

# Bernice E Morrow

## List of Publications by Year in descending order

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133  
papers

11,664  
citations

41258

49  
h-index

30848

102  
g-index

141  
all docs

141  
docs citations

141  
times ranked

10473  
citing authors

#	ARTICLE	IF	CITATIONS
1	The DNA sequence of human chromosome 22. <i>Nature</i> , 1999, 402, 489-495.	13.7	1,086
2	22q11.2 deletion syndrome. <i>Nature Reviews Disease Primers</i> , 2015, 1, 15071.	18.1	954
3	TBX1 Is Responsible for Cardiovascular Defects in Velo-Cardio-Facial/DiGeorge Syndrome. <i>Cell</i> , 2001, 104, 619-629.	13.5	884
4	Schizophrenia susceptibility associated with interstitial deletions of chromosome 22q11.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7612-7616.	3.3	591
5	Meiotic Pachytene Arrest in MLH1-Deficient Mice. <i>Cell</i> , 1996, 85, 1125-1134.	13.5	528
6	Psychotic Illness in Patients Diagnosed with Velo-Cardio-Facial Syndrome and Their Relatives. <i>Journal of Nervous and Mental Disease</i> , 1994, 182, 476-477.	0.5	394
7	A common molecular basis for rearrangement disorders on chromosome 22q11. <i>Human Molecular Genetics</i> , 1999, 8, 1157-1167.	1.4	385
8	Low-Copy Repeats Mediate the Common 3-Mb Deletion in Patients with Velo-cardio-facial Syndrome. <i>American Journal of Human Genetics</i> , 1999, 64, 1076-1086.	2.6	340
9	VEGF: A modifier of the del22q11 (DiGeorge) syndrome?. <i>Nature Medicine</i> , 2003, 9, 173-182.	15.2	288
10	Association of codon 108/158 catechol-O-methyltransferase gene polymorphism with the psychiatric manifestations of velo-cardio-facial syndrome. , 1996, 67, 468-472.		259
11	Genomic Disorders on 22q11. <i>American Journal of Human Genetics</i> , 2002, 70, 1077-1088.	2.6	228
12	Microduplication and Triplication of 22q11.2: A Highly Variable Syndrome. <i>American Journal of Human Genetics</i> , 2005, 76, 865-876.	2.6	221
13	Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. <i>American Journal of Human Genetics</i> , 2010, 86, 850-859.	2.6	217
14	Full spectrum of malformations in velo-cardio-facial syndrome/DiGeorge syndrome mouse models by altering Tbx1 dosage. <i>Human Molecular Genetics</i> , 2004, 13, 1577-1585.	1.4	214
15	AT-Rich Palindromes Mediate the Constitutional t(11;22) Translocation. <i>American Journal of Human Genetics</i> , 2001, 68, 1-13.	2.6	175
16	Suppression of neural fate and control of inner ear morphogenesis by Tbx1. <i>Development (Cambridge)</i> , 2004, 131, 1801-1812.	1.2	150
17	Inactivation of Tbx1 in the pharyngeal endoderm results in 22q11DS malformations. <i>Development (Cambridge)</i> , 2006, 133, 977-987.	1.2	146
18	Velo-cardio-facial syndrome: Frequency and extent of 22q11 deletions. <i>American Journal of Medical Genetics Part A</i> , 1995, 57, 514-522.	2.4	134

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19	Tbx1 affects asymmetric cardiac morphogenesis by regulating Pitx2 in the secondary heart field. <i>Development (Cambridge)</i> , 2006, 133, 1565-1573.	1.2	132
20	Identification of downstream genetic pathways of Tbx1 in the second heart field. <i>Developmental Biology</i> , 2008, 316, 524-537.	0.9	124
21	A Tbx1-Six1/Eya1-Fgf8 genetic pathway controls mammalian cardiovascular and craniofacial morphogenesis. <i>Journal of Clinical Investigation</i> , 2011, 121, 1585-1595.	3.9	123
22	Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. <i>New England Journal of Medicine</i> , 2017, 376, 742-754.	13.9	120
23	Shuffling of Genes Within Low-Copy Repeats on 22q11 (LCR22) by Alu-Mediated Recombination Events During Evolution. <i>Genome Research</i> , 2003, 13, 2519-2532.	2.4	115
24	Molecular and clinical study of 183 patients with conotruncal anomaly face syndrome. <i>Human Genetics</i> , 1998, 103, 70-80.	1.8	114
25	Comparative mapping of the human 22q11 chromosomal region and the orthologous region in mice reveals complex changes in gene organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14608-14613.	3.3	104
26	Identification of a New Human Catenin Gene Family Member (ARVCF) from the Region Deleted in Veloâ€“Cardioâ€“Facial Syndrome. <i>Genomics</i> , 1997, 41, 75-83.	1.3	103
27	A model for transcription termination by RNA polymerase I. <i>Cell</i> , 1994, 79, 527-534.	13.5	102
28	Dual embryonic origin of the mammalian otic vesicle forming the inner ear. <i>Development (Cambridge)</i> , 2011, 138, 5403-5414.	1.2	102
29	Identification, Characterization, and Precise Mapping of a Human Gene Encoding a Novel Membrane-Spanning Protein from the 22q11 Region Deleted in Veloâ€“Cardioâ€“Facial Syndrome. <i>Genomics</i> , 1997, 42, 245-251.	1.3	96
30	Molecular genetics of 22q11.2 deletion syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 2070-2081.	0.7	96
31	Tissue-specific roles of Tbx1 in the development of the outer, middle and inner ear, defective in 22q11DS patients. <i>Human Molecular Genetics</i> , 2006, 15, 1629-1639.	1.4	91
32	Using common genetic variation to examine phenotypic expression and risk prediction in 22q11.2 deletion syndrome. <i>Nature Medicine</i> , 2020, 26, 1912-1918.	15.2	90
33	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. <i>Molecular Psychiatry</i> , 2021, 26, 4496-4510.	4.1	87
34	The Role of Neural Crest during Cardiac Development in a Mouse Model of DiGeorge Syndrome. <i>Developmental Biology</i> , 2002, 251, 157-166.	0.9	85
35	Rare Genome-Wide Copy Number Variation and Expression of Schizophrenia in 22q11.2 Deletion Syndrome. <i>American Journal of Psychiatry</i> , 2017, 174, 1054-1063.	4.0	77
36	Behavior of mice with mutations in the conserved region deleted in velocardiofacial/DiGeorge syndrome. <i>Neurogenetics</i> , 2006, 7, 247-257.	0.7	70

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37	The 22q11 deletion syndrome candidate gene Tbx1 determines thyroid size and positioning. <i>Human Molecular Genetics</i> , 2007, 16, 276-285.	1.4	67
38	Copy-Number Variation of the Glucose Transporter Gene SLC2A3 and Congenital Heart Defects in the 22q11.2 Deletion Syndrome. <i>American Journal of Human Genetics</i> , 2015, 96, 753-764.	2.6	62
39	Mouse and Human CRKL Is Dosage Sensitive for Cardiac Outflow Tract Formation. <i>American Journal of Human Genetics</i> , 2015, 96, 235-244.	2.6	58
40	A Common Breakpoint on 11q23 in Carriers of the Constitutional t(11;22) Translocation. <i>American Journal of Human Genetics</i> , 1999, 65, 1608-1616.	2.6	57
41	T-genes and limb bud development. <i>American Journal of Medical Genetics, Part A</i> , 2006, 140A, 1407-1413.	0.7	57
42	Genotype and cardiovascular phenotype correlations with TBX1 in 1,022 velo-cardio-facial/digeorge/22q11.2 deletion syndrome patients. <i>Human Mutation</i> , 2011, 32, 1278-1289.	1.1	57
43	Isolation of a new clathrin heavy chain gene with muscle-specific expression from the region commonly deleted in velo-cardio-facial syndrome. <i>Human Molecular Genetics</i> , 1996, 5, 617-624.	1.4	55
44	Over-expression of a human chromosome 22q11.2 segment including TXNRD2, COMT and ARVCF developmentally affects incentive learning and working memory in mice. <i>Human Molecular Genetics</i> , 2009, 18, 3914-3925.	1.4	53
45	Enhanced Maternal Origin of the 22q11.2 Deletion in Velocardiofacial and DiGeorge Syndromes. <i>American Journal of Human Genetics</i> , 2013, 92, 439-447.	2.6	53
46	Mesodermal Tbx1 is required for patterning the proximal mandible in mice. <i>Developmental Biology</i> , 2010, 344, 669-681.	0.9	52
47	Detection of an Atypical 22q11 Deletion That Has No Overlap with the DiGeorge Syndrome Critical Region. <i>American Journal of Human Genetics</i> , 1997, 60, 1544-1547.	2.6	52
48	Detection of an Atypical 22q11 Deletion That Has No Overlap with the DiGeorge Syndrome Critical Region. <i>American Journal of Human Genetics</i> , 1997, 60, 1544-1548.	2.6	51
49	Identification of Critical Regions and Candidate Genes for Cardiovascular Malformations and Cardiomyopathy Associated with Deletions of Chromosome 1p36. <i>PLoS ONE</i> , 2014, 9, e85600.	1.1	51
50	A Pedigree-Based Map of Recombination in the Domestic Dog Genome. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3517-3524.	0.8	51
51	Changes in the guanine nucleotide-binding proteins, Giand go, during differentiation of 3T3-L1 cells. <i>FEBS Letters</i> , 1986, 199, 103-106.	1.3	50
52	Der(22) Syndrome and Velo-Cardio-Facial Syndrome/DiGeorge Syndrome Share a 1.5-Mb Region of Overlap on Chromosome 22q11. <i>American Journal of Human Genetics</i> , 1999, 64, 747-758.	2.6	50
53	Mutations inGJB2,GJB6, and mitochondrial DNA are rare in African American and Caribbean Hispanic individuals with hearing impairment. <i>American Journal of Medical Genetics, Part A</i> , 2007, 143A, 830-838.	0.7	50
54	Refinement of causative genes in monosomy 1p36 through clinical and molecular cytogenetic characterization of small interstitial deletions. <i>American Journal of Medical Genetics, Part A</i> , 2010, 152A, 1951-1959.	0.7	50

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55	Frequent translocations occur between low copy repeats on chromosome 22q11.2 (LCR22s) and telomeric bands of partner chromosomes. <i>Human Molecular Genetics</i> , 2003, 12, 1823-1837.	1.4	49
56	Histone Modifier Genes Alter Conotruncal Heart Phenotypes in 22q11.2 Deletion Syndrome. <i>American Journal of Human Genetics</i> , 2015, 97, 869-877.	2.6	49
57	Genetic modifiers of the physical malformations in velo-cardio-facial syndrome/DiGeorge syndrome. <i>Developmental Disabilities Research Reviews</i> , 2008, 14, 19-25.	2.9	48
58	Genotype-phenotype correlation in interstitial 6q deletions: a report of 12 new cases. <i>Neurogenetics</i> , 2012, 13, 31-47.	0.7	48
59	Dissection of Tbx1 and Fgf interactions in mouse models of 22q11DS suggests functional redundancy. <i>Human Molecular Genetics</i> , 2006, 15, 3219-3228.	1.4	47
60	Canonical Wnt signaling modulates <i>Tbx1</i> , <i>Eya1</i> , and <i>Six1</i> expression, restricting neurogenesis in the otic vesicle. <i>Developmental Dynamics</i> , 2010, 239, 1708-1722.	0.8	47
61	Cooperative Function of Tbx1 and Brn4 in the Periotic Mesenchyme is Necessary for Cochlea Formation. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2008, 9, 33-43.	0.9	46
62	Tbx1 and Brn4 regulate retinoic acid metabolic genes during cochlear morphogenesis. <i>BMC Developmental Biology</i> , 2009, 9, 31.	2.1	46
63	A 200-kb region of human chromosome 22q11.2 confers antipsychotic-responsive behavioral abnormalities in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 19132-19137.	3.3	44
64	Rare copy number variants and congenital heart defects in the 22q11.2 deletion syndrome. <i>Human Genetics</i> , 2016, 135, 273-285.	1.8	43
65	Gene expression profile of trisomy 21 placentas: A potential approach for designing noninvasive techniques of prenatal diagnosis. <i>American Journal of Obstetrics and Gynecology</i> , 2002, 187, 457-462.	0.7	42
66	Complete Sequence of the 22q11.2 Allele in 1,053 Subjects with 22q11.2 Deletion Syndrome Reveals Modifiers of Conotruncal Heart Defects. <i>American Journal of Human Genetics</i> , 2020, 106, 26-40.	2.6	42
67	The 22q11 low copy repeats are characterized by unprecedented size and structural variability. <i>Genome Research</i> , 2019, 29, 1389-1401.	2.4	39
68	REGULATION OF GROWTH AND DIFFERENTIATION OF EPITHELIAL CELLS BY HORMONES, GROWTH FACTORS, AND SUBSTRATES OF EXTRACELLULAR MATRIX. <i>Annals of the New York Academy of Sciences</i> , 1981, 372, 354-370.	1.8	36
69	New cases and refinement of the critical region in the 1q41q42 microdeletion syndrome. <i>European Journal of Medical Genetics</i> , 2011, 54, 42-49.	0.7	36
70	Mammalian TBX1 Preferentially Binds and Regulates Downstream Targets Via a Tandem T-site Repeat. <i>PLoS ONE</i> , 2014, 9, e95151.	1.1	33
71	Variance of IQ is partially dependent on deletion type among 1,427 22q11.2 deletion syndrome subjects. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 2172-2181.	0.7	33
72	Hominoid lineage specific amplification of low-copy repeats on 22q11.2 (LCR22s) associated with velo-cardio-facial/digeorge syndrome. <i>Human Molecular Genetics</i> , 2007, 16, 2560-2571.	1.4	32

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73	Tbx1 is required autonomously for cell survival and fate in the pharyngeal core mesoderm to form the muscles of mastication. <i>Human Molecular Genetics</i> , 2014, 23, 4215-4231.	1.4	31
74	A Novel C-Terminal CIB2 (Calcium and Integrin Binding Protein 2) Mutation Associated with Non-Syndromic Hearing Loss in a Hispanic Family. <i>PLoS ONE</i> , 2015, 10, e0133082.	1.1	31
75	Single cell multi-omic analysis identifies a Tbx1-dependent multilineage primed population in murine cardiopharyngeal mesoderm. <i>Nature Communications</i> , 2021, 12, 6645.	5.8	31
76	Traffic of genetic information between segmental duplications flanking the typical 22q11.2 deletion in velo-cardio-facial syndrome/DiGeorge syndrome. <i>Genome Research</i> , 2005, 15, 1487-1495.	2.4	30
77	AT-rich repeats associated with chromosome 22q11.2 rearrangement disorders shape human genome architecture on Yq12. <i>Genome Research</i> , 2007, 17, 451-460.	2.4	30
78	Agnathia-otocephaly complex: A case report and examination of the OTX2 and PRRX1 genes. <i>Gene</i> , 2012, 494, 124-129.	1.0	28
79	Association between autism spectrum disorder in individuals with velocardiofacial (22q11.2 deletion) syndrome and PRODH and COMT genotypes. <i>Psychiatric Genetics</i> , 2014, 24, 269-272.	0.6	28
80	The Role of mGluR Copy Number Variation in Genetic and Environmental Forms of Syndromic Autism Spectrum Disorder. <i>Scientific Reports</i> , 2016, 6, 19372.	1.6	28
81	Incontinentia pigmenti in a newborn male infant with DNA confirmation. , 1998, 75, 159-163.		27
82	Reduced dosage of $\beta$ -catenin provides significant rescue of cardiac outflow tract anomalies in a Tbx1 conditional null mouse model of 22q11.2 deletion syndrome. <i>PLoS Genetics</i> , 2017, 13, e1006687.	1.5	27
83	Tbx1 and Foxi3 genetically interact in the pharyngeal pouch endoderm in a mouse model for 22q11.2 deletion syndrome. <i>PLoS Genetics</i> , 2019, 15, e1008301.	1.5	27
84	Characterization of the past and current duplication activities in the human 22q11.2 region. <i>BMC Genomics</i> , 2011, 12, 71.	1.2	25
85	Characterization and Mutation Analysis of Goosecoid-like (GSCL), a Homeodomain-Containing Gene That Maps to the Critical Region for VCFS/DGS on 22q11. <i>Genomics</i> , 1997, 46, 364-372.	1.3	24
86	Endoderm-specific deletion of <i>Tbx1</i> reveals an FGF-independent role for Tbx1 in pharyngeal apparatus morphogenesis. <i>Developmental Dynamics</i> , 2014, 243, 1143-1151.	0.8	24
87	Isolation and Characterization of a Human Gene Containing a Nuclear Localization Signal from the Critical Region for Velo-Cardio-Facial Syndrome on 22q11. <i>Genomics</i> , 1998, 53, 146-154.	1.3	22
88	Spectrum of elastin sequence variants and cardiovascular phenotypes in 49 patients with Williams-Beuren syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2013, 161, 527-533.	0.7	22
89	Genome-Wide Association Study to Find Modifiers for Tetralogy of Fallot in the 22q11.2 Deletion Syndrome Identifies Variants in the <i>GPR98</i> Locus on 5q14.3. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	22
90	Deletion size analysis of 1680 22q11.2DS subjects identifies a new recombination hotspot on chromosome 22q11.2. <i>Human Molecular Genetics</i> , 2018, 27, 1150-1163.	1.4	22

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91	Mutational analysis of HOXA2 and SIX2 in a Bronx population with isolated microtia. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2010, 74, 878-882.	0.4	21
92	GJB2 mutation spectrum in 209 hearing impaired individuals of predominantly Caribbean Hispanic and African descent. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2010, 74, 611-618.	0.4	20
93	Overt cleft palate phenotype and <i>TBX1</i> genotype correlations in velo-cardio-facial/DiGeorge/22q11.2 deletion syndrome patients. <i>American Journal of Medical Genetics, Part A</i> , 2012, 158A, 2781-2787.	0.7	20
94	Variant discovery and breakpoint region prediction for studying the human 22q11.2 deletion using BAC clone and whole genome sequencing analysis. <i>Human Molecular Genetics</i> , 2016, 25, 3754-3767.	1.4	20
95	Optical mapping of the 22q11.2DS region reveals complex repeat structures and preferred locations for non-allelic homologous recombination (NAHR). <i>Scientific Reports</i> , 2020, 10, 12235.	1.6	20
96	Cleft palate, retrognathia and congenital heart disease in velo-cardio-facial syndrome: A phenotype correlation study. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2011, 75, 1167-1172.	0.4	18
97	Whole-Genome Sequencing and Integrative Genomic Analysis Approach on Two 22q11.2 Deletion Syndrome Family Trios for Genotype to Phenotype Correlations. <i>Human Mutation</i> , 2015, 36, 797-807.	1.1	16
98	Dysregulation of TBX1 dosage in the anterior heart field results in congenital heart disease resembling the 22q11.2 duplication syndrome. <i>Human Molecular Genetics</i> , 2018, 27, 1847-1857.	1.4	16
99	Use of polyestradiol phosphate and anti-17 $\beta$ estradiol antibodies for the localization of estrogen receptors in target tissues: A critique. <i>Cancer</i> , 1980, 46, 2872-2879.	2.0	15
100	Isolation and Characterization of a Novel Gene Containing WD40 Repeats from the Region Deleted in Velo-cardio-facial/ DiGeorge Syndrome on Chromosome 22q11. <i>Genomics</i> , 2001, 73, 264-271.	1.3	15
101	Development of a Targeted Multi-Disorder High-Throughput Sequencing Assay for the Effective Identification of Disease-Causing Variants. <i>PLoS ONE</i> , 2015, 10, e0133742.	1.1	15
102	Gene-based genome-wide association studies and meta-analyses of conotruncal heart defects. <i>PLoS ONE</i> , 2019, 14, e0219926.	1.1	15
103	Identification of putative retinoic acid target genes downstream of mesenchymal <i>Tbx1</i> during inner ear development. <i>Developmental Dynamics</i> , 2012, 241, 563-573.	0.8	14
104	Genetic analysis of nonalcoholic fatty liver disease within a Caribbean-Hispanic population. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2015, 3, 558-569.	0.6	14
105	A candidate gene approach to identify modifiers of the palatal phenotype in 22q11.2 deletion syndrome patients. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2013, 77, 123-127.	0.4	13
106	Expression of Cdcrl-1 (Pnut11), a gene frequently deleted in velo-cardio-facial syndrome/DiGeorge syndrome. <i>Mechanisms of Development</i> , 2000, 96, 121-124.	1.7	12
107	Conditional and constitutive expression of a Tbx1-GFP fusion protein in mice. <i>BMC Developmental Biology</i> , 2013, 13, 33.	2.1	12
108	A normative chart for cognitive development in a genetically selected population. <i>Neuropsychopharmacology</i> , 2022, 47, 1379-1386.	2.8	12

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109	Gene targeting in mammalian cells by homologous recombination. <i>Current Opinion in Biotechnology</i> , 1993, 4, 577-582.	3.3	11
110	Genetic dosage compensation in a family with velo-cardio-facial/DiGeorge/22q11.2 deletion syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 548-554.	0.7	10
111	Molecular characterization of an interstitial deletion of 1p31.3 in a patient with obesity and psychiatric illness and a review of the literature. , 2011, 155, 825-832.		10
112	Biallelic expression of <i>Tbx1</i> protects the embryo from developmental defects caused by increased receptor tyrosine kinase signaling. <i>Developmental Dynamics</i> , 2012, 241, 1310-1324.	0.8	9
113	LPA receptor activity is basal specific and coincident with early pregnancy and involution during mammary gland postnatal development. <i>Scientific Reports</i> , 2016, 6, 35810.	1.6	9
114	Gene-based analyses of the maternal genome implicate maternal effect genes as risk factors for conotruncal heart defects. <i>PLoS ONE</i> , 2020, 15, e0234357.	1.1	8
115	Genetic evaluation of American minority pediatric cochlear implant recipients. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2009, 73, 195-203.	0.4	7
116	<i>Tbx1</i> and <i>Jag1</i> act in concert to modulate the fate of neurosensory cells of the mouse otic vesicle. <i>Biology Open</i> , 2017, 6, 1472-1482.	0.6	7
117	Integrated rare variant-based risk gene prioritization in disease case-control sequencing studies. <i>PLoS Genetics</i> , 2017, 13, e1007142.	1.5	7
118	Atypical chromosome 22q11.2 deletions are complex rearrangements and have different mechanistic origins. <i>Human Molecular Genetics</i> , 2019, 28, 3724-3733.	1.4	7
119	Two Functional Copies of the <i>DGCR6</i> Gene Are Present on Human Chromosome 22q11 Due to a Duplication of an Ancestral Locus. <i>Genome Research</i> , 2001, 11, 208-217.	2.4	6
120	A Novel, Single Nucleotide Polymorphism-Based Assay to Detect 22q11 Deletions. <i>Genetic Testing and Molecular Biomarkers</i> , 2007, 11, 91-100.	1.7	5
121	Interstitial duplication of 22q13.2 in a girl with short stature, impaired speech and language, and dysmorphism. <i>Journal of Pediatric Genetics</i> , 2015, 01, 047-053.	0.3	5
122	NOTCH maintains developmental cardiac gene network through WNT5A. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 125, 98-105.	0.9	4
123	Copy number variations in individuals with conotruncal heart defects reveal some shared developmental pathways irrespective of 22q11.2 deletion status. <i>Birth Defects Research</i> , 2019, 111, 888-905.	0.8	3
124	The Prevalence of Ultrarapid Metabolizers of Codeine in a Diverse Urban Population. <i>Otolaryngology - Head and Neck Surgery</i> , 2019, 160, 420-425.	1.1	3
125	<i>Crk</i> and <i>Crkl</i> have shared functions in neural crest cells for cardiac outflow tract septation and vascular smooth muscle differentiation. <i>Human Molecular Genetics</i> , 2021, , .	1.4	3
126	Common Variation in Cytoskeletal Genes Is Associated with Conotruncal Heart Defects. <i>Genes</i> , 2021, 12, 655.	1.0	2



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127	Genome-Wide Association Studies of Conotruncal Heart Defects with Normally Related Great Vessels in the United States. <i>Genes</i> , 2021, 12, 1030.	1.0	1
128	A Tbx1-Six1/Eya1-Fgf8 genetic pathway controls mammalian cardiovascular and craniofacial morphogenesis. <i>Journal of Clinical Investigation</i> , 2011, 121, 2060-2060.	3.9	0
129	Chromosome 22q11.2 Rearrangement Disorders. , 2006, , 193-206.		0
130	Title is missing!. , 2020, 15, e0234357.		0
131	Title is missing!. , 2020, 15, e0234357.		0
132	Title is missing!. , 2020, 15, e0234357.		0
133	Title is missing!. , 2020, 15, e0234357.		0