

Paal S Andersen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

175
papers

7,139
citations

46
h-index

77
g-index

182
ext. papers

8,271
ext. citations

4.9
avg, IF

5.43
L-index

#	Paper	IF	Citations
175	Temporal and Spatial Variation of the Skin-Associated Bacteria from Healthy Participants and Atopic Dermatitis Patients.. <i>MSphere</i> , 2022 , 7, e0091721	5	1
174	Skin Microbiome in Patients with Hand Eczema and Healthy Controls: A Three-week Prospective Study. <i>Acta Dermato-Venereologica</i> , 2021 ,	2.2	1
173	Hand eczema and temporal variation of Staphylococcus aureus clonal complexes: A prospective observational study. <i>Journal of the American Academy of Dermatology</i> , 2021 ,	4.5	1
172	Changes in Skin and Nasal Microbiome and Staphylococcal Species Following Treatment of Atopic Dermatitis with Dupilumab. <i>Microorganisms</i> , 2021 , 9,	4.9	3
171	Staphylococcal Communities on Skin Are Associated with Atopic Dermatitis and Disease Severity. <i>Microorganisms</i> , 2021 , 9,	4.9	10
170	Large-Scale Staphylococcus aureus Foodborne Disease Poisoning Outbreak among Primary School Children. <i>Microbiology Research</i> , 2021 , 12, 43-52	1	5
169	Complete genome of a methicillin-resistant Staphylococcus vitulinus from Danish ground beef meat carrying a mecA2 resistance gene and a novel ccr allotype. <i>Journal of Global Antimicrobial Resistance</i> , 2020 , 23, 221-223	3.4	
168	Cross-sectional study identifies lower risk of Staphylococcus aureus nasal colonization in Danish blood donors with hidradenitis suppurativa symptoms. <i>British Journal of Dermatology</i> , 2020 , 183, 387-389	4	2
167	Genomic analyses of clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
166	High persister cell formation by clinical strains belonging to clonal complex 30. <i>Microbiology (United Kingdom)</i> , 2020 , 166, 654-658	2.9	2
165	eHealth: Disease activity measures are related to the faecal gut microbiota in adult patients with ulcerative colitis. <i>Scandinavian Journal of Gastroenterology</i> , 2020 , 55, 1291-1300	2.4	1
164	Colonization with Staphylococcus aureus in patients with hand eczema: Prevalence and association with severity, atopic dermatitis, subtype and nasal colonization. <i>Contact Dermatitis</i> , 2020 , 83, 442-449	2.7	5
163	Alteration of Bacterial Communities in Anterior Nares and Skin Sites of Patients Undergoing Arthroplasty Surgery: Analysis by 16S rRNA and Staphylococcal-Specific Gene Sequencing. <i>Microorganisms</i> , 2020 , 8,	4.9	7
162	Effect of Co-inhabiting Coagulase Negative Staphylococci on Quorum Sensing, Host Factor Binding, and Biofilm Formation. <i>Frontiers in Microbiology</i> , 2019 , 10, 2212	5.7	15
161	Prevalence of infective endocarditis in patients with positive blood cultures: a Danish nationwide study. <i>European Heart Journal</i> , 2019 , 40, 3237-3244	9.5	16
160	Temporal variation of Staphylococcus aureus clonal complexes in atopic dermatitis: a follow-up study. <i>British Journal of Dermatology</i> , 2019 , 180, 181-186	4	12
159	Cohort description: The Danish Blood Donor Carriage Study. <i>Clinical Epidemiology</i> , 2019 , 11, 885-900	5.9	5

158	Antimicrobial Resistance and Virulence Gene Profiles of Methicillin-Resistant and -Susceptible From Food Products in Denmark. <i>Frontiers in Microbiology</i> , 2019 , 10, 2681	5.7	18
157	Association of Disease Severity With Skin Microbiome and Filaggrin Gene Mutations in Adult Atopic Dermatitis. <i>JAMA Dermatology</i> , 2018 , 154, 293-300	5.1	62
156	Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression. <i>FEMS Microbiology Letters</i> , 2018 , 365,	2.9	7
155	Genomic analysis reveals different mechanisms of fusidic acid resistance in <i>Staphylococcus aureus</i> from Danish atopic dermatitis patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 856-861	5.1	14
154	Demographic fluctuation of community-acquired antibiotic-resistant <i>Staphylococcus aureus</i> lineages: potential role of flimsy antibiotic exposure. <i>ISME Journal</i> , 2018 , 12, 1879-1894	11.9	6
153	Confirmation of an IRAK3 polymorphism as a genetic marker predicting response to anti-TNF treatment in rheumatoid arthritis. <i>Pharmacogenomics Journal</i> , 2018 , 18, 81-86	3.5	21
152	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. <i>Pharmacogenomics Journal</i> , 2018 , 18, 87-97	3.5	27
151	Associations between functional polymorphisms and response to biological treatment in Danish patients with psoriasis. <i>Pharmacogenomics Journal</i> , 2018 , 18, 494-500	3.5	27
150	Identification of a PVL-negative SCCmec-IVa sublineage of the methicillin-resistant <i>Staphylococcus aureus</i> CC80 lineage: understanding the clonal origin of CA-MRSA. <i>Clinical Microbiology and Infection</i> , 2018 , 24, 273-278	9.5	6
149	Dissemination and Characteristics of a Novel Plasmid-Encoded Carbapenem-Hydrolyzing Class D β -Lactamase, OXA-436, Found in Isolates From Four Patients at Six Different Hospitals in Denmark. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	18
148	Human Genetic Susceptibility to Native Valve Endocarditis in Patients With Bacteremia: Genome-Wide Association Study. <i>Frontiers in Microbiology</i> , 2018 , 9, 640	5.7	8
147	Genetic polymorphisms associated with psoriasis and development of psoriatic arthritis in patients with psoriasis. <i>PLoS ONE</i> , 2018 , 13, e0192010	3.7	23
146	The Skin Microbiome in Atopic Dermatitis – Potential Treatment Target?. <i>Current Dermatology Reports</i> , 2018 , 7, 199-208	1.5	2
145	Human genetic variation in GLS2 is associated with development of complicated <i>Staphylococcus aureus</i> bacteremia. <i>PLoS Genetics</i> , 2018 , 14, e1007667	6	9
144	<i>Staphylococcus aureus</i> Bacteremia in Children Aged 5-18 Years-Risk Factors in the New Millennium. <i>Journal of Pediatrics</i> , 2018 , 203, 108-115.e3	3.6	7
143	Genetically determined high activities of the TNF-alpha, IL23/IL17, and NFkB pathways were associated with increased risk of ankylosing spondylitis. <i>BMC Medical Genetics</i> , 2018 , 19, 165	2.1	31
142	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 908-913	9.7	59
141	<i>Staphylococcus aureus</i> CC395 harbours a novel composite staphylococcal cassette chromosome mec element. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1002-1005	5.1	12

140	Spread of avian pathogenic <i>Escherichia coli</i> ST117 O78:H4 in Nordic broiler production. <i>BMC Genomics</i> , 2017 , 18, 13	4.5	54
139	Methicillin-resistant and -susceptible <i>Staphylococcus aureus</i> from retail meat in Denmark. <i>International Journal of Food Microbiology</i> , 2017 , 249, 72-76	5.8	47
138	A universal primer-independent next-generation sequencing approach for investigations of norovirus outbreaks and novel variants. <i>Scientific Reports</i> , 2017 , 7, 813	4.9	14
137	<i>Staphylococcus aureus</i> colonization in atopic eczema and its association with filaggrin gene mutations. <i>British Journal of Dermatology</i> , 2017 , 177, 1394-1400	4	63
136	Whole-genome comparison of urinary pathogenic <i>Escherichia coli</i> and faecal isolates of UTI patients and healthy controls. <i>International Journal of Medical Microbiology</i> , 2017 , 307, 497-507	3.7	32
135	Genomic characterization, phylogenetic analysis, and identification of virulence factors in <i>Aerococcus sanguinicola</i> and <i>Aerococcus urinae</i> strains isolated from infection episodes. <i>Microbial Pathogenesis</i> , 2017 , 112, 327-340	3.8	9
134	Nasal and pharyngeal carriage of methicillin-resistant <i>Staphylococcus sciuri</i> among hospitalised patients and healthcare workers in a Serbian university hospital. <i>PLoS ONE</i> , 2017 , 12, e0185181	3.7	6
133	Genome analysis of <i>Clostridium perfringens</i> isolates from healthy and necrotic enteritis infected chickens and turkeys. <i>BMC Research Notes</i> , 2017 , 10, 270	2.3	13
132	A broad range quorum sensing inhibitor working through sRNA inhibition. <i>Scientific Reports</i> , 2017 , 7, 9857	4.9	45
131	The associations between socioeconomic status and risk of <i>Staphylococcus aureus</i> bacteremia and subsequent endocarditis - a Danish nationwide cohort study. <i>BMC Infectious Diseases</i> , 2017 , 17, 589	4	16
130	Commercial Biocides Induce Transfer of Prophage ϕ 3 from Human Strains of to Livestock CC398. <i>Frontiers in Microbiology</i> , 2017 , 8, 2418	5.7	15
129	Genomic relatedness of <i>Staphylococcus pettenkoferi</i> isolates of different origins. <i>Journal of Medical Microbiology</i> , 2017 , 66, 601-608	3.2	8
128	Whole-genome sequencing of bloodstream <i>Staphylococcus aureus</i> isolates does not distinguish bacteraemia from endocarditis. <i>Microbial Genomics</i> , 2017 , 3,	4.4	14
127	Use of WGS data for investigation of a long-term NDM-1-producing <i>Citrobacter freundii</i> outbreak and secondary in vivo spread of blaNDM-1 to <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Klebsiella oxytoca</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 3117-3124	5.1	37
126	Vancomycin gene selection in the microbiome of urban <i>Rattus norvegicus</i> from hospital environment. <i>Evolution, Medicine and Public Health</i> , 2016 , 2016, 219-26	3	7
125	Methicillin-Resistant <i>Staphylococcus aureus</i> CC398 in Humans and Pigs in Norway: A "One Health" Perspective on Introduction and Transmission. <i>Clinical Infectious Diseases</i> , 2016 , 63, 1431-1438	11.6	66
124	Adaptation of <i>Escherichia coli</i> traversing from the faecal environment to the urinary tract. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 595-603	3.7	11
123	Draft Genome Sequences of Two Avian Pathogenic <i>Escherichia coli</i> Strains of Clinical Importance, E44 and E51. <i>Genome Announcements</i> , 2016 , 4,		4

122	Cross-Talk between and Other Staphylococcal Species via the Quorum Sensing System. <i>Frontiers in Microbiology</i> , 2016 , 7, 1733	5.7	50
121	Familial Clustering of Staphylococcus aureus Bacteremia in First-Degree Relatives: A Danish Nationwide Cohort Study. <i>Annals of Internal Medicine</i> , 2016 , 165, 390-8	8	9
120	Molecular characterisation of the clonal emergence of high-level ciprofloxacin-mono-resistant Haemophilus influenzae in the Region of Southern Denmark. <i>Journal of Global Antimicrobial Resistance</i> , 2016 , 5, 67-70	3.4	7
119	Copy number variation of scavenger-receptor cysteine-rich domains within DMBT1 and Crohn's disease. <i>European Journal of Human Genetics</i> , 2016 , 24, 1294-300	5.3	6
118	Description and characterization of a penicillin-resistant Streptococcus dysgalactiae subsp. equisimilis clone isolated from blood in three epidemiologically linked patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 3376-3380	5.1	18
117	Evidence for Human Adaptation and Foodborne Transmission of Livestock-Associated Methicillin-Resistant Staphylococcus aureus. <i>Clinical Infectious Diseases</i> , 2016 , 63, 1349-1352	11.6	73
116	In vivo expression of antimicrobial peptides in atopic dermatitis. <i>Experimental Dermatology</i> , 2016 , 25, 3-9	4	22
115	Investigation of a possible outbreak of carbapenem-resistant Acinetobacter baumannii in Odense, Denmark using PFGE, MLST and whole-genome-based SNPs. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1965-8	5.1	42
114	Mapping the Evolution of Hypervirulent Klebsiella pneumoniae. <i>MBio</i> , 2015 , 6, e00630	7.8	194
113	Echocardiographic evaluation of pre-diagnostic development in young relatives genetically predisposed to hypertrophic cardiomyopathy. <i>International Journal of Cardiovascular Imaging</i> , 2015 , 31, 1511-8	2.5	4
112	Surface Glycopolymers Are Crucial for In Vitro Anti-Wall Teichoic Acid IgG-Mediated Complement Activation and Opsonophagocytosis of Staphylococcus aureus. <i>Infection and Immunity</i> , 2015 , 83, 4247-55	3.7	25
111	Non-toxicogenic tox gene-bearing Corynebacterium ulcerans in a traumatic ulcer from a human case and his asymptomatic dog. <i>Microbes and Infection</i> , 2015 , 17, 717-9	9.3	9
110	Use of whole-genome sequencing for detection of the spread of VIM-4-producing Escherichia coli between two patients in Denmark. <i>International Journal of Antimicrobial Agents</i> , 2015 , 45, 327-9	14.3	2
109	Characterisation of an IMP-7-producing ST357 Pseudomonas aeruginosa isolate detected in Denmark using whole genome sequencing. <i>International Journal of Antimicrobial Agents</i> , 2015 , 45, 200-1	14.3	11
108	Meticillin-resistant Staphylococcus aureus CC398 is an increasing cause of disease in people with no livestock contact in Denmark, 1999 to 2011. <i>Eurosurveillance</i> , 2015 , 20,	19.8	106
107	Staphylococcus aureus and the ecology of the nasal microbiome. <i>Science Advances</i> , 2015 , 1, e1400216	14.3	126
106	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. <i>Journal of Global Antimicrobial Resistance</i> , 2015 , 3, 219-221	3.4	23
105	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of Staphylococcus aureus. <i>PLoS ONE</i> , 2015 , 10, e0130955	3.7	27

104	Genetic Variations in Pattern Recognition Receptor Loci Are Associated with Anti-TNF Response in Patients with Rheumatoid Arthritis. <i>PLoS ONE</i> , 2015 , 10, e0139781	3.7	26
103	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. <i>PLoS ONE</i> , 2015 , 10, e0145302	3.7	43
102	Effectiveness of anti-tumour necrosis factor- α therapy in Danish patients with inflammatory bowel diseases. <i>Danish Medical Journal</i> , 2015 , 62,	3.8	4
101	Role of urinary cathelicidin LL-37 and human α -defensin 1 in uncomplicated Escherichia coli urinary tract infections. <i>Infection and Immunity</i> , 2014 , 82, 1572-8	3.7	54
100	Genetic susceptibility and genotype-phenotype association in 588 Danish children with inflammatory bowel disease. <i>Journal of Crohns and Colitis</i> , 2014 , 8, 678-85	1.5	19
99	Selection of unique Escherichia coli clones by random amplified polymorphic DNA (RAPD): Evaluation by whole genome sequencing. <i>Journal of Microbiological Methods</i> , 2014 , 103, 101-3	2.8	15
98	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. <i>PLoS ONE</i> , 2014 , 9, e98815	3.7	75
97	Anti-TNF treatment response in rheumatoid arthritis patients is associated with genetic variation in the NLRP3-inflammasome. <i>PLoS ONE</i> , 2014 , 9, e100361	3.7	43
96	Associations between functional polymorphisms in the NFB signaling pathway and response to anti-TNF treatment in Danish patients with inflammatory bowel disease. <i>Pharmacogenomics Journal</i> , 2014 , 14, 526-34	3.5	98
95	Origin and evolution of European community-acquired methicillin-resistant Staphylococcus aureus. <i>MBio</i> , 2014 , 5, e01044-14	7.8	75
94	Risk factors for Staphylococcus aureus nasal colonization in Danish middle-aged and elderly twins. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013 , 32, 1321-6	5.3	23
93	High-quality and -quantity DNA extraction from frozen archival blood clots for genotyping of single-nucleotide polymorphisms. <i>Genetic Testing and Molecular Biomarkers</i> , 2013 , 17, 501-3	1.6	16
92	Genome Sequence of Staphylococcus aureus Strain CA-347, a USA600 Methicillin-Resistant Isolate. <i>Genome Announcements</i> , 2013 , 1,		20
91	The epidemic of extended-spectrum- β -lactamase-producing Escherichia coli ST131 is driven by a single highly pathogenic subclone, H30-Rx. <i>MBio</i> , 2013 , 4, e00377-13	7.8	288
90	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing H30-Rx Subclone of Escherichia coli ST131. <i>Genome Announcements</i> , 2013 , 1,		38
89	Penetrance of hypertrophic cardiomyopathy in children and adolescents: a 12-year follow-up study of clinical screening and predictive genetic testing. <i>Circulation</i> , 2013 , 127, 48-54	16.7	90
88	Human α -defensin-2 as a marker for disease severity and skin barrier properties in atopic dermatitis. <i>British Journal of Dermatology</i> , 2013 , 169, 587-93	4	34
87	Rapid differentiation between livestock-associated and livestock-independent Staphylococcus aureus CC398 clades. <i>PLoS ONE</i> , 2013 , 8, e79645	3.7	71

86	Genome analysis of <i>Staphylococcus aureus</i> ST291, a double locus variant of ST398, reveals a distinct genetic lineage. <i>PLoS ONE</i> , 2013 , 8, e63008	3.7	15
85	Rapid detection, differentiation and typing of methicillin-resistant <i>Staphylococcus aureus</i> harbouring either <i>mecA</i> or the new <i>mecA</i> homologue <i>mecA(LGA251)</i> . <i>Clinical Microbiology and Infection</i> , 2012 , 18, 395-400	9.5	242
84	Genetic variability in beta-defensins is not associated with susceptibility to <i>Staphylococcus aureus</i> bacteremia. <i>PLoS ONE</i> , 2012 , 7, e32315	3.7	8
83	Screening of congenital heart disease patients using multiplex ligation-dependent probe amplification: early diagnosis of syndromic patients. <i>American Journal of Medical Genetics, Part A</i> , 2012 , 158A, 720-5	2.5	24
82	Influence of host genetics and environment on nasal carriage of <i>staphylococcus aureus</i> in danish middle-aged and elderly twins. <i>Journal of Infectious Diseases</i> , 2012 , 206, 1178-84	7	32
81	Cardiac myosin binding protein-C mutations in families with hypertrophic cardiomyopathy: disease expression in relation to age, gender, and long term outcome. <i>Circulation: Cardiovascular Genetics</i> , 2012 , 5, 156-66		94
80	<i>Staphylococcus aureus</i> CC398: host adaptation and emergence of methicillin resistance in livestock. <i>MBio</i> , 2012 , 3,	7.8	504
79	Effects of a 17q21 chromosome gene variant, tobacco smoke and furred pets on infant wheeze. <i>Genes and Immunity</i> , 2012 , 13, 94-7	4.4	22
78	A novel Myosin essential light chain mutation causes hypertrophic cardiomyopathy with late onset and low expressivity. <i>Biochemistry Research International</i> , 2012 , 2012, 685108	2.4	22
77	Genome sequence of <i>Staphylococcus aureus</i> strain 11819-97, an ST80-IV European community-acquired methicillin-resistant isolate. <i>Journal of Bacteriology</i> , 2012 , 194, 1625-6	3.5	28
76	Human β defensin 3 (DEFB103) and its influence on <i>Staphylococcus aureus</i> nasal carriage. <i>International Journal of Infectious Diseases</i> , 2011 , 15, e388-94	10.5	14
75	Genome wide peripheral blood leukocyte DNA methylation microarrays failed to identify associations with Inflammatory Bowel DiseasesP-176.. <i>Inflammatory Bowel Diseases</i> , 2011 , 17, S65	4.5	
74	Alpha-defensin DEFA1A3 gene copy number elevation in Danish Crohn's disease patients. <i>Digestive Diseases and Sciences</i> , 2011 , 56, 3517-24	4	19
73	The KCNE genes in hypertrophic cardiomyopathy: a candidate gene study. <i>Journal of Negative Results in BioMedicine</i> , 2011 , 10, 12		8
72	Prevalence of infective endocarditis in patients with <i>Staphylococcus aureus</i> bacteraemia: the value of screening with echocardiography. <i>European Journal of Echocardiography</i> , 2011 , 12, 414-20		108
71	Determination of beta-defensin genomic copy number in different populations: a comparison of three methods. <i>PLoS ONE</i> , 2011 , 6, e16768	3.7	37
70	CACNA1C (rs1006737) is associated with schizophrenia. <i>Molecular Psychiatry</i> , 2010 , 15, 119-21	15.1	147
69	Cloning and occurrence of <i>czrC</i> , a gene conferring cadmium and zinc resistance in methicillin-resistant <i>Staphylococcus aureus</i> CC398 isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 3605-8	5.9	102

68	HLA-A alleles and infectious mononucleosis suggest a critical role for cytotoxic T-cell response in EBV-related Hodgkin lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6400-5	11.5	88
67	Detecting 22q11.2 deletions by use of multiplex ligation-dependent probe amplification on DNA from neonatal dried blood spot samples. <i>Journal of Molecular Diagnostics</i> , 2010 , 12, 147-51	5.1	29
66	Fabry disease mimicking hypertrophic cardiomyopathy: genetic screening needed for establishing the diagnosis in women. <i>European Journal of Heart Failure</i> , 2010 , 12, 535-40	12.3	63
65	Associations between COX-2 polymorphisms, blood cholesterol and risk of acute coronary syndrome. <i>Atherosclerosis</i> , 2010 , 209, 155-62	3.1	23
64	Infliximab dependency is related to decreased surgical rates in adult Crohn's disease patients. <i>European Journal of Gastroenterology and Hepatology</i> , 2010 , 22, 1196-203	2.2	12
63	Echocardiographic strain imaging to assess early and late consequences of sarcomere mutations in hypertrophic cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2009 , 2, 314-21		111
62	Diagnostic yield, interpretation, and clinical utility of mutation screening of sarcomere encoding genes in Danish hypertrophic cardiomyopathy patients and relatives. <i>Human Mutation</i> , 2009 , 30, 363-70	4.7	94
61	Sharing data between LSDBs and central repositories. <i>Human Mutation</i> , 2009 , 30, 493-5	4.7	17
60	PPARgamma Pro12Ala polymorphism and risk of acute coronary syndrome in a prospective study of Danes. <i>BMC Medical Genetics</i> , 2009 , 10, 52	2.1	22
59	Infliximab dependency in children with Crohn's disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2009 , 29, 792-9	6.1	19
58	The role of sarcomere gene mutations in patients with idiopathic dilated cardiomyopathy. <i>European Journal of Human Genetics</i> , 2009 , 17, 1241-9	5.3	71
57	Polymorphisms in inflammation genes, tobacco smoke and furred pets and wheeze in children. <i>Pediatric Allergy and Immunology</i> , 2009 , 20, 614-23	4.2	10
56	Micro-exons of the cardiac myosin binding protein C gene: flanking introns contain a disproportionately large number of hypertrophic cardiomyopathy mutations. <i>European Journal of Human Genetics</i> , 2008 , 16, 1062-9	5.3	16
55	A 3.2 Mb deletion on 18q12 in a patient with childhood autism and high-grade myopia. <i>European Journal of Human Genetics</i> , 2008 , 16, 312-9	5.3	14
54	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 2003-2005. <i>Journal of Crohns and Colitis</i> , 2008 , 2, 162-9	1.5	15
53	Multiplex ligation-dependent probe amplification technique for copy number analysis on small amounts of DNA material. <i>Analytical Chemistry</i> , 2008 , 80, 9363-8	7.8	18
52	Idiopathic restrictive cardiomyopathy in children is caused by mutations in cardiac sarcomere protein genes. <i>Heart</i> , 2008 , 94, 1478-84	5.1	148
51	Single-strand conformation polymorphism analysis using capillary array electrophoresis for large-scale mutation detection. <i>Nature Protocols</i> , 2007 , 2, 1458-66	18.8	20

50	Type 1 diabetes risk analysis on dried blood spot samples from population-based newborns: design and feasibility of an unselected case-control study. <i>Paediatric and Perinatal Epidemiology</i> , 2007 , 21, 507-17	2.7	30
49	Rapid tumour-like growth of giant filiform polyposis in a patient without a history of chronic bowel inflammation. <i>Apmis</i> , 2007 , 115, 1306-10	3.4	10
48	Prospective study of interaction between alcohol, NSAID use and polymorphisms in genes involved in the inflammatory response in relation to risk of colorectal cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2007 , 624, 88-100	3.3	61
47	Whole genome amplification on DNA from filter paper blood spot samples: an evaluation of selected systems. <i>Genetic Testing and Molecular Biomarkers</i> , 2007 , 11, 65-71		30
46	Mutations in the Kv1.5 channel gene KCNA5 in cardiac arrest patients. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 354, 776-82	3.4	21
45	Chronic inflammation: importance of NOD2 and NALP3 in interleukin-1beta generation. <i>Clinical and Experimental Immunology</i> , 2007 , 147, 227-35	6.2	607
44	Optimization of capillary array electrophoresis single-strand conformation polymorphism analysis for routine molecular diagnostics. <i>Electrophoresis</i> , 2006 , 27, 3816-22	3.6	19
43	Screening of 99 Danish patients with congenital heart disease for GATA4 mutations. <i>Genetic Testing and Molecular Biomarkers</i> , 2006 , 10, 277-80		16
42	NOD2/CARD15 gene polymorphisms in Crohn's disease: a genotype-phenotype analysis in Danish and Portuguese patients and controls. <i>Digestion</i> , 2005 , 72, 156-63	3.6	33
41	One third of Danish hypertrophic cardiomyopathy patients with MYH7 mutations have mutations [corrected] in MYH7 rod region. <i>European Journal of Human Genetics</i> , 2005 , 13, 161-5	5.3	37
40	Mutations in the HERG K ⁺ -ion channel: a novel link between long QT syndrome and sudden infant death syndrome. <i>American Journal of Cardiology</i> , 2005 , 95, 433-4	3	58
39	High-throughput single-strand conformation polymorphism analysis on a microfabricated capillary array electrophoresis device. <i>Electrophoresis</i> , 2005 , 26, 1834-42	3.6	40
38	High-Throughput Mutation Screening 2005 , 71-100		
37	Potassium Must Be Considered in Congenital Long QT Syndrome. <i>Cardiology</i> , 2005 , 5, 54-58		3
36	Apo E in multiple sclerosis and optic neuritis: the apo E-epsilon4 allele is associated with progression of multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2005 , 11, 511-5	5	29
35	Disease concordance, zygosity, and NOD2/CARD15 status: follow-up of a population-based cohort of Danish twins with inflammatory bowel disease. <i>American Journal of Gastroenterology</i> , 2005 , 100, 2486-92	0.7	81
34	Genetic and environmental factors in monozygotic twins with Crohn's disease and their first-degree relatives: a case report. <i>Digestion</i> , 2005 , 71, 262-5	3.6	5
33	Clinical and genetic characteristics of alpha cardiac actin gene mutations in hypertrophic cardiomyopathy. <i>Journal of Medical Genetics</i> , 2004 , 41, e10	5.8	39

32	Genetic and phenotypic characterization of mutations in myosin-binding protein C (MYBPC3) in 81 families with familial hypertrophic cardiomyopathy: total or partial haploinsufficiency. <i>European Journal of Human Genetics</i> , 2004 , 12, 673-7	5.3	57
31	Does KCNE5 play a role in long QT syndrome?. <i>Clinica Chimica Acta</i> , 2004 , 345, 49-53	6.2	10
30	Outcome of clinical versus genetic family screening in hypertrophic cardiomyopathy with focus on cardiac beta-myosin gene mutations. <i>Cardiovascular Research</i> , 2003 , 57, 347-57	9.9	29
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