.17	1,6166E+11	5,45293E+11	4,54264E+11
			GO:0034641	cellular nitrogen compound metabolic process	626	21	34	231	2.89	1,42612E+11	8,7117E+11	4,00738E+11
			GO:1901360	organic cyclic compound metabolic process	486	19	39	27	3.37	4150054,294	3,66049E+11	1,16617E+11
			GO:0009058	biosynthetic process	452	15	33	229	2.67	1,75342E+11	5,58505E+11	4,92711E+11
			GO:0044249	cellular biosynthetic process	423	13	31	212	2.4	7,0611E+11	1,7405E+11	10
			GO:0065007	biological regulation	461	12	26	18	1.97	3,19753E+11	6,60667E+11	10
			GO:1901566	organonitrogen compound biosynthetic process	284	11	39	267	3.04	2,36431E+11	6,7793E+11	6,64372E+11
			GO:0044271	cellular nitrogen compound biosynthetic process	294	11	37	258	2.92	30997798979	8,37537E+11	8,71038E+11
			GO:1901135	carbohydrate derivative metabolic process	90	8	89	613	7.31	3986105,869	3,66049E+11	1,1201E+11
			GO:0009056	catabolic process	102	7	69	473	5.42	6,22772E+11	2,9835E+11	1,74999E+11
			GO:0034654	nucleobase-containing compound biosynthetic process	103	7	68	469	5.36	6,60516E+11	2,9835E+11	1,85605E+11
			GO:0019438	aromatic compound biosynthetic process	113	7	62	427	4.85	1,1472E+11	4,29818E+11	3,22363E+11
			GO:0018130	heterocycle biosynthetic process	121	7	58	399	4.5	1,71032E+11	5,55251E+11	4,806E+11
			GO:0006082	organic acid metabolic process	124	7	56	389	4.38	1,96974E+11	6,0387E+11	5,53498E+11
			GO:0072522	purine-containing compound biosynthetic process	35	7	200	138	18.64	49202,18866	6912907,507	1,38258E+11
			GO:0019637	organophosphate metabolic process	115	7	61	42	4.76	1,2718E+11	4,52375E+11	3,57376E+11
			GO:1901362	organic cyclic compound biosynthetic process	127	7	55	38	4.27	2,25878E+11	6,54348E+11	6,34717E+11
			GO:0046700	heterocycle catabolic process	34	6	176	1217	15.75	738721,25	1,72984E+11	2,07581E+11
			GO:0005975	carbohydrate metabolic process	70	6	86	591	6.84	4,76674E+11	2,3994E+11	13394542559
			GO:0050794	regulation of cellular process	178	6	34	233	2.49	4,331E+11	8,33569E+11	10
			GO:0019693	ribose phosphate metabolic process	45	6	133	92	11.28	3943208,046	3,66049E+11	11080414609
			GO:0046390	ribose phosphate biosynthetic process	29	5	172	1189	15.1	5064077,381	3,66049E+11	1,42301E+11
			GO:0017144	drug metabolic process	59	5	85	585	6.67	1,52243E+11	5,21711E+11	4,27803E+11
			GO:0044283	small molecule biosynthetic process	79	5	63	437	4.85	5,47715E+11	1,42507E+11	10
			GO:0006508	proteolysis	127	5	39	272	2.91	3,62435E+11	7,38002E+11	10
			GO:0006733	oxidoreduction coenzyme metabolic process	26	4	154	1061	13.0	4,78172E+11	2,3994E+11	1,34366E+11
			GO:0032787	monocarboxylic acid metabolic process	38	4	105	726	8.39	2,07027E+11	6,05985E+11	5,81745E+11
			GO:0042592	homeostatic process	52	4	77	531	5.93	6,51851E+11	1,68046E+11	10
			GO:0051186	cofactor metabolic process	63	4	63	438	4.81	1,27293E+11	3,00583E+11	10
			GO:0006006	glucose metabolic process	8	3	375	2587	42.45	1,55527E+11	9,29854E+11	4,37031E+11
			GO:0009132	nucleoside diphosphate metabolic process	13	3	231	1592	21.2	7,53837E+11	2,9835E+11	2,11828E+11
			GO:0046939	nucleotide phosphorylation	13	3	231	1592	21.2	7,53837E+11	2,9835E+11	2,11828E+11
			GO:0042866	pyruvate biosynthetic process	13	3	231	1592	21.2	7,53837E+11	2,9835E+11	2,11828E+11
			GO:0046434	organophosphate catabolic process	19	3	158	1089	13.24	2,39924E+11	6,80997E+11	6,74187E+11
			GO:0034404	nucleobase-containing small molecule biosynthetic process	24	3	125	862	10.08	4,75772E+11	1,24946E+11	10
			GO:0006091	generation of precursor metabolites and energy	37	3	81	559	6.21	1,59687E+11	3,50564E+11	10
			GO:0016052	carbohydrate catabolic process	18	3	167	115	14.12	20415527053	6,0387E+11	5,73676E+11
			GO:0060249	anatomical structure homeostasis	9	2	222	1533	19.93	6,98837E+11	1,73782E+11	10

## SUBREGULADO

## CELLULAR COMPONENT

GO:0000723	telomere maintenance	9	2	222	1533	19.93	6,98837E+11	1,73782E+11	10
GO:0032200	telomere organization	9	2	222	1533	19.93	6,98837E+11	1,73782E+11	10
GO:0015985	energy coupled proton transport, down electrochemical gradient	6	2	333	230	34.9	2,99514E+11	8,17122E+11	8,41635E+11
GO:0043038	amino acid activation	23	2	87	60	6.62	4,31063E+11	8,33569E+11	10
GO:0006421	asparaginyl-tRNA aminoacylation	1	1	1000	6899	inf	1,44956E+11	3,20728E+11	10
GO:0044091	membrane biogenesis	1	1	1000	6899	inf	1,44956E+11	3,20728E+11	10
GO:0006562	proline catabolic process	1	1	1000	6899	inf	1,44956E+11	3,20728E+11	10
GO:0006275	regulation of DNA replication	1	1	1000	6899	inf	1,44956E+11	3,20728E+11	10
GO:0006434	seryl-tRNA aminoacylation	1	1	1000	6899	inf	1,44956E+11	3,20728E+11	10
GO:0020033	antigenic variation	2	1	500	3449	68.89	2,87837E+11	5,99128E+11	10
GO:0009065	glutamine family amino acid catabolic process	2	1	500	3449	68.89	2,87837E+11	5,99128E+11	10
GO:0043648	dicarboxylic acid metabolic process	3	1	333	230	34.44	4,28675E+11	8,33569E+11	10
GO:0020015	glycosome	115	8	70	48	5.57	2,27556E+11	1,11849E+11	2,50312E+11
GO:0042579	microbody	120	8	67	46	5.32	3,05043E+11	1,11849E+11	3,35547E+11
GO:0005777	peroxisome	120	8	67	46	5.32	3,05043E+11	1,11849E+11	3,35547E+11
GO:0005829	cytosol	61	4	66	452	4.98	1,13961E+11	1,16489E+11	10
GO:0045259	proton-transporting ATP synthase complex	20	3	150	1035	12.46	2,79343E+11	4,38967E+11	3,07277E+11
GO:0016469	proton-transporting two-sector ATPase complex	36	3	83	575	6.4	1,48258E+11	1,16489E+11	10
GO:0098800	inner mitochondrial membrane protein complex	38	3	79	545	6.03	1,716E+11	1,2584E+11	10
GO:0019866	organelle inner membrane	44	3	68	47	5.14	2,53311E+11	1,46654E+11	10
GO:0030863	cortical cytoskeleton	12	2	167	115	13.94	1,24567E+11	1,16489E+11	10
GO:0009897	external side of plasma membrane	1	1	1000	6899	inf	1,44956E+11	1,16489E+11	10
GO:0000015	phosphopyruvate hydratase complex	1	1	1000	6899	inf	1,44956E+11	1,16489E+11	10
GO:0020038	subpellicular network	1	1	1000	6899	inf	1,44956E+11	1,16489E+11	10
GO:0020039	pellicle	2	1	500	3449	68.89	2,87837E+11	1,58311E+11	10
GO:0032153	cell division site	3	1	333	230	34.44	4,28675E+11	1,88617E+11	10
GO:0032155	cell division site part	3	1	333	230	34.44	4,28675E+11	1,88617E+11	10
GO:0003824	catalytic activity	1571	49	31	215	4.43	33,6306725	6423,458448	6423,458448
GO:1901363	heterocyclic compound binding	1214	28	23	159	1.97	4,62357E+11	3,27074E+11	8,83101E+11
GO:0097159	organic cyclic compound binding	1214	28	23	159	1.97	4,62357E+11	3,27074E+11	8,83101E+11
GO:0043167	ion binding	982	27	27	19	2.44	3,62542E+11	69245463339	69245463339
GO:0016787	hydrolase activity	582	22	38	261	3.36	1446825,077	6,90859E+11	2,76344E+11
GO:1901265	nucleoside phosphate binding	730	21	29	198	2.41	1,18116E+11	1,32706E+11	22560079873
GO:0000166	nucleotide binding	730	21	29	198	2.41	1,18116E+11	1,32706E+11	22560079873
GO:0036094	small molecule binding	757	21	28	191	2.31	1,88701E+11	1,60414E+11	3,6042E+11
GO:0043168	anion binding	728	18	25	171	1.95	1,41189E+11	4,03717E+11	10
GO:0097367	carbohydrate derivative binding	669	17	25	175	2.0	13352537266	4,03717E+11	10
GO:0008144	drug binding	585	15	26	177	1.99	1,88673E+11	4,90736E+11	10
GO:0016817	hydrolase activity, acting on acid anhydrides	246	12	49	337	3.96	1,83788E+11	4,38793E+11	3,51035E+11
GO:0016491	oxidoreductase activity	220	10	45	314	3.58	1,15156E+11	1,32706E+11	2,19947E+11
GO:0046872	metal ion binding	285	10	35	242	2.7	75405739228	4,03717E+11	10
GO:0043169	cation binding	290	10	34	238	2.65	8,48866E+11	4,03717E+11	10
GO:0016887	ATPase activity	103	8	78	536	6.29	1,05141E+11	4,01637E+11	2,00819E+11
GO:0000287	magnesium ion binding	22	5	227	1568	21.35	1215486,183	6,90859E+11	2,32158E+11
GO:0070011	peptidase activity, acting on L-amino acid peptides	114	5	44	303	3.27	2,41639E+11	5,91706E+11	10
GO:0008233	peptidase activity	119	5	42	29	3.12	2,84433E+11	6,17719E+11	10

## MOLECULAR FUNCTION

GO:0140097	catalytic activity, acting on DNA	44	4	91	627	7.13	3,56603E+11	2,72445E+11	6,81112E+11
GO:0016874	ligase activity	60	4	67	46	5.07	1,07648E+11	4,03717E+11	10
GO:0008094	DNA-dependent ATPase activity	16	3	188	1294	16.3	1,43056E+11	1,40445E+11	2,73238E+11
GO:0004519	endonuclease activity	17	3	176	1217	15.13	1,7191E+11	1,56357E+11	3,28349E+11
GO:0016757	transferase activity, transferring glycosyl groups	31	3	97	668	7.55	98275826918	4,03717E+11	10
GO:0016829	lyase activity	37	3	81	559	6.21	1,59687E+11	4,23615E+11	10
GO:0005509	calcium ion binding	56	3	54	37	3.97	4690831862	8,95949E+11	10
GO:0004611	phosphoenolpyruvate carboxykinase activity	2	2	1000	6899	inf	2,0736E+11	4,40063E+11	3,96057E+11
GO:0018024	histone-lysine N-methyltransferase activity	3	2	667	4599	139.67	6,16225E+11	8,40707E+11	1,17699E+11
GO:0046933	proton-transporting ATP synthase activity, rotational mechanism	5	2	400	2759	46.54	2,01567E+11	1,60414E+11	3,84993E+11
GO:0008276	protein methyltransferase activity	8	2	250	1725	23.26	5,4867E+11	3,61366E+11	10
GO:0004003	ATP-dependent DNA helicase activity	9	2	222	1533	19.93	6,98837E+11	3,92582E+11	10
GO:0050661	NADP binding	9	2	222	1533	19.93	6,98837E+11	3,92582E+11	10
GO:0016763	transferase activity, transferring pentosyl groups	9	2	222	1533	19.93	6,98837E+11	3,92582E+11	10
GO:0003746	translation elongation factor activity	9	2	222	1533	19.93	6,98837E+11	3,92582E+11	10
GO:0008170	N-methyltransferase activity	11	2	182	1254	15.49	1,04783E+11	4,03717E+11	10
GO:0022853	active ion transmembrane transporter activity	13	2	154	1061	12.67	1,45845E+11	4,03717E+11	10
GO:0016830	carbon-carbon lyase activity	16	2	125	862	9.95	2,18182E+11	5,48326E+11	10
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	22	2	91	627	6.96	3,97237E+11	8,31646E+11	10
GO:0016875	ligase activity, forming carbon-oxygen bonds	23	2	87	60	6.62	4,31063E+11	8,31646E+11	10
GO:0003842	1-pyrroline-5-carboxylate dehydrogenase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004816	asparagine-tRNA ligase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0032451	demethylase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0030337	DNA polymerase processivity factor activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0003920	GMP reductase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0016657	oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004612	phosphoenolpyruvate carboxykinase (ATP) activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004634	phosphopyruvate hydratase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004731	purine-nucleoside phosphorylase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0050242	pyruvate, phosphate dikinase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004748	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0004828	serine-tRNA ligase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0017061	S-methyl-5-thioadenosine phosphorylase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0008398	sterol 14-demethylase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0000310	xanthine phosphoribosyltransferase activity	1	1	1000	6899	inf	1,44956E+11	4,03717E+11	10
GO:0031420	alkali metal ion binding	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0004422	hypoxanthine phosphoribosyltransferase activity	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0003938	IMP dehydrogenase activity	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0016781	phosphotransferase activity, paired acceptors	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0030955	potassium ion binding	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0019904	protein domain specific binding	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0106130	purine phosphoribosyltransferase activity	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0004743	pyruvate kinase activity	2	1	500	3449	68.89	2,87837E+11	6,17719E+11	10
GO:0003909	DNA ligase activity	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10
GO:0004427	inorganic diphosphatase activity	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10

## BIOLOGICAL PROCESS

GO:0016864	intramolecular oxidoreductase activity, transposing S-S bonds	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10
GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reducti	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10
GO:0004618	phosphoglycerate kinase activity	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10
GO:0003756	protein disulfide isomerase activity	3	1	333	230	34.44	4,28675E+11	8,31646E+11	10
GO:0008152	metabolic process	1486	74	50	162	2.22	9897,821532	5531782,479	4,9786E+11
GO:0009987	cellular process	1524	64	42	137	1.64	2,02318E+11	1,92011E+11	10
GO:0071704	organic substance metabolic process	1251	61	49	159	2.0	3727156,68	6,82932E+11	1,87476E+11
GO:0044238	primary metabolic process	1210	56	46	151	1.82	4,10611E+11	5,17876E+11	2,06538E+11
GO:0044237	cellular metabolic process	1137	51	45	146	1.71	1,78572E+11	1,79644E+11	8,98218E+11
GO:0006807	nitrogen compound metabolic process	1077	50	46	151	1.78	9,18394E+11	1,073E+11	4,61952E+11
GO:1901564	organonitrogen compound metabolic process	722	48	66	216	2.79	6103,631267	1535063,264	3070126,527
GO:0009058	biosynthetic process	452	35	77	252	3.11	17008,62849	1711068,026	8555340,131
GO:1901576	organic substance biosynthetic process	436	34	78	254	3.12	22467,25447	1883504,833	1,1301E+11
GO:0044249	cellular biosynthetic process	423	33	78	254	3.11	3492,479105	2195896,237	1,75672E+11
GO:0019538	protein metabolic process	592	33	56	181	2.09	41182962715	5,17876E+11	2,0715E+11
GO:1901566	organonitrogen compound biosynthetic process	284	27	95	309	3.79	9448,359689	1584174,975	4752524,924
GO:0044267	cellular protein metabolic process	524	27	52	168	1.86	4,62285E+11	3,94118E+11	10
GO:0043603	cellular amide metabolic process	186	21	113	367	4.47	16746,1913	1711068,026	8423334,225
GO:0065007	biological regulation	461	21	46	148	1.58	4,21784E+11	1,87919E+11	10
GO:0044271	cellular nitrogen compound biosynthetic process	294	20	68	221	2.49	5,98209E+11	71642660908	3,00899E+11
GO:0043604	amide biosynthetic process	177	18	102	331	3.9	626542,4138	1,57575E+11	3,15151E+11
GO:0044281	small molecule metabolic process	222	18	81	264	3.01	1,34148E+11	1,9279E+11	6,74764E+11
GO:0034645	cellular macromolecule biosynthetic process	270	18	67	217	2.41	1,43451E+11	1,50325E+11	7,21559E+11
GO:0009059	macromolecule biosynthetic process	272	18	66	215	2.39	1,55979E+11	1,60117E+11	7,84573E+11
GO:0010467	gene expression	357	17	48	155	1.65	4,58087E+11	1,87919E+11	10
GO:0019752	carboxylic acid metabolic process	120	15	125	407	4.87	307708,1097	1,03185E+11	1,54777E+11
GO:0055114	oxidation-reduction process	187	15	80	261	2.93	5,58951E+11	68573797572	2,81153E+11
GO:0051186	cofactor metabolic process	63	12	190	62	7.95	321,9073698	2195896,237	16191940701
GO:0050794	regulation of cellular process	178	11	62	201	2.16	2,04216E+11	1,4863E+11	10
GO:0006790	sulfur compound metabolic process	26	10	385	1252	20.97	197,0867019	9913,461107	9913,461107
GO:0044283	small molecule biosynthetic process	79	10	127	412	4.81	1,31239E+11	1,9279E+11	6,6013E+11
GO:0055085	transmembrane transport	135	10	74	241	2.63	8,22351E+11	6,67166E+11	10
GO:0016053	organic acid biosynthetic process	52	9	173	563	6.94	2308697,67	4,83865E+11	1,16127E+11
GO:0006629	lipid metabolic process	126	9	71	232	2.51	1,49271E+11	1,13763E+11	10
GO:1901605	alpha-amino acid metabolic process	34	8	235	766	10.17	613236,168	1,57575E+11	3,08458E+11
GO:0006732	coenzyme metabolic process	45	8	178	579	7.13	5459232,879	9,00361E+11	27459941382
GO:0050896	response to stimulus	130	8	62	20	2.12	4,58613E+11	1,87919E+11	10
GO:0017144	drug metabolic process	59	7	119	386	4.4	2,01841E+11	1,92011E+11	10
GO:0006555	methionine metabolic process	9	5	556	1808	40.67	293664,5288	1,03185E+11	1,47713E+11
GO:0009066	aspartate family amino acid metabolic process	11	5	455	1479	27.1	102410,0406	2,45296E+11	5,15123E+11
GO:0007165	signal transduction	27	5	185	603	7.37	1,20076E+11	1,313E+11	6,03981E+11
GO:0023052	signaling	27	5	185	603	7.37	1,20076E+11	1,313E+11	6,03981E+11
GO:0007154	cell communication	30	5	167	542	6.48	1967721983	1,92011E+11	9,89764E+11
GO:0019725	cellular homeostasis	39	5	128	417	4.76	6,36659E+11	52498306608	10
GO:0006760	folic acid-containing compound metabolic process	4	3	750	2441	96.42	1,1139E+11	16978572795	5,60293E+11
GO:0042398	cellular modified amino acid biosynthetic process	5	3	600	1952	48.2	2,72184E+11	3,60285E+11	1,36908E+11
GO:0043038	amino acid activation	23	3	130	424	4.8	3,21304E+11	1,51043E+11	10

**SOBRERREGULADO**

**CELLULAR COMPONENT**

GO:0006418	tRNA aminoacylation for protein translation	23	3	130	424	4.8	3,21304E+11	1,51043E+11	10
GO:0051187	cofactor catabolic process	3	2	667	2169	63.87	2,75885E+11	2,43456E+11	10
GO:0006730	one-carbon metabolic process	3	2	667	2169	63.87	2,75885E+11	2,43456E+11	10
GO:0006525	arginine metabolic process	5	2	400	1302	21.28	8,82905E+11	6,83233E+11	10
GO:0006882	cellular zinc ion homeostasis	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0009162	deoxyribonucleoside monophosphate metabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0007029	endoplasmic reticulum organization	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0042593	glucose homeostasis	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:1901687	glutathione derivative biosynthetic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:1901685	glutathione derivative metabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0009240	isopentenyl diphosphate biosynthetic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0046490	isopentenyl diphosphate metabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0007067	mitotic nuclear division	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0043171	peptide catabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0006461	protein complex assembly	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0070973	protein localization to endoplasmic reticulum exit site	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0006556	S-adenosylmethionine biosynthetic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0046500	S-adenosylmethionine metabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0044273	sulfur compound catabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0046104	thymidine metabolic process	1	1	1000	3254	inf	3,07306E+11	1,4863E+11	10
GO:0016020	membrane	486	23	47	154	1.66	23061221695	4,81446E+11	10
GO:0016021	integral component of membrane	181	11	61	198	2.12	22811152396	4,81446E+11	10
GO:0020016	ciliary pocket	65	5	77	25	2.68	4,84963E+11	5,69832E+11	10
GO:0031514	motile cilium	24	4	167	542	6.45	5,64427E+11	4,81446E+11	5,30561E+11
GO:0005886	plasma membrane	43	4	93	303	3.29	4,18684E+11	5,62232E+11	10
GO:0030992	intraciliary transport particle B	1	1	1000	3254	inf	3,07306E+11	4,81446E+11	10
GO:0003824	catalytic activity	1571	67	43	139	1.7	9,24134E+11	3,02818E+11	2,16247E+11
GO:0043167	ion binding	982	45	46	149	1.72	2,41358E+11	4,65748E+11	5,64779E+11
GO:0043169	cation binding	290	19	66	213	2.38	1,29738E+11	3,02818E+11	3,03587E+11
GO:0016491	oxidoreductase activity	220	12	55	177	1.89	3,72574E+11	1,16243E+11	10
GO:0003735	structural constituent of ribosome	108	11	102	331	3.77	4,28955E+11	3,02818E+11	1,00375E+11
GO:0005198	structural molecule activity	119	11	92	301	3.38	9,79775E+11	3,02818E+11	2,29267E+11
GO:0046914	transition metal ion binding	117	10	85	278	3.08	2,98557E+11	4,65748E+11	6,98622E+11
GO:0008270	zinc ion binding	89	8	90	293	3.23	5,70083E+11	6,66997E+11	10
GO:0022857	transmembrane transporter activity	106	8	75	246	2.66	1,57161E+11	1,04217E+11	10
GO:0005215	transporter activity	112	8	71	232	2.5	2,12472E+11	1,04217E+11	10
GO:0070011	peptidase activity, acting on L-amino acid peptides	114	8	70	228	2.45	2,3365E+11	1,04217E+11	10
GO:0008233	peptidase activity	119	8	67	219	2.34	2,93024E+11	1,04217E+11	10
GO:0016788	hydrolase activity, acting on ester bonds	122	8	66	213	2.28	3,33269E+11	1,08313E+11	10
GO:0016874	ligase activity	60	6	100	325	3.6	9,74815E+11	9,50444E+11	10
GO:0050662	coenzyme binding	86	6	70	227	2.42	47965105971	1,40221E+11	10
GO:0016829	lyase activity	37	5	135	44	5.06	5,0633E+11	6,65829E+11	10
GO:0008081	phosphoric diester hydrolase activity	16	4	250	814	10.76	1,17072E+11	3,02818E+11	2,73947E+11
GO:0004112	cyclic-nucleotide phosphodiesterase activity	6	3	500	1627	32.13	5,32084E+11	3,02818E+11	12450775568
GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups	10	3	300	976	13.76	2,91494E+11	4,65748E+11	6,82095E+11

## MOLECULAR FUNCTION

GO:0016879	ligase activity, forming carbon-nitrogen bonds	17	3	176	574	6.87	1,41055E+11	1,04217E+11	10
GO:0019842	vitamin binding	26	3	115	375	4.17	4,41358E+11	1,35892E+11	10
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	8	3	375	122	19.27	1,4235E+11	3,02818E+11	3,331E+11
GO:0008172	S-methyltransferase activity	3	2	667	2169	63.87	2,75885E+11	4,65748E+11	6,4557E+11
GO:0016289	CoA hydrolase activity	4	2	500	1627	31.93	5,4063E+11	6,65829E+11	10
GO:0016790	thiolester hydrolase activity	4	2	500	1627	31.93	5,4063E+11	6,65829E+11	10
GO:0016881	acid-amino acid ligase activity	5	2	400	1302	21.28	8,82905E+11	8,9826E+11	10
GO:0005085	guanyl-nucleotide exchange factor activity	5	2	400	1302	21.28	8,82905E+11	8,9826E+11	10
GO:0008194	UDP-glycosyltransferase activity	5	2	400	1302	21.28	8,82905E+11	8,9826E+11	10
GO:0052742	phosphatidylinositol kinase activity	6	2	333	1085	15.96	12977530639	1,04217E+11	10
GO:0019200	carbohydrate kinase activity	8	2	250	814	10.63	2,32648E+11	1,04217E+11	10
GO:0004180	carboxypeptidase activity	8	2	250	814	10.63	2,32648E+11	1,04217E+11	10
GO:0016835	carbon-oxygen lyase activity	9	2	222	723	9.11	2,93155E+11	1,04217E+11	10
GO:0046873	metal ion transmembrane transporter activity	9	2	222	723	9.11	2,93155E+11	1,04217E+11	10
GO:0051020	GTPase binding	10	2	200	651	7.97	3,59157E+11	1,13571E+11	10
GO:0042083	5,10-methylenetetrahydrofolate-dependent methyltransferase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0042084	5-methyltetrahydrofolate-dependent methyltransferase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase act	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0042085	5-methyltetrahydropteroyltri-L-glutamate-dependent methyltransferase activi	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0008097	5S rRNA binding	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0003872	6-phosphofructokinase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0017057	6-phosphogluconolactonase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0003994	aconitate hydratase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004053	arginase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004815	aspartate-tRNA ligase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004817	cysteine-tRNA ligase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004163	diphosphomevalonate decarboxylase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0008199	ferric iron binding	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004322	ferroxidase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004329	formate-tetrahydrofolate ligase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0003839	gamma-glutamylcyclotransferase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004478	methionine adenosyltransferase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0016722	oxidoreductase activity, oxidizing metal ions	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0008113	peptide-methionine (S)-S-oxide reductase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004326	tetrahydrofolylpolyglutamate synthase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0004799	thymidylate synthase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0035251	UDP-glucosyltransferase activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0005385	zinc ion transmembrane transporter activity	1	1	1000	3254	inf	3,07306E+11	1,04217E+11	10
GO:0009987	cellular process	1602	14	9	272	2698	314098,0072	1085065,843	2,38714E+11
GO:0006412	translation	244	13	53	1656	12429	0,000154737	0,004999805	0,011759977
GO:0043603	cellular amide metabolic process	265	13	49	1525	11339	0,000460544	0,007000276	0,03500138
GO:0034645	cellular macromolecule biosynthetic process	363	13	36	1113	7982	0,028658872	0,334307548	2,178074289
GO:0009059	macromolecule biosynthetic process	365	13	36	1107	7933	0,030791485	0,334307548	2,340152835
GO:0044271	cellular nitrogen compound biosynthetic process	386	13	34	1047	745	0,063899442	0,607044697	4,856357575
GO:1901566	organonitrogen compound biosynthetic process	391	13	33	1034	7343	0,075573515	0,638176345	5,743587103
GO:0010467	gene expression	403	13	32	1003	7097	0,112051874	0,851594242	8,515942422

SUBREGULADO

BIOLOGICAL PROCESS

CELLULAR COMPONENT

MOLECULAR FUNCTION

SS

GO:1901576	organic substance biosynthetic process	559	13	23	723	4883	7,7775467	49,25911291	591,1093549
GO:0044267	cellular protein metabolic process	632	13	21	639	4231	3,772268884	204,7803109	2866,924352
GO:0034641	cellular nitrogen compound metabolic process	699	13	19	578	3754	137,1938491	695,1155023	10426,73253
GO:0019538	protein metabolic process	731	13	18	553	3558	243,0826272	1154,642479	18474,27967
GO:0044260	cellular macromolecule metabolic process	780	13	17	518	3289	555,9453484	2485,402734	42251,84648
GO:1901564	organonitrogen compound metabolic process	880	13	15	459	2835	2572,510967	10861,71297	195510,8335
GO:0043170	macromolecule metabolic process	1040	13	13	389	2292	21149,89376	84599,57506	1607391,926
GO:0006807	nitrogen compound metabolic process	1211	13	11	334	1872	141681,2519	538388,7574	10767775148
GO:0044237	cellular metabolic process	1251	13	10	323	179	212097,1707	767589,7607	1,61194E+11
GO:0044238	primary metabolic process	1354	13	10	298	1603	564023,7079	1863730,513	4,28658E+11
GO:0071704	organic substance metabolic process	1404	13	9	288	1522	881105,0454	279016,5977	6,6964E+11
GO:0008152	metabolic process	1650	13	8	245	1196	6297471,261	1,91443E+11	4,78608E+11
GO:0044249	cellular biosynthetic process	546	13	24	74	5018	5,742034003	39,67223493	43,63945843
GO:0009058	biosynthetic process	577	13	23	70	4707	11,70026833	68,40156871	889,2203932
GO:0006449	regulation of translational termination	3	1	333	10362	16593	9,62149E+11	2,21586E+11	7,31233E+11
GO:0009408	response to heat	3	1	333	10362	16593	9,62149E+11	2,21586E+11	7,31233E+11
GO:0006452	translational frameshifting	3	1	333	10362	16593	9,62149E+11	2,21586E+11	7,31233E+11
GO:0034250	positive regulation of cellular amide metabolic process	4	1	250	7772	1106	1,28094E+11	2,70421E+11	9,73514E+11
GO:0043244	regulation of protein complex disassembly	4	1	250	7772	1106	1,28094E+11	2,70421E+11	9,73514E+11
GO:0009891	positive regulation of biosynthetic process	10	1	100	3109	3682	3,17366E+11	5,48178E+11	10
GO:0034248	regulation of cellular amide metabolic process	13	1	77	2391	276	4,10727E+11	65031838737	10
GO:0005737	cytoplasm	2105	14	7	207	1712	1,24039E+11	4,78437E+11	3,34906E+11
GO:0005575	cellular component	2913	14	5	149	845	8,543E+11	1,64758E+11	2,30661E+11
GO:0005840	ribosome	163	12	74	2289	11913	9,26082E-05	0,002500421	0,002500421
GO:1990904	ribonucleoprotein complex	215	12	56	1735	8759	0,000275488	0,037190926	0,074381851
GO:0032991	protein-containing complex	580	12	21	643	2873	394,2985549	2129,212197	10646,06098
GO:0043228	non-membrane-bounded organelle	580	12	21	643	2873	394,2985549	2129,212197	10646,06098
GO:0044444	cytoplasmic part	1268	12	9	294	108	3034995,351	13657479081	8,19449E+11
GO:0043226	organelle	1762	12	7	212	662	1,05234E+11	3,15701E+11	2,84131E+11
GO:0043229	intracellular organelle	1619	12	7	23	757	4,31088E+11	1,45492E+11	1,16394E+11
GO:0003735	structural constituent of ribosome	160	12	75	2332	12162	7,36503E-05	0,001178405	0,001178405
GO:0005198	structural molecule activity	172	12	70	2169	1122	0,000179467	0,001435736	0,002871471
GO:0003676	nucleic acid binding	542	5	9	287	383	2,31613E+11	5,82069E+11	3,70581E+11
GO:0003723	RNA binding	207	4	19	601	796	3,49895E+11	1,8661E+11	5,59831E+11
GO:0032403	protein complex binding	2	1	500	15543	33193	6,42397E+11	2,56959E+11	1,02783E+11
GO:0008097	5S rRNA binding	3	1	333	10362	16593	9,62149E+11	3078875608	1539437804
GO:0019843	rRNA binding	10	1	100	3109	3682	3,17366E+11	6,19699E+11	5,07786E+11
GO:0044877	protein-containing complex binding	15	1	67	2072	2364	4,72501E+11	7,33426E+11	7560008405
GO:0006793	phosphorus metabolic process	372	20	54	179	1.97	7,10201E+11	7,12831E+11	10
GO:0043412	macromolecule modification	404	20	50	165	1.8	1,68395E+11	1,1113E+11	10
GO:0016310	phosphorylation	240	19	79	264	3.06	8195161,133	4,44178E+11	2,22089E+11
GO:0006468	protein phosphorylation	204	19	93	31	3.68	824647,9803	6,13786E+11	2,2348E+11
GO:0007018	microtubule-based movement	90	14	156	518	6.5	32296,68337	8752401,193	8752401,193
GO:0006928	movement of cell or subcellular component	101	14	139	462	5.67	138061,2524	1,87073E+11	3,74146E+11
GO:0007017	microtubule-based process	118	14	119	395	4.72	905956,5673	6,13786E+11	2,45514E+11
GO:0050789	regulation of biological process	228	14	61	205	2.24	7,96369E+11	7,38799E+11	10

**SOBRERREGULADO**

	GO ID	GO Term	SOBRERREGULADO							
			Count	Count	Count	Count	Count	Count	Count	
<b>BIOLOGICAL PROCESSES</b>	GO:0065007	biological regulation	255	14	55	183	1.97	1,99023E+11	1,19856E+11	10
	GO:0019222	regulation of metabolic process	92	8	87	29	3.2	6,00378E+11	6,50809E+11	10
	GO:0050793	regulation of developmental process	15	4	267	888	12.06	8,21042E+11	2,09072E+11	2,22503E+11
	GO:0010608	posttranscriptional regulation of gene expression	34	4	118	392	4.4	1,79481E+11	1,1113E+11	10
	GO:0009372	quorum sensing	8	3	375	1249	19.79	1,32803E+11	2,57069E+11	3,59897E+11
	GO:0010605	negative regulation of macromolecule metabolic process	24	3	125	416	4.69	3,38084E+11	1,60738E+11	10
	GO:0000278	mitotic cell cycle	20	3	150	50	5.8	2,07697E+11	12236065176	10
	GO:0051640	organelle localization	12	2	167	555	6.54	4,85076E+11	2,22806E+11	10
	GO:0072382	minus-end-directed vesicle transport along microtubule	3	2	667	222	65.54	2,6325E+11	3,75478E+11	7,13408E+11
	GO:0099518	vesicle cytoskeletal trafficking	3	2	667	222	65.54	2,6325E+11	3,75478E+11	7,13408E+11
	GO:0048268	clathrin coat assembly	1	1	1000	3331	inf	3,00236E+11	1,45293E+11	10
	GO:0015819	lysine transport	1	1	1000	3331	inf	3,00236E+11	1,45293E+11	10
	GO:0080135	regulation of cellular response to stress	1	1	1000	3331	inf	3,00236E+11	1,45293E+11	10
	GO:0043555	regulation of translation in response to stress	1	1	1000	3331	inf	3,00236E+11	1,45293E+11	10
	GO:0010998	regulation of translational initiation by eIF2 alpha phosphorylation	1	1	1000	3331	inf	3,00236E+11	1,45293E+11	10
<b>CELLULAR COMPONENTS</b>	GO:1902494	catalytic complex	107	10	93	311	3.51	1,26129E+11	5,14886E+11	1,66491E+11
	GO:0071944	cell periphery	64	5	78	26	2.8	4,20545E+11	4,12084E+11	10
	GO:0010494	cytoplasmic stress granule	22	3	136	454	5.19	2,68634E+11	3,6276E+11	10
	GO:0035770	ribonucleoprotein granule	23	3	130	434	4.93	3,023E+11	3,6276E+11	10
	GO:0071439	clathrin complex	1	1	1000	3331	inf	3,00236E+11	3,6276E+11	10
	GO:0097038	perinuclear endoplasmic reticulum	1	1	1000	3331	inf	3,00236E+11	3,6276E+11	10
	GO:1990578	perinuclear endoplasmic reticulum membrane	1	1	1000	3331	inf	3,00236E+11	3,6276E+11	10
	GO:0048471	perinuclear region of cytoplasm	1	1	1000	3331	inf	3,00236E+11	3,6276E+11	10
<b>MOLECULAR FUNCTION</b>	GO:0003674	molecular function	3364	113	34	112	1.64	1,18034E+11	4,51903E+11	10
	GO:0097159	organic cyclic compound binding	1272	68	53	178	2.6	4160,816422	111509,8801	557549,4006
	GO:0043167	ion binding	1080	54	50	167	2.14	2399437,411	2,92295E+11	3,21525E+11
	GO:1901265	nucleoside phosphate binding	814	42	52	172	2.08	1,50011E+11	8,73977E+11	2,01015E+11
	GO:0036094	small molecule binding	842	42	50	166	1.99	3,23349E+11	1,73315E+11	4,33288E+11
	GO:0097367	carbohydrate derivative binding	745	41	55	183	2.25	415999,3235	3,09688E+11	5,57439E+11
	GO:0043168	anion binding	808	41	51	169	2.03	2,70109E+11	1,50811E+11	3,61947E+11
	GO:0035639	purine ribonucleoside triphosphate binding	716	40	56	186	2.28	3774770,862	3,09688E+11	5,05819E+11
	GO:0032555	purine ribonucleotide binding	729	40	55	183	2.23	5754303,332	4,0583E+11	7,71077E+11
	GO:0005524	ATP binding	614	39	64	212	2.65	21913,08235	4893921,724	29363530345
	GO:0008144	drug binding	640	39	61	203	2.52	619163,82	9218661,32	8,2968E+11
	GO:0003676	nucleic acid binding	542	29	54	178	2.04	1,18892E+11	59005774562	1,59316E+11
	GO:0016740	transferase activity	573	29	51	169	1.91	2,81386E+11	1,3002E+11	3,77057E+11
	GO:0140096	catalytic activity, acting on a protein	440	29	66	22	2.61	3120302,309	3,09688E+11	4,18121E+11
	GO:0016772	transferase activity, transferring phosphorus-containing groups	361	21	58	194	2.17	2,27839E+11	1,09037E+11	3,05304E+11
	GO:0004672	protein kinase activity	206	19	92	307	3.64	951171,1698	1,27457E+11	1,27457E+11
	GO:0016817	hydrolase activity, acting on acid anhydrides	295	17	58	192	2.11	6,65879E+11	2,62434E+11	8,92277E+11
	GO:0017111	nucleoside-triphosphatase activity	283	17	60	20	2.21	4,39288E+11	1,96215E+11	5,88646E+11
	GO:0003777	microtubule motor activity	71	14	197	657	8.71	1402,791201	111509,8801	187974,021
	GO:0003774	motor activity	75	14	187	622	8.13	2947,665841	111509,8801	394987,2227
	GO:0019787	ubiquitin-like protein transferase activity	22	6	273	908	12.61	3301972,657	3,09688E+11	4,42464E+11
	GO:0004842	ubiquitin-protein transferase activity	22	6	273	908	12.61	3301972,657	3,09688E+11	4,42464E+11
GO:0004198	calcium-dependent cysteine-type endopeptidase activity	25	4	160	533	6.31	6,02686E+11	2,44727E+11	8,076E+11	



GO:0045182	translation regulator activity	2	2	1000	3331	inf	8,95169E+11	4,61356E+11	1,19953E+11
GO:0008409	5'-3' exonuclease activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0004534	5'-3' exoribonuclease activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0004683	calmodulin-dependent protein kinase activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0032051	clathrin light chain binding	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0004686	elongation factor-2 kinase activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0004694	eukaryotic translation initiation factor 2alpha kinase activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0019002	GMP binding	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0015189	L-lysine transmembrane transporter activity	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0003730	mRNA 3'-UTR binding	1	1	1000	3331	inf	3,00236E+11	8,80614E+11	10
GO:0007017	microtubule-based process	121	14	116	265	2.98	7,31409E+11	3,75108E+11	2,62576E+11
GO:0006508	proteolysis	157	14	89	204	2.21	8,33467E+11	1,87009E+11	10
GO:0055114	oxidation-reduction process	188	14	74	17	1.81	3,47872E+11	4,44875E+11	10
GO:0060285	cilium-dependent cell motility	37	9	243	557	7.27	2124161,095	2,72817E+11	7,62574E+11
GO:0048870	cell motility	40	9	225	515	6.56	4161798,15	2,98817E+11	1,49409E+11
GO:0051674	localization of cell	40	9	225	515	6.56	4161798,15	2,98817E+11	1,49409E+11
GO:0040011	locomotion	42	9	214	49	6.16	628620,0403	3,76124E+11	2,25675E+11
GO:0030030	cell projection organization	45	5	111	254	2.77	4,50196E+11	4,44875E+11	10
GO:0044782	cilium organization	45	5	111	254	2.77	4,50196E+11	4,44875E+11	10
GO:0120036	plasma membrane bounded cell projection organization	45	5	111	254	2.77	4,50196E+11	4,44875E+11	10
GO:0035556	intracellular signal transduction	17	4	235	538	6.83	53961738176	1,49017E+11	10
GO:0023052	signaling	31	4	129	295	3.28	4,43263E+11	4,44875E+11	10
GO:0001578	microtubule bundle formation	6	3	500	1144	22.15	1,49449E+11	5,96135E+11	53652139326
GO:0035082	axoneme assembly	6	3	500	1144	22.15	1,49449E+11	5,96135E+11	53652139326
GO:0009187	cyclic nucleotide metabolic process	7	3	429	981	16.61	2,53121E+11	7,57253E+11	9,08703E+11
GO:0009190	cyclic nucleotide biosynthetic process	7	3	429	981	16.61	2,53121E+11	7,57253E+11	9,08703E+11
GO:1901264	carbohydrate derivative transport	10	3	300	686	9.49	7870798118	1,87009E+11	10
GO:0015931	nucleobase-containing compound transport	17	3	176	404	4.74	35603140637	4,44875E+11	10
GO:0003341	cilium movement	4	2	500	1144	22.06	1,07646E+11	2,14694E+11	10
GO:0060294	cilium movement involved in cell motility	4	2	500	1144	22.06	1,07646E+11	2,14694E+11	10
GO:0015858	nucleoside transport	5	2	400	915	14.7	1,74263E+11	3,12802E+11	10
GO:0007155	cell adhesion	8	2	250	572	7.35	44742085339	4,44875E+11	10
GO:0022610	biological adhesion	8	2	250	572	7.35	44742085339	4,44875E+11	10
GO:0006102	isocitrate metabolic process	1	1	1000	2288	inf	4,37037E+11	4,44875E+11	10
GO:0019918	peptidyl-arginine methylation, to symmetrical-dimethyl arginine	1	1	1000	2288	inf	4,37037E+11	4,44875E+11	10
GO:0033058	directional locomotion	1	1	1000	2288	inf	4,37037E+11	4,44875E+11	10
GO:0043056	forward locomotion	1	1	1000	2288	inf	4,37037E+11	4,44875E+11	10
GO:0046168	glycerol-3-phosphate catabolic process	1	1	1000	2288	inf	4,37037E+11	4,44875E+11	10
GO:0005929	cilium	892	77	86	198	2.58	36,48999353	474,3699158	426,9329243
GO:0042995	cell projection	892	77	86	198	2.58	36,48999353	474,3699158	426,9329243
GO:0120025	plasma membrane bounded cell projection	892	77	86	198	2.58	36,48999353	474,3699158	426,9329243
GO:0099568	cytoplasmic region	665	66	99	227	2.96	2,645288071	51,58311739	309,4987043
GO:0043228	non-membrane-bounded organelle	779	60	77	176	2.11	374972,5649	3133699,293	4,38718E+11
GO:0043232	intracellular non-membrane-bounded organelle	779	60	77	176	2.11	374972,5649	3133699,293	4,38718E+11
GO:0044430	cytoskeletal part	392	59	151	344	4.84	2,56635E-07	1,50131E-05	3,00263E-05
GO:0005856	cytoskeleton	399	59	148	338	4.73	6,20573E-07	2,42024E-05	7,26071E-05

REGULADO

COMPONENT

BIOLOGICAL PROCESS

SUB

CELLULAF

GO:0005930	axoneme	205	50	244	558	8.69	3,97276E-14	4,64813E-12	4,64813E-12
GO:0016021	integral component of membrane	198	16	81	185	1.99	1,23709E+11	7,96828E+11	10
GO:0031224	intrinsic component of membrane	199	16	80	184	1.98	1,29399E+11	7,96828E+11	10
GO:0009331	glycerol-3-phosphate dehydrogenase complex	1	1	1000	2288	inf	4,37037E+11	2,13056E+11	10
GO:0030992	intraciliary transport particle B	1	1	1000	2288	inf	4,37037E+11	2,13056E+11	10
GO:0046930	pore complex	1	1	1000	2288	inf	4,37037E+11	2,13056E+11	10
GO:0005515	protein binding	760	44	58	132	1.42	2,76267E+11	2,43676E+11	10
GO:0016787	hydrolase activity	650	42	65	148	1.62	5,26189E+11	8,05474E+11	10
GO:0140096	catalytic activity, acting on a protein	441	27	61	14	1.48	4,42936E+11	2,51841E+11	10
GO:0017111	nucleoside-triphosphatase activity	261	21	80	184	2.0	4,63889E+11	76928258983	9,23139E+11
GO:0016817	hydrolase activity, acting on acid anhydrides	273	21	77	176	1.9	7,72724E+11	9,61076E+11	10
GO:0016491	oxidoreductase activity	218	16	73	168	1.79	2,81635E+11	2,43676E+11	10
GO:0008233	peptidase activity	147	13	88	202	2.19	1,15808E+11	1,35563E+11	10
GO:0004175	endopeptidase activity	87	11	126	289	3.27	1,30067E+11	3,15075E+11	2,58833E+11
GO:0003774	motor activity	75	10	133	305	3.47	1,42496E+11	3,15075E+11	2,83568E+11
GO:0004197	cysteine-type endopeptidase activity	37	9	243	557	7.27	2124161,095	1,98945E+11	4,22708E+11
GO:0005509	calcium ion binding	62	9	145	332	3.82	1,33366E+11	3,15075E+11	2,65399E+11
GO:0003777	microtubule motor activity	72	8	111	254	2.8	1,26254E+11	1,39581E+11	10
GO:0005516	calmodulin binding	10	6	600	1373	33.65	118603,3793	2,36021E+11	2,36021E+11
GO:0015932	nucleobase-containing compound transmembrane transporter activity	12	4	333	763	11.11	1,33366E+11	3,15075E+11	2,65398E+11
GO:1901505	carbohydrate derivative transmembrane transporter activity	12	4	333	763	11.11	1,33366E+11	3,15075E+11	2,65398E+11
GO:0016849	phosphorus-oxygen lyase activity	7	3	429	981	16.61	2,53121E+11	5,0371E+11	5,0371E+11
GO:0071949	FAD binding	8	3	375	858	13.28	391990415	7,09146E+11	7,80061E+11
GO:0005337	nucleoside transmembrane transporter activity	5	2	400	915	14.7	1,74263E+11	1,73391E+11	10
GO:0016861	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	5	2	400	915	14.7	1,74263E+11	1,73391E+11	10
GO:0004071	aspartate-ammonia ligase activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0004367	glycerol-3-phosphate dehydrogenase [NAD+] activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0004489	methylenetetrahydrofolate reductase (NAD(P)H) activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0004801	sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0008609	alkylglycerone-phosphate synthase activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0009378	four-way junction helicase activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0015288	porin activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0022829	wide pore channel activity	1	1	1000	2288	inf	4,37037E+11	2,51841E+11	10
GO:0009987	cellular process	1627	114	70	14	1.75	1027055,78	2,31088E+11	6,93263E+11
GO:0071704	organic substance metabolic process	1381	89	64	129	1.46	3,23781E+11	6,24435E+11	10
GO:0043170	macromolecule metabolic process	1036	63	61	122	1.3	4,72492E+11	2,08333E+11	10
GO:0044260	cellular macromolecule metabolic process	746	54	72	145	1.6	2,49799E+11	5,10953E+11	10
GO:1901564	organonitrogen compound metabolic process	821	52	63	127	1.35	3,74972E+11	2,08333E+11	10
GO:0034641	cellular nitrogen compound metabolic process	704	45	64	128	1.36	4,5595E+11	2,08333E+11	10
GO:0090304	nucleic acid metabolic process	383	27	70	141	1.49	4,17547E+11	2,08333E+11	10
GO:0071840	cellular component organization or biogenesis	249	22	88	177	1.92	61717028385	1,06145E+11	10
GO:0006996	organelle organization	168	18	107	214	2.37	1,67466E+11	5,10953E+11	10
GO:0019752	carboxylic acid metabolic process	128	15	117	234	2.61	1,66148E+11	5,10953E+11	10
GO:0006082	organic acid metabolic process	132	15	114	227	2.52	2,26215E+11	5,10953E+11	10
GO:0050896	response to stimulus	143	15	105	21	2.3	4,89882E+11	8,93703E+11	10
GO:0055085	transmembrane transport	146	13	89	178	1.9	3,00392E+11	2,08333E+11	10

MOLECULAR FUNCTION

## BIOLOGICAL PROCESS

GO:0006259	DNA metabolic process	118	13	110	22	2.42	5,69491E+11	1,0116E+11	10
GO:0007049	cell cycle	54	12	222	444	5.63	995828,0648	2,31088E+11	6,72184E+11
GO:0007059	chromosome segregation	25	11	440	88	15.52	952,5527617	642973,1142	642973,1142
GO:0006811	ion transport	93	9	97	194	2.07	4,17767E+11	2,08333E+11	10
GO:0000226	microtubule cytoskeleton organization	27	8	296	593	8.21	3404224,243	5,74463E+11	2,29785E+11
GO:0000278	mitotic cell cycle	30	8	267	533	7.09	7870818,107	7,58972E+11	53128022221
GO:0007010	cytoskeleton organization	35	8	229	457	5.77	2,5443E+11	1,7174E+11	1,7174E+11
GO:0006812	cation transport	63	8	127	254	2.82	1,24779E+11	1,7189E+11	10
GO:0018193	peptidyl-amino acid modification	35	7	200	40	4.85	1,4527E+11	5,10953E+11	9,80576E+11
GO:0006260	DNA replication	41	6	146	293	3.31	1,51961E+11	18995137223	10
GO:0070925	organelle assembly	50	6	120	24	2.63	3,70381E+11	2,08333E+11	10
GO:0000413	protein peptidyl-prolyl isomerization	17	4	235	471	5.92	86762965993	1,33102E+11	10
GO:0048285	organelle fission	18	4	222	444	5.5	1,07248E+11	1,54026E+11	10
GO:0051726	regulation of cell cycle	28	4	143	286	3.2	4,8616E+11	2,08333E+11	10
GO:0032502	developmental process	8	4	500	100	19.27	3,64787E+11	2,23847E+11	2,46231E+11
GO:0061640	cytoskeleton-dependent cytokinesis	16	3	188	375	4.42	4,26878E+11	2,08333E+11	10
GO:0048856	anatomical structure development	5	3	600	120	28.81	1,14686E+11	4,38474E+11	7,7413E+11
GO:0070838	divalent metal ion transport	5	3	600	120	28.81	1,14686E+11	4,38474E+11	7,7413E+11
GO:0072511	divalent inorganic cation transport	5	3	600	120	28.81	1,14686E+11	4,38474E+11	7,7413E+11
GO:0009064	glutamine family amino acid metabolic process	12	3	250	50	6.39	1,94285E+11	2,08333E+11	10
GO:0016999	antibiotic metabolic process	15	3	200	40	4.79	3,59779E+11	2,08333E+11	10
GO:0006875	cellular metal ion homeostasis	3	2	667	1333	38.28	7,22624E+11	1,16136E+11	10
GO:0009266	response to temperature stimulus	6	2	333	667	9.56	3,26889E+11	2,08333E+11	10
GO:0009607	response to biotic stimulus	6	2	333	667	9.56	3,26889E+11	2,08333E+11	10
GO:0140014	mitotic nuclear division	6	2	333	667	9.56	3,26889E+11	2,08333E+11	10
GO:0006826	iron ion transport	7	2	286	571	7.65	4,42751E+11	2,08333E+11	10
GO:0015684	ferrous iron transport	2	2	1000	200	inf	2,4912E+11	5,10953E+11	10
GO:0016572	histone phosphorylation	2	2	1000	200	inf	2,4912E+11	5,10953E+11	10
GO:0018105	peptidyl-serine phosphorylation	2	2	1000	200	inf	2,4912E+11	5,10953E+11	10
GO:0018209	peptidyl-serine modification	2	2	1000	200	inf	2,4912E+11	5,10953E+11	10
GO:0072503	cellular divalent inorganic cation homeostasis	2	2	1000	200	inf	2,4912E+11	5,10953E+11	10
GO:0006873	cellular ion homeostasis	4	2	500	100	19.13	1,39761E+11	1,77998E+11	10
GO:0006525	arginine metabolic process	5	2	400	80	12.75	2,25289E+11	2,08333E+11	10
GO:0051805	evasion or tolerance of immune response of other organism involved in symbiosis	5	2	400	80	12.75	2,25289E+11	2,08333E+11	10
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA)	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0001306	age-dependent response to oxidative stress	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0001558	regulation of cell growth	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0001817	regulation of cytokine production	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0005984	disaccharide metabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0005985	sucrose metabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006144	purine nucleobase metabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006429	leucyl-tRNA aminoacylation	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006469	negative regulation of protein kinase activity	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006542	glutamine biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006686	sphingomyelin biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006696	ergosterol biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006874	cellular calcium ion homeostasis	1	1	1000	200	inf	5E+11	2,08333E+11	10

**SOBRERREGULADO**

GO:0006882	cellular zinc ion homeostasis	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0006885	regulation of pH	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0007568	aging	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0009311	oligosaccharide metabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0009313	oligosaccharide catabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0015886	heme transport	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0031297	replication fork processing	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0031929	TOR signaling	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0033260	nuclear DNA replication	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0033261	obsolete regulation of S phase	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0038203	TORC2 signaling	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0048034	heme O biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0051181	cofactor transport	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0051348	negative regulation of transferase activity	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0051452	intracellular pH reduction	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0070627	ferrous iron import	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0097286	iron ion import	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1901678	iron coordination entity transport	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1901685	glutathione derivative metabolic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1901687	glutathione derivative biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1902298	cell cycle DNA replication maintenance of fidelity	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1903426	regulation of reactive oxygen species biosynthetic process	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1990426	mitotic recombination-dependent replication fork processing	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:1990505	mitotic DNA replication maintenance of fidelity	1	1	1000	200	inf	5E+11	2,08333E+11	10
GO:0043228	non-membrane-bounded organelle	779	57	73	146	1.63	1,43265E+11	2,03176E+11	2,23494E+11
GO:0005694	chromosome	83	22	265	53	7.37	4,526920246	706,1995584	706,1995584
GO:0015630	microtubule cytoskeleton	213	20	94	188	2.05	4,54405E+11	5,06337E+11	70887187102
GO:0044427	chromosomal part	74	19	257	514	6.98	181,6619982	1416,963586	28339,27172
GO:0035869	ciliary transition zone	45	10	222	444	5.6	5561207,439	1,44591E+11	8,67548E+11
GO:0071944	cell periphery	67	9	134	269	3.02	5,70007E+11	5,92807E+11	8,89211E+11
GO:0044815	DNA packaging complex	26	7	269	538	7.16	2,09218E+11	4,07974E+11	3,2638E+11
GO:0032993	protein-DNA complex	36	7	194	389	4.68	1,72776E+11	2,24609E+11	2,69531E+11
GO:0005886	plasma membrane	48	7	146	292	3.3	9,13999E+11	8,91149E+11	10
GO:0000922	spindle pole	10	3	300	60	8.22	1,14133E+11	1,04734E+11	10
GO:0032133	chromosome passenger complex	5	2	400	80	12.75	2,25289E+11	1,95251E+11	10
GO:0009317	acetyl-CoA carboxylase complex	1	1	1000	200	inf	5E+11	3E+11	10
GO:0009343	biotin carboxylase complex	1	1	1000	200	inf	5E+11	3E+11	10
GO:0044796	DNA polymerase processivity factor complex	1	1	1000	200	inf	5E+11	3E+11	10
GO:0019908	nuclear cyclin-dependent protein kinase holoenzyme complex	1	1	1000	200	inf	5E+11	3E+11	10
GO:0043626	PCNA complex	1	1	1000	200	inf	5E+11	3E+11	10
GO:0097537	Y-shaped link	1	1	1000	200	inf	5E+11	3E+11	10
GO:1901363	heterocyclic compound binding	1298	95	73	146	1.77	1568805,824	2,28261E+11	4,56522E+11
GO:0097159	organic cyclic compound binding	1298	95	73	146	1.77	1568805,824	2,28261E+11	4,56522E+11
GO:0043167	ion binding	1035	69	67	133	1.48	4931440061	6,8468E+11	10
GO:0003676	nucleic acid binding	593	51	86	172	1.97	5430246,926	4,92355E+11	1,5802E+11

**CELLULAR COMPONENT**

## MOLECULAR FUNCTION

GO:0008144	drug binding	624	43	69	138	1.48	1,64664E+11	1,19793E+11	10
GO:0043169	cation binding	296	27	91	182	2.01	1,56557E+11	4,53087E+11	4,55581E+11
GO:0003723	RNA binding	292	26	89	178	1.95	2,6828E+11	4,59232E+11	7,80695E+11
GO:0046872	metal ion binding	290	25	86	172	1.87	4,94099E+11	6,8468E+11	10
GO:0003729	mRNA binding	125	14	112	224	2.47	35935209107	5,80953E+11	10
GO:0003677	DNA binding	146	14	96	192	2.07	1,38506E+11	10606624967	10
GO:0046914	transition metal ion binding	116	12	103	207	2.25	1,25879E+11	1,02727E+11	10
GO:0005215	transporter activity	123	11	89	179	1.9	4,2771E+11	1,86538E+11	10
GO:0016874	ligase activity	64	9	141	281	3.18	4,18351E+11	6,40737E+11	10
GO:0046983	protein dimerization activity	35	8	229	457	5.77	2,5443E+11	9,25489E+11	7,40391E+11
GO:0022804	active transmembrane transporter activity	48	7	146	292	3.3	9,13999E+11	8,31168E+11	10
GO:0046982	protein heterodimerization activity	27	6	222	444	5.53	1,79635E+11	4,53087E+11	5,22737E+11
GO:0140097	catalytic activity, acting on DNA	46	6	130	261	2.89	2,57397E+11	1,70233E+11	10
GO:0019842	vitamin binding	25	5	200	40	4.82	7,01105E+11	7,00945E+11	10
GO:0016879	ligase activity, forming carbon-nitrogen bonds	18	4	222	444	5.5	1,07248E+11	9,45731E+11	10
GO:0016859	cis-trans isomerase activity	19	4	211	421	5.13	1,30615E+11	1,02727E+11	10
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	19	4	211	421	5.13	1,30615E+11	1,02727E+11	10
GO:0005506	iron ion binding	16	4	250	50	6.41	6,90161E+11	7,00945E+11	10
GO:0030170	pyridoxal phosphate binding	16	4	250	50	6.41	6,90161E+11	7,00945E+11	10
GO:0070279	vitamin B6 binding	16	4	250	50	6.41	6,90161E+11	7,00945E+11	10
GO:0008170	N-methyltransferase activity	11	3	273	545	7.19	1,51212E+11	1,12828E+11	10
GO:0072509	divalent inorganic cation transmembrane transporter activity	3	3	1000	200	inf	1,23683E+11	5,99864E+11	3,59918E+11
GO:0046915	transition metal ion transmembrane transporter activity	3	3	1000	200	inf	1,23683E+11	5,99864E+11	3,59918E+11
GO:0015297	antiporter activity	5	3	600	120	28.81	1,14686E+11	3,70818E+11	3,33736E+11
GO:0031625	ubiquitin protein ligase binding	8	3	375	75	11.52	5,73859E+11	7,00945E+11	10
GO:0015291	secondary active transmembrane transporter activity	10	3	300	60	8.22	1,14133E+11	9,76848E+11	10
GO:0018024	histone-lysine N-methyltransferase activity	3	2	667	1333	38.28	7,22624E+11	7,00945E+11	10
GO:0005381	iron ion transmembrane transporter activity	2	2	1000	200	inf	2,4912E+11	4,53087E+11	7,2494E+11
GO:0003896	DNA primase activity	5	2	400	80	12.75	2,25289E+11	15246323778	10
GO:0004534	5'-3' exoribonuclease activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0043142	single-stranded DNA-dependent ATPase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004053	arginase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0003989	acetyl-CoA carboxylase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0090599	alpha-glucosidase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0033676	double-stranded DNA-dependent ATPase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0043566	structure-specific DNA binding	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004482	mRNA (guanine-N7-)-methyltransferase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004657	proline dehydrogenase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004748	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004766	spermidine synthase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004823	leucine-tRNA ligase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004421	hydroxymethylglutaryl-CoA synthase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0004357	glutamate-cysteine ligase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0008409	5'-3' exonuclease activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0008892	guanine deaminase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10
GO:0009678	hydrogen-translocating pyrophosphatase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10

		GO:0004356	glutamate-ammonia ligase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0004311	farnesyltranstransferase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0004075	biotin carboxylase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0015926	glucosidase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0016885	ligase activity, forming carbon-carbon bonds	1	1	1000	200	inf	5E+11	1,86538E+11	10		
		GO:0000150	recombinase activity	1	1	1000	200	inf	5E+11	1,86538E+11	10		
SUBREGULADO	BIOLOGICAL PROCESS	GO:0009987	cellular process	1249	35	28	148	2.03	3,19841E+11	2,55524E+11	4,95754E+11		
		GO:0071704	organic substance metabolic process	1202	34	28	149	2.02	32970802386	2,55524E+11	5,11047E+11		
		GO:0044238	primary metabolic process	1166	32	27	145	1.88	8,14902E+11	5,57387E+11	10		
		GO:0044237	cellular metabolic process	1011	31	31	162	2.18	1,4905E+11	1,35898E+11	2,31027E+11		
		GO:0009058	biosynthetic process	445	24	54	284	4.03	75058,38162	164160,4198	1,1634E+11		
		GO:1901564	organonitrogen compound metabolic process	792	24	30	16	1.96	8,2709E+11	5,57387E+11	10		
		GO:0044249	cellular biosynthetic process	414	23	56	293	4.11	83042,7142	164160,4198	1,28716E+11		
		GO:1901576	organic substance biosynthetic process	424	23	54	286	3.99	127641,3867	1978441,494	1,97844E+11		
		GO:0044260	cellular macromolecule metabolic process	693	23	33	175	2.18	3,11716E+11	2,55524E+11	4,83161E+11		
		GO:0044267	cellular protein metabolic process	546	21	38	203	2.55	7,639E+11	7,89364E+11	1,18405E+11		
		GO:0034641	cellular nitrogen compound metabolic process	568	21	37	195	2.43	1,29618E+11	1,25568E+11	2,00908E+11		
		GO:0019538	protein metabolic process	678	21	31	163	1.95	1,14072E+11	7,36718E+11	10		
		GO:0034645	cellular macromolecule biosynthetic process	292	19	65	343	4.62	95318,95341	164160,4198	1,47744E+11		
		GO:0009059	macromolecule biosynthetic process	292	19	65	343	4.62	95318,95341	164160,4198	1,47744E+11		
		GO:1901566	organonitrogen compound biosynthetic process	307	19	62	326	4.36	206277,6587	290663,9736	3,1973E+11		
		GO:0043043	peptide biosynthetic process	215	18	84	441	6.09	4300,731538	342344,095	666613,3885		
		GO:0043603	cellular amide metabolic process	228	18	79	416	5.69	10772,45766	417432,7343	1669730,937		
		GO:0044271	cellular nitrogen compound biosynthetic process	323	18	56	294	3.8	1828477,896	2,36178E+11	2,83414E+11		
		GO:0010467	gene expression	326	17	52	275	3.47	7835914,374	9,34282E+11	1,21457E+11		
		GO:0006534	cysteine metabolic process	1	1	1000	5267	inf	1,89855E+11	9,8092E+11	10		
		GO:0006071	glycerol metabolic process	1	1	1000	5267	inf	1,89855E+11	9,8092E+11	10		
		GO:0006435	threonyl-tRNA aminoacylation	1	1	1000	5267	inf	1,89855E+11	9,8092E+11	10		
		GO:0052646	alditol phosphate metabolic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		GO:0044262	cellular carbohydrate metabolic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		GO:0006750	glutathione biosynthetic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		GO:0006072	glycerol-3-phosphate metabolic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		GO:0016042	lipid catabolic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		GO:0019184	nonribosomal peptide biosynthetic process	2	1	500	2634	52.44	3,76159E+11	1,5758E+11	10		
		SUBREGULADO	CELLULAR COMPONENT	GO:0044424	intracellular part	531	23	43	228	3.04	5960898,833	2,50358E+11	2,50358E+11
				GO:0044464	cell part	604	23	38	201	2.59	4,42757E+11	14304450069	1,85958E+11
				GO:0032991	protein-containing complex	357	20	56	295	3.95	493477,3816	3896431,568	20726050029
				GO:0043229	intracellular organelle	368	20	54	286	3.81	789548,3786	4737290,272	3,3161E+11
				GO:0043226	organelle	386	20	52	273	3.6	1635175,437	85846,71043	68677368344
				GO:0043228	non-membrane-bounded organelle	236	19	81	424	5.92	3133,079214	32897,33174	131589,327
GO:0005737	cytoplasm			335	18	54	283	3.64	3022814,542	1,41065E+11	1,26958E+11		
GO:0005840	ribosome			143	16	112	589	8.24	437,1485479	18360,23901	18360,23901		
GO:1990904	ribonucleoprotein complex			161	16	99	523	7.18	2497,174586	32897,33174	104881,3326		
GO:0008537	proteasome activator complex			1	1	1000	5267	inf	1,89855E+11	4,98371E+11	7,97393E+11		
GO:0022624	proteasome accessory complex			1	1	1000	5267	inf	1,89855E+11	4,98371E+11	7,97393E+11		

	MOLECULAR FUNCTION									
	GO ID	Term	Count	Count	Count	Count	Count	Count	Count	Count
	GO:0003735	structural constituent of ribosome	146	16	110	577	8.04	595,0266084	684,2805997	684,2805997
	GO:0005198	structural molecule activity	156	16	103	54	7.44	1577,380915	90699,4026	1813,988052
	GO:0008234	cysteine-type peptidase activity	62	10	161	369	4.35	3,04239E+11	1,51359E+11	6,05435E+11
	GO:0019842	vitamin binding	25	3	120	632	7.33	1,11612E+11	1,09167E+11	10
	GO:0019787	ubiquitin-like protein transferase activity	20	3	150	79	9.5	59188318009	1,09167E+11	6,80666E+11
	GO:0004842	ubiquitin-protein transferase activity	20	3	150	79	9.5	59188318009	1,09167E+11	6,80666E+11
	GO:0008097	5S rRNA binding	3	2	667	3511	106.49	1,05242E+11	4,03429E+11	1,21029E+11
	GO:0019843	rRNA binding	7	2	286	1505	21.27	7,01272E+11	1,09167E+11	8,06462E+11
	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	7	2	286	1505	21.27	7,01272E+11	1,09167E+11	8,06462E+11
	GO:0030170	pyridoxal phosphate binding	17	2	118	62	7.07	4,01994E+11	2,00997E+11	10
	GO:0070279	vitamin B6 binding	17	2	118	62	7.07	4,01994E+11	2,00997E+11	10
	GO:0017061	S-methyl-5-thioadenosine phosphorylase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0008425	2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0008169	C-methyltransferase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0003847	1-alkyl-2-acetyl-glycerophosphocholine esterase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004124	cysteine synthase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004829	threonine-tRNA ligase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004731	purine-nucleoside phosphorylase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004452	isopentenyl-diphosphate delta-isomerase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004371	glycerone kinase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004370	glycerol kinase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004357	glutamate-cysteine ligase activity	1	1	1000	5267	inf	1,89855E+11	1,09167E+11	10
	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	2	1	500	2634	52.44	3,76159E+11	2,00997E+11	10
	CELLULAR PROCESS									
	GO:0006810	transport	238	15	63	182	2.0	1,58832E+11	97012467298	10
	GO:0051179	localization	243	15	62	179	1.95	1,89004E+11	1,05596E+11	10
	GO:0007018	microtubule-based movement	71	10	141	407	4.9	1,30332E+11	1,41688E+11	3,34953E+11
	GO:0006928	movement of cell or subcellular component	73	10	137	396	4.74	1,65395E+11	1,41688E+11	4,25064E+11
	GO:0007017	microtubule-based process	84	10	119	344	4.02	5,32562E+11	2,28114E+11	1,36869E+11
	GO:0055085	transmembrane transport	120	9	75	217	2.36	2,17088E+11	1,18706E+11	10
	GO:0006082	organic acid metabolic process	104	9	87	25	2.78	9,05297E+11	8,94851E+11	10
	GO:0017144	drug metabolic process	53	7	132	382	4.45	2,04039E+11	4,03369E+11	52437908218
	GO:0006811	ion transport	73	7	96	277	3.08	1,21995E+11	9,50085E+11	10
	GO:0006457	protein folding	43	6	140	404	4.71	3223566761	47022050873	8,28457E+11
	GO:0071702	organic substance transport	66	6	91	263	2.89	2,524E+11	1,32381E+11	10
	GO:0065008	regulation of biological quality	56	6	107	31	3.47	1,19193E+11	9,50085E+11	10
	GO:0006575	cellular modified amino acid metabolic process	9	5	556	1808	40.67	293664,5288	1,03185E+11	1,47713E+11
	GO:0044272	sulfur compound biosynthetic process	14	5	357	1033	16.13	709227,761	1,41688E+11	1,82272E+11
	GO:0006790	sulfur compound metabolic process	23	5	217	629	8.05	9,27906E+11	3,38576E+11	2,38472E+11
	GO:0042592	homeostatic process	45	5	111	321	3.6	1,83875E+11	1,05013E+11	10
	GO:0042558	pteridine-containing compound metabolic process	7	4	571	1859	43.11	279732,1457	5,62821E+11	1,40705E+11
	GO:0043900	regulation of multi-organism process	10	4	400	1332	22.14	1,42041E+11	48116469619	3,84932E+11
	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	10	4	400	1332	22.14	1,42041E+11	48116469619	3,84932E+11
	GO:0006820	anion transport	16	4	250	723	9.59	17920436344	4,03369E+11	4,60555E+11
	GO:0032787	monocarboxylic acid metabolic process	27	4	148	429	4.99	1,28844E+11	97012467298	10
	GO:0019725	cellular homeostasis	38	4	105	304	3.36	4,05531E+11	1,70855E+11	10
	GO:0008610	lipid biosynthetic process	38	4	105	304	3.36	4,05531E+11	1,70855E+11	10
	GO:0015858	nucleoside transport	5	3	600	1736	42.92	3,83256E+11	1,96994E+11	9,84968E+11

**SOBRERREGULADO**

**BIOLC**

**CELLULAR COMPONENT**

**ON**

GO:1901264	carbohydrate derivative transport	8	3	375	1085	17.15	1,98805E+11	4,03369E+11	5,1093E+11
GO:0015931	nucleobase-containing compound transport	8	3	375	1085	17.15	1,98805E+11	4,03369E+11	5,1093E+11
GO:0016999	antibiotic metabolic process	12	3	250	723	9.52	7,0563E+11	78846436635	10
GO:0006083	acetate metabolic process	2	2	1000	2893	inf	1,18567E+11	3,38576E+11	3,04718E+11
GO:0019427	acetyl-CoA biosynthetic process from acetate	2	2	1000	2893	inf	1,18567E+11	3,38576E+11	3,04718E+11
GO:0015748	organophosphate ester transport	3	2	667	1928	56.77	3,47634E+11	47022050873	8,93419E+11
GO:0015914	phospholipid transport	3	2	667	1928	56.77	3,47634E+11	47022050873	8,93419E+11
GO:0010876	lipid localization	5	2	400	1157	18.91	1,10702E+11	9,17752E+11	10
GO:0015711	organic anion transport	5	2	400	1157	18.91	1,10702E+11	9,17752E+11	10
GO:0009067	aspartate family amino acid biosynthetic process	6	2	333	964	14.18	1,62317E+11	97012467298	10
GO:0034033	purine nucleoside bisphosphate biosynthetic process	6	2	333	964	14.18	1,62317E+11	97012467298	10
GO:0034030	ribonucleoside bisphosphate biosynthetic process	6	2	333	964	14.18	1,62317E+11	97012467298	10
GO:0009066	aspartate family amino acid metabolic process	8	2	250	723	9.45	2,89566E+11	14041230767	10
GO:0033865	nucleoside bisphosphate metabolic process	8	2	250	723	9.45	2,89566E+11	14041230767	10
GO:0034032	purine nucleoside bisphosphate metabolic process	8	2	250	723	9.45	2,89566E+11	14041230767	10
GO:0033875	ribonucleoside bisphosphate metabolic process	8	2	250	723	9.45	2,89566E+11	14041230767	10
GO:0006429	leucyl-tRNA aminoacylation	1	1	1000	2893	inf	3,45707E+11	1,50588E+11	10
GO:0006556	S-adenosylmethionine biosynthetic process	1	1	1000	2893	inf	3,45707E+11	1,50588E+11	10
GO:0046500	S-adenosylmethionine metabolic process	1	1	1000	2893	inf	3,45707E+11	1,50588E+11	10
GO:0006665	sphingolipid metabolic process	1	1	1000	2893	inf	3,45707E+11	1,50588E+11	10
GO:0016020	membrane	362	23	64	184	2.1	2,51503E+11	1,28896E+11	1,03116E+11
GO:0016021	integral component of membrane	173	15	87	251	2.88	7,58055E+11	4,44004E+11	3,10803E+11
GO:0005875	microtubule associated complex	24	7	292	844	12.14	1054441,354	2,1616E+11	4,32321E+11
GO:0005856	cytoskeleton	35	7	200	579	7.35	1,49199E+11	1,22343E+11	6,11717E+11
GO:1902494	catalytic complex	66	7	106	307	3.45	7,11415E+11	2,65164E+11	29168031096
GO:0005952	cAMP-dependent protein kinase complex	1	1	1000	2893	inf	3,45707E+11	1,18117E+11	10
GO:0003824	catalytic activity	1626	70	43	125	1.6	7,08521E+11	3,59166E+11	10
GO:0043167	ion binding	1002	49	49	141	1.73	2,92942E+11	1,77655E+11	5,50731E+11
GO:0036094	small molecule binding	791	44	56	161	2.01	3,37598E+11	3,34045E+11	6,34685E+11
GO:0043168	anion binding	762	43	56	163	2.03	2,94975E+11	3,34045E+11	5,54554E+11
GO:1901265	nucleoside phosphate binding	766	43	56	162	2.02	3,33087E+11	3,34045E+11	6,26204E+11
GO:0017076	purine nucleotide binding	693	42	61	175	2.22	6734812,596	19910032047	1,26614E+11
GO:0097367	carbohydrate derivative binding	703	42	60	173	2.18	9531398,32	19910032047	1,7919E+11
GO:0008144	drug binding	600	40	67	193	2.48	1108377,545	10700083404	2,08375E+11
GO:0035639	purine ribonucleoside triphosphate binding	682	40	59	17	2.1	2,31631E+11	3,34045E+11	4,35467E+11
GO:0032559	adenyl ribonucleotide binding	586	39	67	193	2.46	1571741,541	10700083404	2,95487E+11
GO:0016787	hydrolase activity	679	33	49	141	1.58	2,03801E+11	9,12252E+11	10
GO:0016817	hydrolase activity, acting on acid anhydrides	291	22	76	219	2.57	3,04251E+11	3,34045E+11	5,71991E+11
GO:0005215	transporter activity	112	12	107	31	3.61	3,97298E+11	3,55677E+11	7,46921E+11
GO:0016887	ATPase activity	93	11	118	342	4.02	2,9496E+11	3,34045E+11	5,54525E+11
GO:0003777	microtubule motor activity	68	10	147	425	5.16	8961139,515	19910032047	1,68469E+11
GO:0003774	motor activity	70	10	143	413	4.98	11530526044	2,08261E+11	2,16774E+11
GO:0004198	calcium-dependent cysteine-type endopeptidase activity	24	6	250	723	9.74	1,21855E+11	2,08261E+11	2,29088E+11
GO:0008234	cysteine-type peptidase activity	48	6	125	362	4.14	5,63728E+11	3,02803E+11	10
GO:0016874	ligase activity	61	6	98	285	3.15	1,77277E+11	8,12879E+11	10
GO:0043492	ATPase activity, coupled to movement of substances	36	5	139	402	4.65	7,25974E+11	3,59166E+11	10



## MOLECULAR FUNCTI

GO:0022804	active transmembrane transporter activity	43	5	116	336	3.79	1,53004E+11	7,19119E+11	10
GO:0015318	inorganic molecular entity transmembrane transporter activity	56	5	89	258	2.81	4,26427E+11	1,27251E+11	10
GO:0051082	unfolded protein binding	34	4	118	34	3.82	2,82986E+11	1,06546E+11	10
GO:0005337	nucleoside transmembrane transporter activity	5	3	600	1736	42.92	3,83256E+11	3,55677E+11	7,20521E+11
GO:0016646	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as	7	3	429	1395	24.09	9,10168E+11	3,02818E+11	2,12979E+11
GO:1901505	carbohydrate derivative transmembrane transporter activity	8	3	375	1085	17.15	1,98805E+11	1,24585E+11	3,73754E+11
GO:0015932	nucleobase-containing compound transmembrane transporter activity	8	3	375	1085	17.15	1,98805E+11	1,24585E+11	3,73754E+11
GO:0016878	acid-thiol ligase activity	2	2	1000	2893	inf	1,18567E+11	7,96095E+11	2,22907E+11
GO:0016208	AMP binding	2	2	1000	2893	inf	1,18567E+11	7,96095E+11	2,22907E+11
GO:0004012	phospholipid-translocating ATPase activity	3	2	667	1928	56.77	3,47634E+11	1,92221E+11	6,53552E+11
GO:0005319	lipid transporter activity	4	2	500	1446	28.38	6,7954E+11	3,54871E+11	10
GO:0005315	inorganic phosphate transmembrane transporter activity	5	2	400	1157	18.91	1,10702E+11	5,33639E+11	10
GO:0015291	secondary active transmembrane transporter activity	9	2	222	643	8.1	3,63993E+11	1,10372E+11	10
GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase act	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0042085	5-methyltetrahydropteroyltri-L-glutamate-dependent methyltransferase activi	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0003989	acetyl-CoA carboxylase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0004019	adenylosuccinate synthase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0008603	cAMP-dependent protein kinase regulator activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0019203	carbohydrate phosphatase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0042132	fructose 1,6-bisphosphate 1-phosphatase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0004375	glycine dehydrogenase (decarboxylating) activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0004823	leucine-tRNA ligase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0016885	ligase activity, forming carbon-carbon bonds	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0004478	methionine adenosyltransferase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0016781	phosphotransferase activity, paired acceptors	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0050242	pyruvate, phosphate dikinase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0042284	sphingolipid delta-4 desaturase activity	1	1	1000	2893	inf	3,45707E+11	1,06546E+11	10
GO:0055114	oxidation-reduction process	175	11	63	22	2.45	1,0194E+11	7,26283E+11	10
GO:0044281	small molecule metabolic process	173	10	58	202	2.22	2,42083E+11	9,27987E+11	10
GO:0005975	carbohydrate metabolic process	53	7	132	462	5.51	6,53066E+11	5,0493E+11	16522581215
GO:0006082	organic acid metabolic process	101	7	69	243	2.66	2,39994E+11	9,27987E+11	10
GO:0006732	coenzyme metabolic process	39	6	154	538	6.54	70511570741	5,0493E+11	1,78394E+11
GO:0017144	drug metabolic process	44	6	136	477	5.67	1,35988E+11	5,0493E+11	3,4405E+11
GO:0051186	cofactor metabolic process	53	6	113	396	4.57	3,59752E+11	5,0493E+11	91017260245
GO:1901135	carbohydrate derivative metabolic process	57	6	105	368	4.21	5,189E+11	5,0493E+11	10
GO:0055086	nucleobase-containing small molecule metabolic process	64	6	94	328	3.69	9,13685E+11	7,00492E+11	10
GO:0019637	organophosphate metabolic process	84	6	71	25	2.73	3,14548E+11	98247597138	10
GO:0019693	ribose phosphate metabolic process	33	5	152	53	6.36	2,15275E+11	5,0493E+11	5,44646E+11
GO:0046390	ribose phosphate biosynthetic process	23	4	174	609	7.43	3,64581E+11	5,0493E+11	9,22391E+11
GO:0032787	monocarboxylic acid metabolic process	24	4	167	583	7.06	42804876567	5,0493E+11	10
GO:0072522	purine-containing compound biosynthetic process	26	4	154	538	6.41	57653107334	5,40231E+11	10
GO:0072521	purine-containing compound metabolic process	33	4	121	424	4.86	1,3554E+11	8,16469E+11	10
GO:0019725	cellular homeostasis	36	4	111	389	4.4	1,82852E+11	8,38424E+11	10
GO:0016999	antibiotic metabolic process	12	3	250	875	11.68	4,11995E+11	5,0493E+11	10
GO:0072524	pyridine-containing compound metabolic process	18	3	167	583	6.99	1,34982E+11	8,16469E+11	10
GO:0006091	generation of precursor metabolites and energy	22	3	136	477	5.51	2,34648E+11	9,27593E+11	10
GO:0006790	sulfur compound metabolic process	23	3	130	457	5.24	26437661625	9,55533E+11	10

## PROCESS

SUBREGULADO

BIOLOGICAL F

CELLULAR COMPONENT

GO:0046700	heterocycle catabolic process	24	3	125	438	4.99	2,9603E+11	9,62026E+11	10
GO:1901361	organic cyclic compound catabolic process	24	3	125	438	4.99	2,9603E+11	9,62026E+11	10
GO:0034033	purine nucleoside bisphosphate biosynthetic process	6	2	333	1167	17.35	1,12408E+11	7,26283E+11	10
GO:0033865	nucleoside bisphosphate metabolic process	8	2	250	875	11.56	2,0215E+11	8,38424E+11	10
GO:0009132	nucleoside diphosphate metabolic process	8	2	250	875	11.56	2,0215E+11	8,38424E+11	10
GO:0046939	nucleotide phosphorylation	8	2	250	875	11.56	2,0215E+11	8,38424E+11	10
GO:0042866	pyruvate biosynthetic process	8	2	250	875	11.56	2,0215E+11	8,38424E+11	10
GO:0016052	carbohydrate catabolic process	9	2	222	778	9.91	2,55123E+11	93545026897	10
GO:0046434	organophosphate catabolic process	11	2	182	636	7.7	3,75602E+11	1,14491E+11	10
GO:0006083	acetate metabolic process	2	2	1000	350	inf	8,07797E+11	5,0493E+11	2,04373E+11
GO:0019427	acetyl-CoA biosynthetic process from acetate	2	2	1000	350	inf	8,07797E+11	5,0493E+11	2,04373E+11
GO:0035383	thioester metabolic process	4	2	500	175	34.73	46678785014	5,0493E+11	10
GO:0015858	nucleoside transport	5	2	400	140	23.14	7,63533E+11	6,03669E+11	10
GO:1901264	carbohydrate derivative transport	7	2	286	100	13.88	1,54462E+11	8,38424E+11	10
GO:0015931	nucleobase-containing compound transport	7	2	286	100	13.88	1,54462E+11	8,38424E+11	10
GO:1901292	nucleoside phosphate catabolic process	10	2	200	70	8.66	3,13047E+11	98247597138	10
GO:0006090	pyruvate metabolic process	10	2	200	70	8.66	3,13047E+11	98247597138	10
GO:0006429	leucyl-tRNA aminoacylation	1	1	1000	350	inf	2,85714E+11	9,62026E+11	10
GO:0006562	proline catabolic process	1	1	1000	350	inf	2,85714E+11	9,62026E+11	10
GO:0010133	proline catabolic process to glutamate	1	1	1000	350	inf	2,85714E+11	9,62026E+11	10
GO:0006556	S-adenosylmethionine biosynthetic process	1	1	1000	350	inf	2,85714E+11	9,62026E+11	10
GO:0046500	S-adenosylmethionine metabolic process	1	1	1000	350	inf	2,85714E+11	9,62026E+11	10
GO:0044464	cell part	539	22	41	143	1.59	4,66358E+11	14553223871	10
GO:1902494	catalytic complex	64	5	78	273	2.99	3,46009E+11	14553223871	10
GO:0044430	cytoskeletal part	34	4	118	412	4.69	1,50322E+11	14553223871	9,31997E+11
GO:0005856	cytoskeleton	34	4	118	412	4.69	1,50322E+11	14553223871	9,31997E+11
GO:0031514	motile cilium	8	2	250	875	11.56	2,0215E+11	14553223871	10
GO:0042995	cell projection	11	2	182	636	7.7	3,75602E+11	14553223871	10
GO:0000785	chromatin	11	2	182	636	7.7	3,75602E+11	14553223871	10
GO:0005929	cilium	11	2	182	636	7.7	3,75602E+11	14553223871	10
GO:0120025	plasma membrane bounded cell projection	11	2	182	636	7.7	3,75602E+11	14553223871	10
GO:0032993	protein-DNA complex	11	2	182	636	7.7	3,75602E+11	14553223871	10
GO:0044815	DNA packaging complex	12	2	167	583	6.93	4,42483E+11	14553223871	10
GO:0005952	cAMP-dependent protein kinase complex	1	1	1000	350	inf	2,85714E+11	14553223871	10
GO:0000015	phosphopyruvate hydratase complex	1	1	1000	350	inf	2,85714E+11	14553223871	10
GO:0022624	proteasome accessory complex	1	1	1000	350	inf	2,85714E+11	14553223871	10
GO:0008537	proteasome activator complex	1	1	1000	350	inf	2,85714E+11	14553223871	10
GO:0016491	oxidoreductase activity	201	11	55	192	2.1	2,64143E+11	1,58525E+11	10
GO:0048037	cofactor binding	123	8	65	228	2.49	22878669764	1,58525E+11	10
GO:0050662	coenzyme binding	85	6	71	247	2.69	3,30875E+11	1,72456E+11	10
GO:0008234	cysteine-type peptidase activity	45	5	111	389	4.43	8,46333E+11	1,45569E+11	10
GO:0003774	motor activity	64	5	78	273	2.99	3,46009E+11	1,7504E+11	10
GO:0004175	endopeptidase activity	66	5	76	265	2.89	3,88025E+11	1,8539E+11	10
GO:0016829	lyase activity	32	4	125	438	5.03	1,21721E+11	1,58525E+11	10
GO:0004197	cysteine-type endopeptidase activity	25	4	160	56	6.72	4,98585E+11	1,22509E+11	8,57566E+11
GO:0009055	electron transfer activity	28	3	107	375	4.18	4,41645E+11	2,00282E+11	10

SOBRERREGULADO	CELLULAR COMPONENT	MOLECULAR FUNCTION									
			GO ID	Term	Count	Count	Count	Count	Count	Count	
		GO:0016830	carbon-carbon lyase activity	14	3	214	75	9.55	6,53978E+11	1,40605E+11	10
		GO:0051920	peroxiredoxin activity	3	2	667	2333	69.47	2,3782E+11	6,8175E+11	4,0905E+11
		GO:0005516	calmodulin binding	6	2	333	1167	17.35	1,12408E+11	1,58525E+11	10
		GO:0016877	ligase activity, forming carbon-sulfur bonds	11	2	182	636	7.7	3,75602E+11	1,84582E+11	10
		GO:0016878	acid-thiol ligase activity	2	2	1000	350	inf	8,07797E+11	2,77882E+11	1,38941E+11
		GO:0016208	AMP binding	2	2	1000	350	inf	8,07797E+11	2,77882E+11	1,38941E+11
		GO:0016744	transferase activity, transferring aldehyde or ketonic groups	2	2	1000	350	inf	8,07797E+11	2,77882E+11	1,38941E+11
		GO:0005337	nucleoside transmembrane transporter activity	5	2	400	140	23.14	7,63533E+11	1,45569E+11	10
		GO:1901505	carbohydrate derivative transmembrane transporter activity	7	2	286	100	13.88	1,54462E+11	1,58525E+11	10
		GO:0015932	nucleobase-containing compound transmembrane transporter activity	7	2	286	100	13.88	1,54462E+11	1,58525E+11	10
		GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	10	2	200	70	8.66	3,13047E+11	1,68263E+11	10
		GO:0003842	1-pyrroline-5-carboxylate dehydrogenase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0008603	cAMP-dependent protein kinase regulator activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0019203	carbohydrate phosphatase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0042132	fructose 1,6-bisphosphate 1-phosphatase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004332	fructose-bisphosphate aldolase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004823	leucine-tRNA ligase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004478	methionine adenosyltransferase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004588	orotate phosphoribosyltransferase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004590	orotidine-5'-phosphate decarboxylase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004612	phosphoenolpyruvate carboxykinase (ATP) activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004634	phosphopyruvate hydratase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0004802	transketolase activity	1	1	1000	350	inf	2,85714E+11	1,58525E+11	10
		GO:0034660	ncRNA metabolic process	64	4	63	535	6.19	6,07851E+11	9,48541E+11	7,90206E+11
		GO:0006396	RNA processing	77	4	52	445	5.07	1,16178E+11	9,48541E+11	10
		GO:0044085	cellular component biogenesis	63	3	48	408	4.51	3,60415E+11	1,61565E+11	10
		GO:0006665	sphingolipid metabolic process	1	1	1000	8566	inf	1,16743E+11	9,48541E+11	10
		GO:0010564	regulation of cell cycle process	1	1	1000	8566	inf	1,16743E+11	9,48541E+11	10
		GO:0032886	regulation of microtubule-based process	1	1	1000	8566	inf	1,16743E+11	9,48541E+11	10
		GO:0051129	negative regulation of cellular component organization	1	1	1000	8566	inf	1,16743E+11	9,48541E+11	10
		GO:0070507	regulation of microtubule cytoskeleton organization	1	1	1000	8566	inf	1,16743E+11	9,48541E+11	10
		GO:0030031	cell projection assembly	2	1	500	4283	86.92	2,32159E+11	1,37185E+11	10
		GO:0120031	plasma membrane bounded cell projection assembly	2	1	500	4283	86.92	2,32159E+11	1,37185E+11	10
		GO:0030030	cell projection organization	3	1	333	2855	43.45	3,46263E+11	1,60765E+11	10
		GO:0033043	regulation of organelle organization	3	1	333	2855	43.45	3,46263E+11	1,60765E+11	10
		GO:0051128	regulation of cellular component organization	3	1	333	2855	43.45	3,46263E+11	1,60765E+11	10
		GO:0120036	plasma membrane bounded cell projection organization	3	1	333	2855	43.45	3,46263E+11	1,60765E+11	10
		GO:0035869	ciliary transition zone	1	1	1000	8566	inf	1,16743E+11	2,62673E+11	5,25346E+11
		GO:0044463	cell projection part	3	1	333	2855	43.45	3,46263E+11	3,11636E+11	10
		GO:0120038	plasma membrane bounded cell projection part	3	1	333	2855	43.45	3,46263E+11	3,11636E+11	10
		GO:0043167	ion binding	949	17	18	153	1.98	2,89905E+11	1,96977E+11	10
		GO:0046872	metal ion binding	260	8	31	264	3.14	8,80565E+11	1,75115E+11	9,24593E+11
		GO:0043169	cation binding	265	8	30	259	3.07	9,84606E+11	1,75115E+11	10
		GO:0046914	transition metal ion binding	105	4	38	326	3.63	3,25285E+11	1,96977E+11	10
		GO:0008233	peptidase activity	118	4	34	29	3.2	4,68992E+11	1,96977E+11	10
		GO:0008168	methyltransferase activity	65	3	46	395	4.36	3,90196E+11	1,96977E+11	10

**MOLECULAR FUNC1**

GO:0016741	transferase activity, transferring one-carbon groups	69	3	43	372	4.09	4,53433E+11	1,96977E+11	10
GO:0004177	aminopeptidase activity	11	2	182	1557	19.8	6,83152E+11	1,75115E+11	7,17309E+11
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reducti	11	2	182	1557	19.8	6,83152E+11	1,75115E+11	7,17309E+11
GO:0008238	exopeptidase activity	21	2	95	816	9.35	2,42396E+11	1,96977E+11	10
GO:0004386	helicase activity	28	2	71	612	6.82	4,14615E+11	1,96977E+11	10
GO:0034701	tripeptidase activity	1	1	1000	8566	inf	1,16743E+11	1,75115E+11	10
GO:0042284	sphingolipid delta-4 desaturase activity	1	1	1000	8566	inf	1,16743E+11	1,75115E+11	10
GO:0045148	tripeptide aminopeptidase activity	1	1	1000	8566	inf	1,16743E+11	1,75115E+11	10
GO:0003909	DNA ligase activity	3	1	333	2855	43.45	3,46263E+11	1,96977E+11	10
GO:0018024	histone-lysine N-methyltransferase activity	3	1	333	2855	43.45	3,46263E+11	1,96977E+11	10
GO:0004749	ribose phosphate diphosphokinase activity	4	1	250	2141	28.95	45906781558	1,96977E+11	10
GO:0017150	tRNA dihydrouridine synthase activity	4	1	250	2141	28.95	45906781558	1,96977E+11	10