variability of IDC site. Based on this, we performed pharmacophore screening of joint library of control AI grope from PDB and FtsZ effectors of deposed in ChEMBL. Pharmacophore screening was performed with PharmIT (https://pharmit.csb.pitt.edu/) and ensemble of individual pharmacophores, constructed individually, based on above-mentioned complexes from RCSB Protein Data Bank.

In general, pharmacophore screening reviled 89 hits. Subsequent docking of these compounds with CCDC GOLD program reviled that 87 of 98 compounds agreed with threshold values of GOLD fitness functions (ChemPLP and ASP) specified for reference grope of ligands. Most of selected compounds were benzamides: 2,6-diflurobenzamides (73 compounds), oxazole-benzamides (2 compounds), 1,3-benzothiazole-5-carboxylates (3 compounds) and alkylbenzamides (2 compounds). However, compounds of new gropes: benzene-1,3-diol derivatives (1 compound), chloropurine amine derivatives (1 compound), carbamoyl-difluorophenoxy acetates (2 compounds), 2,6-difluorobenzenesulfonamides (1 compound), and curcuminoids (2 compounds) were also found.

Modern approaches to the production of recombinant human insulin: analysis and perspectives of expression systems in the pharmaceutical industry

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Recombinant human insulin plays a crucial role in the modern world, providing an essential therapeutic agent for millions of people with diabetes. The choice of the optimal expression system influences product yield, purity and biological activity. Given the complexity of the insulin structure and the high-quality standards for pharmaceuticals, effective expression systems are a key factor in ensuring a stable and high-quality production platform for recombinant human insulin.

The use of bacterial expression systems, particularly *Escherichia coli* strains, for the production of recombinant insulin is based on their high replication rate and ability to rapidly amplify expressed genes. The expression of genetically modified plasmids containing the insulin gene ensures high productivity. This approach also involves optimizing regulatory elements such as promoters and operators to increase expression efficiency. It should be noted that this method has its challenges, such as plasmid loss and a high probability of translation errors, which can cause adverse immune reactions in humans.

Yeast expression systems, including *Saccharomyces cerevisiae* and *Pichia pastoris*, have become an important alternative for recombinant insulin production. Yeasts have the advantage of being able to express and modify the glycosylation of insulin, which determines its biological activity and stability. In addition, yeasts are known for their ability to perform post-translational modifications, such as proper protein folding and disulfide bond formation, which are critical for insulin function. Regulated genetic constructs and optimized cultivation conditions allow high yields of recombinant insulin in yeast systems. However, the high mannose structure and heterogeneity of glycosylation can lead to batch-to-batch variability.

The use of transgenic plants for recombinant insulin production is a promising direction in biotechnology. Plant systems such as *Arabidopsis thaliana* or *Nicotiana benthamiana* can be genetically modified to express insulin. The advantages of using transgenic plants include low production costs, easy purification of the plant body, absence of human pathogens, scalability of cultivation, and the potential for post-translational modifications similar to those found in mammalian organisms. However, it is important to address issues of product stability and purity and to ensure that introduced genes do not affect plant traits. This approach to recombinant insulin production could be crucial in providing access to therapeutic agents in regions with limited technical or economic resources.

The use of stem cells (embryonic, induced pluripotent, bone marrow mesenchymal, adipose-derived, human placental and umbilical cord stem cells) as an expression system is an area of active research in biotechnology. Embryonic and

induced pluripotent stem cells, with their unique capacity for self-renewal and differentiation, offer the potential to generate stable and productive lines expressing insulin. Genetic modification of stem cells aims to achieve optimal insulin gene expression and controlled production regulation. The use of such cells opens up the possibility of post-translational modifications similar to those that occur in natural cells, which can influence the functionality and structure of recombinant insulin and reduce the likelihood of immune rejection. Despite the potential benefits, the use of stem cells in recombinant insulin production faces challenges such as ethical issues, cell line stability and process optimisation. Nevertheless, this approach is attracting the attention of scientists as a promising direction for expanding the possibilities of producing recombinant biological medicines.

Expression systems for insulin production have become diverse and innovative. However, each system has its challenges and limitations, such as ethical issues, production sustainability and the need for process optimization. Overall, the combination of scientific research and technological development is contributing to the further improvement of expression systems for insulin production and defining progress in the production of this important drug.

Cooperative synergies between members of the plant microbiota

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Since the ancestral plant lineages inhabited the land 450 million years ago, plants and their associated microbes have interacted with each other to form a collection of species often referred to as the holobiont. Microbial synergies are presented on an evolutionary scale, showing that interactions between plants and microbes are relatively recent compared to older interactions between bacteria or between different microbial kingdoms. It is generally recognized that the formation