```
G2E6      1    MAKLTALTLLGMGLALFDRQKSSFQTRFNVHREVTPVELPNCNLVKGIDNGSEDLEILPN
HuPON1    1    ----I-------------RNHQ--Y---L-AL---Q-------------ET---–M-----
G3C9      1    ----------L------G--------------------------V----–-------

G2E6      61   GLAFISSGLKYPGIMSFDPDKSGKILLMDLNEKEPAVSELEIIGNTLDISSFNPHGISTF
HuPON1    61   ---------------K--N-NSP----------ED-T-L--G-T-SKF-V-----–-----
G3C9      61   -----------------------------ED-V-L--G-T----------------–-----

G2E6      121  IDDDNTVYLLVVNHPGSSSTVEVFKFQEEEKSLLHLKTIRHKLLPSVNDIVAVGPEHFYA
HuPON1    121  T-E--AM--------DAK----L-----------------------NL–-----------G
G3C9      121  T-E-----------D--------------------------------–-------------

G2E6      181  TNDHYFIDPYLKSWEMHLGLAWSFVTYYSPNDVRVVAEGFDFANGINISPDGKYVYIAEL
HuPON1    181  ------L----Q----Y------Y-V----SE---------–-–---------------–
G3C9      181  ------A------------------------------------–-–---------------–

G2E6      241  LAHKIHVYEKHANWTLTPLRVLSFDTLVDNISVDPVTGDLWVGCHPNGMRIFFYDAENPP
HuPON1    241  --------------------KS-D-N---–-–------E---------–----K-----S----
G3C9      241  --------------------KS-D-----–-–-------------------–-------Y--PK---

G2E6      301  GSEVLRIQDILSEEPKVTVVYAENGTVLQGSTVAAVYKGKLLIGTVFHKALYCDL
HuPON1    301  A-------N--T------Q-------------–--S--------------–-------E-
G3C9      301  -------------------------------–---------------–-------E-
```

Figure S1. Amino acid sequence alignment of G2E6, G3C9, and HuPON1. Protein sequences were aligned using CLUSTAL W (Larkin M.A., Blackshields G., Brown N.P., Chenna R., McGettigan P.A., McWilliam H., Valentin F., Wallace I.M., Wilm A., Lopez R., Thompson J.D., Gibson T.J. and Higgins D.G. (2007) ClustalW and ClustalX version 2. *Bioinformatics 23*, 2947-2948.) using G2E6 as the reference sequence. Amino acid residues that are conserved amino acids between G2E6 and either HuPON1 or G3C9 are indicated by '–' symbol. Residues with atoms within 5 Å of the phosphate ion in the G2E6 crystal are highlighted in yellow.