

Denis C Shields

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

10,329
citations

50276

46
h-index

37204

96
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130
all docs

130
docs citations

130
times ranked

16699
citing authors

#	ARTICLE	IF	CITATIONS
1	Short linear motif candidates in the cell entry system used by SARS-CoV-2 and their potential therapeutic implications. <i>Science Signaling</i> , 2021, 14, .	3.6	61
2	Enriching antimicrobial peptides from milk hydrolysates using pectin/alginate food-gels. <i>Food Chemistry</i> , 2021, 352, 129220.	8.2	18
3	Computational modelling of chromosomally clustering protein domains in bacteria. <i>BMC Bioinformatics</i> , 2021, 22, 593.	2.6	1
4	Prediction of polyproline II secondary structure propensity in proteins. <i>Royal Society Open Science</i> , 2020, 7, 191239.	2.4	12
5	Resolving the Interactome of the Human Macrophage Immunometabolism Regulator (MACIR) with Enhanced Membrane Protein Preparation and Affinity Proteomics. <i>Proteomics</i> , 2020, 20, e2000062.	2.2	4
6	Implications of kappa-casein evolutionary diversity for the self-assembly and aggregation of casein micelles. <i>Royal Society Open Science</i> , 2019, 6, 190939.	2.4	12
7	Computational and experimental analysis of bioactive peptide linear motifs in the integrin adhesome. <i>PLoS ONE</i> , 2019, 14, e210337.	2.5	5
8	Computational Opportunities and Challenges in Finding Cyclic Peptide Modulators of Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019, 2001, 73-95.	0.9	7
9	Casein Hydrolysate with Glycemic Control Properties: Evidence from Cells, Animal Models, and Humans. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 4352-4363.	5.2	28
10	Genetic variants in PPARGC1B and CNTN4 are associated with thromboxane A2 formation and with cardiovascular event free survival in the Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT). <i>Atherosclerosis</i> , 2018, 269, 42-49.	0.8	7
11	Peptides derived from cadherin juxtamembrane region inhibit platelet function. <i>Royal Society Open Science</i> , 2018, 5, 172347.	2.4	8
12	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
13	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	12.8	70
14	Integrating biomarkers across omic platforms: an approach to improve stratification of patients with indolent and aggressive prostate cancer. <i>Molecular Oncology</i> , 2018, 12, 1513-1525.	4.6	41
15	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	21.4	492
16	Peptigram: A Web-Based Application for Peptidomics Data Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 712-719.	3.7	73
17	Functional characterisation of the YIPF protein family in mammalian cells. <i>Histochemistry and Cell Biology</i> , 2017, 147, 439-451.	1.7	18
18	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	8.2	106

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19	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. <i>Journal of Medical Genetics</i> , 2016, 53, 835-845.	3.2	28
20	Impact of genetic variation in the 5-HT transporter and receptor on platelet function in patients with stable CAD taking aspirin. <i>Thrombosis Research</i> , 2016, 146, 51-55.	1.7	7
21	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 4094-4106.	2.9	19
22	Optimal computational comparison of mass spectrometric peptide profiles of alternative hydrolysates from the same starting material. <i>LWT - Food Science and Technology</i> , 2016, 73, 296-302.	5.2	5
23	ProVizâ€”a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. <i>Nucleic Acids Research</i> , 2016, 44, W11-W15.	14.5	68
24	Coarse Master Equation-Based Analysis of N-Methylation and Temperature Effects on the Dynamics of Cyclic Peptides. <i>Biophysical Journal</i> , 2016, 110, 379a.	0.5	1
25	Design and Evaluation of Antimalarial Peptides Derived from Prediction of Short Linear Motifs in Proteins Related to Erythrocyte Invasion. <i>PLoS ONE</i> , 2015, 10, e0127383.	2.5	7
26	Virtual Screening Using Combinatorial Cyclic Peptide Libraries Reveals Protein Interfaces Readily Targetable by Cyclic Peptides. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 600-613.	5.4	14
27	Genome-wide epistatic expression quantitative trait loci discovery in four human tissues reveals the importance of local chromosomal interactions governing gene expression. <i>BMC Genomics</i> , 2015, 16, 109.	2.8	5
28	Discovering Anti-platelet Drug Combinations with an Integrated Model of Activator-Inhibitor Relationships, Activator-Activator Synergies and Inhibitor-Inhibitor Synergies. <i>PLoS Computational Biology</i> , 2015, 11, e1004119.	3.2	4
29	Computational Approaches to Developing Short Cyclic Peptide Modulators of Proteinâ€”Protein Interactions. <i>Methods in Molecular Biology</i> , 2015, 1268, 241-271.	0.9	27
30	SLiMScape 3.x: a Cytoscape 3 app for discovery of Short Linear Motifs in protein interaction networks. <i>F1000Research</i> , 2015, 4, 477.	1.6	1
31	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014, 5, 5068.	12.8	216
32	Cadherin juxtamembrane region derived peptides inhibit TGFÎ²1 induced gene expression. <i>Bioarchitecture</i> , 2014, 4, 103-110.	1.5	4
33	Following the Digestion of Milk Proteins from Mother to Baby. <i>Journal of Proteome Research</i> , 2014, 13, 5777-5783.	3.7	41
34	Computational survey of peptides derived from disulphide-bonded protein loops that may serve as mediators of protein-protein interactions. <i>BMC Bioinformatics</i> , 2014, 15, 305.	2.6	3
35	In silico approaches to predict the potential of milk protein-derived peptides as dipeptidyl peptidase IV (DPP-IV) inhibitors. <i>Peptides</i> , 2014, 57, 43-51.	2.4	113
36	Predicting the Important Enzymes in Human Breast Milk Digestion. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 7225-7232.	5.2	55

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37	Amino acid enrichment and compositional changes among mammalian milk proteins and the resulting nutritional consequences. <i>Journal of Dairy Science</i> , 2014, 97, 1248-1258.	3.4	8
38	Angiotensin converting enzyme and nitric oxide inhibitory activities of novel milk derived peptides. <i>International Dairy Journal</i> , 2014, 35, 38-42.	3.0	7
39	Potential of known and short prokaryotic protein motifs as a basis for novel peptide-based antibacterial therapeutics: a computational survey. <i>Frontiers in Microbiology</i> , 2014, 5, 4.	3.5	18
40	SCL-Epred: a generalised de novo eukaryotic protein subcellular localisation predictor. <i>Amino Acids</i> , 2013, 45, 291-299.	2.7	9
41	Inhibition of dipeptidyl peptidase IV and xanthine oxidase by amino acids and dipeptides. <i>Food Chemistry</i> , 2013, 141, 644-653.	8.2	124
42	CPPpred: prediction of cell penetrating peptides. <i>Bioinformatics</i> , 2013, 29, 3094-3096.	4.1	125
43	PeptideLocator: prediction of bioactive peptides in protein sequences. <i>Bioinformatics</i> , 2013, 29, 1120-1126.	4.1	66
44	SLiMScape: a protein short linear motif analysis plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 224.	2.6	19
45	A genome-wide association study of recipient genotype and medium-term kidney allograft function. <i>Clinical Transplantation</i> , 2013, 27, 379-387.	1.6	39
46	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	21.4	282
47	Genome-Wide Analysis of Blood Pressure Variability and Ischemic Stroke. <i>Stroke</i> , 2013, 44, 2703-2709.	2.0	17
48	Marked Variability in the Extent of Protein Disorder within and between Viral Families. <i>PLoS ONE</i> , 2013, 8, e60724.	2.5	50
49	Predicting Binding within Disordered Protein Regions to Structurally Characterised Peptide-Binding Domains. <i>PLoS ONE</i> , 2013, 8, e72838.	2.5	33
50	Peptide-Binding Domains: Are Limp Handshakes Safest?. <i>Science Signaling</i> , 2012, 5, pe40.	3.6	12
51	Genome-wide association study of genetic determinants of LDL-c response to atorvastatin therapy: importance of Lp(a). <i>Journal of Lipid Research</i> , 2012, 53, 1000-1011.	4.2	97
52	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. <i>Human Genetics</i> , 2012, 131, 565-579.	3.8	180
53	Correlation of disorder between <i>S. cerevisiae</i> interacting proteins. <i>Molecular BioSystems</i> , 2012, 8, 417-425.	2.9	1
54	SLiMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. <i>Nucleic Acids Research</i> , 2012, 40, 10628-10641.	14.5	92

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55	EnzymePredictor: A Tool for Predicting and Visualizing Enzymatic Cleavages of Digested Proteins. Journal of Proteome Research, 2012, 11, 6056-6065.	3.7	48
56	Prediction of Short Linear Protein Binding Regions. Journal of Molecular Biology, 2012, 415, 193-204.	4.2	71
57	Profile-based short linear protein motif discovery. BMC Bioinformatics, 2012, 13, 104.	2.6	14
58	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
59	Structures of YAP protein domains reveal promising targets for development of new cancer drugs. Seminars in Cell and Developmental Biology, 2012, 23, 827-833.	5.0	113
60	Interactome-wide prediction of short, disordered protein interaction motifs in humans. Molecular BioSystems, 2012, 8, 282-295.	2.9	30
61	Platelet signalling networks: Pathway perturbation demonstrates differential sensitivity of ADP secretion and fibrinogen binding. Platelets, 2012, 23, 17-25.	2.3	17
62	Towards the Improved Discovery and Design of Functional Peptides: Common Features of Diverse Classes Permit Generalized Prediction of Bioactivity. PLoS ONE, 2012, 7, e45012.	2.5	322
63	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
64	Predictive modelling of angiotensin converting enzyme inhibitory dipeptides. Food Chemistry, 2012, 133, 1349-1354.	8.2	73
65	Protein Disorder and Short Conserved Motifs in Disordered Regions Are Enriched near the Cytoplasmic Side of Single-Pass Transmembrane Proteins. PLoS ONE, 2012, 7, e44389.	2.5	21
66	CycloPs: Generating Virtual Libraries of Cyclized and Constrained Peptides Including Nonnatural Amino Acids. Journal of Chemical Information and Modeling, 2011, 51, 829-836.	5.4	34
67	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
68	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
69	Shift in the isoelectric-point of milk proteins as a consequence of adaptive divergence between the milks of mammalian species. Biology Direct, 2011, 6, 40.	4.6	35
70	Evolution of the isoelectric point of mammalian proteins as a consequence of indels and adaptive evolution. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1635-1648.	2.6	13
71	A polymorphism in <i>ACE2</i> is associated with a lower risk for fatal cardiovascular events in females: the MORGAM project. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2011, 12, 504-509.	1.7	27
72	SLIMSearch 2.0: biological context for short linear motifs in proteins. Nucleic Acids Research, 2011, 39, W56-W60.	14.5	68

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73	Differences in the Number of Intrinsically Disordered Regions between Yeast Duplicated Proteins, and Their Relationship with Functional Divergence. <i>PLoS ONE</i> , 2011, 6, e24989.	2.5	12
74	Estimation and efficient computation of the true probability of recurrence of short linear protein sequence motifs in unrelated proteins. <i>BMC Bioinformatics</i> , 2010, 11, 14.	2.6	27
75	Meta-Analysis To Test the Association of HIV-1 <i>nef</i> Amino Acid Differences and Deletions with Disease Progression. <i>Journal of Virology</i> , 2010, 84, 3644-3653.	3.4	19
76	SLIMFinder: a web server to find novel, significantly over-represented, short protein motifs. <i>Nucleic Acids Research</i> , 2010, 38, W534-W539.	14.5	64
77	SLIMSearch: A Webserver for Finding Novel Occurrences of Short Linear Motifs in Proteins, Incorporating Sequence Context. <i>Lecture Notes in Computer Science</i> , 2010, , 50-61.	1.3	9
78	Masking residues using context-specific evolutionary conservation significantly improves short linear motif discovery. <i>Bioinformatics</i> , 2009, 25, 443-450.	4.1	60
79	Genetic polymorphisms in platelet-related proteins and coronary artery disease: investigation of candidate genes, including N-acetylgalactosaminyltransferase 4 (GALNT4) and sulphotransferase 1A1/2 (SULT1A1/2). <i>Journal of Thrombosis and Thrombolysis</i> , 2009, 27, 175-184.	2.1	32
80	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. <i>American Journal of Human Genetics</i> , 2009, 85, 628-642.	6.2	183
81	Discovery of Small Molecule Inhibitors of Protein-Protein Interactions Using Combined Ligand and Target Score Normalization. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2708-2717.	5.4	26
82	Ligand Switching in Cell-Permeable Peptides: Manipulation of the β -Integrin Signature Motif. <i>ACS Chemical Biology</i> , 2009, 4, 457-471.	3.4	9
83	Haplotypic analysis of tag SNPs of the interleukin-18 gene in relation to cardiovascular disease events: the MORGAM Project. <i>European Journal of Human Genetics</i> , 2008, 16, 1512-1520.	2.8	12
84	Approved Drug Mimics of Short Peptide Ligands from Protein Interaction Motifs. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1943-1948.	5.4	35
85	Lack of association between NFKBIL1/LTA polymorphisms and hypertension, myocardial infarct, unstable angina and stable angina in a large Irish population sample. <i>Atherosclerosis</i> , 2008, 197, 465-466.	0.8	5
86	Web Server To Identify Similarity of Amino Acid Motifs to Compounds (SAAMCO). <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1524-1529.	5.4	7
87	CompariMotif: quick and easy comparisons of sequence motifs. <i>Bioinformatics</i> , 2008, 24, 1307-1309.	4.1	47
88	The SLIMDisc server: short, linear motif discovery in proteins. <i>Nucleic Acids Research</i> , 2007, 35, W455-W459.	14.5	51
89	Renin Gene Polymorphisms and Haplotypes, Blood Pressure, and Responses to Renin-Angiotensin System Inhibition. <i>Hypertension</i> , 2007, 50, 340-347.	2.7	41
90	Association of Methylenetetrahydrofolate Reductase Polymorphism and the Risk of Squamous Cell Carcinoma in Renal Transplant Patients. <i>Transplantation</i> , 2007, 84, 113-116.	1.0	37

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91	Identification of Potential Small Molecule Peptidomimetics Similar to Motifs in Proteins. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 464-474.	5.4	17
92	SLiMFinder: A Probabilistic Method for Identifying Over-Represented, Convergently Evolved, Short Linear Motifs in Proteins. <i>PLoS ONE</i> , 2007, 2, e967.	2.5	143
93	Bioinformatic discovery of novel bioactive peptides. , 2007, 3, 108-112.		73
94	Absolute Net Charge and the Biological Activity of Oligopeptides. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 2183-2190.	5.4	5
95	The Impact on Coronary Artery Disease of Common Polymorphisms Known to Modulate Responses to Pathogens. <i>Annals of Human Genetics</i> , 2006, 70, 934-945.	0.8	19
96	SLiMDisc: short, linear motif discovery, correcting for common evolutionary descent. <i>Nucleic Acids Research</i> , 2006, 34, 3546-3554.	14.5	101
97	Evaluation of Whether Accelerated Protein Evolution in Chordates Has Occurred before, after, or Simultaneously with Gene Duplication. <i>Molecular Biology and Evolution</i> , 2006, 24, 315-323.	8.9	14
98	The impact of genetic variation in the region of the GPIIIa gene, on PIA2 expression bias and GPIIb/IIIa receptor density in platelets. <i>British Journal of Haematology</i> , 2005, 132, 051220022257002.	2.5	10
99	Overdispersion of allele frequency differences between populations: implications for meta-analyses of genotypic disease associations. <i>European Journal of Human Genetics</i> , 2005, 13, 79-85.	2.8	2
100	Uroplakin III is not a major candidate gene for primary vesicoureteral reflux. <i>European Journal of Human Genetics</i> , 2005, 13, 500-502.	2.8	32
101	Genetic stratification of pathogen-response-related and other variants within a homogeneous Caucasian Irish population. <i>European Journal of Human Genetics</i> , 2005, 13, 798-806.	2.8	13
102	A sequence sub-sampling algorithm increases the power to detect distant homologues. <i>Nucleic Acids Research</i> , 2005, 33, 3772-3778.	14.5	1
103	Preferential Transmission of Paternal Alleles at Risk Genes in Attention-Deficit/Hyperactivity Disorder. <i>American Journal of Human Genetics</i> , 2005, 77, 958-965.	6.2	100
104	Human Tissue Profiling with Multidimensional Protein Identification Technology. <i>Journal of Proteome Research</i> , 2005, 4, 1757-1767.	3.7	81
105	MORGAM (an international pooling of cardiovascular cohorts). <i>International Journal of Epidemiology</i> , 2004, 34, 21-27.	1.9	105
106	Significantly Different Patterns of Amino Acid Replacement After Gene Duplication as Compared to After Speciation. <i>Molecular Biology and Evolution</i> , 2003, 20, 484-490.	8.9	38
107	Genetic variability in the extracellular matrix as a determinant of cardiovascular risk: association of type III collagen COL3A1 polymorphisms with coronary artery disease. <i>Blood</i> , 2002, 100, 1220-1223.	1.4	24
108	Integrating Genotypic Data with Transcriptomic and Proteomic Data. <i>Comparative and Functional Genomics</i> , 2002, 3, 22-27.	2.0	6

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109	Platelet glycoprotein Ib alpha receptor polymorphisms and recurrent ischaemic events in acute coronary syndrome patients. <i>Journal of Thrombosis and Thrombolysis</i> , 2002, 13, 13-19.	2.1	33
110	Genetic variation in glycoprotein IIb/IIIa (GPIIb/IIIa) as a determinant of the responses to an oral GPIIb/IIIa antagonist in patients with unstable coronary syndromes. <i>Blood</i> , 2001, 98, 3256-3260.	1.4	61
111	Acquisition of multiple virulence/avirulence determinants by potato virus X (PVX) has occurred through convergent evolution rather than through recombination. <i>Virus Genes</i> , 2000, 20, 165-172.	1.6	26
112	Gene conversion among chemokine receptors. <i>Gene</i> , 2000, 246, 239-245.	2.2	39
113	A method to predict residues conferring functional differences between related proteins: Application to MAP kinase pathways. <i>Protein Science</i> , 2000, 9, 655-670.	7.6	18
114	Genetic Analysis of the Thermolabile Variant of 5,10-Methylenetetrahydrofolate Reductase as a Risk Factor for Ischemic Stroke. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 1999, 19, 208-211.	2.4	63
115	The Evolution of the MAP Kinase Pathways: Coduplication of Interacting Proteins Leads to New Signaling Cascades. <i>Journal of Molecular Evolution</i> , 1999, 49, 567-582.	1.8	117
116	The "Thermolabile" Variant of Methylenetetrahydrofolate Reductase and Neural Tube Defects: An Evaluation of Genetic Risk and the Relative Importance of the Genotypes of the Embryo and the Mother. <i>American Journal of Human Genetics</i> , 1999, 64, 1045-1055.	6.2	219
117	Evidence for an allelic association between bipolar disorder and a Na ⁺ , K ⁺ adenosine triphosphatase alpha subunit gene (ATP1A3). <i>Biological Psychiatry</i> , 1998, 44, 47-51.	1.3	69
118	Lack of evidence for a major locus for bipolar disorder in the pericentromeric region of chromosome 18 in Irish pedigrees. <i>Biological Psychiatry</i> , 1997, 42, 486-494.	1.3	14
119	Molecular evidence for an ancient duplication of the entire yeast genome. <i>Nature</i> , 1997, 387, 708-713.	27.8	1,702
120	Mapping Genes Within a YAC by Computer-Assisted Interpretation of Partial Restriction Digestions. <i>Nucleic Acids Research</i> , 1996, 24, 4495-4500.	14.5	1
121	Homocysteine and Risk of Premature Coronary Heart Disease. <i>Circulation</i> , 1996, 94, 2154-2158.	1.6	196
122	The evolution of haematopoietic cytokine /receptor complexes. <i>Cytokine</i> , 1995, 7, 679-688.	3.2	20
123	Prediction of Genetic Risks from Segregation Analyses of Morbid Risks. <i>Human Heredity</i> , 1994, 44, 52-55.	0.8	4
124	Coding of pointers in the segregation analysis program POINTER. <i>Genetic Epidemiology</i> , 1994, 11, 385-387.	1.3	3
125	The CEPH consortium linkage map of human chromosome 2. <i>Genomics</i> , 1992, 14, 1055-1063.	2.9	10
126	Switches in species-specific codon preferences: The influence of mutation biases. <i>Journal of Molecular Evolution</i> , 1990, 31, 71-80.	1.8	60

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127	Evidence that mutation patterns vary among <i>Drosophila</i> transposable elements. <i>Journal of Molecular Biology</i> , 1989, 207, 843-846.	4.2	24
128	Codon usage patterns in <i>Escherichia coli</i> , <i>Bacillus subtilis</i> , <i>Saccharomyces cerevisiae</i> , <i>Schizosaccharomyces pombe</i> , <i>Drosophila melanogaster</i> and <i>Homo sapiens</i> ; a review of the considerable within-species diversity. <i>Nucleic Acids Research</i> , 1988, 16, 8207-8211.	14.5	569
129	Synonymous codon usage in <i>Bacillus subtilis</i> reflects both translational selection and mutational biases. <i>Nucleic Acids Research</i> , 1987, 15, 8023-8040.	14.5	277