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online data

SUPPLEMENTARY ONLINE DATA

Mitogen-activated protein kinase-mediated phosphorylation of peroxiredoxin 6 regulates its phospholipase A_2 activity

Yongzheng WU*, Sheldon I. FEINSTEIN*, Yefim MANEVICH*, Ibrul CHOWDHURY*, Jhang Ho PAK*[1], Altaf KAZI*, Chandra DODIA*, David W. SPEICHER† and Aron B. FISHER*[2]

*Institute for Environmental Medicine, University of Pennsylvania School of Medicine, Philadelphia, PA 19104-6068, U.S.A., and †Wistar Institute, 36th and Spruce Streets, Philadelphia, PA 19104, U.S.A.

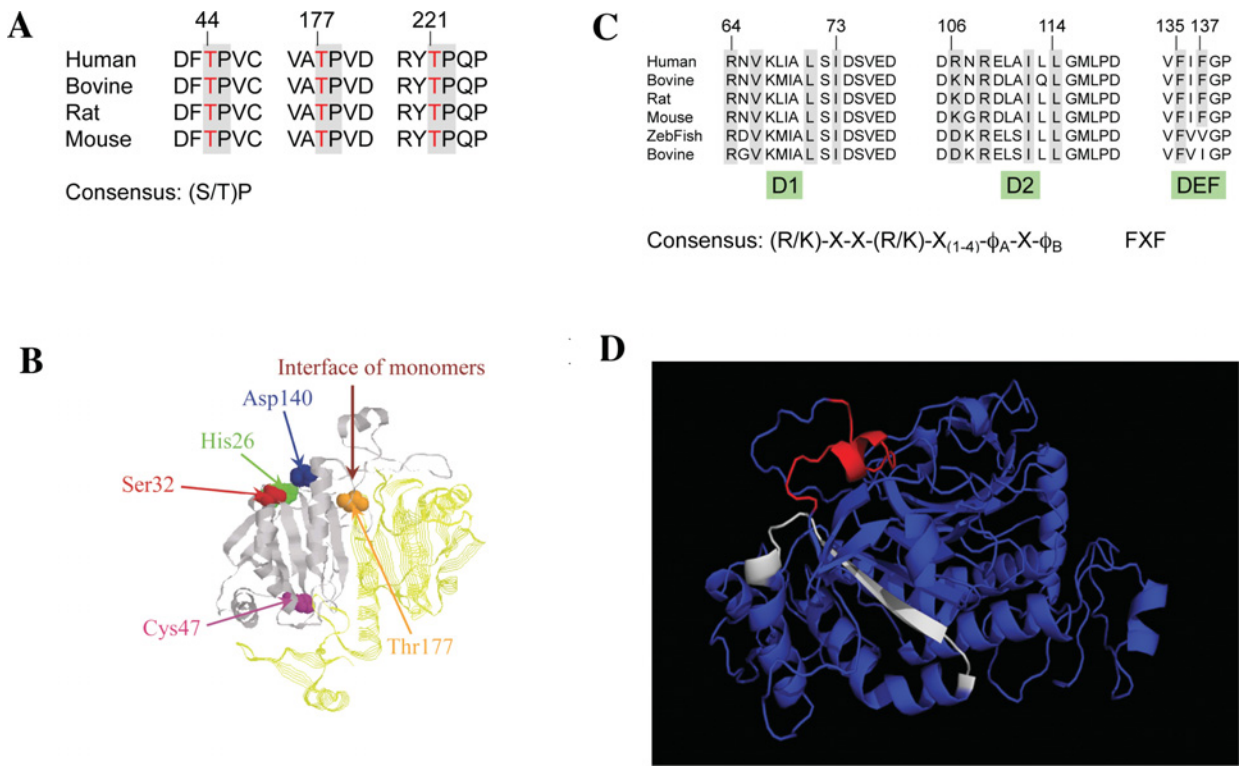

Figure S1 Structural features of Prdx6

(**A**) Prediction of MAPK phosphorylation sites. Conserved MAPK phosphoacceptor sites in the Prdx6 peptide sequence are shaded in grey. Thr (T) residues at position 44, 177 and 220 that are possible phosphorylation sites are shown in red. (**B**) The location of the phosphorylation site in Prdx6. The crystal structure of oxidized Prdx6 is shown as a homodimer [41]. The PLA_2 catalytic triad (Ser-32, His-26 and Asp-140) of Prdx6 [24] and the proposed phosphorylation site (Thr-177) are indicated. (**C**) Predicted sites for MAPK docking to Prdx6. Prdx6 homologues contain D- and DEF-domains for interaction with MAPKs. X is any amino acid and Φ is a hydrophobic amino acid such as leucine/isoleucine. (**D**) Surface accessibility of MAPK docking sites, indicating localization of the D-domain peptides on the Prdx6 structure. D1-domain is in grey (partially accessible) and D2-domain is in red (fully accessible) against the rest of the Prdx6 molecule in blue.

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[1] Present address: University Ulsan College of Medicine, Seoul 138-736, Korea.
[2] To whom any correspondence should be addressed (email abf@mail.med.upenn.edu).