

# Lisa W Seeb

## List of Publications by Year in descending order

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74  
papers

3,038  
citations

117619

34  
h-index

189881

50  
g-index

77  
all docs

77  
docs citations

77  
times ranked

2579  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genotyping by sequencing resolves shallow population structure to inform conservation of Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Evolutionary Applications</i> , 2014, 7, 355-369.	3.1	178
2	Paralogs are revealed by proportion of heterozygotes and deviations in read ratios in genotyping-by-sequencing data from natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 656-669.	4.8	167
3	Use of sequence data from rainbow trout and Atlantic salmon for SNP detection in Pacific salmon. <i>Molecular Ecology</i> , 2005, 14, 4193-4203.	3.9	165
4	Managing fisheries using genetic data: case studies from four species of Pacific salmon. <i>Fisheries Research</i> , 1999, 43, 45-78.	1.7	140
5	RADseq provides unprecedented insights into molecular ecology and evolutionary genetics: comment on Breaking RAD by Lowry et al. (2016). <i>Molecular Ecology Resources</i> , 2017, 17, 356-361.	4.8	112
6	Effects of Crossovers Between Homeologs on Inheritance and Population Genomics in Polyploid-Derived Salmonid Fishes. <i>Journal of Heredity</i> , 2015, 106, 217-227.	2.4	97
7	SNP Genotyping by the 5'-Nuclease Reaction: Advances in High-Throughput Genotyping with Nonmodel Organisms. <i>Methods in Molecular Biology</i> , 2009, 578, 277-292.	0.9	78
8	Single-nucleotide polymorphisms (SNPs) identified through genotyping-by-sequencing improve genetic stock identification of Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ) from western Alaska. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2014, 71, 698-708.	1.4	74
9	Single-Nucleotide Polymorphisms (SNPs) under Diversifying Selection Provide Increased Accuracy and Precision in Mixed-Stock Analyses of Sockeye Salmon from the Copper River, Alaska. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 865-881.	1.4	70
10	Genetic Population Structure of Chum Salmon in the Pacific Rim Inferred from Mitochondrial DNA Sequence Variation. <i>Environmental Biology of Fishes</i> , 2004, 69, 37-50.	1.0	69
11	DNA and allozyme markers provide concordant estimates of population differentiation: analyses of U.S. and Canadian populations of Yukon River fall-run chum salmon ( <i>Oncorhynchus keta</i> ). <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1998, 55, 1748-1758.	1.4	62
12	Single Nucleotide Polymorphisms Provide Rapid and Accurate Estimates of the Proportions of U.S. and Canadian Chinook Salmon Caught in Yukon River Fisheries. <i>North American Journal of Fisheries Management</i> , 2005, 25, 944-953.	1.0	62
13	Genomic islands of divergence linked to ecotypic variation in sockeye salmon. <i>Molecular Ecology</i> , 2017, 26, 554-570.	3.9	62
14	Retention of a chromosomal inversion from an anadromous ancestor provides the genetic basis for alternative freshwater ecotypes in rainbow trout. <i>Molecular Ecology</i> , 2019, 28, 1412-1427.	3.9	58
15	High Genetic Heterogeneity in Chum Salmon in Western Alaska, the Contact Zone between Northern and Southern Lineages. <i>Transactions of the American Fisheries Society</i> , 1999, 128, 58-87.	1.4	54
16	Genetic Diversity of Sockeye Salmon of Cook Inlet, Alaska, and Its Application to Management of Populations Affected by the Exxon Valdez Oil Spill. <i>Transactions of the American Fisheries Society</i> , 2000, 129, 1223-1249.	1.4	53
17	Allozymes and Mitochondrial DNA Discriminate Asian and North American Populations of Chum Salmon in Mixed-Stock Fisheries along the South Coast of the Alaska Peninsula. <i>Transactions of the American Fisheries Society</i> , 1999, 128, 88-103.	1.4	52
18	Number of Alleles as a Predictor of the Relative Assignment Accuracy of Short Tandem Repeat (STR) and Single-Nucleotide Polymorphism (SNP) Baselines for Chum Salmon. <i>Transactions of the American Fisheries Society</i> , 2008, 137, 751-762.	1.4	52

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19	Complementary uses of ecological and biochemical genetic data in identifying and conserving salmon populations. <i>Fisheries Research</i> , 1993, 18, 59-76.	1.7	51
20	Managing mixed-stock fisheries: genotyping multi-SNP haplotypes increases power for genetic stock identification. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 429-434.	1.4	51
21	Multiplex preamplification PCR and microsatellite validation enables accurate single nucleotide polymorphism genotyping of historical fish scales. <i>Molecular Ecology Resources</i> , 2011, 11, 268-277.	4.8	50
22	Divergent life-history races do not represent Chinook salmon coast-wide: the importance of scale in Quaternary biogeography. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 415-435.	1.4	50
23	Sorting duplicated loci disentangles complexities of polyploid genomes masked by genotyping by sequencing. <i>Molecular Ecology</i> , 2016, 25, 2117-2129.	3.9	46
24	Single nucleotide polymorphisms unravel hierarchical divergence and signatures of selection among Alaskan sockeye salmon ( <i>Oncorhynchus nerka</i> ) populations. <i>BMC Evolutionary Biology</i> , 2011, 11, 48.	3.2	45
25	Genetic Variation and Postglacial Dispersal of Populations of Northern Pike ( <i>Esox lucius</i> ) in North America. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1987, 44, 556-561.	1.4	44
26	Spawning Habitat and Geography Influence Population Structure and Juvenile Migration Timing of Sockeye Salmon in the Wood River Lakes, Alaska. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 763-782.	1.4	44
27	Identification of Multiple QTL Hotspots in Sockeye Salmon ( <i>Oncorhynchus nerka</i> ) Using Genotyping-by-Sequencing and a Dense Linkage Map. <i>Journal of Heredity</i> , 2016, 107, 122-133.	2.4	43
28	Rank and Order: Evaluating the Performance of SNPs for Individual Assignment in a Non-Model Organism. <i>PLoS ONE</i> , 2012, 7, e49018.	2.5	42
29	Impacts of Marker Class Bias Relative to Locus-Specific Variability on Population Inferences in Chinook Salmon: A Comparison of Single-Nucleotide Polymorphisms with Short Tandem Repeats and Allozymes. <i>Transactions of the American Fisheries Society</i> , 2007, 136, 1674-1687.	1.4	41
30	Signatures of natural selection among lineages and habitats in <i>Oncorhynchus mykiss</i> . <i>Ecology and Evolution</i> , 2012, 2, 1-18.	1.9	41
31	Genetic Relationships Among <i>Salvelinus</i> Species Inferred from Allozyme Data. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1994, 51, 182-197.	1.4	39
32	Transforming ecology and conservation biology through genome editing. <i>Conservation Biology</i> , 2020, 34, 54-65.	4.7	39
33	Genetic differentiation of Alaska Chinook salmon: the missing link for migratory studies. <i>Molecular Ecology Resources</i> , 2011, 11, 226-246.	4.8	38
34	Genetic Interpretation of Broad-Scale Microsatellite Polymorphism in Odd-Year Pink Salmon. <i>Transactions of the American Fisheries Society</i> , 1998, 127, 535-550.	1.4	37
35	Single-nucleotide polymorphisms reveal distribution and migration of Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ) in the Bering Sea and North Pacific Ocean. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 128-141.	1.4	37
36	Use of the 5â€²-Nuclease Reaction for Single Nucleotide Polymorphism Genotyping in Chinook Salmon. <i>Transactions of the American Fisheries Society</i> , 2005, 134, 207-217.	1.4	34

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37	Genetic variation in allozymes of western larch. Canadian Journal of Forest Research, 1986, 16, 1013-1018.	1.7	33
38	Dense SNP panels resolve closely related Chinook salmon populations. Canadian Journal of Fisheries and Aquatic Sciences, 2020, 77, 451-461.	1.4	33
39	Identification and Characterization of Sex-Associated Loci in Sockeye Salmon Using Genotyping-by-Sequencing and Comparison with a Sex-Determining Assay Based on the sdyGene. Journal of Heredity, 2016, 107, 559-566.	2.4	32
40	Genetic and Ecological Divergence Defines Population Structure of Sockeye Salmon Populations Returning to Bristol Bay, Alaska, and Provides a Tool for Admixture Analysis. Transactions of the American Fisheries Society, 2007, 136, 82-94.	1.4	31
41	Signals of heterogeneous selection at an MHC locus in geographically proximate ecotypes of sockeye salmon. Molecular Ecology, 2014, 23, 5448-5461.	3.9	30
42	Temporally Isolated Lineages of Pink Salmon Reveal Unique Signatures of Selection on Distinct Pools of Standing Genetic Variation. Journal of Heredity, 2014, 105, 835-845.	2.4	30
43	Resolving allele dosage in duplicated loci using genotyping-by-sequencing data: A path forward for population genetic analysis. Molecular Ecology Resources, 2018, 18, 570-579.	4.8	28
44	Temporal and Geographic Genetic Divergence: Characterizing Sockeye Salmon Populations in the Chignik Watershed, Alaska, Using Single-Nucleotide Polymorphisms. Transactions of the American Fisheries Society, 2011, 140, 749-762.	1.4	26
45	High-Resolution Melting Analysis for the Discovery of Novel Single-Nucleotide Polymorphisms in Rainbow and Cutthroat Trout for Species Identification. Transactions of the American Fisheries Society, 2010, 139, 676-684.	1.4	25
46	Network Analysis of Linkage Disequilibrium Reveals Genome Architecture in Chum Salmon. G3: Genes, Genomes, Genetics, 2020, 10, 1553-1561.	1.8	24
47	Landscape heterogeneity and local adaptation define the spatial genetic structure of Pacific salmon in a pristine environment. Conservation Genetics, 2013, 14, 483-498.	1.5	22
48	Parallel signatures of selection in temporally isolated lineages of pink salmon. Molecular Ecology, 2014, 23, 2473-2485.	3.9	22
49	Development of Genomic Resources for Pacific Herring through Targeted Transcriptome Pyrosequencing. PLoS ONE, 2012, 7, e30908.	2.5	22
50	Thirty-eight single nucleotide polymorphism markers for high-throughput genotyping of chum salmon. Molecular Ecology Notes, 2007, 7, 1211-1215.	1.7	19
51	Recombination patterns reveal information about centromere location on linkage maps. Molecular Ecology Resources, 2016, 16, 655-661.	4.8	19
52	The application of genomics to inform conservation of a functionally important reef fish (Scarus) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 1	1.5	19
53	Single-Nucleotide Polymorphic Genotypes Reveal Patterns of Early Juvenile Migration of Sockeye Salmon in the Eastern Bering Sea. Transactions of the American Fisheries Society, 2011, 140, 734-748.	1.4	18
54	Screening of duplicated loci reveals hidden divergence patterns in a complex salmonid genome. Molecular Ecology, 2017, 26, 4509-4522.	3.9	18

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55	Genetic signals of artificial and natural dispersal linked to colonization of South America by non-native Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Ecology and Evolution</i> , 2018, 8, 6192-6209.	1.9	17
56	Fine-scale sampling reveals distinct isolation by distance patterns in chum salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Evolution</i> , 2018, 8, 273-285.	1.5	16
57	A general model for salmon run reconstruction that accounts for interception and differences in availability to harvest. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 439-451.	1.4	16
58	Low allozyme heterozygosity in North Pacific and Bering Sea populations of red king crab ( <i>Paralithodes camtschaticus</i> ): adaptive specialization, population bottleneck, or metapopulation structure?. <i>ICES Journal of Marine Science</i> , 2011, 68, 499-506.	2.5	15
59	Chum Salmon Genetic Diversity in the Northeastern Pacific Ocean Assessed with Single Nucleotide Polymorphisms (SNPs): Applications to Fishery Management. <i>North American Journal of Fisheries Management</i> , 2015, 35, 974-987.	1.0	14
60	Parallel signatures of selection at genomic islands of divergence and the major histocompatibility complex in ecotypes of sockeye salmon across Alaska. <i>Molecular Ecology</i> , 2019, 28, 2254-2271.	3.9	14
61	The pink salmon genome: Uncovering the genomic consequences of a two-year life cycle. <i>PLoS ONE</i> , 2021, 16, e0255752.	2.5	14
62	Genetic Structure and Diversity of Japanese Chum Salmon Populations Inferred from Single-Nucleotide Polymorphism Markers. <i>Transactions of the American Fisheries Society</i> , 2014, 143, 1231-1246.	1.4	13
63	Allozyme polymorphisms permit the identification of larval and juvenile rockfishes of the genus <i>Sebastes</i> . <i>Environmental Biology of Fishes</i> , 1991, 30, 191-201.	1.0	12
64	Y-chromosome haplotypes are associated with variation in size and age at maturity in male Chinook salmon. <i>Evolutionary Applications</i> , 2020, 13, 2791-2806.	3.1	12
65	How Stock of Origin Affects Performance of Individuals across a Meta-Ecosystem: An Example from Sockeye Salmon. <i>PLoS ONE</i> , 2013, 8, e58584.	2.5	11
66	Consequences of Emergence Timing for the Growth and Relative Survival of Steelhead Fry from Naturally Spawning Wild and Hatchery Parents. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 977-989.	1.4	10
67	Contrasting genetic metrics and patterns among naturalized rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Evolution</i> , 2018, 8, 273-285.	1.9	10
68	Hierarchical biogeographical processes largely explain the genomic divergence pattern in a species complex of sea anemones (Metridioidea: Sagartiidae: Anthothoe). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 217-228.	2.7	8
69	Temporal Genetic Variance and Propagule-Driven Genetic Structure Characterize Naturalized Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) from a Patagonian Lake Impacted by Trout Farming. <i>PLoS ONE</i> , 2015, 10, e0142040.	2.5	7
70	Deep sequencing of the transcriptome and mining of single nucleotide polymorphisms (SNPs) provide genomic resources for applied studies in Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Conservation Genetics Resources</i> , 2014, 6, 807-811.	0.8	6
71	Novel RAD sequence data reveal a lack of genomic divergence between dietary ecotypes in a landlocked salmonid population. <i>Conservation Genetics Resources</i> , 2018, 10, 169-171.	0.8	5
72	Mixed-stock analyses of migratory, non-native Chinook salmon at sea and assignment to natal sites in fresh water at their introduced range in South America. <i>Biological Invasions</i> , 2020, 22, 3175-3182.	2.4	5

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73	“Chromosomes and genes, spawned these fateful scenes” Rapid adaptation in an introduced fish. <i>Molecular Ecology</i> , 2018, 27, 3965-3967.	3.9	1
74	Response to May and Delany: We Never Said Wright was Wrong. <i>Journal of Heredity</i> , 2015, 106, esv072.	2.4	0