

Supplementary Tables

Term	Count	%	P-Value	Bonferroni	Benjamini
cellular macromolecule biosynthetic process	26	72.2	1.80E-07	2.30E-04	3.30E-05
nucleic acid-templated transcription	23	63.9	1.60E-07	2.00E-04	3.30E-05
regulation of RNA metabolic process	23	63.9	1.50E-07	1.90E-04	3.80E-05
gene expression	27	75	9.50E-08	1.20E-04	4.00E-05
regulation of gene expression	24	66.7	3.80E-07	4.80E-04	4.00E-05
cellular biosynthetic process	28	77.8	3.70E-07	4.70E-04	4.30E-05
transcription, DNA-templated	23	63.9	6.70E-08	8.50E-05	4.30E-05
cellular nitrogen compound biosynthetic process	26	72.2	1.40E-07	1.70E-04	4.40E-05
RNA metabolic process	26	72.2	3.60E-08	4.50E-05	4.50E-05
macromolecule biosynthetic process	26	72.2	3.60E-07	4.60E-04	4.60E-05
nucleic acid metabolic process	26	72.2	3.40E-07	4.30E-04	4.70E-05
RNA biosynthetic process	23	63.9	3.00E-07	3.80E-04	4.80E-05
regulation of nitrogen compound metabolic process	24	66.7	5.00E-07	6.30E-04	4.80E-05
biosynthetic process	28	77.8	7.90E-07	9.90E-04	6.60E-05
regulation of nucleobase-containing compound metabolic process	23	63.9	7.60E-07	9.70E-04	6.90E-05
nitrogen compound metabolic process	29	80.6	1.20E-06	1.50E-03	9.10E-05
cellular nitrogen compound metabolic process	28	77.8	1.50E-06	1.90E-03	1.10E-04
aromatic compound biosynthetic process	23	63.9	3.00E-06	3.80E-03	1.50E-04
negative regulation of RNA metabolic process	13	36.1	3.00E-06	3.70E-03	1.60E-04
regulation of RNA biosynthetic process	21	58.3	2.90E-06	3.60E-03	1.60E-04
regulation of transcription, DNA-templated	21	58.3	2.40E-06	3.00E-03	1.60E-04
regulation of nucleic acid-templated transcription	21	58.3	2.60E-06	3.30E-03	1.60E-04
nucleobase-containing compound biosynthetic process	23	63.9	2.30E-06	2.90E-03	1.60E-04
organic substance biosynthetic process	27	75	3.30E-06	4.20E-03	1.60E-04

regulation of cellular macromolecule biosynthetic process	22	61.1	2.50E-06	3.20E-03	1.60E-04
heterocycle biosynthetic process	23	63.9	2.80E-06	3.60E-03	1.60E-04
nucleobase-containing compound metabolic process	26	72.2	3.90E-06	4.90E-03	1.80E-04
regulation of macromolecule metabolic process	26	72.2	4.20E-06	5.30E-03	1.80E-04
regulation of macromolecule biosynthetic process	22	61.1	4.20E-06	5.30E-03	1.90E-04
organic cyclic compound biosynthetic process	23	63.9	4.70E-06	5.90E-03	2.00E-04
transcription from RNA polymerase II promoter	15	41.7	5.00E-06	6.30E-03	2.00E-04
heterocycle metabolic process	26	72.2	6.00E-06	7.60E-03	2.40E-04
cellular aromatic compound metabolic process	26	72.2	7.00E-06	8.90E-03	2.70E-04
regulation of cellular biosynthetic process	22	61.1	8.50E-06	1.10E-02	3.10E-04
negative regulation of nucleobase-containing compound metabolic process	13	36.1	8.40E-06	1.10E-02	3.10E-04
regulation of biosynthetic process	22	61.1	1.10E-05	1.30E-02	3.70E-04
organic cyclic compound metabolic process	26	72.2	1.30E-05	1.60E-02	4.50E-04
regulation of metabolic process	26	72.2	1.40E-05	1.80E-02	4.70E-04
regulation of primary metabolic process	25	69.4	1.90E-05	2.40E-02	6.10E-04
negative regulation of gene expression	13	36.1	1.90E-05	2.40E-02	6.20E-04
negative regulation of nitrogen compound metabolic process	13	36.1	2.20E-05	2.70E-02	6.70E-04
regulation of cellular metabolic process	25	69.4	2.20E-05	2.80E-02	6.80E-04
COPI coating of Golgi vesicle	3	8.3	2.40E-05	3.00E-02	7.00E-04
COPI-coated vesicle budding	3	8.3	2.40E-05	3.00E-02	7.00E-04
Golgi transport vesicle coating	3	8.3	2.40E-05	3.00E-02	7.00E-04
macromolecule metabolic process	31	86.1	2.70E-05	3.30E-02	7.70E-04

regulation of transcription from RNA polymerase II promoter	14	38.9	3.10E-05	3.80E-02	8.70E-04
positive regulation of gene expression	13	36.1	7.00E-05	8.40E-02	1.90E-03
cellular metabolic process	32	88.9	8.10E-05	9.70E-02	2.20E-03
cellular macromolecule metabolic process	29	80.6	9.40E-05	1.10E-01	2.50E-03
metabolic process	33	91.7	1.20E-04	1.40E-01	3.10E-03
regulation of mRNA metabolic process	5	13.9	1.50E-04	1.70E-01	3.70E-03
Golgi vesicle budding	3	8.3	1.80E-04	2.00E-01	4.40E-03
organic substance metabolic process	32	88.9	2.90E-04	3.10E-01	7.10E-03
negative regulation of transcription, DNA-templated	10	27.8	3.10E-04	3.20E-01	7.40E-03
positive regulation of RNA metabolic process	11	30.6	3.50E-04	3.60E-01	8.20E-03
negative regulation of macromolecule metabolic process	14	38.9	3.60E-04	3.70E-01	8.20E-03
regulation of mRNA splicing, via spliceosome	4	11.1	3.80E-04	3.80E-01	8.50E-03
negative regulation of cellular metabolic process	14	38.9	3.90E-04	3.90E-01	8.60E-03
negative regulation of nucleic acid-templated transcription	10	27.8	4.20E-04	4.10E-01	9.10E-03
negative regulation of RNA biosynthetic process	10	27.8	4.70E-04	4.50E-01	9.90E-03
positive regulation of nitrogen compound metabolic process	12	33.3	4.90E-04	4.60E-01	1.00E-02
iron-sulfur cluster assembly	3	8.3	5.30E-04	4.90E-01	1.10E-02
metallo-sulfur cluster assembly	3	8.3	5.30E-04	4.90E-01	1.10E-02
negative regulation of transcription from RNA polymerase II promoter	8	22.2	6.30E-04	5.50E-01	1.30E-02
negative regulation of metabolic process	14	38.9	8.00E-04	6.40E-01	1.60E-02
sulfur compound metabolic process	6	16.7	8.50E-04	6.60E-01	1.70E-02
positive regulation of macromolecule biosynthetic process	11	30.6	9.10E-04	6.90E-01	1.80E-02

negative regulation of cellular macromolecule biosynthetic process	10	27.8	9.90E-04	7.10E-01	1.90E-02
RNA splicing	6	16.7	1.20E-03	7.80E-01	2.20E-02
regulation of mRNA processing	4	11.1	1.20E-03	7.80E-01	2.20E-02
positive regulation of nucleobase-containing compound metabolic process	11	30.6	1.20E-03	7.90E-01	2.20E-02
regulation of RNA splicing	4	11.1	1.40E-03	8.20E-01	2.50E-02
negative regulation of biological process	19	52.8	1.50E-03	8.50E-01	2.60E-02
negative regulation of macromolecule biosynthetic process	10	27.8	1.60E-03	8.70E-01	2.80E-02
positive regulation of cellular biosynthetic process	11	30.6	1.70E-03	8.80E-01	2.90E-02
positive regulation of biosynthetic process	11	30.6	1.90E-03	9.10E-01	3.20E-02
primary metabolic process	30	83.3	2.00E-03	9.20E-01	3.20E-02
RNA processing	8	22.2	2.00E-03	9.20E-01	3.20E-02
negative regulation of cellular process	18	50	1.90E-03	9.10E-01	3.20E-02
negative regulation of cellular biosynthetic process	10	27.8	2.20E-03	9.40E-01	3.40E-02
mRNA processing	6	16.7	2.40E-03	9.50E-01	3.80E-02
negative regulation of biosynthetic process	10	27.8	2.40E-03	9.50E-01	3.80E-02
negative regulation of mRNA metabolic process	3	8.3	2.50E-03	9.60E-01	3.90E-02
positive regulation of macromolecule metabolic process	14	38.9	2.60E-03	9.60E-01	3.90E-02

Table S1. Gene ontology enrichment of 37 cellular genes in the Zta-interactome.