



2023年第1期总1期

饲料用酶工程

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1. 微生物生产饲料氨基酸研究进展

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政策法规

1. **Mycotoxin Handbook Published by USDA (美国农业部发布最新版本用于测定谷物及其加工商品中真菌毒素的官方案程序信息)**

简介: The Mycotoxin Handbook illustrates step-by-step procedures for sample preparation and for certifying grain and commodities for mycotoxins, as well as safety information for testing and storing test chemicals. All official inspection personnel authorized or licensed to perform official mycotoxin testing shall reference this Handbook for procedures. This handbook has been updated to incorporate FGIS's agency move to AMS, the inclusion of Policy Bulletin Board #275 Mycotoxin Testing in Grain: Sample Preparation Guidance, the removal of qualitative testing, updated test kit ranges, as well as general revisions and formatting. In addition, definitions, tables, and processes were updated to the current standards. The specific technical updates are listed in Chapter 7 of this handbook. This handbook supersedes the Mycotoxin Handbook, dated June 28, 2016.

来源: USDA

发布日期: 2023-01-06

全文链接: <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GV0PMiAFLP2ABFoPxGk80c113.pdf>

前沿资讯

1. **An e-nose could be a powerful tool in the feed chain for quality and safety control and mycotoxin monitoring (电子鼻可以成为饲料链中质量和安全控制以及霉菌毒素监测的有力工具)**

简介: Dr Matteo Ottoboni, from the Department of Veterinary Medicine and Animal Sciences, at the University of Milan, presented on the application of electronic noses for feed safety and animal nutrition at the World Mycotoxin Forum in Antwerp in Belgium last month.

来源: FEED NAVIGATOR

发布日期: 2023-11-30

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoSK-AOPD6AAnjd668cww681.pdf>

2. **KAIST-UCSD researchers build an enzyme discovering AI (KAIST-UCSD研究人员构建了一种人工智能识别酶的系统)**

简介: KAIST (President Kwang-Hyung Lee) announced on the 24th that a joint research team comprised of Gi Bae Kim, Ji Yeon Kim, Dr. Jong An Lee and Distinguished Professor Sang Yup Lee of the Department of Chemical and Biomolecular Engineering at KAIST, and Dr. Charles J. Norsigian and Professor Bernhard O. Palsson of the Department of Bioengineering at UCSD has developed DeepEctransformer, an artificial intelligence that can predict the enzyme functions from the protein sequence, and has established a prediction system by utilizing the AI to quickly and accurately identify the enzyme function. The joint team developed DeepEctransformer, an AI that utilizes deep learning and a protein homology analysis module to predict the enzyme function of a given protein sequence. To better understand the features of protein sequences, the transformer architecture, which is commonly

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used in natural language processing, was additionally used to extract important features about enzyme functions in the context of the entire protein sequence, which enabled the team to accurately predict the EC number of the enzyme. The developed DeepEctransformer can predict a total of 5360 EC numbers.

来源: EurekaAlert

发布日期: 2023-11-24

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoTDWAKGYfAAW01-mR1ZE443.pdf>

3. FSU researchers capture high-resolution images of magnesium ions interacting with CRISPR gene-editing enzyme (FSU研究人员捕获了镁离子与CRISPR基因编辑酶相互作用的高分辨率图像)

简介: In research published in Nature Catalysis, scientists at Florida State University produced the first high-resolution, time-lapsed images showing magnesium ions interacting with the CRISPR-Cas9 enzyme while it cut strands of DNA, providing clear evidence that magnesium plays a role in both chemical bond breakage and near-simultaneous DNA cutting. The researchers used the cryo-electron microscope at FSU's Biological Science Imaging Resource, which can produce images with near-atomic resolution, to observe metal ions and other atoms at work within the CRISPR-Cas9 enzyme. That allowed them to collect data that not only confirmed their earlier hypotheses but also led to the surprising discovery about how magnesium coordinates double-stranded breaks.

来源: EurekaAlert

发布日期: 2023-11-02

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoT7iAOz11AAp2gGEyGq8424.pdf>

学术文献

1. Diet medication and beta-glucanase affect ileal digesta soluble beta-glucan molecular weight, carbohydrate fermentation, and performance of coccidiosis vaccinated broiler chickens given wheat-based diets (饲料药物和 β -葡聚糖酶对接种球虫病肉鸡回肠消化、可溶性 β -葡聚糖分子量、碳水化合物发酵和生产性能的影响)

简介: Exogenous enzymes as alternatives to feed antibiotics in poultry has become an emerging research area with the emergence of antibiotic resistance. The objective was to evaluate the effects of diet medication (antibiotics) and β -glucanase (BGase) on digesta soluble β -glucan depolymerization, carbohydrate fermentation, and performance of coccidiosis-vaccinated broiler chickens fed wheat-based diets. A total of 1,782 broilers were raised on litter floor pens, and each treatment was assigned to 1 pen in each of the 9 rooms. The 3 dietary treatments were based on wheat as the sole grain (control, control þ medication and control þ 0.1% BGase), and the birds were fed the respective treatments ad libitum from 0 to 33 d. Treatments were arranged in a randomized complete block design and analyzed as a one-way ANOVA. Beta-glucanase reduced the peak molecular weight, weight average molecular weight (Mw) and maximum molecular weight for the smallest 10% β -glucan molecules (MW-10%) in ileal digesta at d 11 and 33, whereas diet medication reduced Mw and MW-10% at d 33 compared to the control ($P < 0.01$). Beta-glucanase and medication reduced the ileal viscosity at d 11

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compared to the control ($P < 0.010$). Ileal propionic acid concentration at d 11 and caecal total SCFA, acetic, and butyric acid concentrations at d 33 were lower in the BGase-supplemented diet than in the control ($P < 0.05$). The BGase-added diet had higher duodenal pH compared to the control at d 33 ($P < 0.026$). The effect of medication on carbohydrate fermentation was minimal. Diet medication increased weight gain after d 11, whereas BGase increased the gain for the total trial period compared to the control ($P < 0.001$). Feed intake was not affected by the dietary treatment. Medication and BGase improved feed efficiency after d 11 compared to the control ($P < 0.001$). The response to diet medication was larger than BGase, considering weight gain and feed efficiency after d 11 ($P < 0.001$). In conclusion, diet medication and BGase depolymerized high molecular weight ileal soluble β -glucan and increased overall bird performance. Dietary BGase may benefit bird health in broilers fed wheat-based diets without medication.

来源: Science Direct

发布日期: 2023-11-16

全文链接: <https://doi.org/10.1016/j.aninu.2023.03.013>

2. Mycotoxins in food and feed: toxicity, preventive challenges, and advanced detection techniques for associated diseases (食品和饲料中的真菌毒素: 毒性、预防挑战和相关疾病的先进检测技术)

简介: Mycotoxins are produced primarily as secondary fungal metabolites. Mycotoxins are toxic in nature and naturally produced by various species of fungi, which usually contaminate food and feed ingredients. The growth of these harmful fungi depends on several environmental factors, such as pH, humidity, and temperature; therefore, the mycotoxin distribution also varies among global geographical areas. Various rules and regulations regarding mycotoxins are imposed by the government bodies of each country, which are responsible for addressing global food and health security concerns. Despite this legislation, the incidence of mycotoxin contamination is continuously increasing. In this review, we discuss the geographical regulatory guidelines and recommendations that are implemented around the world to control mycotoxin contamination of food and feed products. Researchers and inventors from various parts of the world have reported several innovations for controlling mycotoxin-associated health consequences. Unfortunately, most of these techniques are restricted to laboratory scales and cannot reach users. Consequently, to date, no single device has been commercialized that can detect all mycotoxins that are naturally available in the environment. Therefore, in this study, we describe severe health hazards that are associated with mycotoxin exposure, their molecular signaling pathways and processes of toxicity, and their genotoxic and cytotoxic effects toward humans and animals. We also discuss recent developments in the construction of a sensitive and specific device that effectively implements mycotoxin identification and detection methods. In addition, our study comprehensively examines the recent advancements in the field for mitigating the health consequences and links them with the molecular and signaling pathways that are activated upon mycotoxin exposure.

来源: Critical Reviews in Food Science and Nutrition

发布日期: 2023-10-25

全文链接: <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GV0KY2Ad8YrAH1CZApfp7M626.pdf>

3. The LIKE SEX FOUR 1–malate dehydrogenase complex functions as a scaffold to recruit β -amylase to promote starch degradation (LIKE SEX 4–1–苹果酸脱氢酶复合物作为支架招募 β -淀粉酶促进淀粉降解)

简介: In plant leaves, starch is composed of glucan polymers that accumulate in chloroplasts as the products of photosynthesis during the day; starch is mobilized at night to continuously provide sugars to sustain plant growth and development. Efficient starch degradation requires the involvement of several enzymes, including β -amylase and glucan phosphatase. However, how these enzymes cooperate remains largely unclear. Here, we show that the glucan phosphatase LIKE SEX FOUR 1 (LSF1) interacts with plastid NAD-dependent malate dehydrogenase (MDH) to recruit β -amylase (BAM1), thus reconstituting the BAM1-LSF1-MDH complex. The starch hydrolysis activity of BAM1 drastically increased in the presence of LSF1-MDH in vitro. We determined the structure of the BAM1-LSF1-MDH complex by a combination of cryo-electron microscopy, crosslinking mass spectrometry, and molecular docking. The starch-binding domain of the dual-specificity phosphatase (DSP) and carbohydrate-binding module (CBM) of LSF1 were docked in proximity to BAM1, thus facilitating BAM1 access to and hydrolysis of the polyglucans of starch, thus revealing the molecular mechanism by which the LSF1-MDH complex improves the starch degradation activity of BAM1. Moreover, LSF1 is phosphatase-inactive, and the enzymatic activity of MDH was dispensable for starch degradation, suggesting non-enzymatic scaffold functions for LSF1-MDH in starch degradation. These findings provide important insights into the precise regulation of starch degradation.

来源: Plant Cell

发布日期: 2023-10-06

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoUweAP3SqAB4IrUTbIVI807.pdf>

4. The effect of enzymatically-modified canola meal on growth performance, nutrient utilization, and gut health and function of broiler chickens (酶修饰菜籽粕对肉鸡生长性能、营养物质利用及肠道健康和功能的影响)

简介: Enzymatically-modified canola meal (ECM) is a product obtained from the incubation of canola meal (CM) with a blend of specific carbohydrase enzymes. Incubation of CM with multi-carbohydrase enzymes resulted in a significant decrease in non-starch polysaccharides (NSP) content, production of potentially bioactive NSP hydrolysis products, and the spontaneous lactic acid bacteria fermentation. The latter resulted in the production of lactic acid, phytate hydrolysis, and the reduction in the product pH from 5.9 to 4.0. The main objective of this study was to evaluate the effects of ECM on growth performance, nutrient utilization, and gut health and function of broiler chickens. Four-day-old as hatched Ross 308 broilers were assigned to 5 dietary treatments, each consisting of 8 cages of 8 birds. Birds were fed the starter (414d of age, 100 g/kg CM) and grower (1421d of age, 200 g/kg of CM) Control diet, and Control diets supplemented with ECM (Low and High) or enzymes (E1 and E2). In the ECM-containing diets, ECM replaced either 50 g/kg (Low ECM diet) or entire CM (High ECM diet) of the Control diets. In the E1 and E2 diets, the enzyme blend was supplemented at 1.25 g/kg and 12.5 g/kg of the starter Control diet and 2.5 g/kg and 25 g/kg of the grower Control diet, respectively. Replacing CM with ECM did not affect growth performance, but significantly increased the apparent total tract

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NSP digestibility and nitrogen-corrected apparent metabolizable energy content. The ECM-containing diets decreased sialic acids secretion on day 21 and increased the abundance of Lactobacillus ($P < 0.01$) in ileum and ceca compared to Control, E1, and E2 during the whole trial. The abundance of Escherichia coli was significantly lower in ceca of birds fed the High ECM grower diets compared to the Control. Total short chain fatty acids in cecal digesta of birds fed High ECM starter diet significantly increased compared with the Control. Replacing CM with ECM improved nutrient digestibility and increased the presence of probiotic organisms which was not observed in the enzyme supplemented diets. Therefore, ECM can improve gut health and could be used as a valuable feed ingredient or additive.

来源: Science Direct

发布日期: 2023-09-04

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoNp-AH9L4AAjZaSxuoYo405.pdf>

5. Enzyme function prediction using contrastive learning (利用对比学习预测酶功能)

简介: Enzyme function annotation is a fundamental challenge, and numerous computational tools have been developed. However, most of these tools cannot accurately predict functional annotations, such as enzyme commission (EC) number, for less-studied proteins or those with previously uncharacterized functions or multiple activities. We present a machine learning algorithm named CLEAN (contrastive learning-enabled enzyme annotation) to assign EC numbers to enzymes with better accuracy, reliability, and sensitivity compared with the state-of-the-art tool BLASTp. The contrastive learning framework empowers CLEAN to confidently (i) annotate understudied enzymes, (ii) correct mislabeled enzymes, and (iii) identify promiscuous enzymes with two or more EC numbers—functions that we demonstrate by systematic *in silico* and *in vitro* experiments. We anticipate that this tool will be widely used for predicting the functions of uncharacterized enzymes, thereby advancing many fields, such as genomics, synthetic biology, and biocatalysis.

来源: Science

发布日期: 2023-03-31

全文链接: <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn6p6ANpo6ABLRbwI6JHc343.pdf>

6. Large language models generate functional protein sequences across diverse families (大型语言模型生成跨不同家族的功能性蛋白质序列)

简介: Deep-learning language models have shown promise in various biotechnological applications, including protein design and engineering. Here we describe ProGen, a language model that can generate protein sequences with a predictable function across large protein families, akin to generating grammatically and semantically correct natural language sentences on diverse topics. The model was trained on 280 million protein sequences from >19,000 families and is augmented with control tags specifying protein properties. ProGen can be further fine-tuned to curated sequences and tags to improve controllable generation performance of proteins from families with sufficient homologous samples. Artificial proteins fine-tuned to five distinct lysozyme families showed similar catalytic efficiencies as natural lysozymes, with sequence identity to natural proteins as low as 31.4%. ProGen is readily adapted to diverse protein families, as we demonstrate with chorismate mutase and malate dehydrogenase.

来源: Nature Biotechnology

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发布日期:2023-01-26

全文链接:<http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn9RuABDqdADt8eH1-Kjg206.pdf>

➤ 科技图书

1. **Advances in microbial production of feed amino acid (微生物生产饲料氨基酸研究进展)**

简介: Feed amino acids have numerous applications, and the market demand for them is likely to grow. Microbial cell factories promise the sustainable production of feed amino acids; however, their performance is significantly affected by the availability of precursors, carbon metabolic flux, and transporter systems. To circumvent these potential roadblocks, high-performance microbial cell factories have been constructed by strengthening the supply of precursors, increasing metabolic pathway flux, and engineering transporters. In this review, limiting factors and recent technical advances affecting the production of feed amino acids in microbial cell factories are discussed. In addition, existing challenges and potential strategies for increasing the output of these amino acids are described.

来源: Advances in Applied Microbiology

发布日期:2022-12-31

全文链接:<http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVoJmSAax58AB-PvTFgwSk761.pdf>