Multiplexed phosphoproteomic profiling using titanium dioxide and immuno-affinity enrichments reveals complementary phosphorylation events

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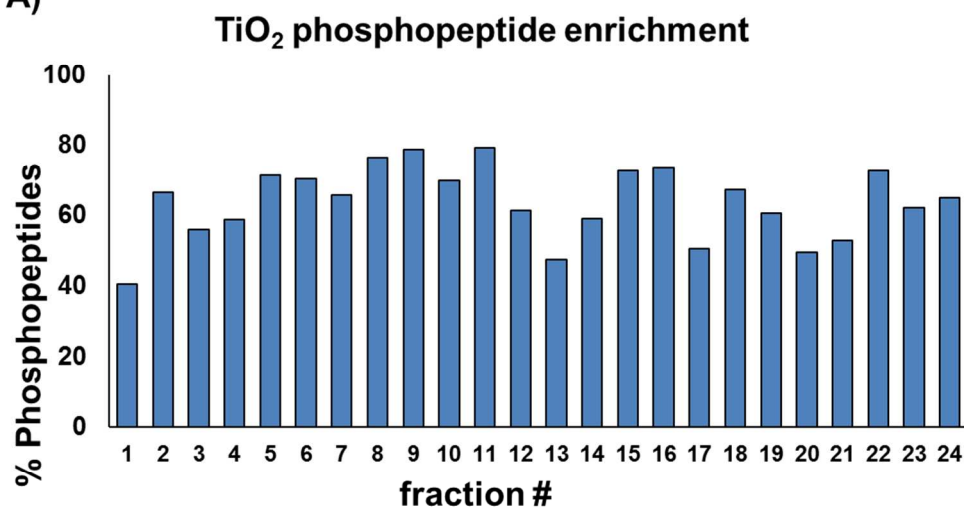[‡] These authors contributed to this work equally

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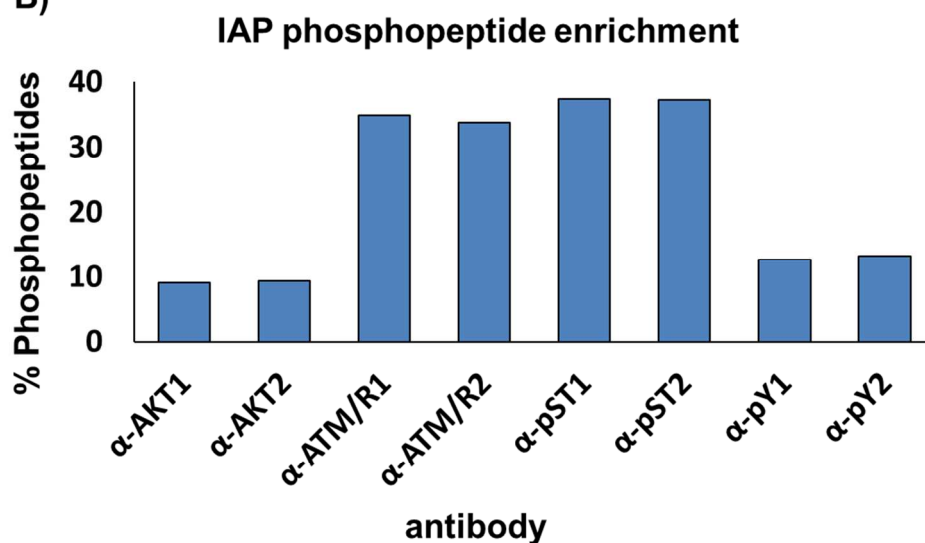
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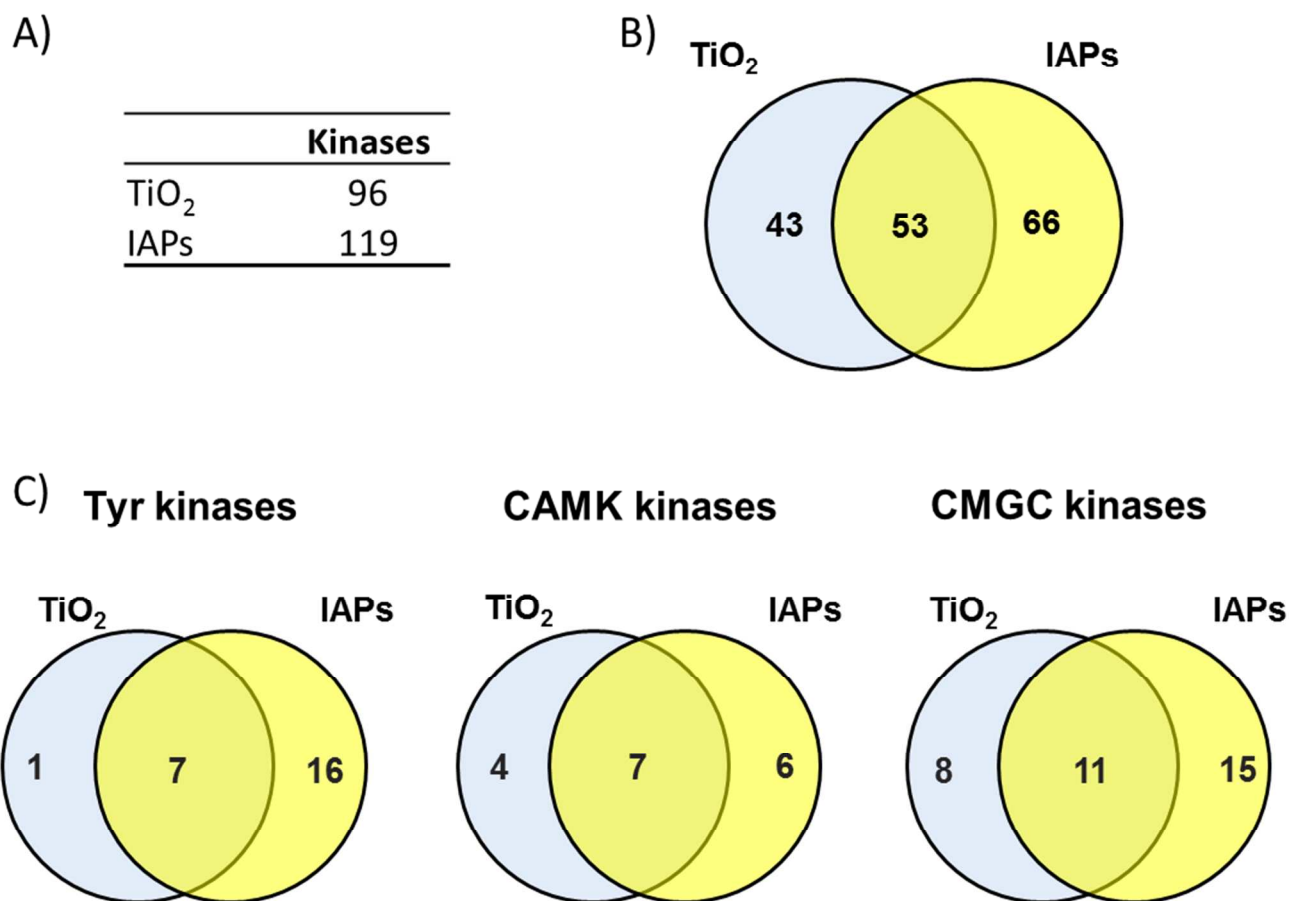
Supplemental Figure 1

A)

B)

Supplemental Figure 1: Analysis of phosphopeptide enrichment. A) Phosphopeptide enrichment for each of the 24 fractions using the TiO_2 method. B) Phosphopeptide enrichment for each IAP (replicate 1 and 2).

Supplemental Figure 2

A)

	Kinases
TiO$_2$	96
IAPs	119

B)

TiO$_2$ IAPs

43   53   66

C) **Tyr kinases**   **CAMK kinases**   **CMGC kinases**

TiO$_2$ IAPs   TiO$_2$ IAPs   TiO$_2$ IAPs
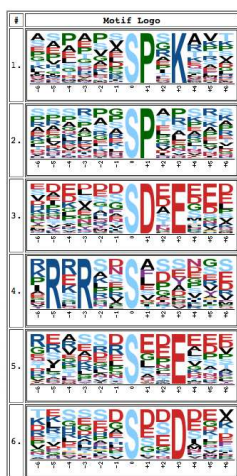
1   7   16   4   7   6   8   11   15

Supplemental Figure 2: Kinases identified by TiO$_2$ and IAP enrichments A) Tally of kinases identified with each enrichment strategy. **B)** Venn diagram of corresponding overlap. **C)** Venn diagrams for Tyrosine, CAMK and CMGC kinases for each enrichment strategy.
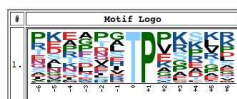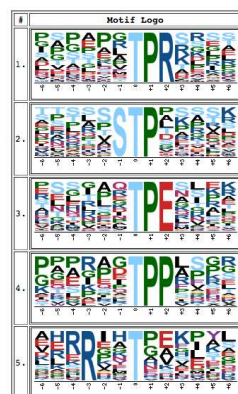
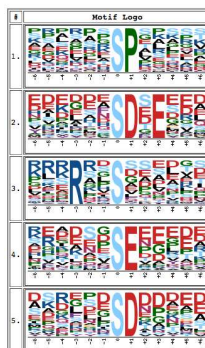**Supplemental Figure 3**

A) BEZ-235

TiO$_2$ pS IAP pS
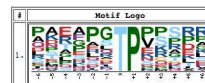

TiO$_2$ pT IAP pT

B) GSK1120212

TiO$_2$ pS IAP pS
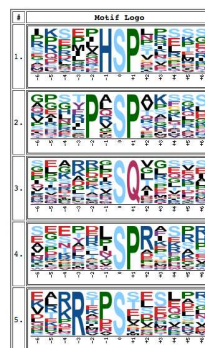
TiO$_2$ pT IAP pT
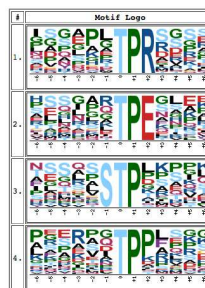
C) Staurosporine
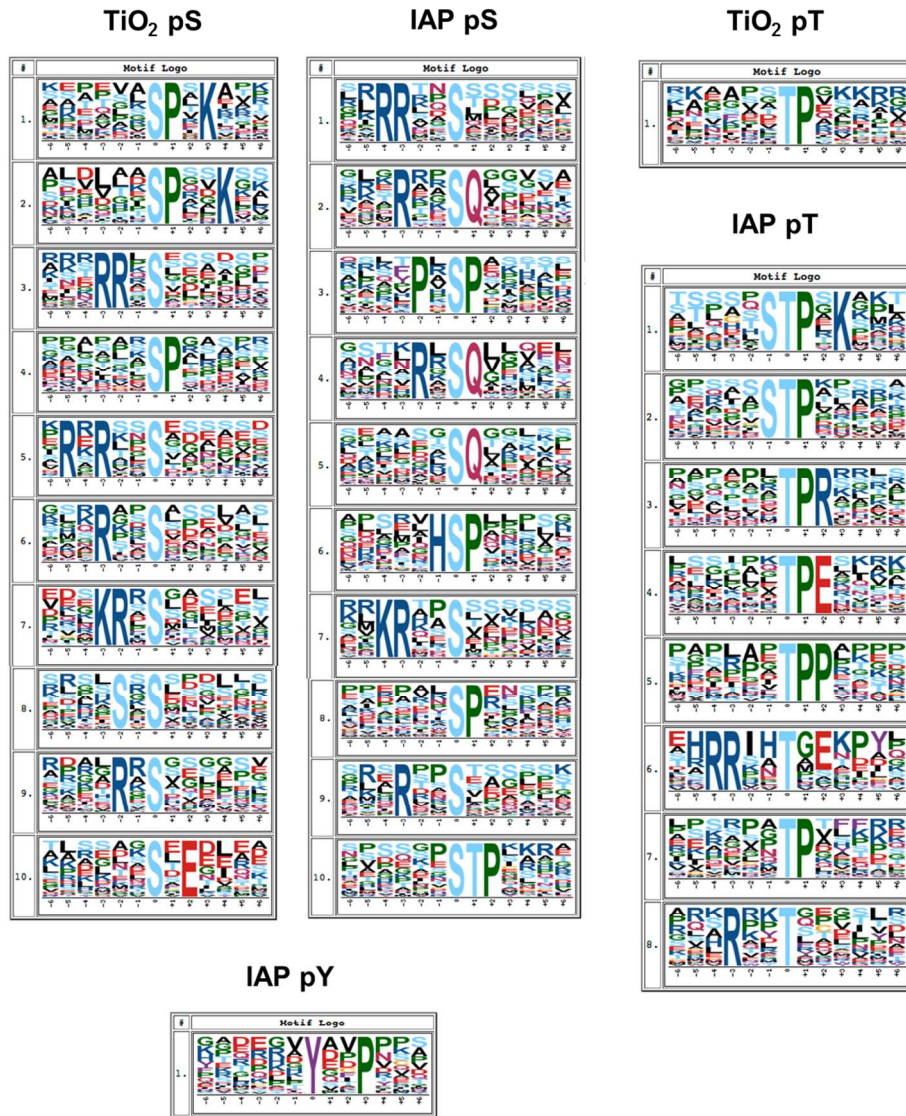
Supplemental Figure 3: Sequence logos for phosphorylation sites. PhosphoSitePlus (http://www.phosphosite.org) motif analysis (38) of quantified phosphorylation events inhibited following treatment with A) BEZ-235, B) GSK 1120212, and C) Staurosporine. Sequences were centered at the phosphorylated residue and extended six amino acids on each side, thereby resulting in a 13-amino acid long motif for each phosphorylation site.