Paal S Andersen

List of Publications by Year
in descending order

176	9,259	38742 50	49909 87
papers	citations	h-index	g-index

182	182	182	13713
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Hand eczema and temporal variation of Staphylococcus aureus clonal complexes: A prospective observational study. Journal of the American Academy of Dermatology, 2022, 87, 1006-1013.	1.2	4
2	Temporal and Spatial Variation of the Skin-Associated Bacteria from Healthy Participants and Atopic Dermatitis Patients. MSphere, 2022, 7, e0091721.	2.9	5
3	Colonization with Staphylococcus aureus in healthcare workers: consequences of hand eczema. British Journal of Dermatology, 2022, 187, 609-611.	1.5	1
4	Staphylococcal Communities on Skin Are Associated with Atopic Dermatitis and Disease Severity. Microorganisms, 2021, 9, 432.	3.6	25
5	Large-Scale Staphylococcus aureus Foodborne Disease Poisoning Outbreak among Primary School Children. Microbiology Research, 2021, 12, 43-52.	1.9	25
6	Changes in Skin and Nasal Microbiome and Staphylococcal Species Following Treatment of Atopic Dermatitis with Dupilumab. Microorganisms, 2021, 9, 1487.	3.6	29
7	Skin Microbiome in Patients with Hand Eczema and Healthy Controls: A Three-week Prospective Study. Acta Dermato-Venereologica, 2021, 102, adv00633.	1.3	3
8	eHealth: Disease activity measures are related to the faecal gut microbiota in adult patients with ulcerative colitis. Scandinavian Journal of Gastroenterology, 2020, 55, 1291-1300.	1.5	5
9	Colonization with <scp>Staphylococcus aureus</scp> in patients with hand eczema: Prevalence and association with severity, atopic dermatitis, subtype and nasal colonization. Contact Dermatitis, 2020, 83, 442-449.	1.4	13
10	Alteration of Bacterial Communities in Anterior Nares and Skin Sites of Patients Undergoing Arthroplasty Surgery: Analysis by 16S rRNA and Staphylococcal-Specific tuf Gene Sequencing. Microorganisms, 2020, 8, 1977.	3.6	10
11	Complete genome of a methicillin-resistant Staphylococcus vitulinus from Danish ground beef meat carrying a mecA2 resistance gene and a novel ccr allotype. Journal of Global Antimicrobial Resistance, 2020, 23, 221-223.	2.2	0
12	Crossâ€sectional study identifies lower risk of Staphylococcus aureus nasal colonization in Danish blood donors with hidradenitis suppurativa symptoms. British Journal of Dermatology, 2020, 183, 387-389.	1.5	5
13	Genomic analyses of Staphylococcus aureus clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. Microbial Genomics, 2020, 6, .	2.0	6
14	High persister cell formation by clinical Staphylococcus aureus strains belonging to clonal complex 30. Microbiology (United Kingdom), 2020, 166, 654-658.	1.8	5
15	Temporal variation of Staphylococcus aureus clonal complexes in atopic dermatitis: a followâ€up study. British Journal of Dermatology, 2019, 180, 181-186.	1.5	17
16	Cohort description: The Danish Blood Donor Staphylococcus aureus Carriage Study . Clinical Epidemiology, 2019, Volume 11, 885-900.	3.0	17
17	Antimicrobial Resistance and Virulence Gene Profiles of Methicillin-Resistant and -Susceptible Staphylococcus aureus From Food Products in Denmark. Frontiers in Microbiology, 2019, 10, 2681.	3.5	33
18	Effect of Co-inhabiting Coagulase Negative Staphylococci on S. aureus agr Quorum Sensing, Host Factor Binding, and Biofilm Formation. Frontiers in Microbiology, 2019, 10, 2212.	3.5	27

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19	Prevalence of infective endocarditis in patients with positive blood cultures: a Danish nationwide study. European Heart Journal, 2019, 40, 3237-3244.	2.2	40
20	Association of Disease Severity With Skin Microbiome and Filaggrin Gene Mutations in Adult Atopic Dermatitis. JAMA Dermatology, 2018, 154, 293.	4.1	108
21	Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression. FEMS Microbiology Letters, 2018, 365, .	1.8	11
22	Genomic analysis reveals different mechanisms of fusidic acid resistance in Staphylococcus aureus from Danish atopic dermatitis patients. Journal of Antimicrobial Chemotherapy, 2018, 73, 856-861.	3.0	27
23	Demographic fluctuation of community-acquired antibiotic-resistant Staphylococcus aureus lineages: potential role of flimsy antibiotic exposure. ISME Journal, 2018, 12, 1879-1894.	9.8	11
24	Confirmation of an IRAK3 polymorphism as a genetic marker predicting response to anti-TNF treatment in rheumatoid arthritis. Pharmacogenomics Journal, 2018, 18, 81-86.	2.0	26
25	Genetically determined high activity of IL-12 and IL-18 in ulcerative colitis and TLR5 in Crohns disease were associated with non-response to anti-TNF therapy. Pharmacogenomics Journal, 2018, 18, 87-97.	2.0	42
26	Associations between functional polymorphisms and response to biological treatment in Danish patients with psoriasis. Pharmacogenomics Journal, 2018, 18, 494-500.	2.0	51
27	Identification of a PVL-negative SCC mec -IVa sublineage of the methicillin-resistant Staphylococcus aureus CC80 lineage: understanding the clonal origin of CA-MRSA. Clinical Microbiology and Infection, 2018, 24, 273-278.	6.0	15
28	Dissemination and Characteristics of a Novel Plasmid-Encoded Carbapenem-Hydrolyzing Class D Î²-Lactamase, OXA-436, Found in Isolates from Four Patients at Six Different Hospitals in Denmark. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	24
29	The Skin Microbiome in Atopic Dermatitisâ€"a Potential Treatment Target?. Current Dermatology Reports, 2018, 7, 199-208.	2.1	3
30	Human genetic variation in GLS2 is associated with development of complicated Staphylococcus aureus bacteremia. PLoS Genetics, 2018, 14, e1007667.	3.5	16
31	Staphylococcus aureus Bacteremia in Children Aged 5-18 Yearsâ€"Risk Factors in the New Millennium. Journal of Pediatrics, 2018, 203, 108-115.e3.	1.8	12
32	Genetically determined high activities of the TNF-alpha, IL23/IL17, and NFkB pathways were associated with increased risk of ankylosing spondylitis. BMC Medical Genetics, 2018, 19, 165.	2.1	44
33	Human Genetic Susceptibility to Native Valve Staphylococcus aureus Endocarditis in Patients With S. aureus Bacteremia: Genome-Wide Association Study. Frontiers in Microbiology, 2018, 9, 640.	3.5	14
34	Genetic polymorphisms associated with psoriasis and development of psoriatic arthritis in patients with psoriasis. PLoS ONE, 2018, 13, e0192010.	2.5	34
35	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	3.9	75
36	Staphylococcus aureusCC395 harbours a novel composite staphylococcal cassette chromosomemecelement. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw544.	3.0	16

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37	Spread of avian pathogenic Escherichia coli ST117 O78:H4 in Nordic broiler production. BMC Genomics, 2017, 18, 13.	2.8	80
38	Methicillin-resistant and -susceptible Staphylococcus aureus from retail meat in Denmark. International Journal of Food Microbiology, 2017, 249, 72-76.	4.7	83
39	A universal primer-independent next-generation sequencing approach for investigations of norovirus outbreaks and novel variants. Scientific Reports, 2017, 7, 813.	3.3	19
40	Staphylococcus aureus colonization in atopic eczema and its association with filaggrin gene mutations. British Journal of Dermatology, 2017, 177, 1394-1400.	1.5	101
41	Whole-genome comparison of urinary pathogenic Escherichia coli and faecal isolates of UTI patients and healthy controls. International Journal of Medical Microbiology, 2017, 307, 497-507.	3.6	57
42	Genomic characterization, phylogenetic analysis, and identification of virulence factors in Aerococcus sanguinicola and Aerococcus urinae strains isolated from infection episodes. Microbial Pathogenesis, 2017, 112, 327-340.	2.9	14
43	Commercial Biocides Induce Transfer of Prophage Î¦13 from Human Strains of Staphylococcus aureus to Livestock CC398. Frontiers in Microbiology, 2017, 8, 2418.	3.5	23
44	Nasal and pharyngeal carriage of methicillin-resistant Staphylococcus sciuri among hospitalised patients and healthcare workers in a Serbian university hospital. PLoS ONE, 2017, 12, e0185181.	2.5	11
45	Genome analysis of Clostridium perfringens isolates from healthy and necrotic enteritis infected chickens and turkeys. BMC Research Notes, 2017, 10, 270.	1.4	21
46	A broad range quorum sensing inhibitor working through sRNA inhibition. Scientific Reports, 2017, 7, 9857.	3.3	60
47	The associations between socioeconomic status and risk of Staphylococcus aureus bacteremia and subsequent endocarditis â€“ a Danish nationwide cohort study. BMC Infectious Diseases, 2017, 17, 589.	2.9	26
48	Genomic relatedness of Staphylococcus pettenkoferi isolates of different origins. Journal of Medical Microbiology, 2017, 66, 601-608.	1.8	10
49	Whole-genome sequencing of bloodstream Staphylococcus aureus isolates does not distinguish bacteraemia from endocarditis. Microbial Genomics, 2017, 3, .	2.0	21
50	Draft Genome Sequences of Two Avian Pathogenic Escherichia coli Strains of Clinical Importance, E44 and E51. Genome Announcements, 2016, 4, .	0.8	7
51	Cross-Talk between Staphylococcus aureus and Other Staphylococcal Species via the agr Quorum Sensing System. Frontiers in Microbiology, 2016, 7, 1733.	3.5	67
52	Familial Clustering ofStaphylococcus aureusBacteremia in First-Degree Relatives. Annals of Internal Medicine, 2016, 165, 390.	3.9	15
53	Molecular characterisation of the clonal emergence of high-level ciprofloxacin-monoresistant Haemophilus influenzae in the Region of Southern Denmark. Journal of Global Antimicrobial Resistance, 2016, 5, 67-70.	2.2	11
54	Copy number variation of scavenger-receptor cysteine-rich domains within DMBT1 and Crohnâ€™s disease. European Journal of Human Genetics, 2016, 24, 1294-1300.	2.8	10

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55	Description and characterization of a penicillin-resistant Streptococcus dysgalactiae subsp . equisimilis clone isolated from blood in three epidemiologically linked patients. Journal of Antimicrobial Chemotherapy, 2016, 71, 3376-3380.	3.0	30
56	Evidence for Human Adaptation and Foodborne Transmission of Livestock-Associated Methicillin-ResistantStaphylococcus aureus: Table 1.. Clinical Infectious Diseases, 2016, 63, 1349-1352.	5.8	89
57	In vivo expression of antimicrobial peptides in atopic dermatitis. Experimental Dermatology, 2016, 25, 3-9.	2.9	37
58	Use of WGS data for investigation of a long-term NDM-1-producingCitrobacter freundiioutbreak and secondaryin vivospread ofblaNDM-1toEscherichia coli,Klebsiella pneumoniaeandKlebsiella oxytoca. Journal of Antimicrobial Chemotherapy, 2016, 71, 3117-3124.	3.0	44
59	Vancomycin gene selection in the microbiome of urbanRattus norvegicusfrom hospital environment. Evolution, Medicine and Public Health, 2016, 2016, 219-226.	2.5	9
60	Methicillin-ResistantStaphylococcus aureusCC398 in Humans and Pigs in Norway: A â€œOne Healthâ€•Perspective on Introduction and Transmission. Clinical Infectious Diseases, 2016, 63, 1431-1438.	5.8	86
61	Adaptation of Escherichia coli traversing from the faecal environment to the urinary tract. International Journal of Medical Microbiology, 2016, 306, 595-603.	3.6	16
62	Meticillin-resistant Staphylococcus aureus CC398 is an increasing cause of disease in people with no livestock contact in Denmark, 1999 to 2011. Eurosurveillance, 2015, 20, .	7.0	130
63	Staphylococcus aureus and the ecology of the nasal microbiome. Science Advances, 2015, 1, e1400216.	10.3	189
64	Investigation of a possible outbreak of NDM-5-producing ST16 Klebsiella pneumoniae among patients in Denmark with no history of recent travel using whole-genome sequencing. Journal of Global Antimicrobial Resistance, 2015, 3, 219-221.	2.2	25
65	Investigation of a possible outbreak of carbapenem-resistant Acinetobacter baumannii in Odense, Denmark using PFGE, MLST and whole-genome-based SNPs. Journal of Antimicrobial Chemotherapy, 2015, 70, 1965-1968.	3.0	54
66	Mapping the Evolution of Hypervirulent Klebsiella pneumoniae. MBio, 2015, 6, e00630.	4.1	270
67	Echocardiographic evaluation of pre-diagnostic development in young relatives genetically predisposed to hypertrophic cardiomyopathy. International Journal of Cardiovascular Imaging, 2015, 31, 1511-1518.	1.5	6
68	Surface Glycopolymers Are Crucial for In Vitro Anti-Wall Teichoic Acid IgG-Mediated Complement Activation and Opsonophagocytosis of Staphylococcus aureus. Infection and Immunity, 2015, 83, 4247-4255.	2.2	29
69	Non-toxigenic tox gene-bearing Corynebacterium ulcerans in a traumatic ulcer from a human case and his asymptomatic dog. Microbes and Infection, 2015, 17, 717-719.	1.9	18
70	Use of whole-genome sequencing for detection of the spread of VIM-4-producing Escherichia coli between two patients in Denmark. International Journal of Antimicrobial Agents, 2015, 45, 327-329.	2.5	2
71	Characterisation of an IMP-7-producing ST357 Pseudomonas aeruginosa isolate detected in Denmark using whole genome sequencing. International Journal of Antimicrobial Agents, 2015, 45, 200-201.	2.5	11
72	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of Staphylococcus aureus. PLoS ONE, 2015, 10, e0130955.	2.5	40

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73	Genetic Variations in Pattern Recognition Receptor Loci Are Associated with Anti-TNF Response in Patients with Rheumatoid Arthritis. PLoS ONE, 2015, 10, e0139781.	2.5	34
74	Polymorphisms in the Toll-Like Receptor and the IL-23/IL-17 Pathways Were Associated with Susceptibility to Inflammatory Bowel Disease in a Danish Cohort. PLoS ONE, 2015, 10, e0145302.	2.5	47
75	Effectiveness of anti-tumour necrosis factor-Î± therapy in Danish patients with inflammatory bowel diseases. Danish Medical Journal, 2015, 62, .	0.5	5
76	Polymorphisms in the Inflammatory Pathway Genes TLR2, TLR4, TLR9, LY96, NFKBIA, NFKB1, TNFA, TNFRSF1A, IL6R, IL10, IL23R, PTPN22, and PPARG Are Associated with Susceptibility of Inflammatory Bowel Disease in a Danish Cohort. PLoS ONE, 2014, 9, e98815.	2.5	102
77	Anti-TNF Treatment Response in Rheumatoid Arthritis Patients Is Associated with Genetic Variation in the NLRP3-Inflammasome. PLoS ONE, 2014, 9, e100361.	2.5	55
78	Associations between functional polymorphisms in the NFÎºB signaling pathway and response to anti-TNF treatment in Danish patients with inflammatory bowel disease. Pharmacogenomics Journal, 2014, 14, 526-534.	2.0	118
79	Origin and Evolution of European Community-Acquired Methicillin-Resistant Staphylococcus aureus. MBio, 2014, 5, e01044-14.	4.1	112
80	Role of Urinary Cathelicidin LL-37 and Human Î²-Defensin 1 in Uncomplicated Escherichia coli Urinary Tract Infections. Infection and Immunity, 2014, 82, 1572-1578.	2.2	70
81	Genetic susceptibility and genotypeâ€“phenotype association in 588 Danish children with inflammatory bowel disease. Journal of Crohn's and Colitis, 2014, 8, 678-685.	1.3	26
82	Selection of unique Escherichia coli clones by random amplified polymorphic DNA (RAPD): Evaluation by whole genome sequencing. Journal of Microbiological Methods, 2014, 103, 101-103.	1.6	20
83	Risk factors for Staphylococcus aureus nasal colonization in Danish middle-aged and elderly twins. European Journal of Clinical Microbiology and Infectious Diseases, 2013, 32, 1321-1326.	2.9	25
84	High-Quality and -Quantity DNA Extraction from Frozen Archival Blood Clots for Genotyping of Single-Nucleotide Polymorphisms. Genetic Testing and Molecular Biomarkers, 2013, 17, 501-503.	0.7	18
85	Genome Sequence of Staphylococcus aureus Strain CA-347, a USA600 Methicillin-Resistant Isolate. Genome Announcements, 2013, 1, .	0.8	40
86	The Epidemic of Extended-Spectrum-Î²-Lactamase-Producing Escherichia coli ST131 Is Driven by a Single Highly Pathogenic Subclone, H 30-Rx. MBio, 2013, 4, e00377-13.	4.1	380
87	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing H 30-Rx Subclone of Escherichia coli ST131. Genome Announcements, 2013, 1, .	0.8	42
88	Penetrance of Hypertrophic Cardiomyopathy in Children and Adolescents. Circulation, 2013, 127, 48-54.	1.6	121
89	Human Î²-defensin-2 as a marker for disease severity and skin barrier properties in atopic dermatitis. British Journal of Dermatology, 2013, 169, 587-593.	1.5	44
90	Rapid Differentiation between Livestock-Associated and Livestock-Independent Staphylococcus aureus CC398 Clades. PLoS ONE, 2013, 8, e79645.	2.5	78

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91	Genome Analysis of Staphylococcus aureus ST291, a Double Locus Variant of ST398, Reveals a Distinct Genetic Lineage. PLoS ONE, 2013, 8, e63008.	2.5	18
92	Influence of Host Genetics and Environment on Nasal Carriage of Staphylococcus aureus in Danish Middle-Aged and Elderly Twins. Journal of Infectious Diseases, 2012, 206, 1178-1184.	4.0	41
93	Cardiac Myosin Binding Protein-C Mutations in Families With Hypertrophic Cardiomyopathy. Circulation: Cardiovascular Genetics, 2012, 5, 156-166.	5.1	121
94	Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. MBio, 2012, 3, .	4.1	638
95	Effects of a 17q21 chromosome gene variant, tobacco smoke and furred pets on infant wheeze. Genes and Immunity, 2012, 13, 94-97.	4.1	28
96	A Novel Myosin Essential Light Chain Mutation Causes Hypertrophic Cardiomyopathy with Late Onset and Low Expressivity. Biochemistry Research International, 2012, 2012, 1-6.	3.3	27
97	Genome Sequence of Staphylococcus aureus Strain 11819-97, an ST80-IV European Community-Acquired Methicillin-Resistant Isolate. Journal of Bacteriology, 2012, 194, 1625-1626.	2.2	31
98	Rapid detection, differentiation and typing of methicillin-resistant Staphylococcus aureus harbouring either mecA or the new mecA homologue mecALGA251. Clinical Microbiology and Infection, 2012, 18, 395-400.	6.0	322
99	Genetic Variability in Beta-Defensins Is Not Associated with Susceptibility to Staphylococcus aureus Bacteremia. PLoS ONE, 2012, 7, e32315.	2.5	8
100	Screening of congenital heart disease patients using multiplex ligationâ€dependent probe amplification: Early diagnosis of syndromic patients. American Journal of Medical Genetics, Part A, 2012, 158A, 720-725.	1.2	27
101	Prevalence of infective endocarditis in patients with Staphylococcus aureus bacteraemia: the value of screening with echocardiography. European Journal of Echocardiography, 2011, 12, 414-420.	2.3	138
102	Human Î²-defensin 3 (DEFB103) and its influence on Staphylococcus aureus nasal carriage. International Journal of Infectious Diseases, 2011, 15, e388-e394.	3.3	16
103	Genome wide peripheral blood leukocyte DNA methylation microarrays failed to identify associations with Inflammatory Bowel Diseases. Inflammatory Bowel Diseases, 2011, 17, S65.	1.9	0
104	Alpha-Defensin DEFA1A3 Gene Copy Number Elevation in Danish Crohnâ€™s Disease Patients. Digestive Diseases and Sciences, 2011, 56, 3517-3524.	2.3	21
105	The KCNE genes in hypertrophic cardiomyopathy: a candidate gene study. Journal of Negative Results in BioMedicine, 2011, 10, 12.	1.4	9
106	Determination of Beta-Defensin Genomic Copy Number in Different Populations: A Comparison of Three Methods. PLoS ONE, 2011, 6, e16768.	2.5	39
107	Infliximab dependency is related to decreased surgical rates in adult Crohn's disease patients. European Journal of Gastroenterology and Hepatology, 2010, 22, 1196-1203.	1.6	12
108	CACNA1C (rs1006737) is associated with schizophrenia. Molecular Psychiatry, 2010, 15, 119-121.	7.9	167

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109	Cloning and Occurrence of czrC , a Gene Conferring Cadmium and Zinc Resistance in Methicillin-Resistant Staphylococcus aureus CC398 Isolates. Antimicrobial Agents and Chemotherapy, 2010, 54, 3605-3608.	3.2	132
110	HLA-A alleles and infectious mononucleosis suggest a critical role for cytotoxic T-cell response in EBV-related Hodgkin lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6400-6405.	7.1	102
111	Detecting 22q11.2 Deletions by Use of Multiplex Ligation-Dependent Probe Amplification on DNA from Neonatal Dried Blood Spot Samples. Journal of Molecular Diagnostics, 2010, 12, 147-151.	2.8	34
112	Fabry disease mimicking hypertrophic cardiomyopathy: genetic screening needed for establishing the diagnosis in women. European Journal of Heart Failure, 2010, 12, 535-540.	7.1	75
113	Associations between COX-2 polymorphisms, blood cholesterol and risk of acute coronary syndrome. Atherosclerosis, 2010, 209, 155-162.	0.8	24
114	Echocardiographic Strain Imaging to Assess Early and Late Consequences of Sarcomere Mutations in Hypertrophic Cardiomyopathy. Circulation: Cardiovascular Genetics, 2009, 2, 314-321.	5.1	140
115	Diagnostic yield, interpretation, and clinical utility of mutation screening of sarcomere encoding genes in Danish hypertrophic cardiomyopathy patients and relatives. Human Mutation, 2009, 30, 363-370.	2.5	110
116	Sharing data between LSDBs and central repositories. Human Mutation, 2009, 30, 493-495.	2.5	18
117	PPARÎ³ Pro12Ala polymorphism and risk of acute coronary syndrome in a prospective study of Danes. BMC Medical Genetics, 2009, 10, 52.	2.1	25
118	Infliximab dependency in children with Crohnâ€™s disease. Alimentary Pharmacology and Therapeutics, 2009, 29, 792-799.	3.7	21
119	The role of sarcomere gene mutations in patients with idiopathic dilated cardiomyopathy. European Journal of Human Genetics, 2009, 17, 1241-1249.	2.8	79
120	Polymorphisms in inflammation genes, tobacco smoke and furred pets and wheeze in children. Pediatric Allergy and Immunology, 2009, 20, 614-623.	2.6	11
121	Micro-exons of the cardiac myosin binding protein C gene: flanking introns contain a disproportionately large number of hypertrophic cardiomyopathy mutations. European Journal of Human Genetics, 2008, 16, 1062-1069.	2.8	21
122	A 3.2â€‰Mb deletion on 18q12 in a patient with childhood autism and high-grade myopia. European Journal of Human Genetics, 2008, 16, 312-319.	2.8	15
123	Genetic and environmental factors as predictors of disease severity and extent at time of diagnosis in an inception cohort of inflammatory bowel disease, Copenhagen County and City 2003â€“2005. Journal of Crohn's and Colitis, 2008, 2, 162-169.	1.3	19
124	Multiplex Ligation-Dependent Probe Amplification Technique for Copy Number Analysis on Small Amounts of DNA Material. Analytical Chemistry, 2008, 80, 9363-9368.	6.5	27
125	Idiopathic restrictive cardiomyopathy in children is caused by mutations in cardiac sarcomere protein genes. Heart, 2008, 94, 1478-1484.	2.9	188
126	Whole Genome Amplification on DNA from Filter Paper Blood Spot Samples: An Evaluation of Selected Systems. Genetic Testing and Molecular Biomarkers, 2007, 11, 65-71.	1.7	31

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127	Mutations in the Kv1.5 channel gene KCNA5 in cardiac arrest patients. Biochemical and Biophysical Research Communications, 2007, 354, 776-782.	2.1	26
128	Single-strand conformation polymorphism analysis using capillary array electrophoresis for large-scale mutation detection. Nature Protocols, 2007, 2, 1458-1466.	12.0	20
129	Type 1 diabetes risk analysis on dried blood spot samples from population-based newborns: design and feasibility of an unselected caseâ€“control study. Paediatric and Perinatal Epidemiology, 2007, 21, 507-517.	1.7	34
130	Rapid tumourâ€like growth of giant filiform polyposis in a patient without a history of chronic bowel inflammation. Apmis, 2007, 115, 1306-1310.	2.0	13
131	Prospective study of interaction between alcohol, NSAID use and polymorphisms in genes involved in the inflammatory response in relation to risk of colorectal cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 624, 88-100.	1.0	70
132	Screening of 99 Danish Patients with Congenital Heart Disease for GATA4 Mutations. Genetic Testing and Molecular Biomarkers, 2006, 10, 277-280.	1.7	24
133	Chronic inflammation: importance of NOD2 and NALP3 in interleukin-1? generation. Clinical and Experimental Immunology, 2006, 147, 061127015327006-???.	2.6	832
134	Optimization of capillary array electrophoresis single-strand conformation polymorphism analysis for routine molecular diagnostics. Electrophoresis, 2006, 27, 3816-3822.	2.4	21
135	One third of Danish hypertrophic cardiomyopathy patients have mutations in MYH7 rod region. European Journal of Human Genetics, 2005, 13, 161-165.	2.8	42
136	Mutations in the HERG K+-ion channel: A novel link between long QT syndrome and sudden infant death syndrome. American Journal of Cardiology, 2005, 95, 433-434.	1.6	65
137	High-throughput single-strand conformation polymorphism analysis on a microfabricated capillary array electrophoresis device. Electrophoresis, 2005, 26, 1834-1842.	2.4	43
138	High-Throughput Mutation Screening. , 2005, , 71-100.		0
139	Potassium Must Be Considered in Congenital Long QT Syndrome. Cardiology, 2005, 5, 54-58.	0.3	5
140	Apo E in multiple sclerosis and optic neuritis: the Apo E-o4 allele is associated with progression of multiple sclerosis. Multiple Sclerosis Journal, 2005, 11, 511-515.	3.0	33
141	Disease Concordance, Zygosity, and NOD2/CARD15 Status: Follow-Up of a Population-Based Cohort of Danish Twins with Inflammatory Bowel Disease. American Journal of Gastroenterology, 2005, 100, 2486-2492.	0.4	89
142	Genetic and Environmental Factors in Monozygotic Twins with Crohnâ€™s Disease and Their First-Degree Relatives: A Case Report. Digestion, 2005, 71, 262-265.	2.3	7
143	NOD2/CARD15 Gene Polymorphisms in Crohnâ€™s Disease: A Genotype-Phenotype Analysis in Danish and Portuguese Patients and Controls. Digestion, 2005, 72, 156-163.	2.3	35
144	Clinical and genetic characteristics of Â cardiac actin gene mutations in hypertrophic cardiomyopathy. Journal of Medical Genetics, 2004, 41, 10e-10.	3.2	46

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145	Genetic and phenotypic characterization of mutations in myosin-binding protein C (MYBPC3) in 81 families with familial hypertrophic cardiomyopathy: total or partial haploinsufficiency. European Journal of Human Genetics, 2004, 12, 673-677.	2.8	64
146	Does KCNE5 play a role in long QT syndrome?. Clinica Chimica Acta, 2004, 345, 49-53.	1.1	10
147	High-throughput single strand conformation polymorphism mutation detection by automated capillary array electrophoresis: validation of the method. Human Mutation, 2003, 21, 116-122.	2.5	52
148	Capillary electrophoresis-based single strand DNA conformation analysis in high-throughput mutation screening. Human Mutation, 2003, 21, 455-465.	2.5	87
149	Singleâ€Strand Conformation Polymorphism Analysis Using Capillary Electrophoresis. Current Protocols in Human Genetics, 2003, 36, Unit 7.12.	3.5	2
150	Outcome of clinical versus genetic family screening in hypertrophic cardiomyopathy with focus on cardiac Î²-myosin gene mutations. Cardiovascular Research, 2003, 57, 347-357.	3.8	38
151	Recent developments in high-throughput mutation screening. Pharmacogenomics, 2001, 2, 387-399.	1.3	40
152	Predictors of coronary in-stent restenosis: importance of angiotensin-converting enzyme gene polymorphism and treatment with angiotensin-converting enzyme inhibitors. Journal of the American College of Cardiology, 2001, 38, 1434-1439.	2.8	42
153	Screening for Mutations and Polymorphisms in the Genes KCNH2 and KCNE2 Encoding the Cardiac HERG/MiRP1 Ion Channel: Implications for Acquired and Congenital Long Q-T Syndrome. Clinical Chemistry, 2001, 47, 1390-1395.	3.2	76
154	Automated mutation screening using dideoxy fingerprinting and capillary array electrophoresis. Human Mutation, 2001, 18, 451-457.	2.5	21
155	The val606met mutation in the cardiac beta-myosin heavy chain gene in patients with familial hypertrophic cardiomyopathy is associated with a high risk of sudden death at young age. American Journal of Cardiology, 2001, 87, 1315-1317.	1.6	30
156	A Response Calculus for Immobilized T Cell Receptor Ligands. Journal of Biological Chemistry, 2001, 276, 49125-49132.	3.4	25
157	Role of the T Cell Receptor Ligand Affinity in T Cell Activation by Bacterial Superantigens. Journal of Biological Chemistry, 2001, 276, 33452-33457.	3.4	58
158	Myosin light chain mutations in familial hypertrophic cardiomyopathy: phenotypic presentation and frequency in Danish and South African populations. Journal of Medical Genetics, 2001, 38, 43e-43.	3.2	70
159	Development and application of linkage analysis in genetic diagnosis of familial hypertrophic cardiomyopathy. Journal of Medical Genetics, 2001, 38, 193-198.	3.2	6
160	Long QT syndrome with a high mortality rate caused by a novel G572R missense mutation in KCNH2. Clinical Genetics, 2000, 57, 125-130.	2.0	12
161	A Novel Missense Mutation, Leu390Val, in the Cardiac ÃŸ-myosin Heavy Chain Associated with Pronounced Septal Hypertrophy in Two Families with Hypertrophic Cardiomyopathy. Scandinavian Cardiovascular Journal, 2000, 34, 558-563.	1.2	9
162	High Throughput Mutation Screening by Automated Capillary Electrophoresis. Combinatorial Chemistry and High Throughput Screening, 2000, 3, 393-409.	1.1	25

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