Wesley C Warren

List of Publications by Year in Descending Order

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155 papers	17,338 citations	59 h-index	131 g-index
164 ext. papers	21,656 ext. citations	15.7 avg, IF	5.44 L-index

#	Paper	IF	Citations
155	Single Circulating-Tumor-Cell-Targeted Sequencing to Identify Somatic Variants in Liquid Biopsies in Non-Small-Cell Lung Cancer Patients. *Current Issues in Molecular Biology*, **2022**, 44, 750-763	2.9	1
154	Avian genomics **2022**, 7-16		
153	Tumorigenic circulating tumor cells from xenograft mouse models of non-metastatic NSCLC patients reveal distinct single cell heterogeneity and drug responses.. *Molecular Cancer*, **2022**, 21, 73	42.1	1
152	The Evolution of Viviparity in Vertebrates. *Advances in Anatomy, Embryology and Cell Biology*, **2021**, 234, 7-19	1.2	0
151	Ultracontinuous Single Haplotype Genome Assemblies for the Domestic Cat (Felis catus) and Asian Leopard Cat (Prionailurus bengalensis). *Journal of Heredity*, **2021**, 112, 165-173	2.4	5
150	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. *BMC Biology*, **2021**, 19, 41	7.3	9
149	Mining the 99 Lives Cat Genome Sequencing Consortium database implicates genes and variants for the Ticked locus in domestic cats (Felis catus). *Animal Genetics*, **2021**, 52, 321-332	2.5	3
148	A domestic cat whole exome sequencing resource for trait discovery. *Scientific Reports*, **2021**, 11, 7159	4.9	3
147	A chromosome-level genome of Astyanax mexicanus surface fish for comparing population-specific genetic differences contributing to trait evolution. *Nature Communications*, **2021**, 12, 1447	17.4	13
146	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	50.4	161
145	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. *Science*, **2021**, 372, 984-989	33.3	33
144	Explainable artificial intelligence in high-throughput drug repositioning for subgroup stratifications with interventionable potential. *Journal of Biomedical Informatics*, **2021**, 118, 103792	10.2	0
143	Epigenetic Regulation of Cancer Immune Cells. *Seminars in Cancer Biology*, **2021**,	12.7	3
142	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. *Current Biology*, **2021**, 31, 911-922.e4	6.3	10
141	Fixation of allelic gene expression landscapes and expression bias pattern shape the transcriptome of the clonal Amazon molly. *Genome Research*, **2021**, 31, 372-379	9.7	3
140	Chromosome-scale genome assembly of the sea louse Caligus rogercresseyi by SMRT sequencing and Hi-C analysis. *Scientific Data*, **2021**, 8, 60	8.2	4
139	The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	14

138	Genome Assemblies across the Diverse Evolutionary Spectrum of Protozoan Parasites. *Microbiology Resource Announcements*, **2021**, 10, e0054521	1.3	0
137	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. *American Journal of Human Genetics*, **2020**, 106, 893-904	11	14
136	Neuronal Ceroid Lipofuscinosis in a Domestic Cat Associated with a DNA Sequence Variant That Creates a Premature Stop Codon in. *G3: Genes, Genomes, Genetics*, **2020**, 10, 2741-2751	3.2	2
135	The quail genome: insights into social behaviour, seasonal biology and infectious disease response. *BMC Biology*, **2020**, 18, 14	7.3	19
134	The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. *Nature Ecology and Evolution*, **2020**, 4, 841-852	12.3	65
133	A new domestic cat genome assembly based on long sequence reads empowers feline genomic medicine and identifies a novel gene for dwarfism. *PLoS Genetics*, **2020**, 16, e1008926	6	29
132	A 50K SNP array reveals genetic structure for bald eagles (Haliaeetus leucocephalus). *Conservation Genetics*, **2020**, 21, 65-76	2.6	4
131	Global assessment of organ specific basal gene expression over a diurnal cycle with analyses of gene copies exhibiting cyclic expression patterns. *BMC Genomics*, **2020**, 21, 787	4.5	
130	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. *Science*, **2020**, 370,	33.3	28
129	Sequence analysis in reveals pervasiveness of X-Y arms races in mammalian lineages. *Genome Research*, **2020**, 30, 1716-1726	9.7	6
128	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. *Genome Biology*, **2019**, 20, 187	18.3	39
127	Expression Signatures of Cisplatin- and Trametinib-Treated Early-Stage Medaka Melanomas. *G3: Genes, Genomes, Genetics*, **2019**, 9, 2267-2276	3.2	5
126	A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. *Molecular Ecology Resources*, **2019**, 19, 997-1014	8.4	11
125	The Piranha Genome Provides Molecular Insight Associated to Its Unique Feeding Behavior. *Genome Biology and Evolution*, **2019**, 11, 2099-2106	3.9	7
124	Dramatic changes in gene expression in different forms of Crithidia fasciculata reveal potential mechanisms for insect-specific adhesion in kinetoplastid parasites. *PLoS Neglected Tropical Diseases* , **2019**, 13, e0007570	4.8	7
123	Antarctic blackfin icefish genome reveals adaptations to extreme environments. *Nature Ecology and Evolution*, **2019**, 3, 469-478	12.3	62
122	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. *Genome Research*, **2019**, 29, 576-589	9.7	15
121	Human-specific tandem repeat expansion and differential gene expression during primate evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 23243-23253	11.5	37

120	Characterizing the Major Structural Variant Alleles of the Human Genome. *Cell*, **2019**, 176, 663-675.e19	56.2	205
119	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. *Nature Ecology and Evolution*, **2018**, 2, 669-679	12.3	60
118	Comparison of Xiphophorus and human melanoma transcriptomes reveals conserved pathway interactions. *Pigment Cell and Melanoma Research*, **2018**, 31, 496-508	4.5	7
117	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. *Genome Biology and Evolution*, **2018**, 10, 2110-2129	3.9	48
116	Diversity of Immunoglobulin Light Chain Genes in Non-Teleost Ray-Finned Fish Uncovers IgL Subdivision into Five Ancient Isotypes. *Frontiers in Immunology*, **2018**, 9, 1079	8.4	5
115	Applications and efficiencies of the first cat 63K DNA array. *Scientific Reports*, **2018**, 8, 7024	4.9	26
114	High-resolution comparative analysis of great ape genomes. *Science*, **2018**, 360,	33.3	178
113	Expression signatures of early-stage and advanced medaka melanomas. *Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology*, **2018**, 208, 20-28	3.2	8
112	Gene expression variation and parental allele inheritance in a Xiphophorus interspecies hybridization model. *PLoS Genetics*, **2018**, 14, e1007875	6	4
111	Long-term experimental hybridisation results in the evolution of a new sex chromosome in swordtail fish. *Nature Communications*, **2018**, 9, 5136	17.4	14
110	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, Astyanax mexicanus. *Molecular Ecology*, **2018**, 27, 4397-4416	5.7	77
109	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. *Nature Genetics*, **2017**, 49, 387-394	36.3	92
108	Building and Improving Reference Genome Assemblies. *Proceedings of the IEEE*, **2017**, 1-14	14.3	4
107	Complexities of gene expression patterns in natural populations of an extremophile fish (Poecilia mexicana, Poeciliidae). *Molecular Ecology*, **2017**, 26, 4211-4225	5.7	15
106	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. *G3: Genes, Genomes, Genetics*, **2017**, 7, 109-117	3.2	143
105	Molecular genetic analysis of the melanoma regulatory locus in Xiphophorus interspecies hybrids. *Molecular Carcinogenesis*, **2017**, 56, 1935-1944	5	9
104	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. *Nature Genetics*, **2017**, 49, 1705-1713	36.3	76
103	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. *Nature Genetics*, **2017**, 49, 1714-1721	36.3	43

102	A Resource of Genome-Wide Single Nucleotide Polymorphisms (Snps) for the Conservation and Management of Golden Eagles. *Journal of Raptor Research*, **2017**, 51, 368-377	0.9	6
101	The practical use of genome sequencing data in the management of a feline colony pedigree. *BMC Veterinary Research*, **2017**, 13, 225	2.7	1
100	Tsetse fly (Glossina pallidipes) midgut responses to Trypanosoma brucei challenge. *Parasites and Vectors*, **2017**, 10, 614	4	7
99	The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. *Molecular Ecology*, **2017**, 26, 6384-6399	5.7	18
98	The Cyprinodon variegatus genome reveals gene expression changes underlying differences in skull morphology among closely related species. *BMC Genomics*, **2017**, 18, 424	4.5	18
97	The Novel Evolution of the Sperm Whale Genome. *Genome Biology and Evolution*, **2017**, 9, 3260-3264	3.9	27
96	The landscape of extreme genomic variation in the highly adaptable Atlantic killifish. *Genome Biology and Evolution*, **2017**, 9, 659-676	3.9	34
95	The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. *Genome Biology and Evolution*, **2017**, 9, 3525-3530	3.9	16
94	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). *GigaScience*, **2017**, 6, 1-6	7.6	16
93	Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. *Nature Communications*, **2016**, 7, 12997	17.4	22
92	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. *Science Advances*, **2016**, 2, e1600633	14.3	49
91	A proteinaceous organic matrix regulates carbonate mineral production in the marine teleost intestine. *Scientific Reports*, **2016**, 6, 34494	4.9	8
90	A High-Resolution SNP Array-Based Linkage Map Anchors a New Domestic Cat Draft Genome Assembly and Provides Detailed Patterns of Recombination. *G3: Genes, Genomes, Genetics*, **2016**, 6, 1607-16	3.2	32
89	Evolutionary signals of selection on cognition from the great tit genome and methylome. *Nature Communications*, **2016**, 7, 10474	17.4	125
88	Divergence and Functional Degradation of a Sex Chromosome-like Supergene. *Current Biology*, **2016**, 26, 344-50	6.3	183
87	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. *Genome Research*, **2016**, 26, 108-18	9.7	81
86	Patterns of Genome-Wide Variation in Glossina fuscipes fuscipes Tsetse Flies from Uganda. *G3: Genes, Genomes, Genetics*, **2016**, 6, 1573-84	3.2	9
85	The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. *Science*, **2016**, 354, 1305-1308	33.3	250

84	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of Limulus polyphemus (Arthropoda: Chelicerata). *Genome Biology and Evolution*, **2016**, 8, 1571-89	3.9	33
83	Germ cell and tumor associated piRNAs in the medaka and Xiphophorus melanoma models. *BMC Genomics*, **2016**, 17, 357	4.5	9
82	X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. *BMC Genomics*, **2016**, 17, 37	4.5	18
81	Pangolin genomes and the evolution of mammalian scales and immunity. *Genome Research*, **2016**, 26, 1312-1322	9.7	54
80	Developing tools for the study of molluscan immunity: The sequencing of the genome of the eastern oyster, Crassostrea virginica. *Fish and Shellfish Immunology*, **2015**, 46, 2-4	4.3	49
79	Third Report on Chicken Genes and Chromosomes 2015. *Cytogenetic and Genome Research*, **2015**, 145, 78-179	1.9	57
78	Physical Mapping and Refinement of the Painted Turtle Genome (Chrysemys picta) Inform Amniote Genome Evolution and Challenge Turtle-Bird Chromosomal Conservation. *Genome Biology and Evolution*, **2015**, 7, 2038-50	3.9	32
77	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. *BMC Biology*, **2015**, 13, 41	7.3	36
76	The genome of the vervet (Chlorocebus aethiops sabaeus). *Genome Research*, **2015**, 25, 1921-33	9.7	84
75	The Physarum polycephalum Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. *Genome Biology and Evolution*, **2015**, 8, 109-25	3.9	63
74	Identification and analysis of divergent immune gene families within the Tasmanian devil genome. *BMC Genomics*, **2015**, 16, 1017	4.5	10
73	Response to Hron et al. *Genome Biology*, **2015**, 16, 165	18.3	10
72	Whole Body Melanoma Transcriptome Response in Medaka. *PLoS ONE*, **2015**, 10, e0143057	3.7	13
71	Genome of Rhodnius prolixus, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 14936-41	11.5	220
70	Joint MiRNA/mRNA expression profiling reveals changes consistent with development of dysfunctional corpus luteum after weight gain. *PLoS ONE*, **2015**, 10, e0135163	3.7	37
69	Genome of the human hookworm Necator americanus. *Nature Genetics*, **2014**, 46, 261-269	36.3	139
68	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. *Nature*, **2014**, 508, 494-9	50.4	406
67	Genome sequence of the tsetse fly (Glossina morsitans): vector of African trypanosomiasis. *Science*, **2014**, 344, 380-6	33.3	192

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66	Elephant shark genome provides unique insights into gnathostome evolution. *Nature*, **2014**, 505, 174-9	50.4	498
65	Sequencing the mouse Y chromosome reveals convergent gene acquisition and amplification on both sex chromosomes. *Cell*, **2014**, 159, 800-13	56.2	192
64	Single haplotype assembly of the human genome from a hydatidiform mole. *Genome Research*, **2014**, 24, 2066-76	9.7	98
63	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 17230-5	11.5	184
62	A RAD-tag genetic map for the platyfish (Xiphophorus maculatus) reveals mechanisms of karyotype evolution among teleost fish. *Genetics*, **2014**, 197, 625-41	4	68
61	High-coverage sequencing and annotated assemblies of the budgerigar genome. *GigaScience*, **2014**, 3, 11	7.6	67
60	Gibbon genome and the fast karyotype evolution of small apes. *Nature*, **2014**, 513, 195-201	50.4	241
59	On the origin of SCPP genes. *Evolution & Development*, **2014**, 16, 125-6	2.6	3
58	Extensive error in the number of genes inferred from draft genome assemblies. *PLoS Computational Biology*, **2014**, 10, e1003998	5	180
57	Venkatesh et al. reply. *Nature*, **2014**, 511, E9-10	50.4	8
56	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
55	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
54	Comparative analysis of cancer driver genes between human and six non-human primates (LB182). *FASEB Journal*, **2014**, 28, LB182	0.9	
53	Independent specialization of the human and mouse X chromosomes for the male germ line. *Nature Genetics*, **2013**, 45, 1083-7	36.3	111
52	Convergence in feeding posture occurs through different genetic loci in independently evolved cave populations of Astyanax mexicanus. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 16933-8	11.5	84
51	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 20645-50	11.5	203
50	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. *Nature Genetics*, **2013**, 45, 415-21, 421e1-2	36.3	465
49	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetics*, **2013**, 45, 776-783	36.3	240

48	The genome of the platyfish, Xiphophorus maculatus, provides insights into evolutionary adaptation and several complex traits. *Nature Genetics*, **2013**, 45, 567-72	36.3	201
47	No bull: upholding community standards in public sharing of biological datasets. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, E4277	11.5	1
46	Systems biology of the vervet monkey. *ILAR Journal*, **2013**, 54, 122-43	1.7	93
45	Basal vertebrates clarify the evolutionary history of ciliopathy-associated genes Tmem138 and Tmem216. *Molecular Biology and Evolution*, **2013**, 30, 62-5	8.3	4
44	To the Root of the Curl: A Signature of a Recent Selective Sweep Identifies a Mutation That Defines the Cornish Rex Cat Breed. *PLoS ONE*, **2013**, 8, e67105	3.7	26
43	Echidna venom gland transcriptome provides insights into the evolution of monotreme venom. *PLoS ONE*, **2013**, 8, e79092	3.7	14
42	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. *Nature*, **2012**, 483, 82-6	50.4	181
41	Specifying and sustaining pigmentation patterns in domestic and wild cats. *Science*, **2012**, 337, 1536-41	33.3	84
40	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
39	A limited role for gene duplications in the evolution of platypus venom. *Molecular Biology and Evolution*, **2012**, 29, 167-77	8.3	30
38	A non-human primate system for large-scale genetic studies of complex traits. *Human Molecular Genetics*, **2012**, 21, 3307-16	5.6	43
37	Proteomics and deep sequencing comparison of seasonally active venom glands in the platypus reveals novel venom peptides and distinct expression profiles. *Molecular and Cellular Proteomics*, **2012**, 11, 1354-64	7.6	35
36	Transcriptome analysis of female and male Xiphophorus maculatus Jp 163 A. *PLoS ONE*, **2011**, 6, e18379	3.7	31
35	A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). *Standards in Genomic Sciences*, **2011**, 4, 257-70		24
34	The draft genome of the parasitic nematode Trichinella spiralis. *Nature Genetics*, **2011**, 43, 228-35	36.3	230
33	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
32	A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*, **2011**, 478, 476-82	50.4	802
31	Digital gene expression for non-model organisms. *Genome Research*, **2011**, 21, 1905-15	9.7	44

30	The genome sequence of the leaf-cutter ant Atta cephalotes reveals insights into its obligate symbiotic lifestyle. *PLoS Genetics*, **2011**, 7, e1002007	6	191
29	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. *Nature*, **2010**, 463, 536-9	50.4	286
28	The genome of a songbird. *Nature*, **2010**, 464, 757-62	50.4	655
27	The genome of the Western clawed frog Xenopus tropicalis. *Science*, **2010**, 328, 633-6	33.3	579
26	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. *Nature*, **2010**, 466, 612-6	50.4	168
25	A catalog of reference genomes from the human microbiome. *Science*, **2010**, 328, 994-9	33.3	508
24	Genome sequence of Cronobacter sakazakii BAA-894 and comparative genomic hybridization analysis with other Cronobacter species. *PLoS ONE*, **2010**, 5, e9556	3.7	166
23	Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. *Chromosoma*, **2009**, 118, 53-69	2.8	18
22	The enigma of the platypus genome. *Australian Journal of Zoology*, **2009**, 57, 157	0.5	2
21	Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, **2008**, 453, 175-83	50.4	545
20	Evolutionary toggling of the MAPT 17q21.31 inversion region. *Nature Genetics*, **2008**, 40, 1076-83	36.3	138
19	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods*, **2008**, 5, 247-52	21.6	458
18	Gene discovery and comparative analysis of X-degenerate genes from the domestic cat Y chromosome. *Genomics*, **2008**, 92, 329-38	4.3	43
17	Defensins and the convergent evolution of platypus and reptile venom genes. *Genome Research*, **2008**, 18, 986-94	9.7	101
16	Origin of INSL3-mediated testicular descent in therian mammals. *Genome Research*, **2008**, 18, 974-85	9.7	48
15	Evolutionary and biomedical insights from the rhesus macaque genome. *Science*, **2007**, 316, 222-34	33.3	1072
14	Characterizing the chromosomes of the platypus (Ornithorhynchus anatinus). *Chromosome Research*, **2007**, 15, 961-74	4.4	13
13	Physical map-assisted whole-genome shotgun sequence assemblies. *Genome Research*, **2006**, 16, 768-75	9.7	24

12	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature*, **2005**, 434, 724-31	50.4	61
11	Profiling of gender-regulated gene transcripts in the filarial nematode Brugia malayi by cDNA oligonucleotide array analysis. *Molecular and Biochemical Parasitology*, **2005**, 143, 49-57	1.9	38
10	Glucose and insulin treatment of insulinoma cells results in transcriptional regulation of a common set of genes. *Diabetes*, **2004**, 53, 1496-508	0.9	46
9	Fosmid-based physical mapping of the Histoplasma capsulatum genome. *Genome Research*, **2004**, 14, 1603-9	9.7	20
8	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. *Nature Genetics*, **2004**, 36, 1268-74	36.3	308
7	A physical map of the chicken genome. *Nature*, **2004**, 432, 761-4	50.4	166
6	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. *Nature*, **2004**, 432, 717-22	50.4	341
5	Construction and characterization of a new bovine bacterial artificial chromosome library with 10 genome-equivalent coverage. *Mammalian Genome*, **2000**, 11, 662-3	3.2	48
4	Cloning of the cDNAs coding for cat growth hormone and prolactin. *Gene*, **1996**, 168, 247-9	3.8	5
3	Increased production of peptide deformylase eliminates retention of formylmethionine in bovine somatotropin overproduced in Escherichia coli. *Gene*, **1996**, 174, 235-8	3.8	13
2	Towards complete and error-free genome assemblies of all vertebrate species		38
1	The evolution of ecological flexibility, large brains, and long lives: capuchin monkey genomics revealed with fecalFACS		2