

Functional enrichment in lynxes

Sp.	Term	Annotated	Significant	Expected	Fisher	p.adj	ontology	
Lp	GO:1902236	negative regulation of endoplasmic retic...	16	3	0.12	0.00023	0.0178	BP
Lp	GO:0006334	nucleosome assembly	74	5	0.57	0.00026	0.0178	BP
Lp	GO:0030527	structural constituent of chromatin	89	14	0.79	4.7E-14	0	MF
Lp	GO:0046982	protein heterodimerization activity	279	13	2.49	1.3E-06	1E-04	MF
Lp	GO:0003677	DNA binding	1813	35	16.16	2.2E-05	0.0011	MF
Lp	GO:0000786	nucleosome	118	14	1.02	1.7E-12	0	CC
Lp	GO:0005634	nucleus	7772	76	67.04	2.6E-05	0.002	CC
Lr	GO:0061099	negative regulation of protein tyrosine ...	20	4	0.29	0.00032	0.048	BP
Lr	GO:0009435	NAD biosynthetic process	12	3	0.17	0.00058	0.048	BP
Lr	GO:0042537	benzene-containing compound metabolic pr...	13	3	0.19	0.00075	0.048	BP
Lr	GO:0009074	aromatic amino acid family catabolic pro...	13	3	0.19	0.00075	0.048	BP
LI	GO:1902236	negative regulation of endoplasmic retic...	16	2	0.03	0.00034	0.0105	BP
LI	GO:0001755	neural crest cell migration	37	2	0.06	0.00187	0.0196	BP
LI	GO:0097237	cellular response to toxic substance	74	2	0.13	0.00505	0.0196	BP
LI	GO:0045927	positive regulation of growth	162	2	0.28	0.00676	0.0196	BP
LI	GO:0043632	modification-dependent macromolecule cat...	542	3	0.94	0.01000	0.0196	BP
LI	GO:1903599	positive regulation of autophagy of mito...	10	1	0.02	0.01722	0.0196	BP
LI	GO:0032353	negative regulation of hormone biosynthe...	10	1	0.02	0.01722	0.0196	BP
LI	GO:0016078	tRNA catabolic process	10	1	0.02	0.01722	0.0196	BP
LI	GO:0045822	negative regulation of heart contraction	10	1	0.02	0.01722	0.0196	BP
LI	GO:0006596	polyamine biosynthetic process	10	1	0.02	0.01722	0.0196	BP
LI	GO:0045475	locomotor rhythm	10	1	0.02	0.01722	0.0196	BP
LI	GO:0010992	ubiquitin recycling	10	1	0.02	0.01722	0.0196	BP
LI	GO:0010831	positive regulation of myotube different...	10	1	0.02	0.01722	0.0196	BP
LI	GO:0030007	intracellular potassium ion homeostasis	10	1	0.02	0.01722	0.0196	BP
LI	GO:0043144	sno(s)RNA processing	10	1	0.02	0.01722	0.0196	BP
LI	GO:0006206	pyrimidine nucleobase metabolic process	10	1	0.02	0.01722	0.0196	BP
LI	GO:1903377	negative regulation of oxidative stress-...	10	1	0.02	0.01722	0.0196	BP
LI	GO:0071027	nuclear RNA surveillance	10	1	0.02	0.01722	0.0196	BP
LI	GO:0031943	regulation of glucocorticoid metabolic p...	10	1	0.02	0.01722	0.0196	BP
LI	GO:0071044	histone mRNA catabolic process	10	1	0.02	0.01722	0.0196	BP
LI	GO:0051580	regulation of neurotransmitter uptake	10	1	0.02	0.01722	0.0196	BP
LI	GO:0032341	aldosterone metabolic process	11	1	0.02	0.01892	0.0196	BP
LI	GO:0071233	cellular response to leucine	11	1	0.02	0.01892	0.0196	BP
LI	GO:0042415	norepinephrine metabolic process	11	1	0.02	0.01892	0.0196	BP
LI	GO:0003096	renal sodium ion transport	11	1	0.02	0.01892	0.0196	BP
LI	GO:1904925	positive regulation of autophagy of mito...	11	1	0.02	0.01892	0.0196	BP
LI	GO:0048484	enteric nervous system development	11	1	0.02	0.01892	0.0196	BP
LI	GO:0044793	negative regulation by host of viral pro...	11	1	0.02	0.01892	0.0196	BP
LI	GO:0036376	sodium ion export across plasma membrane	11	1	0.02	0.01892	0.0196	BP
LI	GO:0051590	positive regulation of neurotransmitter ...	11	1	0.02	0.01892	0.0196	BP
LI	GO:0097254	renal tubular secretion	12	1	0.02	0.02062	0.0206	BP
Lc	GO:0007186	G protein-coupled receptor signaling pat...	1333	44	15.59	1.6E-11	0	BP
Lc	GO:0050911	detection of chemical stimulus involved ...	408	23	4.77	4.9E-10	0	BP
Lc	GO:0004984	olfactory receptor activity	688	38	8.3	2.5E-15	0	MF
Lc	GO:0004930	G protein-coupled receptor activity	1071	42	12.92	1.6E-11	0	MF
Lc	GO:0005886	plasma membrane	3774	80	44.66	2.5E-08	0	CC
Lc	GO:0043198	dendritic shaft	13	3	0.15	0.00043	0.046	CC