Jeffrey C Murray

List of Publications by Year
in descending order

136	16,645	61984 43	18647 119
papers	citations	h-index	g-index

143	143	143	22151
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Variant analyses of candidate genes in orofacial clefts in multiâ€ethnic populations. Oral Diseases, 2022, 28, 1921-1935.	3.0	3
2	Targeted newborn metabolomics: prediction of gestational age from cord blood. Journal of Perinatology, 2022, 42, 181-186.	2.0	2
3	Genomeâ€wide association study of multiethnic nonsyndromic orofacial cleft families identifies novel loci specific to family and phenotypic subtypes. Genetic Epidemiology, 2022, , .	1.3	4
4	Genetic predictors of severe intraventricular hemorrhage in extremely low-birthweight infants. Journal of Perinatology, 2021, 41, 286-294.	2.0	3
5	Using an aquatic model, <scp>Xenopus laevis</scp>, to uncover the role of chromodomain 1 in craniofacial disorders. Genesis, 2021, 59, e23394.	1.6	10
6	Cost-effectiveness of a gestational age metabolic algorithm for preterm and small-for-gestational-age classification. American Journal of Obstetrics & Gynecology MFM, 2021, 3, 100279.	2.6	7
7	Coâ€occurrence of orofacial clefts and clubfoot phenotypes in a subâ€Saharan African cohort: Wholeâ€exome sequencing implicates multiple syndromes and genes. Molecular Genetics & Genomic Medicine, 2021, 9, e1655.	1.2	3
8	Genome-Wide Association Study of Non-syndromic Orofacial Clefts in a Multiethnic Sample of Families and Controls Identifies Novel Regions. Frontiers in Cell and Developmental Biology, 2021, 9, 621482.	3.7	16
9	Interactions between PDA-associated polymorphisms and genetic ancestry alter ductus arteriosus gene expression. Pediatric Research, 2021, , .	2.3	0
10	The PAX1 locus at 20p11 is a potential genetic modifier for bilateral cleft lip. Human Genetics and Genomics Advances, 2021, 2, 100025.	1.7	9
11	FAT4 identified as a potential modifier of orofacial cleft laterality. Genetic Epidemiology, 2021, 45, 721-735.	1.3	14
12	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. PLoS Genetics, 2021, 17, e1009584.	3.5	18
13	Integrative genetic, genomic and transcriptomic analysis of heat shock protein and nuclear hormone receptor gene associations with spontaneous preterm birth. Scientific Reports, 2021, 11, 17115.	3.3	12
14	Genome-Wide Scan for Parent-of-Origin Effects in a sub-Saharan African Cohort With Nonsyndromic Cleft Lip and/or Cleft Palate (CL/P). Cleft Palate-Craniofacial Journal, 2021, , 105566562110363.	0.9	1
15	Association of maternal prenatal selenium concentration and preterm birth: a multicountry meta-analysis. BMJ Global Health, 2021, 6, e005856.	4.7	13
16	Re-evaluating surgery and re-irradiation for locally recurrent pediatric ependymoma â€“ a multi-institutional study. Neuro-Oncology Advances, 2021, 3, vdab158.	0.7	5
17	Whole genome sequencing of orofacial cleft trios from the Gabriella Miller Kids First Pediatric Research Consortium identifies a new locus on chromosome 21. Human Genetics, 2020, 139, 215-226.	3.8	19
18	Dissecting maternal and fetal genetic effects underlying the associations between maternal phenotypes, birth outcomes, and adult phenotypes: A mendelian-randomization and haplotype-based genetic score analysis in 10,734 motherâ€“infant pairs. PLoS Medicine, 2020, 17, e1003305.	8.4	37

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19	Reply to â€œDiversity is essential for good science and Reproductive science is no different: A response to the recent formulation of the Burroughs Welcome Fund Pregnancy Think-Tankâ€. American Journal of Obstetrics and Gynecology, 2020, 223, 951-952.	1.3	0
20	Advancing human health in the decade ahead: pregnancy as a key window for discovery. American Journal of Obstetrics and Gynecology, 2020, 223, 312-321.	1.3	13
21	Nonâ€random distribution of deleterious mutations in the DNA and proteinâ€binding domains of IRF6 are associated with Van Der Woude syndrome. Molecular Genetics & Genomic Medicine, 2020, 8, e1355.	1.2	13
22	Genome-wide Enrichment of De Novo Coding Mutations in Orofacial Cleft Trios. American Journal of Human Genetics, 2020, 107, 124-136.	6.2	48
23	SPECC1L regulates palate development downstream of IRF6. Human Molecular Genetics, 2020, 29, 845-858.	2.9	18
24	CDH1 Mutation Distribution and Type Suggests Genetic Differences between the Etiology of Orofacial Clefting and Gastric Cancer. Genes, 2020, 11, 391.	2.4	11
25	A phase 2 study of valproic acid and radiation, followed by maintenance valproic acid and bevacizumab in children with newly diagnosed diffuse intrinsic pontine glioma or highâ€grade glioma. Pediatric Blood and Cancer, 2020, 67, e28283.	1.5	40
26	Multiomics Characterization of Preterm Birth in Low- and Middle-Income Countries. JAMA Network Open, 2020, 3, e2029655.	5.9	53
27	Title is missing!. , 2020, 17, e1003305.		0
28	Title is missing!. , 2020, 17, e1003305.		0
29	Title is missing!. , 2020, 17, e1003305.		0
30	Title is missing!. , 2020, 17, e1003305.		0
31	Title is missing!. , 2020, 17, e1003305.		0
32	Title is missing!. , 2020, 17, e1003305.		0
33	Detection of de novo copy number deletions from targeted sequencing of trios. Bioinformatics, 2019, 35, 571-578.	4.1	2
34	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	12.8	49
35	Mutations in GDF11 and the extracellular antagonist, Follistatin, as a likely cause of Mendelian forms of orofacial clefting in humans. Human Mutation, 2019, 40, 1813-1825.	2.5	26
36	A systematic genetic analysis and visualization of phenotypic heterogeneity among orofacial cleft GWAS signals. Genetic Epidemiology, 2019, 43, 704-716.	1.3	36

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37	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
38	Deletions and loss-of-function variants in TP63 associated with orofacial clefting. European Journal of Human Genetics, 2019, 27, 1101-1112.	2.8	16
39	Front Cover, Volume 40, Issue 10. Human Mutation, 2019, 40, i.	2.5	0
40	Association of lowâ€frequency genetic variants in regulatory regions with nonsyndromic orofacial clefts. American Journal of Medical Genetics, Part A, 2019, 179, 467-474.	1.2	18
41	Genomic analyses in African populations identify novel risk loci for cleft palate. Human Molecular Genetics, 2019, 28, 1038-1051.	2.9	61
42	Genetic variants associated with patent ductus arteriosus in extremely preterm infants. Journal of Perinatology, 2019, 39, 401-408.	2.0	16
43	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. Genetic Epidemiology, 2019, 43, 37-49.	1.3	6
44	Genetic Variants and the Cortisol Response in Children: An Exploratory Study. Biological Research for Nursing, 2019, 21, 157-165.	1.9	1
45	Novel GREM1 Variations in Sub-Saharan African Patients With Cleft Lip and/or Cleft Palate. Cleft Palate-Craniofacial Journal, 2018, 55, 736-742.	0.9	9
46	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
47	Polymorphisms in urea cycle enzyme genes are associated with persistent pulmonary hypertension of the newborn. Pediatric Research, 2018, 83, 142-147.	2.3	22
48	Genomeâ€wide interaction studies identify sexâ€specific risk alleles for nonsyndromic orofacial clefts. Genetic Epidemiology, 2018, 42, 664-672.	1.3	15
49	Identification of paternal uniparental disomy on chromosome 22 and a de novo deletion on chromosome 18 in individuals with orofacial clefts. Molecular Genetics & Genomic Medicine, 2018, 6, 924-932.	1.2	4
50	Mutations in the Epithelial Cadherin-p120-Catenin Complex Cause Mendelian Non-Syndromic Cleft Lip with or without Cleft Palate. American Journal of Human Genetics, 2018, 102, 1143-1157.	6.2	94
51	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at PLEKHG1. Hypertension, 2018, 72, 408-416.	2.7	46
52	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. PLoS Genetics, 2018, 14, e1007394.	3.5	35
53	Genome-wide meta-analyses of nonsyndromic orofacial clefts identify novel associations between FOXE1 and all orofacial clefts, and TP63 and cleft lip with or without cleft palate. Human Genetics, 2017, 136, 275-286.	3.8	139
54	Genome-wide association study of sepsis in extremely premature infants. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2017, 102, F439-F445.	2.8	32

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55	Association of candidate gene polymorphisms with clinical subtypes of preterm birth in a Latin American population. Pediatric Research, 2017, 82, 554-559.	2.3	8
56	Association studies of lowâ€frequency coding variants in nonsyndromic cleft lip with or without cleft palate. American Journal of Medical Genetics, Part A, 2017, 173, 1531-1538.	1.2	36
57	Relationship of Genetic Variants With Procedural Pain, Anxiety, and Distress in Children. Biological Research for Nursing, 2017, 19, 339-349.	1.9	13
58	DNA methylation of a novel PAK4 locus influences ototoxicity susceptibility following cisplatin and radiation therapy for pediatric embryonal tumors. Neuro-Oncology, 2017, 19, 1372-1379.	1.2	7
59	Whole exome association of rare deletions in multiplex oral cleft families. Genetic Epidemiology, 2017, 41, 61-69.	1.3	10
60	Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. Genetic Epidemiology, 2017, 41, 244-250.	1.3	24
61	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, 109, 1030-1038.	1.5	41
62	Identification of 16q21 as a modifier of nonsyndromic orofacial cleft phenotypes. Genetic Epidemiology, 2017, 41, 887-897.	1.3	24
63	Genome-wide analysis of parent-of-origin interaction effects with environmental exposure (PoOxE): An application to European and Asian cleft palate trios. PLoS ONE, 2017, 12, e0184358.	2.5	16
64	Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. Birth Defects Research, 2017, , .	1.5	0
65	Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. PLoS Genetics, 2016, 12, e1006149.	3.5	140
66	A multi-ethnic genome-wide association study identifies novel loci for non-syndromic cleft lip with or without cleft palate on 2p24.2, 17q23 and 19q13. Human Molecular Genetics, 2016, 25, ddw104.	2.9	163
67	Maternal and neonatal epidemiological features in clinical subtypes of preterm birth. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 3153-3161.	1.5	22
68	Polymorphisms in NR5A2, gene encoding liver receptor homolog-1 are associated with preterm birth. Pediatric Research, 2016, 79, 776-780.	2.3	8
69	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. American Journal of Human Genetics, 2016, 98, 744-754.	6.2	146
70	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
71	Common Genetic Variants in FOXP2 Are Not Associated with Individual Differences in Language Development. PLoS ONE, 2016, 11, e0152576.	2.5	18
72	Determining the prevalence of cytomegalovirus infection in a cohort ofÂpreterm infants. Journal of Neonatal-Perinatal Medicine, 2015, 8, 137-141.	0.8	12

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73	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
74	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
75	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
76	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. American Journal of Human Genetics, 2015, 96, 397-411.	6.2	150
77	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. PLoS Genetics, 2015, 11, e1005059.	3.5	82
78	Integrated Genomic Analyses in Bronchopulmonary Dysplasia. Journal of Pediatrics, 2015, 166, 531-537.e13.	1.8	93
79	Replication of 13q31.1 association in nonsyndromic cleft lip with cleft palate in Europeans. American Journal of Medical Genetics, Part A, 2015, 167, 1054-1060.	1.2	31
80	Antioxidant response genes sequence variants and BPD susceptibility in VLBW infants. Pediatric Research, 2015, 77, 477-483.	2.3	52
81	Genetic variation in CYB5R3 is associated with methemoglobin levels in preterm infants receiving nitric oxide therapy. Pediatric Research, 2015, 77, 472-476.	2.3	5
82	Evidence of Geneâ^'Environment Interaction for Two Genes on Chromosome 4 and Environmental Tobacco Smoke in Controlling the Risk of Nonsyndromic Cleft Palate. PLoS ONE, 2014, 9, e88088.	2.5	33
83	A LINE-1 Insertion in DLX6 Is Responsible for Cleft Palate and Mandibular Abnormalities in a Canine Model of Pierre Robin Sequence. PLoS Genetics, 2014, 10, e1004257.	3.5	49
84	Identification of single nucleotide polymorphisms in hematopoietic cell transplant patients affecting early recognition of, and response to, endotoxin. Innate Immunity, 2014, 20, 697-711.	2.4	9
85	2013 Presidential Address: Just Another Presidentâ€™s Speech (but Itâ€™s All about You). American Journal of Human Genetics, 2014, 94, 319-323.	6.2	0
86	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
87	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. Genetics, 2014, 197, 1039-1044.	2.9	79
88	Dominant Mutations in GRHL3 Cause Van der Woude Syndrome and Disrupt Oral Periderm Development. American Journal of Human Genetics, 2014, 94, 23-32.	6.2	195
89	Search for genetic modifiers of IRF6 and genotypeâ€“phenotype correlations in Van der Woude and popliteal pterygium syndromes. American Journal of Medical Genetics, Part A, 2013, 161, 2535-2544.	1.2	21
90	A solution pathway for preterm birth: accelerating a priority research agenda. The Lancet Global Health, 2013, 1, e328-e330.	6.3	44

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91	Clinical and environmental influences on metabolic biomarkers collected for newborn screening. Clinical Biochemistry, 2013, 46, 133-138.	1.9	62
92	Polymorphisms of CYP51A1 from Cholesterol Synthesis: Associations with Birth Weight and Maternal Lipid Levels and Impact on CYP51 Protein Structure. PLoS ONE, 2013, 8, e82554.	2.5	24
93	Genetics of Nonsyndromic Orofacial Clefts. Cleft Palate-Craniofacial Journal, 2012, 49, 73-91.	0.9	212
94	Assessing the impact of nicotine dependence genes on the risk of facial clefts: An example of the use of national registry and biobank data. Norsk Epidemiologi, 2012, 21, 241-250.	0.3	5
95	Cleft lip and palate: understanding genetic and environmental influences. Nature Reviews Genetics, 2011, 12, 167-178.	16.3	1,435
96	Temporal lobe pleomorphic xanthoastrocytoma and acquired BRAF mutation in an adolescent with the constitutional 22q11.2 deletion syndrome. Journal of Neuro-Oncology, 2011, 102, 509-514.	2.9	16
97	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	145
98	Mapping a New Spontaneous Preterm Birth Susceptibility Gene, IGF1R, Using Linkage, Haplotype Sharing, and Association Analysis. PLoS Genetics, 2011, 7, e1001293.	3.5	61
99	Recurrence risk for offspring of twins discordant for oral cleft: A populationâ€based cohort study of the Danish 1936â€“2004 cleft twin cohort. American Journal of Medical Genetics, Part A, 2010, 152A, 2468-2474.	1.2	28
100	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. Nature Genetics, 2010, 42, 525-529.	21.4	518
101	A cohort study of recurrence patterns among more than 54 000 relatives of oral cleft cases in Denmark: support for the multifactorial threshold model of inheritance. Journal of Medical Genetics, 2010, 47, 162-168.	3.2	188
102	Genome Scan, Fine-Mapping, and Candidate Gene Analysis of Non-Syndromic Cleft Lip with or without Cleft Palate Reveals Phenotype-Specific Differences in Linkage and Association Results. Human Heredity, 2009, 68, 151-170.	0.8	113
103	Maternal Contributions to Preterm Delivery. American Journal of Epidemiology, 2009, 170, 1358-1364.	3.4	133
104	FOXE1 association with both isolated cleft lip with or without cleft palate, and isolated cleft palate. Human Molecular Genetics, 2009, 18, 4879-4896.	2.9	136
105	Disruption of an AP-2Î± binding site in an IRF6 enhancer is associated with cleft lip. Nature Genetics, 2008, 40, 1341-1347.	21.4	382
106	Cancer Risk in Persons with Oral Cleftâ€”A Population-based Study of 8,093 Cases. American Journal of Epidemiology, 2005, 161, 1047-1055.	3.4	111
107	Direct Sequencing of Candidate Genes for Nonsyndromic Cleft Lip and Palate. PLoS Genetics, 2005, preprint, e64.	3.5	1
108	Long term follow up study of survival associated with cleft lip and palate at birth. BMJ: British Medical Journal, 2004, 328, 1405.	2.3	205

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109	Cleft palate: players, pathways, and pursuits. Journal of Clinical Investigation, 2004, 113, 1676-1678.	8.2	93
110	Novel IRF6 mutations in Japanese patients with Van der Woude Syndrome: two missense mutations (R45Q and P396S) and a 17-kb deletion. Journal of Human Genetics, 2003, 48, 622-628.	2.3	31
111	Mutations in IRF6 cause Van der Woude and popliteal pterygium syndromes. Nature Genetics, 2002, 32, 285-289.	21.4	784
112	Clinical Pathology Case: Hyperimmunoglobulin E Syndrome (Job's Syndrome). Fetal and Pediatric Pathology, 2001, 20, 223-226.	0.3	0
113	Matroshka and ectopic polymorphisms: Two new classes of DNA sequence variation identified at the Van der Woude syndrome locus on 1q32-q41. Human Mutation, 2001, 18, 422-434.	2.5	2
114	Time for T. Nature Genetics, 2001, 29, 107-109.	21.4	8
115	Pitx2 Regulates Procollagen Lysyl Hydroxylase (Plod) Gene Expression. Journal of Cell Biology, 2001, 152, 545-552.	5.2	78
116	Mutations in the human forkhead transcription factor FOXE3 associated with anterior segment ocular dysgenesis and cataracts. Human Molecular Genetics, 2001, 10, 231-236.	2.9	184
117	CLINICAL PATHOLOGY CASE: HYPERIMMUNOGLOBULIN E SYNDROME (JOB'S SYNDROME). Fetal and Pediatric Pathology, 2001, 20, 223-226.	0.3	0
118	The Pitx2 protein in mouse development. Developmental Dynamics, 2000, 218, 195-200.	1.8	126
119	Exclusion of the branchio-oto-renal syndrome locus (EYA1) from patients with branchio-oculo-facial syndrome. , 2000, 91, 387-390.		19
120	Domain-specific mutations in TGFB1 result in Camurati-Engelmann disease. Nature Genetics, 2000, 26, 19-20.	21.4	239
121	Genomic structure of the human retinoic acid receptor-alpha1 gene. Mammalian Genome, 1999, 10, 528-529.	2.2	8
122	Microdeletions at chromosome bands 1q32-q41 as a cause of Van der Woude syndrome. , 1999, 84, 145-150.		65
123	Candidate genes for nonsyndromic cleft lip and palate and maternal cigarette smoking and alcohol consumption: Evaluation of genotype-environment interactions from a population-based case-control study of orofacial clefts. , 1999, 59, 39-50.		198
124	Analysis of select folate pathway genes,PAX3, and humanT in a midwestern neural tube defect population. Teratology, 1999, 59, 331-341.	1.6	88
125	Analysis of select folate pathway genes, PAX3, and human T in a midwestern neural tube defect population. Teratology, 1999, 59, 331-341.	1.6	3
126	The effect of follow-up on limiting non-participation bias in genetic epidemiologic investigations. European Journal of Epidemiology, 1998, 14, 129-138.	5.7	23

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127	Cloning and chromosomal localization of two novel human genes encoding LIM-domain binding factors CLIM1 and CLIM2/LDB1/NLI. Mammalian Genome, 1998, 9, 921-924.	2.2	10
128	Assignment of gene responsible for progressive pseudorheumatoid dysplasia to chromosome 6 and examination of COL10A1 as candidate gene. European Journal of Human Genetics, 1998, 6, 251-256.	2.8	22
129	A novel homeobox gene PITX3 is mutated in families with autosomal-dominant cataracts and ASMD. Nature Genetics, 1998, 19, 167-170.	21.4	371
130	A new human homeobox gene OGI2X is a member of the most conserved homeobox gene family and is expressed during heart development in mouse. Human Molecular Genetics, 1998, 7, 415-422.	2.9	40
131	Exclusion of Ifa and Ifb as the Lps gene and mapping of three markers near the Lps locus. Mammalian Genome, 1997, 8, 785-786.	2.2	3
132	Genomic structure, sequence, and mapping of humanFGF8 with no evidence for its role in craniosynostosis/limb defect syndromes. , 1997, 72, 354-362.		16
133	Cloning and characterization of a novel bicoid-related homeobox transcription factor gene, RIEG, involved in Rieger syndrome. Nature Genetics, 1996, 14, 392-399.	21.4	852
134	Integrated human genomeâ€“wide maps constructed using the CEPH reference panel. Nature Genetics, 1994, 6, 391-393.	21.4	216
135	The chromosome 4 workshop report. Genomics, 1992, 12, 857-858.	2.9	0
136	Characterization of the calcitonin/CGRP gene in Williams syndrome. American Journal of Medical Genetics Part A, 1991, 39, 28-33.	2.4	6