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The structural basis of orotidine-5'-phosphate decarboxylase catalysis: Ground-state destabilisation by electrostatic repulsion is not a driving force

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I will present crystallographic snapshots of the human enzyme orotidine-5-monophosphate decarboxylase in complex with the genuine substrate, substrate analogs, transition state analogs and product - all at true atomic resolution. These snapshots of catalysis defy the proposed mechanism of ground-state destabilization by revealing that the substrate carboxylate is protonated and forms a favorable low-barrier hydrogen bond with a negatively charged amino acid.

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