Wesam Kurdi

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1417423/publications.pdf

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25	1,614	516710	552781
papers	citations	16 h-index	26 g-index

27	27	27	3959
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prenatal exome sequencing and chromosomal microarray analysis in fetal structural anomalies in a highly consanguineous population reveals a propensity of ciliopathy genes causing multisystem phenotypes. Human Genetics, 2022, 141, 101-126.	3.8	6
2	Efficacy of hyoscine in pain management during hysteroscopy: a systematic review and meta-analysis. Journal of the Turkish German Gynecology Association, 2022, 23, 51-57.	0.6	1
3	The Evolution of Fetal Procedures. Innovations in Surgery and Interventional Medicine, 2022, 2, 15-16.	0.1	0
4	Bleeding and thrombotic risk in pregnant women with Fontan physiology. Heart, 2021, 107, 1390-1397.	2.9	9
5	Novel loss of function variants in FRAS1 AND FREM2 underlie renal agenesis in consanguineous families. Journal of Nephrology, 2021, 34, 893-900.	2.0	11
6	Lethal variants in humans: lessons learned from a large molecular autopsy cohort. Genome Medicine, 2021, 13, 161.	8.2	13
7	Efficacy of hyoscine in pain management during hysteroscopy: a systematic review and meta-analysis. Journal of the Turkish German Gynecology Association, 2021, .	0.6	1
8	Fetal Anomalies Associated with Novel Pathogenic Variants in TMEM94. Genes, 2020, 11, 967.	2.4	4
9	The effect of hyoscine-N-butylbromide on pain perception during and after hysterosalpingography in infertile women: a systematic review and meta-analysis of randomised controlled trials. Human Fertility, 2020, , 1-8.	1.7	2
10	Absence of GP130 cytokine receptor signaling causes extended StÃ¼ve-Wiedemann syndrome. Journal of Experimental Medicine, 2020, 217, .	8.5	41
11	Lessons Learned from Large-Scale, First-Tier Clinical Exome Sequencing in a Highly Consanguineous Population. American Journal of Human Genetics, 2019, 104, 1182-1201.	6.2	184
12	Bialleleic PKD1 mutations underlie early-onset autosomal dominant polycystic kidney disease in Saudi Arabian families. Pediatric Nephrology, 2019, 34, 1615-1623.	1.7	21
13	Autozygome and high throughput confirmation of disease genes candidacy. Genetics in Medicine, 2019, 21, 736-742.	2.4	81
14	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. American Journal of Human Genetics, 2018, 102, 116-132.	6.2	46
15	Molecular autopsy in maternalâ€“fetal medicine. Genetics in Medicine, 2018, 20, 420-427.	2.4	84
16	The genetic landscape of familial congenital hydrocephalus. Annals of Neurology, 2017, 81, 890-897.	5.3	108
17	The landscape of genetic diseases in Saudi Arabia based on the first 1000 diagnostic panels and exomes. Human Genetics, 2017, 136, 921-939.	3.8	209
18	Autozygosity reveals recessive mutations and novel mechanisms in dominant genes: implications in variant interpretation. Genetics in Medicine, 2017, 19, 1144-1150.	2.4	77

#	Article	IF	Citations
19	Expanding the genetic heterogeneity of intellectual disability. Human Genetics, 2017, 136, 1419-1429.	3.8	122
20	Genetic spectrum of Saudi Arabian patients with antenatal cystic kidney disease and ciliopathy phenotypes using a targeted renal gene panel. Journal of Medical Genetics, 2016, 53, 338-347.	3.2	28
21	Identification of embryonic lethal genes in humans by autozygosity mapping and exome sequencing in consanguineous families. Genome Biology, 2015, 16, 116.	8.8	91
22	Accelerating Novel Candidate Gene Discovery in Neurogenetic Disorders via Whole-Exome Sequencing of Prescreened Multiplex Consanguineous Families. Cell Reports, 2015, 10, 148-161.	6.4	375
23	Identification of a novel MKS locus defined byTMEM107mutation. Human Molecular Genetics, 2015, 24, 5211-5218.	2.9	42
24	Robot-assisted surgical staging for ovarian cancer in pregnant women. Journal of Robotic Surgery, 2012, 6, 163-166.	1.8	1
25	Delayed normalisation of uterine artery doppler waveforms is not a benign phenomenon. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2004, 117, 20-23.	1.1	23