Electronic Supplementary Material (ESI) for RSC Advances.

Assessment of interacting mechanism between *Candida rugosa* lipases and hydroxyapatite and identification of hydroxyapatite-binding sequence through proteomics and molecular modelling

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Supporting information

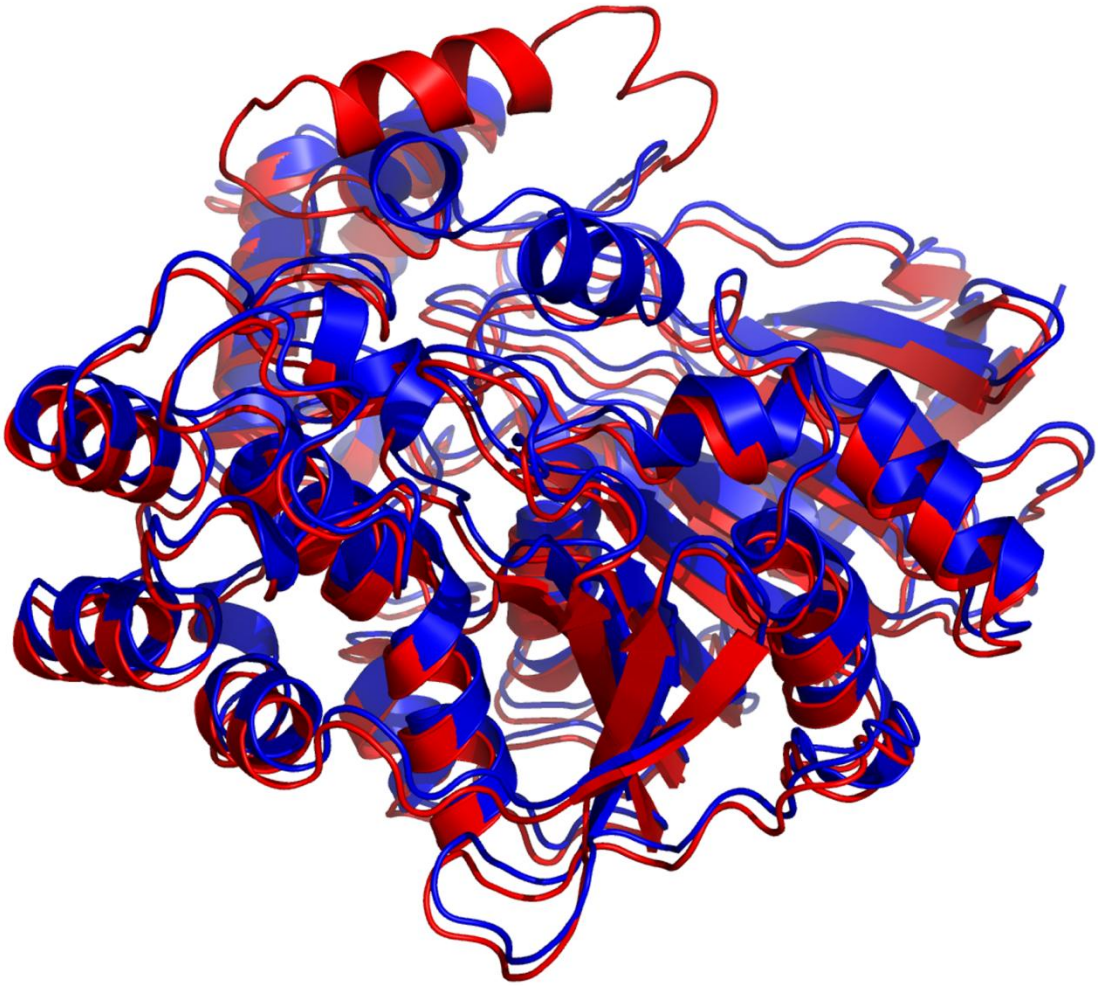

Fig S1. Superimposed structures of Candida rugosa lipase, isoform I, in ‘open’ (PDB entry 1CRL, red) and in ‘closed’ conformation (PDB entry 1THR, blue).

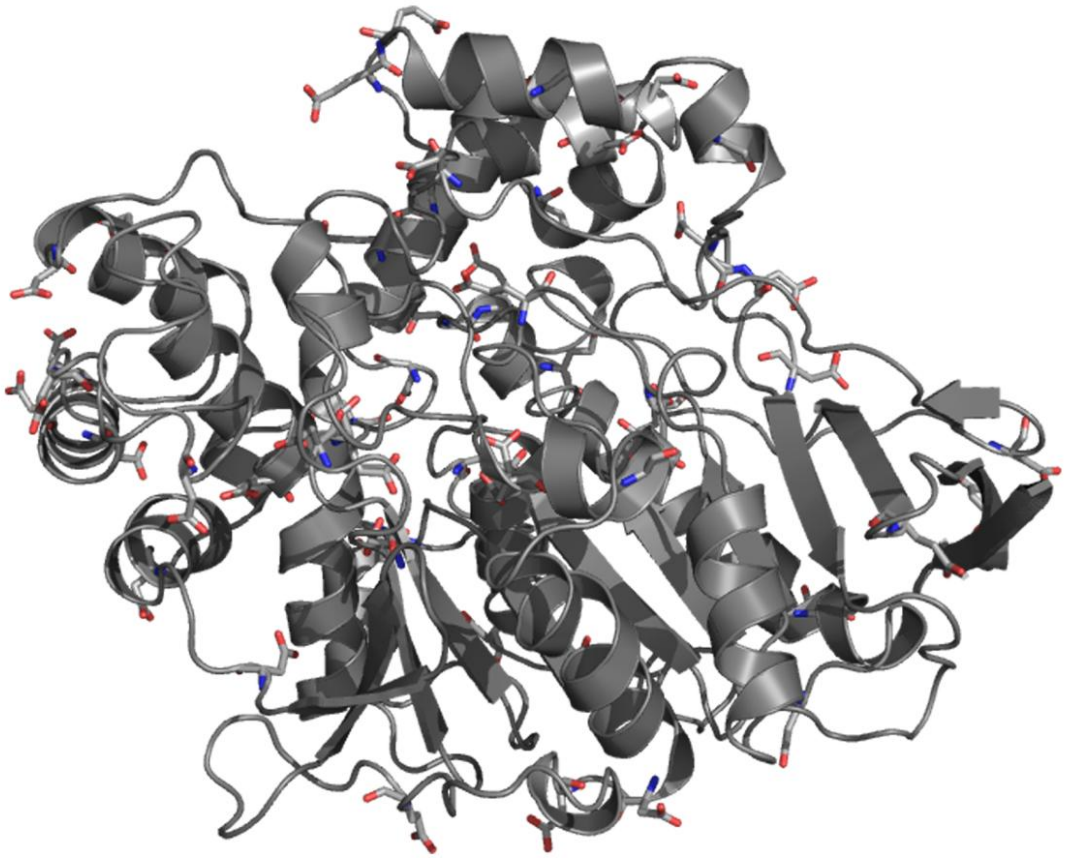

Figure S2. Asp and Glu residues, depicted as stick representation, in structure of Candida rugosa lipase, isoform I, in 'open' conformation (PDB entry 1CRL)

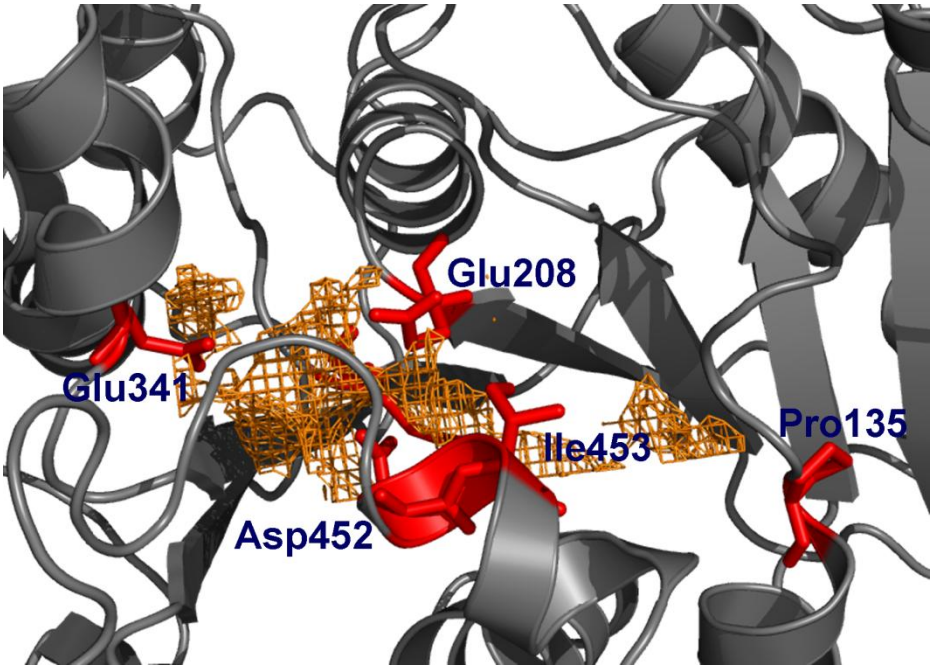

Figure S3. Molecular interaction field of Ca2+ probe (orange, mesh representation) on isocontour level of -75 kcal/mol in the cleft of 1CRL, near the active site. Representative residues proximal to MIF are shown in stick presentation.