

Response of *Sclerotinia sclerotiorum* to long exposure of isothiocyanates by transcriptomics approach

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GO terms of Biological Processes with p value lower than 0.05 and log2>1 in the treatment of <i>Sclerotinia sclerotiorum</i> with AITC versus Control					
GO term	description	pvalue	downregulated	ratio	upregulated
GO:1901564	organonitrogen compound metabolic process	0.0000	53	1.2379	125
GO:0022607	cellular component assembly	0.0000	38	1.3067	94
GO:0002181	cytoplasmic translation	0.0000	6	2.3219	30
GO:1901989	positive regulation of cell cycle phase transition	0.0000	4	1.9069	15
GO:1901992	positive regulation of mitotic cell cycle phase transition	0.0000	4	1.9069	15
GO:0044281	small molecule metabolic process	0.0000	60	1.2630	144
GO:1903047	mitotic cell cycle process	0.0000	21	1.7162	69
GO:0034622	cellular macromolecular complex assembly	0.0000	19	1.8395	68
GO:0000278	mitotic cell cycle	0.0000	22	1.6491	69
GO:0065003	macromolecular complex assembly	0.0000	23	1.7618	78
GO:0051301	cell division	0.0000	17	1.6939	55
GO:1902101	positive regulation of metaphase/anaphase transition of cell cycle	0.0001	1	3.8074	14
GO:0045842	positive regulation of mitotic metaphase/anaphase transition	0.0001	1	3.8074	14
GO:1901970	positive regulation of mitotic sister chromatid separation	0.0001	1	3.8074	14
GO:0008154	actin polymerization or depolymerization	0.0001	3	1.7370	10
GO:0006461	protein complex assembly	0.0001	16	1.5236	46
GO:1903364	positive regulation of cellular protein catabolic process	0.0001	2	2.8074	14
GO:1901800	positive regulation of proteasomal protein catabolic process	0.0001	2	2.8074	14
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0001	2	2.8074	14
GO:0045732	positive regulation of protein catabolic process	0.0001	2	2.8074	14
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	0.0001	2	2.8074	14
GO:0070271	protein complex biogenesis	0.0001	16	1.5236	46
GO:0055086	nucleobase-containing small molecule metabolic process	0.0002	16	1.8074	56

GO:0009896	positive regulation of catabolic process	0.0002	2	2.8074	14
GO:0031331	positive regulation of cellular catabolic process	0.0002	2	2.8074	14
GO:0045862	positive regulation of proteolysis	0.0002	2	2.8074	14
GO:0030866	cortical actin cytoskeleton organization	0.0002	5	1.3785	13
GO:0030865	cortical cytoskeleton organization	0.0002	5	1.3785	13
GO:0030832	regulation of actin filament length	0.0002	3	1.2224	7
GO:0008064	regulation of actin polymerization or depolymerization	0.0002	3	1.2224	7
GO:0030029	actin filament-based process	0.0003	9	1.3536	23
GO:0032956	regulation of actin cytoskeleton organization	0.0003	3	1.8745	11
GO:0032970	regulation of actin filament-based process	0.0003	3	1.8745	11
GO:0051984	positive regulation of chromosome segregation	0.0004	1	3.9069	15
GO:0043254	regulation of protein complex assembly	0.0004	2	2.8074	14
GO:0030036	actin cytoskeleton organization	0.0005	8	1.5236	23
GO:0071822	protein complex subunit organization	0.0005	24	1.2224	56
GO:0006412	translation	0.0005	21	1.9475	81
GO:2001252	positive regulation of chromosome organization	0.0005	2	2.9069	15
GO:0043603	cellular amide metabolic process	0.0005	6	2.2224	28
GO:0030041	actin filament polymerization	0.0006	2	2.0000	8
GO:0000910	cytokinesis	0.0006	8	1.5236	23
GO:0045840	positive regulation of mitotic nuclear division	0.0007	1	3.9069	15
GO:0030833	regulation of actin filament polymerization	0.0007	2	1.8074	7
GO:0032271	regulation of protein polymerization	0.0007	2	1.8074	7
GO:0090068	positive regulation of cell cycle process	0.0008	5	2.0000	20
GO:0045931	positive regulation of mitotic cell cycle	0.0008	5	2.0000	20
GO:0007015	actin filament organization	0.0008	6	1.1155	13
GO:0010638	positive regulation of organelle organization	0.0008	3	2.6630	19
GO:0000915	actomyosin contractile ring assembly	0.0010	3	1.5850	9

GO:0044837	actomyosin contractile ring organization	0.0010	3	1.5850	9
GO:0031032	actomyosin structure organization	0.0010	3	1.5850	9
GO:0000912	assembly of actomyosin apparatus involved in cytokinesis	0.0010	3	1.5850	9
GO:1902407	assembly of actomyosin apparatus involved in mitotic cytokinesis	0.0010	3	1.5850	9
GO:1903475	mitotic actomyosin contractile ring assembly	0.0010	3	1.5850	9
GO:0061640	cytoskeleton-dependent cytokinesis	0.0011	8	1.4594	22
GO:0000281	mitotic cytokinesis	0.0011	8	1.4594	22
GO:0051785	positive regulation of nuclear division	0.0011	1	3.9069	15
GO:1901987	regulation of cell cycle phase transition	0.0012	6	2.1155	26
GO:1901605	alpha-amino acid metabolic process	0.0013	18	1.1520	40
GO:0043623	cellular protein complex assembly	0.0013	13	1.2065	30
GO:0043933	macromolecular complex subunit organization	0.0013	40	1.3785	104
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	0.0014	1	2.0000	4
GO:0051493	regulation of cytoskeleton organization	0.0014	3	2.0000	12
GO:1901990	regulation of mitotic cell cycle phase transition	0.0020	6	2.0589	25
GO:0051494	negative regulation of cytoskeleton organization	0.0020	2	1.0000	4
GO:0007067	mitotic nuclear division	0.0020	8	2.5236	46
GO:0044770	cell cycle phase transition	0.0021	8	1.7549	27
GO:0051306	mitotic sister chromatid separation	0.0021	1	4.2479	19
GO:0009117	nucleotide metabolic process	0.0022	14	1.6189	43
GO:0006996	organelle organization	0.0024	68	1.1414	150
GO:0006753	nucleoside phosphate metabolic process	0.0026	14	1.6189	43
GO:0006518	peptide metabolic process	0.0031	3	1.8745	11
GO:0051781	positive regulation of cell division	0.0032	2	3.2479	19
GO:0044772	mitotic cell cycle phase transition	0.0034	8	1.7004	26
GO:0031334	positive regulation of protein complex assembly	0.0036	1	3.0000	8

GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	0.0039	1	4.1699	18
GO:0044784	metaphase/anaphase transition of cell cycle	0.0039	1	4.1699	18
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	0.0039	1	4.1699	18
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	0.0039	1	4.1699	18
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.0039	1	4.1699	18
GO:0010965	regulation of mitotic sister chromatid separation	0.0039	1	4.1699	18
GO:0032270	positive regulation of cellular protein metabolic process	0.0041	7	1.5146	20
GO:0051247	positive regulation of protein metabolic process	0.0041	7	1.5146	20
GO:0044087	regulation of cellular component biogenesis	0.0042	5	2.2630	24
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0042	2	3.1699	18
GO:0009144	purine nucleoside triphosphate metabolic process	0.0045	2	3.2479	19
GO:0044712	single-organism catabolic process	0.0046	25	1.1110	54
GO:0006082	organic acid metabolic process	0.0051	35	1.1186	76
GO:0045787	positive regulation of cell cycle	0.0052	5	2.0704	21
GO:0046128	purine ribonucleoside metabolic process	0.0054	4	2.6439	25
GO:0042255	ribosome assembly	0.0056	3	2.0000	12
GO:0033043	regulation of organelle organization	0.0056	12	1.8074	42
GO:0046034	ATP metabolic process	0.0058	2	3.1699	18
GO:0061136	regulation of proteasomal protein catabolic process	0.0058	2	3.1699	18
GO:0072521	purine-containing compound metabolic process	0.0060	6	2.4594	33
GO:0006544	glycine metabolic process	0.0062	0	inf	6
GO:0043436	oxoacid metabolic process	0.0062	34	1.1414	75
GO:0022402	cell cycle process	0.0062	24	1.6818	77
GO:0009116	nucleoside metabolic process	0.0063	5	2.6323	31
GO:0009123	nucleoside monophosphate metabolic process	0.0068	7	1.6521	22
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	0.0079	9	1.5305	26

GO:0009205	purine ribonucleoside triphosphate metabolic process	0.0079	2	3.1699	18
GO:1903362	regulation of cellular protein catabolic process	0.0079	2	3.1699	18
GO:0030162	regulation of proteolysis	0.0079	2	3.1699	18
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	0.0079	2	3.1699	18
GO:0022618	ribonucleoprotein complex assembly	0.0083	4	2.8074	28
GO:0006575	cellular modified amino acid metabolic process	0.0084	5	1.7655	17
GO:0009141	nucleoside triphosphate metabolic process	0.0084	2	3.3219	20
GO:0042278	purine nucleoside metabolic process	0.0086	4	2.6439	25
GO:0009066	aspartate family amino acid metabolic process	0.0086	8	1.0875	17
GO:0009126	purine nucleoside monophosphate metabolic process	0.0086	5	2.0000	20
GO:0009167	purine ribonucleoside monophosphate metabolic process	0.0086	5	2.0000	20
GO:0042775	mitochondrial ATP synthesis coupled electron transport	0.0091	2	2.0000	8
GO:0010498	proteasomal protein catabolic process	0.0096	9	1.5305	26
GO:0071826	ribonucleoprotein complex subunit organization	0.0098	6	2.2224	28
GO:0051304	chromosome separation	0.0105	1	4.2479	19
GO:0009199	ribonucleoside triphosphate metabolic process	0.0105	2	3.1699	18
GO:1901565	organonitrogen compound catabolic process	0.0107	6	1.9386	23
GO:0042176	regulation of protein catabolic process	0.0107	2	3.2479	19
GO:0019752	carboxylic acid metabolic process	0.0115	32	1.2095	74
GO:0044262	cellular carbohydrate metabolic process	0.0116	11	1.1255	24
GO:0051258	protein polymerization	0.0128	2	2.3219	10
GO:0007346	regulation of mitotic cell cycle	0.0129	9	1.9175	34
GO:0009161	ribonucleoside monophosphate metabolic process	0.0136	6	1.8074	21
GO:0006730	one-carbon metabolic process	0.0143	0	inf	6
GO:0007049	cell cycle	0.0147	34	1.2701	82
GO:0009119	ribonucleoside metabolic process	0.0154	4	2.7549	27
GO:0000028	ribosomal small subunit assembly	0.0159	0	inf	8

GO:0009308	amine metabolic process	0.0161	5	1.0000	10
GO:0044089	positive regulation of cellular component biogenesis	0.0161	2	2.7004	13
GO:0006103	2-oxoglutarate metabolic process	0.0176	1	2.0000	4
GO:0032506	cytokinetic process	0.0177	7	1.1926	16
GO:1902410	mitotic cytokinetic process	0.0177	7	1.1926	16
GO:1901657	glycosyl compound metabolic process	0.0190	5	2.6323	31
GO:0051130	positive regulation of cellular component organization	0.0200	4	2.5850	24
GO:0006531	aspartate metabolic process	0.0203	1	1.5850	3
GO:0002182	cytoplasmic translational elongation	0.0203	1	1.5850	3
GO:0031333	negative regulation of protein complex assembly	0.0203	1	1.5850	3
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.0203	0	inf	4
GO:0051186	cofactor metabolic process	0.0211	15	1.0473	31
GO:0000070	mitotic sister chromatid segregation	0.0216	4	2.8074	28
GO:0000819	sister chromatid segregation	0.0216	4	2.8074	28
GO:0031329	regulation of cellular catabolic process	0.0228	2	3.1699	18
GO:0006508	proteolysis	0.0228	22	1.3735	57
GO:0007088	regulation of mitotic nuclear division	0.0261	2	3.5236	23
GO:0019637	organophosphate metabolic process	0.0276	28	1.0000	56
GO:0009894	regulation of catabolic process	0.0283	2	3.2479	19
GO:0022900	electron transport chain	0.0284	3	1.8745	11
GO:1902600	hydrogen ion transmembrane transport	0.0287	1	4.2479	19
GO:0033047	regulation of mitotic sister chromatid segregation	0.0287	1	4.2479	19
GO:0033045	regulation of sister chromatid segregation	0.0287	1	4.2479	19
GO:0010604	positive regulation of macromolecule metabolic process	0.0291	16	1.0000	32
GO:0006144	purine nucleobase metabolic process	0.0301	2	1.8074	7
GO:0007010	cytoskeleton organization	0.0316	9	1.7370	30

GO:0044283	small molecule biosynthetic process	0.0332	23	1.2313	54
GO:0006520	cellular amino acid metabolic process	0.0334	22	1.0324	45
GO:0042773	ATP synthesis coupled electron transport	0.0349	2	2.1699	9
GO:0051983	regulation of chromosome segregation	0.0356	1	4.2479	19
GO:1901606	alpha-amino acid catabolic process	0.0362	4	1.0000	8
GO:0045010	actin nucleation	0.0366	1	2.0000	4
GO:0030838	positive regulation of actin filament polymerization	0.0366	1	2.0000	4
GO:0032273	positive regulation of protein polymerization	0.0366	1	2.0000	4
GO:0006465	signal peptide processing	0.0366	1	2.0000	4
GO:0009069	serine family amino acid metabolic process	0.0369	5	1.3785	13
GO:0009112	nucleobase metabolic process	0.0376	2	2.5850	12
GO:1901607	alpha-amino acid biosynthetic process	0.0378	11	1.2955	27
GO:0051128	regulation of cellular component organization	0.0442	19	1.2756	46
GO:0032268	regulation of cellular protein metabolic process	0.0448	16	1.1699	36
GO:0044723	single-organism carbohydrate metabolic process	0.0448	17	1.0418	35
GO:0031048	chromatin silencing by small RNA	0.0474	2	1.0000	4
GO:0009113	purine nucleobase biosynthetic process	0.0474	2	1.0000	4
GO:0030148	sphingolipid biosynthetic process	0.0474	1	2.3219	5
GO:0010564	regulation of cell cycle process	0.0476	9	1.8745	33
GO:1902969	mitotic DNA replication	0.0476	0	inf	11
GO:0006119	oxidative phosphorylation	0.0476	2	2.1699	9
GO:0051246	regulation of protein metabolic process	0.0479	16	1.2095	37
GO:0019400	alditol metabolic process	0.0480	1	1.5850	3
GO:0006268	DNA unwinding involved in DNA replication	0.0480	0	inf	4
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.0480	0	inf	4
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	0.0480	0	inf	4

GO terms of Biological Processes with p value lower than 0.05 and log2<-1 in the treatment of <i>Sclerotinia sclerotiorum</i> with AITC versus Control					
GO term	description	pvalue	downregulated	ratio	upregulated
GO:1901376	organic heteropentacyclic compound metabolic process	0.0000	6	-1.5850	2
GO:1901378	organic heteropentacyclic compound biosynthetic process	0.0001	5	-1.3219	2
GO:0045461	sterigmatocystin biosynthetic process	0.0004	5	-2.3219	1
GO:0045460	sterigmatocystin metabolic process	0.0004	5	-2.3219	1
GO:0009403	toxin biosynthetic process	0.0004	5	-2.3219	1
GO:0009404	toxin metabolic process	0.0004	5	-2.3219	1
GO:0006915	apoptotic process	0.0007	6	-1.5850	2
GO:0012501	programmed cell death	0.0007	6	-1.5850	2
GO:0008219	cell death	0.0019	6	-1.5850	2
GO:0016265	death	0.0019	6	-1.5850	2
GO:1990542	mitochondrial transmembrane transport	0.0036	13	-1.3785	5
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.0203	4	-inf	0
GO:0043504	mitochondrial DNA repair	0.0203	3	-1.5850	1
GO:0045041	protein import into mitochondrial intermembrane space	0.0203	3	-1.5850	1
GO:0006783	heme biosynthetic process	0.0210	5	-1.3219	2
GO:0000470	maturation of LSU-rRNA	0.0210	5	-1.3219	2
GO:0071470	cellular response to osmotic stress	0.0276	9	-1.1699	4
GO:0071482	cellular response to light stimulus	0.0277	4	-1.0000	2
GO:1901679	nucleotide transmembrane transport	0.0277	4	-1.0000	2
GO:0036180	filamentous growth of a population of unicellular organisms in response to biotic stimulus	0.0351	5	-1.3219	2
GO:0042168	heme metabolic process	0.0351	5	-1.3219	2
GO:0071241	cellular response to inorganic substance	0.0366	4	-2.0000	1

GO:0071248	cellular response to metal ion	0.0366	4	-2.0000	1
GO:0016226	iron-sulfur cluster assembly	0.0403	6	-1.5850	2
GO:0031163	metallo-sulfur cluster assembly	0.0403	6	-1.5850	2
GO:0017004	cytochrome complex assembly	0.0474	4	-1.0000	2
GO:0006862	nucleotide transport	0.0474	4	-1.0000	2
GO:0032042	mitochondrial DNA metabolic process	0.0480	3	-1.5850	1
GO:0042981	regulation of apoptotic process	0.0480	4	-inf	0
GO:0043067	regulation of programmed cell death	0.0480	4	-inf	0
GO:0016114	terpenoid biosynthetic process	0.0480	3	-1.5850	1
GO terms of Biological Processes with p value lower than 0.05 and log2>1 in the treatment of <i>Sclerotinia sclerotiorum</i> with I3C versus Control					
GO term	description	pvalue	downregulated	ratio	upregulated
GO:0009070	serine family amino acid biosynthetic process	0.0144	3	1.2224	7
GO:0000097	sulfur amino acid biosynthetic process	0.0162	4	1.0000	8
GO:0043162	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	0.0206	0	inf	4
GO:0000096	cellular amino acid biosynthetic process	0.0442	4	1.0000	8
GO:0046487	glyoxylate metabolic process	0.0462	0	inf	3
GO:0009088	threonine biosynthetic process	0.0462	0	inf	3
GO:0009092	homoserine metabolic process	0.0484	1	1.5850	3
GO terms of Biological Processes with p value lower than 0.05 and log2<-1 in the treatment of <i>Sclerotinia sclerotiorum</i> with I3C versus Control					
GO term	description	pvalue	downregulated	ratio	upregulated
GO:0002181	cytoplasmic translation	0.0000	24	-3.0000	3
GO:0042273	ribosomal large subunit biogenesis	0.0000	20	-inf	0
GO:0044281	small molecule metabolic process	0.0000	89	-1.2278	38
GO:0042254	ribosome biogenesis	0.0000	51	-4.6724	2

GO:1901700	response to oxygen-containing compound	0.0000	13	-1.7004	4
GO:0042255	ribosome assembly	0.0000	13	-3.7004	1
GO:0022613	ribonucleoprotein complex biogenesis	0.0000	57	-4.2479	3
GO:0002182	cytoplasmic translational elongation	0.0001	5	-inf	0
GO:1901564	organonitrogen compound metabolic process	0.0001	71	-1.1497	32
GO:0071470	cellular response to osmotic stress	0.0001	12	-3.5850	1
GO:0042221	response to chemical	0.0002	33	-2.0444	8
GO:1901701	cellular response to oxygen-containing compound	0.0002	10	-1.3219	4
GO:0006970	response to osmotic stress	0.0002	13	-3.7004	1
GO:0055086	nucleobase-containing small molecule metabolic process	0.0002	37	-2.0395	9
GO:0044712	single-organism catabolic process	0.0002	41	-1.6571	13
GO:0009124	nucleoside monophosphate biosynthetic process	0.0003	15	-inf	0
GO:0009117	nucleotide metabolic process	0.0003	33	-2.4594	6
GO:0044723	single-organism carbohydrate metabolic process	0.0003	33	-2.2370	7
GO:0009408	response to heat	0.0003	8	-inf	0
GO:0009266	response to temperature stimulus	0.0003	8	-inf	0
GO:0044237	cellular metabolic process	0.0003	324	-1.6816	101
GO:0006753	nucleoside phosphate metabolic process	0.0003	33	-2.4594	6
GO:0006412	translation	0.0003	58	-3.2730	6
GO:0009123	nucleoside monophosphate metabolic process	0.0004	19	-2.6630	3
GO:0070887	cellular response to chemical stimulus	0.0005	27	-2.1699	6
GO:0034605	cellular response to heat	0.0006	7	-inf	0
GO:0000470	maturation of LSU-rRNA	0.0006	7	-inf	0
GO:0044724	single-organism carbohydrate catabolic process	0.0007	12	-2.5850	2
GO:1901566	organonitrogen compound biosynthetic process	0.0008	44	-1.0671	21
GO:0019693	ribose phosphate metabolic process	0.0009	23	-2.9386	3
GO:0072593	reactive oxygen species metabolic process	0.0009	7	-1.2224	3

GO:0000302	response to reactive oxygen species	0.0010	8	-1.4150	3
GO:0010035	response to inorganic substance	0.0012	10	-1.3219	4
GO:0009156	ribonucleoside monophosphate biosynthetic process	0.0013	13	-inf	0
GO:0044085	cellular component biogenesis	0.0014	93	-2.9542	12
GO:0006457	protein folding	0.0015	19	-4.2479	1
GO:0009161	ribonucleoside monophosphate metabolic process	0.0015	17	-2.5025	3
GO:1901135	carbohydrate derivative metabolic process	0.0016	47	-2.7472	7
GO:1990542	mitochondrial transmembrane transport	0.0017	10	-1.7370	3
GO:0009311	oligosaccharide metabolic process	0.0018	8	-3.0000	1
GO:0006979	response to oxidative stress	0.0019	13	-1.7004	4
GO:0030702	chromatin silencing at centromere	0.0019	8	-2.0000	2
GO:0009628	response to abiotic stimulus	0.0020	22	-4.4594	1
GO:0097306	cellular response to alcohol	0.0021	3	-1.5850	1
GO:0097308	cellular response to farnesol	0.0021	3	-1.5850	1
GO:0071396	cellular response to lipid	0.0021	3	-1.5850	1
GO:0046351	disaccharide biosynthetic process	0.0021	4	-inf	0
GO:0009312	oligosaccharide biosynthetic process	0.0021	4	-inf	0
GO:0097305	response to alcohol	0.0021	3	-1.5850	1
GO:0097307	response to farnesol	0.0021	3	-1.5850	1
GO:0033993	response to lipid	0.0021	3	-1.5850	1
GO:0005992	trehalose biosynthetic process	0.0021	4	-inf	0
GO:0044248	cellular catabolic process	0.0024	53	-1.0841	25
GO:0034599	cellular response to oxidative stress	0.0027	11	-1.8745	3
GO:1901376	organic heteropentacyclic compound metabolic process	0.0027	5	-inf	0
GO:0006414	translational elongation	0.0027	10	-inf	0
GO:0044262	cellular carbohydrate metabolic process	0.0032	17	-1.2801	7
GO:0019637	organophosphate metabolic process	0.0034	47	-2.5546	8

GO:0071704	organic substance metabolic process	0.0035	332	-1.6202	108
GO:0070925	organelle assembly	0.0036	16	-3.0000	2
GO:0071826	ribonucleoprotein complex subunit organization	0.0038	21	-3.3923	2
GO:0000460	maturation of 5.8S rRNA	0.0039	9	-inf	0
GO:0005975	carbohydrate metabolic process	0.0041	45	-1.5850	15
GO:0000027	ribosomal large subunit assembly	0.0044	6	-inf	0
GO:1901293	nucleoside phosphate biosynthetic process	0.0044	21	-3.3923	2
GO:0006364	rRNA processing	0.0049	32	-inf	0
GO:0009126	purine nucleoside monophosphate metabolic process	0.0051	14	-2.2224	3
GO:0009167	purine ribonucleoside monophosphate metabolic process	0.0051	14	-2.2224	3
GO:0009127	purine nucleoside monophosphate biosynthetic process	0.0051	10	-inf	0
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	0.0051	10	-inf	0
GO:0009651	response to salt stress	0.0054	5	-inf	0
GO:0019323	pentose catabolic process	0.0057	3	-1.5850	1
GO:0045461	sterigmatocystin biosynthetic process	0.0057	4	-inf	0
GO:0045460	sterigmatocystin metabolic process	0.0057	4	-inf	0
GO:0009403	toxin biosynthetic process	0.0057	4	-inf	0
GO:0009404	toxin metabolic process	0.0057	4	-inf	0
GO:0005991	trehalose metabolic process	0.0057	4	-inf	0
GO:0022618	ribonucleoprotein complex assembly	0.0062	19	-3.2479	2
GO:0006091	generation of precursor metabolites and energy	0.0062	15	-1.9069	4
GO:0044249	cellular biosynthetic process	0.0065	179	-1.8400	50
GO:0019538	protein metabolic process	0.0068	145	-2.0924	34
GO:0009165	nucleotide biosynthetic process	0.0070	20	-3.3219	2
GO:0015986	ATP synthesis coupled proton transport	0.0071	6	-inf	0
GO:0005984	disaccharide metabolic process	0.0071	5	-2.3219	1
GO:0015985	energy coupled proton transport, down electrochemical gradient	0.0071	6	-inf	0

GO:1902582	single-organism intracellular transport	0.0073	41	-1.3576	16
GO:0009259	ribonucleotide metabolic process	0.0083	18	-2.5850	3
GO:0044267	cellular protein metabolic process	0.0083	136	-2.2801	28
GO:0016072	rRNA metabolic process	0.0087	32	-inf	0
GO:0006915	apoptotic process	0.0094	4	-2.0000	1
GO:0051156	glucose 6-phosphate metabolic process	0.0094	5	-inf	0
GO:0042743	hydrogen peroxide metabolic process	0.0094	4	-2.0000	1
GO:0012501	programmed cell death	0.0094	4	-2.0000	1
GO:0071214	cellular response to abiotic stimulus	0.0098	13	-3.7004	1
GO:0051169	nuclear transport	0.0100	18	-4.1699	1
GO:0006913	nucleocytoplasmic transport	0.0100	18	-4.1699	1
GO:0006006	glucose metabolic process	0.0106	7	-2.8074	1
GO:0006754	ATP biosynthetic process	0.0109	6	-inf	0
GO:0000028	ribosomal small subunit assembly	0.0109	5	-2.3219	1
GO:0072521	purine-containing compound metabolic process	0.0112	19	-1.9260	5
GO:0005996	monosaccharide metabolic process	0.0114	10	-1.7370	3
GO:0009150	purine ribonucleotide metabolic process	0.0116	16	-2.4150	3
GO:0031506	cell wall glycoprotein biosynthetic process	0.0117	4	-inf	0
GO:0000032	cell wall mannoprotein biosynthetic process	0.0117	4	-inf	0
GO:1901378	organic heteropentacyclic compound biosynthetic process	0.0117	4	-inf	0
GO:0031647	regulation of protein stability	0.0117	4	-inf	0
GO:0016052	carbohydrate catabolic process	0.0117	16	-1.1926	7
GO:0046128	purine ribonucleoside metabolic process	0.0118	15	-2.3219	3
GO:0044238	primary metabolic process	0.0120	312	-1.6415	100
GO:0009119	ribonucleoside metabolic process	0.0130	17	-2.5025	3
GO:0006163	purine nucleotide metabolic process	0.0134	16	-2.4150	3
GO:0006839	mitochondrial transport	0.0138	10	-1.7370	3

GO:0051168	nuclear export	0.0141	13	-3.7004	1
GO:0046390	ribose phosphate biosynthetic process	0.0141	14	-inf	0
GO:0009058	biosynthetic process	0.0145	185	-1.7765	54
GO:0008219	cell death	0.0152	4	-2.0000	1
GO:0016265	death	0.0152	4	-2.0000	1
GO:0043269	regulation of ion transport	0.0152	5	-inf	0
GO:0042278	purine nucleoside metabolic process	0.0158	15	-2.3219	3
GO:0002183	cytoplasmic translational initiation	0.0160	5	-2.3219	1
GO:0006739	NADP metabolic process	0.0160	5	-2.3219	1
GO:0009145	purine nucleoside triphosphate biosynthetic process	0.0160	6	-inf	0
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.0160	6	-inf	0
GO:1901576	organic substance biosynthetic process	0.0184	180	-1.9069	48
GO:0051656	establishment of organelle localization	0.0190	9	-2.1699	2
GO:0042455	ribonucleoside biosynthetic process	0.0190	11	-inf	0
GO:0071472	cellular response to salt stress	0.0206	4	-inf	0
GO:0006057	mannoprotein biosynthetic process	0.0206	4	-inf	0
GO:0006056	mannoprotein metabolic process	0.0206	4	-inf	0
GO:0046365	monosaccharide catabolic process	0.0206	3	-1.5850	1
GO:1901137	carbohydrate derivative biosynthetic process	0.0216	32	-5.0000	1
GO:0042274	ribosomal small subunit biogenesis	0.0222	15	-3.9069	1
GO:0009201	ribonucleoside triphosphate biosynthetic process	0.0224	6	-inf	0
GO:0009163	nucleoside biosynthetic process	0.0230	11	-inf	0
GO:0046034	ATP metabolic process	0.0234	10	-2.3219	2
GO:0009890	negative regulation of biosynthetic process	0.0250	18	-1.5850	6
GO:0031327	negative regulation of cellular biosynthetic process	0.0250	18	-1.5850	6
GO:0006458	'de novo' protein folding	0.0259	3	-inf	0
GO:0006112	energy reserve metabolic process	0.0259	3	-inf	0

GO:0005977	glycogen metabolic process	0.0259	3	-inf	0
GO:0042159	lipoprotein catabolic process	0.0259	2	-1.0000	1
GO:0098734	macromolecule depalmitoylation	0.0259	2	-1.0000	1
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	0.0259	2	-1.0000	1
GO:0010620	negative regulation of transcription by transcription factor catabolism	0.0259	2	-1.0000	1
GO:0002084	protein depalmitoylation	0.0259	2	-1.0000	1
GO:0072530	purine-containing compound transmembrane transport	0.0259	2	-1.0000	1
GO:0043462	regulation of ATPase activity	0.0259	3	-inf	0
GO:0036369	transcription factor catabolic process	0.0259	2	-1.0000	1
GO:0042451	purine nucleoside biosynthetic process	0.0259	9	-inf	0
GO:0046129	purine ribonucleoside biosynthetic process	0.0259	9	-inf	0
GO:0009116	nucleoside metabolic process	0.0263	17	-2.0875	4
GO:0044710	single-organism metabolic process	0.0273	191	-1.2376	81
GO:0009260	ribonucleotide biosynthetic process	0.0274	13	-inf	0
GO:0009205	purine ribonucleoside triphosphate metabolic process	0.0277	10	-2.3219	2
GO:0072524	pyridine-containing compound metabolic process	0.0277	10	-2.3219	2
GO:1901657	glycosyl compound metabolic process	0.0279	17	-1.7655	5
GO:0090407	organophosphate biosynthetic process	0.0285	30	-2.9069	4
GO:0015980	energy derivation by oxidation of organic compounds	0.0312	10	-1.3219	4
GO:0009141	nucleoside triphosphate metabolic process	0.0320	11	-2.4594	2
GO:0051640	organelle localization	0.0326	9	-1.5850	3
GO:0009144	purine nucleoside triphosphate metabolic process	0.0326	10	-2.3219	2
GO:0009199	ribonucleoside triphosphate metabolic process	0.0326	10	-2.3219	2
GO:0010256	endomembrane system organization	0.0327	8	-2.0000	2
GO:0019682	glyceraldehyde-3-phosphate metabolic process	0.0328	4	-inf	0
GO:0042744	hydrogen peroxide catabolic process	0.0328	4	-inf	0
GO:0006098	pentose-phosphate shunt	0.0328	4	-inf	0

GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	0.0328	4	-inf	0
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	0.0328	4	-inf	0
GO:0006986	response to unfolded protein	0.0328	5	-inf	0
GO:0033753	establishment of ribosome localization	0.0349	7	-inf	0
GO:0071426	ribonucleoprotein complex export from nucleus	0.0349	7	-inf	0
GO:0071166	ribonucleoprotein complex localization	0.0349	7	-inf	0
GO:0000054	ribosomal subunit export from nucleus	0.0349	7	-inf	0
GO:0033750	ribosome localization	0.0349	7	-inf	0
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	0.0349	7	-inf	0
GO:0044699	single-organism process	0.0356	292	-1.1345	133
GO:0010033	response to organic substance	0.0359	13	-3.7004	1
GO:0019318	hexose metabolic process	0.0387	7	-1.8074	2
GO:1901659	glycosyl compound biosynthetic process	0.0388	11	-inf	0
GO:0009152	purine ribonucleotide biosynthetic process	0.0388	11	-inf	0
GO:0010038	response to metal ion	0.0400	4	-1.0000	2
GO:0009987	cellular process	0.0405	379	-1.4265	141
GO:0072528	pyrimidine-containing compound biosynthetic process	0.0440	7	-inf	0
GO:1901617	organic hydroxy compound biosynthetic process	0.0448	12	-2.0000	3
GO:0006164	purine nucleotide biosynthetic process	0.0454	11	-inf	0
GO:0050821	protein stabilization	0.0462	3	-inf	0
GO:0044070	regulation of anion transport	0.0462	3	-inf	0
GO:0006096	glycolytic process	0.0484	4	-inf	0
GO:0051050	positive regulation of transport	0.0484	4	-inf	0
GO:0008152	metabolic process	0.0491	375	-1.3808	144
GO terms of Biological Processes with p value lower than 0.05 and log2>1 in the comparison of <i>Sclerotinia sclerotiorum</i> treated with AITC versus I3C					
GO term	description	pvalue	downregulated	ratio	upregulated

GO:0044281	small molecule metabolic process	0.0000	44	1.8715	161
GO:1901564	organonitrogen compound metabolic process	0.0000	37	1.8458	133
GO:0044711	single-organism biosynthetic process	0.0000	50	1.5850	150
GO:0006082	organic acid metabolic process	0.0000	35	1.3301	88
GO:0043436	oxoacid metabolic process	0.0000	35	1.2970	86
GO:0019752	carboxylic acid metabolic process	0.0000	34	1.3219	85
GO:0044283	small molecule biosynthetic process	0.0000	26	1.3219	65
GO:0044249	cellular biosynthetic process	0.0000	94	1.6451	294
GO:0009058	biosynthetic process	0.0000	103	1.5709	306
GO:1903364	positive regulation of cellular protein catabolic process	0.0000	1	4.0875	17
GO:1901800	positive regulation of proteasomal protein catabolic process	0.0000	1	4.0875	17
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0000	1	4.0875	17
GO:0045732	positive regulation of protein catabolic process	0.0000	1	4.0875	17
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	0.0000	1	4.0875	17
GO:0009896	positive regulation of catabolic process	0.0000	1	4.0875	17
GO:0031331	positive regulation of cellular catabolic process	0.0000	1	4.0875	17
GO:0045862	positive regulation of proteolysis	0.0000	1	4.0875	17
GO:1901576	organic substance biosynthetic process	0.0000	94	1.6549	296
GO:1902101	positive regulation of metaphase/anaphase transition of cell cycle	0.0000	0	inf	16
GO:0045842	positive regulation of mitotic metaphase/anaphase transition	0.0000	0	inf	16
GO:1901970	positive regulation of mitotic sister chromatid separation	0.0000	0	inf	16
GO:0046394	carboxylic acid biosynthetic process	0.0000	22	1.0324	45
GO:0016053	organic acid biosynthetic process	0.0000	22	1.0324	45
GO:0043254	regulation of protein complex assembly	0.0000	2	3.0000	16
GO:1901566	organonitrogen compound biosynthetic process	0.0000	27	1.5305	78

GO:0044710	single-organism metabolic process	0.0000	114	1.6017	346
GO:0055086	nucleobase-containing small molecule metabolic process	0.0000	10	2.5850	60
GO:1901135	carbohydrate derivative metabolic process	0.0000	12	2.6630	76
GO:1901989	positive regulation of cell cycle phase transition	0.0000	0	inf	18
GO:1901992	positive regulation of mitotic cell cycle phase transition	0.0000	0	inf	18
GO:0044723	single-organism carbohydrate metabolic process	0.0000	12	2.0297	49
GO:0008154	actin polymerization or depolymerization	0.0000	2	2.4594	11
GO:1901605	alpha-amino acid metabolic process	0.0000	18	1.1876	41
GO:0009116	nucleoside metabolic process	0.0000	5	2.8074	35
GO:0030041	actin filament polymerization	0.0000	2	2.1699	9
GO:0030833	regulation of actin filament polymerization	0.0000	2	2.0000	8
GO:0032271	regulation of protein polymerization	0.0000	2	2.0000	8
GO:0006412	translation	0.0000	11	2.9835	87
GO:0045840	positive regulation of mitotic nuclear division	0.0000	0	inf	17
GO:0010638	positive regulation of organelle organization	0.0000	1	4.4594	22
GO:0007015	actin filament organization	0.0000	5	1.5850	15
GO:0044264	cellular polysaccharide metabolic process	0.0000	4	2.3923	21
GO:0044237	cellular metabolic process	0.0000	159	1.6871	512
GO:0051785	positive regulation of nuclear division	0.0001	0	inf	17
GO:0006520	cellular amino acid metabolic process	0.0001	23	1.1203	50
GO:0019637	organophosphate metabolic process	0.0001	15	2.3026	74
GO:0030832	regulation of actin filament length	0.0001	2	2.0000	8
GO:0008064	regulation of actin polymerization or depolymerization	0.0001	2	2.0000	8
GO:0009119	ribonucleoside metabolic process	0.0001	3	3.4150	32
GO:0051984	positive regulation of chromosome segregation	0.0001	0	inf	16
GO:1901657	glycosyl compound metabolic process	0.0001	5	2.8074	35
GO:0009123	nucleoside monophosphate metabolic process	0.0002	3	3.2224	28

GO:0009161	ribonucleoside monophosphate metabolic process	0.0002	3	3.1699	27
GO:1901607	alpha-amino acid biosynthetic process	0.0002	14	1.0506	29
GO:0032787	monocarboxylic acid metabolic process	0.0002	9	1.9175	34
GO:0031334	positive regulation of protein complex assembly	0.0002	1	3.1699	9
GO:0042278	purine nucleoside metabolic process	0.0002	3	3.2224	28
GO:0044255	cellular lipid metabolic process	0.0003	17	1.5564	50
GO:0043244	regulation of protein complex disassembly	0.0003	2	1.3219	5
GO:0034622	cellular macromolecular complex assembly	0.0003	9	2.8962	67
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0003	1	4.3219	20
GO:0044262	cellular carbohydrate metabolic process	0.0003	7	2.0995	30
GO:0009144	purine nucleoside triphosphate metabolic process	0.0003	1	4.3923	21
GO:0030036	actin cytoskeleton organization	0.0003	7	1.6521	22
GO:0046128	purine ribonucleoside metabolic process	0.0003	3	3.1699	27
GO:0009117	nucleotide metabolic process	0.0003	7	2.7776	48
GO:0044763	single-organism cellular process	0.0004	159	1.3310	400
GO:0090066	regulation of anatomical structure size	0.0004	3	1.4150	8
GO:0032535	regulation of cellular component size	0.0004	3	1.4150	8
GO:0006753	nucleoside phosphate metabolic process	0.0004	7	2.7776	48
GO:0006091	generation of precursor metabolites and energy	0.0004	2	3.8074	28
GO:0051306	mitotic sister chromatid separation	0.0004	0	inf	20
GO:0032956	regulation of actin cytoskeleton organization	0.0004	2	2.4594	11
GO:0032970	regulation of actin filament-based process	0.0004	2	2.4594	11
GO:0030029	actin filament-based process	0.0004	7	1.6521	22
GO:0046034	ATP metabolic process	0.0004	1	4.3219	20
GO:0061136	regulation of proteasomal protein catabolic process	0.0004	1	4.3219	20
GO:2001252	positive regulation of chromosome organization	0.0004	0	inf	16
GO:1902600	hydrogen ion transmembrane transport	0.0005	0	inf	23

GO:0022618	ribonucleoprotein complex assembly	0.0005	4	2.8580	29
GO:0019693	ribose phosphate metabolic process	0.0005	3	3.5025	34
GO:0072521	purine-containing compound metabolic process	0.0006	5	2.7655	34
GO:0002181	cytoplasmic translation	0.0006	1	4.8074	28
GO:0044087	regulation of cellular component biogenesis	0.0006	5	2.2630	24
GO:0006790	sulfur compound metabolic process	0.0006	11	1.2955	27
GO:0009126	purine nucleoside monophosphate metabolic process	0.0006	3	2.9386	23
GO:0009167	purine ribonucleoside monophosphate metabolic process	0.0006	3	2.9386	23
GO:0051781	positive regulation of cell division	0.0006	2	3.2479	19
GO:0009205	purine ribonucleoside triphosphate metabolic process	0.0006	1	4.3219	20
GO:1903362	regulation of cellular protein catabolic process	0.0006	1	4.3219	20
GO:0030162	regulation of proteolysis	0.0006	1	4.3219	20
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	0.0006	1	4.3219	20
GO:0009141	nucleoside triphosphate metabolic process	0.0006	1	4.4594	22
GO:0006084	acetyl-CoA metabolic process	0.0007	0	inf	9
GO:0051130	positive regulation of cellular component organization	0.0007	4	2.7004	26
GO:0022607	cellular component assembly	0.0007	23	1.9027	86
GO:0009259	ribonucleotide metabolic process	0.0008	3	3.3219	30
GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	0.0009	0	inf	19
GO:0044784	metaphase/anaphase transition of cell cycle	0.0009	0	inf	19
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	0.0009	0	inf	19
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	0.0009	0	inf	19
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.0009	0	inf	19
GO:0010965	regulation of mitotic sister chromatid separation	0.0009	0	inf	19
GO:0044712	single-organism catabolic process	0.0009	12	2.3923	63
GO:0009199	ribonucleoside triphosphate metabolic process	0.0009	1	4.3219	20

GO:0065003	macromolecular complex assembly	0.0010	13	2.4894	73
GO:0043624	cellular protein complex disassembly	0.0010	4	1.0000	8
GO:0071704	organic substance metabolic process	0.0011	166	1.6775	531
GO:0051258	protein polymerization	0.0013	2	2.4594	11
GO:0051493	regulation of cytoskeleton organization	0.0014	2	2.5850	12
GO:0000915	actomyosin contractile ring assembly	0.0015	3	1.4150	8
GO:0044837	actomyosin contractile ring organization	0.0015	3	1.4150	8
GO:0031032	actomyosin structure organization	0.0015	3	1.4150	8
GO:0000912	assembly of actomyosin apparatus involved in cytokinesis	0.0015	3	1.4150	8
GO:1902407	assembly of actomyosin apparatus involved in mitotic cytokinesis	0.0015	3	1.4150	8
GO:1903475	mitotic actomyosin contractile ring assembly	0.0015	3	1.4150	8
GO:0006163	purine nucleotide metabolic process	0.0016	3	3.1699	27
GO:0006073	cellular glucan metabolic process	0.0017	2	2.8074	14
GO:0009112	nucleobase metabolic process	0.0017	2	2.8074	14
GO:0006631	fatty acid metabolic process	0.0017	6	1.4150	16
GO:0071822	protein complex subunit organization	0.0020	12	2.2730	58
GO:0090068	positive regulation of cell cycle process	0.0023	2	3.3219	20
GO:0045931	positive regulation of mitotic cell cycle	0.0023	2	3.3219	20
GO:0030866	cortical actin cytoskeleton organization	0.0024	4	1.4594	11
GO:0030865	cortical cytoskeleton organization	0.0024	4	1.4594	11
GO:0031329	regulation of cellular catabolic process	0.0024	1	4.3219	20
GO:0042176	regulation of protein catabolic process	0.0024	1	4.3219	20
GO:0051304	chromosome separation	0.0025	0	inf	20
GO:0006526	arginine biosynthetic process	0.0026	0	inf	7
GO:0000395	mRNA 5'-splice site recognition	0.0026	1	2.5850	6
GO:0071826	ribonucleoprotein complex subunit organization	0.0026	4	2.8580	29
GO:0006818	hydrogen transport	0.0027	2	3.7549	27

GO:0015992	proton transport	0.0027	2	3.7549	27
GO:0009150	purine ribonucleotide metabolic process	0.0027	3	3.1155	26
GO:0001731	formation of translation preinitiation complex	0.0029	0	inf	9
GO:0033692	cellular polysaccharide biosynthetic process	0.0029	4	1.0000	8
GO:0051128	regulation of cellular component organization	0.0030	14	1.8651	51
GO:0006085	acetyl-CoA biosynthetic process	0.0032	0	inf	6
GO:0045010	actin nucleation	0.0032	1	2.3219	5
GO:0030838	positive regulation of actin filament polymerization	0.0032	1	2.3219	5
GO:0032273	positive regulation of protein polymerization	0.0032	1	2.3219	5
GO:0046459	short-chain fatty acid metabolic process	0.0032	1	2.3219	5
GO:0033043	regulation of organelle organization	0.0033	8	2.3923	42
GO:0060627	regulation of vesicle-mediated transport	0.0034	3	1.8745	11
GO:0043648	dicarboxylic acid metabolic process	0.0034	5	1.4854	14
GO:0044042	glucan metabolic process	0.0036	2	2.8074	14
GO:0009064	glutamine family amino acid metabolic process	0.0036	4	1.7004	13
GO:0044724	single-organism carbohydrate catabolic process	0.0036	0	inf	17
GO:0042775	mitochondrial ATP synthesis coupled electron transport	0.0036	1	3.1699	9
GO:0006984	ER-nucleus signaling pathway	0.0037	1	2.0000	4
GO:0019541	propionate metabolic process	0.0037	1	2.0000	4
GO:0044085	cellular component biogenesis	0.0037	32	1.9425	123
GO:0015986	ATP synthesis coupled proton transport	0.0040	0	inf	8
GO:0015985	energy coupled proton transport, down electrochemical gradient	0.0040	0	inf	8
GO:0061640	cytoskeleton-dependent cytokinesis	0.0042	8	1.1699	18
GO:0000281	mitotic cytokinesis	0.0042	8	1.1699	18
GO:0006575	cellular modified amino acid metabolic process	0.0043	4	2.0875	17
GO:1901617	organic hydroxy compound biosynthetic process	0.0044	6	1.6630	19
GO:1901137	carbohydrate derivative biosynthetic process	0.0045	7	2.6845	45

GO:0043604	amide biosynthetic process	0.0049	2	2.9069	15
GO:0009124	nucleoside monophosphate biosynthetic process	0.0049	1	4.0000	16
GO:0009156	ribonucleoside monophosphate biosynthetic process	0.0050	1	3.9069	15
GO:0006637	acyl-CoA metabolic process	0.0052	0	inf	9
GO:0035383	thioester metabolic process	0.0052	0	inf	9
GO:0000910	cytokinesis	0.0052	8	1.1699	18
GO:0006376	mRNA splice site selection	0.0056	1	2.5850	6
GO:0009084	glutamine family amino acid biosynthetic process	0.0061	1	3.1699	9
GO:0044238	primary metabolic process	0.0065	154	1.6932	498
GO:0043241	protein complex disassembly	0.0070	4	1.0000	8
GO:0006629	lipid metabolic process	0.0070	23	1.1489	51
GO:0016126	sterol biosynthetic process	0.0071	2	2.4594	11
GO:0009894	regulation of catabolic process	0.0073	1	4.3219	20
GO:0006525	arginine metabolic process	0.0075	0	inf	8
GO:0006754	ATP biosynthetic process	0.0075	0	inf	8
GO:0006090	pyruvate metabolic process	0.0075	0	inf	8
GO:0000245	spliceosomal complex assembly	0.0075	1	2.8074	7
GO:0032270	positive regulation of cellular protein metabolic process	0.0076	3	2.8074	21
GO:0051247	positive regulation of protein metabolic process	0.0076	3	2.8074	21
GO:0071616	acyl-CoA biosynthetic process	0.0077	0	inf	6
GO:0006730	one-carbon metabolic process	0.0077	0	inf	6
GO:0035384	thioester biosynthetic process	0.0077	0	inf	6
GO:0044699	single-organism process	0.0081	200	1.2630	480
GO:0009165	nucleotide biosynthetic process	0.0082	5	2.3785	26
GO:0046165	alcohol biosynthetic process	0.0086	3	2.3219	15
GO:0044108	cellular alcohol biosynthetic process	0.0096	0	inf	10
GO:0097384	cellular lipid biosynthetic process	0.0096	0	inf	10

GO:0006696	ergosterol biosynthetic process	0.0096	0	inf	10
GO:0008204	ergosterol metabolic process	0.0096	0	inf	10
GO:0016129	phytosteroid biosynthetic process	0.0096	0	inf	10
GO:0016128	phytosteroid metabolic process	0.0096	0	inf	10
GO:0034314	Arp2/3 complex-mediated actin nucleation	0.0103	1	2.0000	4
GO:0051494	negative regulation of cytoskeleton organization	0.0103	1	2.0000	4
GO:0015672	monovalent inorganic cation transport	0.0108	4	2.8074	28
GO:0072330	monocarboxylic acid biosynthetic process	0.0112	4	1.8074	14
GO:0007088	regulation of mitotic nuclear division	0.0117	2	3.4594	22
GO:1901293	nucleoside phosphate biosynthetic process	0.0117	5	2.3785	26
GO:0051301	cell division	0.0120	11	2.0324	45
GO:0006793	phosphorus metabolic process	0.0122	39	1.5972	118
GO:0009250	glucan biosynthetic process	0.0127	2	1.5850	6
GO:0006563	L-serine metabolic process	0.0127	2	1.5850	6
GO:0009145	purine nucleoside triphosphate biosynthetic process	0.0127	0	inf	8
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.0127	0	inf	8
GO:0030042	actin filament depolymerization	0.0130	1	1.5850	3
GO:0071501	cellular response to sterol depletion	0.0130	1	1.5850	3
GO:0002182	cytoplasmic translational elongation	0.0130	0	inf	4
GO:0006112	energy reserve metabolic process	0.0130	0	inf	4
GO:0005977	glycogen metabolic process	0.0130	0	inf	4
GO:0031333	negative regulation of protein complex assembly	0.0130	1	1.5850	3
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.0130	0	inf	4
GO:0006991	response to sterol depletion	0.0130	1	1.5850	3
GO:0032933	SREBP signaling pathway	0.0130	1	1.5850	3
GO:0043933	macromolecular complex subunit organization	0.0133	24	2.0444	99

GO:0019538	protein metabolic process	0.0135	53	2.0534	220
GO:0043603	cellular amide metabolic process	0.0136	2	3.6439	25
GO:0044089	positive regulation of cellular component biogenesis	0.0137	3	1.8745	11
GO:0006694	steroid biosynthetic process	0.0141	2	2.4594	11
GO:0044107	cellular alcohol metabolic process	0.0145	0	inf	10
GO:0015980	energy derivation by oxidation of organic compounds	0.0147	2	3.2479	19
GO:1901615	organic hydroxy compound metabolic process	0.0150	8	1.7004	26
GO:0006096	glycolytic process	0.0154	0	inf	6
GO:0000387	spliceosomal snRNP assembly	0.0154	1	2.3219	5
GO:0033047	regulation of mitotic sister chromatid segregation	0.0170	0	inf	19
GO:0033045	regulation of sister chromatid segregation	0.0170	0	inf	19
GO:0005975	carbohydrate metabolic process	0.0179	14	2.3424	71
GO:0051186	cofactor metabolic process	0.0180	5	2.8875	37
GO:0051495	positive regulation of cytoskeleton organization	0.0185	1	2.5850	6
GO:0006415	translational termination	0.0185	2	1.3219	5
GO:0016051	carbohydrate biosynthetic process	0.0196	5	1.2630	12
GO:0070085	glycosylation	0.0196	4	2.0000	16
GO:0006732	coenzyme metabolic process	0.0198	3	3.4594	33
GO:0009127	purine nucleoside monophosphate biosynthetic process	0.0200	1	3.4594	11
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	0.0200	1	3.4594	11
GO:0015991	ATP hydrolysis coupled proton transport	0.0202	0	inf	8
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	0.0202	0	inf	8
GO:0009201	ribonucleoside triphosphate biosynthetic process	0.0202	0	inf	8
GO:0045787	positive regulation of cell cycle	0.0205	2	3.3219	20
GO:0009272	fungal-type cell wall biogenesis	0.0209	1	3.0000	8
GO:0009142	nucleoside triphosphate biosynthetic process	0.0209	0	inf	9

GO:0043650	dicarboxylic acid biosynthetic process	0.0210	2	2.0000	8
GO:0051983	regulation of chromosome segregation	0.0212	0	inf	19
GO:0006544	glycine metabolic process	0.0221	0	inf	5
GO:0030100	regulation of endocytosis	0.0221	0	inf	5
GO:0042455	ribonucleoside biosynthetic process	0.0225	0	inf	15
GO:0007010	cytoskeleton organization	0.0228	9	1.5850	27
GO:0009101	glycoprotein biosynthetic process	0.0229	3	2.3219	15
GO:0009100	glycoprotein metabolic process	0.0229	3	2.3219	15
GO:0043413	macromolecule glycosylation	0.0229	3	2.3219	15
GO:0006486	protein glycosylation	0.0229	3	2.3219	15
GO:0098662	inorganic cation transmembrane transport	0.0241	5	2.4330	27
GO:0098660	inorganic ion transmembrane transport	0.0248	7	2.0000	28
GO:0008610	lipid biosynthetic process	0.0264	10	1.6781	32
GO:0034637	cellular carbohydrate biosynthetic process	0.0269	4	1.0000	8
GO:1901565	organonitrogen compound catabolic process	0.0275	3	2.8745	22
GO:0044267	cellular protein metabolic process	0.0278	46	2.1275	201
GO:0006414	translational elongation	0.0282	0	inf	11
GO:0009163	nucleoside biosynthetic process	0.0287	0	inf	15
GO:0044396	actin cortical patch organization	0.0295	2	1.3219	5
GO:0009225	nucleotide-sugar metabolic process	0.0295	2	1.3219	5
GO:0042558	pteridine-containing compound metabolic process	0.0295	0	inf	7
GO:0006206	pyrimidine nucleobase metabolic process	0.0295	0	inf	7
GO:1903047	mitotic cell cycle process	0.0304	12	2.2224	56
GO:0000278	mitotic cell cycle	0.0309	13	2.1069	56
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	0.0315	0	inf	4
GO:0006491	N-glycan processing	0.0315	1	1.5850	3
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.0315	0	inf	4

GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	0.0315	0	inf	4
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	0.0315	0	inf	4
GO:0009173	pyrimidine ribonucleoside monophosphate metabolic process	0.0315	0	inf	4
GO:0006222	UMP biosynthetic process	0.0315	0	inf	4
GO:0046049	UMP metabolic process	0.0315	0	inf	4
GO:0006066	alcohol metabolic process	0.0327	4	2.2479	19
GO:0005976	polysaccharide metabolic process	0.0331	5	2.3219	25
GO:0030447	filamentous growth	0.0334	4	1.5850	12
GO:0006461	protein complex assembly	0.0340	4	3.3923	42
GO:0090407	organophosphate biosynthetic process	0.0341	7	2.6189	43
GO:0009260	ribonucleotide biosynthetic process	0.0348	1	4.0875	17
GO:0042546	cell wall biogenesis	0.0354	2	2.3219	10
GO:0070271	protein complex biogenesis	0.0379	4	3.3923	42
GO:0006796	phosphate-containing compound metabolic process	0.0391	38	1.5465	111
GO:0042773	ATP synthesis coupled electron transport	0.0399	1	3.1699	9
GO:0046854	phosphatidylinositol phosphorylation	0.0400	1	2.0000	4
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	0.0400	0	inf	5
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	0.0400	0	inf	5
GO:0046653	tetrahydrofolate metabolic process	0.0400	0	inf	5
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	0.0416	3	3.1155	26
GO:0046390	ribose phosphate biosynthetic process	0.0423	1	4.0875	17
GO:0044772	mitotic cell cycle phase transition	0.0430	2	3.6439	25
GO:0006144	purine nucleobase metabolic process	0.0435	2	1.5850	6
GO:0006446	regulation of translational initiation	0.0435	0	inf	8
GO:0070592	cell wall polysaccharide biosynthetic process	0.0435	2	1.0000	4
GO:0006760	folic acid-containing compound metabolic process	0.0435	0	inf	6

GO:0098655	cation transmembrane transport	0.0473	8	1.7549	27
GO:0010498	proteasomal protein catabolic process	0.0477	3	3.1155	26
GO:0006487	protein N-linked glycosylation	0.0491	2	2.1699	9
GO:0044770	cell cycle phase transition	0.0495	2	3.6439	25
GO:0043623	cellular protein complex assembly	0.0496	3	3.3219	30
GO terms of Biological Processes with p value lower than 0.05 and log2<-1 in the comparison of <i>Sclerotinia sclerotiorum</i> treated with AITC versus I3C					
GO term	description	pvalue	downregulated	ratio	upregulated
GO:0043504	mitochondrial DNA repair	0.0130	3	-1.5850	1
GO:0071482	cellular response to light stimulus	0.0154	4	-1.0000	2
GO:0032042	mitochondrial DNA metabolic process	0.0315	3	-1.5850	1
GO:0009416	response to light stimulus	0.0442	5	-1.3219	2