## Chuan Gao

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3065623/publications.pdf

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1163117 1372567 1,361 11 8 10 citations h-index g-index papers 12 12 12 2742 citing authors all docs docs citations times ranked

#	Article	IF	CITATIONS
1	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
2	XX Disorder of Sex Development is associated with an insertion on chromosome 9 and downregulation of RSPO1 in dogs (Canis lupus familiaris). PLoS ONE, 2017, 12, e0186331.	2.5	12
3	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. PLoS Computational Biology, 2016, 12, e1004791.	3.2	46
4	HEFT: eQTL analysis of many thousands of expressed genes while simultaneously controlling for hidden factors. Bioinformatics, 2014, 30, 369-376.	4.1	22
5	Vitamin D-responsive SGPP2 variants associated with lung cell expression and lung function. BMC Medical Genetics, 2013, 14, 122.	2.1	9
6	Differential Expression of Vitamin E and Selenium-Responsive Genes by Disease Severity in Chronic Obstructive Pulmonary Disease. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2013, 10, 450-458.	1.6	7
7	<i>IQCB1</i> and <i>PDE6B</i> Mutations Cause Similar Early Onset Retinal Degenerations in Two Closely Related Terrier Dog Breeds., 2013, 54, 7005.		40
8	An ADAM9 mutation in canine cone-rod dystrophy 3 establishes homology with human cone-rod dystrophy 9. Molecular Vision, 2010, 16, 1549-69.	1.1	39
9	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
10	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. BMC Genetics, 2008, 9, 37.	2.7	95
11	Whole genome linkage disequilibrium maps in cattle. BMC Genetics, 2007, 8, 74.	2.7	201