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Artificial Intelligence applied to Biotechnology

Inteligencia Artificial aplicada a la Biotecnologia

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Abstract

We are living the last technological revolution with artificial intelligence (AI), whose basis and techniques have precisely now deserved Nobel Prizes in Physics and Chemistry. This computing technology mimic aspects of human intelligence such as solving complex problems, communicating with humans, and learning from data and experience. Generative AI is entering quickly in our lives, and AI is already used in many economic sectors, and especially in research and its applications, as in Biotechnology. The revolution of biotechnological advances in genomic sequencing, together with those of protein structures, has given rise to an exponential growth of data, which requires automatic tools such as AI. Here the main applications of AI to biotechnology are reviewed, being the biomedical and pharmaceutical the most common. It is worth noting for instance the diagnosis of diseases as cancer, or the prediction of Alzheimer's. There is also the relevant Alphafold software, a deep learning system which can predict protein structures, their folding, and interactions protein-drugs. IA applications to other biotechnology fields are also reviewed, such as plant biotechnology —for instance selecting suitable genes for transgenic proteins—, or environmental biotechnology —for optimization of removal of pollutants—, or for genome editing.

Keywords. Artificial intelligence; biotechnology; machine learning; deep learning; data mining; genomics; disease diagnosis; algorithm; molecular; environment.

What is Artificial Intelligence?

There are many definitions for "Artificial Intelligence" (AI), as the term **intelligence** has a complex and variable meaning. Human intelligence, according an agreed-upon definition [1], is the mental capacity that involves the ability to reason, plan, solve problems, think abstractly, understand complex ideas, and learn quickly from experience and the environment.

Apart from this "natural" human intelligence, **artificial** intelligence (**AI**, from now on) can be defined as a part of computing dedicated to the development of algorithms —sets of instructions for executing a task or solving a problem— that allow a machine —usually a computer— having some reasoning abilities that mimic aspects of human intelligence.

Historically, aside from the previous development of logic and mathematics from the classical Greeks through the medieval philosopher Ramon Llull, or Pascal and Leibniz in the 17th century, AI properly began with the computational models of the English mathematician Alan Turing in 1936, father of computer science, and AI was established as an academic discipline in the late 1950s in British and American universities.

In the years that followed, AI went through cycles of optimism followed by periods of disappointment and loss of funding, known as the AI winter. However, in the 1980s, the pioneering methods of neural networks that are the basis of today's machine learning were proposed by the recent winners of the 2024 Nobel Prize in Physics, the American John Hopfield, and the British Geoffrey Hinton [2]. The 1990s saw a revolution in computing with personal computers and the Internet for almost everyone, another basis of today's AI. An important milestone then was IBM's Deep Blue supercomputer, specialized in playing chess, which in 1997 managed to beat the world champion Garry Kaspàrov [3], and was therefore the first time that a machine with a very specific AI outperformed humans in complex operations.

Until the beginning of the 21st century, many computer programs were developed applied to various sectors such as finance, medical diagnosis, research, and games (such as Deep Blue) that are based on logical-mathematical deductive reasoning: this is what is called **symbolic AI**, where algorithms developed by programmers have explicit formulation rules [4].

However, the most well-known AI today is **non-symbolic or connectionist AI**, which is based on statistical inductive methods. In this case, the key are the artificial **neural networks**, the mathematical models of **machine learning**, inspired by the biological nervous system, with interconnected nodules, among which stand out the so-called **deep learning** neural networks in multilayers, connected to each other. Learning is based on algorithms that process examples from a huge set of data giving possible answers that gradually change in successive iterations as the hits increase, learning to classify the input data within a fixed set of possible output categories [5]. In summary, machine learning can be defined as the science of programming computers in such a way that they learn from data [6].

This development of the software has gone in parallel with the great improvement in the efficiency of the architecture of the transformers, that is the **hardware**, with **supercomputers**. All this has given rise to the current boom since 2020, with companies, universities and laboratories dedicated to AI, mainly in California, but with tools and applications used globally.

The most well-known tools are those of **generative AI** which can create text and images, but also many applications commonly used by almost everyone, such as advanced Internet search engines, recommendation and advertising systems, interaction with human speech, automatic translation of text and voice, maps using, virtual assistants, conversational chatbots, autonomous cars and so many others. In fact, many cutting-edge AI applications are not perceived as AI, and often when one has become useful and common enough it is no longer labeled as AI [7]. Current AI, and not only generative AI, is also applied in many economic sectors, including administrations, education, communication, industries of all kinds, and especially at the level of research and its applications, as we will see with biotechnology.

For a better understanding of how AI works in general I recommend Melanie Mitchell's book [8].

Relationship of Artificial Intelligence with Biotechnology

Computer technology —the basis of AI— has had an extremely rapid exponential growth in the last 50 years, like no other discipline. The number of transistors in each electronic chip has been doubling every 2 years, a phenomenon known as Moore's law. The only other area that has gone at the same rate, and even faster, is biotechnology. The revolution of biotechnological advances in genomic sequencing, together with those of protein structures and other molecules, has given rise to an exponential growth of data, which are deposited by the thousands every day in databases such as GenBank (NCBI), at a rate of doubling its number every year, now exceeding 10^{16} bytes of information [9].

To work with this enormous amount of biotechnological information, automatic tools are needed that integrate data from different sources, and process the relevant information in order to generate new knowledge and be able to use this to develop new processes, compounds, products and services, or to improve the existing ones In fact, it is unthinkable that any significant advances in biotechnology can be made in the future without the large volumes of data stored online. We can see for example some of the databases used by the European Bioinformatics Institute of the European Molecular Biology Laboratory (EMBL-EBI) in the review by Cook *et al.* [10].

This **data mining** has become one of the pillars of biotechnological research. In many cases, the complete process includes integrating information from multiple sources, applying statistical and machine learning techniques to explore and extract insights from that integrated information, and using those insights for the design, control, and improvement of bioprocesses [9]. A large part of these techniques is considered artificial intelligence.

It must be emphasized that AI is entirely based on digital technology, and therefore **digitization** is the first step for any application to any biotechnological research or process. AI systems are integrated in many cases with other digital technologies such as sensors, cyber-physical systems (robots), and techniques that allow the automation of tasks and the collection and analysis of multiple data [11].

The use of AI tools in biotechnological research practically began in 2000, as reflected in the publications in indexed international scientific journals and since then it has been increasing exponentially (Table 1). Most of a total of 3500 articles have been published in recent years. The keywords related to AI most referenced in these articles are Machine Learning and Deep Learning, that is, the most used methods. Apart from these, some of the most cited keywords specific to the biotechnological field are Microarray and Gene expression, which indicate that gene expression studies are one of the fields where AI techniques are used the most.

Table 1. Number of annual biotechnological research publications using AI tools (Modified from Xu *et al.* [12]).

Year of publication	No. of publications
2000	0
2005	40
2010	110
2015	130
2020	670

According to Xu *et al.* [12], two of the three most referenced from those 3500 articles are about improving AI methods themselves and the third —published in Nature Biotechnology, on the identification of specific gene sequences— is more specific to biotechnology [13]. AI is widely used in biotechnology to solve a wide variety of problems. However, the most popular topics are those related to the field of health, that is, biomedical and pharmaceutical applications.

Biomedical and pharmaceutical applications of Artificial Intelligence

As we have seen, some of the most common are those related to genomics, and especially for the **genetic diagnosis of diseases**, as is the case with **cancer** [14]. For example, Cristiano *et al.* [15] developed a very interesting work to detect cancer at an early stage based on the profiles of the sequences of the free DNA fragments (cell-free DNA, cfDNA) found in the blood plasma, a method called DELFI by the authors. This method has the clear advantage of not being invasive since a small blood sample is enough. Cancer patients have some altered sequences of cfDNA fragments due to various mutations compared to healthy individuals, but it is very difficult and laborious to detect these changes by genetic markers or other common techniques. In this work, detection has been achieved by comparing cfDNA fragmentation profiles of 208 patients with 7 types of cancer and 215 healthy individuals, using machine learning techniques combined with other techniques.

The machine learning model used was the gradient tree boosting algorithm, which includes both the characteristics of the fragmentation profiles in certain genomic intervals, as well as the numbers of copies of chromosomes and mitochondrial DNA. With this algorithm, validation is done with multiple layers of training data and test data in different combinations, as in other machine learning techniques. Finally, a score is obtained (DELFI score) that can be used to classify individuals as healthy or having cancer, with a good probability.

With the samples correctly identified from cancer patients with 90% specificity, another similar algorithm trained to predict the type of cancer —breast, colorectal, lung, ovarian, pancreatic, gastric, or bile duct— was applied, and the result was 75% specific of the type of cancer. Therefore, this method is very promising for the early detection and control of human cancer [15].

Apart from cancer, there are many applications of AI in the **diagnosis and prognosis of other diseases**. Some examples are the detection of tumoral lymph nodes [16] or the prediction of Alzheimer's [17]. In addition, the AI tools can analyze medical images —such as X-rays, CT scans, and MRIs— to detect signs of disease with high accuracy. They can also combine clinical data to predict disease course and assess response to treatment [18]. AI helps identify biomarkers, which are biological indicators of diseases or health conditions. Machine learning models analyze omics data (genomics, proteomics, metabolomics) to find patterns that indicate the presence of diseases or response to therapies [19].

Another case that needs to be commented on is the **Alphafold software** for the field of **molecular biology**, designed as a deep learning system, and specifically the AlphaFold3 version [20], which has the prediction of the protein structure as its main function, and depending on the molecules that surround it. Consequently, this software can predict the interactions of proteins and other biomolecules with drugs. In this way, AlphaFold can predict in three dimensions how proteins fold and what form they take when they interact with other smaller molecules, be it one or many. These can be drugs, and this is how their effects can be seen, since these depend on the form adopted by the proteins with which they interact.

AlphaFold was developed in 2018 by DeepMind, a company based in London —founded by Demis Hassabis—, which is a subsidiary of Alphabet Inc. (Google) of California. The version AlphaFold2 already had a large protein database and can be used online at their free web. Now DNA, RNA and many other ligand molecules have also been added to Alphafold3, such as antibodies, ions, or many drugs, in addition to the fact that the database already has 200 million protein structures [21]. Just these days the Nobel Prize in Chemistry 2024 has been awarded to Demis Hassabis and John Jumper, both from Deep Mind, together with David Baker from Seattle (USA) for their predictions in structure and the computational design of proteins [22].

The main feature of AlphaFold's algorithms is their very high machine learning capacity. The software was started by training it on about 170,000 proteins from public databases of sequences and structures and uses a machine-learning neural network that takes a piecemeal approach and then puts them together into a joint solution. Based on the genetic sequences and ligands and covalent bonds, the possible alignments of multiple sequences are performed by pairs in different modules with trial-and-error recycling, generating the positions of each atom, and in comparative modules the different sections of the protein are being predicted, until reaching the final module of the total structure [20].

AlphaFold is being used in many studies to design new drugs and to find several disease antigens to fight. For example, it has been used to predict the structure of some proteins of SARS-CoV-2, the agent of COVID-19, before being confirmed experimentally. One of the predicted proteins participates in the lysis of the host cell to release the replicated virions [23].

Apart from AlphaFold, there are quite a few other applications of machine learning for drug discovery, which identify potential therapeutic compounds more efficiently than traditional methods. As mentioned, large amounts of biological data are analyzed to predict drug-target interaction, reducing the time and cost of new drug development [24, 25].

AI applications to other fields of Biotechnology

AI has strongly entered **precision agriculture**, but especially with non-biotech applications, such as the use of AI to predict crop yields, detect diseases from images, optimize the use of resources such as water and fertilizers, or the use of fruit harvesting robots with built-in digital vision and controlled by AI [26]. For example, deep learning with multilayer neural networks, called convolutional ones, is applied to the processing of images taken by drones or satellites, in a similar way to facial image recognition or searches for images from common browsers. There is a good review of the use of these convolutional networks in agriculture by Kamilaris & Prenafeta-Boldú [27].

AI applied to Biotechnological agriculture

The properly speaking biotechnological agriculture or **plant biotechnology** includes a range of biological techniques, both traditional and more modern, in which agricultural species are modified and with the possible use of microorganisms, to improve the yield of crops or obtain new products, while guaranteeing food safety and sustainability. These techniques include selection and crossing of varieties, mutations and genetic modifications or the introduction of foreign genes by recombinant DNA and other advanced techniques [28].

Improved yield can be achieved through disease control by making plants resistant to disease-causing microorganisms, whether bacteria, fungi, or viruses. Another field of improvement is to achieve tolerance to abiotic stress such as drought, and other applications are phytoremediation, to remove harmful compounds such as heavy metals, and the production of secondary metabolites and other compounds of industrial interest [29].

The applications of **AI in plant biotechnology** are very diverse and include, among others, the prediction of parental combinations in hybridizations or the classification of genotypes and genetic diversity. However, most applications carried out are modeling and prediction studies of various parameters, such as seed yield or other plant characteristics or disease predictions, or estimation of water stress tolerance [6].

AI can also be used to identify and select suitable genes to synthesize transgenic proteins and produce them in plants, in what is called **molecular agriculture**. The most interesting thing in this field is to produce animal proteins in plants, in a more sustainable and less polluting way than obtaining them with animals in intensive farms. There are currently several companies that produce pig, cow, or egg proteins, as well as enzymes and other molecules, in plant cells [30].

An example is the synthesis of cow's milk casein in potatoes, a transgenic protein [31]. To make this possible, the Israeli computational biology R&D company Evogene used an AI program called GeneRator-AI, that identifies and selects relevant genes linked to certain phenotypes or characters from the NCBI databases, which can be used to clone them into organisms that are easy to work with. In this case, with GeneRator-AI the genes of the 4 subtypes of cow's milk casein were selected and the potato plant was chosen as the optimal organism to clone them. With this, plants were obtained that accumulate casein in their leaves. Once the casein is extracted, cheeses can be made, as is done by the company Finally Foods [32, 31].

AI applied to Environmental Biotechnology

This includes many different microbial processes with the aim of preserving the environment, such as the biodegradation of organic waste in water and soil, the elimination of pollutants —especially xenobiotic compounds—, restoration of biodiversity, and use of some biodegradable waste to produce sustainable fuels, such as biogas or biofuel. As in all other industries, AI techniques are also useful for working with lots of dates and drawing more reliable conclusions from them.

An example is the optimization of the **removal of the pollutant 2,4,6-trinitrotoluene** (TNT) by activated sludge with aeration, using artificial neural networks, published by Karimi *et al.* (2023)[33]. TNT or 2-methyl-1,3,5-trinitrobenzene (IUPAC name) is an explosive, toxic, irritating and carcinogenic aromatic hydrocarbon. In addition to being used as an explosive in mines and military industries, it is also used for the synthesis of many different compounds such as drugs, biocides, dyes, and others, and for this reason it is often found in contaminated wastewater. TNT can be removed from these with the usual biological treatments of activated sludge from sewage treatment plants, but it has a high oxygen demand (BOD) for its biodegradation and the removal efficiency is not very high. That is why it is necessary to adjust the parameters of the purification systems well to achieve biodegradation of TNT, and AI mathematical models are a good option.

To eliminate TNT, the authors [33] have used the ANFIS model (adaptive neural fuzzy inference system), which allows modeling of input-output relationships in complex systems. These algorithms involve learning with the training data and then solve it in a fuzzy inference system —where the variables can have partial values, between 0 and 1—, while ignoring the deeper layers, without complex mathematical models, and more flexible and faster for biological treatment processes. The result was very good, with a 97% removal of TNT, at optimal conditions for the parameters of the treatment plant [33].

AI applied to genome editing

Various AI tools can be applied to improve genome editing, a type of genetic engineering in which a piece of DNA is inserted, modified, or replaced in the genome of a living being. The best known and valued editing system is CRISPR (clustered regularly interspaced short palindromic repeats), consisting of a guide RNA component and an endonuclease, such as Cas9. In nature **CRISPR-Cas9** is used by bacteria to defend themselves from viral attacks. This genomic DNA editor is being successfully used in various biotechnological sectors, both in research and applied to biomedicine, agriculture or environmental or others [34].

However, since CRISPR-Cas9 is an editor derived from bacteria, often presents some drawbacks when brought to other organisms, such as human cells. A good alternative to overcome these evolutionary constraints is to design genome editors with AI [35], using a **large language model**, that is, a neural network with many trained parameters, like the well-known AI programs that generate texts or images. In this case the parameters are genetic data of the entire biological scale, and they have prepared a database of one million CRISPR operons through systematic data mining of 26 terabases (10^{12}) extracted from genomes and metagenomes. In this way, the AI models [35] can generate many more RNA sequences for CRISPR-Cas than are currently available, and with that human genes can be edited much more efficiently.

Conclusions

Currently we are experiencing a digital revolution, especially in the world of communications, and the term **Artificial Intelligence** (AI) is on everyone's lips largely due to generative AI with virtual assistants, conversational chatbots and generators of texts and images. In addition, AI is being applied to all business economic sectors and administrations to automate processes, perform data analysis and predictive market analysis, create content of all kinds, personalize advertising recommendations, and many other possibilities. This boom is generating a lot of expectations, even financial ones, sometimes exaggerated, and at the same time AI, as a new tool that it is, generates fears and misgivings regarding the risks and frauds that its use can entail.

Despite this, as a very useful new technology, more and more profit will be drawn from it, and with the right controls, it will lead to further advances for humanity. This is very clear in the world of **science and technology**. AI tools are being used in many research laboratories and technology centers as tools that allow better analysis of experimental results and easier design of new ones.

The relevance of AI is evident with the **Nobel prizes** awarded these days, the one in Physics to the pioneers who developed the bases of neural networks and the one in Chemistry precisely for the application of AI to Biotechnology, specifically in the protein structure.

Within science and technology, precisely **biotechnology** is the field that is providing the most advances and benefits in recent times. The two last revolutions since the end of the 20th century are the digital one —including AI lately— and biotechnology, especially that related to health. Advances in biotechnology, with genomic sequencing and protein structure resolution, and all related omics, are increasingly dependent on the extensive use of massive amounts of data, requiring AI tools to analyze them and draw reliable results and conclusions.

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References

1. Gottfredson, L.S. Mainstream science on intelligence: an editorial with 52 signatories, history and bibliography. *Intelligence*, **1997**, 13-23. https://doi.org/10.1016/S0160-2896(97)90011-8
2. The Nobel Prize in Physics. Nobel Prize Outreach AB. *NobelPrize.org*, **2024**. https://www.nobelprize.org/prizes/physics/2024/summary/
3. Espeso, P. Deep Blue, el ordenador con una sola misión: ganar al humano. *Xataka*, **2024**. https://www.xataka.com/otros/deep-blue-el-ordenador-con-una-sola-mision-ganar-al-humano
4. Wikipedia contributors. Symbolic artificial intelligence. *Wikipedia, The Free Encyclopedia*, 2024. https://en.wikipedia.org/w/index.php?title=Symbolic_artificial_intelligence&oldid=123563212
5. Caudai, C., Galizia, A., Geraci, F. *et al.* AI applications in functional genomics. *Comput Struct Biotech J*, **2021**, 19, 5762-5790. https://doi.org/10.1016/j.csbj.2021.10.009
6. Niazian, M. & Niedbala, G. Machine Learning for Plant Breeding and Biotechnology. *Agriculture*, **2020**, 10, 436. https://doi.org/10.3390/agriculture10100436
7. Kaplan, A. & Haenlein, M. Siri, Siri, in my hand: Who's the fairest in the land? On the interpretations, illustrations, and implications of artificial intelligence. *Business Horizons*, **2019**, 62, 15–25. https://doi.org/10.1016/j.bushor.2018.08.004
8. Mitchell, M. Artificial Intelligence: a guide for thinking humans. **2019**, Farrar, Strauss and Giroux, USA. https://melaniemitchell.me/aibook/
9. Oliveira, A.L. Biotechnology, Big Data and Artificial Intelligence. *Biotech J*, **2019**, 1800613, 1-6. https://doi.org/10.1002/biot.201800613
10. Cook, C.E., Bergan, M.T., Cochrane, G. *et al*. The European Bioinformatics Institute in 2017: data coordination and integration, *Nucleic Acids Research*, **2018**, 46, D21–D29. https://doi.org/10.1093/nar/gkx1154
11. Holzinger, A., Keiblinger, K., Holub, P. *et al.* AI for life: Trends in artificial intelligence for biotechnology. *New Biotechnol*, **2023**, 74, 16-24. https://doi.org/10.1016/j.nbt.2023.02.001
12. Xu, D., Liu, B., Wang, J & *et al*. Bibliometric analysis of artificial intelligence for biotechnology and applied microbiology: Exploring research hotspots and frontiers. *Front Bioeng Biotechnol*, **2022**, 10.3389. https://doi.org/10.3389/fbioe.2022.998298

13. Alipanahi, B., Delong, A., Weirauch, M. *et al*. Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. *Nature Biotechnol*, **2015**, 33, 831–838. https://doi.org/10.1038/nbt.3300
14. NIH. AI, Machine Learning and Genomics. National Human Genome Res Inst, *National Institute of Health*, USA, **2024**. https://www.genome.gov/about-genomics/educational-resources/fact-sheets/artificial-intelligence-machine-learning-and-genomics
15. Cristiano, S., Leal, A., Phallen, J. *et al*. Genome-wide cell-free DNA fragmentation in patients with cancer. *Nature*, **2019**, 570, 385. https://doi.org/10.1038/s41586-019-1272-6
16. Wu, S., Wang, Y., Hong, G. *et al*. An AI model for detecting pathological lymph node metastasis in prostate cancer using whole slide images. *Clinical Med Lancet*, **2024**, 71, 102580. https://doi.org/10.1016/j.eclinm.2024.102580
17. Nield, D. Breakthrough AI can now predict Alzheimer's up to 7 years in advance. *Science Alert Health*, **2024**, 3, 14. https://www.sciencealert.com/breakthrough-ai-can-now-predict-alzheimers-up-to-7-years-in-advance
18. Savage, N. AI's keen diagnostic eye. *Nature Outlook*, **2024**, 4, 18. https://www.nature.com/articles/d41586-024-01132-2
19. Chudzik, A., Sledzianowski, A. & Przybyszweski, A.W. Machine Learning and Digital Biomarkers Can Detect Early Stages of Neurodegenerative Diseases. *Sensors*, **2024**, 24:1572. https://doi.org/10.3390/s24051572
20. Abramson, J., Adler, J., Dunger, J. *et al*. Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*, **2024**, 10.1038. https://www.nature.com/articles/s41586-024-07487-w
21. Camps, J.M. La IA de Google que vol revolucionar la indústria farmacèutica: com funciona. *3Cat*, **2024**, 5, 9. https://www.ccma.cat/324/la-ia-de-google-que-vol-revolucionar-la-industria-farmaceutica-com-funciona/noticia/3291709/
22. The Nobel Prize in Chemistry 2024. Nobel Prize Outreach AB. *NobelPrize.org*, **2024**, 10, 9. https://www.nobelprize.org/prizes/chemistry/2024/summary
23. Google Deep Mind. Computational predictions of protein structures associated with COVID-19. *Deep Mind, Google*, **2020**, 8, 4. https://deepmind.google/discover/blog/computational-predictions-of-protein-structures-associated-with-covid-19/
24. Jiménez-Luna, J., Grisoni, F., Weskamp, N. *et al*. Artificial intelligence in drug discovery: recent advances and future perspectives. *Expert Opinion on Drug Discovery*, **2021**, 16(9), 949–959. https://doi.org/10.1080/17460441.2021.1909567

25. Noto, M. Machine learning uncovers new ways to kill bacteria with non-antibiotic drugs. *Science Alert*, **2024**, Health, 4, 17. https://www.sciencealert.com/machine-learning-uncovers-new-ways-to-kill-bacteria-with-non-antibiotic-drugs
26. Chebrolu, N., Lottes, P., Schaeffer, A. *et al*. Agricultural robot dataset for plant classification, localization, and mapping on sugar beet fields. *Int J Robot Res*, **2017**, 36, 1045–1052. https://doi.org/10.1177/0278364917720510
27. Kamilaris, A. & Prenafeta-Boldú, F.X. A review of the use of convolutional neural networks in agriculture. *J Agric Sci* **2018**, 156, 312-322. https://www.cambridge.org/core/journals/journal-of-agricultural-science/article/review-of-the-use-of-convolutional-neural-networks-in-agriculture/15B08C5CDD85F21EEEFAFE7387536149
28. Liu, W., Yuan, J.S. & Stewart, C.N. Advanced genetic tools for plant biotechnology. *Nat Rev Genet*, **2013**, 14, 781–793. https://doi.org/10.1038/nrg3583
29. Altman, A. & Hasegawa, P.M., eds. Plant Biotechnology and Agriculture; Prospects for the 21st century. *Academic Press*, **2012**.
30. Romanos, B. Agricultura molecular en plantas: ¿proteína animal en vegetales? *TechFood Magazine*, **2023**, 10, 16. https://www.techfoodmag.com/agricultura-molecular-en-plantas-producir-proteina-animal-en-plantas/
31. Watson, E. Casein ... from potatoes ? Molecular farming startup Finally Foods emerges from stealth. *AgFunderNews*, **2024**, 4, 2. https://agfundernews.com/casein-from-potatoes-molecular-farming-startup-finally-foods-emerges-from-stealth
32. Gavilán, M. & Muniesa, J. Plantas de patatas productoras de caseína gracias a la agricultura celular. *Gastronomía y Cia*, **2024**, 4, 3. https://www.gastronomiaycia.com/2024/04/03/plantas-de-patatas-productoras-de-caseina-gracias-a-la-agricultura-celular/
33. Karimi, H., Mohammadi, F., Rajabi, S. *et al*. Biological 2,4,6-trinitrotoluene removal by extended aeration activated sludge: optimization using artificial neural network. *Sci Reports*, **2023**, 13, 9053. https://doi.org/10.1038/s41598-023-34657-z
34. Zhang, F., Wen, Y. & Guo, X. CRISPR/Cas9 for genome editing: progress, implications and challenges. *Hum Mol Genet*, **2014**, 23, R40–R46. https://doi.org/10.1093/hmg/ddu125
35. Ruffolo, J.A., Nayfach, S., Gallagher, J. *et al*. Design of highly functional genome editors by modeling the universe of CRISPR-Cas sequences. *bioRxiv*, **2024**, 4, 22, Cold Spring Harbor Lab. https://doi.org/10.1101/2024.04.22.590591

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