

Sunday Evening News No. 113

Week 06 (2019-04-02 – 2019-10-02)

Selected and edited by **BGF** Jany

„Politik bedeutet ein starkes langsames Bohren von harten Brettern mit Leidenschaft und Augenmaß zugleich.“ Max Weber (1864-1920)

Gilt sicherlich auch für die Wissenschaft!

"Politics means a strong slow drilling of hard boards with passion and a sense of proportion at the same time." Max Weber (1864-1920)

That`s probably also true for science!

Dear all,

Here again my subjective selection of press releases and publications.

EU-Zulassung von gentechnisch veränderten Pflanzen

Informationsdienst Gentechnik: **EU-Kommission erlaubt Import von Mais mit acht gentechnischen Veränderungen**

<https://www.keine-gentechnik.de/nachricht/33527/#gsc.tab=0>

Deter A.: **EU-Parlament gegen neue Importzulassungen von gentechnisch veränderten Pflanzen**

Das Europäische Parlament hat gegen den Import neuer gentechnisch veränderter Sorten der Firmen Bayer und Syngenta gestimmt.

<https://www.topagrar.com/acker/news/eu-parlament-gegen-neue-importzulassungen-von-gentechnisch-veraenderten-pflanzen-10281219.html>

hier auch: GVO-Zulassungen 2019: Komitologieverfahren - Stufe 1 und Stufe 2

<https://www.biotech-gm-food.com/aktuelles>

Wess L.: **Mehr Eurythmie in der Pflanzenforschung?**

<https://www.salonkolumnisten.com/mehr-eurythmie-in-der-pflanzenforschung/>

BDP-Position: **Landwirtschaft benötigt Fortschritt**

Nutzung neuer Züchtungsmethoden muss möglich sein

https://www.bdp-online.de/de/Ueber_uns/Our_positions/2018-12-21_BDP-Position_NBT_nach_EuGH_.pdf

BDP Neue Züchtungsmethoden: **Pauschale Bewertung ist falsch**

Seit mehr als 100 Jahren verbessern Züchter die landwirtschaftlichen und gärtnerischen Pflanzen. Dafür entwickeln sie ihre Züchtungswerkzeuge kontinuierlich weiter. Der Europäische Gerichtshof (EuGH) hat im Juli 2018 ein folgenschweres Urteil gefällt. Hiernach sind Pflanzen aus neuen Züchtungsmethoden als gentechnisch veränderte Organismen (GVO) eingestuft. Die damit verbundenen unverhältnismäßig hohen Auflagen machen eine Anwendung der Methoden unwahrscheinlich – zum Nachteil von Landwirtschaft und Gesellschaft.

https://www.bdp-online.de/de/Ueber_uns/Our_positions/2018-12-21_Kompaktinformation_neue_Zuechtungsmethoden.pdf

Informationsdienst Gentechnik: **Umstritten: Wie (un)sichtbar schneidet die Gen-Schere?**

<https://www.keine-gentechnik.de/nachricht/33574/>

Osterkamp J.: **Die nächsten Generationen der CRISPR-Genschere**

Weiterentwickelte Cas-Enzyme sollen das Genwerkzeug CRISPR genauer, sicherer und vielseitiger machen - so wie CasX, das neueste Modell. Das scheint aber noch einmal anders zu funktionieren als andere Alternativen.

<https://www.spektrum.de/news/die-naechsten-generationen-der-crispr-genschere/1622082>

de La Hamaide S.: **French, German farmers destroy crops after GMOs found in Bayer seeds**

<https://www.reuters.com/article/us-france-gmo-bayer/french-german-farmers-destroy-crops-after-gmos-found-in-bayer-seeds-idUSKCN1PV1RG>

Fischer N.: From Ancient to Heirloom — The History of the Humble Bean
Similarly pleasing to see and to taste, heirloom beans have a long and colourful past.
<https://medium.com/nannie-appleseed/ancient-and-heirloom-beans-4c17353fb76b>

Lallensack R.: **The Reason These Poisonous Butterflies Don't Mate Is Written in Their DNA**
Wing color and mate preference seem to be genetically bound, leading these tropical butterflies to only choose mates that look like them
<https://www.smithsonianmag.com/science-nature/reason-butterflies-dont-mate-genetics-written-dna-180971456/>

Brainard J.: **Mexico's monarch population booms**
https://www.sciencemagazinedigital.org/sciencemagazine/08_february_2019_Main/MobilePagedArticle.action?articleId=1462723&app=false#articleId1462723

The daily up-date of the press releases: <https://www.biotech-gm-food.com/presse>

Publications:

Only if now yet seen:

Akcakaya P. et al. (2018): **In vivo CRISPR editing with no detectable genome-wide off-target mutations.** Nature 561, 416–419 | doi: 10.1038/s41586-018-0500-9

CRISPR-Cas genome-editing nucleases hold substantial promise for developing human therapeutic applications¹⁻⁶ but identifying unwanted off-target mutations is important for clinical translation⁷. A well-validated method that can reliably identify off-targets in vivo has not been described to date, which means it is currently unclear whether and how frequently these mutations occur. Here we describe 'verification of in vivo off-targets' (VIVO), a highly sensitive strategy that can robustly identify the genome-wide off-target effects of CRISPR-Cas nucleases in vivo. We use VIVO and a guide RNA deliberately designed to be promiscuous to show that CRISPR-Cas nucleases can induce substantial off-target mutations in mouse livers in vivo. More importantly, we also use VIVO to show that appropriately designed guide RNAs can direct efficient in vivo editing in mouse livers with no detectable off-target mutations. VIVO provides a general strategy for defining and quantifying the off-target effects of gene-editing nucleases in whole organisms, thereby providing a blueprint to foster the development of therapeutic strategies that use in vivo gene editing.
<https://www.nature.com/articles/s41586-018-0500-9>

Literature Review: Bianca van Beugen (2019): **Estimation of Human Risk from Animal Toxicity Tests: How realistic are uncertainty factors?**
https://www.academia.edu/38285576/Estimation_of_Human_Risk_from_Animal_Toxicity_Tests_How_realistic_are_uncertainty_factors_definitief.pdf?email_work_card=thumbnail-desktop

Tigue D.A., Kriese-Anderson L. and Pacumbaba R. (2019): **General Public Education of Food Myths and Urban Legends: Hormones, Antibiotics and GMOs.** MMB 1 (3), 21
<https://dl.sciencesocieties.org/publications/mmb/pdfs/1/3/21>

Herman R.A., Zhuang M., Storer N.P., Cnudde P., Delaney B. (2019): **Risk-Only Assessment of Genetically Engineered Crops Is Risky.** Trends in Plant Science, 24 (1), 58–68 | DOI:<https://doi.org/10.1016/j.tplants.2018.10.001>

The risks of not considering benefits in risk assessment are often overlooked. Risks are also often evaluated without consideration of the broader context. We discuss these two concepts in relation to genetically engineered (GE) crops. The health, environmental, and economic risks and benefits of GE crops are exemplified and presented in the context of modern agriculture. Misattribution of unique risks to GE crops are discussed. It is concluded that the scale of modern agriculture is its distinguishing characteristic and that the greater knowledge around GE crops allows for a more thorough characterization of risk. By considering the benefits and risks in the context of modern agriculture, society will be better served and benefits will be less likely to be forgone.
<https://www.cell.com/action/showPdf?pii=S1360-1385%2818%2930230-9>

Arora S. et al. (2019): **Resistance gene cloning from a wild crop relative by sequence capture and association genetics.** Nature Biotechnology 37. 139-143 | DOI: [10.1038/s41587-018-0007-9](https://doi.org/10.1038/s41587-018-0007-9),

Disease resistance (R) genes from wild relatives could be used to engineer broad-spectrum resistance in domesticated crops. We combined association genetics with R gene enrichment sequencing (AgRenSeq) to exploit pan-genome variation in wild diploid wheat and rapidly clone four stem rust resistance genes. AgRenSeq enables R gene cloning in any crop that has a diverse germplasm panel.
<https://www.nature.com/articles/s41587-018-0007-9>

John Innes Centre: Rapid gene cloning technique will transform crop disease protection
<https://phys.org/news/2019-02-rapid-gene-cloning-technique-crop.html#jCp>

Liu J-J. et al. (2019): **CasX enzymes comprise a distinct family of RNA-guided genome editors.** *Nature* | DOI: [10.1038/s41586-019-0908-x](https://doi.org/10.1038/s41586-019-0908-x)

The RNA-guided CRISPR-associated (Cas) proteins Cas9 and Cas12a provide adaptive immunity against invading nucleic acids, and function as powerful tools for genome editing in a wide range of organisms. Here we reveal the underlying mechanisms of a third, fundamentally distinct RNA-guided genome-editing platform named CRISPR–CasX, which uses unique structures for programmable double-stranded DNA binding and cleavage. Biochemical and in vivo data demonstrate that CasX is active for *Escherichia coli* and human genome modification. Eight cryo-electron microscopy structures of CasX in different states of assembly with its guide RNA and double-stranded DNA substrates reveal an extensive RNA scaffold and a domain required for DNA unwinding. These data demonstrate how CasX activity arose through convergent evolution to establish an enzyme family that is functionally separate from both Cas9 and Cas12a.
<https://www.nature.com/articles/s41586-019-0908-x>

Sanders R., University of California – Berkeley: Scientists find new and smaller CRISPR gene editor: CasX
<https://phys.org/news/2019-02-scientists-smaller-crispr-gene-editor.html#jCp>

Vicencio J., Martínez-Fernández C., Serrat X., Cerón J. (2019): **Efficient Generation of Endogenous Fluorescent Reporters by Nested CRISPR in *Caenorhabditis elegans*.** *Genetics* (2019). | <https://doi.org/10.1534/genetics.119.301965>

CRISPR-based genome editing methods in model organisms are evolving at an extraordinary speed. Whereas the generation of deletion or missense mutants is quite straightforward, the production of endogenous fluorescent reporters is more challenging. We have developed Nested CRISPR, a cloning-free ribonucleoprotein-driven method that robustly produces endogenous fluorescent reporters with EGFP, mCherry, or wrmScarlet in *Caenorhabditis elegans*. This method is based on the division of the fluorescent protein (FP) sequence in three fragments. In the first step, ssDNA donors (≤200 bp) are used to insert the 5' and 3' fragments of the FP in the locus of interest. In the second step, these sequences act as homology regions for homology-directed repair using a dsDNA donor (PCR product) containing the middle fragment, thus completing the FP sequence. In Nested CRISPR, the first step involving ssDNA donors is a well-established method that yields high editing efficiencies, and the second step is reliable because it uses universal crRNAs and PCR products. We have also used Nested CRISPR in a non-essential gene to produce a deletion mutant in the first step and a transcriptional reporter in the second step. In the search for modifications to optimize the method, we tested synthetic sgRNAs, but did not observe a significant increase in efficiency. To streamline the approach, we combined all Step 1 and Step 2 reagents in a single injection and were successful in 3 of 5 loci tested with editing efficiencies of up to 20%. Finally, we discuss the prospects of this method in the future.
<http://www.genetics.org/content/early/2019/01/31/genetics.119.301965>

IDIBELL-Bellvitge Biomedical Research Institute: Nested CRISPR enables efficient genome editing using long DNA fragments
<https://phys.org/news/2019-02-crispr-enables-efficient-genome-dna.html#jCp>

Zhang Z.; Hua L., Gupta A., Tricoli D., Edwards K.J., Yang B., Li L. (2019): **Development of an *Agrobacterium*-delivered CRISPR/Cas9 system for wheat genome editing.** *Plant Biotechnology Journal*: <https://doi.org/10.1111/pbi.13088>

CRISPR/Cas9 has been widely used for genome editing in many organisms, including important crops like wheat. Despite the tractability in designing CRISPR/Cas9, efficacy in the application of this powerful genome editing tool also depends on DNA delivery methods. In wheat, the biolistics based transformation is the most used method for delivery of the CRISPR/Cas9 complex. Due to the high frequency of gene silencing associated with high copy transgenes and low edit rate in wheat, a large T₀ transgenic plant population are required for recovery of desired mutations, which poses a bottleneck for many genome editing projects. Here, we report an *Agrobacterium*-delivered CRISPR/Cas9 system in wheat, which includes a wheat codon optimized Cas9 driven by a maize ubiquitin gene promoter and a guide RNA cassette driven by wheat U6 promoters in a single binary vector. Using this CRISPR/Cas9 system, we have developed 69 edit mutants for four grain-regulatory genes, *TaCKX2-1*, *TaGLW7*, *TaGW2*, and *TaGW8*, in T₀, T₁, and T₂ generation plants at an average edit rate of 10% without detecting off-target mutations in the most Cas9-active plants. Homozygous mutations can be recovered from a large population in a single generation. Different from most plant species, deletions over 10 bp are the dominant mutation types in wheat. Plants homozygous of 1,160-bp deletion in *TaCKX2-D1* significantly increased grain number per spikelet. In conclusion, our *Agrobacterium*-delivered CRISPR/Cas9 system provides an alternative option for wheat genome editing, which requires a small number of transformation events because CRISPR/Cas9 remains active for novel mutations through generations.
<https://onlinelibrary.wiley.com/doi/abs/10.1111/pbi.13088>
<https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbi.13088>

Burgarella C., Barnaud A., Kane N.A., Jankowski F., Scarcelli N., Billot C., Vigouroux Y., Berthouly-Salazar C. (2019): **Adaptive Introgression: An Untapped Evolutionary Mechanism for Crop Adaptation.** *Front. Plant Sci.* 10:4. doi: 10.3389/fpls.2019.00004
Global environmental changes strongly impact wild and domesticated species biology and their associated ecosystem services. For crops, global warming has led to significant changes in terms of phenology and/or

yield. To respond to the agricultural challenges of this century, there is a strong need for harnessing the genetic variability of crops and adapting them to new conditions. Gene flow, from either the same species or a different species, may be an immediate primary source to widen genetic diversity and adaptions to various environments. When the incorporation of a foreign variant leads to an increase of the fitness of the recipient pool, it is referred to as “adaptive introgression”. Crop species are excellent case studies of this phenomenon since their genetic variability has been considerably reduced over space and time but most of them continue exchanging genetic material with their wild relatives. In this paper, we review studies of adaptive introgression, presenting methodological approaches and challenges to detecting it. We pay particular attention to the potential of this evolutionary mechanism for the adaptation of crops. Furthermore, we discuss the importance of farmers’ knowledge and practices in shaping wild-to-crop gene flow. Finally, we argue that screening the wild introgression already existing in the cultivated gene pool may be an effective strategy for uncovering wild diversity relevant for crop adaptation to current environmental changes and for informing new breeding directions.

<https://www.frontiersin.org/articles/10.3389/fpls.2019.00004/full>

Sánchez-Bayo F., Wyckhuys K.A.G. (2019): **Worldwide decline of the entomofauna: A review of its drivers.** *Biological Conservation* 232 (2019) 8–27 |

<https://doi.org/10.1016/j.biocon.2019.01.020>

Biodiversity of insects is threatened worldwide. Here, we present a comprehensive review of 73 historical reports of insect declines from across the globe, and systematically assess the underlying drivers. Our work reveals dramatic rates of decline that may lead to the extinction of 40% of the world's insect species over the next few decades. In terrestrial ecosystems, Lepidoptera, Hymenoptera and dung beetles (Coleoptera) appear to be the taxa most affected, whereas four major aquatic taxa (Odonata, Plecoptera, Trichoptera and Ephemeroptera) have already lost a considerable proportion of species. Affected insect groups not only include specialists that occupy particular ecological niches, but also many common and generalist species. Concurrently, the abundance of a small number of species is increasing; these are all adaptable, generalist species that are occupying the vacant niches left by the ones declining. Among aquatic insects, habitat and dietary generalists, and pollutant-tolerant species are replacing the large biodiversity losses experienced in waters within agricultural and urban settings. The main drivers of species declines appear to be in order of importance: i) habitat loss and conversion to intensive agriculture and urbanisation; ii) pollution, mainly that by synthetic pesticides and fertilisers; iii) biological factors, including pathogens and introduced species; and iv) climate change. The latter factor is particularly important in tropical regions, but only affects a minority of species in colder climates and mountain settings of temperate zones. A rethinking of current agricultural practices, in particular a serious reduction in pesticide usage and its substitution with more sustainable, ecologically-based practices, is urgently needed to slow or reverse current trends, allow the recovery of declining insect populations and safeguard the vital ecosystem services they provide. In addition, effective remediation technologies should be applied to clean polluted waters in both agricultural and urban environments.

<https://www.sciencedirect.com/science/article/abs/pii/S0006320718313636>

Hiltpold I. and Hibbard B.E. (2018): **Indirect Root Defenses Cause Induced Fitness Costs in Bt-Resistant Western Corn Rootworm.** *Journal of Economic Entomology* 111 (5), 2349 - 2358. DOI: [10.1093/jee/toy220](https://doi.org/10.1093/jee/toy220)

Plants genetically modified to produce insecticidal toxins from the bacterium *Bacillus thuringiensis* Berliner (Bt) have been extensively used to manage the western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae) in the United States. Evolution of WCR resistance to Bt toxins has forced the consideration of alternative pest management and improved insect resistance management. Entomopathogenic nematodes (EPNs), obligate insect parasites, are attracted toward volatile organic compounds (VOCs) emitted by maize roots after WCR herbivory. The production of VOCs of two types of Bt maize (MON88017 and MIR604) and their near-isolines was evaluated after induction with Bt-susceptible and resistant WCR. The attraction of EPNs toward the Bt hybrids was tested in the laboratory and the field. Bt hybrids emitted VOCs when induced by Bt-resistant insects whereas induction by Bt-susceptible WCR did not elicit a plant response. Survival of Bt-resistant WCR was lower on the hybrid attracting EPNs and similar to the survival of Bt-susceptible WCR without EPNs. This trade-off of Bt-resistance is defined here as an induced fitness cost, and offers a viable tool to management of Bt-resistant WCR.

<https://academic.oup.com/jee/article-abstract/111/5/2349/5063818?redirectedFrom=fulltext>

University of Delaware: Researchers discover corn plants call in hungry nematodes when resistant rootworms attack

<https://phys.org/news/2019-02-corn-hungry-nematodes-resistant-rootworms.html#jCp>

Pett W., Adamski, M., Adamska M., Warren W.R., Eitel M., Pisani D., Wörheide G. (2019):

The role of homology and orthology in the phylogenomic analysis of metazoan gene content. *Molecular Biology and Evolution*, msz013, <https://doi.org/10.1093/molbev/msz013>

Resolving the relationships of animals (Metazoa) is crucial to our understanding of, for example, the origin of key traits such as muscles, guts and nerves. However, a broadly accepted metazoan consensus phylogeny has yet to emerge. In part this is because the genomes of deeply-diverging and fast-evolving lineages may undergo significant gene turnover, reducing the number of orthologs shared with related phyla. This can limit the usefulness of traditional phylogenetic methods that rely on alignments of orthologous sequences. Phylogenetic analysis of gene content has the potential to circumvent this orthology requirement, with binary

presence/absence of homologous gene families representing a source of phylogenetically informative characters. Applying binary substitution models to the gene content of 26 complete animal genomes, we demonstrate that patterns of gene conservation differ markedly depending on whether gene families are defined by orthology or homology, i.e. whether paralogs are excluded or included. We conclude that the placement of some deeply-diverging lineages may exceed the limit of resolution afforded by the current methods based on comparisons of orthologous protein sequences, and novel approaches are required to fully capture the evolutionary signal from genes within genomes.

<https://academic.oup.com/mbe/advance-article-abstract/doi/10.1093/molbev/msz013/5303344?redirectedFrom=fulltext>

Bradley P., den Bakker H.C., Eduardo P. C. Rocha E.P,C., McVean G. & Iqbal Z. (2019): **Ultrafast search of all deposited bacterial and viral genomic data.** *Nature Biotechnology* 37, 152–159 | . DOI: [10.1038/s41587-018-0010-1](https://doi.org/10.1038/s41587-018-0010-1)

Exponentially increasing amounts of unprocessed bacterial and viral genomic sequence data are stored in the global archives. The ability to query these data for sequence search terms would facilitate both basic research and applications such as real-time genomic epidemiology and surveillance. However, this is not possible with current methods. To solve this problem, we combine knowledge of microbial population genomics with computational methods devised for web search to produce a searchable data structure named Blitsliced Genomic Signature Index (BIGSI). We indexed the entire global corpus of 447,833 bacterial and viral whole-genome sequence datasets using four orders of magnitude less storage than previous methods. We applied our BIGSI search function to rapidly find resistance genes *MCR-1*, *MCR-2*, and *MCR-3*, determine the host-range of 2,827 plasmids, and quantify antibiotic resistance in archived datasets. Our index can grow incrementally as new (unprocessed or assembled) sequence datasets are deposited and can scale to millions of datasets.

<https://www.nature.com/articles/s41587-018-0010-1>

European Molecular Biology Laboratory: The web meets genomics: a DNA search engine for microbes

<https://phys.org/news/2019-02-web-genomics-dna-microbes.html#jCp>

Lutzoni F. et al.(2018): **Contemporaneous radiations of fungi and plants linked to symbiosis.** *Nature Communications*, 9 (5451) DOI: [10.1038/s41467-018-07849-9](https://doi.org/10.1038/s41467-018-07849-9)

Interactions between fungi and plants, including parasitism, mutualism, and saprotrophy, have been invoked as key to their respective macroevolutionary success. Here we evaluate the origins of plant-fungal symbioses and saprotrophy using a time-calibrated phylogenetic framework that reveals linked and drastic shifts in diversification rates of each kingdom. Fungal colonization of land was associated with at least two origins of terrestrial green algae and preceded embryophytes (as evidenced by losses of fungal flagellum, ca. 720 Ma), likely facilitating terrestriality through endomycorrhizal and possibly endophytic symbioses. The largest radiation of fungi (Leotiomyceta), the origin of arbuscular mycorrhizae, and the diversification of extant embryophytes occurred ca. 480 Ma. This was followed by the origin of extant lichens. Saprotrophic mushrooms diversified in the Late Paleozoic as forests of seed plants started to dominate the landscape. The subsequent diversification and explosive radiation of Agaricomycetes, and eventually of ectomycorrhizal mushrooms, were associated with the evolution of Pinaceae in the Mesozoic, and establishment of angiosperm-dominated biomes in the Cretaceous.

<https://www.nature.com/articles/s41467-018-07849-9.pdf>

Blumenthal, K. G., Wolfson, A. R., Li, Y.; Seguin, C. M., Phadke, N. A., Banerji, A.; Mort, E. (2019): **Allergic Reactions Captured by Voluntary Reporting.** *Journal of Patient Safety:*

[January 31, 2019 - Volume Publish Ahead of Print - Issue - p](https://journals.lww.com/journalpatientsafety/Abstract/publishahead/Allergic_Reactions_Captured_by_Voluntary_Reporting.99286.aspx)

[https://journals.lww.com/journalpatientsafety/Abstract/publishahead/Allergic Reactions Captured by Voluntary Reporting.99286.aspx](https://journals.lww.com/journalpatientsafety/Abstract/publishahead/Allergic_Reactions_Captured_by_Voluntary_Reporting.99286.aspx)

Ng, T.L., Rohac R., Mitchell A.J., Boal A.K. & Balskus E.P (2019): **An N-nitrosating metalloenzyme constructs the pharmacophore of streptozotocin.** *Nature* 566, 94 – 99 | DOI: [10.1038/s41586-019-0894-z](https://doi.org/10.1038/s41586-019-0894-z)

Small molecules containing the *N*-nitroso group, such as the bacterial natural product streptozotocin, are prominent carcinogens^{1,2} and important cancer chemotherapeutics^{3,4}. Despite the considerable importance of this functional group to human health, enzymes dedicated to the assembly of the *N*-nitroso unit have not been identified. Here we show that SznF, a metalloenzyme from the biosynthesis of streptozotocin, catalyses an oxidative rearrangement of the guanidine group of *N*^ω-methyl-L-arginine to generate an *N*-nitroso urea product. Structural characterization and mutagenesis of SznF reveal two separate active sites that promote distinct steps in this transformation using different iron-containing metallocofactors. This biosynthetic reaction, which has little precedent in enzymology or organic synthesis, expands the catalytic capabilities of non-haem-iron-dependent enzymes to include N–N bond formation. We find that biosynthetic gene clusters that encode SznF homologues are widely distributed among bacteria—including environmental organisms, plant symbionts and human pathogens—which suggests an unexpectedly diverse and uncharacterized microbial reservoir of bioactive *N*-nitroso metabolites.

<https://www.nature.com/articles/s41586-019-0894-z>

Harvard University: Study unravels how microbes produce key compound used to fight cancer

<https://phys.org/news/2019-02-unravels-microbes-key-compound-cancer.html#jCp>

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de.

As always, I thank you all for hints and for publications. Most of the pdf files can be downloaded directly from the links.

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