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ProxiMAX and MAX randomization: Precision protein engineering

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ProxiMAX and MAX randomization technologies are defined saturation mutagenesis processes that deliver precision control of both identity and relative ratio of amino acids at specified locations within a protein library. Both processes are non-degenerate, meaning that encoding DNA libraries are as small as is physically possible. ProxiMAX is the technology that lies behind Isogenica's Colibra™ offering and is ideal for saturating contiguous codons, as required in antibody libraries. In contrast, 'MAX' randomization targets codons at disparate locations within a gene and is therefore more applicable to other scaffolds or proteins. Since no constraints are imposed by the genetic code, both technologies can eliminate unwanted amino acids such as cysteine and methionine from libraries or encode desired subsets of amino acids with ease. Yet their underlying processes are quite different. This presentation will examine the development of both ProxiMAX and MAX randomization process and give examples of libraries created to date.

Biography

Anna V Hine has studied at the University of Manchester (UK) and Harvard Medical School. She is a Reader and Associate Dean Enterprise at Aston University (UK). In March 2013, she was named BBSRC Commercial Innovator of the Year 2013, for her work in transferring 'ProxiMAX randomisation' into SME Isogenica Ltd. She is a Molecular Biologist by training.

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