```
At RBX1          1  -MATLDSDVTMIPAGEASSSVAASSSNKKAKRFEIKKWSAVALWAWDIVVDNCAICRNHI
Pi RBX1          1  -MASPDIDVPMVPAGEGSTGVGPST--KKPKRFEIKKWNAVSLWAWDIVVDNCAICRNHI
Human  Rbx1      1  MAAAMDVDT---PSG---TNSGAGK-----KRFEVKKWNAVALWAWDIVVDNCAICRNHI
                                                   ●●●●●●●●●●●●●●●●      ○  ○

At RBX1         60  MDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH
Pi RBX1         58  MDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH
Human  Rbx1     50  MDLCIECQANQASATSEECTVAWGVCNHAFHFHCISRWLKTRQVCPLDNREWEFQKYGH
                       ○  ○           ●○   ●  ○●○ ●○ ○○    ●●    ○  ○      ●●●
```

**Supplemental Figure 6. Alignment of Amino Acid Sequences of Pi RBX1 of *P. inflata*, At RBX1 of *Arabidopsis*, and an Rbx1 of human.** For a given site, the amino acid that is present in at least two of the sequences is highlighted in dark shading, and the amino acid that is similar to the residue in dark shading is highlighted in gray shading. The black dots show the CUL1 binding residues and the open circles represent the Zinc chelating residues in human Rbx1 (Zheng et al., 2002).