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HTSeq--a Python framework to work with  
high-throughput sequencing data

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2047	Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cell state. <b>2015</b> , 6, 6683		235
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2045	SC3-seq: a method for highly parallel and quantitative measurement of single-cell gene expression. <b>2015</b> , 43, e60		79
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2038	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. <b>2015</b> , 12, 37		49
2037	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <b>2015</b> , 16, 712-24		286
2036	X Chromosome and Autosome Dosage Responses in <i>Drosophila melanogaster</i> Heads. <b>2015</b> , 5, 1057-63		14
2035	A New Bioinformatic Pipeline to Address the Most Common Requirements in RNA-seq Data Analysis. <b>2015</b> , 117-125		
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2031	Transcriptome profile of liver at different physiological stages reveals potential mode for lipid metabolism in laying hens. <b>2015</b> , 16, 763		57

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2029	Roles of Defense Hormones in the Regulation of Ozone-Induced Changes in Gene Expression and Cell Death. <b>2015</b> , 8, 1776-94	38
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2023	Assessing the prevalence of mycoplasma contamination in cell culture via a survey of NCBI's RNA-seq archive. <b>2015</b> , 43, 2535-42	58
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1634	Using Next-Generation Sequencing to Develop Molecular Diagnostics for <i>Pseudoperonospora cubensis</i> , the Cucurbit Downy Mildew Pathogen. <b>2016</b> , 106, 1105-1116	32
1633	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation. <b>2016</b> , 30, 1731-46	68
1632	Zinc finger protein 407 overexpression upregulates PPAR target gene expression and improves glucose homeostasis in mice. <b>2016</b> , 311, E869-E880	9
1631	Vine nitrogen status and volatile thiols and their precursors from plot to transcriptome level. <b>2016</b> , 16, 173	16
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1626	TRPM2 SNP genotype previously associated with susceptibility to <i>Rhodococcus equi</i> pneumonia in Quarter Horse foals displays differential gene expression identified using RNA-Seq. <b>2016</b> , 17, 993	4
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1624	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <b>2016</b> , 7, 11764	82
1623	Identification of candidate genes associated with porcine meat color traits by genome-wide transcriptome analysis. <b>2016</b> , 6, 35224	18
1622	The AS-RBM15 lncRNA enhances RBM15 protein translation during megakaryocyte differentiation. <b>2016</b> , 17, 887-900	46
1621	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <b>2016</b> , 6, 20316	17
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1484	Multiple mutualist effects on genomewide expression in the tripartite association between <i>Medicago truncatula</i> , nitrogen-fixing bacteria and mycorrhizal fungi. <b>2016</b> , 25, 4946-62	30
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1478	NeuroD1 reprograms chromatin and transcription factor landscapes to induce the neuronal program. <b>2016</b> , 35, 24-45	134
1477	Expression profiling identifies Sertoli and Leydig cell genes as Fsh targets in adult zebrafish testis. <b>2016</b> , 437, 237-251	34
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1445	Combined physiological, transcriptome, and cis-regulatory element analyses indicate that key aspects of ripening, metabolism, and transcriptional program in grapes ( <i>Vitis vinifera</i> L.) are differentially modulated accordingly to fruit size. <b>2016</b> , 17, 416	45
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1436	Cortisol-treated zebrafish embryos develop into pro-inflammatory adults with aberrant immune gene regulation. <b>2016</b> , 5, 1134-41			38
1435	Contextual fear conditioning induces differential alternative splicing. <b>2016</b> , 134 Pt B, 221-35			17
1434	Expression-level support for gene dosage sensitivity in three Glycine subgenus Glycine polyploids and their diploid progenitors. <b>2016</b> , 212, 1083-1093			20
1433	HIF-1 $\beta$ s an Essential Mediator of IFN- $\gamma$ Dependent Immunity to Mycobacterium tuberculosis. <b>2016</b> , 197, 1287-97			116
1432	Leveraging Genetic-Background Effects in Saccharomyces cerevisiae To Improve Lignocellulosic Hydrolysate Tolerance. <b>2016</b> , 82, 5838-49			16
1431	Flow-based sorting of neonatal lymphocyte populations for transcriptomics analysis. <b>2016</b> , 437, 13-20			10
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1427	A subpopulation model to analyze heterogeneous cell differentiation dynamics. <i>Bioinformatics</i> , <b>2016</b> , 32, 3306-3313	7.2	4	
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1421	RNA-seq analysis for detecting quantitative trait-associated genes. <b>2016</b> , 6, 24375			28
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1415	The DNA methyltransferase DNMT3C protects male germ cells from transposon activity. <b>2016</b> , 354, 909-912	192
1414	Partial exhaustion of CD8 T cells and clinical response to teplizumab in new-onset type 1 diabetes. <b>2016</b> , 1,	88
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1388	Akkermansia muciniphila mediates negative effects of IFN $\gamma$ on glucose metabolism. <b>2016</b> , 7, 13329	144
1387	DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. <b>2016</b> , 22, 1488-1495	140
1386	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <b>2016</b> , 7,	21
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1373	An integrated omic analysis of hepatic alteration in medaka fish chronically exposed to cyanotoxins with possible mechanisms of reproductive toxicity. <b>2016</b> , 219, 119-131	31
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1370	Microenvironmental Gene Expression Plasticity Among Individual <i>Drosophila melanogaster</i> . <b>2016</b> , 6, 4197-4210	20
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1338	Preparing for Winter: The Transcriptomic Response Associated with Different Day Lengths in <i>Drosophila montana</i> . <b>2016</b> , 6, 1373-81	26
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1327	Dual leucine zipper kinase regulates expression of axon guidance genes in mouse neuronal cells. <b>2016</b> , 11, 13	4
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1323	Transcriptional profiling of subcutaneous adipose tissue in Italian Large White pigs divergent for backfat thickness. <b>2016</b> , 47, 306-23	27
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1317	Transcriptome Profiling Strategies. <b>2016</b> , 69-104	
1316	Differential mRNA Alternative Splicing. <b>2016</b> , 105-119	4
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1110	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. <b>2017</b> , 168, 442-459.e20	274
1109	Transcriptomic and anatomic parcellation of 5-HTR expressing cortical interneuron subtypes revealed by single-cell RNA sequencing. <b>2017</b> , 8, 14219	30
1108	THZ1 targeting CDK7 suppresses STAT transcriptional activity and sensitizes T-cell lymphomas to BCL2 inhibitors. <b>2017</b> , 8, 14290	58
1107	Characterization of a nuclear pore protein sheds light on the roles and composition of the <i>Toxoplasma gondii</i> nuclear pore complex. <b>2017</b> , 74, 2107-2125	7
1106	Epigenomic landscape of 5-hydroxymethylcytosine reveals its transcriptional regulation of lncRNAs in colorectal cancer. <b>2017</b> , 116, 658-668	24
1105	MicroRNA-125a promotes resistance to BRAF inhibitors through suppression of the intrinsic apoptotic pathway. <b>2017</b> , 30, 328-338	23
1104	Identification and evolutionary analysis of long non-coding RNAs in zebra finch. <b>2017</b> , 18, 117	10
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1102	Potential molecular consequences of transgene integration: The R6/2 mouse example. <b>2017</b> , 7, 41120	8
1101	Impact of Nonalcoholic Fatty Liver Disease on Toxicokinetics of Tetrachloroethylene in Mice. <b>2017</b> , 361, 17-28	17
1100	Meta-analysis of polycystic kidney disease expression profiles defines strong involvement of injury repair processes. <b>2017</b> , 312, F806-F817	19
1099	Genome-Wide Prioritization and Transcriptomics Reveal Novel Signatures Associated With Thiazide Diuretics Blood Pressure Response. <b>2017</b> , 10,	5
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1097	A computational interactome for prioritizing genes associated with complex agronomic traits in rice ( <i>Oryza sativa</i> ). <b>2017</b> , 90, 177-188	20
1096	A Fluorophore Fusion Construct of Human Profilin I with Non-Compromised Poly(L-Proline) Binding Capacity Suitable for Imaging. <b>2017</b> , 429, 964-976	7
1095	Praja1 E3 ubiquitin ligase promotes skeletal myogenesis through degradation of EZH2 upon p38 $\beta$ activation. <b>2017</b> , 8, 13956	32

1094	Metabolically Active Three-Dimensional Brown Adipose Tissue Engineered from White Adipose-Derived Stem Cells. <b>2017</b> , 23, 253-262	12
1093	Identification of a conserved gene signature associated with an exacerbated inflammatory environment in the hippocampus of aging rats. <b>2017</b> , 27, 435-449	11
1092	Divergent functional isoforms drive niche specialisation for nutrient acquisition and use in rumen microbiome. <b>2017</b> , 11, 932-944	31
1091	Identification of endoribonuclease specific cleavage positions reveals novel targets of RNase III in <i>Streptococcus pyogenes</i> . <b>2017</b> , 45, 2329-2340	10
1090	Human Blood CD1c+ Dendritic Cells Encompass CD5high and CD5low Subsets That Differ Significantly in Phenotype, Gene Expression, and Functions. <b>2017</b> , 198, 1553-1564	58
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1088	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <b>2017</b> , 541, 536-540	226
1087	Identifying a gene expression signature of cluster headache in blood. <b>2017</b> , 7, 40218	17
1086	Distinct 5-methylcytosine profiles in poly(A) RNA from mouse embryonic stem cells and brain. <b>2017</b> , 18, 1	268
1085	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <b>2017</b> , 214, 808-819	49
1084	Genome-Wide Transcriptional Response to Varying RpoS Levels in <i>Escherichia coli</i> K-12. <b>2017</b> , 199,	40
1083	The Long Noncoding RNA Landscape of the Ischemic Human Left Ventricle. <b>2017</b> , 10,	20
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1080	Transcriptome sequencing reveals prenatal PFOS exposure on liver disorders. <b>2017</b> , 223, 416-425	20
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1078	RNA-Seq Analysis of Developing Pecan ( <i>Carya illinoensis</i> ) Embryos Reveals Parallel Expression Patterns among Allergen and Lipid Metabolism Genes. <b>2017</b> , 65, 1443-1455	21
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1073	Short bowel syndrome results in increased gene expression associated with proliferation, inflammation, bile acid synthesis and immune system activation: RNA sequencing a zebrafish SBS model. <b>2017</b> , 18, 23	18
1072	Dataset for distribution of SIDER2 elements in the genome and transcriptome. <b>2017</b> , 11, 39-43	
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1070	Transcriptomic analysis of common carp anterior kidney during Cyprinid herpesvirus 3 infection: Immunoglobulin repertoire and homologue functional divergence. <b>2017</b> , 7, 41531	18
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1064	Expression level is a key determinant of E2F1-mediated cell fate. <b>2017</b> , 24, 626-637	26
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1059	Transcriptomic dynamics of breast cancer progression in the MMTV-PyMT mouse model. <b>2017</b> , 18, 185	23

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1054	Mutation of a nucleosome compaction region disrupts Polycomb-mediated axial patterning. <b>2017</b> , 355, 1081-1084	88
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1050	Transcriptome analysis of IL-10-stimulated (M2c) macrophages by next-generation sequencing. <b>2017</b> , 222, 847-856	92
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1046	The T-ALL related gene BCL11B regulates the initial stages of human T-cell differentiation. <b>2017</b> , 31, 2503-2514	32
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1042	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <b>2017</b> , 23, 493-500	225
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1040	cis-Acting Complex-Trait-Associated lincRNA Expression Correlates with Modulation of Chromosomal Architecture. <b>2017</b> , 18, 2280-2288	52
1039	ENL links histone acetylation to oncogenic gene expression in acute myeloid leukaemia. <b>2017</b> , 543, 265-269	124
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510	558. Unravelling regulatory variants affecting gene expression in four porcine tissues. <b>2022</b> ,	o
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508	SLC-0111, an inhibitor of carbonic anhydrase IX, attenuates hepatoblastoma cell viability and migration. 13,	1
507	Blood transcriptome responses in patients correlate with severity of COVID-19 disease. 13,	o
506	Microbially produced vitamin B12 contributes to the lipid-lowering effect of silymarin. <b>2023</b> , 14,	o
505	YTHDF2 orchestrates tumor-associated macrophage reprogramming and controls antitumor immunity through CD8+ T cells. <b>2023</b> , 24, 255-266	o
504	Identification of molecular signatures and pathways involved in Rett syndrome using a multi-omics approach.	o
503	An RNA-seq time series of the medaka pituitary gland during sexual maturation. <b>2023</b> , 10,	o
502	Pathway and Network Analyses Identify Growth Factor Signaling and MMP9 as Potential Mediators of Mitochondrial Dysfunction in Severe COVID-19. <b>2023</b> , 24, 2524	o
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