Poster Presentation

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X-ray diffraction analysis of homodimeric yeast hexokinases

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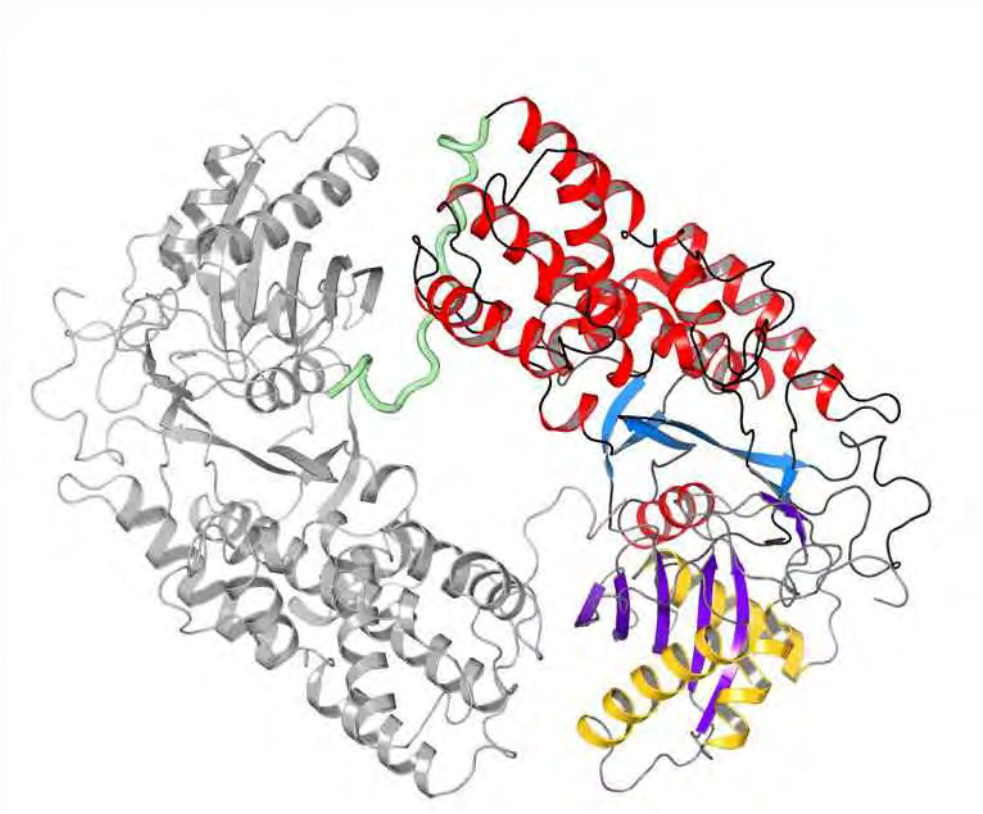
Yeast hexokinases are described in textbooks as classical open/close-switch monomeric enzymes. The hexokinase isoenzymes ScHxk1 and ScHxk2 of the budding yeast Saccharomyces cerevisiae share 77 % sequence identity. They exist in either an open or closed conformation, however, the published states were not of the same isoform. Crystal structures of the hexokinase KlHxk1 of the milk yeast Kluyvermyces lactis demonstrated open/close states of the same yeast hexokinase isoenzyme for the first time. KlHxk1 has 70 or 73 % sequence identity with ScHxk1 or 2, respectively. ScHxk2 and KlHxk1 contain an N-terminal binding stretch for the transcriptional repressor Mig1 which is the structural link to their function in glucose repression. They also exhibit monomer-dimer equilibria depending on protein concentration and phosphorylation of an N-terminal serine residue (S15). Experimental evidence for an expected ring-shaped homodimer of ScHxk2 was still missing to explain the phosphorylation-dependent oligomerization as demonstrated for KlHxk1 (figure). Structural data of other yeast glucose kinases were also limited in order to support a similar phenomenon. Therefore, we comparatively explored the oligomeric structure of ScHxk2 and K. lactis glucokinase 1 (KlGlk1) by means of X-ray diffraction in solution and in the crystalline state. The crystal structure of ScHxk2 was solved at high resolution (<1.5Å), and small-angle X-ray data of ScHxk2 were collected. Data analysis indicated that all three glucose-phosphorylating enzymes share a similar oligomeric architecture.



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