The GeneCards Suite: From Gene Data Mining to Diseas

Citation Report

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1	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	6.5	308
2	Integrated Identification of Disease-Gene Links and their Utility in Next-Generation Sequencing Interpretation. , 2016, , .		0
3	Zebrafish small molecule screens: Taking the phenotypic plunge. Computational and Structural Biotechnology Journal, 2016, 14, 350-356.	1.9	24
4	Higher scores in the extraversion personality trait are associated with a functional polymorphism in the<i>PER3</i>gene in healthy subjects. Chronobiology International, 2017, 34, 280-286.	0.9	11
5	Pharos: Collating protein information to shed light on the druggable genome. Nucleic Acids Research, 2017, 45, D995-D1002.	6.5	271
6	MalaCards: an amalgamated human disease compendium with diverse clinical and genetic annotation and structured search. Nucleic Acids Research, 2017, 45, D877-D887.	6.5	398
7	ChiTaRS-3.1â€"the enhanced chimeric transcripts and RNA-seq database matched with proteinâ€"protein interactions. Nucleic Acids Research, 2017, 45, D790-D795.	6.5	44
8	Holistic Approach to Determine Cause of Autopsy-Negative Sudden Natural Death. Journal of the American College of Cardiology, 2017, 69, 2146-2148.	1.2	11
9	The human retinoblastoma susceptibility gene (RB1): an evolutionary story in primates. Mammalian Genome, 2017, 28, 198-212.	1.0	3
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16	Exploring genome-wide DNA methylation patterns in Aicardi syndrome. Epigenomics, 2017, 9, 1373-1386.	1.0	8
17	Whole exome sequencing in inborn errors of immunity: use the power but mind the limits. Current Opinion in Allergy and Clinical Immunology, 2017, 17, 421-430.	1.1	12
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19	A novel method for genome-wide profiling of dynamic host-pathogen interactions using 3â€² end enriched RNA-seq. Scientific Reports, 2017, 7, 8681.	1.6	3
20	Proteomic analysis of the secretome of human bone marrow-derived mesenchymal stem cells primed by pro-inflammatory cytokines. Journal of Proteomics, 2017, 166, 115-126.	1.2	80
21	Defining a Cancer Dependency Map. Cell, 2017, 170, 564-576.e16.	13.5	1,794
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25	Ensemble Modeling Approach Targeting Heterogeneous RNA-Seq data: Application to Melanoma Pseudogenes. Scientific Reports, 2017, 7, 17344.	1.6	2
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30	Dupuytrenâ€™s and Ledderhose Diseases in a Family with LMNA-Related Cardiomyopathy and a Novel Variant in the ASTE1 Gene. Cells, 2017, 6, 40.	1.8	5
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32	Bronchial Epithelial Cells from Cystic Fibrosis Patients Express a Specific Long Non-coding RNA Signature upon Pseudomonas aeruginosa Infection. Frontiers in Cellular and Infection Microbiology, 2017, 7, 218.	1.8	31
33	Exome-Wide Meta-Analysis Identifies Rare 3â€²-UTR Variant in ERCC1/CD3EAP Associated with Symptoms of Sleep Apnea. Frontiers in Genetics, 2017, 8, 151.	1.1	7
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38	From gene networks to drugs: systems pharmacology approaches for AUD. Psychopharmacology, 2018, 235, 1635-1662.	1.5	15
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41	lncRNA-based study of epigenetic regulations in diabetic peripheral neuropathy. In Silico Pharmacology, 2018, 6, 7.	1.8	9
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44	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	5.8	59
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