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Compiling and utilising a Rubisco mutagenic database - Research training/internship

We are looking for a student with an interest in carbon fixation and protein sequence-structure-function for a project to create a database of Rubisco mutagenic data from the literature, and relate it to results obtained in our laboratory from computational modeling.

Nature's carbon-fixing enzyme Ribulose-1,5-bisphosphate (Rubisco) exhibits a slow catalytic turnover rate and poor affinity for substrate CO_2 that its catalysis often limits the growth rate of photosynthetic organisms. Rubisco exhibits substantial natural diversity, with Rubiscos from certain species having higher substrate specificities. However, the reason for this diversity is largely unknown, and thus we cannot exploit this information in engineering strategies to enhance Rubisco kinetic performance.

Using molecular dynamics (MD) simulations, we have identified "pockets" in Rubisco that may selectively accumulate CO_2. The characteristics of the amino acid residues that define the CO_2 pockets are generally highly conserved between all organisms. We would like to know what data exists about the influence of these identified residues on Rubisco's kinetic performance.

In this project you will (i) perform extensive literature searches to find and document Rubisco mutations and their effect on enzyme solubility and kinetic performance, (ii) perform sequence-structure alignments to "normalise" residue numbering between Rubiscos from different species, and (iii) compare your new Rubisco mutagenic database with our recently obtained MD data.

If you find this project of interest, please contact: Laura Gunn, laura.gunn@icm.uu.se Department of Cell and Molecular Biology, Laboratory of Molecular Biophysics, Uppsala University
Group website: https://www.icm.uu.se/molecular-biophysics