## William W Laegreid

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. Mammalian Genome, 2002, 13, 272-281.	2.2	199
2	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. Applied and Environmental Microbiology, 2010, 76, 4858-4862.	3.1	146
3	Genotypic Analyses of Escherichia coli O157:H7 and O157 Nonmotile Isolates Recovered from Beef Cattle and Carcasses at Processing Plants in the Midwestern States of the United States. Applied and Environmental Microbiology, 2001, 67, 3810-3818.	3.1	114
4	Immune Evasion of Porcine Reproductive and Respiratory Syndrome Virus through Glycan Shielding Involves both Glycoprotein 5 as Well as Glycoprotein 3. Journal of Virology, 2011, 85, 5555-5564.	3.4	107
5	Prion gene sequence variation within diverse groups of U.S. sheep, beef cattle, and deer. Mammalian Genome, 2003, 14, 765-777.	2.2	104
6	A highly attenuated host range-restricted vaccinia virus strain, NYVAC, encoding the prM, E, and NS1 genes of Japanese encephalitis virus prevents JEV viremia in swine. Virology, 1992, 190, 454-458.	2.4	103
7	Sequence Evaluation of Four Pooled-Tissue Normalized Bovine cDNA Libraries and Construction of a Gene Index for Cattle. Genome Research, 2001, 11, 626-630.	5.5	98
8	Association of neonatal serum immunoglobulin G1 concentration with health and performance in beef calves. Journal of the American Veterinary Medical Association, 2006, 228, 914-921.	0.5	88
9	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. PLoS Genetics, 2012, 8, e1002467.	3.5	78
10	A mechanically-induced colon cancer cell population shows increased metastatic potential. Molecular Cancer, 2014, 13, 131.	19.2	65
11	Association of Escherichia coli O157:H7 tirpolymorphisms with human infection. BMC Infectious Diseases, 2007, 7, 98.	2.9	64
12	Bovine Immune Response to Shiga-Toxigenic Escherichia coli O157:H7. Vaccine Journal, 2006, 13, 1322-1327.	3.1	63
13	Single nucleotide polymorphism (SNP) discovery and linkage mapping of bovine cytokine genes. Mammalian Genome, 1999, 10, 1062-1069.	2.2	61
14	Estimation of DNA sequence diversity in bovine cytokine genes. Mammalian Genome, 2001, 12, 32-37.	2.2	51
15	Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. Journal of the American Veterinary Medical Association, 2005, 226, 1311-1314.	0.5	46
16	Prevalence of the prion protein gene E211K variant in U.S. cattle. BMC Veterinary Research, 2008, 4, 25.	1.9	46
17	Location of T-cell epitopes in nonstructural proteins 9 and 10 of type-II porcine reproductive and respiratory syndrome virus. Virus Research, 2012, 169, 13-21.	2.2	45
18	Association of bovine neonatal Fc receptor a-chain gene (FCGRT) haplotypes with serum IgG concentration in newborn calves. Mammalian Genome, 2002, 13, 704-710	2.2	42

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19	Interleukin-8 haplotype structure from nucleotide sequence variation in commercial populations of U.S. beef cattle. Mammalian Genome, 2001, 12, 219-226.	2.2	38
20	Prion gene haplotypes of U.S. cattle. BMC Genetics, 2006, 7, 51.	2.7	36
21	A Synthetic Porcine Reproductive and Respiratory Syndrome Virus Strain Confers Unprecedented Levels of Heterologous Protection. Journal of Virology, 2015, 89, 12070-12083.	3.4	36
22	Association of a Bovine Prion Gene Haplotype with Atypical BSE. PLoS ONE, 2008, 3, e1830.	2.5	34
23	Beta-2-microglobulin haplotypes in U.S. beef cattle and association with failure of passive transfer in newborn calves. Mammalian Genome, 2004, 15, 227-236.	2.2	33
24	Distribution of Shiga-Toxigenic <i>Escherichia coli</i> O157 in the Gastrointestinal Tract of Naturally O157-Shedding Cattle at Necropsy. Applied and Environmental Microbiology, 2010, 76, 5278-5281.	3.1	29
25	Evaluation of a Real-Time PCR Kit for Detecting Escherichia coli O157 in Bovine Fecal Samples. Applied and Environmental Microbiology, 2004, 70, 1855-1857.	3.1	25
26	Gene expression profiling of bovine macrophages in response to O157:H7 lipopolysaccharide. Developmental and Comparative Immunology, 2004, 28, 635-645.	2.3	25
27	A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20.	2.7	22
28	Ranking viruses: measures of positional importance within networks define core viruses for rational polyvalent vaccine development. Bioinformatics, 2012, 28, 1624-1632.	4.1	20
29	PRNP Haplotype Associated with Classical BSE Incidence in European Holstein Cattle. PLoS ONE, 2010, 5, e12786.	2.5	20
30	Small ruminant lentivirus genetic subgroups associate with sheep TMEM154 genotypes. Veterinary Research, 2013, 44, 64.	3.0	19
31	Development of a Blocking Enzyme-Linked Immunosorbent Assay for Detection of Serum Antibodies to O157 Antigen of <i>Escherichia coli</i> . Vaccine Journal, 1998, 5, 242-246.	2.6	18
32	Identification and genetic mapping of bovine chemokine genes expressed in epithelial cells. Mammalian Genome, 1999, 10, 128-133.	2.2	13
33	Ovine reference materials and assays for prion genetic testing. BMC Veterinary Research, 2010, 6, 23.	1.9	12
34	In-Depth Global Analysis of Transcript Abundance Levels in Porcine Alveolar Macrophages Following Infection with Porcine Reproductive and Respiratory Syndrome Virus. Advances in Virology, 2010, 2010, 1-12.	1.1	12
35	Prevalence of and risk factors associated with ovine progressive pneumonia in Wyoming sheep flocks. Journal of the American Veterinary Medical Association, 2015, 247, 932-937.	0.5	8
36	Optimization of Brucella abortus Protocols for Downstream Molecular Applications. Journal of Clinical Microbiology, 2018, 56, .	3.9	8

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37	Linkage disequilibrium across six prion gene regions spanning 20 kbp in U.S. sheep. Mammalian Genome, 2006, 17, 1121-1129.	2.2	6
38	Correlation of amino acid preference and mammalian viral genome type. Bioinformatics, 2005, 21, 1349-1357.	4.1	3
39	A sequencing strategy for identifying variation throughout the prion gene of BSE-affected cattle. BMC Research Notes, 2008, 1, 32.	1.4	2