REFERENCIAS

Abremski, K; Hoess, R (1984) Bacteriophage P1: site-specific recombination, purification and properties of Cre recombinase protein. Journal of Biological Chemistry. Vol 259, pp. 1509-1514

Arnold, F; Wintrodes, P; Miyazaki, K; Gershenson, A (2001) How enzymes adapt: lessons from directed evolution. Trends in Biochemical Sciences Vol. 26, pp. 100-106

Bloom, J; Labthavikul, S; Otey, C; Arnold, F (2006) Protein stability promotes evolvability. PNAS Vol. 103, pp. 5869-5874

Chen, R (2001) Enzyme engineering: rational redesign versus directed evolution. Trends in biotechnology Vol. 19, pp. 13

Delby, P (2003) Optimizing enzyme function by directed evolution. Current Opinion in Chemical Biology Vol. 13, pp. 500-505

Gerlt, J; Raustel, F (2003) Evolution of function in (b/a)8- barrel enzymes. Current Opinion in Chemical Biology Vol. 7, pp. 252-264

Gerlt, J; Babbit, P (2001) Barrels in pieces. Nature Structural Biology. Vol. 8, pp. 5-7

Glick B, Pasternak J (2003) Biotechnolgy, Principles and Applications of Recombinant DNA, Ed. ASM Press, Washington

Gopaul, D; Guo, F; Van Duyne, G (1998) Structure of the Holliday junction intermediate in Cre-loxP site-specific recombination. Oxford University Press. Vol 17, pp.. 4175-4187

Henn-Sat, M; Thoma, R; Schmidt, S; Henning, M; Kirscher, K; Sterner, R (2002) Two (ba)8- barrel enzymes of histidine and tryptophan biosynthesis have similar reaction mechanisms and common strategies. Biochemistry Vol 41, pp. 12032-12042

Höcker, B (2005) Directed evolution of (ba)8- barrel enzymes. Science

Höcker, B; Deismann-Drieneger, S; Hettwer, S; Lustig, A; Sterner, R (2001) Dissection of a (ba)8- barrel enzyme into two folded halves. Nature structural biology Vol. 8, pp. 32-36

Höcker, B; Jürgens, C; Wilmanns, M; Sterner, R (2001) Stability, catalytic versatility and evolution of the (ba)8- barrel fold. Current Opinion in Biotechnology Vol. 12, pp. 376-381

Höcker, B; Schmidt, S; Sterner, R (2001) A common evolutionary origin of two elementary enzyme folds. FEBS Letters Vol 510, pp. 133-135

http://www.basic.northwestern.edu/biotools/oligocalc.html

Jürgens, C; Strom, A; Wegener, D; Hettwer, S; Wilmanns, M; Sterner, R (2000) Directed evolution of a (ba)8- barrel enzyme to catalyse related reactions in two different metabolic pathways. PNAS Vol. 97, pp. 9925-9930

Kay, B; Winter, J; McCaffertg, J (1996) Phage display of peptides and proteins. A laboratory manual. Ed. Academic Press.

Kazlauskas, R (2005) Enzymes in focus. Nature Vol. 436, pp. 1096-1097

Kuchner O, Arnold F (1997) Directed evolution of enzyme catalysts, Tib Tech Reviews, Vol. 15, p.p. 523 – 530.

Kuper, J; Doenges, C; Wilmanns, M (2005) Two-fold repeated (ba)4 half-barrels may provide a molecular tool for dual substrate specificity. EMBO reports Vol. 6, pp. 134-139

Lang, D; Thoma, R; Henn-Sax, M; Sterner, R; Wilmanns, M (2000) Structural evidence for evolution of the b/a barrel scaffold by gene duplication and fusion. Science Vol. 289, pp. 1546-1549

Lockless, S; Ranganathan, R (1999) Evolutionary conserved pathways of energetic connectivity in protein families. Science Vol. 286, p. 299

Miozzari, G; Niederberger, P(XXX) Tryptophan biosynthesis in *Saccharomyces cereviciae*: control of the flux through the pathway. XXX Vol 134, pp. 48-59

Moore, J; Jin, HM; Kuchner, O; Arnold, FH (1997) Strategies for the in vitro evolution of protein function: enzyme evolution by random recombination of improved sequences. Journal of Molecular Biology Vol. 272, p. 336

Nelson D, Cox M (2000) Lenhinger, Principles of Biochemistry, Ed. Worth Publishers, NY

Ostermeier, M; Hoon Shin, J; Benkovic, S (1999). A combinatorial approach to hybrid enzymes independent of DNA homology. Nature Biotechnology Vol 17, pp. 1209

Park H, Nam S, Lee C, Yoon C, Mannervik B, Benkovic S, Kim H (2006) Design and evolution of new catalytic activity with an existing protein scaffold, Science Vol. 311 p.p. 535 – 538

Patrick, W; Blackburn, J (2005) In vitro selection and characterization of a stable-subdomain of phosphoribosylanthranilate isomerase. FEBS Journal Vol 272, pp. 3684-3697

Sblattero, D; Bradbury, A (2000) Exploiting recombination in single bacteria to make large phage antibody libraries. Nature Biotechnology. Vol. 18, pp. 75-80

Sblattero, D; Lou, J; Mazari, R; Bradbury, A (2001). In vivo recombination as a tool to generate molecular diversity in phage antibody libraries. Review in molecular biotechnology Vol 74, pp. 303-315

Shukla, A; Guptsarama, P (2004) Folding of b/a- unit scrambled form of *S. cerevisiae* triosephosphat isomerase: evidence for autonomy of substructure formation and plasticity of hydrophobic and hydrogen bond interactions in core of (b/a)8 barrel. Proteins: structure, function and bioinformatics. Vol 55, pp. 548-557

Siegel, R; Velappan, N; Pavlik, P; Chasteen, L; Bradbury, A (2005) Recombinatorial cloning using heterologous lox sites. Vol. 14, pp. 1119-1129

Theobald, D; Wutthe, D (2005) Divergent evolution within protein superfolds inferred from profile-based phylogenetics. Journal of Molecular Biology Vol. 354, pp. 722-737

Vega, MC; Lorentzen, E; Linden, A; Wilmanns, M (2003). Evolutionary markers in the (b/a)8- barrel fold. Current opinion in chemical biology. Vol 7, pp. 694-707

Wierenga, RK (2001). The TIM-barrel fold: a versatile framework for efficient enzymes. FEBS Letters. Vol 492, pp. 193-198