

## Supplemental Information

### Supplemental Figure Legends

**Figure S1.** Alignment of protein phosphatase 5 of different species. The protein sequence of PPH-5 of *Caenorhabditis elegans* (CE), PP5 of *Rattus norvegicus* (RN), of *Mus musculus* (MM) and of *Homo sapiens* (HS) and Ppt1 of *Saccharomyces cerevisiae* (SC) were aligned using ClustalW. The alignment was processed by Jalview and Blosum62 for visualization of the sequence homology.

**Figure S2.** Dose-dependent activation of PPH-5 by the identified compounds. Titration of PPH-5 with P5SA-1 (A), P5SA-2 (B), P5SA-4 (C) and P5SA-5 (D) in a pNPP-based phosphatase assay in a buffer of 40 mM HEPES, pH 7.5, 20 mM KCl, 5 mM MnCl<sub>2</sub>, 1 mM DTT and 60 mM pNPP. With P5SA-3 no saturation curve could be obtained due to low affinity and stability.

**Figure S3.** The P5SAs neither influence the ATPase activity of *C. elegans* Hsc70/HSP-1 and *C. elegans* Hsp90/DAF-21 nor interfere with the interaction sites between the chaperones and their cochaperones. Concentrations well above the K<sub>D</sub> of P5SA-1 (yellow), P5SA-2 (orange), P5SA-4 (red) and P5SA-5 (blue) were tested for their influence on the ATPase rates of the nematode chaperone systems. DMSO controls are shown in grey. Addition of the nucleotide exchange factor BAG-1 and the J protein DNJ-13 increases the activity of Hsc70/HSP-1, but the P5SAs have no effect on this system. The activator of Hsp90 AHA-1 acts as predicted by increasing the ATPase rate. P5SAs have again no effect on this chaperone system. Results are expressed as mean ± SD (n ≥ 3).

**Figure S4.** The P5SAs only weakly influence the apparent K<sub>M</sub> of pNPP. Substrate titrations of pNPP were done with 100 nM of PPH-5. The substrate binding curve in absence of activators is depicted in black. P5SAs were applied at their maximal soluble concentrations. Results are expressed as mean ± SD (n ≥ 3).

**Figure S5.** The P5SAs are not able to activate in an additive manner. Concentrations of three times the  $K_D$  were used for each compound (P5SA-1 was 40 $\mu$ M, P5SA-2 was 23  $\mu$ M, P5SA-4 was 70  $\mu$ M and P5SA-5 was 16  $\mu$ M. P5SA-3 was not used for solubility problems). Compounds were added in different combinations as indicated. Results are expressed as mean  $\pm$  SD ( $n \geq 3$ ).

**Figure S6:** Overlay of the human PP5 with the structures of the rat PP5. Stereo view of the backbone superposition of three molecules shown as ribbon plots: human apo PP5 (dark grey) with  $\alpha$ J-helix in cyan, rat apo PP5 (intermediate grey) with  $\alpha$ J-helix in green and PP5:P5SA-2 with  $\alpha$ J-helix in light grey and yellow.

Figure S1.

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CE_PPH-5 1 MAATITDDIVATVLESIEEKSYEDEKEKAGMIKDEANQFFKQVYDVDAADLYSVAIEIHP-TAVLYGNRAQAYLKKELYGSAL ED 84
RN_PP5 1 -MAMAEGERTCAEPPRDEPPAEGTLKRAEELKTQANDYFKAKDYENAIFKYSQAI ELNPSNAIYYGNRSLAYLRTECYGALGD 84
MM_PP5 1 -MAMAEGERTCAEPPRDEPPADGALKRAEELKTQANDYFKAKDYENAIFKYSQAI ELNPGNAIYYGNRSLAYLRTECYGALGD 84
HS_PP5 1 -MAMAEGERTCAEPPRDEPPADGALKRAEELKTQANDYFKAKDYENAIFKYSQAI ELNPSNAIYYGNRSLAYLRTECYGALGD 84
SC_Ppt1 1 -----MSTPTAADRAKALERKNEGNVFVKEKHFLLKAI EKYTEAIDL DSTQSIYFSNRAF AHFKVDNFGSALND 68

CE_PPH-5 85 ADNAIAIDPSYVKGFYRRATANMALGRFKKALT DYQAVVVKCPNDKDKARAFDECSKIVRRQKFEAAIST--DHDKKTVAETLDI 167
RN_PP5 85 ATRAIELDKKYIKGYRRAASNALGKFRRAALRDYETVVVKVPNDKDAKMKYQECISKIVKQKAFERA IAG--DEHRRSVVDSLDI 167
MM_PP5 85 ATRAIELDKKYIKGYRRAASNALGKFRRAALRDYETVVVKVPNDKDAKMKYQECISKIVKQKAFERA IAG--DEHRRSVVDSLDI 167
HS_PP5 85 ATRAIELDKKYIKGYRRAASNALGKFRRAALRDYETVVVKVPNDKDAKMKYQECISKIVKQKAFERA IAG--DEHRRSVVDSLDI 167
SC_Ppt1 69 CDEAIKLDPKNIKAYHRRALS CMALLEFKKARKDLNVLLKAKPNPAATKALLTDRFI REERERKAI GGAENEAKISLQCTLNL 153

CE_PPH-5 168 NAMAIED---SYDGRPLED-----KITKEFVLQII-KTFKNGQKLHKKYAFKMLLEFYNYVKSIP TMVEITVPT 232
RN_PP5 168 ESMTIED---EYSGPKLEDG-----KVTITFMKDLI-QWYKDKKLRKCAQYILVQKKEVLCKLSTLVETTLKE 233
MM_PP5 168 ESMTIED---EYSGPKLEDG-----KVTITFMKDLI-QWYKDKKLRKCAQYILVQKKEVLCKLSTLVETTLKE 233
HS_PP5 168 ESMTIED---EYSGPKLEDG-----KVTISFMKELM-QWYKDKKLRKCAQYILVQKKEVLSKLSLTVETTLKE 233
SC_Ppt1 154 SFDANADLANYEGPKLEFEQLYDDKNAFKGAIKNMSQEFISKMVNDLELKGKYL PKKYVAAIISHADTLFRQEPSMVELNNS 238

CE_PPH-5 233 G--KKF TICGDVHGQFYDL CNIFEI NGYPSSETNPYLFNGDFVDRGSFSVETIF TMIGFKLLYPNHFFMSRGNHESDVMNMYGFE 315
RN_PP5 234 T--EKITVCGDTHGQFYDLLNIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDFHLLRGNHETDNMNOIYGF 316
MM_PP5 234 T--EKITVCGDTHGQFYDLLNIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDFHLLRGNHETDNMNOIYGF 316
HS_PP5 234 T--EKITVCGDTHGQFYDLLNIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDFHLLRGNHETDNMNOIYGF 316
SC_Ppt1 239 TPDKVLSVCGDTHGQFYDLNLFRKFGKVGPKHTYLENGDFVDRGSWSCEVALLFYCLKILHPNNEFLRGNHESDMNMIYGF 323

CE_PPH-5 316 GEVKAKYTQDMCFETETFCWLP LCHL I NEKIFVCHGGLFEKEDGVTLEDIRKTDNRQPPDEGIMCDLLWSDPOP INGRSFSKRG 400
RN_PP5 317 GEVKAKYTAQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRKIERNRQPPDSGPMCDLLWSDPOPQNGRSVSKRG 401
MM_PP5 317 GEVKAKYTAQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRKIERNRQPPDSGPMCDLLWSDPOPQNGRSVSKRG 401
HS_PP5 317 GEVKAKYTAQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRKIERNRQPPDSGPMCDLLWSDPOPQNGRSI SKRG 401
SC_Ppt1 324 DECKYKYSQRI FNMF AQSFEESLPLATL I NNDYLVMHGGLPSDPSATLSDFKNIDRFAPPRDGA FEMELLWADPQEA NGMPSQRG 408

CE_PPH-5 401 VGCQFGPDVTSKWCETNGIEYVRSHEVKPEGYEMHNGOCTVFSAPNYCDQMNGKAFITIT-----GDNLT PRFTPF 475
RN_PP5 402 VSCQFGPDVTKAFLEENQLDYI I RSHEVKAEGYEV AHGGRCVTVFSAPNYCDQMGNKASYIHLO-----GSDLRPOFHQF 476
MM_PP5 402 VSCQFGPDVTKAFLEENQLDYI I RSHEVKAEGYEV AHGGRCVTVFSAPNYCDQMGNKASYIHLO-----GSDLRPOFHQF 476
HS_PP5 402 VSCQFGPDVTKAFLEENQLDYI I RSHEVKAEGYEV AHGGRCVTVFSAPNYCDQMGNKASYIHLO-----GSDLRPOFHQF 476
SC_Ppt1 409 LGHAFGPDITDRFLRNKLRK I FRSHELRMGGVQFEQKGLMTVFSAPNYCDSQGNLGGV I HVVPGHGLQAGRNDQNL I IET 493

CE_PPH-5 476 DAVPHRKLPPMAYANSLFGFN-- 496
RN_PP5 477 TAVPHPNVKPMAYANTLLQLGMM 499
MM_PP5 477 TAVPHPNVKPMAYANTLLQLGMM 499
HS_PP5 477 TAVPHPNVKPMAYANTLLQLGMM 499
SC_Ppt1 494 EAV EHPDIKPMAYNSGGFGL--- 513

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Figure S2.

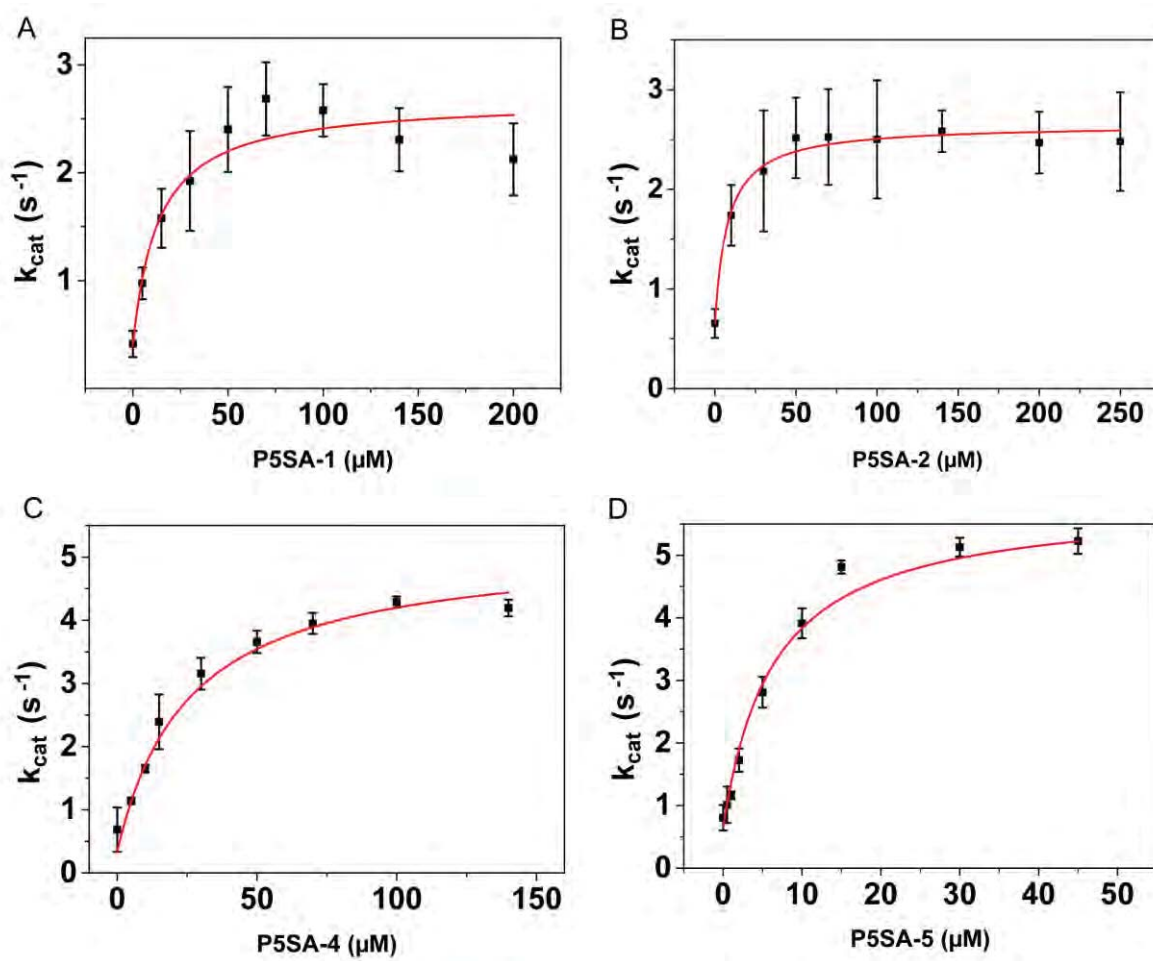


Figure S3.

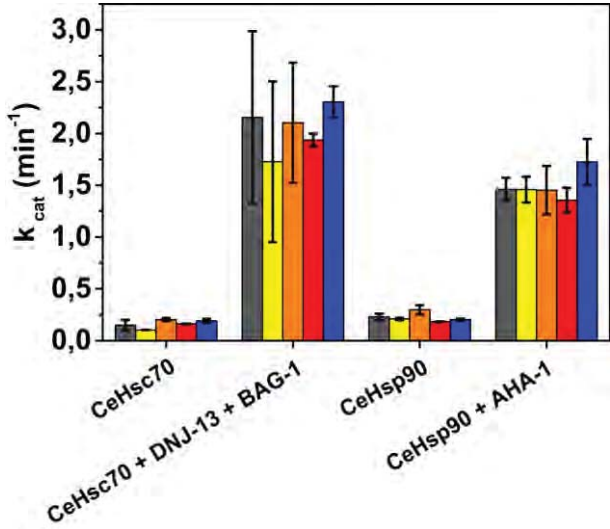


Figure S4.

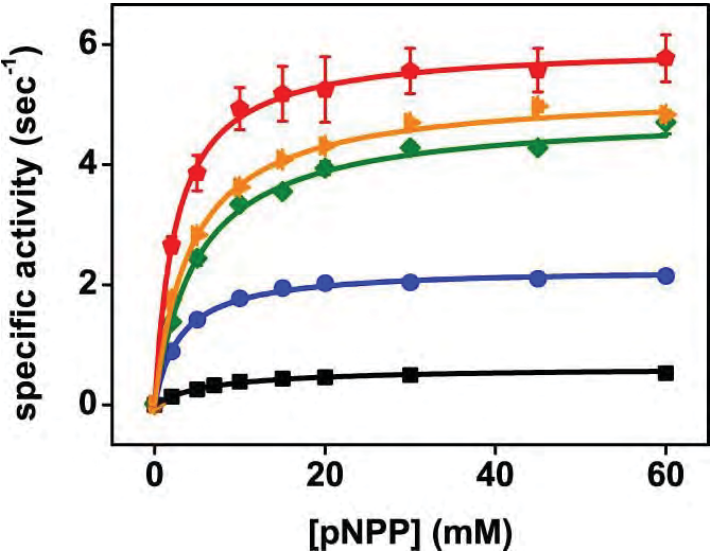


Figure S5.

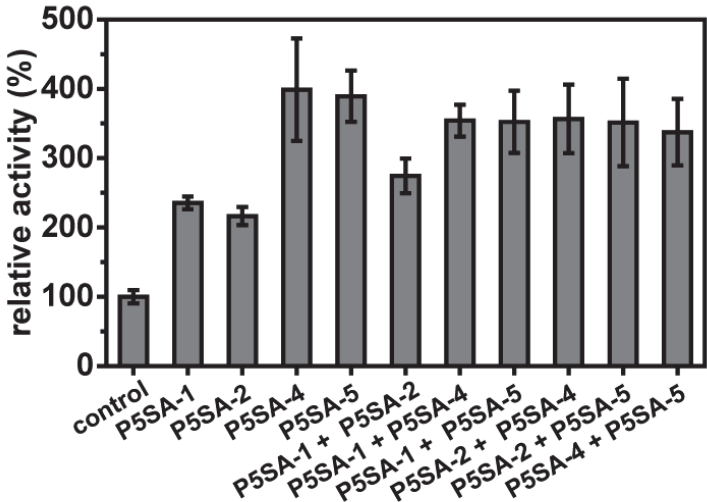


Figure S6.

