

Molecular Function - CET Treatment

Ontology	Genes	Up	Down	Array	z-up	z-down
catalytic activity	494	270	224	3999	-1.22	2.52
nucleotide binding	207	110	97	1641	-0.76	2.03
DNA binding	204	140	64	1709	1.81	-2.41
hydrolase activity	183	98	85	1695	-2.37	0.22
molecular transducer activity	151	111	40	1318	1.9	-3.34
signal transducer activity	151	111	40	1318	1.9	-3.34
receptor activity	117	90	27	994	2.44	-3.35
oxidoreductase activity	77	36	41	545	-0.51	2.9
RNA binding	72	30	42	567	-1.76	2.83
transmembrane receptor activity	70	58	12	617	2.23	-3.5
all	69	32	37	505	-0.73	2.57
molecular_function	68	32	36	493	-0.58	2.52
cytoskeletal protein binding	59	44	15	361	3.77	-0.67
actin binding	40	31	9	253	3.18	-1
iron ion binding	37	15	22	217	-0.14	3.6
transferase activity, transferring glycosyl groups	35	22	13	198	2.18	1.09
G-protein coupled receptor activity	30	26	4	306	0.93	-2.95
metal ion transmembrane transporter activity	30	25	5	223	2.38	-1.86
rhodopsin-like receptor activity	22	18	4	236	0.29	-2.31
cation channel activity	21	18	3	179	1.52	-2.02
manganese ion binding	21	15	6	119	2.32	0.07
cysteine-type peptidase activity	20	8	12	113	-0.03	2.82
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	17	6	11	86	-0.06	3.4
transmembrane receptor protein kinase activity	15	13	2	73	3.54	-0.86
monooxygenase activity	14	7	7	69	0.97	2.02
UDP-glycosyltransferase activity	14	12	2	79	2.78	-0.98
diacylglycerol binding	13	10	3	51	3.46	0.32
oxidoreductase activity, acting on CH-OH group of donors	13	4	9	95	-1.12	2.07
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	13	4	9	87	-0.93	2.36
lipid transporter activity	12	5	7	61	0.32	2.38
transmembrane receptor protein tyrosine kinase activity	12	10	2	61	2.81	-0.59
tubulin binding	12	9	3	54	2.72	0.22
protein transporter activity	11	2	9	63	-1.23	3.46
transferase activity, transferring pentosyl groups	11	5	6	38	1.44	3.11
unfolded protein binding	11	2	9	90	-1.82	2.25
microtubule binding	10	8	2	42	3	-0.04

Z-scores were determined using GeneSifter software. Criteria for inclusion in the table were an ontology having a z-score = 2 or = -2 in z-up or z-down column and gene list column containing 10 genes. Genes - number of genes differentially expressed within the assigned Molecular Function ontology; Array- the number of genes on the microarray assigned to the particular gene ontology. Significant z-scores and corresponding numbers of genes in each category are shown in bold.

Molecular Function – CET + LH Treatment

Ontology	Genes	Up	Down	Array	z-up	z-down
catalytic activity	389	163	226	3999	-0.99	-4.46
molecular transducer activity	188	70	118	1318	1.85	2.76
signal transducer activity	188	70	118	1318	1.85	2.76
receptor activity	153	51	102	994	1.29	4.03
transferase activity	130	58	72	1337	0.01	-2.62
transmembrane receptor activity	100	30	70	617	0.66	4.2
transferase activity, transferring phosphorus-containing groups	70	33	37	737	0.2	-2.29
cytoskeletal protein binding	51	15	36	361	-0.17	2.14
G-protein coupled receptor activity	50	14	36	306	0.21	3.21
structural molecule activity	48	11	37	507	-2.45	0.16
identical protein binding	44	8	36	338	-1.8	2.57
rhodopsin-like receptor activity	41	13	28	236	0.9	2.87
hydrolase activity, acting on acid anhydrides	39	12	27	487	-2.07	-1.38
actin binding	38	11	27	253	0.01	2.22
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	38	12	26	485	-2.05	-1.54
pyrophosphatase activity	38	12	26	484	-2.05	-1.53
alkali metal ion binding	29	12	17	159	2	1.77
peptide binding	24	9	15	124	1.61	2.17
cytokine activity	23	12	11	141	2.45	0.32
magnesium ion binding	23	10	13	326	-1.14	-2.23
enzyme activator activity	21	12	9	256	0.28	-2.27
sodium ion binding	19	7	12	91	1.58	2.26
protein binding, bridging	15	6	9	67	1.86	2.02
cysteine-type peptidase activity	12	10	2	113	2.37	-2.22
growth factor binding	12	7	5	63	2.65	0.25
kinase binding	12	2	10	75	-0.71	2.1
phosphoric diester hydrolase activity	12	7	5	63	2.65	0.25

Z-scores were determined using GeneSifter software. Criteria for inclusion in the table were an ontology having a z-score = 2 or = -2 in z-up or z-down column and gene list column containing 10 genes. Genes - number of genes differentially expressed within the assigned Molecular Function ontology; Array- the number of genes on the microarray assigned to the particular gene ontology. Significant z-scores and corresponding numbers of genes in each category are shown in bold.

Molecular Function –PGF_{2α} Treatment

Ontology	Genes	Up	Down	Array	z-up	z-down
protein binding	417	267	150	5570	3.8	-2.67
catalytic activity	286	140	146	3999	-2.26	2.29
molecular transducer activity	138	96	42	1318	6.27	0.1
signal transducer activity	138	96	42	1318	6.27	0.1
transition metal ion binding	132	70	62	2148	-2.11	-0.75
nucleic acid binding	113	57	56	2474	-5.02	-2.82
receptor activity	108	75	33	994	5.8	0.34
zinc ion binding	97	53	44	1795	-2.61	-1.82
DNA binding	74	43	31	1709	-3.53	-3.41
calcium ion binding	70	49	21	694	4.11	-0.18
receptor binding	67	50	17	550	6.1	-0.07
transmembrane receptor activity	62	39	23	617	2.91	0.86
oxidoreductase activity	52	21	31	545	-0.26	3.49
carbohydrate binding	30	24	6	212	5.39	-0.26
RNA binding	30	13	17	567	-2.2	-0.2
actin binding	26	17	9	253	2.15	0.38
iron ion binding	26	9	17	217	0.06	4
gated channel activity	25	14	11	206	2	1.83
cytokine activity	23	21	2	141	6.54	-1.18
electron carrier activity	20	8	12	182	0.22	2.69
sugar binding	18	14	4	130	3.89	-0.04
voltage-gated channel activity	17	10	7	128	2.15	1.52
voltage-gated ion channel activity	17	10	7	128	2.15	1.52
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	16	6	10	86	1.37	4.53
pattern binding	15	13	2	85	5.25	-0.42
protein complex binding	15	14	1	81	6.04	-0.99
receptor signaling protein activity	15	12	3	110	3.65	-0.25
vitamin binding	15	6	9	105	0.86	3.21
glycosaminoglycan binding	14	12	2	78	5.07	-0.29
polysaccharide binding	14	12	2	78	5.07	-0.29
growth factor activity	13	10	3	120	2.37	-0.4
heme binding	13	3	10	91	-0.38	4.31
monooxygenase activity	13	4	9	69	0.73	4.73
protease inhibitor activity	13	9	4	103	2.41	0.43
tetrapyrrole binding	13	3	10	91	-0.38	4.31
endopeptidase inhibitor activity	12	9	3	100	2.5	-0.08
exopeptidase activity	11	5	6	77	1.08	2.35
transmembrane receptor protein kinase activity	11	5	6	73	1.2	2.5
G-protein-coupled receptor binding	10	9	1	52	4.84	-0.5
growth factor binding	10	9	1	63	4.11	-0.71
heparin binding	10	9	1	61	4.23	-0.67

Z-scores were determined using GeneSifter software. Criteria for inclusion in the table were an ontology having a z-score = 2 or = -2 in z-up or z-down column and gene list column containing 10 genes. Genes - number of genes differentially expressed within the assigned Molecular Function ontology; Array- the number of genes on the microarray assigned to the particular gene ontology. Significant z-scores and corresponding numbers of genes in each category are shown in bold.