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ProxiMAX randomization: Precision antibody engineering

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ProxiMAX' randomization is the technology that lies behind Isogenica's Colibra™ offering. It is a defined saturation mutagenesis process that delivers precision control of both identity and relative ratio of amino acids at specified locations within a protein/antibody library. Thus unwanted amino acids such as cysteine and methionine can be eliminated from libraries because no constraints are imposed by the genetic code. Moreover, the process is non-degenerate, which means that encoding DNA libraries are as small as is physically possible. ProxiMAX relies on a process of saturation cycling comprising ligation, amplification and digestion for each cycle and is the science behind the commercial "Colibra™" technology. With achieved diversities of >99% (6 and 11 saturated codons) and the potential to generate libraries of up to 1014 components, we contest that ProxiMAX randomization is a vital tool in engineering antibody libraries of the highest quality. This presentation will examine the development of the ProxiMAX process and give examples of antibody 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. A Molecular Biologist by training, she relishes interdisciplinary work.

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