

**COMPARATIVE STUDIES OF SUGAR AND PROTEIN KINASES:  
GENETIC RELATIONSHIPS AND CONSENSUS SEQUENCES**ANNA ZDYB<sup>1</sup> and JACEK LELUK<sup>2</sup>

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Sequences of forty five sugar and protein kinases homologous to human hexokinase (NP\_277042) were aligned. Multiple alignment was carried out and verified with the use of a genetic semihomology algorithm [1-3].

A high degree of conservativity for structurally and functionally important locations, including the catalytic site, was observed. The genetically justified multiple alignment procedure led to a consensus sequence which accounts for all typical features for this protein family at the primary level. Over 20% of all positions revealed an extremely high degree of identity, i.e. in 90% sequences or more they were occupied by the same amino acid residues.

Based on the most optimal alignment, diagrams of genetic relationships were constructed.

The diagrams of genetic relationships show the most possible mechanism of evolutionary differentiation, the mutational processes involved and the variability extensions at non-conservative positions with the aid of synonymous six-codon amino acids. Very often positions of high variability contain six-codon amino acids. The frequency of amino acid occurrence is not convergent with the number of synonymous codons for them. This suggests an important role of cryptic mutations in the evolutionary differentiation mechanism.

**REFERENCES**

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