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Isolation and sequence analysis of the gene for arginine kinase from the chelicerate arthropod, *Limulus polyphemus*: insights into catalytically important residues

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Abstract

The gene for arginine kinase (AK; EC 2.7.3.3) from the horseshoe crab, *Limulus polyphemus*, was cloned and the complete cDNA sequence was determined. An open reading frame with 1071 nucleotides was detected that encodes a 357 amino-acid protein with a calculated M(r) of 40,238. The coding transcript is flanked by 13 and 512 nucleotides of 5' and 3' untranslated regions, respectively. The deduced amino-acid sequence of *Limulus* AK displays extensive similarity to other arginine kinases, vertebrate and invertebrate creatine kinases (CK) and a glycoamine kinase (GK). Consensus AK and consensus CK sequences, as well as a GK sequence, were compared to CK peptide regions containing residues presumed to be important in catalysis and/or located in close proximity to the active site. Our comparisons revealed some inconsistencies with hypothesized roles of particular residues in catalytic function.

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