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P013 ParaMAX: non-degenerative saturation mutagenesis applied to an alpha helical repeat protein

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Alpha helical repeat proteins possess alpha solenoid motifs, which comprise repeating alpha helical modules arrayed in a highly structured and uniformed manner. They, thus create a desirable interface for high affinity and specific protein/ligand interactions due to the modularity's predictability and reproducibility in target binding. Engineering of such repeatproteins is most efficient using a high-throughput, library-based approach. Saturation mutagenesis allows synthesis of massively diverse gene libraries via codon randomisation. The resulting libraries are then expressed and screened via either cloning (e.g.phage display) or purely *in vitro* display technologies. Saturation mutagenesis is itself most efficient when minimising use of the genetic code and we have previously presented non-degenerate methodologies to saturate either contiguous or non-contiguous (ProxiMAX and MAX randomisations respectively). However, ProxiMAX, which is predominantly used to engineer antibodies, is best-suited to an automated format, whilst MAX randomisation is primarily for engineering active sites. Alpha helical repeat proteins require a combination of both contiguous and non-contiguous codons to be saturated. We therefore present ParaMAX randomisation, an extension of MAX randomisation, but with the added benefit of being able to saturate contiguous codons. ParaMAX randomisation is currently in the experimental stages of saturating up to 8 contiguous codons. Results to date and accompanying quality control data will be presented.