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Press Releases -Media / Presse- und Medienberichte

ARC: **Leak – Draft NGT Regulation and Impact Assessment revealed**
https://www.arc2020.eu/leak-draft-ngt-regulation-and-impact-assessment-revealed/

Bruhns A.: **Neue Gentechnik: EU-Vorschlag sieht keine Kennzeichnungspflicht vor**
https://table.media/berlin/analyse/neue-gentechnik-eu-vorschlag-sieht-keine-kennzeichnungspflicht-vor/

GLP Team**: Leaked European Commission document recommends softening EU regulations of gene edited crops and other products of New Genomic Techniques: "The current EU GMO regulation is not fit for purpose"**
https://geneticliteracyproject.org/2023/06/16/leaked-european-council-document-recommends-deregulation-of-gene-edited-crops-the-current-eu-gmo-regulation-is-not-fit-for-purpose/

Taylor K.: **Umkämpftes EU-Renaturierungsgesetz überlebt Abstimmung im Parlament**
https://www.euractiv.de/section/energie-und-umwelt/news/umkaempftes-eu-renaturierungsgesetz-ueberlebt-abstimmung-im-parlament/

EU's embattled nature restoration law survives Parliament rejection
https://www.euractiv.com/section/energy-environment/news/eus-embattled-nature-restoration-law-survives-parliament-rejection/?_ga=2.268530033.1073813683.1686924919-1161537847.1686754289

Miller H.I., Altman D.W.: **Regulation of Molecular Genetic Engineering Must Be Evidence-Based**
https://www.europeanscientist.com/en/features/regulation-of-molecular-genetic-engineering-must-be-evidence-based/

European Parliament: **Ensuring food security and the long-term resilience of EU agriculture**
https://www.europarl.europa.eu/doceo/document/TA-9-2023-0238_EN.pdf

Deutscher Bundestag: **Kampf gegen den Hunger: Forschung muss intensiviert werden**
https://www.bundestag.de/dokumente/textarchiv/2023/kw24-pa-nachhaltigkeitsbeirat-agrarsysteme-951670

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ▶here: June week 24

Publications – Publikationen

Bottini, S., Fuoco, C., Schiavo, N. et al. (2023): A call for an 'Asilomar' for cultivated meat and seafood. *Nat Biotechnol* (2023). https://doi.org/10.1038/s41587-023-01849-x

Li, Y., Zhong, H., Shan, Y. et al. (2023): Changes in global food consumption increase GHG emissions despite efficiency gains along global supply chains. Nat Food | https://doi.org/10.1038/s43016-023-00768-z
Greenhouse gas (GHG) emissions related to food consumption complement production-based or territorial accounts by capturing carbon leaked through trade. Here we evaluate global consumption-based food emissions between 2000 and 2019 and underlying drivers using a physical trade flow approach and structural decomposition analysis. In 2019, emissions throughout global food supply chains reached 30 ±9% of anthropogenic GHG emissions, largely triggered by beef and dairy consumption in rapidly developing countries—while per capita emissions in developed countries with a high percentage of animal-based food declined. Emissions outsourced through international food trade dominated by beef and oil crops increased by ~1 Gt CO_2 equivalent, mainly driven by increased imports by developing countries. Population growth and per capita demand increase were key drivers to the global emissions increase (+30% and +19%, respectively) while decreasing emissions intensity from land-use activities was the major factor to offset emissions growth (−39%). Climate change mitigation may depend on incentivizing consumer and producer choices to reduce emissions-intensive food products.
https://www.nature.com/articles/s43016-023-00768-z

Stokstad E. (2023): **EPA decision to tighten oversight of gene-edited crops draws mixed response**
U.S. agency will require evidence that introduced traits don't increase health risks before exempting modified plants from regulation
https://www.science.org/content/article/epa-decision-tighten-oversight-gene-edited-crops-draws-mixed-response

Environmental Protection Agency: **Pesticides: Exemptions of Certain Plant-Incorporated Protectants Derived from Newer Technologies**
The Environmental Protection Agency (EPA) is exempting a class of plant-incorporated protectants (PIPs) that have been created using genetic engineering from certain registration requirements under the Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA), and from the requirements to establish a tolerance or tolerance exemption for residues of these substances on food or feed under the Federal Food, Drug, and Cosmetic Act (FFDCA). Specifically, EPA is finalizing its exemptions as described in its October 2020 proposal for PIPs now termed "PIPs created through genetic engineering from a sexually compatible plant" and "loss-of-function PIPs," finalizing the process through which the Agency determines their eligibility for exemption, and finalizing the associated recordkeeping requirements. This set of exemptions reflects the biotechnological advances made since 2001, when EPA first exempted PIPs derived through conventional breeding and excluded from the exemptions those PIPs that are created through biotechnology. EPA anticipates that today's exemptions will benefit the public by ensuring that human health and the environment are adequately protected, while also reducing the regulatory burden for the regulated community. These exemptions may also result in increased research and development activities, commercialization of new pest control options for farmers, particularly in minor crops, and increase the diversity of options for pest and disease management, which could provide environmental benefits.
https://www.regulations.gov/document/EPA-HQ-OPP-2019-0508-0122

Impens L., Lorenzo C.D., Vandeputte W., Wytynck P. et al. (2023): **Combining multiplex gene editing and doubled haploid technology in maize.** New Phytologist | https://doi.org/10.1111/nph.19021
A major advantage of using CRISPR/Cas9 for gene editing is multiplexing, that is, the simultaneous targeting of many genes. However, primary transformants typically contain hetero-allelic mutations or are genetic mosaic, while genetically stable lines that are homozygous are desired for functional analysis. Currently, a dedicated and labor-intensive effort is required to obtain such higher-order mutants through several generations of genetic crosses and genotyping.
We describe the design and validation of a rapid and efficient strategy to produce lines of genetically identical plants carrying various combinations of homozygous edits, suitable for replicated analysis of phenotypical differences. This approach was achieved by combining highly multiplex gene editing in *Zea mays* (maize) with *in vivo* haploid induction and efficient *in vitro* generation of doubled haploid plants using embryo rescue doubling. By combining three CRISPR/Cas9 constructs that target in total 36 genes potentially involved in leaf growth, we generated an array of homozygous lines with various combinations of edits within three generations. Several genotypes show a reproducible 10% increase in leaf size, including a septuple mutant combination.
We anticipate that our strategy will facilitate the study of gene families via multiplex CRISPR mutagenesis and the identification of allele combinations to improve quantitative crop traits.
https://nph.onlinelibrary.wiley.com/doi/abs/10.1111/nph.19021

Chen, J., Wang, Z., Tan, K. et al. (2023): **A complete telomere-to-telomere assembly of the maize genome.** Nat Genet | https://doi.org/10.1038/s41588-023-01419-6
A complete telomere-to-telomere (T2T) finished genome has been the long pursuit of genomic research. Through generating deep coverage ultralong Oxford Nanopore Technology (ONT) and PacBio HiFi reads, we report here a complete genome assembly of maize with each chromosome entirely traversed in a single contig. The 2,178.6 Mb T2T Mo17 genome with a base accuracy of over 99.99% unveiled the structural features of all repetitive regions of the genome. There were several super-long simple-sequence-repeat arrays having consecutive thymine–adenine–guanine (TAG) tri-nucleotide repeats up to 235 kb. The assembly of the entire nucleolar organizer region of the 26.8 Mb array with 2,974 45S rDNA copies revealed the enormously complex patterns of rDNA duplications and transposon insertions. Additionally, complete assemblies of all ten centromeres enabled us to precisely dissect the repeat compositions of both CentC-rich and CentC-poor centromeres. The complete Mo17 genome represents a major step forward in understanding the complexity of the highly recalcitrant repetitive regions of higher plant genomes.
https://www.nature.com/articles/s41588-023-01419-6

Sha, G., Sun, P., Kong, X. et al. (2023): **Genome editing of a rice CDP-DAG synthase confers multipathogen resistance**. Nature | https://doi.org/10.1038/s41586-023-06205-2
The discovery and application of genome editing introduced a new era of plant breeding by giving researchers efficient tools for the precise engineering of crop genomes[1]. Here we demonstrate the power of genome editing for engineering broad-spectrum disease resistance in rice (*Oryza sativa*). We first isolated a lesion mimic mutant (LMM) from a mutagenized rice population. We then demonstrated that a 29-base-pair deletion in a gene we named *RESISTANCE TO BLAST1* (*RBL1*) caused broad-spectrum disease resistance and showed that this mutation caused an approximately 20-fold reduction in yield. *RBL1* encodes a cytidine diphosphate diacylglycerol

synthase that is required for phospholipid biosynthesis[2]. Mutation of *RBL1* results in reduced levels of phosphatidylinositol and its derivative phosphatidylinositol 4,5-bisphosphate (PtdIns(4,5)P_2). In rice, PtdIns(4,5)P_2 is enriched in cellular structures that are specifically associated with effector secretion and fungal infection, suggesting that it has a role as a disease-susceptibility factor[3]. By using targeted genome editing, we obtained an allele of *RBL1*, named *RBL1*$^{\Delta 12}$, which confers broad-spectrum disease resistance but does not decrease yield in a model rice variety, as assessed in small-scale field trials. Our study has demonstrated the benefits of editing an LMM gene, a strategy relevant to diverse LMM genes and crops.
https://www.nature.com/articles/s41586-023-06205-2

Berthelier, J., Furci, L., Asai, S. et al. (2023): **Long-read direct RNA sequencing reveals epigenetic regulation of chimeric gene-transposon transcripts in *Arabidopsis thaliana***. Nat Commun 14, 3248 | https://doi.org/10.1038/s41467-023-38954-z
Transposable elements (TEs) are accumulated in both intergenic and intragenic regions in plant genomes. Intragenic TEs often act as regulatory elements of associated genes and are also co-transcribed with genes, generating chimeric TE-gene transcripts. Despite the potential impact on mRNA regulation and gene function, the prevalence and transcriptional regulation of TE-gene transcripts are poorly understood. By long-read direct RNA sequencing and a dedicated bioinformatics pipeline, ParasiTE, we investigated the transcription and RNA processing of TE-gene transcripts in *Arabidopsis thaliana*. We identified a global production of TE-gene transcripts in thousands of *A. thaliana* gene loci, with TE sequences often being associated with alternative transcription start sites or transcription termination sites. The epigenetic state of intragenic TEs affects RNAPII elongation and usage of alternative poly(A) signals within TE sequences, regulating alternative TE-gene isoform production. Co-transcription and inclusion of TE-derived sequences into gene transcripts impact regulation of RNA stability and environmental responses of some loci. Our study provides insights into TE-gene interactions that contributes to mRNA regulation, transcriptome diversity, and environmental responses in plants.
https://www.nature.com/articles/s41467-023-38954-z

Rai G.K., Khanday D.M., Kumar P., Magotra I. et al. (2023): **Enhancing Crop Resilience to Drought Stress through CRISPR-Cas9 Genome Editing**. Plants 12 (12), 2306 | https://doi.org/10.3390/plants12122306
With increasing frequency and severity of droughts in various parts of the world, agricultural productivity may suffer major setbacks. Among all the abiotic factors, drought is likely to have one of the most detrimental effects on soil organisms and plants. Drought is a major problem for crops because it limits the availability of water, and consequently nutrients which are crucial for plant growth and survival. This results in reduced crop yields, stunted growth, and even plant death, according to the severity and duration of the drought, the plant's developmental stage, and the plant's genetic background. The ability to withstand drought is a highly complex characteristic that is controlled by multiple genes, making it one of the most challenging attributes to study, classify, and improve. Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) technology has opened a new frontier in crop enhancement, revolutionizing plant molecular breeding. The current review provides a general understanding of principles as well as optimization of CRISPR system, and presents applications on genetic enhancement of crops, specifically in terms of drought resistance and yield. Moreover, we discuss how innovative genome editing techniques can aid in the identification and modification of genes conferring drought tolerance.
https://www.mdpi.com/2223-7747/12/12/2306

Yang Z-W., Lian, Z.-H., Liu L. Fang B.-Z. et al. (2023): **Cultivation strategies for prokaryotes from extreme environments.** iMeta | https://doi.org/10.1002/imt2.123
The great majority of microorganisms are as-yet-uncultivated, mostly found in extreme environments. High-throughput sequencing provides data-rich genomes from single-cell and metagenomic techniques, which has enabled researchers to obtain a glimpse of the unexpected genetic diversity of "microbial dark matter." However, cultivating microorganisms from extreme environments remains essential for dissecting and utilizing the functions of extremophiles. Here, we provide a straightforward protocol for efficiently isolating prokaryotic microorganisms from different extreme habitats (thermal, xeric, saline, alkaline, acidic, and cryogenic environments), which was established through previous successful work and our long-term experience in extremophile resource mining. We propose common processes for extremophile isolation at first and then summarize multiple cultivation strategies for recovering prokaryotic microorganisms from extreme environments and meanwhile provide specific isolation tips that are always overlooked but important. Furthermore, we propose the use of multi-omics-guided microbial cultivation approaches for culturing these as-yet-uncultivated microorganisms and two examples are provided to introduce how these approaches work. In summary, the protocol allows researchers to significantly improve the isolation efficiency of pure cultures and novel taxa, which therefore paves the way for the protection and utilization of microbial resources from extreme environments.
https://onlinelibrary.wiley.com/doi/full/10.1002/imt2.123

Afzal, S. *et al.* (2023). **Modern Breeding Approaches for Climate Change**. In: Jatoi, W.N., Mubeen, M., Hashmi, M.Z., Ali, S., Fahad, S., Mahmood, K. (eds) Climate Change Impacts on Agriculture. Springer, Cham. https://doi.org/10.1007/978-3-031-26692-8_17
Climate-smart agriculture is the emerging and sustainable option to mitigate the adverse effects of climate change (on crop adaptability) before it significantly influences global crop production. Crop development

through modern breeding techniques, effective agronomic practices and exploitation of natural variability in neglected and popular crops are all good ways to meet future food demands. However, the rapidly changing environment requires technological interventions to improve crop climate resilience. Technological advances such as genome-edited transgenic plants, high-throughput phenotyping technologies combined with next-generation sequencing techniques, big data analytics and advances in modern breeding techniques help modern agriculture progress towards robotics or digital conversion to face future environmental adversaries. For example, speed breeding in combination with genomic and phenomic methods can lead to quicker identification of genetic factors and, as a result, speed up crop development programmes.
Furthermore, combining next-generation interdisciplinary breeding platforms might open up new opportunities for developing climate-ready crops. Several integrated modern breeding platforms were created in the last few decades and are now employed worldwide. Africa and Asia have adopted these most frequently used crop improvement platforms with advanced techniques like multitrait association studies using genome-wide association studies (GWASs). These have permitted precise exploration of the genetic make-up of agricultural attributes in most crops. This chapter explores various ways to increase crop output by developing climate-resilient superior genotypes. Further, we discussed how combinatorial advanced breeding technologies and biotechnological approaches would be used for managing climate change's consequences to promote crops with climate resilience.
https://link.springer.com/chapter/10.1007/978-3-031-26692-8_17

Yuan, G., Lu, H., De, K. et al. (2023): **Split selectable marker systems utilizing inteins facilitate gene stacking in plants.** Commun Biol 6, 567 | https://doi.org/10.1038/s42003-023-04950-8
The ability to stack multiple genes in plants is of great importance in the development of crops with desirable traits but can be challenging due to limited selectable marker options. Here we establish split selectable marker systems using protein splicing elements called "inteins" for *Agrobacterium*-mediated co-transformation in plants. First, we show that such a split selectable marker system can be used effectively in plants to reconstitute a visible marker, RUBY, from two non-functional fragments through tobacco leaf infiltration. Next, to determine the general applicability of our split selectable marker systems, we demonstrate the utility of these systems in the model plants *Arabidopsis* and poplar by successfully stacking two reporters *eYGFPuv* and *RUBY*, using split Kanamycin or Hygromycin resistance markers. In conclusion, this method enables robust plant co-transformation, providing a valuable tool for the simultaneous insertion of multiple genes into both herbaceous and woody plants efficiently.
https://www.nature.com/articles/s42003-023-04950-8

Bai, X., Huang, Z., Duraj-Thatte, A.M. et al. (2023): **Engineering the gut microbiome**. Nat Rev Bioeng | https://doi.org/10.1038/s44222-023-00072-2
The role of the gut microbiome in human health and disease is being increasingly recognized. Gut microbes (including bacteria, fungi and viruses) can be genetically modified to diagnose (as biosensors) and treat (detoxification, controlled biosynthesis and precision targeting) the dysbiosis of the microbiome, which has been linked to several cancers and metabolic, autoimmune and infectious diseases. However, conventional manipulation of single microbial strains is often insufficient, and engineering a mutually supportive and collaborative network of gut microbes — 'a keystone consortium' — could be more effective. In this Review, we summarize gut microbiome engineering strategies against selected diseases and critically discuss their translational potential. We focus mainly on genetic engineering approaches, but we also discuss complementary strategies such as encapsulation, coupling with electronic devices, orthogonal diet engineering and faecal microbiota transplantation.
https://www.nature.com/articles/s44222-023-00072-2

Akinduro, A., Onyekwelu, C.I., Oyelumade, T. et al. (2023): **Impact of soil supplemented with pig manure on the abundance of antibiotic resistant bacteria and their associated genes**. J Antibiot | https://doi.org/10.1038/s41429-023-00633-y
This study was conducted to evaluate the abundance of antibiotic resistant bacteria and their resistance genes from agriculture soil supplemented with pig manure. Uncultivable soil sample was supplemented with pig manure samples under microcosm experimental conditions and plated on Luria-Bertani (LB) agar incorporated with commercial antibiotics. The supplementation of soil with 15% pig manure resulted in the highest increase in the population of antibiotic resistant bacteria (ARB)/multiple antibiotic resistant bacteria (MARB). Seven genera that included *Pseudomonas*, *Escherichia*, *Providencia*, *Salmonella*, *Bacillus*, *Alcaligenes* and *Paenalcaligenes* were the cultivable ARB identified. A total of ten antibiotic resistant bacteria genes (ARGs) frequently used in clinical or veterinary settings and two mobile genetic elements (MGEs) (Class 1 and Class 2 integrons) were detected. Eight heavy metal, copper, cadmium, chromium, manganese, lead, zinc, iron, and cobalt were found in all of the manure samples at different concentrations. Tetracycline resistance genes were widely distributed with prevalence of 50%, while aminoglycoside and quinolone-resistance gene had 16% and 13%, respectively. Eighteen ARB isolates carried more than two ARGs in their genome. Class 1 integron was detected among all the 18 ARB with prevalence of 90–100%, while Class 2 integron was detected among 11 ARB. The two classes of integron were found among 10 ARB. Undoubtedly, pig manure collected from farms in Akure metropolis are rich in ARB and their abundance might play a vital role in the dissemination of resistance genes among clinically-relevant pathogens.
https://www.nature.com/articles/s41429-023-00633-y

Huang Q., Lariviere P.J., Powell J.E., Moran N.A. (2023): **Engineered gut symbiont inhibits microsporidian parasite and improves honey bee survival.** PNAS 120 (25) e2220922120 | https://doi.org/10.1073/pnas.222092212
Honey bees (*Apis mellifera*) are critical agricultural pollinators as well as model organisms for research on development, behavior, memory, and learning. The parasite *Nosema ceranae*, a common cause of honey bee colony collapse, has developed resistance to small-molecule therapeutics. An alternative long-term strategy to combat *Nosema* infection is therefore urgently needed, with synthetic biology offering a potential solution. Honey bees harbor specialized bacterial gut symbionts that are transmitted within hives. Previously, these have been engineered to inhibit ectoparasitic mites by expressing double-stranded RNA (dsRNA) targeting essential mite genes, via activation of the mite RNA interference (RNAi) pathway. In this study, we engineered a honey bee gut symbiont to express dsRNA targeting essential genes of *N. ceranae* via the parasite's own RNAi machinery. The engineered symbiont sharply reduced *Nosema* proliferation and improved bee survival following the parasite challenge. This protection was observed in both newly emerged and older forager bees. Furthermore, engineered symbionts were transmitted among cohoused bees, suggesting that introducing engineered symbionts to hives could result in colony-level protection.
https://www.pnas.org/doi/10.1073/pnas.2220922120

Helander M., Jeevannavar A., Kaakinen K.,Mathew S.A. et al. (2023): **Glyphosate and a glyphosate-based herbicide affect bumblebee gut microbiota.** FEMS Microbiology Ecology, fiad065 | https://doi.org/10.1093/femsec/fiad065
Pollinator decline is one of the gravest challenges facing the world today, and the overuse of pesticides may be among its causes. Here we studied whether glyphosate, the world's most widely used pesticide, affects the bumblebee gut microbiota. We exposed the bumblebee diet to glyphosate and a glyphosate-based herbicide and quantified the microbiota community shifts using 16S ribosomal RNA gene sequencing. Furthermore, we estimated the potential sensitivity of bee gut microbes to glyphosate based on previously reported presence of target enzyme. Glyphosate increased, whereas the glyphosate-based herbicide decreased gut microbiota diversity, indicating that negative effects are attributable to co-formulants. Both glyphosate and the glyphosate-based herbicide treatments significantly decreased the relative abundance of potentially glyphosate-sensitive bacterial species *Snodgrasella alvi.* However, the relative abundance of potentially glyphosate-sensitive *Candidatus Schmidhempelia* genera increased in bumblebees treated with glyphosate. Overall, 50% of the bacterial genera detected in the bee gut microbiota were classified as potentially resistant to glyphosate, while 36% were classified as sensitive. Healthy core microbiota have been shown to protect bees from parasite infections, change metabolism, and decrease mortality. Thus, the heavy use of glyphosate-based herbicides may have implications on bees and ecosystems.
https://academic.oup.com/femsec/advance-article/doi/10.1093/femsec/fiad065/7198109?login=false

Boukid F., Ganeshan S., Wang Y., Tülbek M.C., Nickerson M.D. (2023): **Bioengineered Enzymes and Precision Fermentation in the Food Industry.** Int. J. Mol. Sci. *24* (12), 10156 | https://doi.org/10.3390/ijms241210156
Enzymes have been used in the food processing industry for many years. However, the use of native enzymes is not conducive to high activity, efficiency, range of substrates, and adaptability to harsh food processing conditions. The advent of enzyme engineering approaches such as rational design, directed evolution, and semi-rational design provided much-needed impetus for tailor-made enzymes with improved or novel catalytic properties. Production of designer enzymes became further refined with the emergence of synthetic biology and gene editing techniques and a plethora of other tools such as artificial intelligence, and computational and bioinformatics analyses which have paved the way for what is referred to as precision fermentation for the production of these designer enzymes more efficiently. With all the technologies available, the bottleneck is now in the scale-up production of these enzymes. There is generally a lack of accessibility thereof of large-scale capabilities and know-how. This review is aimed at highlighting these various enzyme-engineering strategies and the associated scale-up challenges, including safety concerns surrounding genetically modified microorganisms and the use of cell-free systems to circumvent this issue. The use of solid-state fermentation (SSF) is also addressed as a potentially low-cost production system, amenable to customization and employing inexpensive feedstocks as substrate.
Int. J. Mol. Sci. *24* (12), 10156 | https://doi.org/10.3390/ijms241210156

Drakonaki A., Mathioudaki E., Geladas E.D., Konsolaki E. et al. (2023): **Production of Polyhydroxybutyrate by Genetically Modified Pseudomonas sp. phDV1: A Comparative Study of Utilizing Wine Industry Waste as a Carbon Source.** Microorganisms *11* (6), 1592; https://doi.org/10.3390/microorganisms11061592
Pseudomonas sp. phDV1 is a polyhydroxyalkanoate (PHA) producer. The presence of the endogenous PHA depolymerase (phaZ) responsible for the degradation of the intracellular PHA is one of the main shortages in the bacterial production of PHA. Further, the production of PHA can be affected by the regulatory protein phaR, which is important in accumulating different PHA-associated proteins. PHA depolymerase phaZ and phaR knockout mutants of Pseudomonas sp. phDV1 were successfully constructed. We investigate the PHA production from 4.25 mM phenol and grape pomace of the mutants and the wild type. The production was screened by fluorescence microscopy, and the PHA production was quantified by HPLC chromatography. The PHA is composed of Polydroxybutyrate (PHB), as confirmed by ^{1}H-nuclear magnetic resonance analysis. The wildtype strain produces approximately 280 µg PHB after 48 h in grape pomace, while the phaZ knockout

mutant produces 310 µg PHB after 72 h in the presence of phenol per gram of cells, respectively. The ability of the phaZ mutant to synthesize high levels of PHB in the presence of monocyclic aromatic compounds may open the possibility of reducing the costs of industrial PHB production.
https://www.mdpi.com/2076-2607/11/6/1592

EFSA (European Food Safety Authority), Bottex, B, Gkrintzali, G, Garcia Matas, R, Georgiev, M, Maggiore, A, Merten, C, Rortais, A, Afonso, A and Robinson, T, 2023. Technical report on EFSA's activities on emerging risks in 2020. *EFSA supporting publication* 2023: 20(5):EN-8024. 51 pp. doi:10.2903/sp.efsa.2023.EN-8024
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2023.EN-8024

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.
*As always, I thank you all for hints and for publications. M*ost of *the pdf files can be downloaded directly from the links.*

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