Robin S Waples

List of Publications by Year
in descending order

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125 papers	18,506 citations	30070 54 h-index	17592 121 g-index
136 all docs	136 docs citations	136 times ranked	12556 citing authors

#	Article	IF	Citations
1	Pseudoreplication in genomicâ€scale data sets. Molecular Ecology Resources, 2022, 22, 503-518.	4.8	16
2	Closeâ€kin methods to estimate census size and effective population size. Fish and Fisheries, 2022, 23, 273-293.	5.3	25
3	Implications of Large-Effect Loci for Conservation: A Review and Case Study with Pacific Salmon. Journal of Heredity, 2022, 113, 121-144.	2.4	25
4	What IsNe, Anyway?. Journal of Heredity, 2022, 113, 371-379.	2.4	40
5	<scp><scp>TheWeight</scp></scp>: A simple and flexible algorithm for simulating nonâ€ideal, ageâ€structured populations. Methods in Ecology and Evolution, 2022, 13, 2030-2041.	5.2	6
6	Comparison of three techniques for genetic estimation of effective population size in a critically endangered parrot. Animal Conservation, 2021, 24, 491-498.	2.9	11
7	Detecting population declines via monitoring the effective number of breeders (N_b). Molecular Ecology Resources, 2021, 21, 379-393.	4.8	24
8	Big Data in Conservation Genomics: Boosting Skills, Hedging Bets, and Staying Current in the Field. Journal of Heredity, 2021, 112, 313-327.	2.4	10
9	Relative Precision of the Sibship and LD Methods for Estimating Effective Population Size With Genomics-Scale Datasets. Journal of Heredity, 2021, 112, 535-539.	2.4	8
10	Conservation and Management of Salmon in the Age of Genomics. Annual Review of Animal Biosciences, 2020, 8, 117-143.	7.4	34
11	An estimator of the Opportunity for Selection that is independent of mean fitness. Evolution; International Journal of Organic Evolution, 2020, 74, 1942-1953.	2.3	16
12	Serendipity and me. ICES Journal of Marine Science, 2020, 77, 1658-1665.	2.5	3
13	AgeStrucNb: Software for Simulating and Detecting Changes in the Effective Number of Breeders (Nb). Journal of Heredity, 2020, 111, 491-497.	2.4	3
14	Genomic signatures and correlates of widespread population declines in salmon. Nature Communications, 2019, 10, 2996.	12.8	52
15	Life history and temporal variability of escape events interactively determine the fitness consequences of aquaculture escapees on wild populations. Theoretical Population Biology, 2019, 129, 93-102.	1.1	10
16	The evolution of microendemism in a reef fish (Hypoplectrus maya). Molecular Ecology, 2019, 28, 2872-2885.	3.9	10
17	Rigorous monitoring of a large-scale marine stock enhancement program demonstrates the need for comprehensive management of fisheries and nursery habitat. Scientific Reports, 2019, 9, 5290.	3.3	27
18	Estimating effective population size of large marine populations, is it feasible?. Fish and Fisheries, 2019, 20, 189-198.	5.3	51

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19	Accounting for Age Structure and Spatial Structure in Eco-Evolutionary Analyses of a Large, Mobile Vertebrate. Journal of Heredity, 2018, 109, 709-723.	2.4	17
20	Null Alleles and FIS Ã— FST Correlations. Journal of Heredity, 2018, 109, 457-461.	2.4	18
21	Consequences of sex change for effective population size. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181702.	2.6	13
22	Genomics and conservation units: The genetic basis of adult migration timing in Pacific salmonids. Evolutionary Applications, 2018, 11, 1518-1526.	3.1	62
23	Robust estimates of a high N _e / N ratio in a top marine predator, southern bluefin tuna. Science Advances, 2018, 4, eaar7759.	10.3	47
24	Is the Red Wolf a Listable Unit Under the US Endangered Species Act?. Journal of Heredity, 2018, 109, 585-597.	2.4	44
25	Purging putative siblings from population genetic data sets: a cautionary view. Molecular Ecology, 2017, 26, 1211-1224.	3.9	134
26	Humanâ€mediated evolution in a threatened species? Juvenile lifeâ€history changes in Snake River salmon. Evolutionary Applications, 2017, 10, 667-681.	3.1	19
27	Performance of IUCN proxies for generation length. Conservation Biology, 2017, 31, 883-893.	4.7	15
28	Genotype-based estimates of local abundance and effective population size for Hector's dolphins. Biological Conservation, 2017, 211, 150-160.	4.1	9
29	Consistent Extinction Risk Assessment under the U.S. Endangered Species Act. Conservation Letters, 2017, 10, 328-336.	5.7	11
30	Effective number of breeders from sibship reconstruction: empirical evaluations using hatchery steelhead. Evolutionary Applications, 2017, 10, 146-160.	3.1	54
31	Fisheryâ€induced evolution provides insights into adaptive responses of marine species to climate change. Frontiers in Ecology and the Environment, 2016, 14, 217-224.	4.0	37
32	Making sense of genetic estimates of effective population size. Molecular Ecology, 2016, 25, 4689-4691.	3.9	48
33	Tiny estimates of the N_e/N ratio in marine fishes: Are they real?. Journal of Fish Biology, 2016, 89, 2479-2504.	1.6	70
34	Harvestâ€induced evolution and effective population size. Evolutionary Applications, 2016, 9, 658-672.	3.1	29
35	Sex change and effective population size: implications for population genetic studies in marine fish. Heredity, 2016, 117, 251-258.	2.6	20
36	Estimating contemporary effective population size in non-model species using linkage disequilibrium across thousands of loci. Heredity, 2016, 117, 233-240.	2.6	181

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37	Climate science strategy of the US National Marine Fisheries Service. Marine Policy, 2016, 74, 58-67.	3.2	54
38	Life-history traits and effective population size in species with overlapping generations revisited: the importance of adult mortality. Heredity, 2016, 117, 241-250.	2.6	38
39	Evaluating the Rymanâ€“Laikre effect for marine stock enhancement and aquaculture. Environmental Epigenetics, 2016, 62, 617-627.	1.8	41
40	Trends and management implications of humanâ€influenced lifeâ€history changes in marine ectotherms. Fish and Fisheries, 2016, 17, 1005-1028.	5.3	76
41	Effectiveness of managed gene flow in reducing genetic divergence associated with captive breeding. Evolutionary Applications, 2015, 8, 956-971.	3.1	47
42	Temporal correlations in population trends: Conservation implications from time-series analysis of diverse animal taxa. Biological Conservation, 2015, 192, 247-257.	4.1	52
43	Testing for Hardyâ€“Weinberg Proportions: Have We Lost the Plot?. Journal of Heredity, 2015, 106, 1-19.	2.4	290
44	Artificial propagation of freshwater fishes: benefits and risks to recipient ecosystems from stocking, translocation and re-introduction. , 2015, , 399-436.		4
45	Effects of Overlapping Generations on Linkage Disequilibrium Estimates of Effective Population Size. Genetics, 2014, 197, 769-780.	2.9	299
46	<scp>NeEstimator</scp> v2: reâ€implementation of software for the estimation of contemporary effective population size (N_e) from genetic data. Molecular Ecology Resources, 2014, 14, 209-214.	4.8	1,584
47	INTERMITTENT BREEDING AND CONSTRAINTS ON LITTER SIZE: CONSEQUENCES FOR EFFECTIVE POPULATION SIZE PER GENERATION (N_e) AND PER REPRODUCTIVE CYCLE (N_b). Evolution; International Journal of Organic Evolution, 2014, 68, 1722-1734.	2.3	48
48	Combining demographic and genetic factors to assess population vulnerability in stream species. Ecological Applications, 2014, 24, 1505-1524.	3.8	34
49	Genetic Monitoring of Threatened Chinook Salmon Populations: Estimating Introgression of Nonnative Hatchery Stocks and Temporal Genetic Changes. North American Journal of Fisheries Management, 2013, 33, 693-706.	1.0	15
50	Simple life-history traits explain key effective population size ratios across diverse taxa. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131339.	2.6	173
51	Accounting for missing data in the estimation of contemporary genetic effective population size (N_e). Molecular Ecology Resources, 2013, 13, 243-253.	4.8	62
52	Estimation of effective population size in continuously distributed populations: there goes the neighborhood. Heredity, 2013, 111, 189-199.	2.6	112
53	A Tale of Two Acts: Endangered Species Listing Practices in Canada and the United States. BioScience, 2013, 63, 723-734.	4.9	84
54	A Tale of Two Acts: Endangered Species Listing Practices in Canada and the United States. BioScience, 2013, 63, 723-734.	4.9	56

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55	Introduction. Conservation Biology, 2013, 27, 1137-1137.	4.7	3
56	Genetic diversity in the Snake River sockeye salmon captive broodstock program as estimated from broodstock records. Conservation Genetics, 2012, 13, 1183-1193.	1.5	21
57	Detecting population recovery using gametic disequilibrium-based effective population size estimates. Conservation Genetics Resources, 2012, 4, 987-989.	0.8	8
58	Red flags: correlates of impaired species recovery. Trends in Ecology and Evolution, 2012, 27, 542-546.	8.7	34
59	Effective size of a wild salmonid population is greatly reduced by hatchery supplementation. Heredity, 2012, 109, 254-260.	2.6	104
60	Population Genetic Structure and Life History Variability in Oncorhynchus nerka from the Snake River Basin. Transactions of the American Fisheries Society, 2011, 140, 716-733.	1.4	15
61	Genetic Monitoring Reveals Genetic Stability within and among Threatened Chinook Salmon Populations in the Salmon River, Idaho. North American Journal of Fisheries Management, 2011, 31, 96-105.	1.0	24
62	Inbreeding effective population size and parentage analysis without parents. Molecular Ecology Resources, 2011, 11, 162-171.	4.8	42
63	Time to Evolve? Potential Evolutionary Responses of Fraser River Sockeye Salmon to Climate Change and Effects on Persistence. PLoS ONE, 2011, 6, e20380.	2.5	94
64	CalculatingN_eandN_e/Nin age-structured populations: a hybrid Felsenstein-Hill approach. Ecology, 2011, 92, 1513-1522.	3.2	87
65	Interacting Effects of Phenotypic Plasticity and Evolution on Population Persistence in a Changing Climate. Conservation Biology, 2011, 25, 56-63.	4.7	245
66	Understanding and Estimating Effective Population Size for Practical Application in Marine Species Management. Conservation Biology, 2011, 25, 438-449.	4.7	270
67	Estimating Contemporary Effective Population Size on the Basis of Linkage Disequilibrium in the Face of Migration. Genetics, 2011, 189, 633-644.	2.9	201
68	Early detection of population fragmentation using linkage disequilibrium estimation of effective population size. Conservation Genetics, 2010, 11, 2425-2430.	1.5	44
69	Linkage disequilibrium estimates of contemporary N_e using highly variable genetic markers: a largely untapped resource for applied conservation and evolution. Evolutionary Applications, 2010, 3, 244-262.	3.1	777
70	Highâ€grading bias: subtle problems with assessing power of selected subsets of loci for population assignment. Molecular Ecology, 2010, 19, 2599-2601.	3.9	26
71	Integrating evolutionary considerations into recovery planning for Pacific salmon. , 2010, , 239-266.		3
72	Phenotypic plasticity and population viability: the importance of environmental predictability. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 3391-3400.	2.6	352

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73	When are genetic methods useful for estimating contemporary abundance and detecting population trends?. Molecular Ecology Resources, 2010, 10, 684-692.	4.8	82
74	Spatialâ€temporal stratifications in natural populations and how they affect understanding and estimation of effective population size. Molecular Ecology Resources, 2010, 10, 785-796.	4.8	105
75	Compromising genetic diversity in the wild: unmonitored large-scale release of plants and animals. Trends in Ecology and Evolution, 2010, 25, 520-529.	8.7	454
76	Eco-evolutionary dynamics: fluctuations in population growth rate reduce effective population size in chinook salmon. Ecology, 2010, 91, 902-914.	3.2	15
77	Modelling evolutionary processes in small populations: not as ideal as you think. Molecular Ecology, 2009, 18, 1834-1847.	3.9	22
78	Sex change and the genetic structure of marine fish populations. Fish and Fisheries, 2009, 10, 329-343.	5.3	33
79	Genetic and Evolutionary Considerations in Fishery Management: Research Needs for the Future. , 2009, , 427-451.		21
80	Legal Viability, Societal Values, and SPOIR: Response to D'Elia et al.. Conservation Biology, 2008, 22, 1075-1077.	4.7	4
81	Integrating genetic data into management of marine resources: how can we do it better?. Fish and Fisheries, 2008, 9, 423-449.	5.3	256
82	Evolutionary responses by native species to major anthropogenic changes to their ecosystems: Pacific salmon in the Columbia River hydropower system. Molecular Ecology, 2008, 17, 84-96.	3.9	122
83	Evolutionary history of Pacific salmon in dynamic environments. Evolutionary Applications, 2008, 1, 189-206.	3.1	133
84	Potential for anthropogenic disturbances to influence evolutionary change in the life history of a threatened salmonid. Evolutionary Applications, 2008, 1, 271-285.	3.1	50
85	<scp>ldne</scp>: a program for estimating effective population size from data on linkage disequilibrium. Molecular Ecology Resources, 2008, 8, 753-756.	4.8	1,071
86	An improved method for predicting the accuracy of genetic stock identification. Canadian Journal of Fisheries and Aquatic Sciences, 2008, 65, 1475-1486.	1.4	210
87	Temporal Estimates of Effective Population Size in Species With Overlapping Generations. Genetics, 2007, 175, 219-233.	2.9	162
88	Genetic monitoring as a promising tool for conservation and management. Trends in Ecology and Evolution, 2007, 22, 25-33.	8.7	934
89	Effective population size of steelhead trout: influence of variance in reproductive success, hatchery programs, and genetic compensation between life-history forms. Molecular Ecology, 2007, 16, 953-966.	3.9	125
90	Evaluating the performance of a multilocus Bayesian method for the estimation of migration rates. Molecular Ecology, 2007, 16, 1149-1166.	3.9	324

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91	A potential bias in the temporal method for estimating Nein admixed populations under natural selection. Molecular Ecology, 2007, 16, 2261-2271.	3.9	15
92	Pacific Salmon Extinctions: Quantifying Lost and Remaining Diversity. Conservation Biology, 2007, 21, 1009-1020.	4.7	260
93	A Biological Framework for Evaluating Whether a Species Is Threatened or Endangered in a Significant Portion of Its Range. Conservation Biology, 2007, 21, 964-974.	4.7	37
94	Normativity Redux. Conservation Biology, 2007, 21, 1649-1650.	4.7	7
95	Empirical Results of Salmon Supplementation in the Northeast Pacific: A Preliminary Assessment. , 2007, , 383-403.		34
96	salmonnb: a program for computing cohort-specific effective population sizes (Nb) in Pacific salmon and other semelparous species using the temporal method. Molecular Ecology Notes, 2006, 7, 21-24.	1.7	13
97	What is a population? An empirical evaluation of some genetic methods for identifying the number of gene pools and their degree of connectivity. Molecular Ecology, 2006, 15, 1419-1439.	3.9	1,266
98	A bias correction for estimates of effective population size based on linkage disequilibrium at unlinked gene loci*. Conservation Genetics, 2006, 7, 167-184.	1.5	667
99	Seed Banks, Salmon, and Sleeping Genes: Effective Population Size in Semelparous, Ageâ€Structured Species with Fluctuating Abundance. American Naturalist, 2006, 167, 118-135.	2.1	45
100	Genetic estimates of contemporary effective population size: to what time periods do the estimates apply?. Molecular Ecology, 2005, 14, 3335-3352.	3.9	255
101	Assignment methods: matching biological questions with appropriate techniques. Trends in Ecology and Evolution, 2005, 20, 136-142.	8.7	645
102	LIFE-HISTORY DIVERGENCE IN CHINOOK SALMON: HISTORIC CONTINGENCY AND PARALLEL EVOLUTION. Evolution; International Journal of Organic Evolution, 2004, 58, 386.	2.3	73
103	LIFE-HISTORY DIVERGENCE IN CHINOOK SALMON: HISTORIC CONTINGENCY AND PARALLEL EVOLUTION. Evolution; International Journal of Organic Evolution, 2004, 58, 386-403.	2.3	196
104	Life-history divergence in Chinook salmon: historic contingency and parallel evolution. Evolution; International Journal of Organic Evolution, 2004, 58, 386-403.	2.3	43
105	Understanding and confronting species uncertainty in biology and conservation. Trends in Ecology and Evolution, 2003, 18, 597-603.	8.7	263
106	Evaluating the effect of stage-specific survivorship on theNe/Nratio. Molecular Ecology, 2002, 11, 1029-1037.	3.9	89
107	Relationship of Effective to Census Size in Fluctuating Populations. Conservation Biology, 2002, 16, 129-136.	4.7	114
108	Effective Size of Fluctuating Salmon Populations. Genetics, 2002, 161, 783-791.	2.9	96

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109	Characterizing diversity in salmon from the Pacific Northwest*. Journal of Fish Biology, 2001, 59, 1-41.	1.6	49
110	Evolution of Sockeye Salmon Ecotypes. Science, 2001, 291, 251b-252.	12.6	7
111	Dispelling Some Myths about Hatcheries. Fisheries, 1999, 24, 12-21.	0.8	214
112	Prioritizing Pacific Salmon Stocks for Conservation: Response to Allendorf et al.. Conservation Biology, 1998, 12, 1144-1147.	4.7	13
113	Separating the wheat from the chaff: patterns of genetic differentiation in high gene flow species. , 1998, 89, 438-450.		1,016
114	Evolutionarily Significant Units, Distinct Population Segments, and the Endangered Species Act: Reply to Pennock and Dimmick. Conservation Biology, 1998, 12, 718-721.	4.7	19
115	Allozyme Variability ofOncorhynchus nerkain the Pacific Northwest, with Special Consideration to Populations of Redfish Lake, Idaho. Transactions of the American Fisheries Society, 1996, 125, 645-663.	1.4	49
116	Conservation and Genetics of Salmonid Fishes. , 1996, , 238-280.		204
117	Genetic Risk Associated with Supplementation of Pacific Salmonids: Captive Broodstock Programs. Canadian Journal of Fisheries and Aquatic Sciences, 1994, 51, 310-329.	1.4	119
118	Effective population numbers of shellfish broodstocks estimated from temporal variance in allelic frequencies. Aquaculture, 1992, 108, 215-232.	3.5	148
119	Genetic interactions Between Hatchery and Wild Salmonids: Lessons from the Pacific Northwest. Canadian Journal of Fisheries and Aquatic Sciences, 1991, 48, 124-133.	1.4	347
120	Conservation Genetics of Pacific Salmon. II. Effective Population Size and the Rate of Loss of Genetic Variability. Journal of Heredity, 1990, 81, 267-276.	2.4	130
121	Conservation Genetics of Pacific Salmon I. Temporal Changes in Allele Frequency. Conservation Biology, 1990, 4, 144-156.	4.7	145
122	Conservation Genetics of Pacific Salmon. III. Estimating Effective Population Size. Journal of Heredity, 1990, 81, 277-289.	2.4	111
123	TEMPORAL VARIATION IN ALLELE FREQUENCIES: TESTING THE RIGHT HYPOTHESIS. Evolution; International Journal of Organic Evolution, 1989, 43, 1236-1251.	2.3	95
124	A generalized approach for estimating effective population size from temporal changes in allele frequency.. Genetics, 1989, 121, 379-391.	2.9	695
125	Estimation of allele frequencies at isoloci.. Genetics, 1988, 118, 371-384.	2.9	64