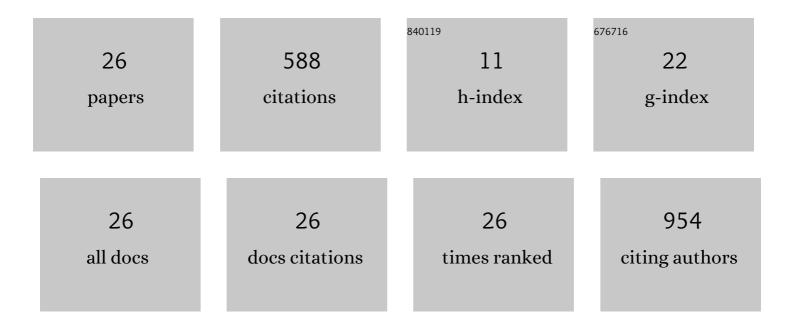
Christine Flury

List of Publications by Year in descending order

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CHDISTINE FILIDY

#	Article	IF	CITATIONS
1	Runs of homozygosity in Swiss goats reveal genetic changes associated with domestication and modern selection. Genetics Selection Evolution, 2022, 54, 6.	1.2	14
2	Identification of two new recessive <i>MC1R</i> alleles in redâ€coloured Evolèner cattle and other breeds. Animal Genetics, 2022, 53, 427-435.	0.6	1
3	Introgression of ASIP and TYRP1 Alleles Explains Coat Color Variation in Valais Goats. Journal of Heredity, 2021, 112, 452-457.	1.0	7
4	Big dairy data to unravel effects of environmental, physiological and morphological factors on milk production of mountain-pastured Braunvieh cows. Royal Society Open Science, 2020, 7, 200638.	1.1	3
5	The LCORL Locus Is under Selection in Large-Sized Pakistani Goat Breeds. Genes, 2020, 11, 168.	1.0	25
6	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. Genes, 2019, 10, 826.	1.0	14
7	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. PLoS Genetics, 2019, 15, e1008536.	1.5	50
8	Title is missing!. , 2019, 15, e1008536.		0
9	Title is missing!. , 2019, 15, e1008536.		Ο
10	Title is missing!. , 2019, 15, e1008536.		0
11	Title is missing!. , 2019, 15, e1008536.		Ο
12	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. Journal of Dairy Science, 2018, 101, 1292-1296.	1.4	35
13	Crossed beaks in a local Swiss chicken breed. BMC Veterinary Research, 2018, 14, 68.	0.7	8
14	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. Genetics Selection Evolution, 2017, 49, 83.	1.2	49
15	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. BMC Genomics, 2017, 18, 999.	1.2	22
16	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. BMC Genomics, 2017, 18, 910.	1.2	36
17	A WebGIS platform for the monitoring of Farm Animal Genetic Resources (GENMON). PLoS ONE, 2017, 12, e0176362.	1.1	10
18	Identification of key contributors in complex population structures. PLoS ONE, 2017, 12, e0177638.	1.1	13

CHRISTINE FLURY

#	Article	IF	CITATIONS
19	A Non-Synonymous HMGA2 Variant Decreases Height in Shetland Ponies and Other Small Horses. PLoS ONE, 2015, 10, e0140749.	1.1	73
20	A Chromosomal Region on ECA13 Is Associated with Maxillary Prognathism in Horses. PLoS ONE, 2014, 9, e86607.	1.1	12
21	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. BMC Genomics, 2014, 15, 948.	1.2	44
22	A Genome-Wide Association Study Reveals Loci Influencing Height and Other Conformation Traits in Horses. PLoS ONE, 2012, 7, e37282.	1.1	138
23	Alopecia areata in Eringer cows. Veterinary Dermatology, 2010, 21, 545-553.	0.4	10
24	Haplotype kinship for three populations of the Goettingen minipig. Genetics Selection Evolution, 2007, 39, 159.	1.2	8
25	Extension of the concept of kinship, relationship, and inbreeding to account for linked epistatic complexes. Livestock Science, 2006, 103, 131-140.	0.6	6
26	Haplotype Reconstruction and Estimation of Haplotype Frequencies from Nuclear Families with Only One Parent Available. Human Heredity, 2006, 62, 12-19.	0.4	10