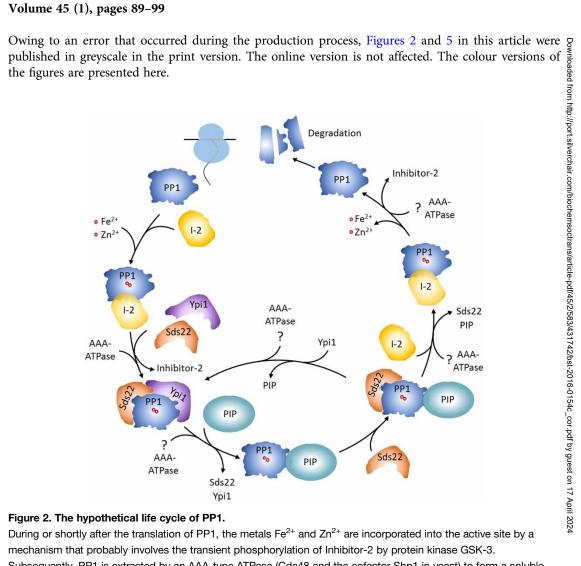




Correction: Biogenesis and activity regulation of protein phosphatase 1

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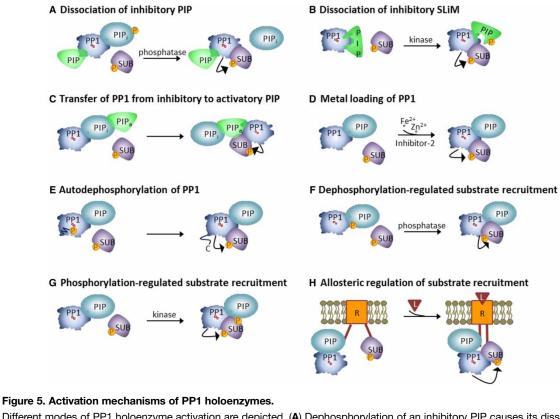
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mechanism that probably involves the transient phosphorylation of Inhibitor-2 by protein kinase GSK-3. Subsequently, PP1 is extracted by an AAA-type ATPase (Cdc48 and the cofactor Shp1 in yeast) to form a soluble, inhibited trimeric complex with Sds22 and Ypi1 (Inhibitor-3 in vertebrates). This complex serves as the source of PP1 for the assembly of PP1 holoenzymes. At least some PP1 holoenzymes can recruit Sds22 as a third subunit. It is suggested that Sds22 mediates the recruitment of an AAA-ATPase to extract PP1 from these holoenzymes, either for (phosphorylation-independent) metal unloading by Inhibitor-2 and its subsequent proteolytic degradation or for recycling to form a trimeric complex with Sds22 and Ypi1/Inhibitor-3.

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Different modes of PP1 holoenzyme activation are depicted. (A) Dephosphorylation of an inhibitory PIP causes its dissociation and activation of a PP1 holoenzyme. (B) Phosphorylation-dependent dissociation of an inhibitory SLiM activates a PP1 complex. (C) A PP1 holoenzyme can be activated by transfer of PP1 from an inhibitory to an activatory PIP. (D and E) Targeting of the catalytic subunit of PP1 itself can modulate activation, for example, by metal loading of PP1 (D) or by autodephosphorylation of an inhibitory site in the C-terminus of PP1 (E). (F) The phosphorylation state of PIPs determines their binding affinity for substrates. (G) Substrate recruitment can depend on its prior phosphorylation state. (H) Ligand binding to a receptor complex can induce conformational changes that bring PP1 within reach of its substrate. P, phosphorylation; SUB,

substrate; i, inhibitory; a, activatory; R, receptor; L, ligand.