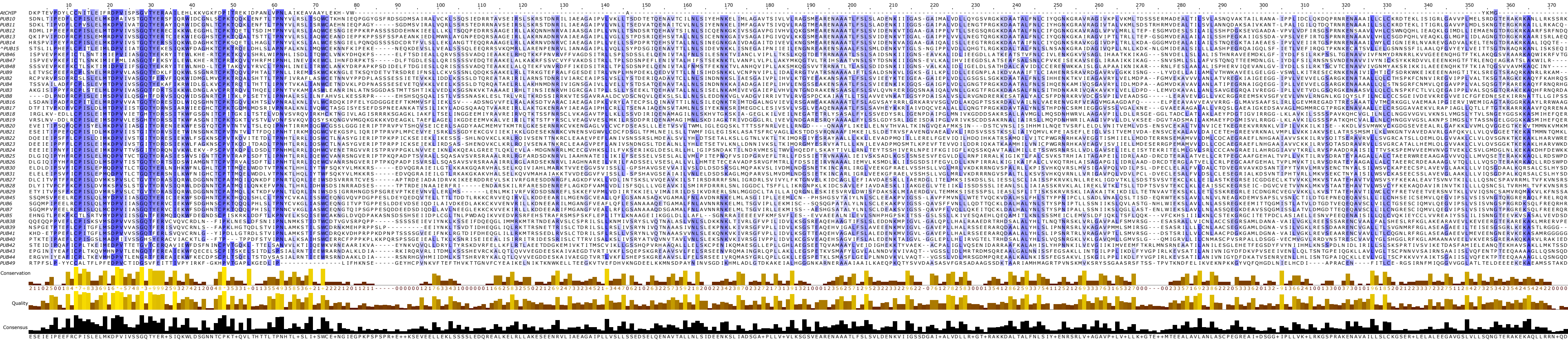
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PUB41
PUB40
PUB42
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Conservation
Quality
Consensus

Multiple Sequence Alignment of Class II and III PUBs

Shown is the amino acid sequence alignment of 42 PUBs. Alignment was curated manually and gaps occurring in the alignment were deleted if more than 75% of the aligned sequences contained a gap in the same position. Highest residue conservation is indicated by dark blue, lighter shades indicate lower conservation. The phosphorylated residues Thr62 and Thr88 of PUB22 are highlighted in red.

Sequences used for the alignment:

>AtCHIP At3G07370 /180-262 (outgroup)
DKPTEVPDYLCCNITLEIFRDPVISPSGVTYERAAILEHLKKVGKFDPITREKIDPANLVPNLAIKE
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--YKMG-----------------

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RILIAEAGAIPVLVKLLTSDDTETQENAVTCILNLSIYEHNKELIMLAGAVTSIVLVLRAGSMEARE
NAAATLFSLSLADENKIIIGAS-
GAIMALVDLLQYGSVRGKKDAATALFNLCIYQGNKGRAVRAGIVKPLVKMLTDSSSERMADEA
LTILSVLASNQVAKTAILRANA-
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>PUB11 AT1g23030 /225-590
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GAIPALVDLLENGTPRGKKDAATALFNLCIYHGNKGRAVRAGIVTALVKMLSDSTRHRMVDEA
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ACQ-

>PUB12 AT2g28830 /236-606
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ARENAAATLFSLSVIDENKVTIGAA-
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GAIPPLVVLLNEGTQRGKKDAATALFNLCIYQGNKGKAIRAGVIPTLTRLLTEP-
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>PUB46 AT5g18320 /61-424
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EAVKALIDLIEEGDLLATKEATSTVFNLCIVLENKGKVVSAGLIHAATKKIKAG---
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IKRFVTG

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IYDLFSILRNSNSVNDENAVVIVYNICKSYKKRDVVLEEENKHGTFTRLENQEAGRATSLAKWIL
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>PUB45 AT1g27910 /227-596
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