Supplementary Data 1

Input sequences for AlphaFold analysis

Label

Bold: Gpx active site

Yellow highlight: Gpx catalytic triad

Green highlight: Gpx protein sequences used in MD simulation

Blue highlight: CK2β protein sequences used in MD simulation

Gpx (197 aa)

>EEA19957.1 glutathione peroxidase Hyr1, putative [*Talaromyces marneffei* ATCC 18224]

MASATTFYDFSPPDKKGNPYPLTDYK**GKVVLVVNTASKCGFT**PQFAGLEKLYKSIEAKH
PGAFTILGFPCNQFGNQDPGSNDEIQSFCQVNYGVTFPVLGKIDVNGSKAEPLFEWIKSE
KPGLLGVKRVLWNFEKALINGKGEVVGRWRSITKPESLEATILKEIDIASKDVKGVEVVP
TATETAASAAPAEEAKEA

CK2β (215 aa)
>NP_001311.3 casein kinase II subunit beta isoform 1 [Homo sapiens]

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEPD
EELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQP
MLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYRP
KRPANQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTIR