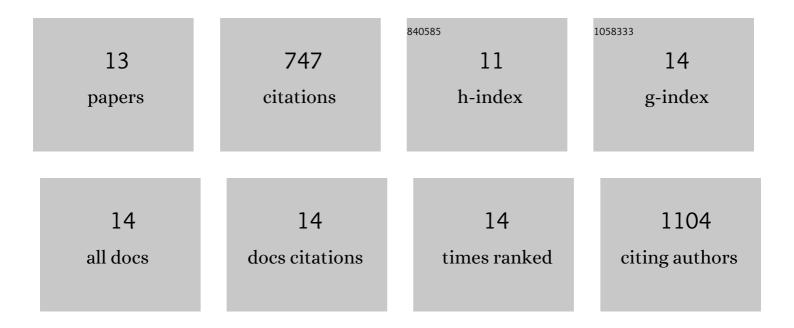
Kay-Uwe Götz

List of Publications by Year in descending order

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KAY-LIWE CÃOTZ

#	Article	IF	CITATIONS
1	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	9.4	286
2	Genome-Wide Association Study Identifies Two Major Loci Affecting Calving Ease and Growth-Related Traits in Cattle. Genetics, 2011, 187, 289-297.	1.2	96
3	A Nonsense Mutation in TMEM95 Encoding a Nondescript Transmembrane Protein Causes Idiopathic Male Subfertility in Cattle. PLoS Genetics, 2014, 10, e1004044.	1.5	88
4	Imputation of high-density genotypes in the Fleckvieh cattle population. Genetics Selection Evolution, 2013, 45, 3.	1.2	85
5	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. Genetics Selection Evolution, 2014, 46, 40.	1.2	59
6	Identification of QTL for UV-Protective Eye Area Pigmentation in Cattle by Progeny Phenotyping and Genome-Wide Association Analysis. PLoS ONE, 2012, 7, e36346.	1.1	53
7	Genomeâ€wide association study uncovers four <scp>QTL</scp> predisposing to supernumerary teats in cattle. Animal Genetics, 2012, 43, 689-695.	0.6	19
8	Syndrome of arachnomelia in Simmental cattle. BMC Veterinary Research, 2008, 4, 39.	0.7	16
9	Systematic genotyping of groups of cows to improve genomic estimated breeding values of selection candidates. Genetics Selection Evolution, 2016, 48, 73.	1.2	13
10	A simple method to separate base population and segregation effects in genomic relationship matrices. Genetics Selection Evolution, 2015, 47, 53.	1.2	12
11	Arachnomelia syndrome in Simmental cattle is caused by a homozygous 2-bp deletion in the molybdenum cofactor synthesis step 1 gene (MOCS1). BMC Genetics, 2011, 12, 11.	2.7	11
12	Precision of genetic parameters and breeding values estimated in marker assisted BLUP genetic evaluation. Genetics Selection Evolution, 2009, 41, 26.	1.2	6
13	Genotyping of groups of cows to improve genomic breeding values of new traits. Journal of Animal Breeding and Genetics, 2018, 135, 286-292.	0.8	1