

The diagram illustrates the process of translation. An mRNA strand is shown with the following sequence: **mRNA AUG (Start) AAC GUV CUC UUC AAG AAG FLAG UAA (Stop)**. Ribosomes are shown translating the mRNA. The first ribosome is at the **AAC** codon, and the second ribosome is at the **FLAG** codon. The third ribosome is at the **UAA** codon, which is the stop codon. The amino acids being added to the growing polypeptide chain are **Met**, **Lys**, and **Asp**. The completed polypeptide chain is shown below the ribosomes, with the sequence **Met-His-Lys-Asp**.

In this issue, Ohta et al. report the ribosomal polymerization of α -hydroxy acids by means of genetic code reprogramming. The flexizyme system, a ribozyme-based tRNA acylation tool, was used to reassign individual codons to seven types of α -hydroxy acids. Next, polyesters were synthesized under controls of the reprogrammed genetic code using a reconstituted cell-free translation system. The sequence and length of the polyester segments were specified by the mRNA template, indicating that high fidelity ribosome expression of polyesters was possible. This work represents an exciting, not previously described example of mRNA-directed synthesis of polyesters consisting of several different α -hydroxy acids (Figure credits: Ohta et al.).

The image displays the chemical structure of a complex steroid derivative, likely a triterpene. The molecule features a multi-ring steroid nucleus with various functional groups, including hydroxyl groups (OH), a carboxylic acid group (HOOC), and a ketone group (C=O). The structure is highly branched and includes several methyl groups (CH₃) and a long side chain with multiple hydroxyl groups. The background of the slide shows a close-up of several red, gilled mushrooms, suggesting a natural source for the compound.

Inhibition of Monoacylglycerol Lipase in Intact Brain Neurons

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The *N*-aryl carbamate URB602 is an inhibitor of monoacylglycerol lipase (MGL), a serine hydrolase involved in the biological deactivation of the endocannabinoid 2-arachidonoylglycerol (2-AG). Using purified recombinant MGL and intact brain neurons, King and colleagues demonstrate the selective inhibitory effects of URB602 on MGL activity. The authors further show that this inhibition occurs through a partially reversible, noncompetitive mechanism using an approach that combines kinetic, dialysis, and structure-activity relationship (SAR) analyses. Thus, URB602 remains a useful tool to investigate the roles of 2-AG and validate MGL as a pharmacological target.

From Targeting Gravitropism to Understanding ABC Transporters



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P-glycoproteins (PGPs) are ATP-binding cassette (ABC) transporters that translocate a myriad of molecules across biological membranes. In plants, a few PGP proteins together with PIN proteins transport the plant hormone auxin and participate in the physiological changes required for the response to gravitropic stimuli. Using a genetic and biochemical approach, Rojas-Pierce et al. identified PGP19 as a target of the gravitropic inhibitor Gravacin in *Arabidopsis thaliana*. The authors analyzed the effect of Gravacin on the transport activity of PGP19 and PGP19-PIN complexes, as well as the physical interaction between Gravacin and PGP19-containing microsomal membranes. Better understanding of the Gravacin/PGP19 system might lead to a better understanding of ABC transporters, in general. (Photo credits: Rojas-Pierce et al.)

New Way to Build a Double Hot-Dog

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Eukaryotic fatty acid megasynthases utilize a dehydratase to catalyze one of the β -carbon processing reactions that follow each chain extension step. Expression, mutagenesis and structural modeling studies by Pasta et al. suggest that the dehydratase of the animal megasynthase has evolved from a freestanding, prokaryotic, homodimeric counter-

part that exhibits a typical double hot-dog fold, with two active-sites located at the subunit interface. However, in this megasynthase, the double hot-dog is formed by two "pseudosubunits" derived from contiguous regions of the same polypeptide, and only one active site is retained. This architecture differs from that of fungal megasynthase dehydratases, even though the enzymes utilize similar catalytic mechanisms.

Emetine Regulates *Bcl-x* Splicing

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Emetine, the ipecac alkaloid, has been used for treatment of different human disease for centuries. More recently, it was established that emetine acts as a eukaryotic protein synthesis inhibitor. Moreover, emetine has been evaluated as a potential chemotherapeutic agent. However, molecular details of emetine mechanism of action are still lacking. Boon-Unge et al. present evidence that emetine regulates alternative splicing of exon 2 in the *Bcl-x* gene, leading to a decrease in the amount of anti-apoptotic Bcl-xL and an increase of proapoptotic Bcl-xS protein levels. Interestingly, authors show that emetine exerts the effects on *Bcl-x* splicing in a phosphorylation-dependent manner, with protein phosphatase-1 mediating these effects. Specific control of the alternative splicing of *Bcl-x* gene is an emerging target for anti-cancer treatment, and emetine is a new piece that starts to complete the puzzle.

