```
                 Kinase domain
ScVIP1 354 - DGEDHNIYIYYHSKNGGGGRRLFRKVGNKSSEFDPTLVHPRTEGSYIYEQFMDTDNFEDV - 413
SpASP1 200 - YGEDHNIYIYFPKSVGGGGRKLFRKVANKSSDYDPDLCAPRTEGSFIYEEFMNVDNAEDV - 259
HsVIP2 162 - SAEDHNVYIYYPTSAGGGSQRLFRKIGSRSSVYSPES-NVRKTGSYIYEEFMPTDG-TDV - 247
AtVIH1 159 - NGDDHSIMIYYPSSAGGGMKELFRKVGNRSSEFHPDVRRVRREGSYIYEEFMPTGG-TDV - 217
AtVIH2 160 - NGDDHSIMIYYPSSAGGGMKELFRKIGNRSSEFHPDVRRVRREGSYIYEEFMATGG-TDV - 218
              .:**.: **: .. *** :.****:..:** : *     *  **:***:** ...  **
                 Kinase domain
ScVIP1 414 - KAYTIGENFCHAETRKSPVVDGIVRRNTHGKEVRYITELSDEEKTIAGKVSKAFSQMICG - 473
SpASP1 260 - KVYTVGPHYSHAETRKSPVVDGIVRRNPHGKEIRFITNLSEEEKNMASKISIAFEQPVCG - 319
HsVIP2 248 - KVYTVGPDYAHAEARKSPALDGKVERDSEGKEVRYPVILNAREKLIAWKVCLAFKQTVCG - 307
AtVIH1 218 - KVYTVGPEYAHAEARKSPVVDGVVMRNPDGKEVRYPVLLTPAEKQMAREVCIAFRQAVCG - 277
AtVIH2 219 - KVYTVGPEYAHAEARKSPVVDGVVMRNTDGKEVRYPVLLTPAEKQMAREVCIAFRQAVCG - 278
             *.**:* .:.***:****.:** * *: .***:*: . *.  ** :* ::. ** * :**
                 Kinase domain
ScVIP1 474 - FDLLRVSGKSYVIDVNGFSFVKDNKAYYDSCANILRSTFIEAKKKMDM-EKKN------- - 525
SpASP1 320 - FDLLRVSGQSYVIDVNGWSFVKDNNDYYDNAARILKQMFHVAERHRRN-RVPSVQ----- - 373
HsVIP2 308 - FDLLRANGQSYVCDVNGFSFVKNSMKYYDDCAKILGNIVMRELAPQFH------IPWSIP - 361
AtVIH1 278 - FDLLRSEGSSYVCDVNGWSFVKNSYKYYDDAACVLRKMFLDAKAPHLSSTIPPILPWKIN - 337
AtVIH2 279 - FDLLRSEGCSYVCDVNGWSFVKNSYKYYDDAACVLRKMCLDAKAPHLSSTLPPTLPWKVN - 338
             ***** .* *** ****:****:.  ***..* :* .
                 phosphatase domain
ScVIP1 526 - ------------LPIIREEKEQKWVFKGLAIIIRHADRTPKQKFKHSFTSPIFISLLKGH - 573
SpASP1 374 - -----------EVLNPPPRESEAWRLKSLVGVLRHADRTPKQKFKFSFTSDPFVKLLQGH - 422
HsVIP2 362 - LEAEDI-------PIVPTTSGTMMELRCVIAVIRHGDRTPKQKMKMEVRHQKFFDLFEKC - 414
AtVIH1 338 - EPVQSNEGLTRQGSGIIGTFGQSEELRCVIAIVRHGDRTPKQKVKLKVTEEKLLNLMLKY - 397
AtVIH2 339 - EPVQSNEGLTRQGSGIIGTFGQSEELRCVIAVVRHGDRTPKQKVKLKVTEEKLLNLMLKY - 398
                                        :: :  ::**.*******.* ..    :..*:
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