Bibliography

[1]   Meyer R., Höfelein C., Lüthy J., Candrian U. Polymerase chain reaction-restriction fragment length polymorphism analysis: a simple method for species identification on food. *J. AOAC Int*. 1995, 78 (6) pp. 1542–1551

[2]   Palumbi S., Martin A., Romano S., Mcmillan W.O., Stice L., Grabowski G. The Simple Fool's Guide To PCR, Honolulu, HI: Dept. of Zoology and Kewalo Marine Laboratory, University of Hawaii, 2, 2002

[3]   Cornish-Bowden A. Nomenclature for incompletely specified bases in nucleic acid sequences: recommendations 1984. *Nucleic Acids Res*. 1985, 13 pp. 3021–3030

[4]   ISO 21571:2005, *Foodstuffs — Methods of analysis for the detection of genetically modified organisms and derived products — Nucleic acid extraction*

[5]   ISO 22949-1:2021, *Molecular biomarker analysis — Methods of analysis for the detection and identification of animal species in food and feed products (nucleotide sequencing-based methods) — Part 1: General requirements*

[6]   Matthes N., Pietsch K., Rullmann A., Näumann G., Pöpping B., Szabo K. The Barcoding Table of Animal Species (BaTAnS): a new tool to select appropriate methods for animal species identification using DNA barcoding. *Mol. Biol. Rep*. 2020, 47 pp. 6457–6461. DOI:10.1007/s11033-020-05675-1

[7]   Harrison R.G., Larson E.L. Hybridization, Introgression, and the Nature of Species Boundaries. *J. Hered*. 2014, 105 pp. 795–809. DOI:10.1093/jhered/esu033

[8]   Ratnasingham S., Hebert P.D.N. BOLD: The Barcode of Life Data System. *Mol. Ecol. Notes*. 2007, 7 pp. 355–364

[9]   Benson D.A., Cavanaugh M., Clark K., Karsch-Mizrachi I., Lipman D.J., Ostell J. et al. GenBank. *Nucleic Acids Res*. 2013, 41 pp. D36–D42. DOI:10.1093/nar/gks1195

[10]   Denay G., Preckel L., Petersen H., Pietsch K., Wöhlke A., Brünen-Nieweler C. Benchmarking and validation of a bioinformatics workflow for meat species identification using 16S rDNA metabarcoding. *Foods*. 2023, DOI:10.3390/foods12050968