EvaGreen® References

Characterization of EvaGreen dye for qPCR

Mao, F., Leung, W.Y., and Xin, X. (2007). Characterization of EvaGreen and the implication of its physicochemical properties for qPCR applications. BMC Biotechnology, 7, 76. doi:10.1186/1472-6750-7-76

EvaGreen in ddPCR

Athamanolap, P.,Shin, D. J., and Wang, T. H. (2013). Droplet Array Platform for High-Resolution Melt Analysis of DNA Methylation Density. J Lab Autom. 10.1177/2211068213507923 (HRM, DNA methylation)

Fraley, S. I.,Hardick, J.,Jo Masek, B.,Athamanolap, P.,Rothman, R. E.,Gaydos, C. A.,Carroll, K. C.,Wakefield, T.,Wang, T. H., and Yang, S. (2013). Universal digital high-resolution melt: a novel approach to broad-based profiling of heterogeneous biological samples. Nucleic Acids Res 41, e175. 10.1093/nar/gkt684 (U-dHRM bacteria diagnostics)

McDermott, G. P.,Do, D.,Litterst, C. M.,Maar, D.,Hindson, C. M.,Steenblock, E. R.,Legler, T. C.,Jouvenot, Y.,Marrs, S. H.,Bemis, A., et al. (2013). Multiplexed target detection using DNA-binding dye chemistry in droplet digital PCR. Anal Chem 85, 11619-11627. 10.1021/ac403061n (Evagreen multiplex in biorad ddPCR)

Miotke, L. K.,Lau, B. T.,Rumma, R. T., and Ji, H. P. (2014). High Sensitivity Detection and Quantitation of DNA Copy Number and Single Nucleotide Variants with Single Color Droplet Digital PCR. Anal Chem. 10.1021/ac403843j

EvaGreen in High Resolution Melt analysis

Athamanolap, P.,Shin, D. J., and Wang, T. H. (2013). Droplet Array Platform for High-Resolution Melt Analysis of DNA Methylation Density. J Lab Autom. 10.1177/2211068213507923 (HRM, DNA methylation)

Cai, X. Q.,Yu, H. Q.,Ruan, Z. X.,Yang, L. L.,Bai, J. S.,Qiu, D. Y.,Jian, Z. H.,Xiao, Y. Q.,Yang, J. Y.,Le, T. H., et al. (2013). Rapid detection and simultaneous genotyping of Cronobacter spp. (formerly Enterobacter sakazakii) in powdered infant formula using real-time PCR and high resolution melting (HRM) analysis. PLoS One 8, e67082. 10.1371/journal.pone.0067082

Dhami, M. K., and Kumarasinghe, L. (2014). A HRM real-time PCR assay for rapid and specific identification of the emerging pest spotted-wing drosophila (Drosophila suzukii). PLoS One 9, e98934. 10.1371/journal.pone.0098934

Fraley, S. I.,Hardick, J.,Jo Masek, B.,Athamanolap, P.,Rothman, R. E.,Gaydos, C. A.,Carroll, K. C.,Wakefield, T.,Wang, T. H., and Yang, S. (2013). Universal digital high-resolution melt: a novel approach to broad-based profiling of heterogeneous biological samples. Nucleic Acids Res 41, e175. 10.1093/nar/gkt684 (U-dHRM bacteria diagnostics)

Hanson, E. K., and Ballantyne, J. (2013). Rapid and inexpensive body fluid identification by RNA profiling-based multiplex High Resolution Melt (HRM) analysis. F1000Res 2, 281. 10.12688/f1000research.2-281.v2

Kozina, V.,Cappallo-Obermann, H.,Gromoll, J., and Spiess, A. N. (2011). A one-step real-time multiplex PCR for screening Y-chromosomal microdeletions without downstream amplicon size analysis. PLoS One 6, e23174. 10.1371/journal.pone.0023174

Li, Y. D.,Chu, Z. Z.,Liu, X. G.,Jing, H. C.,Liu, Y. G., and Hao, D. Y. (2010). A cost-effective high-resolution melting approach using the EvaGreen dye for DNA polymorphism detection and genotyping in plants. J Integr Plant Biol 52, 1036-1042. 10.1111/j.1744-7909.2010.01001.x

Liyanage, K. E.,Hooper, A. J.,Defesche, J. C.,Burnett, J. R., and van Bockxmeer, F. M. (2008). High-resolution melting analysis for detection of familial ligand-defective apolipoprotein B-100 mutations. Ann Clin Biochem 45, 170-176. 10.1258/acb.2007.007077

Mader, E.,Ruzicka, J.,Schmiderer, C., and Novak, J. (2011). Quantitative high-resolution melting analysis for detecting adulterations. Anal Biochem 409, 153-155. 10.1016/j.ab.2010.10.009

Maltese, P.,Canestrari, E.,Palma, L.,Ruzzo, A.,Corini, F.,Menotta, M.,Andreoni, F.,Latiano, A.,Annese, V., and Magnani, M. (2009). High resolution melting (HRM) analysis for the detection of ER22/23EK, BclI, and N363S polymorphisms of the glucocorticoid receptor gene. J Steroid Biochem Mol Biol 113, 269-274. 10.1016/j.jsbmb.2009.01.012

Rao, P.,Wu, H.,Jiang, Y.,Opriessnig, T.,Zheng, X.,Mo, Y., and Yang, Z. (2014). Development of an EvaGreen-based multiplex real-time PCR assay with melting curve analysis for simultaneous detection and differentiation of six viral pathogens of porcine reproductive and respiratory disorder. J Virol Methods 208, 56-62. 10.1016/j.jviromet.2014.06.027

Tanaka, M.,Takahahi, J.,Hirayama, F., and Tani, Y. (2011). High-resolution melting analysis for genotyping Duffy, Kidd and Diego blood group antigens. Leg Med (Tokyo) 13, 1-6. 10.1016/j.legalmed.2010.08.004

Twist, G. P.,Gaedigk, R.,Leeder, J. S., and Gaedigk, A. (2013). High-resolution melt analysis to detect sequence variations in highly homologous gene regions: application to CYP2B6. Pharmacogenomics 14, 913-922. 10.2217/pgs.13.66 (HRM, SNP genotyping)

Valenzuela-Munoz, V.,Araya-Garay, J. M., and Gallardo-Escarate, C. (2013). SNP discovery and High Resolution Melting Analysis from massive transcriptome sequencing in the California red abalone Haliotis rufescens. Mar Genomics 10, 11-16. 10.1016/j.margen.2012.12.003

White, H. E.,Hall, V. J., and Cross, N. C. (2007). Methylation-sensitive high-resolution melting-curve analysis of the SNRPN gene as a diagnostic screen for Prader-Willi and Angelman syndromes. Clin Chem 53, 1960-1962. 10.1373/clinchem.2007.093351

You, C. G.,Li, X. J.,Li, Y. M.,Wang, L. P.,Li, F. F.,Guo, X. L., and Gao, L. N. (2013). Association analysis of single nucleotide polymorphisms of proinflammatory cytokine and their receptors genes with rheumatoid arthritis in northwest Chinese Han population. Cytokine 61, 133-138. 10.1016/j.cyto.2012.09.007

EvaGreen for Fluidigm

Adamski, M. G.,Li, Y.,Wagner, E.,Yu, H.,Seales-Bailey, C.,Soper, S. A.,Murphy, M., and Baird, A. E. (2013). Next-generation qPCR for the high-throughput measurement of gene expression in multiple leukocyte subsets. J Biomol Screen 18, 1008-1017. 10.1177/1087057113489882 (Fluidigm rt-pcr)

Allen, E. K.,Manichaikul, A.,Chen, W. M.,Rich, S. S.,Daly, K. A., and Sale, M. M. (2014). Evaluation of replication of variants associated with genetic risk of otitis media. PLoS One 9, e104212. 10.1371/journal.pone.0104212

Barribeau, S. M., and Schmid-Hempel, P. (2013). Qualitatively different immune response of the bumblebee host, Bombus terrestris, to infection by different genotypes of the trypanosome gut parasite, Crithidia bombi. Infect Genet Evol 20, 249-256. 10.1016/j.meegid.2013.09.014

Brunner, F. S.,Schmid-Hempel, P., and Barribeau, S. M. (2013). Immune gene expression in Bombus terrestris: signatures of infection despite strong variation among populations, colonies, and sister workers. PLoS One 8, e68181. 10.1371/journal.pone.0068181

Bugarel, M.,Vignaud, M. L.,Moury, F.,Fach, P., and Brisabois, A. (2012). Molecular identification in monophasic and nonmotile variants of Salmonella enterica serovar Typhimurium. Microbiologyopen 1, 481-489. 10.1002/mbo3.39

Citri, A.,Pang, Z. P.,Sudhof, T. C.,Wernig, M., and Malenka, R. C. (2012). Comprehensive qPCR profiling of gene expression in single neuronal cells. Nat Protoc 7, 118-127. 10.1038/nprot.2011.430

Diepeveen, E. T.,Roth, O., and Salzburger, W. (2013). Immune-related functions of the Hivep gene family in East African cichlid fishes. G3 (Bethesda) 3, 2205-2217. 10.1534/g3.113.008839

Flynn, J. M.,Spusta, S. C.,Rosen, C. J., and Melov, S. (2013). Single cell gene expression profiling of cortical osteoblast lineage cells. Bone 53, 174-181. 10.1016/j.bone.2012.11.043

Guo, G.,Luc, S.,Marco, E.,Lin, T. W.,Peng, C.,Kerenyi, M. A.,Beyaz, S.,Kim, W.,Xu, J.,Das, P. P., et al. (2013). Mapping cellular hierarchy by single-cell analysis of the cell surface repertoire. Cell Stem Cell 13, 492-505. 10.1016/j.stem.2013.07.017

Ho, D. W.,Yang, Z. F.,Yi, K.,Lam, C. T.,Ng, M. N.,Yu, W. C.,Lau, J.,Wan, T.,Wang, X.,Yan, Z., et al. (2012). Gene expression profiling of liver cancer stem cells by RNA-sequencing. PLoS One 7, e37159. 10.1371/journal.pone.0037159

Isom, S. C.,Stevens, J. R.,Li, R.,Spollen, W. G.,Cox, L.,Spate, L. D.,Murphy, C. N., and Prather, R. S. (2013). Transcriptional profiling by RNA-Seq of peri-attachment porcine embryos generated by a variety of assisted reproductive technologies. Physiol Genomics 45, 577-589. 10.1152/physiolgenomics.00094.2012

Jasnos, L.,Aksoy, F. B.,Hersi, H. M.,Wantuch, S., and Sawado, T. (2013). Identifying division symmetry of mouse embryonic stem cells: negative impact of DNA methyltransferases on symmetric self-renewal. Stem Cell Reports 1, 360-369. 10.1016/j.stemcr.2013.08.005

Jasnos, L., and Sawado, T. (2014). Determining cell division symmetry through the dissection of dividing cells using single-cell expression analysis. Nat Protoc 9, 505-516. 10.1038/nprot.2014.032

Johnston, W. T.,Mutalima, N.,Sun, D.,Emmanuel, B.,Bhatia, K.,Aka, P.,Wu, X.,Borgstein, E.,Liomba, G. N.,Kamiza, S., et al. (2014). Relationship between Plasmodium falciparum malaria prevalence, genetic diversity and endemic Burkitt lymphoma in Malawi. Sci Rep 4, 3741. 10.1038/srep03741

Kerenyi, M. A.,Shao, Z.,Hsu, Y. J.,Guo, G.,Luc, S.,O'Brien, K.,Fujiwara, Y.,Peng, C.,Nguyen, M., and Orkin, S. H. (2013). Histone demethylase Lsd1 represses hematopoietic stem and progenitor cell signatures during blood cell maturation. Elife 2, e00633. 10.7554/eLife.00633

Khan, S. A.,Schaart, J. G.,Beekwilder, J.,Allan, A. C.,Tikunov, Y. M.,Jacobsen, E., and Schouten, H. J. (2012). The mQTL hotspot on linkage group 16 for phenolic compounds in apple fruits is probably the result of a leucoanthocyanidin reductase gene at that locus. BMC Res Notes 5, 618. 10.1186/1756-0500-5-618

Laurell, H.,Iacovoni, J. S.,Abot, A.,Svec, D.,Maoret, J. J.,Arnal, J. F., and Kubista, M. (2012). Correction of RT-qPCR data for genomic DNA-derived signals with ValidPrime. Nucleic Acids Res 40, e51. 10.1093/nar/gkr1259

May-Panloup, P.,Ferre-L'Hotellier, V.,Moriniere, C.,Marcaillou, C.,Lemerle, S.,Malinge, M. C.,Coutolleau, A.,Lucas, N.,Reynier, P.,Descamps, P., et al. (2012). Molecular characterization of corona radiata cells from patients with diminished ovarian reserve using microarray and microfluidic-based gene expression profiling. Hum Reprod 27, 829-843. 10.1093/humrep/der431

Murima, P.,de Sessions, P. F.,Lim, V.,Naim, A. N.,Bifani, P.,Boshoff, H. I.,Sambandamurthy, V. K.,Dick, T.,Hibberd, M. L.,Schreiber, M., et al. (2013). Exploring the mode of action of bioactive compounds by microfluidic transcriptional profiling in mycobacteria. PLoS One 8, e69191. 10.1371/journal.pone.0069191

Pasca, S. P.,Portmann, T.,Voineagu, I.,Yazawa, M.,Shcheglovitov, A.,Pasca, A. M.,Cord, B.,Palmer, T. D.,Chikahisa, S.,Nishino, S., et al. (2011). Using iPSC-derived neurons to uncover cellular phenotypes associated with Timothy syndrome. Nat Med 17, 1657-1662. 10.1038/nm.2576

Pedersen, R.,Ingerslev, H. C.,Sturek, M.,Alloosh, M.,Cirera, S.,Christoffersen, B. O.,Moesgaard, S. G.,Larsen, N., and Boye, M. (2013). Characterisation of gut microbiota in Ossabaw and Gottingen minipigs as models of obesity and metabolic syndrome. PLoS One 8, e56612. 10.1371/journal.pone.0056612

Piazza, R. M.,Delannoy, S.,Fach, P.,Saridakis, H. O.,Pedroso, M. Z.,Rocha, L. B.,Gomes, T. A.,Vieira, M. A.,Beutin, L., and Guth, B. E. (2013). Molecular and phenotypic characterization of Escherichia coli O26:H8 among diarrheagenic E. coli O26 strains isolated in Brazil. Appl Environ Microbiol 79, 6847-6854. 10.1128/AEM.01693-13

Rodgaard, T.,Skovgaard, K.,Stagsted, J., and Heegaard, P. M. (2013). Cloning changes the response to obesity of innate immune factors in blood, liver, and adipose tissues in domestic pigs. Cell Reprogram 15, 185-194. 10.1089/cell.2012.0091

Rusnakova, V.,Honsa, P.,Dzamba, D.,Stahlberg, A.,Kubista, M., and Anderova, M. (2013). Heterogeneity of astrocytes: from development to injury - single cell gene expression. PLoS One 8, e69734. 10.1371/journal.pone.0069734

Schunter, C.,Garza, J. C.,Macpherson, E., and Pascual, M. (2014). SNP development from RNA-seq data in a nonmodel fish: how many individuals are needed for accurate allele frequency prediction? Mol Ecol Resour 14, 157-165. 10.1111/1755-0998.12155

Shcheglovitov, A.,Shcheglovitova, O.,Yazawa, M.,Portmann, T.,Shu, R.,Sebastiano, V.,Krawisz, A.,Froehlich, W.,Bernstein, J. A.,Hallmayer, J. F., et al. (2013). SHANK3 and IGF1 restore synaptic deficits in neurons from 22q13 deletion syndrome patients. Nature 503, 267-271. 10.1038/nature12618 (fluidigm single cell pcr)

Skovgaard, K.,Cirera, S.,Vasby, D.,Podolska, A.,Breum, S. O.,Durrwald, R.,Schlegel, M., and Heegaard, P. M. (2013). Expression of innate immune genes, proteins and microRNAs in lung tissue of pigs infected experimentally with influenza virus (H1N2). Innate Immun 19, 531-544. 10.1177/1753425912473668

Sreenivasan, R.,Jiang, J.,Wang, X.,Bartfai, R.,Kwan, H. Y.,Christoffels, A., and Orban, L. (2013). Gonad Differentiation in Zebrafish Is Regulated by the Canonical Wnt Signaling Pathway. Biol Reprod. 10.1095/biolreprod.113.110874

Weinstein, J. A.,Zeng, X.,Chien, Y. H., and Quake, S. R. (2013). Correlation of gene expression and genome mutation in single B-cells. PLoS One 8, e67624. 10.1371/journal.pone.0067624

Wopereis, S.,Wolvers, D.,van Erk, M.,Gribnau, M.,Kremer, B.,van Dorsten, F. A.,Boelsma, E.,Garczarek, U.,Cnubben, N.,Frenken, L., et al. (2013). Assessment of inflammatory resilience in healthy subjects using dietary lipid and glucose challenges. BMC Med Genomics 6, 44. 10.1186/1755-8794-6-44

EvaGreen in isothermal amplification

Duarte, C.,Salm, E.,Dorvel, B.,Reddy, B., Jr., and Bashir, R. (2013). On-chip parallel detection of foodborne pathogens using loop-mediated isothermal amplification. Biomed Microdevices. 10.1007/s10544-013-9769-5

Fukuta, S.,Takahashi, R.,Kuroyanagi, S.,Ishiguro, Y.,Miyake, N.,Nagai, H.,Suzuki, H.,Tsuji, T.,Hashizume, F.,Watanabe, H., et al. (2014). Development of loop-mediated isothermal amplification assay for the detection of Pythium myriotylum. Lett Appl Microbiol 59, 49-57. 10.1111/lam.12244

Goldmeyer, J.,Kong, H., and Tang, W. (2007). Development of a novel one-tube isothermal reverse transcription thermophilic helicase-dependent amplification platform for rapid RNA detection. J Mol Diagn 9, 639-644. 10.2353/jmoldx.2007.070012

Li, Y.,Kim, H. J.,Zheng, C.,Chow, W. H.,Lim, J.,Keenan, B.,Pan, X.,Lemieux, B., and Kong, H. (2008). Primase-based whole genome amplification. Nucleic Acids Res 36, e79. 10.1093/nar/gkn377

Liu, C.,Mauk, M.,Gross, R.,Bushman, F. D.,Edelstein, P. H.,Collman, R. G., and Bau, H. H. (2013). Membrane-based, sedimentation-assisted plasma separator for point-of-care applications. Anal Chem 85, 10463-10470. 10.1021/ac402459h

Loo, J. F. C.,Lau, P. M.,Ho, H. P., and Kong, S. K. (2013). An aptamer-based bio-barcode assay with isothermal recombinase polymerase amplification for cytochrome-c detection and anti-cancer drug screening. Talanta 115, 159-165. 10.1016/j.talanta.2013.04.051

Montgomery, J. L.,Rejali, N., and Wittwer, C. T. (2013). Stopped-flow DNA polymerase assay by continuous monitoring of dNTP incorporation by fluorescence. Anal Biochem 441, 133-139. 10.1016/j.ab.2013.07.008

Salm, E.,Zhong, Y.,Reddy, B., Jr.,Duarte-Guevara, C.,Swaminathan, V.,Liu, Y. S., and Bashir, R. (2014). Electrical detection of nucleic acid amplification using an on-chip quasi-reference electrode and a PVC REFET. Anal Chem 86, 6968-6975. 10.1021/ac500897t

Schaerli, Y.,Stein, V.,Spiering, M. M.,Benkovic, S. J.,Abell, C., and Hollfelder, F. (2010). Isothermal DNA amplification using the T4 replisome: circular nicking endonuclease-dependent amplification and primase-based whole-genome amplification. Nucleic Acids Res 38, e201. 10.1093/nar/gkq795

Wang, D. and Liu, Y. (2015). Development of Primer Sets for Loop-Mediated Isothermal Amplification that Enables Rapid and Specific Detection of *Streptococcus dysgalactiae*, *Streptococcus uberis* and *Streptococcus agalactiaeInt.* J. Environ. Res. Public Health, 12, 5735-5742; doi:10.3390/ijerph120605735

Zhou, Q. J.,Wang, L.,Chen, J.,Wang, R. N.,Shi, Y. H.,Li, C. H.,Zhang, D. M.,Yan, X. J., and Zhang, Y. J. (2014). Development and evaluation of a real-time fluorogenic loop-mediated isothermal amplification assay integrated on a microfluidic disc chip (on-chip LAMP) for rapid and simultaneous detection of ten pathogenic bacteria in aquatic animals. J Microbiol Methods 104, 26-35. 10.1016/j.mimet.2014.06.008

EvaGreen in capillary electrophoresis

Sang, F.,Ren, H., and Ren, J. (2006). Genetic mutation analysis by CE with LIF detection using inverse-flow derivatization of DNA fragments. Electrophoresis 27, 3846-3855. 10.1002/elps.200600160

Sang, F., and Ren, J. (2006). Capillary electrophoresis of double-stranded DNA fragments using a new fluorescence intercalating dye EvaGreen. J Sep Sci 29, 1275-1280

Fast EvaGreen Master Mix

Adamski, M. G.,Li, Y.,Wagner, E.,Yu, H.,Seales-Bailey, C.,Soper, S. A.,Murphy, M., and Baird, A. E. (2013). Next-generation qPCR for the high-throughput measurement of gene expression in multiple leukocyte subsets. J Biomol Screen 18, 1008-1017. 10.1177/1087057113489882

Almeida, L. O.,Garcia, C. B.,Matos-Silva, F. A.,Curti, C., and Leopoldino, A. M. (2014). Accumulated SET protein up-regulates and interacts with hnRNPK, increasing its binding to nucleic acids, the Bcl-xS repression, and cellular proliferation. Biochem Biophys Res Commun 445, 196-202. 10.1016/j.bbrc.2014.01.175

Chan, L. T.,Zhong, S.,Naqvi, A. R.,Self-Fordham, J.,Nares, S.,Bair, E., and Khan, A. A. (2013). MicroRNAs: new insights into the pathogenesis of endodontic periapical disease. J Endod 39, 1498-1503. 10.1016/j.joen.2013.08.032

Choi, W. G.,Toyota, M.,Kim, S. H.,Hilleary, R., and Gilroy, S. (2014). Salt stress-induced Ca2+ waves are associated with rapid, long-distance root-to-shoot signaling in plants. Proc Natl Acad Sci U S A 111, 6497-6502. 10.1073/pnas.1319955111

Li, J.,Wu, R.,Chen, H.,Zhou, Y.,Li, Y.,Wang, Y.,Liu, Y., and Liu, M. (2013). The Cloning and Characterization of the Enolase2 Gene of Gekko japonicus and Its Polyclonal Antibody Preparation. Int J Mol Sci 14, 8787-8800. 10.3390/ijms14058787

Naqvi, A. R.,Fordham, J. B.,Khan, A., and Nares, S. (2013). MicroRNAs responsive to Aggregatibacter actinomycetemcomitans and Porphyromonas gingivalis LPS modulate expression of genes regulating innate immunity in human macrophages. Innate Immun 20, 540-551. 10.1177/1753425913501914

Oliveira-Pelegrin, G. R.,Basso, P. J.,Soares, A. S.,Martinez, M. R.,Riester, K. D., and Rocha, M. J. (2013). Cleaved caspase-3 expression in hypothalamic magnocellular neurons may affect vasopressin secretion during experimental polymicrobial sepsis. J Neuroimmunol 258, 10-16. 10.1016/j.jneuroim.2013.02.007

Rodrigues, E. F.,Santos-Reboucas, C. B.,Goncalves Pimentel, M. M.,Mencalha, A. L.,Dobbin, J.,Da Costa, E. S.,Fernandez Cde, S.,Bouzas, L. F.,Abdelhay, E., and De Souza Fernandez, T. (2010). Epigenetic alterations of p15(INK4B) and p16(INK4A) genes in pediatric primary myelodysplastic syndrome. Leuk Lymphoma 51, 1887-1894. 10.3109/10428194.2010.505820

Timon-Gomez, A.,Proft, M., and Pascual-Ahuir, A. (2013). Differential regulation of mitochondrial pyruvate carrier genes modulates respiratory capacity and stress tolerance in yeast. PLoS One 8, e79405. 10.1371/journal.pone.0079405

Valenzuela-Munoz, V.,Araya-Garay, J. M., and Gallardo-Escarate, C. (2013). SNP discovery and High Resolution Melting Analysis from massive transcriptome sequencing in the California red abalone Haliotis rufescens. Mar Genomics 10, 11-16. 10.1016/j.margen.2012.12.003

Vig, P. J.,Hearst, S. M.,Shao, Q., and Lopez, M. E. (2014). Knockdown of acid-sensing ion channel 1a (ASIC1a) suppresses disease phenotype in SCA1 mouse model. Cerebellum 13, 479-490. 10.1007/s12311-014-0563-6

Wei, C.,Li, L.,Su, H.,Xu, L.,Lu, J.,Zhang, L.,Liu, W.,Ren, H., and Du, L. (2014). Identification of the crucial molecular events during the large-scale myoblast fusion in sheep. Physiol Genomics 46, 429-440. 10.1152/physiolgenomics.00184.2013

You, C. G.,Li, X. J.,Li, Y. M.,Wang, L. P.,Li, F. F.,Guo, X. L., and Gao, L. N. (2013). Association analysis of single nucleotide polymorphisms of proinflammatory cytokine and their receptors genes with rheumatoid arthritis in northwest Chinese Han population. Cytokine 61, 133-138. 10.1016/j.cyto.2012.09.007

Zhang, Q.,Zhang, J.,Jiang, C.,Qin, J.,Ke, K., and Ding, F. (2014). Involvement of ERK1/2 pathway in neuroprotective effects of pyrroloquinoline quinine against rotenone-induced SH-SY5Y cell injury. Neuroscience 270, 183-191. 10.1016/j.neuroscience.2014.04.022

Fast Plus EvaGreen Master Mix

Babelova, A.,Jansen, F.,Sander, K.,Lohn, M.,Schafer, L.,Fork, C.,Ruetten, H.,Plettenburg, O.,Stark, H.,Daniel, C., et al. (2013). Activation of Rac-1 and RhoA contributes to podocyte injury in chronic kidney disease. PLoS One 8, e80328. 10.1371/journal.pone.0080328

Cai, X. Q.,Yu, H. Q.,Ruan, Z. X.,Yang, L. L.,Bai, J. S.,Qiu, D. Y.,Jian, Z. H.,Xiao, Y. Q.,Yang, J. Y.,Le, T. H., et al. (2013). Rapid detection and simultaneous genotyping of Cronobacter spp. (formerly Enterobacter sakazakii) in powdered infant formula using real-time PCR and high resolution melting (HRM) analysis. PLoS One 8, e67082. 10.1371/journal.pone.0067082

Camargo Lde, L.,Babelova, A.,Mieth, A.,Weigert, A.,Mooz, J.,Rajalingam, K.,Heide, H.,Wittig, I.,Lopes, L. R., and Brandes, R. P. (2013). Endo-PDI is required for TNFalpha-induced angiogenesis. Free Radic Biol Med 65, 1398-1407. 10.1016/j.freeradbiomed.2013.09.028

Garcia, D. C.,Miceli, D. C.,Valdecantos, P. A.,Garcia, E. V., and Roldan-Olarte, M. (2014). Expression of urokinase type plasminogen activator receptor (uPAR) in the bovine oviduct: Relationship with uPA effect on oviductal epithelial cells. Res Vet Sci 97, 118-123. 10.1016/j.rvsc.2014.05.012

Kropotova, E. S.,Zinovieva, O. L.,Zyryanova, A. F.,Dybovaya, V. I.,Prasolov, V. S.,Beresten, S. F.,Oparina, N. Y., and Mashkova, T. D. (2014). Altered expression of multiple genes involved in retinoic acid biosynthesis in human colorectal cancer. Pathol Oncol Res 20, 707-717. 10.1007/s12253-014-9751-4

Wang, C. P.,Li, J. L.,Zhang, L. Z.,Zhang, X. C.,Yu, S.,Liang, X. M.,Ding, F., and Wang, Z. W. (2013). Isoquercetin protects cortical neurons from oxygen-glucose deprivation-reperfusion induced injury via suppression of TLR4-NF-small ka, CyrillicB signal pathway. Neurochem Int 63, 741-749. 10.1016/j.neuint.2013.09.018