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# Aquaporins and CO<sub>2</sub> diffusion across biological membrane

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Despite the physiological significance of effective  $CO_2$  diffusion across biological membranes, the underlying mechanism behind this process is not yet resolved. Particularly debatable is the existence of  $CO_2$ -permeable aquaporins. The lipophilic characteristic of  $CO_2$  should, according to Overton's rule, result in a rapid flux across lipid bilayers. However, experimental evidence of limited membrane permeability poses a challenge to this idea of free diffusion. In this review, we summarized recent progress with regard to  $CO_2$  diffusion, and discussed the physiological effects of altered aquaporin expression, the molecular mechanisms of  $CO_2$  transport via aquaporins, and the function of sterols and other membrane proteins in  $CO_2$  permeability and end up with perspectives on resolving such argument either by determining the atomic resolution structure of  $CO_2$  permeable aquaporins or by developing new methods for measuring permeability.

#### KEYWORDS

carbon dioxide, aquaporin, biological membranes, diffusion, physiological relevance

#### Introduction

More than 30 years ago, aquaporin was found to be a highly specialized water channel protein in erythrocytes (Preston et al., 1992; Agre, 2004). The discovery of aquaporins changed our perspective on the highly controlled permeability of biological membranes, which had previously been explained by the paradigm of free diffusion of water transport across membranes (Edidin, 2003). Aquaporins are a class of structurally conserved proteins that have been shown to function as channels for a wide range of neutral chemicals since their discovery. These molecules include glycerol (Jensen et al., 2001; Nollert et al., 2001), urea (Ishibashi et al., 1994; Ma et al., 1997), hydrogen peroxide (Almasalmeh et al., 2014), ammonia (Jahn et al., 2004; Kirscht et al., 2016), and even the gas molecule-carbon dioxide (Uehlein et al., 2003). Such a wide range of substrate selectivity suggests that biological membrane permeability is tightly controlled and is not just based on passive diffusion across the lipid bilayer. More than a century ago, Meyer and Overton proposed that the membrane permeability of a given solute is closely associated with its lipid solubility [also known as Overton's rule (Missner and Pohl, 2009)]. For many molecules, experimental evidence confirmed this rule (Missner et al., 2008a), but some did not follow the prediction. The appearance of these molecules begs the question of whether or not Overton's rule alone can account for the passage of molecules through biological membranes. Among those molecules that deviated from the prediction by Overton's rule, CO2 was intensively investigated due to

its role as a physiological component for essential process, i.e., respiration and photosynthesis. Despite the predicted high permeability of CO2, accumulated evidences from biologists found that certain cell membranes are remarkably resistant to CO<sub>2</sub>, which could not be explained solely by Overton's rule due to its high lipophilic property. To address this challenge, Pohl's team has introduced the effect of unstirred layers (USLs) and buffer, which account for a significant portion of the diffusion barrier of the lipid bilayer (Missner and Pohl, 2009). While research directed by Kaldenhoff and Boron independently demonstrated the existence of aquaporin-mediated CO<sub>2</sub> transport in regulating the CO<sub>2</sub> diffusion across biological membranes (Nakhoul et al., 1998; Uehlein et al., 2003). Since then, discussion has been continued with regard to the potential biological significance of CO<sub>2</sub> channels in regulating CO<sub>2</sub> transport across biological membranes. As more relevant results continue to uncover the complexities of CO2 movement across biological membranes, several questions have emerged: Why do some biological membranes have such low intrinsic CO2 permeability? How do biological systems deal with the conflict between the need for fast gas exchange and the low intrinsic permeability of the CO<sub>2</sub> membrane? Is there a CO<sub>2</sub> channel protein that exists in addition to free diffusion?

Baring the above open questions, we focused in this review on recent updates since our last systematic review article in 2014 (Kaldenhoff et al., 2014). We began with discussing the classical theory of  $CO_2$  solubility-diffusion of  $CO_2$  transport across lipid bilayers and the physiological influence of altered aquaporin expression. We then delved into the molecular details of aquaporin-mediated  $CO_2$  transport, as well as the role of sterols and nonrelevant membrane proteins on the overall  $CO_2$ permeability of biological membranes. Finally, we summarized the current limitations of the different methods used to measure  $CO_2$  permeability and offered a perspective on the current understanding of  $CO_2$  diffusion across biological membranes.

#### Meyer overton's rule and the CO<sub>2</sub> solubilitydiffusion model

As the basic principle for mass transportation through diffusive means, Adolf Fick described that the diffusive flux (*J*) was related to the diffusion coefficient (*D*) and gradient of the substrate (in case of two phases, rewritten as the concentration difference between the two phases  $\nabla \varphi$ ) concentration:

$$J = -D\nabla\varphi \tag{1}$$

Later, Meyer and Overton established the rule of spontaneous permeation of solutes and solvents across membranes, stating that the flux of the substance across a membrane, J, was linearly dependent on the permeability of the membrane,  $P_{\rm m}$ , with a concentration difference  $\Delta c_s$  at two surfaces of the membrane, when the partition coefficient of the substance,  $K_{\rm p}$ , was given.

Eq. 1 can be rewritten as following:

$$J = -P_m \cdot \Delta c_s \tag{2}$$

Where  $P_m = K_p \cdot D_m / d$ ,  $D_m$  is the diffusion coefficient, *d* is the thickness of the membrane.

As indicated by the rule, the permeability of a given molecule is related to the partition coefficient  $K_p$ . Therefore, gas molecules, such as  $\mathrm{CO}_2$  would have a membrane permeability as fast as permeating a water layer, with a  $K_p \ge 1$ . However, experimental data has shown contradictory results with extremely low gas permeability from certain biological membranes. As proposed by Pohl's group, the existence of an unstirred layer, which dominates the resistance of CO2 diffusion, and the variation in the thickness of this layer could explain for this discrepancy (Missner et al., 2008b). In 2011, a joint correspondence letter was published that summarized the main agreement and disagreement on channel protein-mediated CO<sub>2</sub> diffusion by the research groups Boron, Gros and Pohl (Boron et al., 2011). In summary, they agreed that channel-mediated  $CO_2$ transport would require a high resistance of the non-channel part of the membrane to CO<sub>2</sub> diffusion and relatively low resistance to CO<sub>2</sub> from USLs. In 2015, further cross-talk was initiated to collect new comments or views on CO2 transport mediated by channel proteins under physiological conditions by Cooper, Occhipinti, and Boron (Cooper et al., 2015). In this proposal, a new "access-solubilitydiffusion-egress" model was proposed, where resistance of nonchannel proteins, different headgroup of lipids, the role of cholesterol, as well as USLs, all accounted for the apparent CO<sub>2</sub> permeability of biological membranes. While the disagreement still remains, Pohl pointed out the concern of data generated by both stopped flow and mass spectrometry, due to the fast process of CO<sub>2</sub> diffusion in the range of milliseconds. Furthermore, it could be the limited availability of carbonic anhydrases (CAs), which led to extremely low CO2 permeability to the apical membranes. Finally, new points were raised: 1) How to explain the role of sterols and high percentage of membrane proteins, on the diffusion of diffusion of CO2 of biological membranes? 2) Mutation work that influences the function of certain aquaporin, resulting in the change of  $P_{M,CO_2}$ , could not be correctly mapped to the change in thickness of USLs. 3) The altered activity CA activity of certain cells was not correlated with CO<sub>2</sub> permeability. 4) The existence of USLs still challenged the proponents of CO<sub>2</sub> channels.

### Physiological roles for aquaporin-mediated CO<sub>2</sub> membrane diffusion

 $CO_2$  and  $O_2$  are gas molecules that play crucial roles in respiration by providing energy through oxidative phosphorylation reactions. Both gases need to be exchanged efficiently between the cellular organelles and the atmosphere, guided by their osmotic gradients. Unlike animals, plant cells or other photosynthesis microorganisms take up  $CO_2$  as a substrate for photosynthesis, and the concentration gradient is less significant compared to animals (Uehlein et al., 2017). Therefore, a higher efficient diffusion of  $CO_2$  from the atmosphere to the chloroplast stroma, where photosynthesis occurred, would be more beneficial for photosynthesis-active organisms (Kaldenhoff et al., 2014).

For quite a long time, the resistance of the mesophyll to  $CO_2$  was overlooked for green-leaf plants. Instead, the regulation of stroma and  $CO_2$  interconversion to bicarbonate and protons catalyzed by carbonic anhydrases (CA) was considered to be the limiting factor in  $CO_2$  availability (Kaldenhoff, 2012). However, even with complete

Names	Origins	Validation methods	References
NtAQP1	Nicotiana tabacum	<i>X. laevis</i> oocytes <sup>a</sup> , Yeast <sup>b</sup> , Black lipid membrane/ copolymers <sup>c</sup>	Uehlein et al. (2003), Otto et al. (2010), Uehlein et al. (2012a), Kai and Kaldenhoff (2014)
AtPIP1;2	Arabidopsis thaliana	Leaf <sup>d</sup> , Yeast, In vivo <sup>e</sup>	Heckwolf et al. (2011), Uehlein et al. (2012b)
HaPIP1;1	Helianthemum almeriense	Yeast	Navarro-Rodenas et al. (2013)
ZmPIP1;5	Zea mays	Yeast	Heinen et al. (2014)
ZmPIP1;6	Zea mays	Yeast	Heinen et al. (2014)
OsPIP1;2	Oryza sativa L.	In vivo	Xu et al. (2019)
OsPIP1;3	Oryza sativa L.	In vivo	Chen et al. (2021)
SlPIP1;2	Solanum lycopersicum	In vivo	Zhang et al. (2021)
NtPIP2;1	Nicotiana tabacum	Black lipid membrane	Uehlein et al. (2003), Uehlein et al. (2012a), Kai and Kaldenhoff (2014)
HvPIP2;1	Hordeum vulgare L.	X. laevis Oocytes	Mori et al. (2014)
HvPIP2;2			
HvPIP2;3			
HvPIP2;5			
AtPIP2;1	Arabidopsis thaliana	X. laevis oocytes	Wang et al. (2016)
AtPIP2;5	Arabidopsis thaliana	Yeast	Israel et al. (2021)
SiPIP2;7	Setaria italica	Yeast, In vivo	Ermakova et al. (2021)
PtAQP2	Phaeodactylum tricornutum	Mass spectrometry <sup>f</sup>	Matsui et al. (2018)
AQP1	Homo sapiens	X. laevis oocytes, Proteoliposome <sup>g</sup>	Nakhoul et al. (1998), Prasad et al. (1998), Musa-Aziz et al. (2009), Geyer et al. (2013)
AQP5	Homo sapiens	X. laevis oocytes	Wang and Boron (2019)
AQP5	Rattus norvegicus	X. laevis oocytes	Musa-Aziz et al. (2009), Geyer et al. (2013)
AQP6			
AQP9			
AQP0	Bos taurus	X. laevis oocytes	Geyer et al. (2013)
AQP1a1	Danio rerio	In situ <sup>h</sup>	Talbot et al. (2015)
SsAqpZ	Synechococcus sp.	Yeast	Ding et al. (2013)

#### TABLE 1 Summary of CO<sub>2</sub> permeable aquaporins.

<sup>a</sup>X.*laevis* oocytes: CO<sub>2</sub> permeability was determined by a pH electrode that recorded the change in pH value when AQP was expressed in *X. laevis* oocytes (Geyer et al., 2013).

<sup>b</sup>Yeast: CO<sub>2</sub> permeability was determined by a stopped flow spectrophotometer when AQP was expressed in the yeast protoplast (Otto et al., 2010).

<sup>c</sup>Black lipid membrane/copolymers: The permeability of CO<sub>2</sub> permeability was determined by scanning the pH electrode when AQP was incorporated into a triblock copolymer or phospholipid bilayer (Uehlein et al., 2012a; Kai and Kaldenhoff, 2014).

<sup>d</sup>Leaf: The same setup as the black lipid membrane except that a leaf patch instead of an artificial bilayer was measured (Uehlein et al., 2012b).

<sup>e</sup>*in vivo*: the CO<sub>2</sub> permeability was determined by the altered mesophyII conductance or photosynthesis related parameters via aquaporin overexpression or knockout mutant lines. <sup>f</sup>Mass spectrometry: The CO<sub>2</sub> permeability was determined by following the O<sup>18</sup> exchange monitored by mass spectrometry.

<sup>g</sup>Proteoliposome: CO<sub>2</sub> permeability was determined using a stopped flow spectrophotometer using aquaporin reconstituted liposomes.

<sup>h</sup>in situ: aquaporin knockdown mutant zebrafish larvae were monitored by CO<sub>2</sub> excretion using a custom-built total CO<sub>2</sub> analyzer.

deletion of CA activity in the chloroplast stroma, photosynthesis decreased by only about 7% (Price et al., 1994; Kaldenhoff, 2012). Furthermore, the mesophyll CO<sub>2</sub> conductance varied rapidly in response to temperature, light, or water stress, instead of having a relatively constant value. This contradicted the pure physical model of mesophyll CO<sub>2</sub> diffusion. Together, these shreds of evidence pointed to the existence of other major factors that regulated CO<sub>2</sub> diffusion, such as aquaporin-mediated transportation.

The physiological influence of altered expression of potential permeable  $CO_2$  aquaporins was recently systematically evaluated and reviewed by Evans' group (Groszmann et al., 2017). To understand the role of certain putative permeable aquaporins with  $CO_2$ , transgenic plants were generated and the impact on parameters relevant to photosynthesis was determined. In general, the change of mesophyII conductance was correlated with the tuned expression level of corresponding aquaporins. However, the

mesophyII drawdown should be negatively correlated with the mesophyII conductance and the CO<sub>2</sub> assimilation rate, where causal links between AQP and mesophyII conductance can be established. To provide the general ranges of photosyntheticrelated parameters under varied mesophyII conductance, they performed simulations by changing the mesophyII conductance, when either stomatal conductance or  $C_i$  was set to be constant. They gave an estimated range of mesophyII drawdown, CO2 assimilation rates, transpiration rate, and transpiration efficiency based on consistent literature data (Groszmann et al., 2017). Furthermore, mesophyII conductance is a combined feature that could be influenced by many factors other than membrane permeability, such as the chloroplast surface area, adjacent to the intercellular air space per unit of leaf area and cell wall thickness (Evans, 2021). Since 2014, more direct or indirect evidence accumulated, supporting the aquaporin-facilitated CO2 transportation, i.e., AtPIP2;5, SlPIP1;2 (from tomato), OsPIP1;2 and OsPIP1;3 (from rice), HvPIP2;1, 2;2, 2; 3, 2;5 (from Barley), ZmPIP1;5, 1;6 (from Maize), as well as SiPIP2; 7 from C4 plant-foxtail millet (see Table 1).

Recent studies have shown that the influence of altered expression of potential CO<sub>2</sub> permeable aquaporins on the mesophyII conductance and photosynthesis rate should be calibrated by growth and environmental conditions, as well as the oligomeric/phosphorylation status of the corresponding aquaporins. Although there are accumulated evidences for aquaporin-mediated CO<sub>2</sub> transportation, there have also been studies that have shown that simple manipulation of these aquaporins did not lead to changes in mesophyII conductance or photosynthetic efficiency. In one study, the knockout of three aquaporin genes-AtPIP1;2, AtPIP1;3, AtPIP2;6 from Arabidopsis thaliana did not result in changes in mesophyII conductance nor photosynthetic efficiency. The authors discussed possible reasons for these results: i) functional redundancy within aquaporin families; ii) the possible change in hydraulic conductance together with the higher light intensities (200  $\mu mol \; m^{-2} \; s^{-1})$  altered the photosynthetic capacity, which would be sufficient to remove the effect on both  $g_m$ and g<sub>s</sub>; iii) altered the hydraulic conductance of mutant lines through functional stimulation by colocalization of PIP1s and PIP2s on the plasma membrane (Kromdijk et al., 2020). However, the hydraulic conductance of mutant lines was not measured in the above study, which left this question to be further investigated. In another case, the ectopic expression of either AtPIP1;2 or AtPIP1;4 in tobacco did not further increase mesophyII conductance nor the rate of assimilation of CO<sub>2</sub>. Similarly, the authors pointed out the influence of plant growth and environmental conditions on the ability of certain CO<sub>2</sub> permeable aquaporins to alter mesophyII conductance, particularly, when a high basal gm was observed in control wild-type control plants (Clarke et al., 2022). This effect was also observed from rice PIPs (Huang et al., 2021) and tomato SiPIP1; 2 knockout mutants (Kelly et al., 2014), where  $g_m$  was affected only when grown in a CO<sub>2</sub> enriched environment. Other studies have pointed out that the oligomeric or phosphorylation state of overexpressed CO<sub>2</sub> permeable aquaporins can directly impact their function (Otto et al., 2010; Maurel et al., 2015; Groszmann et al., 2017). Additionally, aquaporins can act as signaling molecules, responding to different environmental stimuli and regulating stomatal dynamics in response to changes in ambient CO<sub>2</sub> concentration (Ding and Chaumont, 2020) or ABA-mediated biotic stress (Fang et al., 2019). Finally, one important aspect to consider is the relative humidity within the substomatal cavity, which was assumed to be saturated when calculating the intercellular CO<sub>2</sub> concentration determined by the gas exchange experiment (Cernusak et al., 2018). As recently investigated by Farquhar's group, the relative humidity within the substomatal cavity could drop down to around 80%, with the saturation edge retreating to the mesophyII cell walls. Surprisingly, the mesophyII conductance to  $CO_2$  remained less affected when alter the  $\Delta w$  (the difference between saturated humidity and the humidity in the air) if compared to uncorrected data, which might be controlled by the aquaporins within the mesophyII cell membranes (Wong et al., 2022). Although there are several aquaporins reported to function as both water and CO<sub>2</sub> channels, the detailed mechanism of such potential dual functions still needs to be investigated, which could be investigated with new methods such as in situ measurement of water potentials within leaves using the fluorescent powder-hydrogel nanoreporters (Jain et al., 2021), as well as cell specific overexpress experiment to avoid functional redundancy from endogenous aquaporins using plant leave single cell RNA sequence data base (Kim et al., 2021).

To conclude, the impact of changes in  $CO_2$  permeable aquaporins on mesophyll conductance and photosynthesis rate should be considered, with respect to growth and environmental conditions, in particular the relative humidity within the substomatal cavity, as well as the oligomeric and phosphorylation status of the corresponding aquaporins.

#### Molecular mechanism of aquaporinmediated CO<sub>2</sub> diffusion

Since the discovery of the CO<sub>2</sub> channel protein: aquaporin-1 from humans and NtAQP1 from tobacco, many aquaporins from different organisms were reported to mediate CO2 transport, covering many members from mammals, plants, microalgae, and fish (see Table 1). The family of aquaporins has a relatively conserved structure, with six membrane-spanning helices, two reentrant short helices with NPA motifs, and flexible N-/ C-termini heading towards the cytosol. The six bundle-like membrane-spanning alpha helices were tightly arranged in a circle, constituting the solute conduction pore/channel. Although aquaporins function as the water channel in monomers, they often form a quaternary tetramer assembly in native membranes and even large orthogonal arrays in the case of AQP4 (Ho et al., 2009). Until now, the physiological relevance of such a tetrameric assembly is not completely clear; however, a few cases showed that the central pore formed by the aquaporin tetramer was likely to be the  $CO_2$  channel. Early work based on X. laevis oocytes with low intrinsic CO2 permeabilities provided experimental evidence that AQP1 acts as a permeable CO<sub>2</sub> channel (Nakhoul et al., 1998). Later, a molecular simulation based on the high-resolution structure of AQP1 gave the atomic level of details that the central pore of the AQP1 tetramer could mediate fast CO<sub>2</sub> diffusion in low intrinsic CO<sub>2</sub>-permeable membranes (Hub and de Groot, 2006). This hypothesis was further demonstrated by the yeast protoplast system to determine the altered permeability of CO2 when the assembly of the artificial tetramer with a fixed ratio of NtPIP1;2 and NtPIP2;1, connected by a

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NIPIP2:1	AtPIP2:1 1	1 MAK DVEAVPGEGFQTRDYODPPPAPFIDGAEL	KKWSFYR 39
HMPP2:1         MA         DEVME TGGGDFAADY TD PPPAF LUDAAE LASKGLYR         41           HMPP2:1         MA         KD IE AAPGGE FSK SK DS OPPAF LUDAAE LASKGLYR         40           HMPP2:3         MA         KD IE AAPGGE FSK SK DS OPPAF LUDAE LASKGLYR         40           ZmPP1:6         61         AG IAEF IA FT FL FLY IS MUNKYKS         PSK GT VG I OG I AVA FGGM FA LVVC TA         11           HandPi SK GLAEF MA FT FL FLY IS MUNKYKS         PSK GT VG I OG I AVA FGGM FA LVVC TA         110           MACH         SK GLAEF MA FT FLY IS LVT MUKYKS         PSK GT VG I OG I AVA FGGM FA LVVC TA         110           JAPP1:2         SK GLAEF MA FT FLY IS LVT MUKYKS         PSK GT VG I OG I AVA FGGM FA LVVC TA         110           JAPP1:2         SK GLAEF VA FT FLY IS LLTVMQVKRS         SSK GT VG I OG I AVA FGGM FA LVVC TA         110           ZmPP1:5         SK GLAEF VA FT FLY IS LLTVMQVKRS         SSK GT VG I OG I AVA FGGM FA LVVC TA         110           ZmPP1:4         SK I AFY OT I FLY IS LLTVMQVKRS         SSK GT VG I OG I AVA FGGM FA LVVC TA         110           ZmPP1:4         SK I AFY OT I FLY I VI TV VI VI VK VKRS         SSK GT VG I OG I AVA FGGM FA LVVC TA         110           ZmPP1:4         I AVA FFGM FA LL FLY I TV TVI VY VKRS         SSK GT VG I AVA FGGM FA LVVC TA         110           ZmPP1:4         I AVA FGGM FA LF FLY TV TVI VY VKRG VFM			
Hump21         1         MA         NDIEAAPPGGEFSSIDYSDEPPARIEDOFEET TKKGLYR         40           HumpP23         1         MA         KDIEAAPPGGEYGAKDSSDEPPARIEDOFEET TKKGLYR         40           ZmiPirf, 6         1         AGIAEFVATFLELLYTVLTVMGVSKS         PSK GTVGI OG I AVA FGGMI FALVYCTA         114           ZmiPirf, 5         SG LAEFNATFLELLYTVLTVMGVSKS         PSK GTVGI OG I AVA FGGMI FALVYCTA         116           NAGP         54         AGIAEFNATFLELLYTVLTVMGVSKS         PSK GTVGI OG I AVA FGGMI FALVYCTA         116           SWIPIZ         52         AGIAEFNATFLELLYTVLTVMGVSKS         PNKGASGGI FALVYCTA         116           SWIPIZ         52         AGIAEFNATFLELLYTVLTVMGVSKS         PSK GTVGI OG I AVA FGGMI FALVYCTA         116           SWIPIZ         52         AGIAEFNATFLELLYTVLTVLTVVKYKS         SSK GTVGI OG I AVA FGGMI FALVYCTA         116           SWIPIZZ         40         LAEFNATLELFLYTVLTVVKYKS         SSK GTVGI OG I AVA FGGMI FALVYCTA         117           SWIPIZZ         40         LAEFNATLELFLYTVLTVVKYKS         SSK GTVGI OG I AVA FGGMI FALVYCTA         117           SWIPIZZ         40         LAEFNATLEFLYTVTVV I VYKNGSA         SSK GTVGI OG I AVA FGGMI FLVVCTA         117           SWIPIZZ         40         LAEFNATLEFLYTVTVV I VYKNGSA         SSWIPIZZ         104 </td <td></td> <td></td> <td></td>			
HypP2:3         1         MA         KD IEAAPPGGEYGAKD& SDEPEAELEDAE ELITYKELIY         VI         HI           ZmPP1:6         61         ACI AEF IATE LELIY TVLTVMØVKS.         PSK GTVGI OGI AWA FGGMI FALVYCTA         HI           MADP1:         56         ACI AEF IATE LELIY TVLTVMØVKS.         PSK GTVGI OGI AWA FGGMI FALVYCTA         HI           MADP1:         56         ACI AEF IATE LELIY TVLTVMØVKRS.         PSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           MADP1:         56         ACI AEF IATE LELIY TVLTVMØVKRS.         PSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         56         ACI AEF IATE LELIY TVLTVMØVKRS.         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         55         ACI AEF IATE LELIY IS LITYMØVKRS.         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         16         AEF ATTE LELIY IS LITYMØVKRS.         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         16         AEF ATTE LELIY ITVLI TVVKI VIKSS         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         16         AEF ATTE LELIY ITVLI TVVKI VIKSS         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI           APPI2:         16         AEF ATTE LELIY ITVLI TVVKI VIKSS         SSK GSTVGI OGI AWA FGGMI FALVYCTA         HI         HI         HI			
Hit         ZmPIPI16       611       GCI A EFVÄT F FLUY TVLTVMÖVSKS       PSK GGTVG I GGI AVA FGGMI FA LVVCTA 114         NAGP12       57       AGI A EFNÄT FLUY TVLTVMÖVSKS       PSK GGTVG I GGI AVA FGGMI FA LVVCTA 107         NAGP12       58       AGI A EFNÄT FLUY TVLTVMÖVSKS       PSK GGTVG I GGI AVA FGGMI FA LVVCTA 107         SIPP12       58       AGI A EFNÄT FLUY TVLTVMÖVSKS       PSK GGTVG I GGI AVA FGGMI FA LVVCTA 105         SIPP12       58       AGI A EFNÄT FLUY TVLTVMÖVSKS       SSK FGTVG I GGI AVA FGGMI FA LVVCTA 108         SIPP12       58       AGI A EFNÄT FLUY TVLTVMÖVSKS       SSK FGTVG I GGI AVA FGGMI FA LVVCTA 108         SIPP12       58       AGI A EFNÄT FLUY TVLTVI VVVVVVVAGCA       SSK FGTVG I GGI AVA FGGMI FLUVCTA 101         SIPP12       38       AL A EFNÄT FLUY TVLTVI VVVVVVGGA       SSK FGTVG I GGI AVA FGGMI FLUVCTA 101         SIPP22       40       VI A EFNÄT L FLUY TVLTVI VVVVVVGGA       SSK FGTVG I GGI AVA FGGMI FLUVCTA 101         SIPP22       41       VI A EFNÄT L FLUY TVLTVI VVVVVVGGA       SGV FGTVG I GGI AVA FGGMI FLUVCTA 101         PMPP23       41       VI A EFNÄT L FLUY TVLTVI VVVVVVGGA       SGV FGTGMI FA VTFVVVVVVVCVGA       SGV FGTGMI FA VTFVVVVVVVCVCC AVA FGTMA         SIPP23       41       VI A EFNÄT L FLUY TVLTVVVVVVVGC L GA V GGAV SVKA FGGN FVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV	HVPIP2, I I	NDTEAAFQGGEF3SKDT3DFFFAFTVDFEEL	TRVOLTR 40
2mPIP16       61       ACIAE INTELELYTVULTVMÖVSKS       PSK GTVG I GEIAWAFGGMI FALVYCTA       114         halppip1       57       ACIAE INTELELYTSUMTVMÖVKKS       PSK GTVG I GEIAWAFGGMI FALVYCTA       110         AMDP1       54       ACIAE MAIFELYTSUMTVMÖVKKS       PSK GSTVG I GEIAWAFGGMI FALVYCTA       100         AMDP1       54       ACIAE MAIFELYTTUTUTVMÖVKKS       PSK GSTVG I GEIAWAFGGMI FALVYCTA       100         2mPIP15       55       ACIAE VATELELYTSUTVTVVVVVVVVSS       PSK GSTVG I GEIAWAFGGMI FALVYCTA       100         2mPIP15       55       ACIAEVATELELYTSUTVTVUVVVVVVVVSS       PSK GSTVGI GEIAWAFGGMI FALVYCTA       100         2mPIP15       55       ACIAEVATELELYTSUTVTVUVVVVVVVVTGTGTOAS       PSPD2AGGVGU E I AWFGGMI FALVYCTA       100         40       AEEVATLELYTSUTVTVTVVVVVVVVTGTOTOAS       SOPDAGGVGU E I AWFGGMI FALVYCTA       100         40       AEEVATLELYTVTVTVTVVVVVVVVVVVTGTO COASAGAVVCI E I AWFGGMI FALVYCTA       100         41       AEEVATLELYTTVTVTVVVVVVVVTGTO COASAGAVVCI E I AWFGGMI FALVYCTA       100         41       AEEVATLELYTVTVTVVVVVVVVTGTO COASAGAVVCI E I AWFGGMI FALVYCTA       100         41       AEEVATLELYTTVTVTVVVVVVVVTGTO COASAGAVVCI E I AWFGGMI FALVYCTA       100         41       AEEVATLELYTTVTVTVVVVVVVVVTGTO COASAGAVVCI E I AWFGGMI FALVYCTA       100         <	HvPIP2;3 1	1 MA KD I EAAPPGGEYGAKDYSDPPPAPLFDAEEL	IKWSLYR 40
HalPPI;1 57 AG IAEE IATELE LY IS WITVIG VUKAPSK GOTVG I QG IAW FGGM FALVYCTA 10 AIPPI;2 53 AG IAEE IATELE LY ITUL TVM QVKRSPSK GS TVG I QG IAW FGGM FALVYCTA 10 SPIPI;2 53 AG IAEE IATELE LY ITUL TVM QVKRS			H1
HalPPI;1 57 AG IAEE IATELE LY IS WITVIG VUKAPSK GOTVG I QG IAW FGGM FALVYCTA 10 AIPPI;2 53 AG IAEE IATELE LY ITUL TVM QVKRSPSK GS TVG I QG IAW FGGM FALVYCTA 10 SPIPI;2 53 AG IAEE IATELE LY ITUL TVM QVKRS	7mDID1:6 61		
NAAP17: 54 AG LAELMATELELY ITULIVMOUKRS       DISLOSS GLOGIAWA FEGMI FALVYCTA 107         SIPP7: 25 AG LAELMATELELY ITULIVMOVKRS       NIKKS TVGVOGIAWA FEGMI FALVYCTA 105         SIPP7: 25 AG LAELMATELELY ITULIVMOVKRS       NIKKS TVGVOGIAWA FEGMI FALVYCTA 105         CAPP7: 55 AG LAELMATELELY ITULIVMOVKS       SIKKATVGIOGIAWA FEGMI FALVYCTA 108         CAPP7: 55 AG LAELWATELELY ITULIVMOVKS       SIKKATVGIOGIAWA FEGMI FALVYCTA 108         SIPP7: 40 AV LAELVATLELY ISILIVMOVKS       ASKGATVGIOGIAWA FEGMI FALVYCTA 108         SIPP7: 40 AV LAELVATLELY ITULIV IVKNOTSKAS       ASKGATVGIOGIAWA FEGMI FALVYCTA 108         SIPP7: 40 AV LAELVATLELY ITULIV IVKNOTSKAS       ASKGATVGIOGIAWA FEGMI FALVYCTA 104         APP7: 21 AL AELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 40 AV LAELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AL AELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AV LAELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AV LAELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AL AELVATLELY ITULIV IVKNOTSKAS       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AL AELVATLELY ITULIVIN IVKNOSCIAO ILAIWA FEGMI FALVYCTA 104       NEDVAGOVGIAU ILAIWA FEGMI FALVYCTA 104         APP7: 21 AL AELVATLELY ITULIVIN IVKNOSCIAO ILAIWA FEGMI FALVYCTA 107       NEDVA			
AIPIPI2:       25       AG LAEE IN ATELETY ITUL TWOKKRS	HaPIP1;1 5/	AGTAEFTATFLFLYTSVMTVMGVVKAPSKCQTVGTQGTAVAFGGMTF	ALVYCIA 110
SIPIPT:       25 AG LAEEMATELELY ITVUL TVMOYNON       TSK GTYGYOB LAWAFGGMI FALYYCTA 105         OEPIPT:       55 AG LAEEWATELELY ITVUL TVMOYNON       TSK GTYGYOB LAWAFGGMI FALYYCTA 105         OEPIPT:       55 AG LAEEWATELELY ISUL TVMOYNS       ASK GTYG I OB LAW FGGMI FALYYCTA 105         OEPIPT:       55 AG LAEEWATELELY ISUL TVMOYNS       ASK GTYG I OB LAW FGGMI FALYYCTA 105         MPIPZ:       14 AEEVATULELY ISUL TVMOYNS       ASK GTYG I DG LAW FGGMI FALYYCTA 104         MPIPZ:       14 AEEVATULELY ITVUTU IV INYK HGTDASAS SOPDAAG GOVGU LG LAW FGGMI FELYYCTA 104         MPIPZ:       14 AEEVATULELY ITVUTU IV INYK HGTDASASADAAG GOVGU LG LAW FGGMI FELYYCTA 104         MPIPZ:       14 AEEVATULELY ITVUTU IV INYK HGTDASASADAAG GOVGU LG LAW FGGMI FELYYCTA 104         MPIPZ:       14 NAEEVATULELY ITVUTU IV INYK HGTDASASADAAG GOVGU LG LAW FGGMI FELYYCTA 104         MPIPZ:       14 NAEEVATULELY ITVUTU IV INYK HGTDASASADAAG GOVGU LG LAW FGGMI FELYYCTA 104         MPIPZ:       14 NAEEVATULELY ITVUTU IV INYK HGTDASASADAAG GOVGU LG LAW FGGMI FELYYCTA 104         MAINAGTI 105 GG HINAYTFGL LLARKI SUTRAVY VVVUGU CLAAVGG AVK FGSAVKE FMAN FGLWI IVYCTA 104         MAINAGTI 105 GG HINAYTFGL LLARKI SUTRAVY VVVUGU CLAAVGG AVK FGSAVKE FMAN FGLWI IVYCTA 104         MAINAGTI 105 GG HINAYTFGL LLARKI SUTRAVY VVVUGU CLAAVGG AVK FGAVKE FMAN FGLWI IVYCTA 104         MAINAGTI 105 GG HINAYTFGL LLARKI SUTRAVY VVVUGU CLAAVGG AVK FGAVKE FMAN FGLWI IVYCTA 105         MIAPIPZ: <td< td=""><td></td><td></td><td></td></td<>			
SIPIP12:       24: AG LAEEMATFLETY TTVLTUVMGYSRA	AtPIP1;2 53	3 AGIAEFIATFLFLYITVLTVMGVKRSPNMCASVGIQGIAWAFGGMIF/	ALVYCTA 100
0 <i>cPiP1</i> : 2 5 AG I AE FMATF_LLY TXL TYMOVXSS			
ZmPP1;5       55       AG IA EF VAT FLEY IS LLTWØYNKS			
0 0 0 0 0 0 0 0 0 0 0 0 0 			
Hu/P/22         241         AL LAEEYANTLEFLYITAAT VI GYKHOTSASADP & ACYGYLGI AWA FGGMI FL VYCTTA 101           APIP27         40         AV AEEYANTLEFLYITAAT VI GYKHOTSASSOPDAA GCYG'GI LGI AWA FGGMI FL VYCTA 101           APIP27         40         AV AEEYANTLEFLYITAAT VI GYKHOTSASSOPDAA GCYG'GI LGI AWA FGGMI FV VYCTA 101           APIP27         40         AV AEEYANTLEFLYITVAT VI GYKHOTDPAVNSAADAA GCYG'LGI AWA FGGMI FV VYCTA 102           Hu/P23         41         AV EEYANTLEFLYITVAT VI GYKHOSDPAVNSAADAAG SCYG'LGI AWA FGGMI FV VYCTA 102           Hu/P23         41         VI AEEYANTLEFLYITVAT VI GYKHOSDPAVNSAADAAG SCYG'LGI AWA FGGMI FV VYCTA 102           TMPP13         14         VI AEEYANTLEFLYITVAT VI GYKHOSDPAVANSAADAAG SCYG'LGI AWA FGGMI FV VYCTA 102           TMPP23         41         VI AEEYANTLEFLYITVAT VI GYKHOSDPAVANSAADAAG SCYG'LGI AWA FGGMI FV VYCTA 102           TMPP13         15         SCHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKA MCGMO PY OLLBOGAN VV 168           GI SCGHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKA GYCA, PY OLBOGAN VV 168         SCHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKA GYCA, PY OLBOGANAV 170           AMPP13         16         SCGHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKA GYCA, PY OLBOGANAV 170           AMPP13         10         SCGHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKA GYCA, PY OLBOGANAV 170           AMPP13         10         SCGHINPAYTFGILLARKI SI TRAY FV WAOCLGA TCAGAVVKAG GYCA, PY OLBOGANAV 170<			
SIPIP27 40 AV I AEFVATLE FLY TIXATVI GYKHGTDASA-SGPDAA GOGYG ILGI AWAFGGMI FL VYCTA 101 MIPIP24 13 AA I AEFI ATLE FLY TIXATVI GYKHGSDVDANGDV GOGYG ILGI AWAFGGMI FV VYCTA 102 HVPIP25 42 AV I AEFVATLE FLY TIXATVI GYKHGSDVDANGDV GOGYG ILGI AWAFGGMI FV VYCTA 102 HVPIP25 42 AV I AEFVATLE FLY TIXATVI GYKHGSDVDANGDV GOGYG ILGI AWAFGGMI FV VYCTA 102 HVPIP23 41 AV I AEFVATLE FLY TIXATVI GYKHGSDVDANGDV GOGYG ILGI AWAFGGMI FV VYCTA 103 TITTATVI AEFVATLE FLY TIXATVI GYKHGSDVDANGDV GOGYG ILGI AWAFGGMI FV VYCTA 103 TITTATVI AEFVATLE FLY TIXATVI GYKHGSDVDA-A-SGVG ILGI AWAFGGMI FV VYCTA 103 TITTATVI AEFVATLE FLY TIXATVI GYKHGSDVDA-AG SGVG ILGI AWAFGGMI FV VYCTA 103 TITTATVI AEFVATLE FLY TIXATVI GYKHGSDVCAGAV GAGV KKA GGA-LYES AGGGMAV 176 HAPIP21 111 GI SGGHI NPAV TFG ILEARKLSI TRA YFYI VIWQCLGA CGAGV KKA GGA-V KG MGGO VL INGGNY VI 73 AINACH108 IS GGHI NPAV TFG ILEARKLSI TRA YFYI VIWQCLGA ICGAGV KKAFGGA FV CAGAG GGANV 170 GAPIP1 2106 GI SGGHI NPAV TFG ILEARKLSI TRA YFYI WWQCLGA ICGAGV KKAFGGA - LYES AGGGANV 170 GAPIP1 2106 GI SGGHI NPAV TFG ILEARKLSI TRA YFYI WWQCLGA ICGAGV KKAFGGA - LYES AGGGANV 170 GAPIP1 2106 GI SGGHI NPAV TFG ILEARKLSI TRA YFYI MWQCLGA ICGAGV KKAFGGA - LYENAGGGANV 170 GAPIP1 2106 GI SGGHI NPAV TFG ILEARKLSI TRA YFYIMWQCLGA ICGAGV KKAFGGA - LYENAGGGANV 170 GAPIP1 2106 GI SGHI NPAV TFG ILEARKLSI TRA YFYMMQCLGA ICGAGV KKAFGGA - LYENAGGGANN 170 GAPIP1 2106 GI SGHI NPAV TFG ILEARKV SU RA LIY WAGCAGI GGA GV KKAFGGA - LYENAGGGANN 170 GAPIP1 2108 GI SGHI NPAV TFG ILEARKV SU RA LIYMAQCGA ICGAGV KKAFGGA - LYENAGGGANN 170 GAPIP1 101 AVAGAG ICGAGV KKAFGGA - LYENAGGGANN 170 GAPIP1 101 AVAGAG ICGAGV KKAFGGA - LYENAGGGANN 170 GAPIP1 101 AVAGAG ICGAG IV GYENAGY MPIP2 101 GI SGHI NPAV TFG ILEARKV SU RA LIYMA ACCGA ICGA GV KKAFGGA - LYENAGGGANN 170 GAPIP1 101 AVAGAG ICGA I INFOLVINT FG ILARKV SU RA LIYMA ACCGA ICGA GV KKAFGGA - LYENAGGGANN 170 GAPIP1 101 AVAGY KGGA ICGAE V GYENAGY MPIP1 101 101 101 101 101 101 101 101 101 1			
AIPIP21       40       VI AEEVATLEFLYTVLTV IGVK IGSUTDAGGVDEGGVI LGIAWA FGGMI FLVVYCTA         MPIP23       40       ALEFIATLEFLYTVLTV IGVK MGDVDANGVCGGVI LGIAWA FGGMI FVLVYCTA         MHPP25       42       VI AEEVATLEFLYTVATV IGVK MGDVPAVNSAADAACGVV LGIAWA FGGMI FVLVYCTA         MHPP23       41       VI AEEVATLEFLYTVATV IGVK MGDVPAVNSAADAACGVV LGIAWA FGGMI FVLVYCTA       103         MHP23       41       VI AEEVATLEFLYTVATV IGVK MGDVAGAVGAAVGGAVGAVK GFMGEPOVLLNGGAN FVLVYCTA       103         MH0P13       41       IV       ISGGMI NAVTFGLEFLARK LSUTRAVY VVMQCLGAVGGAVK GFMGPOVLLNGGAN FVLVYCTA       103         MIAGP1105       ISGGMI NAVTFGLEFLARK LSUTRAVY VVMQCLGAVGGAVK GFMG-PVORL GGGANV       160       104       104         MIAPP12130       ISGGMI NAVTFGLEFLARK LSUTRAVY VVMQCLGAVGGAVK GFQG-LVETNGGAVK GFQGAL LWGN VGGAVK GFQG-LVETNGGANV       107         GAPP12100       ISGGMI NAVTFGLEFLARK LSUTRAVF MMMCLGAI GGAVK GFQG-LVETNGGGANV       107         GAPP12100       ISGGMI NAVTFGLEFLARK LSUTRAVF MMMCLGAI GGAVK GFQG-LVETNGGGANAV       107         GAPP12100       ISGGMI NAVTFGLEFLARK VSUKALLFMMM2 LGAI GGAVK GFQG-LVETNGGGANAV       107         GAPP12100       ISGGMI NAVTFGLEFLARK VSUKALLFMMM2 LGAI GGAVK GFQG-LVETNGGGANAV       107         GAPP12100       ISGGMI NAVTFGLEFLARK VSUKALLFMMM2 LGAI GGAVK GFQG-LVETNGGGANAV       108         GAPP12100       ISGGMI NAV	HvPIP2;2 41	1 ALIAEFVATLLFLYITVATVIGYKVQSA ADPCAGVGVLGIAWAFGGMIF	VLVYCTA 96
ALPIP2:1       40       AV   AE EYATLL FLYTULT VIETV IGYK IOSDTDAGGVDCGVG ULDIAM FGGMI FLUVYCTA         MPIP2:3       40       AL EFI ATLL FLYTUATV IGYK MGDVDAGCVCGVULDIAM FGGMI FLUVYCTA         MHPP2:3       41       VILAEFVATLL FLYTUATV IGYK MGDVPAVNSAADAACGVVULDIAM FGGMI FLUVYCTA         MHPP2:3       41       VILAEFVATLL FLYTUATV IGYK MGDVPAVNSAADAACGVVULDIAM FGGMI FLUVYCTA         MH       III       IIII         TMPP1:3       41       VILAEFVATLL FLYTUATV IGYK MGDVPAGPNAADAACSGVULDIAM FGGMI FLUVYCTA         MMGP1:10       GVSGCHINPAVTFGLELARK LSUTRAINV VVMOCLGAVGGAVWG FMGGPOVLDIAM FGGMI FLUVYCTA         MMGP1:10       GVSGCHINPAVTFGLELARK LSUTRAINV VVMOCLGAVGGAVWG FMG-PVORL GGGANV         SIPP1:2:10       GISGGMINPAVTFGLELARK LSUTRAINV VVMOCLGAVGGAVWG FGG-LVETT GGGANV         SIPP1:2:10       GISGGMINPAVTFGLELARK LSUTRAINV         SIPP1:2:10       GISGGMINPAVTFGLELARK LSUTRAINV         SIPP1:3:10       GISGGMINPAVTFGLELARK LSUTRAINV         SIPP1:3:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:2:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:3:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:3:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:2:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:2:10       GISGGMINPAVTFGLELARK SUTRAINV         SIPP1:2:10       GISGGMI	SiPIP2:7 40	AVIAE FVATLLFLY I TVA TVI GYKHQTDASA - SGPDAACGGVGI LGI AWA FGGMI F	ILVYCTA 101
NIPIP21         38         AI         AEE         I AT         I E V I VI T VI T VI T VI T VI T VI T VI			
HvPP22       42       VI AEE ITATLE LEYTIYATVI GYKHADDPAVNSADAACGGVGVLGIAWAFGGMI FVLVYCTA 102         HvPP23       41       VI AEEVATLE LEYTIYATVI GYKHADDPAGPNAADAACSGVGILGIAWAFGGMI FVLVYCTA 102         Hu       P2         ZmPIP1;6115       GVSGGHINPAVTFGLFLARKLSLTRA VYVVVQCLGAVCGAVVKAFGSA-LYESAGGANAV 176         HahPir;1111       GISGGHINPAVTFGLFLARKLSLTRA VYVVVQCLGAVCGAVVKAFGSA-LYESAGGANAV 176         JAPIP1;2105       GISGGHINPAVTFGLFLARKLSLTRA VYVVVQCLGAVCGAVVKAFGSA-LYESAGGANAV 176         JAPIP1;2105       GISGGHINPAVTFGLFLARKLSLTRA YVVVVQLGALGAVVKAFGSA-LYETK GGGAVVV         SIPIP1;2105       GISGGHINPAVTFGLFLARKLSLTRA YVVVVQLGALGAVCKAFGSA-LYETK GGGAVVV         SIPIP1;2105       GISGGHINPAVTFGLFLARKLSLTRA YVVVVQLGALGAVCKAG-LYETK GGGAVVV         ZmPIP1;2105       GISGGHINPAVTFGLFLARKLSLTRA YVVVVQLGALGAVCKAG-LYETK GGGAVV         SIPIP2;2102       GISGGHINPAVTFGLFLARKLSLTRA YVVVVQLGALGAVCKAG-LYETK GGGAVV         SIPIP2;2102       GISGGHINPAVTFGLFLARKVSLVRA LYMMADCLGAICGAVKGGAVCLUKAGASA-YV070         SIPIP2;2102       GISGGHINPAVTFGLFLARKVSLVRA LYMMADCLGAICGAVKGGAVCGAVKGFGSA-YW7NGGGANV 158         HvP12;3104       GSGGHINPAVTFGLFLARKVSLVRA LYMAADCLGAICGVLKAGSA-YVRYRGGANV 158         HvP12;3104       GSGHINPAVTFGLFLARKVSLVRA LYMAADCLGAICGVLKAGSA-YVRYR GGANSLE 164         HvP12;3104       GSGHINPAVTFGLFLARKVSLVRA LYMAADCLGAICGVLKAGSA-YVRYR GGANSLE 164         HvP12;3104        GSGHINPAVTFGLFLARK			
HyPP21 41 AV I AE EVATLLE LY ITVA TV IGYKHOSD PTV-NTTDA CSGVG I LGI AM FGGMI FV LYVCTA 102 HyPP23 41 AV I AE EVATLLE LY ITVA TV IGYKHOSD PAPNADAACS GVG I LGI AM FGGMI FV LYVCTA 103 TMACP1 103 GVGHI NPAVTFGL LARK LSI TRA IY WV MQCLGA VGA VV KA FGSA - LY ESA GGANA V 176 HaPP17 111 GI SGGHI NPAVTFGL LARK LSI TRA IY WW MQCLGA VGA VV KA FGSA - LY ESA GGANA V 176 HaPP17 111 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KA FGSA - LY ESA GGANA V 176 HAPP17 2107 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KGFQP - VARL EGA VKA FGYA VI B9 APP17 2107 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KGFQP - VARL EGA VKA FGYA VI B9 APP17 2107 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KGFQP - VET LGGA VV KGFQA VX FT GGA VV KGFQA VI TTG GEA VV KGFQ - VT TGGA VKA FGYA VI B9 APP17 2107 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KGFQG - LY MGA GGA VV 167 OSPIP17 2108 GI SGGHI NPAVTFGL FLARK LSI TRA IY WW MQCLGA VGA VV KGFQG - LY MGA GGA VV 167 OSPIP17 2109 GI SGGHI NPAVTFGL FLARK VSI LRA VY WI VI AQAACG GGA VV KGFQG - LY MGA GGA VV 170 OSPIP17 103 GI SGGHI NPAVTFGL FLARK VSI LRA VY MA MOLGA VK GGA S. YY TRY GGAN VI 168 APP12 103 GI SGGHI NPAVTFGL FLARK VSI LRA VY MA VI A A OCGA VK KGFQS - YV RY GGAN VI 168 APP12 103 GI SGGHI NPAVTFGL FLARK VSI LRA LY MAAOCLGA VK GGY FVA FGSA - YV RY GGAN VI 168 APP12 103 GV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY GY VA FGSA - YV RY GGAN VI 168 APP12 103 GV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY FVA FGSA - YV RY GGAN VI 168 APP12 104 GV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY GY VA FGSA - YV RY GGAN VI 168 APP12 105 AV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY GU VA FGSA - YV RY GGAN VI 168 APP12 104 GV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY GU VA FGSA - YV RY GGAN VI 168 APP12 105 AV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA VGY GU VA FGSA - YV RY GGAN VI 168 APP12 104 GV SGGHI NPAVTFGL FLARK VSI VRA LLY MAAOCLGA MCY ELV LAT LY LY TY SGA TO KANAON VY LA LY			
HypP2:3       41       VI AEEVATLLELYI ITVATV IĞYKHQADPAGPNAADAAĞ SGVGI LGI AWAFGGMI FVLVYCTA 103         H1       H2         ZmPP1:615       GVSGCHI NPAVTFGL FLARKLSI TRAVY VVVVQCLGAVGGAVVKGFMGGPQY OLLNGGANFV 176         HaPP1:1111       GISGGHI NPAVTFGL FLARKLSI TRAVY VVVQCLGAVGGAVVKGFMGGPQY OLLNGGANFV 178         SPIP1:2105       GISGGHI NPAVTFGL FLARKLSI TRAVY VVVQCLGA ICGAVVKGFMGGPQY OLLNGGANFV 170         SPIP1:2105       GISGGHI NPAVTFGL FLARKLSI TRAVY VVVQCLGA ICGAVVKGFQK-LYETTGGGANVV 170         ZmPP1:5105       GISGGHI NPAVTFGL FLARKLSI TRAVY VVVQCLGA ICGAVVKGFQK-LYETTGGGANVV 170         ZmPP1:5106       GISGGHI NPAVTFGL FLARKLSI TRAVY MVVQCLGA ICGAVVKGFQK-LYETTGGGANV 170         ZmPP1:5107       GISGGHI NPAVTFGL FLARKVSI VRA 1LWMVQCLGA ICGAVVKGFQK-LYETTGGGANV 170         MIP2:2195       GISGGHI NPAVTFGL FLARKVSI VRA 1LWMAQCLGA ICGAVKGFQKG-LYETTGGGANV 170         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVL VKGFGSA-YVRY GGANV 150         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVL VKGFSA-YVRY GGANTU 160         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVL VKGFSA-YVRY GGANTU 160         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVG VKA FGSA-YVRY GGANTU 160         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVG VKA FGSA-YVRY GGANTU 160         MIP2:110       GISGGHI NPAVTFGL FLARKVSI VRA 1LWAQACLGA ICGVG VKA FGSA-YVRY GGANTU 160			
H1 H2 DESCRIPTION OF THE SAGGGANAV 16 HaPIPI: 1111 GISGGH INPAVTFGL LARK LSLTRAVY VVVVQL GAV CGAVKAFCSA - LIESAGGGANAV 16 HAPIPI: 1016 GISGGH INPAVTFGL FLARK LSLTRAVY VVVVQL GAV CGAVKOFMGFOY OLL NGGANVV 16 AIPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY IVVVQL GAV CGA CGA 6VVKOFMYG - PY QRL GGANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY IVVVQL GAV CGA 6VKOFGYF - VGAL GGAANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY IVVVQL GAV CGA 6VKOFGYF - LFETK GGANAVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY MVVQL GAV CGA 6VKOFGYF - LFETK GGAANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY MVVQL GAV CGA 6VKOFGYF - LFETK GGAANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK LSLTRAVY MVVL CAGAG (CGA 6VKOFGYF - LFETK GGAANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK SLTRAVY MVVL CAGAG (CGA 6VKOFGYF - LFETK GGAANVV 170 CAPIPI: 2107 GISGGH INPAVTFGL FLARK SLTRAVY MVVL CAGAG (CGA 6VKOFGFG - LVMGS GGAANAV 170 HPIP2: 2103 GISGGH INPAVTFGL FLARKVSLVRA ILY MVADCLGA CGA 6VKOFGFG - LVMGS GGAANAV 170 HPIP2: 101 GISGGH INPAVTFGL FLARKVSLVRA ILY MADCLGA CGA 6VKOFGFG - VVRO GGANEV 163 SIPIP2: 102 GISGGH INPAVTFGL FLARKVSLVRA ILY MADCLGA CGA CGA 6VKOFG FG - VVRO GGANEV 163 HPIP2: 103 GVSGGH INPAVTFGL FLARKVSLVRA ILY ILACLGA CGV 6VKAFOSS - YVRO GGANEL 164 HPIP2: 103 GVSGGH INPAVTFGL FLARKVSLVRA ILY ILACLGA CGV 6LVKGFGSS - YVRO GGANEL 164 HPIP2: 103 GVSGGH INPAVTFGL FLARKVSLVRA ILY ILACLGA CGV 6LVKGFGSS - YVRO GGANEL 164 HPIP2: 103 AVSGGH INPAVTFGL FLARKVSLVRA ILY ILACLGA CGV 6LVKGFGSS - YVRO GGANEL 164 HPIP2: 104 AVKGD GLGAE VGTFVLVYTVFSA TDAKRARDSHVP I LAFL PI GFAVFLVHLATIP ITG 230 ZMPIP1: 111 ANGV TKGD GLGAE IVGTFVLVYTVFSA TDAKRARDSHVP I LAFL PI GFAVFLVHLATIP ITG 230 ZMPIP1: 111 ANGV TKGD GLGAE IVGTFVLVYTVFSA TDAKRARDSHVP I LAFL PI GFAVFLVHLATIP ITG 231 APP1: 2109 AHGY TKGD GLGAE IVGTFVLVYTVFSA TDAKRARDSHVP I LAFL PI GFAVFLVHLATIP ITG 232 ZMPIP1: 111 APG TKGD GLGAE IVGTFVLVYTVFSA TDAKRARDSHVP I LAFL PI GFAVFLVHLATIP ITG 232 ZMPIP1: 111 APG TKGD GLGAE IVGTFVLVYTVFSA TDAKRARDSHVPI LAFL PI GFAVFLVHLAT	HvPIP2;1 41	1 AVIAEFVATLLFLYITVATVIGYKHQSDPTV-NTTDAACSGVGILGIAWAFGGMIF	VLVYCTA 102
ZmPiP1:6115 GV SGGH INPAVTFGL LARK LSL TRAVYYVVMQCLGAV CGAGVVKAFGSA - LYESA GGANAV 176 HaPP1:1111 GI SGGH INPAVTFGL FLARK LSL TRAI YYMVMQCLGAI CGAGVVKAFGSA - LYESA GGANAV 176 HaPP1:2107 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVVKAFGWG - PY QRL GGANV 160 AIPP1:2107 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVVKAFGWG - PY QRL GGANV 170 JZmPiP1:5108 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVVKAFGWG - LYETT SGGANV 170 JZmPiP1:5108 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVVKAFGWG - LYETT SGGANV 170 JZmPiP1:5108 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVKAFGWG - LYETT SGGANV 170 JZmPiP1:2109 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVKAFGWG - LYETT SGGANV 170 JZmPiP1:2109 GI SGGH INPAVTFGL FLARK LSL TRAVY I VMQCLGAI CGAGVKAFGWG - LYMGS GGAANAV 170 JMPiP2:29 GI SGGH INPAVTFGL FLARK VSL IRAI LYMAQCLGAI CGAGVKAFGWG - YMGA QGAGMAV 170 JMPiP2:29 GI SGGH INPAVTFGL FLARK VSL IRAI LYMAQCLGAI CGAGVKAFGWG - YWR QGANSE LISI JMPiP2:100 GI SGGH INPAVTFGL FLARKVSL IRAI LY II AQCLGAI CGAGVKAFGSG - FY KY GGANSE LISI JMPiP2:100 GI SGGH INPAVTFGL FLARKVSL IRAI LY II AQCLGAI CGA CYKAFGSG - YWR YGGANY 1169 HuPiP2:5105 GI SGGH INPAVTFGL FLARKVSL VRA LLY MAQCLGAI CGA CYKAFGSG - YWR YGGANY 1169 HuPiP2:3104 GV SGGH INPAVTFGL FLARKVSL VRA LLY MAQCLGAI CGA CYKAFGSG - YWR YGGANE LI 41 HuPiP1:1174 ANGY TKGDGLGAE VYGT FVLYVY TSA TDAKR TARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 230 JMPiP1:100 HAGY TKGDGLGAE VYGT FVLYVY TSA TDAKR TARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 230 JMPiP1:100 HAGY TKGDGLGAE VGT FVLYVY TSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPiP1:101 HGY TKGDGLGAE IVGT FVLYVY TSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPiP1:101 HQY TKGDGLGAE IVGT FVLYVY TSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPIP1:101 HGY TKGDGLGAE IVGT FVLYVY TSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPIP1:101 HGY TKGDGLGAE IVGT FVLYVTY FSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPIP1:2180 AHGY TKGDGLGAE IVGT FVLYVTY FSA TDAKRARDSHYPI LAFL PI GFAVFL VHLAT IP ITG 233 JMPIP1:2180 AHGY TK	HvPIP2;3 41	1 <mark>AVIAEFVATLLFLYITVATVIG</mark> YKHQADPAGPNAADAA <mark>C</mark> SG <mark>VGILGIAWAFGGMIF</mark>	V <mark>LVYCTA</mark> 103
HapPri:1111 Gi SGGH INPAVTEGLE LARKLSLTRA I Y YMMOCL GA I CGA VVKGFMGCP V QLLINGGAN Y 137 MAQP108 GI SGGH INPAVTEGLE LARKLSLTRA YFY IVMOCL GA I CGA VVKGFMOC. PY QRL GGAN Y 167 OPPR: 2105 GI SGGH INPAVTEGLE LARKLSLTRAVFY IVMOCL GA I CGA VVKGFMOC. PY QRL GGAN Y 167 OPPR: 2106 GI SGGH INPAVTEGLE LARKLSLTRAVFY IVMOCL GA I CGA VVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKLSLTRAVFY IVMOCL GA I CGA VVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKLSLTRAVFY IVMOCL GA I CGA VVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKLSLTRAVFY IVMOCL GA I CGA VVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKSLTRAVFY MAMOCL GA I CGA VVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKVSLTRAVFY MAMOCL GA I CGA GVVKGFMOC. VMGGAGAN V 170 OPPR: 2106 GI SGGH INPAVTEGLE LARKVSLTRAVFY MAMOCL GA I CGA GVVKGFMOC. VMGGAGAN V 170 OPPR: 2107 GI SGGH INPAVTEGLE LARKVSLTPR LLY MAAOLC GA I CGA FVKAF GSS FVRY GGANST. 161 HVPP2: 101 GI SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA FVKAF GSS YFRY GGANST. 161 HVPP2: 102 GI SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA GV KAF GSS YFRY GGANE LI 164 HVPP2: 103 GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA GV KAF GSS YFRY GGANE LI 164 HVPP2: 103 GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA GV KAF GSS YFRY GGANE LI 164 HVPP2: 104 GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA GV KAF GSS YFRY GGANE LI 164 HVPP2: 105 AVG GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC GA I CGA GV KAF GSS YFVRY GGANE LI 164 HVPP2: 105 AVG GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC HALC GA I CGA VE KAF GSS YFVRY GGANE LI 164 HVPP2: 105 AVG GV SGGH INPAVTEGLE LARKVSL VRA LLY MAAOLC HALC GA I CGA VE KAF GSS YFVRY GGANE LI 164 HVPP2: 105 AVG GV SGGL GAE VG TFVLYTYFSA TDAKRARDSHVP I LAFL PI GFAVFL VHLATI PI TG 233 CMPP1: 104 AVG TKGDGL GAE I VG TFVLYTYFSA TDAKRARDSHVP I LAFL PI GFAVFL VHLATI PI TG 233 CMPP1: 105 ANGY TKGDGL GAE I VG TFVLYTYFSA TDAKRARDSHVP I LAFL PI GFAVFL VHLATI PI TG 233 CMPP1: 107 NHGY TKGDGL GAE I VG TFVLYTYFSA TDAKRARDSH		H1 H2	
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NMAQP1108 GI S GGH IN PAVTFGL FLARK LS LTRA I FY IVMOCL GA I CGA EVVK GFOPS - L FE TK GGAN VY 189 AIPIP1: 210 GI S GGH IN PAVTFGL FLARK LS LTRA LY FY IVMOCL GA I CGA EVVK GFOPS - L FE TK GGAN VY 197 OsPIP1: 210 GI S GGH IN PAVTFGL FLARK LS LTRA LY MWIACL GA I CGA EVVK GFOPS - L FE TK GGAN VY 197 OsPIP1: 310 GI S GGH IN PAVTFGL FLARK LS LTRA LY MWIACL GA I CGA EVVK GFOPS - L FE TK GGAN VY 107 OsPIP1: 310 GI S GGH IN PAVTFGL FLARK LS LTRA LY MWIACL GA I CGA EVVK GFOPS - L FE TK GGA GGA AV 170 OsPIP1: 310 GI S GGH IN PAVTFGL FLARK LS LTRA VY MACL GA I CGA EVVK GFOPS - L YMCS GGAAAV 170 OsPIP1: 310 GI S GGH IN PAVTFGL FLARK VS LY RA LY MAOCL GA I CGA EVVK GFOPS - L YMCS GGAAAV 170 OsPIP1: 310 GI S GGH IN PAVTFGL FLARK VS LY RA LLY MAOCL GA I CGA EVVK GFORS - YV RY GGGANE VI 63 SIPIP2: 100 GI S GGH IN PAVTFGL FLARK VS LY RA LLY MAOCL GA I CGA EVVK GFORS - YV RY GGGANE 1169 HVPIP2: 310 GI S GGH IN PAVTFGL FLARK VS LY RA LLY MAOCL GA I CGA EVVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LLY MAOCL GA I CGA EVVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LLY MAOCL GA I CGA EVVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LLY MAOCL GA I CGA EVVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LV MAOCL GA I CGA EVVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LV MAOCL GA I CGA EVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 GV S GGH IN PAVTFGL FLARK VS LV RA LV MAOCL GA I CGA EVK FFORS - YV RY GGGANE 1169 HVPIP2: 310 FA GGA EV TY FFOR TO AKR SARDS HVP I LAF LP I GFAVF LVHLAT I P I TG 230 ZMPIP1: 311 N FOYTK GO GL GA E I YT FV LY VY FSA TD AKR NARDS HVP I LAF LP I GFAVF LVHLAT I P I TG 230 ZMPIP1: 311 N FOYTK GO GL GA E I YT FV LY VY FSA TD AKR NARDS HVP I LAF LP I GFAVF LVHLAT I P I TG 230 ZMPIP1: 311 N FOYTK GO GL GA E I YT FV LY TY FSA TD AKR NARDS HVP I LAF LP I GFAVF LVHLAT I P I TG 230 ZMPIP1: 311 N FOYTK GO GL GA E I YT TY VY TSA TD AKR NARDS HVP I LAF LP I GFAVF LVHLAT I P I TG 23			
AIPIP12:107       GI S GGH IN PAVTFGL FLARK LS LTRAVY FI VMOCL GA I CGA GVVK GFORS - L FETK GGANVV 167         OSPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORS - L FETK GGANVV 170         OsPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORS - L YEAS GGANAV 170         OsPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:29       GI S GGH IN PAVTFGL FLARK LS LTRALY FY MMOCL GA I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:29       GI S GGH IN PAVTFGL FLARK VS LLRAVW 1VA GCA GG I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:100       GI S GGH IN PAVTFGL FLARK VS LLRAVW 1VA GCA GG I CGA GVVK GFORS - Y YRY GGGANEV 183         AIPIP2:100       GI S GGH IN PAVTFGL FLARK VS LVRA LLY VIA GCA GI CGA GVKK GFORS - Y YRY GGGANE L 164         HVP:2:5105       GI S GGH IN PAVTFGL FLARK VS LVRA LLY MVA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:103       GV S GGH IN PAVTFGL FLARK VS LVRA LLY MVA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:103       GV S GGH IN PAVTFGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:104       HAVTTGGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:105       GI S GGH INPAVTFGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 165         MIP:2:104       HAVTTGGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 165         MIP:2:10	HaPIP1;1 111	1 GISGGHINPAVTFGLFLARKLSLTRAIYYMVMQCLGAICGAGVVKGFMGGPQYQLLI	N <mark>GGAN</mark> FV 173
AIPIP12:107       GI S GGH IN PAVTFGL FLARK LS LTRAVY FI VMOCL GA I CGA GVVK GFORS - L FETK GGANVV 167         OSPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORS - L FETK GGANVV 170         OsPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORS - L YEAS GGANAV 170         OsPIP1:2109       GI S GGH IN PAVTFGL FLARK LS LTRAL FY MVMOCL GA I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:29       GI S GGH IN PAVTFGL FLARK LS LTRALY FY MMOCL GA I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:29       GI S GGH IN PAVTFGL FLARK VS LLRAVW 1VA GCA GG I CGA GVVK GFORG - L YMGS GGANAV 170         IMP:2:100       GI S GGH IN PAVTFGL FLARK VS LLRAVW 1VA GCA GG I CGA GVVK GFORS - Y YRY GGGANEV 183         AIPIP2:100       GI S GGH IN PAVTFGL FLARK VS LVRA LLY VIA GCA GI CGA GVKK GFORS - Y YRY GGGANE L 164         HVP:2:5105       GI S GGH IN PAVTFGL FLARK VS LVRA LLY MVA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:103       GV S GGH IN PAVTFGL FLARK VS LVRA LLY MVA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:103       GV S GGH IN PAVTFGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:104       HAVTTGGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 164         MIP:2:105       GI S GGH INPAVTFGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 165         MIP:2:104       HAVTTGGL FLARK VS LVRA LVY MA GCL GA I CGA GVKK GFORS - Y YRY GGGANE L 165         MIP:2:10	NtAQP1 108	3 GISGGHINPAVTFGLFLARKLSLTRAIFYIVMQCLGAICGAGVVKGFMVG-PYQRL	GGGANVV 169
SIPIP:12 106 G I SGGH INPAVTFGL FLARK LS LTRAVFY IVMOCLGA I CGA EVVKG FORS - LYE TK GGGANV V 170 CAPIP:1309 G I SGGH INPAVTFGL FLARK LS LTRAVFY MAOL GA I CGA EVVKG FORG - LY MGA GGGANV V 170 CAPIP:1309 G I SGGH INPAVTFGL FLARK LS LTRAVFY MAOL GA I CGA EVVKG FORG - LYMGA GGGANV V 170 CAPIP:1309 G I SGGH INPAVTFGL FLARK LS LTRAVFY MAOL GA I CGA EVVKG FORG - LYMGA GGGANV 180 SIPIP:27102 G I SGGH INPAVTFGL FLARK VS LYRA LYMA AC GA G I VGA IVKG FORG - LYMGA GGGANV 180 SIPIP:27102 G I SGGH INPAVTFGL FLARK VS LYRA LYMA AC GA G I VGA IVKG FORG - Y VRY GGGANE V 183 SIPIP:27102 G I SGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGYKA FORS - Y VRY GGGANV 189 SIPIP:27102 G I SGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGYKA FORS - Y VRY GGGANV 159 HPIP:25105 G I SGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGYKA FORS - Y VRY GGGANV 119 SIPIP:27103 G I SGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGYKA FORS - Y VRY GGGANE L 164 HVPIP:23104 G VSGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGYKA FORS - Y VRY GGGANE L 164 HVPIP:23104 G VSGGH INPAVTFGL FLARK VS LYRA LLY MA AC CG A I CYGY FA FORS - Y VRY GGGANE L 165 SIPIP:11174 ANCYTKGD CLGAE I I GTFV LYV TVFSA TDAKR TARDSHVP A LAFL P I GFAVF LVHLATI PI TG 230 HAPIPI:1174 ANCYTKGD CLGAE I I GTFV LYV TVFSA TDAKR SARDSHVP I LAFL P I GFAVF LVHLATI PI TG 231 SIPIP:2169 AHCYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL P I GFAVF LVHLATI PI TG 231 SIPIP:2169 AHCYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL P I GFAVF LVHLATI PI TG 231 SIPIP:2169 AHCYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL P I GFAVF LVHLATI PI TG 232 SIPIP:2169 AHCYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLATI PI TG 232 SIPIP:2169 AGYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLATI PI TG 232 SIPIP:2169 AGYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLATI PI TG 232 SIPIP:21169 AAGYTKG SOLGAE I I GTFV LYV TVFSA TDAKR SARDSHVP I LAFL PI GFAVF LVHLATI PI TG 232 SIPIP:21169 AAGYTKG SOLGAE I I GTFV LYV TVFSA TDAKR NARDSHVP I LAFL P			
CaPPE 12 109 GI SCGHI NPAVTFGL FLARK LS LTRALF KWVMOCLGA I CGA GVVK GFQG-L VET TGGGANVV 170 CaPPE 13 109 GI SCGHI NPAVTFGL FLARK LS LTRAV FYM MOCLGA I CGA GVVK GFQG-LMGS GGANAV 170 HVPP2 2 97 GI SCGHI NPAVTFGL FLARK LS LTRAV FYM MOCLGA I CGA GVVK GFQG-LMGS GGANAV 170 HVPP2 3 05 GI SCGHI NPAVTFGL FLARK VS LRAVKY IVA CCGA GVVK GFQG-LMGS GGANAV 170 HVPP2 100 GI SCGHI NPAVTFGL FLARK VS LRAVKY IVA CCGA I CGA GVVK GFQG-LMGS GGANAV 170 HVPP2 100 GI SCGHI NPAVTFGL FLARK VS LVRA LLYMA CCGA I CGA GVVK GFQG-VK FVK PGGA SS - YV RY GGGA SS 1 HVPP2 100 GI SCGHI NPAVTFGL FLARK VS LVRA LLYM VA CCGA I CGA GVVK GFQS - YV RY GGGA SS 1 HVPP2 100 GI SCGHI NPAVTFGL FLARK VS LVRA LLYM VA CCGA I CGA GVG VK GFQS - YV RY GGGA SS 1 HVPP2 100 GI SCGHI NPAVTFGL FLARK VS LVRA LLYM VA CCGA I CGA GVG VK GFQS - YV RY GGGA SS 1 HVPP2 100 GV SCGHI NPAVTFGL FLARK VS LVRA LLYM VA CCGA I CGA GVG VK GFQS - YV RY GGGA SS 1 HVPP2 100 GV SCGHI NPAVTFGL FLARK VS LVRA LLYM VA CCGA I CGA GVG VK GFQS - YV RY GGGA SS 1 HVPP2 100 HV TGD GL GA EV GTFV LVY TVFS A TDAKK TARDS HVP I LAFL PI GFAV FLVHLATTPI TG 29 HaPP1 117 NHQ YT KCDGL GA EI GTFV LVY TVFS A TDAKK SARDS HVP I LAFL PI GFAV FLVHLATTPI TG 20 APP19 117 NHQ YT KCDGL GA EI GTFV LVY TVFS A TDAKK SARDS HVP I LAFL PI GFAV FLVHLATTPI TG 23 APP19 12 110 AHQ YTK GDGL GA EI GTFV LVY TVFS A TDAKK SARDS HVP I LAFL PI GFAV FLVHLATTPI TG 23 APP19 12 111 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK SARDS HVP I LAFL PI GFAV FLVHLATTPI TG 23 APP19 12 111 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP I LAFL PI GFAV FLVHLATTPI TG 23 APP19 12 111 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP I LAFL PI GFAV FLVHLATTPI TG 23 APP19 12 111 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP LAFL PI GFAV FLVHLATTPI TG 22 APP19 12 11 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP LAFL PI GFAV FLVHLATTPI TG 22 APP19 12 11 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP LAFL PI GFAV FLVHLATTPI TG 22 APP19 12 11 AP GYTK GDGL GA EI GTFV LVY TVFS A TDAKK ARDS HVP LAFL PI GFAV FWHLATTPI TG 22 APP19 12 12 1 GN DAKS GAA I VN N			
2mPiP1;5109 G1 SGGH NPAVTFGL FLARK LS LTRA LFYMVMQC LGA I CGAĞV KG FGG - LYMGA GGGANAV 170 HvPiP2;2 97 G1 SGGH NPAVTFGL FLARK US LLARV FYMANQC LGA I CGAĞV KG FQG - LYMGS GGANAV 170 HvPiP2;2 97 G1 SGGH NPAVTFGL FLARK US LLARV SLVRA LLYMAQC LGA I CGVALVKG FQG - LYMGS GGANAV 178 SiPiP2;7102 G1 SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGA I CGVG FVKA FQS - FYVRY GGGANEV 163 NPiP2;1 98 G1 SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGA I CGVG FVKA FQS - YVRY GGGANEV 163 NPiP2;1 98 G1 SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGA I CGVG FVKA FQS - YVRY GGGANEV 164 HvPiP2;1 51 G1 SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGA I CGVG FVKA FQS - YVRY GGGANE L 164 HvPiP2;1 93 G1 SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGA I CGVG LVKA FQS - YVRY GGGANE L 164 HvPiP2;1 93 GV SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGAMC GVG LVKA FQS - YVRY GGGANE L 164 HvPiP2;1 103 GV SGGH NPAVTFGL FLARK VS LVRA LLYMAQC LGAMC GVG LVKA FQS - YVRY GGGANE L 165 UT TMAQU TO NHQYTK GDGL GAE VG TFV LVY VFS AT DAKR TARDS HVP LAFL P1 GFAV FLVHLAT I P1 TG 239 HaPIP1;1 174 ANGYTK GDGL GAE I GTFV LVY VFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 230 NIAQP1 170 NHGYTK GDGL GAE I GTFV LVY VFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 230 SIPIP1;21 180 AHGYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 233 ZmPIP1;5171 NP GYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 233 ZmPIP1;5171 NP GYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 233 ZmPIP1;5171 NP GYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 233 ZmPIP1;5171 NP GYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 233 ZmPIP1;5171 NP GYTK GDGL GAE I GTFV LVY TVFS AT DAKR ARDS HVP I LAFL P1 GFAV FLVHLAT I P1 TG 234 ZmPIP1;237 TG I NPARS LGAA I I GTFV LVY TVFS AT DPKRS ARDS HVP LAFL P1 GFAV FLVHLAT I P1 TG 234 ZmPIP1;237 TG I NPARS LGAA I I YNDY HY SAT DPKRS ARDS HVP LAFL P1 GFAV FWHLAT I P1 TG 224 HvPIP2;1520 TG AA G1 KG KG LAAE I GTFV LVY TVFS AT DPKRS ARDS HVP LAFL P1 GFAV FWHLA			
0.SPIP1: 1109 GI S GGH I NPAVTFGL FLARK IS L TRAV F I WAMOC LGA I CGA GV VCGFORG - LY MGS GGGA AV 170 HVPIP2: 20 GI S GGH I NPAVTFGL FLARK VS L VRA I LY MAA OC LGA I CGV AL VK GFOSG - FV VR YG GGANE V 183 AIPIP2: 100 GI S GGH I NPAVTFGL FLARK VS L VRA I LY MAA OC LGA I CGV GF VKA FGSS - Y VR YG GGANE V 183 AIPIP2: 100 GI S GGH I NPAVTFGL FLARK VS L VRA I LY MAA OC LGA I CGV GF VKA FGSS - Y VR YG GGANE V 169 HVPIP2: 105 GI S GGH I NPAVTFGL FLARK VS L VRA LLY II A OC LGA I CGV GF VKA FGSS - Y VR YG GGANE L 164 HVPIP2: 105 GI S GGH I NPAVTFGL FLARK VS L VRA LLY MAA OC LGA I CGV GL VKA FGSS - Y VR YG GGANE L 164 HVPIP2: 103 GV S GGH I NPAVTFGL FLARK VS L VRA LLY II A OC LGA I CGV GL VKA FGSS - Y VR YG GGANE L 164 HVPIP2: 103 GV S GGH I NPAVTFGL FLARK VS L VRA VLY I I A OC LGA I CGV GL VKA FGSS - Y VR YG GGANE L 164 HVPIP2: 104 GV S GGH I NPAVTFGL FLARK VS L VRA VLY I I A OC LGA I CGV GL VKA FGSS - Y VR YG GGANE L 164 HVPIP2: 105 H Y KGDGL GAE I V GTFV LVY T VFS A TDAKR NARDS HVP A LAFL PI GFAV F L VHLAT I PI TG 239 I MAPPI : 107 NH GY TK GDGL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 230 I MAPPI : 108 AH GY TK GDGL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 230 I MAPPI : 108 AH GY TK GDGL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 230 I MAPPI : 108 AH GY TK GDGL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 230 I MPIP2: 119 A OGY TK GDGL GAE I V GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 230 I MPIP2: 1108 A OGY I GGAL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 232 I MPIP2: 1108 A OGY I GGAL GAE I V GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 228 I MPIP2: 1108 A OGY I GGAL GAE I I GTFV LVY TY FS A TDAKR NARDS HVP I LAFL PI GFAV F L VHLAT I PI TG 228 I MPIP2: 1109 A OGY I GGAL GAE I V GTFV LVY TY FS A TDAKR NARDS HVP V LAFL PI GFAV F M VHLAT I PI TG 228 I MPIP2: 1217 T M PY TK GDGL GAE I V GTFV LVY TY FS			
HvPP2:2       97       GISGGHINPAVTFGLLLARKYSLVRAILYMAACCAGIVKGFUKA-VKGFUKA-YQANGGGANKV 168         SiPIP2:7       100       GISGGHINPAVTFGLFLARKYSLVRAILYMAACCAGAIGVALVKGFUKA-GSS-YVTRYGGGANSL         MIPP2:1       00       GISGGHINPAVTFGLFLARKYSLVRAILYMAACCAGAIGVALVKGFUKA-GSS-YVTRYGGGANKM         MIPP2:100       GISGGHINPAVTFGLFLARKYSLVRALLYMAACCAAIGVAFWAAGSS-YVTRYGGGANKM         MIPP2:100       GISGGHINPAVTFGLFLARKYSLVRALLYMAACCAAIGVAFWAAGSS-YVTRYGGGANEL         MIPP2:101       GVSGGHINPAVTFGLFLARKYSLVRALLYMAACCAAGUAGVAFWAAGSS-YVTRYGGGANEL         MIPP2:101       GVSGGHINPAVTFGLFLARKYSLVRALLYMAACCAAGVAFWAAGSS-YVTRYGGGANEL         MIPP2:101       GVSGGHINPAVTFGLFLARKYSLVRAVLYIIACCAGUAGVAFWAAGSS-YVTRYGGGANEL         MIADP1100       NAACPITARWYTGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPLALGFLPIGFAVFLVHLATIPITG         MAAPTITONHGYTKGDGLGAEI       GTFVLVYTVFSATDAKRARDSYVPLAFLPIGFAVFLVHLATIPITG         NAAPTITONHGYTKGDGLGAEI       GTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG         NAAPTITONHGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG       231         SIPIP1:111       NPYKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG       232         SIPIP1:111       NPYKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG       233         SIPIP1:111       NPYKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG       233         SIPIP1:1111       NPYKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPI			
SiPP2: 7102 GI SGGH I NPAVT FGL FLARKV SLVRA I LYMAA OC LGA I CGV GFVKA FQS - FYVRY GGANEV 183 AIPIP2: 198 GI SGGH I NPAVT FGL FLARKV SLVRA LLY I I AOC LGA I CGV GFVKA FQS - YY RRY GGAN SL 181 MPIP2: 198 GI SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGA I CGV GFVKA FQS - YY RRY GGAN TH 194 MPIP2: 100 GI SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN LL 186 MPIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN EL 186 MPIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN EL 186 MIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA VLY I I AOC LGA I CGV GFVKA FQS - YY RRY GGAN EL 186 MIAPPI: 117 SP GY TKGDGLGAE V GT FVLVY TVFS AT DAKR TARDSHVPA LAF P I GFAVFL VHLAT I PI TG 239 ANAPPI 170 NHGY TKGDGLGAE I GT FVLVY TVFS AT DAKR NARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 232 AIPIP1: 2169 AHGY TKGDGLGAE I GT FVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 234 MPIP2: 2159 AS GFS RG TA LGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 234 MPIP2: 2150 AS GFS RG TA LGAE I VG TFVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 1160 AAG HTKGV GLAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2150 AS GFS RG TA LGAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2157 AAGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2157 AAGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 227 MPIP2: 2157 AGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 228 MPIP2: 2157 AGY SKG TG LAAE I	OsPIP1;3 109	JGISGGHINPAVTFGLFLARKLSLTRAVFYMAMQCLGAICGAGVVKGFQRG-LYMGS	GGGANAV 170
SiPP2: 7102 GI SGGH I NPAVT FGL FLARKV SLVRA I LYMAA OC LGA I CGV GFVKA FQS - FYVRY GGANEV 183 AIPIP2: 198 GI SGGH I NPAVT FGL FLARKV SLVRA LLY I I AOC LGA I CGV GFVKA FQS - YY RRY GGAN SL 181 MPIP2: 198 GI SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGA I CGV GFVKA FQS - YY RRY GGAN TH 194 MPIP2: 100 GI SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN LL 186 MPIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN EL 186 MPIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA LLYMVA OC LGAMCGV GFVKA FQS - YY RRY GGAN EL 186 MIP2: 100 GV SGGH I NPAVT FGL FLARKV SLVRA VLY I I AOC LGA I CGV GFVKA FQS - YY RRY GGAN EL 186 MIAPPI: 117 SP GY TKGDGLGAE V GT FVLVY TVFS AT DAKR TARDSHVPA LAF P I GFAVFL VHLAT I PI TG 239 ANAPPI 170 NHGY TKGDGLGAE I GT FVLVY TVFS AT DAKR NARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 232 AIPIP1: 2169 AHGY TKGDGLGAE I GT FVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 233 CSPIP1: 2171 APGY TKGDGLGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 234 MPIP2: 2159 AS GFS RG TA LGAE I VG TFVLVY TVFS AT DAKRNARDSHVP I LAF LP I GFAVFL VHLAT I PI TG 234 MPIP2: 2150 AS GFS RG TA LGAE I VG TFVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 1160 AAG HTKGV GLAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2150 AS GFS RG TA LGAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2157 AAGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 224 MPIP2: 2157 AAGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 227 MPIP2: 2157 AGY SKG TG LAAE I I GT FVLVY TVFS AT DPKRSARDSHVP VLAF LP I GFAVFNWHLAT I PI TG 228 MPIP2: 2157 AGY SKG TG LAAE I	HvPIP2:2 97	7 GISGGHINPAVTFGLLLARKVSLLRAVMYIVAQCAGGIVGAGIVKGIMKD-AYQAN	GGGANMV 158
AIPIP2:1100       CISCGH INPAVTEGLE LARKVSL PRALLY I LACCLGA I COV GEVKA FQSA - Y MDRY GGGANSL 161         NIPIP2:1105       GISCGH INPAVTEGLE LARKVSL VRALLYMVA OCLGA LCOV GEVKA FQSA - Y MDRY GGGAN LL 164         HVPIP2:105       GISCGH INPAVTEGLE LARKVSL VRALLYMVA OCLGA I COV GEVKA FQSA - Y FVRY GGGANEL 164         HVPIP2:105       GISCGH INPAVTEGLE LARKVSL VRALLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 164         HVPIP2:105       GISCGH INPAVTEGLE LARKVSL VRALLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP1:210       GVSCGH INPAVTEGLE LARKVSL VRALVI I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP1:210       GVSCGH INPAVTEGLE LARKVSL VRAVLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP1:210       GVSCGH INPAVTEGLE LARKVSL VRAVLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP1:210       GVSCGH INPAVTEGLE LARKVSL VRAVLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP1:210       GVSCGH INPAVTEGLE LARKVSL VRAVLY I LACLGA I COV GEVKA FQSA - Y FVRY GGGANEL 165         TMAPIP2:105       GVSCGH INPAVTEGLE LARKVSL VRAVLY I LACLGA I COV GEVKAFQSA - Y VYR GGGANEL 165         TMPIP2:1105       GVSCGGA I I GTFVLVY TVFSA TDAKRNARDSHVP I LAF LP I GFAVEL VHLAT IPI TG 230         JPIP1:2110       GVKTKGDGLGAE I VGTFVLVY TVFSA TDAKRNARDSHVPI LAF LP I GFAVEL VHLAT IPI TG 233         JPIP1:2111       NPG Y TKGDGLGAE I VGTFVLVY TVFSA TDAKRNARDSHVPI LAF LP I GFAVEL VHLAT IPI TG 236         JPIP1:21111       NPG Y TKGDGLGAE I VGTFVLVY			
NIPIP2:1       96       GISGGHINPAVTFGLFLARKVSLIRALLYMVADCLGALGOVGLVKAFQSA-YFVRYGGGANVM 159         HvPIP2:103       GVSGGHINPAVTFGLFLARKVSLVRALLYMVADCLGALGOVGLVKAFQSA-YFVRYGGGANVL 169         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALLYMVADCLGALGOVGLVKAFQSA-YFVRYGGGANEL 164         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALCGALGOVGLVKAFQSA-YFVRYGGGANEL 164         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALCGAICGVGLVKAFQSA-FYVRYGGGANEL 164         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALCGAICGVGLVKAFQSA-FYVRYGGGANEL 164         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALCGAICGVGLVKAFQSA-FYVRYGGGANEL 164         HvPIP2:3104       GVSGGHINPAVTFGLFLARKVSLVRAVLYIIALCGAICGVGLVKAFQSA-FYVRYGGGANEL 164         HvPIP2:117       ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRADSHVPILAFLPIGFAFLVHLATIPITG 230         JNIP1:2171       ANGYTKGDGLGAEI IGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG 231         JNIP1:2171       APGYTKGDGLGAEI VGTFULVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHLATIPITG 233         JNPIP1:2171       APGYTKGDGLGAEI VGTFULVYTVFSATDAKRSADSHVPILAFLPIGFAVFLVHLATIPITG 234         JNPIP1:2171       APGYTKGDGLGAEI VGTFULVYTVFSATDAKRSADSHVPILAFLPIGFAVFLVHLATIPITG 233         JNPIP1:2171       APGYTKGDGLGAEI VGTFULVYTVFSATDPKRSADSHVPILAFLPIGFAVFLVHLATIPITG 234         JNPIP1:2171       APGYTKGDGLGAEI VGTFULVYTVFSATDPKRSADSHVPILAFLPIGFAVFLVHLATIPITG 234         JNPIP1:2171       APGYTGGGANCHVVVTYTYSATDPKRSADSHVPILAFLPIGF			
HvPiP2: 5105       GI S GGH I NPAVT FGL FLARKVSL VRA LL YMVA CCLGAMCGVGL VKAF COSA - YVRY GGAN TL 166         HvPiP2: 1103       GV S GGH I NPAVT FGL FLARKVSL I RALLY YI I ACCLGAT CGV GL VKAF COSA - YVVRY GGAN FL 164         JMPIP1: 1074       GV S GGH I NPAVT FGL FLARKVSL VRAVLY YI I ACCLGAT CGV GL VKAF COSA - YVVRY GGAN FL 165         JMAPPI 107       SP GY TK GDGL GAE VV GT FVL VY TV FSA TDAKR TARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 239         HaPIP1: 1174       AN GY TK GDGL GAE I V GT FVL VY TV FSA TDAKR SARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 232         AHPIP1: 2169       AH GY TK GDGL GAE I I GT FVL VY TV FSA TDAKR NARDS YVP I LAFL PI GFAVF LVHLAT I PI TG 231         SIPIP1: 717       AP GY TK GDGL GAE I I GT FVL VY TV FSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 233         SIPIP1: 717       AP GY TK GDGL GAE I I GT FVL VY TV FSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 233         OSPIP1: 2171       AP GY TK GDGL GAE I V GT FVL VY TV FSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 233         DAFIP1: 717       AP GY TK GDGL GAE I V GT FVL VY TV FSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 233         DAFIP1: 2171       AP GY TK GDGL GAE I V GT FVL VY TV FSA TDAKR NARDSHVP I LAFL PI GFAVF LVHLAT I PI TG 234         MPIP2: 164       A GY S GT GL AAE I I G TFVL VY TV FSA TDP KR SARDSHVP VL AFL PI GFAVF MVHLAT I PI TG 234         MPIP2: 164       A GY S GT GL AAE I I G TFVL VY TV FSA TDP KR SARDSHVP VL AFL PI GFAVF MVHLAT I PI TG 224         MIPIP2: 166       A GY S K GT GL AAE I I G TFVL VY TV FSA TDP			
HvPIP2:1103       GV SGGH I NPAVT FGL FLARKVSLI RALLY I I AQCLGA I CGVGLVKGFQSS - YYVRY GGANEL 184         HvPIP2:3104       GV SGGH I NPAVT FGL FLARKVSLVRAVLY I I AQCLGA I CGVGLVKGFQSA - FYVRY GGANEL 185         SmPIP1:6177       SP GY TKGDGLGAE VV GT FVLVY TV FSA TDAKR TARDSHVP LAFL P I GFAVF LVHLAT I P I TG 239         JamPiP1:7174       AN GY TKGDGLGAE I V GT FVLVY TV FSA TDAKR SARDSHVP I LAFL P I GFAVF LVHLAT I P I TG 230         AMPIP1:70       NHGY TKGDGLGAE I I GT FVLVY TV FSA TDAKR NARDS YVP I LAFL P I GFAVF LVHLAT I P I TG 231         SIPIP1:2169       AHGY TKGDGLGAE I I GT FVLVY TV FSA TDAKRNARDS YVP I LAFL P I GFAVF LVHLAT I P I TG 231         SIPIP1:2168       AHGY TKGDGLGAE I I GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 231         SIPIP1:2171       APG TK CDGLGAE I V GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 233         OsPIP1:2171       APG TK CDGLGAE I V GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 233         SomPIP1:2171       APG TK CDGLGAE I V GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 233         JSIPP2:164       AS TG ST GT GLAAE I V GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 234         MVPI2:2150       AS GFSR GT ALGAE I V GT FVLVY TV FSA TDAKRNARDS HVP I LAFL P I GFAVF LVHLAT I P I TG 234         MVPI2:2160       AS TG ST GT GLAAE I I GT FVLVY TV FSA TDAKRNARDS HVP V LAFL P I GFAVF MVHLAT I P I TG 224         MVPI2:1162       AG GS ST GT GLAAE I I GT FVLVY TV FSA TD KRSARDS HVP V LAFL P I GFAVF MVH			
HvPIP2;3104 GV SGGH I NPAVT FGL FLARKV SLVRAVLY I I AQCLGA I CGV GL VKG FQSA - FYVRY GGGANEL 165 H3 ZmPIP1;6177 SP GYTKGD GLGAE V GTF VLVY TV FSA TDAKR TARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 230 NAQP1170 NHGYTKGD GLGAE I GTF VLVY TV FSA TDAKR SARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 232 AIPIP1;2169 AHGYTKGD GLGAE I I GTF VLVY TV FSA TDAKR NARDSYVP I LAFL P I GFAVF L VHLAT I P I TG 232 AIPIP1;2169 AHGYTKGD GLGAE I I GTF VLVY TV FSA TDAKR NARDSYVP I LAFL P I GFAVF L VHLAT I P I TG 232 AIPIP1;2171 AP GYTKGD GLGAE I I GTF VLVY TV FSA TDAKR NARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 233 ZmPIP1;3171 NF GYTKGD GLGAE I VGTF I LVY TV FSA TDAKR NARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 233 ZmPIP1;5171 NF GYTKGD GLGAE I VGTF VLVY TV FSA TDAKR NARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 233 ZmPIP1;2171 NF GYTKGD GLGAE I VGTF VLVY TV FSA TDAKR SARDSHVP I LAFL P I GFAVF L VHLAT I P I TG 233 AVPIP2;2159 ÅS GFSRG TA LGAE I VGTF VLVY TV FSA TDAKR SARDSHVP VLAFL P I GFAVF L VHLAT I P I TG 233 HVPIP2;2169 ÅS GFSRG TA LGAE I VGTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAVF MVHLAT I P I TG 224 MIPIP2;160 ÅAGHT KGY GLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 HVPIP2;160 ÅAGHT KGY GLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 HVPIP2;165 AGYSKG TGLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 HVPIP2;166 SAGYSKG TGLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 225 HVPIP2;3166 SAGYSKG TGLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 226 HVPIP2;3166 SAGYSKG TGLAAE I I GTF VLVY TV FSA TDPKR SARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 226 HVPIP2;3217 GI NPARS LGAAI I FNKDR MDHWI FW GPF I GAAL AA VHQV VLAFL P I GFAV FMVHLAT I P I TG 227 HVPIP2;3217 GI NPARS LGAAI I YN TDOAMDHWI FW GPF I GAAL AA VHVV VLAFL P I FKSS - 226 GSPIP1;233 TG I NPARS LGAAI I YN NDAWDDHWI FW GPF I GAAL AA VHVV VLAFL P FKSS - 226 GSPIP1;234 TG I NPARS LGAAI I YN KEH AWDDHWI FW GPF I GAAL AA LAV VV VI R A I			<mark>GGGAN</mark> VM 159
H3         ZmPIP1;6 177 SP GY TKGDGLGAE IVGTFVLVYTVFSATDAKR TARDSHVPALAFL P IGFAVFLVHLATIP ITG 239         HaPIP1;1 174 ANGY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 236         NAOP1 170 NHGY TKGDGLGAE I IGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 231         SIPIP1;2:10 AHGY TKGDGLGAE I IGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 231         SIPIP1;2:11 AP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 233         OSPIP1;2:171 AP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 233         OSPIP1;2:171 AP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P IGFAVFLVHLATIP ITG 233         OSPIP1;2:171 AP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP VLAFL P I GFAVFLVHLATIP I TG 231         OSPIP1;2:171 AP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP VLAFL P I GFAVFLVHLATIP I TG 231         OSPIP1;2:171 AP GY TKGDGLGAE I VGTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 231         OSPIP1;2:162 ADGYS TG TGLAAE I VGTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222         HVPIP2;1:162 ADGYS TG TGLAAE I IGTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222         HPIP2;1:162 ADGYS KGT GLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222         HVPIP2;1:165 SAGYS KGT GLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222         HPIP2;2:165 SAGYS KGT GLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL	HvPIP2;5 105	5 <mark>GISGGHINPAVTFGLFLARKVSLVRALLY</mark> MVAQCLGAMCGV <mark>GLVKA</mark> FQSA-YFVRY	<mark>GGGAN</mark> VM 159 <mark>GGGAN</mark> TL 166
ZmPiP1;6 177 SP GY TKGDGLGAE VVGTFVLVYTVFSATDAKR TARDSHVPALAFLP I GFAVFLVHLATIP I TG 239 HaPiP1;1 174 ANGY TKGDGLGAE I VGTFVLVYTVFSATDAKRARDSHVP I LAFL P I GFAVFLVHLATIP I TG 236 MAQP1 170 NHGY TKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 231 SiPiP1;2 180 AHGY TKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 231 SiPiP1;2 188 AHGY TKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 231 SiPiP1;2 171 AP GY TKGDGLGAE I VGTFI LVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 233 OSPIP1;3 171 NP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 233 OSPIP1;3 171 NP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 233 OSPIP1;3 171 NP GY TKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVP I LAFL P I GFAVFLVHLATIP I TG 233 HVPIP2;1 162 AGGYSTGTGLAAE I VGTFVLVYTVFSATDAKRNARDSHVP VLAFL P I GFAVFLVHLATIP I TG 224 HVPIP2;1 162 AGGYSTGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 224 HVPIP2;1 163 AGFSRGTALGAE I VGTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222 HVPIP2;1 164 STGYSTGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222 HVPIP2;1 165 SAGYSKGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222 HVPIP2;1 165 SAGYSKGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 222 HVPIP2;1 165 SAGYSKGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 229 HVPIP2;1 165 SAGYSKGTGLAAE I GTFVLVYTVFSATDPKRSARDSHVPVLAFL P I GFAVFMVHLATIP I TG 229 HVPIP2;2 125 TG INPARSLGAAI I FNKDRÅWDDHVI FWGPF I GAALAA VYHQVVLR I P I FSSSHY SAG SIPIP1;2 231 TG INPARSLGAAI I FNKDRÅWDDHVI FWGPF I GAALAA VYHQVVLR I P I FSSS SIPIP1;2 231 TG INPARSLGAAI I FNKDRÅWDDHVI FWGPF I GAALAA VYHQVVLR I P FKSSS SIPIP1;2 231 TG INPARSLGAAI I FNKDRÅWDDHVI FWGPF I GAALAALAY VHQVVLR AI I P FKSSS SIPIP1;2 231 TG INPARSLGAAI I YNKKHAWDDHVI FWGPF I GAALAALAA VHQVVLR AI I P FKSSS SISSSN 284 HVPIP2;2 222 TG INPARSLGAAI I YNKKHAWDDHVI FWGPF I GAALAALAA VHQVVLR AI I P FKSSS - 286 SIPIP1;2 231 TG INPARSLGA	HvPIP2;1 103	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVAQCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIAQCLGAICGVGLVKGFQSS-YYVRY	GGGANVM 159 GGGANTL 166 GGGAN <mark>EL 16</mark> 4
HaPIP1;1 114 AN BY TK GOGLGAET VGTY LVY TV FSA TDAK RSARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 236 NAQP1 170 NH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSYVP I LAF LP I GFAV FLVHLAT I P I TG 231 SIPIP1;2 169 AH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 231 SIPIP1;2 168 AH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 ZMPIP1;2 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 ZMPIP1;2 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 OSPIP1;3 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 OSPIP1;3 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 I VPIP2;2 159 ÅS GFSR GTALGAET V GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 HVPIP2;1 162 AD GYS TG TGLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 I VPIP2;1 162 AD GYS TG TGLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 HVPIP2;1 163 AA GYK GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 226 HVPIP2;1 165 SA GYS KGT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 227 HVPIP2;1 165 SA GYS KGT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 227 HVPIP2;1 163 SA GYS GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 228 HVPIP2;2 165 SA GYS GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 228 HVPIP2;2 123 TG I NPARS LGAAI I Y NN HM W WY WF GP FI GAALAA V Y HQV V LRA I P FK SS	HvPIP2;1 103	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVAQCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIAQCLGAICGVGLVKGFQSS-YYVRY	GGGANVM 159 GGGANTL 166 GGGAN <mark>EL 16</mark> 4
HaPIP1;1 114 AN BY TK GOGLGAET VGTY LVY TV FSA TDAK RSARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 236 NAQP1 170 NH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSYVP I LAF LP I GFAV FLVHLAT I P I TG 231 SIPIP1;2 169 AH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 231 SIPIP1;2 168 AH GY TK GOGLGAET I GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 ZMPIP1;2 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 ZMPIP1;2 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 OSPIP1;3 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 OSPIP1;3 171 NP GY TK GOGLGAET V GTFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 233 I VPIP2;2 159 ÅS GFSR GTALGAET V GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 HVPIP2;1 162 AD GYS TG TGLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 I VPIP2;1 162 AD GYS TG TGLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 224 HVPIP2;1 163 AA GYK GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 226 HVPIP2;1 165 SA GYS KGT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 227 HVPIP2;1 165 SA GYS KGT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 227 HVPIP2;1 163 SA GYS GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 228 HVPIP2;2 165 SA GYS GT GLAAET I GTFV LVY TV FSA TDPK RSARDSHVP V LAF LP I GFAV FMVHLAT I P I TG 228 HVPIP2;2 123 TG I NPARS LGAAI I Y NN HM W WY WF GP FI GAALAA V Y HQV V LRA I P FK SS	HvPIP2;1 103	5 G I SGGH I NPAVTFGL FLARKVSLVRA LLYMVAOCLGAMCGVGLVKA FQSA - YFVRY 3 GVSGGH I NPAVTFGL FLARKVSL I RALLY I I AOCLGA I CGVGLVKGFQSS - YFVRY 4 GVSGGH I NPAVTFGL FLARKVSLVRAVLY I I AOCLGA I CGVGLVKGFQSA - FYVRYI	GGGANVM 159 GGGANTL 166 GGGAN <mark>EL 16</mark> 4
NAOP1 170 NHEY TK GOCLGAEI I GTFVLVYTVFSA TDAKRNARDSYVPILAFLP I GFAVFLVHLATIPITG 220 AIPIP12 168 AHGYTKGOCLGAEI I GTFVLVYTVFSA TDAKRNARDSHVPILAFLP I GFAVFLVHLATIPITG 230 OSPIP12 171 APGYTKGOCLGAEI VGTFLVVYTVFSA TDAKRNARDSHVPILAFLP I GFAVFLVHLATIPITG 233 ZmPIP15 171 NPGYTKGOCLGAEI VGTFLVVYTVFSA TDAKRNARDSHVPILAFLP I GFAVFLVHLATIPITG 233 OSPIP13 171 NPGYTKGOCLGAEI VGTFVLVYTVFSA TDAKRNARDSHVPILAFLP I GFAVFLVHLATIPITG 233 AVPIP22 159 ASGFSRGTALGAEI VGTFVLVYTVFSA TDAKRNARDSHVPILAFLP I GFAVFLVHLATIPITG 233 HVPIP22 159 ASGFSRGTALGAEI VGTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFLVHLATIPITG 234 HVPIP22 164 ADGYSTGTGLAAEI VGTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 224 HVPIP21 162 ADGYSTGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 224 HVPIP25 164 STGYSTGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 224 HVPIP25 165 ASGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 229 HVPIP25 166 SAGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 229 HVPIP25 1162 ADGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 229 HVPIP25 1163 SAGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 229 HVPIP25 1163 SAGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 229 HVPIP25 1163 SAGYSKGTGLAAEI I GTFVLVYTVFSA TDPKRSARDSHVPVLAFLP I GFAVFMVHLATIPITG 228 H44LoopD	<i>HvPIP2;1</i> 103 <i>HvPIP2;3</i> 104	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVADCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIADCLGAICGVGLVKGFQSS-YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIADCLGAICGVGLVKGFQSA-FYVRY H3	GGGANVM 159 GGGANTL 166 GGGANEL 164 GGGANEL 165
AIPIP12: 169 AHGYTKGSCLGAEI I GTFVLVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 231 SIPIP1: 2168 AHGYTKGDCLGAEI VGTFILVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 233 ZmPIP1: 5171 NPGYTKGDCLGAEI VGTFILVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 233 ZmPIP1: 5171 NPGYTKGDCLGAEI VGTFULVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 233 SMPIP1: 2159 ASGFSRTALGAEI VGTFVLVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 233 JMPIP2: 2159 ASGFSRTALGAEI VGTFVLVYTVFSATDAKRNARDSHVPILAFLPI GFAVFLVHLATIPITG 231 SIPIP2: 7164 STGYSTGTGLAAEI VGTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 221 SIPIP2: 7164 STGYSTGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 222 HVPIP2: 1162 ADGYSTGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 222 HVPIP2: 5167 AAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 222 HVPIP2: 5167 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 222 HVPIP2: 3166 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 228 HVPIP2: 3166 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPI GFAVFLVHLATIPITG 228 HVPIP2: 231 TGI NPARSLGAAI I YNNDAWDHWI FWGPFI GAALAALYHQVVLRFLPI FKSSS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177	5 G I SGGH I NPAVTFGL FLARKVSLVRA LLYMVAOCLGAMCGVGLVKA FQSA - YFVRY 3 GVSGGH I NPAVTFGL FLARKVSLI RALLY I I AQCLGA I CGVGLVKGFQSS - YFVRY 4 GVSGGH I NPAVTFGL FLARKVSLVRAVLY I I AQCLGA I CGVGLVKGFQSA - FYVRY H3 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLP I GFAVFLVHL/	GGGANVM 159 GGGANTL 166 GGGANEL 164 GGGANEL 165 ATIPITG 239
SIPIP1:2 168 AH GY TK GO GLGAE I IGT FULVY TV FSA TDAK RNARDSHVP I LAFL P IGFAV FLVHLAT IP ITG 230 OSPIP1:2 171 AP GY TK GO GLGAE I VGT FLLVY TV FSA TDAK RNARDSHVP I LAFL P IGFAV FLVHLAT IP ITG 233 OSPIP1:3 171 NP GY TK GO GLGAE I VGT FULVY TV FSA TDAK RSARDSHVP I LAFL P IGFAV FLVHLAT IP ITG 233 OSPIP1:3 171 NP GY TK GO GLGAE I VGT FULVY TV FSA TDAK RSARDSHVP I LAFL P IGFAV FLVHLAT IP ITG 233 OSPIP1:3 171 NP GY TK GO GLGAE I VGT FULVY TV FSA TDAK RSARDSHVP I LAFL P IGFAV FLVHLAT IP ITG 233 HVPIP2:1 58 AS GFSR GT ALGAE I VGT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FLVHLAT IP ITG 224 AVENDEX:1 100 AG HT KOY ST GT GLAAE I VGT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP ITG 224 HVPIP2:1 162 AD GY ST GT GLAAE I I GT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP I TG 224 HVPIP2:1 163 AA GH KOY GLAAE I I GT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP I TG 224 HVPIP2:1 165 SA GY SKGT GLAAE I I GT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP I TG 227 HVPIP2:3 166 SA GY SKGT GLAAE I I GT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP I TG 227 HVPIP2:3 167 SA GY SKGT GLAAE I I GT FULVY TV FSA TDP KRSARDSHVP VLAFL P I GFAV FMVHLAT IP I TG 228 H4 TO T - 1 COOPD H5 ZMPIP1:2 323 TG I NPARS LGAA I I FM KDR WDDHWI FW GP FI GAA LAA VYHQV VLRA I P FK SSAHY 290 NLAQP1 233 TG I NPARS LGAA I I FM KDR WDDHWI FW GP FI GAA LAA VYHQV VLRA I P FK SS 200 NLAQP1 233 TG I NPARS LGAA I I FM KDR WDDHWI FW GP FI GAA LAA VYHQV VLRA I P FK SS 287 AIPIP1:2 324 TG I NPARS LGAA I I FM KDR WDDHWI FW GP FI GAA LAA LYHVV VL I RA I P FK SS 288 ZMPIP1:2 324 TG I NPARS LGAA I I YN KCHAWDDHWI FW GP FI GAA LAA LYHVV VL I RA I P FK SS 288 ZMPIP1:2 324 TG I NPARS LGAA I I YN KCHAWDDHWI FW GP FI GAA LAA LYHQV I I RA I P FK SS 288 ZMPIP1:2 324 TG I NPARS LGAA I I YN KKHAWDDHWI FW GP FI GAA LAA LYHQV I I RA I P FK SS 288 ZMPIP1:2 324 TG I NPARS LGAA I I YN KKHAWDDHWI FW GP FI GAA LAA LYHQV I I RA I P FK SS 288 ZMPIP1:2 324 TG I NPARS LGAA I I YN KK	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVAOCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFQSS-YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFQSA-FYVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/	GGGANVM 159 GGGANTL 166 GGGANEL 164 GGGANEL 165 ATIPITG 238 ATIPITG 236
0. <i>SPIP</i> 1:2 111 AP 6Y TK GDGLGAE I VGTF I LVYTV FSA TDAK RNARDSHVP I LAFL P I GFAV FLVHLAT I P I TG 233 <i>ZmPIP</i> 1:5 171 NP 6Y TK GDGLGAE I VGTFV LVYTV FSA TDAK RNARDSHVP I LAFL P I GFAV FLVHLAT I P I TG 233 <i>HVPIP</i> 2:2 159 AS GFSR GTALGAE I VGTFV LVYTV FSA TDPK RSARDSHVP I LAFL P I GFAV FLVHLAT I P I TG 233 <i>HVPIP</i> 2:2 159 AS GFSR GTALGAE I VGTFV LVYTV FSA TDPK RSARDSHVP I LAFL P I GFAV FMVHLAT I P I TG 233 <i>HVPIP</i> 2:1 162 AD 6YS TG TGLAAE I VGTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 <i>HVPIP</i> 2:1 162 AD 6YS TG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 <i>HVPIP</i> 2:1 160 AA GH TKGV GLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 224 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 229 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 229 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 229 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 229 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 229 <i>HVPIP</i> 2:1 165 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVP VLAFL P I GFAV FMVHLAT I P I TG 227 <i>HVPIP</i> 2:3 166 SAGYSKG TGLAAE I I GTFV LVYTV FSA TDPK RSARDSHVV LAFL P I GFAV FMVHLAT I P I TG 228 <i>HVPIP</i> 2:3 23 TG I NPARS LGAAI I YDNPHGWHGHWI FW GP F I GAALAA VYVLAFL P I FKSS SAHY 260 <i>NIAQP1</i> 233 TG I NPARS LGAAI I YDNDAWDDHWI FW GP F I GAALAA LAY VVV LRA I P FKSS S 45 <i>SIPIP</i> 1:2 232 TG I NPARS LGAAI I YN KCHAWDDHWI FW GP F I GAALAAL Z YHVV V I RA I P FKSS S	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVADCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFQSS-YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFQSSA-FYVRY H3 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSYVPILAFLPIGFAVFLVHL/	GGGANVM 158 GGGANTL 166 GGGANEL 164 GGGANEL 165 ATIPITG 238 ATIPITG 238 ATIPITG 232
ZmPiPi;5:11       NP GY TK GD GL GAE I VG TFV LVY TV FSA TD AK RS ARD SHVP I LAFL PIGFAV FLVHLAT I PITG       233         OsPiPi;3:17:       INP GY TK GD GL GAE I VG TFV LVY TV FSA TD AK RNARD SHVP I LAFL PIGFAV FLVHLAT I PITG       233         OSPIPi;3:17:       INF GY TK GD GL GAE I VG TFV LVY TV FSA TD AK RNARD SHVP VLAFL PIGFAV FLVHLAT I PITG       221         SiPiPi2:7:       164       ST GY ST GT GL AAE I VG TFV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       222         AlPiPi2:1:       162       AD GY ST GT GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       222         HvPiP2:5:       167       AAG YS KG T GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       222         HvPiP2:5:       167       AAG YS KG T GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       222         HvPiP2:3:       166       SAG YS KG T GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       228         MVPIP2:1:       165       SAG YS KG T GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       228         MVPIP2:1:       16       SAG YS KG T GL AAE I I GT FV LVY TV FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       228         CmPIP1:2:       16       FL V VT V FSA TD PK RSARD SHVP VLAFL PIGFAV FMVHLAT I PITG       228         ZmPIP1:2:       16       NT V VT FSA TD PK RSARD SHVP VLAFL PIGFAV FM	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVAQCLGAMCGVGLVKAFQSS-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIAQCLGATCGVGLVKGFQSS-YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIAQCLGATCGVGLVKGFQSS-YFVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/	GGGANVM 158 GGGANTL 166 GGGANEL 164 GGGANEL 166 ATIPITG 236 ATIPITG 236 ATIPITG 237
0 <i>sPiP1</i> :3 111 NF 9Y TK GOCLGAE I VG TFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 231 <i>HVPIP2</i> :2 159 AS GFSR GT ALGAE I VG TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 221 <i>SIPIP2</i> :7 164 S TGYS TG TG LAAE I I GTFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 226 <i>AIPIP2</i> :1 162 AD GYS TG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 222 <i>HVPIP2</i> :1 160 AA GH TK OV GLAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 222 <i>HVPIP2</i> :1 163 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 229 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 229 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 227 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 228 <i>H4</i>	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169 SIPIP1;2 168	5 GISGGH I NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGGH I NPAVTFGL FLARKVSL I RALLY I I A OCLGA I CGVGLVKGFOSS - YFVRY 4 GVSGGH I NPAVTFGL FLARKVSLVRAVLY I A OCLGA I CGVGLVKGFOSA - FYVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKR TARDSHVPA LAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAEI VGTFVLVYTVFSATDAKR SARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSYVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/	GGGANVM 155 GGGANTL 166 GGGANEL 164 GGGANEL 164 ATIPITG 235 ATIPITG 235 ATIPITG 237 ATIPITG 237
0 <i>sPiP1</i> :3 111 NF 9Y TK GOCLGAE I VG TFV LVY TV FSA TDAK RNARDSHVP I LAF LP I GFAV FLVHLAT I P I TG 231 <i>HVPIP2</i> :2 159 AS GFSR GT ALGAE I VG TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 221 <i>SIPIP2</i> :7 164 S TGYS TG TG LAAE I I GTFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 226 <i>AIPIP2</i> :1 162 AD GYS TG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 222 <i>HVPIP2</i> :1 160 AA GH TK OV GLAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 222 <i>HVPIP2</i> :1 163 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 229 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 229 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 227 <i>HVPIP2</i> :1 165 SA GYS KG TG LAAE I I G TFV LVY TV FSA TDPKRSARDSHVP VLAF LP I GFAV FMVHLAT I P I TG 228 <i>H4</i>	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169 SIPIP1;2 168 OsPIP1;2 171	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVADCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFQSS-YVRYY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFQSA-FYVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/	GGGANVM 155 GGGANTL 166 GGGANEL 164 GGGANEL 166 GGGANEL 165 ATIPITG 235 ATIPITG 235 ATIPITG 233 ATIPITG 233 ATIPITG 233
HvPIP2:2159       AS GFSRGTALGAEIVGTFVLVYTVFSATDPKRSARDSHVPVLAFL       LP I GFAVFMVHLATIPITG       221         SIPIP2:7164       STGYSTGTGLAAEIVGTFVLVYTVFSATDPKRSARDSHVPVLAFL       LP I GFAVFMVHLATIPITG       222         AIPIP2:162       ACGYSTGTGLAAEI       I GTFVLVYTVFSATDPKRSARDSHVPVLAFL       LP I GFAVFMVHLATIPITG       222         HVPIP2:1610       AAGHTKGVGLAAEI       I GTFVLVYTVFSATDPKRSARDSHVPVLAFL       LP I GFAVFMVHLATIPITG       222         HVPIP2:1615       SAGYSKGTGLAAEI       I GTFVLVYTVFSATDPKRSARDSHVPVLAFL       LP I GFAVFMVHLATIPITG       222         HVPIP2:165       SAGYSKGTGLAAEI       I GTFVLVYTVFSATDPKRSARDSHIPVLAFL       LP I GFAVFMVHLATIPITG       222         HVPIP2:3165       SAGYSKGTGLAAEI       I GTFVLVYTVFSATDPKRSARDSHIPVLAFL       LP I GFAVFMVHLATIPITG       222         MVPIP2:3165       SAGYSKGTGLAAEI       I GTFVLVYTVFSATDPKRSARDSHIPVLAFL       LP I GFAVFMVHLATIPITG       228         ZmPIP1:5231       TG INPARSLGAAII YDNPHGWHGHWI FW GPFIGAALAALAAV YHQVVLAFL       LP I GFAVFMVHLATIPITG       228         MUP12:2       TG INPARSLGAAII FNKDRAWDDHWI FW GPFIGAALAALAY HQVVLAFL       LP I GFAVFMVHLATIPITG       228         ZmPIP1:5231       TG INPARSLGAAII YDNPHGWHGHWI FW GPFIGAALAALYHQVVLAFL       LP FKSS       286         SIPIP1:2231       TG INPARSLGAAII YNKEHAWDDHWI FW GPFIGAALAALYHQVVI RAIPFKSRS       286	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169 SIPIP1;2 168 OsPIP1;2 171	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVADCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFQSS-YVRYY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFQSA-FYVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFILVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/	GGGANVM 155 GGGANTL 166 GGGANEL 164 GGGANEL 166 GGGANEL 165 ATIPITG 235 ATIPITG 235 ATIPITG 233 ATIPITG 233 ATIPITG 233
SiPiP:2:1162 ADGYSTGTGLAAEI VGTFVLVYTVFSATDPKRSARDSHIPVLAFLP I GFAVFMVHLAT I P I TG 226 AIPiP2:1162 ADGYSTGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 222 HVPIP2:1160 AAGHTKGVGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 222 HVPIP2:1165 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 222 HVPIP2:1165 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 222 HVPIP2:1165 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 227 HVPIP2:1162 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHLAT I P I TG 228 H4 CONTRACTION OF CONTRACTION OF CO	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169 SiPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171	5 GLSGGH I NPAVTFGL FLARKVSLVRA LLYMVACCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGGH I NPAVTFGL FLARKVSL I RA LLY I I AQCLGA I CGVGLVKGFQSS - YFVRYI 4 GVSGGH I NPAVTFGL FLARKVSLVRAVLY I I AQCLGA I CGVGLVKGFQSS - YFVRYI 7 SPGYTKGDGLGAE VGTFVLVYTVFSA TDAKR TARDSHVP ALAF LP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I VGTFVLVYTVFSA TDAKR TARDSHVP ALAF LP I GFAVFLVHL/ 0 NHGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 9 AHGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 8 AHGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/	GGGANVM 150 GGGANTL 166 GGGANEL 166 GGGANEL 165 ATIPITG 230 ATIPITG 230 ATIPITG 237 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233
ALPIP2;1 162 AD GYS TG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 224 NIPI2;1 160 AAG HTKGV GLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 222 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 229 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 229 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 229 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 227 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 227 HVPI2;1 165 SAGYSKG TGLAAEI I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 227 HVPI2;1 123 TGI NPARS LGAAI I FNKDRÅWDDHWI FW GPF I GAALAA VYHQV LRA I P FKSSAHY 290 NIAQP1 233 TGI NPARS LGAAI I FNKDRÅWDDHWI FW GPF I GAALAALYHVVV LRA I P FKSSS 280 NIAQP1 233 TGI NPARS LGAAI I FNKDRÅWDDHWI FW GPF I GAALAALYHVVV I RA I P FKSS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 169 SIPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 OsPIP1;3 171	5 GISGGHINPAVTFGLFLARKVSLVRALLYMVAOCLGAMCGVGLVKAFQSA-YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFQSA-YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFQSA-FYVRY 7 SPGYTKGDGLGAEVVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 5 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFULVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NFGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NFGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NFGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NFGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NFGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/	GGGANVM 155 GGGANL 166 GGGANEL 167 GGGANEL 167 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237
NIPIP2:1100       AA GH TK GV GLAAE I I GTFVLVY TV FSA TDPKRSARDSHVPVLAF LP I GFAV FMVHLAT IP I TG 222         HVPIP2:1105       SAGYSKG TGLAAE I I GTFVLVY TV FSA TDPKRSARDSHVPVLAF LP I GFAV FMVHLAT IP I TG 222         HVPIP2:1105       SAGYSKG TGLAAE I I GTFVLVY TV FSA TDPKRSARDSH IPVLAF LP I GFAV FMVHLAT IP I TG 227         HVPIP2:1105       SAGYSKG TGLAAE I I GTFVLVY TV FSA TDPKRSARDSH IPVLAF LP I GFAV FMVHLAT IP I TG 227         HVPIP2:1105       SAGYSKG TGLAAE I I GTFVLVY TV FSA TDPKRSARDSHVPVLAF LP I GFAV FMVHLAT IP I TG 227         H4      LoopD         H5         ZmPIP1:6 240       TGI NPARS LGAAI I YDNPHGWHGHWI FW GPFI GAALAAL YHQVVLRA I P FKSSAHY       286         NIAQP1 233       TGI NPARS LGAAI I FNKDNAWDDHWI FW GPFI GAALAAL YHQVV I RA I P FKSSS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtIPIP1;2 169 SIPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;2 159	5 G L SGGH I NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGL VKA FOSA - Y FVRY 3 GVSGGH I NPAVTFGL FLARKVSL I RALLY I I A OCLGA I CGVGL VKGFQSS - Y VRYY 4 GVSGGH I NPAVTFGL FLARKVSL VRAVLY I I A OCLGA I CGVGL VKGFQSS - Y VRYY 7 SP GY TKGDGLGAE VGTFVL VY TV FSA TDAKR TARDSHVP A LAF LP I GFAVFL VHL/ 4 ANGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRSARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I VGTFI LVY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NPGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL// 1 NFGY TKGDGLGAE I VGTFVL VY TV FSA	GGGANVM 155 GGGANEL 164 GGGANEL 164 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233
HvPIP2;5167       AA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 229         HvPIP2;165       SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 227         HvPIP2;3166       SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAA I I SN SAN AVDD HWI FW GP FI GAA LAA V YHQV V I RA I P FK SS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 OsPIP1;3 171 HvPIP2;2 159 SiPIP2;7 164	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACCLGAICGVGLVKGFOSA - YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACCLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEINGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEINGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIVGTFVLVYTVFSATDAKRNARDSHVPLAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIVGTFVLVYTVFSATDAKRNARDSHVPLAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIVGTFVLVYTVFSATDPKRNARDSHVPLAFLPIGFAVFLVHL/	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 165 A T I P I TG 233 A T I P I TG 234
HvPIP2;5167       AA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 229         HvPIP2;165       SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 227         HvPIP2;3166       SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GY SK GT GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAAE I I GT FV LVY TV FSA TDP KRSARDSHVPVLAF LP I GFAV FMVHLAT I P I TG 228         TG I SA GLAA I I SN SAN AVDD HWI FW GP FI GAA LAA V YHQV V I RA I P FK SS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NIAQP1170 AtPIP1;2 169 SIPIP1;2 169 SIPIP1;2 168 ZmPIP1;5 171 OsPIP1;3 171 HvPIP2;2 169 SIPIP2;7 164 AtPIP2;1 162	5 GISGGH I NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGGH I NPAVTFGL FLARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSA - YFVRY 4 GVSGGH I NPAVTFGL FLARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSA - YFVRY 7 SPGYTKGDGLGAE VGTFVLVYTVFSATDAKR TARDSHVPALAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I VGTFVLVYTVFSATDAKRARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 8 AHGYTKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 A PGYTKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 A PGYTKGDGLGAE I I GTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 A PGYTKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 NFGYTKGDGLGAE I VGTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 3 GSGSRGTALGAE I VGTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 4 STGYSTGTGLAAE I VGTFVLVYTVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 4 STGYSTGTGLAAE I VGTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHL/ 4 STGYSTGTGLAAE I I GTFVLVYTVFSATDPKRSARDSHVPVLAFLP I GFAVFMVHL/	GGGANVM 155 GGGANEL 164 GGGANEL 164 GGGANEL 165 ATIPITG 235 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPITG 227
HvPIP2:1165       SAGYSKGTGLAAEI       IGTFVLVYTVFSATDPKRNARDSHIPVLAFLPIGFAVFMVHLATIPITG         HvPIP2:3166       SAGYSKGTGLAAEI       IGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHLATIPITG       222         H4      LoopD       H5         ZmPIP1:6240       TGINPARSLGAAII       FNKDRÄWDHWIFWQPFIGAALAALVHOVVLRAIPFKSSAHY296         NIAQP1233       TGINPARSLGAAII       FNKDRÄWDDHWIFWQPFIGAALAALVHOVVLRAIPFKSSAHY290         NIAQP1233       TGINPARSLGAAII       FNKDRÄWDDHWIFWQPFIGAALAALVHVVVLRAIPFKSS285         SIPIP1:231       TGINPARSLGAAII       FNKDRÄWDDHWIFWQPFIGAALAALVHVIVIRAIPFKSS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 OsPIP1;3 171 HvPIP2;2 159 SiPIP2;7 164 AtPIP2;1 160	5 G I SGGH I NPAVTFGL F LARKVSL VRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGGH I NPAVTFGL F LARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSS - YFVRY 4 GVSGGH I NPAVTFGL F LARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSA - FYVRY 7 SP GYTKGDGLGAE VGTFVL VY TV FSA TDAKR TARDSHVPA LAF LP I GFAVFL VHL/ 4 ANGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRSARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VG TFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPG YTKGDGLGAE I VG TFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 4 STGYS TG TGLAAE I VG TFVL VY TV FSA TDAKRNARDSHVP VLAF LP I GFAVFL VHL/ 4 STGYS TG TGLAAE I VG TFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LPI GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVL	GGGANVM 155 GGGANL 166 GGGANEL 164 GGGANEL 164 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 224 ATIPITG 224 ATIPITG 224 ATIPITG 224 ATIPITG 224
HvPIP2;3166       SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGF064VFMVHLATIPITG       228         H4      LoopD       H5         ZmPIP1;6       240       TGINPARSLGAAIIYDNPHGWHGHWIFWGPFAGAALAAVYHQVVLRAIPFKSSAHY296         HaPIP1;1       237       TGINPARSLGAAIIFNCRÄWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSS287         NIAQP1233       TGINPARSLGAAIIFNCRÄWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSS	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 OsPIP1;3 171 HvPIP2;2 159 SiPIP2;7 164 AtPIP2;1 160	5 G I SGGH I NPAVTFGL F LARKVSL VRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGGH I NPAVTFGL F LARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSS - YFVRY 4 GVSGGH I NPAVTFGL F LARKVSL I RALLY I I A OCLGA I CGVGL VKGFOSA - FYVRY 7 SP GYTKGDGLGAE VGTFVL VY TV FSA TDAKR TARDSHVPA LAF LP I GFAVFL VHL/ 4 ANGY TKGDGLGAE I VGTFVL VY TV FSA TDAKRSARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 AP GY TKGDGLGAE I I GTFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VG TFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPG YTKGDGLGAE I VG TFVL VY TV FSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 4 STGYS TG TGLAAE I VG TFVL VY TV FSA TDAKRNARDSHVP VLAF LP I GFAVFL VHL/ 4 STGYS TG TGLAAE I VG TFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVLAF LPI GFAVFMVHL/ 5 ANGYS TG TGLAAE I I GTFVL VY TV FSA TDPKRSARDSHVPVL	GGGANVM 155 GGGANL 166 GGGANEL 164 GGGANEL 164 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 224 ATIPITG 224 ATIPITG 224 ATIPITG 224 ATIPITG 224
H4      LoopD       H5         ZmPIP1;6 240       TGI NPARS LGAA I I YDNPHGWHGHWI FW GP F AGAA LAA V HQVVLRA I P FKSSAHY       296         HaPIP1;1 237       TGI NPARS LGAA I I FNKDRAWDDHWI FW GP F I GAA LAA LYHVVV I RA I P FKSSA-       290         MAOP1 233       TGI NPARS LGAA I I YN TDOAWDDHWI FW GP F I GAA LAA LYHVVV I RA I P FKSS       290         MAOP1 233       TGI NPARS LGAA I I YN TDOAWDDHW F WG GP FI GAA LAA LYHVV I RA I P FKSS       286         SIPIP1;2 231       TGI NPARS LGAA I I YN ROHAWDDHW F WG GP FI GAA LAA LYHVV I RA I P FKSS       286         SIPIP1;2 231       TGI NPARS LGAA I I YN ROHAWDDHW F WG GP FI GAA LAA LYHVV I RA I P FKSR S       286         OSPIP1;2 344       TGI NPARS LGAA I VY NKEHAWDDHWI F WG GP FI GAA LAA LYHVVV I RA I P FKSR S       288         OSPIP1;3 234       TGI NPARS LGAA I VY NSHAWDDHWI F WG GP FI GAA LAA I YHVVV I RA I P FKSR D       288         OSPIP1;3 234       TGI NPARS LGAA VY NRAHAWDHWI F WG GP FI GAA LAA I YHVVV I RA I P FKSR D       288         OSPIP2;2 222       TGI NPARS LGAAV VY NNKAAWDOWI F WG GP FI GAA LAA I YHVVV I RA I P FKSR SNA - 286       288         OFIP2;2 222       TGI NPARS LGAAV VY NNKAAWDOWI F WG GP FI GAA LAA A I YHVV I RA I FK SGS KS LGS FRSS NSN 24       288         HVPIP2;2 223       TGI NPARS FGAAV VY NNKAWDOWI F WG GP FI GAA I AA LYHQY I LRAAA I KA LGS FRSS NA - 286       288         MIPIP2;1 223       TGI NPARS FGAAV I YNCKA WOHWI	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NIAQP1 170 AIPIP1;2 169 SIPIP1;2 169 SIPIP1;2 171 ZmPIP1;5 171 OsPIP1;3 171 HvPIP2;2 159 SIPIP2;7 164 AIPIP2;1 160 HvPIP2;5 167	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGHINPAVTFGLFLARKVSLIRALLYIIACCLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLYIIACCLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 SFGYTGGGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFWHL// 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPVLAFLPIGFAVFWHL// 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 7 AAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 7 AAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 7 AAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 7 AAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL//	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 A T I P I TG 233 A T I P I TG 224 A T I P I TG 224 A T I P I TG 224 A T I P I TG 222 A T I P I TG 225
ZmPIP1;6 240       TG I NPARS L GAA I I YDNPHGWHGHWI FW GP F A GAA L AA V YHQVV L RA I P FK SSAHY       296         HaPIP1;1 237       TG I NPARS L GAA I I FNKDRAWDDHWI FW GP F I GAA L AA L YHVVV I RA I P FK SSA       290         NIAOP1 233       TG I NPARS L GAA I I YN TDOA WDDHWI FW GP F I GAA L AA L YHVVV I RA I P FK SS       290         AIPIP1;2 232       TG I NPARS L GAA I I YN TDOA WDDHWI FW GP F I GAA L AA L YHV V I RA I P FK SSS       286         SIPIP1;2 231       TG I NPARS L GAA I I YN KEHAWDDHWI FW GP F I GAA L AA L YHOV I I RA I P FK SSS       286         OSPIP1;2 234       TG I NPARS L GAA I I YN KEHAWDDHWI FW GP F I GAA L AA L YHOV I I RA I P FK SSS       286         OSPIP1;2 234       TG I NPARS L GAA I VYN KEHAWDDHWI FW GP F I GAA L AA I YHOV I RA I P FK SSS       288         OSPIP1;2 234       TG I NPARS L GAA I VYN RSHAWDDHWI FW GP F I GAA L AA I YHOV I RA I P FK SSS       288         OSPIP1;2 324       TG I NPARS L GAA I VYN RSHAWDDHWI FW GP F I GAA L AA I YHVV I RA I P FK SSS       288         OSPIP1;2 324       TG I NPARS L GAA V YN NKAA WONHWI FW GP F I GAA L AA I YHVV I RA I P FK SSS       288         SiPIP2;2 222       TG I NPARS L GAA V YN NNKA WONHWI FW GP F I GAA I AA A L YHQ Y I L RAAA I KA L GS FRSS SSN 284       284         HVPIP2;2 223       TG I NPARS F GAA V I YN SK FWODHWI FW GP F I GAA I AA L YHQ Y I L RAAA I KA L GS FRSS A - 286       286         MIPIP2;1 223       TG I NPARS F GAA V I YN NKA WO DWI FW GP F I GAA I AA	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;1 162 SiPIP2;7 164 AtPIP2;1 162 HvPIP2;1 165 HvPIP2;1 165	5 GISGHI NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGHI NPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL VRAVLY I AQCLGA I CGVGL VKGFOSA - FYVRY 7 SPGY TKGDGLGAE VGTFVL VY TVFSA TDAKR TARDSHVP I LAF LP I GFAVFL VHL/ 4 ANGY TKGDGLGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 5 AHGY TKGDGLGAE I I GTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 8 AHGY TKGDGLGAE I I GTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NPGY TKGDGLGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 2 ASGFSRGTALGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 2 ASGFSRGTALGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 2 ASGFSRGTALGAE I VGTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 2 ADGYS TGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 3 ASGFSRGTALGAE I VGTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYS TGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/	GGGANVM 155 GGGANEL 164 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227
HaPiP1;1 237 TGI NPARS LGAA I I FNKDRAWDDHWI FWGPF I GAA LAA LYHUYU I RA I P FKSK 280         NIAQP1 233 TGI NPARS LGAA I I FNKDRAWDDHWI FWGPF I GAA LAA LYHUYU I RA I P FKSK 287         AIPIP1;2 232 TGI NPARS LGAA I I FNKDRAWDDHWI FWGPF I GAA LAA LYHU I I RA I P FKSK 286         SIPIP1;2 231 TGI NPARS LGAA I I FNKDRAWDDHWI FWGPF I GAA LAA LYHU I I RA I P FKSK 286         SIPIP1;2 231 TGI NPARS LGAA I I YNKHAWDDHWI FWGPF I GAA LAA LYHU I I RA I P FKSK	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;1 162 SiPIP2;7 164 AtPIP2;1 162 HvPIP2;1 165 HvPIP2;1 165	5 GISGHI NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGHI NPAVTFGL FLARKVSL I RALLY I I ACLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL I RALLY I I ACLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL VRAVLY I ACLGA I CGVGL VKGFOSA - YFVRY 7 SPGYTKGDGLGAE I VGTFVLVY TV FSATDAKR TARDSHVPALAF LP I GFAVFLVHL/ 4 ANGY TKGDGLGAE I VGTFVLVY TV FSATDAKR TARDSHVPALAF LP I GFAVFLVHL/ 5 AHGY TKGDGLGAE I I GTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 8 AHGY TKGDGLGAE I I GTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I I GTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I VGTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I VGTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 NFGY TKGDGLGAE I VGTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 2 AGSFSRGTALGAE I VGTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I VGTFVLVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I VGTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 4 STGYSTGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 4 STGYSTGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 7 AGGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE I I GTFVLVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL// 5 SAGYSKGTGLAAE	GGGANVM 155 GGGANEL 164 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227
NIAOP1 233 TGI NPARS LGAA I I YN TDOAWDDHWL FW GP FI GAA LAAV YHQI I I RA I PFHKSS 286 AIPIP1; 2 232 TGI NPARS LGAA I I YN KHAWDDHW FW GP FI GAA LAA LYHQI I I RA I PFKSRS 286 SIPIP1; 2 231 TGI NPARS LGAA I I YN KHAWDDHW FW GP FI GAA LAA LYHQV I RA I PFKSRS 285 OSPIP1; 2 234 TGI NPARS LGAA I I YN KHAWDDHW FW GP FI GAA LAA LYHQV I RA I PFKSRS 288 SIPIP; 2 234 TGI NPARS LGAA I I YN RSHAWDDHW FW GP FI GAA LAA LYHQV I RA I PFKSRS 288 OSPIP1; 2 334 TGI NPARS LGAA I I YN RSHAWDDHW FW GP FI GAA LAA I YHQV I RA I PFKSRD 288 OSPIP1; 2 324 TGI NPARS LGAA I VY NRAHAWDDHW FW GP FI GAA LAA I YHQV I RA I PFKSRD 288 OSPIP1; 2 324 TGI NPARS LGAA I VY NRAHAWDDHW FW GP FI GAA LAA I YHQV I LRAAA I KA LGS FRSSRSN 284 HVPIP2; 2 222 TGI NPARS LGAA VI YN KKAA WONHW FW GP FI GAA LAA A LYHQV I LRAAA I KA LGS FRSSRSN 284 AIPIP2; 1 225 TGI NPARS LGAA VI YN KKAA WONHW FW GP FI GAA I AA LYHQV I LRAAA I KA LGS FRSSRSN 284 HVPIP2; 223 TGI NPARS FGAA VI YN KKA WONHW FW GP FI GAA I AA LYHQV I LRAAA I KA LGS FRSSRSN 284 HVPIP2; 223 TGI NPARS FGAA VI YN KKA WODHW FW GP FI GAA I AA LYHQY I LRAAG I KA LGS FRSSA 288 HVPIP2; 223 TGI NPARS FGAA VI YN KKA WODHW FW GP FI GAA I AA FYHQY I LRAGA KA LGS FRSNA 289 HVPIP2; 223 TGI NPARS LGAA VI YN KDK AWDD WI FW GP FI GAA I AA FYHQY I LRAGA KA LGS FRSNA 280 HVPIP2; 223 TGI NPARS LGAA VI YN KDK AWDD WI FW GP MI GAA I AA FYHQY I LRAGA KA LGS FRSNA 280 HVPIP2; 223 TGI NPARS LGAA VI YN KDK AWDD WI FW GP MI GAA I AA FYHQY I LRAGA KA LGS FRSNA 280 HVPIP2; 320 TGI NPARS LGAA VI YN NKKAWDD WI FW GP FI GAA I AA AYHQY LRAGA KA LGS FRSNA 280 HVPIP2; 322 TGI NPARS LGAA VI YN NKKAWDD WI FW GP MI GAA I AA AYHQY LRASA K - LGSYRSN 286 HVPIP2; 322 TGI NPARS FGAA VI YN NKKAWDD WI FW GP FI GAA I AAAYHQY U LRASA K - LGSYRSN 286 HVPIP2; 322 TGI NPARS FGAA VI YN NKKAWDD WI FW GP FI GAA I AAAYHQY U LRASA K - LGSYRSN 286 HVPIP2; 322 TGI NPARS FGAA VI YN NKAWDD WI FW GP FI GAA I AAAYHQY U LRASA K - LGSSAS FGRS 290	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;1 150 SiPIP2;7 164 AtPIP2;1 160 HvPIP2;1 165 HvPIP2;3 166	5 GISGHI NPAVTFGLFLARKVSLVRALLYMVA OCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGHI NPAVTFGLFLARKVSLI RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRY 4 GVSGHI NPAVTFGLFLARKVSLI RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRY 4 GVSGHI NPAVTFGLFLARKVSLI RALLY I I AQCLGA I CGVGLVKGFOSA - FYVRY 7 SPGYTKGDGLGAE I VGTFVLVY TVFSATDAKR TARDSHVPALAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I VGTFVLVY TVFSATDAKRARDSHVPI LAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 8 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 2 AGGYSGTGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 2 ADGYSTGTGLAAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFWHL// 2 ADGYSTGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 3 AGGYSKGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 5 AGYSKGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL/// 5 AGYSKGTGLAAE I I GTFVLVY TVFSATDPK	GGGANVM 155 GGGANL 166 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227 ATIPITG 227
NIAOP1 233 TGI NPARS LGAA I I YN TDOAWDDHWL FW GP FI GAA LAAV YHOI I I RA I P FHKSS 286 AIPIP1; 2 232 TGI NPARS LGAA I I YN KHAWDDHWL FW GP FI GAA LAA LYHO'I VI RA I P FKSRS 286 SIPIP1; 2 231 TGI NPARS LGAA I I YN KEHAWDDHWI FW GP FI GAA LAA LYHO'I I RA I P FKSRS 285 OsPIP1; 2 234 TGI NPARS LGAA I I YN KEHAWDDHWI FW GP FI GAA LAA LYHO'VI RA I P FKSRS 288 SIPIP; 2 234 TGI NPARS LGAA I VY NRHAWDDHWI FW GP FI GAA LAA LYHO'VI RA I P FKSRS 288 OSPIP1; 2 334 TGI NPARS LGAA I VY NRHAWDDHWI FW GP FI GAA LAA I YHO'VI RA I P FKSRD 288 OSPIP1; 2 324 TGI NPARS LGAA I VY NRHAWDDHWI FW GP FI GAA LAA I YHO'VI RA I P FKSRD 288 OSPIP1; 2 324 TGI NPARS LGAA I VY NRHAWDDHWI FW GP FI GAA LAA I YHO'VI RA I P FKSRD 288 SIPIP2; 2 222 TGI NPARS LGAA VI YN KAA WONHWI FW GP FI GAA LAA I YHO'VI RA I A FKSRD 288 SIPIP2; 2 225 TGI NPARS LGAA VI YN KKAA WONHWI FW GP FI GAA I AA ALYHO'I LRAAA I KA LGS FRSSRSN 284 AIPIP2; 1 225 TGI NPARS FGAA VI YN KKAA WONHWI FW GP FI GAA I AA LYHO'I LRAAA I KA LGS FRSSRSN 284 HVPIP2; 2 227 TGI NPARS FGAA VI YN KKA WODHWI FW GP FI GAA I AA LYHO'I LRAAS K LGS FRSSRSN 284 HVPIP2; 223 TGI NPARS FGAA VI YN KKAWDDHWI FW GP FI GAA I AA FYHOY I LRAGA I KA LGS FRSSNA - 286 HVPIP2; 223 TGI NPARS LGAA VI YN KDKAWDDOWI FW GP MI GAA I AA FYHOY I LRAGA I KA LGS FRSNA - 280 HVPIP2; 223 TGI NPARS LGAA VI YN KDKAWDDOWI FW GP MI GAA I AA FYHOY I LRAGA I KA LGS FRSNA - 280 HVPIP2; 228 TGI NPARS LGAA VI YN NKKAWDDWI FW GP MI GAA I AA FYHOY I LRAGA I KA LGS FRSNA - 280 HVPIP2; 329 TGI NPARS LGAA VI YN NKKAWDDWI FW GP FI GAA I AA AYHOY I LRAGA I KA LGS FRSNA - 286 HVPIP2; 3229 TGI NPARS LGAA VI YN NKKAWDDWI FW GP FI GAA I AA AYHOY I LRAGA I KA LGS FRSNA - 286 HVPIP2; 3229 TGI NPARS LGAA VI YN NKKAWDDWI FW GP FI GAA I AA AYHOY U LRASAAK - LGSYRSN 286 HVPIP2; 3229 TGI NPARS FGAA VI YN NKKAWDDWI FW GP FI GAA I AAAYHOY U RASAAK - LGSYRSN 286 HVPIP2; 3229 TGI NPARS FGAA VI YN NKAWDDWI FW GP FI GAA I AAAYHOY U RASAAK - LGSYRSN 286 HVPIP2; 3229 TGI NPAR	HvPIP2;1 103 HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 OsPIP1;5 171 HvPIP2;1 150 SiPIP2;7 164 AtPIP2;1 162 NtPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240	5 GISGHI NPAVTFGL FLARKVSLVRA LLYMVA CCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGHI NPAVTFGL FLARKVSL I RA LLY I I AQCLGA I CGVGL VKGFQSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL I RA LLY I I AQCLGA I CGVGL VKGFQSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL VRAVLY I I AQCLGA I CGVGL VKGFQSA - YFVRY 7 SPGY TKGDGLGAE I VGTFV LVY TV FSATDAKR TARDSHVP ALAF LP I GFAVFL VHL/ 4 ANGY TKGDGLGAE I VGTFV LVY TV FSATDAKR TARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 9 AHGY TKGDGLGAE I I GTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I I GTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 APGY TKGDGLGAE I VGTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 1 NFGY TKGDGLGAE I VGTFV LVY TV FSATDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 2 AGGFSR TALGAE I VGTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 2 AGGYSG TALGAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 2 AGGYSG TALGAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 3 AGFSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVP VLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 AGYSKG TGLAAE I I GTFV LVY TV FSATDPKRSARDS	GGGANVM 155 GGGAN L 164 GGGAN E L 164 GGGAN E L 164 A T I P I TG 233 A T I P I TG 232 A T I P I TG 224 A T I P I TG 225 A T I
AIPIP1;2       232       TG I NPARS LGAA I L FNKDNAWDDHWV FWW GP F I GAA LAA L YHV I VI RA I P FKSRS       286         SIPIP1;2       231       TG I NPARS LGAA I VYNKEHAWDDHWI FWW GP F I GAA LAA L YHVV I I RA I P FKSRS       285         SIPIP1;2       234       TG I NPARS LGAA I VYNKEHAWDDHWI FWW GP F I GAA LAA L YHQV I RA I P FKSRS       288         ZmPIP1;5       234       TG I NPARS LGAA I VYNRSHAWNDHWI FWW GP F I GAA LAA I YHVV I RA I P FKSRS       288         OsPIP1;2       234       TG I NPARS LGAA I VYNRSHAWNDHWI FWW GP F I GAA LAA I YHVV I RA I P FKSRD       288         OsPIP1;2       234       TG I NPARS LGAA I VYNRSHAWNDHWI FWW GP F I GAA LAA I YHVV I RA I P FKSRD       288         OsPIP1;2       234       TG I NPARS LGAA I VYNRSHAWNDHWI FWW GP F I GAA LAA I YHVV I RA I P FKSRD       288         OSPIP1;2       234       TG I NPARS LGAA V YNRKAAWDNHWI FWW GP F I GAA LAA I YHVV I RA I P FKSRD       288         SIPIP2;2       227       TG I NPARS LGAA V YNKKAAWDNHWI FWW GP F I GAA LAA LYHQ V I L RAAAI KALGS FRSNA       286         AIPIP2;1       225       TG I NPARS F GAAV I YNKKAWDDHWI FWW GP F I GAA I AA FHQFV L RASGK SLGS FRSNA V 287       286         NIPIP2;1       225       TG I NPARS F GAAV I YNKOK AWDE HWI FWW GP F I GAA I AA FHQY I L RAGAI KA LGS FRSNA - 280       290         HVPIP2;1       228       TG I NPARS LGAAV I YNKOK AWDDOWI FWW GP I GAA I AA FHQY I L RAGAI KA LGS FRSN	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AIPIP1;2 169 OsPIP1;2 171 OsPIP1;2 171 OsPIP1;3 171 HvPIP2;1 165 SiPIP2;7 164 AIPIP2;1 165 HvPIP2;3 166 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 237	5 GLSGH I NPAVTFGL FLARKVSLVRA LLYMVACCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGH INPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGLVKGFQSS - YFVRY 4 GVSGH INPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGLVKGFQSS - YFVRY 4 GVSGH INPAVTFGL FLARKVSL VRAVLY I I AQCLGA I CGVGLVKGFQSS - YFVRY 7 SPGY TKGDGLGAE I VGTFVLVYTVFSA TDAKR TARDSHVP ALAF LP I GFAVFLVHL/ 4 ANGY TKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 0 NHGY TKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 9 AHGY TKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 1 APGY TKGDGLGAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I VGTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I I GTFVLVYTVFSA TDAKRNARDSHVP I LAF LP I GFAVFLVHL/ 4 STGYSTGTGLAAE I I GTFVLVYTVFSA TDPKRSARDSHVPLAF LP I GFAVFLVHL/ 5 SAGYSKGTGLAAE I I GTFVLVYTVFSA TDPKRSARDSHVPLAF LP I GFAVFMVHL/ 5 SAGYSKGTGLAAE I I GTFVLVYTVFSA TDPKRSARDSHVPVLAF LP I GFAVFMVHL/ 5 GAGYSKGTGLAAE I I GTFVLVYTVFSA TDPKRSARDSHVPVLAF	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 GGGAN E L 165 A TIPITG 233 A TIPITG 224 A TIPITG 225 A TI
SIPIP1:2 231       TGI NPARS LGAA I VYNKE HAWDDHWI FW GPF I GAA LAA LYHQV I I RA I PFK SGN 285         OSFIP1:2 234       TGI NPARS LGAA I VYNKE HAWDDHWI FW GPF I GAA LAA I YHQV I I RA I PFK SGN 285         OSFIP1:2 234       TGI NPARS LGAA I VYNRGHAWDDHWI FW GPF I GAA LAA I YHQV I I RA I PFK SRS 288         OSFIP1:3 234       TGI NPARS LGAA I VYNRGHAWDDHWI FW GPF I GAA LAA I YHVV I I RA I PFK SRS 288         OSFIP1:3 234       TGI NPARS LGAA I VYNRGHAWDDHWI FW GPF I GAA LAA I YHVV I RA I PFK SRD 288         OSFIP1:3 234       TGI NPARS LGAA I VYNRAHAWHDHWI FW GPF I GAA LAA I YHVV I RA I PFK SRD 288         OSFIP1:2 227       TGI NPARS LGAAV I YNKKAAWDNHWI FW GPF I GAA LAA I YHVV I RA SAR GYG SFR SNA - 286         AIPIP2:1 225       TGI NPARS LGAAV I YNKKAAWDONHWI FW GPF I GAA I AA LYHQ I LRASAR GYG SFR SNA - 286         AIPIP2:1 225       TGI NPARS FGAAV I YNKSK PWDDHWI FW GPF I GAA I AA FYHQY L RASGSK SLGS FR SAANV 287         NIPIP2:1 223       TGI NPARS FGAAV I YNKOKAWDE HWI FW GPF I GAFAAA YHQY L RAGAVKA LGS FR SNA 280         HVPIP2:2 223       TGI NPARS LGAAV I YNKOKAWDE WI FW GPF I GAFAAA YHQY L RAGAVKA LGS FR SNA 280         HVPIP2:2 223       TGI NPARS LGAAV I YNKOKAWDE WI FW GPM I GAA I AA FYHQY I LRAGA I KA LGS FR SNA 280         HVPIP2:2 228       TGI NPARS LGAAV I YN TOKAWDDOWI FW GPL I GAA I AA YHQY U LRASAK - LGS TR SNA 286         HVPIP2:3 229       TGI NPARS FGAAV I YN TOKAWDDOWI FW GPL I GAA I AA YHQY U LRASAK - LGS TR SNA 286	HvPIP2:1 103 HvPIP2:3 104 ZmPIP1:6 177 HaPIP1:1 174 NtAQP1 170 AtPIP1:2 168 OsPIP1:2 171 ZmPIP1:5 171 HvPIP2:1 160 HvPIP2:1 160 HvPIP2:1 160 HvPIP2:1 165 HvPIP2:3 166 ZmPIP1:6 240 HaPIP1:1 237 NtAQP1 233	5 GISGHI NPAVTFGLFLARKVSLVRALLYMVA OCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGHI NPAVTFGLFLARKVSL I RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRYI 4 GVSGHI NPAVTFGLFLARKVSL I RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRYI 6 GVSGHI NPAVTFGLFLARKVSL VRAVLYI I AQCLGA I CGVGLVKGFOSA - FYVRYI 7 SPGYTKGDGLGAE VGTFVLVY TVFSATDAKR TARDSHVPALAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I VGTFVLVY TVFSATDAKRARDSHVPI LAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 8 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 2 AGGYSTGTGLAAE I VGTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 2 ADGYSTGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 5 AGYSKGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 10 TGINPARSLGAAI I YDNPHGWHGHWI FWGPFI GAALAALAAVYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YDNPAGWDHWI WWGPFI GAALAALAAVYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YDNDQAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YNTDGAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH/// 7 TGINPARSLGAAI I YNTDGAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH/// 7 TGINPARSLGAAI I YNTDGAWDDHW	GGGANVM 155 GGGANEL 164 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPIT
OSPIP1;2 234 TG INPARS LGAA I LYN RGHAWDDHWI FW GP FIGAA LAA I YHQVVI RA I P FKSRS 288 ZmPiP1;5 234 TG INPARS LGAA I VYN RSHAWDDHWI FW GP FIGAA LAA I YHVV I RA LP FKSRD 288 HVPIP2:2 224 TG INPARS LGAA I VYN RSHAWDDHWI FW GP FIGAA LAA I YHVV I RA LP FKSRD 288 HVPIP2:2 222 TG INPARS LGAAVI YN KKAA WONHWI FW GP FIGAA LAA I YHVV I RAAP KA LOS FRSSRSN 284 SIPIP2:7 227 TG INPARS LGAAVI YN KKAA WONHWI FW GP FIGAA I AA LYHQ YI LRAAA I KA LOS FRSSRSN 284 APIP2:1 225 TG INPARS FGAAVI YN KKAA WONHWI FW GP FIGAA I AA LYHQ YI LRAASA KA LOS FRSSRSN 287 NIPIP2:1 223 TG INPARS FGAAVI YN KSK PWDDHWI FW GP FIGAA I AA FYHQ FV LRASGSK SLGS FRSSAANV 287 NIPIP2:1 223 TG INPARS FGAAVI YN KSK PWDDHWI FW GP FIGAA I AA FYHQY I LRAGAV KA LOS FRSNA 288 HVPIP2:2 228 TG INPARS FGAAVI YN KDK AWDD WI FW GP FIGAA I AA FYHQY I LRAGAV KA LOS FRSNA 280 HVPIP2:2 228 TG INPARS LGAAVI YN KDK AWDD WI FW GP FIGAA I AA FYHQY I LRAGAV KA LOS FRSNA 280 HVPIP2:3 229 TG INPARS LGAAVI YN KDK AWDD WI FW GP FIGAA I AA AYHQY U LRAGAV KA LOS FRSNA 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD WI FW GP FIGAA I AA AYHQY U LRASAK - LGSYRSNA 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD WI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD WI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD WI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD WI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA - 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD HVI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA - 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD HVI FW GP FIGAA I AAAYHQY U LRASAK - LGSYRSNA - 280 HVPIP2:3 229 TG INPARS FGAAVI YN NK KAWDD HVI FW GP FIGAA I AAAYHQY U LRASAK - LGSSAS FGRS 290	HvPIP2:1 103 HvPIP2:3 104 ZmPIP1:6 177 HaPIP1:1 174 NtAQP1 170 AtPIP1:2 168 OsPIP1:2 171 ZmPIP1:5 171 HvPIP2:1 160 HvPIP2:1 160 HvPIP2:1 160 HvPIP2:1 165 HvPIP2:3 166 ZmPIP1:6 240 HaPIP1:1 237 NtAQP1 233	5 GISGHI NPAVTFGLFLARKVSLVRALLYMVA OCLGAMCGVGLVKA FOSA - YFVRY 3 GVSGHI NPAVTFGLFLARKVSL I RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRYI 4 GVSGHI NPAVTFGLFLARKVSL I RALLY I I AQCLGA I CGVGLVKGFOSA - YFVRYI 6 GVSGHI NPAVTFGLFLARKVSL VRAVLYI I AQCLGA I CGVGLVKGFOSA - FYVRYI 7 SPGYTKGDGLGAE VGTFVLVY TVFSATDAKR TARDSHVPALAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I VGTFVLVY TVFSATDAKRARDSHVPI LAFLP I GFAVFLVHL/ 4 ANGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 9 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 8 AHGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I I GTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 1 APGYTKGDGLGAE I VGTFVLVY TVFSATDAKRNARDSHVPI LAFLP I GFAVFLVHL/ 2 AGGYSTGTGLAAE I VGTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 2 ADGYSTGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 5 AGYSKGTGLAAE I I GTFVLVY TVFSATDPKRSARDSHVPVLAFLP I GFAVFWHL// 10 TGINPARSLGAAI I YDNPHGWHGHWI FWGPFI GAALAALAAVYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YDNPAGWDHWI WWGPFI GAALAALAAVYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YDNDQAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH// 7 TGINPARSLGAAI I YNTDGAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH/// 7 TGINPARSLGAAI I YNTDGAWDDHWI FWGPFI GAALAALAAYYHQVVLRAI PFKSSAH/// 7 TGINPARSLGAAI I YNTDGAWDDHW	GGGANVM 155 GGGANEL 164 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG 227 ATIPIT
OSPIPI:3 234 TGI NPARS LGAA I VYNRAHAWHDHWI FWYGP F LGAA LAA I YHVVV I RA I P FKSRD 288 HvPIP2:2 222 TGI NPARS LGAAV I YNKKAAWDNHWI FWYGP F VGALAAA YHVVV I LRAAA I KALGS FRSSRSN 284 SIPIP2:7 227 TGI NPARS LGAAV VYNNKKAWDDWI FWYGP F I GAA I AA LYHO I VLRASAR - GYGS FRSNA - 286 AIPIP2:1 225 TGI NPARS FGAAV I YNKSK PWDDHWI FWYGP F I GAA I AA FYHQF VLRASGK SLGS FRSAANV 287 NIPIP2:1 223 TGI NPARS FGAAV I YNKSK PWDDHWI FWYGP F I GAFAAA YHQY I LRAGAV KA LGS FRSNA - 280 HvPIP2:503 TGI NPARS LGAAV I YNKDK AWDDWI FWYGP I GAFAAAYHQY I LRAGAV KA LGS FRSNA - 280 HvPIP2:2123 TGI NPARS LGAAV I YNKDK AWDDWI FWYGPI GAFAAAYHQY LRAGAV KA LGS FRSNA - 280 HvPIP2:223 TGI NPARS LGAAV I YNKDK AWDDWI FWYGPI LGAA I AA FYHQY LRAGAV KA LGS FRSNA - 280 HvPIP2:3229 TGI NPARS LGAAV I YN NCK AWDDWI FWYGPI LGAA I AA AYHQY VLRASAK - LGSYRSN 286 HvPIP2:3229 TGI NPARS FGAAV I YNNK AWDDHWL FWYGPI GAA I AA AYHQY VLRASAK - LGSSAS FGRS 290	HvPIP2;1 103 HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;1 150 SIPIP2;7 164 AtPIP2;1 162 NtPIP2;1 162 NtPIP2;1 163 VPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 237 NtAQP1 233 AtPIP1;2 232	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGHINPAVTFGLFLARKVSLVRALLYIACCLGAICGVGLVKGFQSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLYIACCLGAICGVGLVKGFQSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIACCLGAICGVGLVKGFQSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 AGGYSGTALGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 5 AGGYSGTALGAEIVGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFLVHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 AGGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GINPARSLGAAIIYDNDAWDHWFWGPFIGAALAALYHVVVIRAIPFKSSAH	GGGANVM 155 GGGANL 166 GGGANEL 164 GGGANEL 164 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 233 ATIPITG 224 ATIPITG 225 ATIPITG
OSPIPI:3 234 TGI NPARS LGAA I VYNRAHAWHDHWI FWYGP F LGAA LAA I YHVVV I RA I P FKSRD 288 HvPIP2:2 222 TGI NPARS LGAAV I YNKKAAWDNHWI FWYGP F VGALAAA YHVVV I LRAAA I KALGS FRSSRSN 284 SIPIP2:7 227 TGI NPARS LGAAV VYNNKKAWDDWI FWYGP F I GAA I AA LYHO I VLRASAR - GYGS FRSNA - 286 AIPIP2:1 225 TGI NPARS FGAAV I YNKSK PWDDHWI FWYGP F I GAA I AA FYHQF VLRASGK SLGS FRSAANV 287 NIPIP2:1 223 TGI NPARS FGAAV I YNKSK PWDDHWI FWYGP F I GAFAAA YHQY I LRAGAV KA LGS FRSNA - 280 HvPIP2:503 TGI NPARS LGAAV I YNKDK AWDDWI FWYGP I GAFAAAYHQY I LRAGAV KA LGS FRSNA - 280 HvPIP2:2123 TGI NPARS LGAAV I YNKDK AWDDWI FWYGPI GAFAAAYHQY LRAGAV KA LGS FRSNA - 280 HvPIP2:223 TGI NPARS LGAAV I YNKDK AWDDWI FWYGPI LGAA I AA FYHQY LRAGAV KA LGS FRSNA - 280 HvPIP2:3229 TGI NPARS LGAAV I YN NCK AWDDWI FWYGPI LGAA I AA AYHQY VLRASAK - LGSYRSN 286 HvPIP2:3229 TGI NPARS FGAAV I YNNK AWDDHWL FWYGPI GAA I AA AYHQY VLRASAK - LGSSAS FGRS 290	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OSPIP1;2 171 OSPIP1;5 171 OSPIP1;5 171 OSPIP1;5 171 SIPIP2;1 165 NtPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 233 AtPIP1;2 233	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGHINPAVTFGLFLARKVSLVRALLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 TGINPARSLGAAIIFNDNAWDHWFFWGPFIGAALAAVYHQVVLRAIPFKSSA' 7 TGINPARSLGAAIIFNDNAWDHWFFWGPFIGAALAAVYHQVVLRAIPFKSS- 2 TGINPARSLGAAIIFNDNAWDHWFFWGPFIGAALAALYHVVVIRAIPFKSS- 2 TGINPARSLGAAIIFNDAWDDHWFFWGPFIGAALAALYHVVIVIRAIPFKSS- 2 TGINPARSLGAAIIFNDAWDDHWFFWGPFIGAALAALYHVVIVIRAIPFKSSC- 2 TGINPARSLGAAIIFNDAWDDHWFFWGPFIGAALAALYHVVIVIRAIPFKSSC- 2 TGINP	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 GGGAN E L 165 A T I P I TG 233 A T I P I TG 224 A T I P I TG 225 A T I P
HVPIP2:2 222 TGINPARS LGAAVI YNKKAAWONHWI FWUGP FUGALAAAAYHQY ILRAAAI KALGS FRSSRSN 284 SIPIP2:7 227 TGINPARS LGAAVI YNNKAWSDOWI FWUGP FIGAAIAA LYHQI VLRASAR - GYGS FRSNA - 286 AIPIP2:1 225 TGINPARS FGAAVI YNNSK PWDDHWI FWUGP FIGAAIAA FYHQFVLRASGSKSLGS FRSAANV 287 NIPIP2:1 223 TGINPARS FGAAVI YNNSK PWDDHWI FWUGP FIGAFAAAYHQY ILRAGAVKALGS FRSNA - 288 HVPIP2:5 230 TGINPARS LGAAVI YNNKKAWDDQWI FWUGP FIGAFAAAAYHQY ILRAGAVKALGS FRSNA - 280 HVPIP2:3 228 TGINPARS LGAAVI YN TDKAWDDQWI FWUGP FIGAFAAAYHQY ILRAGAVKALGS FRSNA - 280 HVPIP2:3 229 TGINPARS LGAAVI YN TDKAWDDQWI FWUGP FIGAFAAAYHQY ILRASAK - LGSYRSN 286 HVPIP2:3 229 TGINPARS FGAAVI YN TDKAWDDWI FWUGP FIGAFIAAAYHQY LRASAK - LGSYRSN 286	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OSPIP1;2 171 OSPIP1;5 171 OSPIP1;5 171 OSPIP1;5 171 SIPIP2;1 165 NtPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 233 AtPIP1;2 233	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGHINPAVTFGLFLARKVSLVRALLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFMVHL/ 5 TGINPARSLGAAIIFNDNMWDHWFFWGPFIGAALAAVYHQVVLRAIPFKSSA' 7 TGINPARSLGAAIIFNDNMWDHWFFWGPFIGAALAAVYHQVVLRAIPFKSS- 2 TGINPARSLGAAIIFNDNAWDDHWFFWGPFIGAALAALYHVVVIRAIPFKSS- 2 TGINPARSLGAAIIFNDAWDDHWFFWGPFIGAALAALYHVVIVIRAIPFKSS- 2 TGINPARSLGAAIIFNNDAWDDHWFFWGPFIGAALAALYHVVIVIRAIPFKSSC- 2 TGINPARSLGAAIIFNNDAWDDHWFFWGPFIGAALAALYHVIVIRAIPFKSSC- 2 TGI	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 GGGAN E L 165 A T I P I TG 233 A T I P I TG 224 A T I P I TG 225 A T I P
HVPIP2:2 222 TGINPARS LGAAVI YNKKAAWONHWI FWUGP FUGALAAAAYHQY ILRAAAI KALGS FRSSRSN 284 SIPIP2:7 227 TGINPARS LGAAVI YNNKAWSDOWI FWUGP FIGAAIAA LYHQI VLRASAR - GYGS FRSNA - 286 AIPIP2:1 225 TGINPARS FGAAVI YNNSK PWDDHWI FWUGP FIGAAIAA FYHQFVLRASGSKSLGS FRSAANV 287 NIPIP2:1 223 TGINPARS FGAAVI YNNSK PWDDHWI FWUGP FIGAFAAAYHQY ILRAGAVKALGS FRSNA - 288 HVPIP2:5 230 TGINPARS LGAAVI YNNKKAWDDQWI FWUGP FIGAFAAAAYHQY ILRAGAVKALGS FRSNA - 280 HVPIP2:3 228 TGINPARS LGAAVI YN TDKAWDDQWI FWUGP FIGAFAAAYHQY ILRAGAVKALGS FRSNA - 280 HVPIP2:3 229 TGINPARS LGAAVI YN TDKAWDDQWI FWUGP FIGAFAAAYHQY ILRASAK - LGSYRSN 286 HVPIP2:3 229 TGINPARS FGAAVI YN TDKAWDDWI FWUGP FIGAFIAAAYHQY LRASAK - LGSYRSN 286	HvPIP2:1 103 HvPIP2:1 103 HvPIP2:3 104 ZmPIP1:6 177 MaPIP1:6 177 MaPIP1:2 168 OsPIP1:2 168 OsPIP1:2 171 ZmPIP1:5 171 HvPIP2:1 162 NtPIP2:1 162 NtPIP2:1 165 HvPIP2:1 165 HvPIP2:3 166 ZmPIP1:6 240 HaPIP1:1 237 NtAQP1 233 OsPIP1:2 232 OsPIP1:2 234 ZmPIP1:5 234	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFQSS-YFVRY 3 GVSGHINPAVTFGLFLARKVSLIRALLYIACCLGAICGVGLVKGFQSS-YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLYIACCLGAICGVGLVKGFQSS-YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIACCLGAICGVGLVKGFQSS-YFVRY 14 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 ACGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 AGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 GINPARSLGAAIIYDNPHGWHGHWIFWGPFIGAALAAVYHQVVLRAIPFKSSAH 7 TGINPARSLGAAIIYDNPHGWHGHWIFWGPFIGAALAAVYHQVVLRAIPFKSSAH 7 TGINPARSLGAAIIYNDNPHGWHGHWIFWGPFIGAALAALYHQVVLRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNKEHAWDDHWIFWGPFIGAALAALYHQVVIRAIPFKSSAH 7 TGINPARSLGAAIIYNRSHAWDHWIFWGPFIGAALAALAHYHQVVIRAIPFKSSAH	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 A T I P I TG 233 A T I P I TG 232 A T I P I TG 222 A T I P I TG 22 A T I P I T
SIPIP2;7 227 TG I NPARS LGAAV VYNNKAWS DQWI FW GP F I GAA I AA LYHQ I V LRASAR - GYGS FRSNA 286 AIPIP2;1 225 TG I NPARS FGAAV I YNKSK PWDDHWI FW GP F I GAA I AA FYHQY L LRASGK SLGS FRSANV 287 NIPIP2;1 223 TG I NPARS FGAAV I YNCKAWDEHWI FW GP F I GAFAAAYHQY L LRAGAVKALGS FRSNA 288 HVPIP2;5 230 TG I NPARS LGAAV I YNKDKAWDDWI FW GPMI GAA I AA FYHQY L LRAGAI KALGS FRSNA 290 HVPIP2;1 228 TG I NPARS LGAAV I YNKDKAWDDWI FW GPLI GAA I AAAYHQY V LRASAK - LGSYRSNA 286 HVPIP2;3 229 TG I NPARS LGAAV I YNKDKAWDDWI FW GPFI GAA I AAAYHQY V LRASAK - LGSYRSN 286	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 117 OsPIP1;2 168 OsPIP1;2 117 OsPIP1;5 171 OsPIP1;5 171 OsPIP1;5 171 OsPIP1;5 171 HvPIP2;1 165 HvPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 233 AtPIP1;2 233 OsPIP1;2 234 ZmPIP1;5 234	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGGHINPAVTFGLFLARKVSLVRALVI I LAUCLGAICGVGLVKGFOSA - YFVRY 4 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACCLGAICGVGLVKGFOSA - YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFWHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 3 ASGFSRGTALGAEIVGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 GINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAAVYHQVVLRAIPFKSSAT 7 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 2 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 2 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 4 TGINPARSLGAAIIYNKSHAWDDHWIFWGPFIGAALAALYHVVVIRAIPFKSS- 4 TGINPARSLGAAIIYNKSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAALYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAAIYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAAIYHVVVRAIPFKSSS-	GGGANVM 155 GGGAN L 164 GGGAN L 164 GGGAN L 164 GGGAN L 164 A T I P I TG 233 A T I P I TG 224 A T I P I TG 225 A T I P I TG 2
APPI2:1 225 TGINPARSFGAAVIYNKSKPWDDHWIFWGPFIGAAIAAYHQYLRASGKSLGSFRSAANV 287 NPIP2:1 223 TGINPARSFGAAVIYNQDKAWDEHWIFWGPFIGAFAAAYHQYILRAGAVKALGSFRSNA- 283 HVPIP2:5 230 TGINPARSLGAAVIYNKDKAWDDQWIFWGPMIGAAIAAFYHQYILRAGAIKALGSFRSNA- 290 HVPIP2:1 228 TGINPARSLGAAVIYNTDKAWDDQWIFWGPLIGAAIAAYHQYVLRASAKK- LGSYRSNA - 286 HVPIP2;3 229 TGINPARSFGAAVIYNNKKAWDDHWLFWGPFIGAAIAAYHQYVLRASAKK- LGSSASFGRS 290	HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 117 OsPIP1;2 168 OsPIP1;2 117 OsPIP1;5 171 OsPIP1;5 171 OsPIP1;5 171 OsPIP1;5 171 HvPIP2;1 165 HvPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 233 AtPIP1;2 233 OsPIP1;2 234 ZmPIP1;5 234	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGGHINPAVTFGLFLARKVSLVRALVI I LAUCLGAICGVGLVKGFOSA - YFVRY 4 GVSGGHINPAVTFGLFLARKVSLIRALLYIIACCLGAICGVGLVKGFOSA - YFVRY 4 GVSGGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFWHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 3 ASGFSRGTALGAEIVGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 GINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAAVYHQVVLRAIPFKSSAT 7 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 2 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 2 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVIRAIPFKSS- 4 TGINPARSLGAAIIYNKSHAWDDHWIFWGPFIGAALAALYHVVVIRAIPFKSS- 4 TGINPARSLGAAIIYNKSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALYHVVVRAIPFKSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAALYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAAIYHVVVRAIPFKSSS- 4 TGINPARSLGAAIIYNRSHAWDDHWIFWGPFIGAALAALAAIYHVVVRAIPFKSSS-	GGGANVM 155 GGGAN L 164 GGGAN L 164 GGGAN L 164 GGGAN L 164 A T I P I TG 233 A T I P I TG 224 A T I P I TG 225 A T I P I TG 2
NtPIP2;1 223 TG I NPARS FGAAV I YNQDKAWDEHWI FW GPF I GAFAAAAYHQY I LRAGAVKALGS FRSNA 283 HvPIP2;5 230 TG I NPARS LGAAV I YNKDKAWDDQWI FW GPM I GAA I AA FYHQY I LRAGA I KALGS FRSNA 290 HvPIP2;1 228 TG I NPARS LGAAV I YN TDKAWDDQWI FW GPL I GAA I AAAYHQYVLRASAAK - LGSYRSN 286 HvPIP2;3 229 TG I NPARS FGAAV I YN NEKAWDDHWL FW GPF I GAA I AAAYHQYVLRASAAK - LGSYRSN 286	HvPIP2:1 103 HvPIP2:1 103 HvPIP2:3 104 ZmPIP1:6 177 HaPIP1:1 174 NtAQP1 170 AtPIP1:2 168 OsPIP1:2 171 ZmPIP1:5 171 HvPIP2:1 150 SiPIP2:7 164 HvPIP2:1 160 HvPIP2:1 160 HvPIP2:1 165 HvPIP2:1 165 HvPIP2:3 166 ZmPIP1:6 240 HaPIP1:1 237 NtAQP1 233 AtPIP1:2 232 SIPIP1:2 234 ZmPIP1:2 234 ZmPIP1:2 234	5 GISGHI NPAVTFGL FLARKVSLVRA LLYMVA OCLGAMCGVGL VKA FOSA - YFVRY 3 GVSGHI NPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL I RALLY I I AQCLGA I CGVGL VKGFOSA - YFVRY 4 GVSGHI NPAVTFGL FLARKVSL VRAVLY I AQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I AQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I AQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I AQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I FAQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I FAQCLGA I CGVGL VKGFOSA - FYVRY 14 GVSGHI NPAVTFGL FLARKVSL VRAVLY I FAQCLGA I CGVGL VKGFOSA - FYVRY 15 SPGY TKGDGLGAE I VGTFVL VY TVFSA TDAKRARDSHVP I LAF LP I GFAVFL VHL/ 10 NHYTKGDGLGAE I I GTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 10 NFOYTKGDGLGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 11 NFOYTKGDGLGAE I VGTFVL VY TVFSA TDAKRNARDSHVP I LAF LP I GFAVFL VHL/ 11 NFOYTKGDGLGAE I VGTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFWHL/ 22 ADGYS TGTGLAAE I VGTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFWHL/ 23 AGSTSRTALGAE I VGTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFWHL/ 24 AGYS KGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFWHL/ 36 AGYS KGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVP VLAF LP I GFAVFWHL/ 36 AGYS KGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFWHL/ 36 AGYS KGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFWHL/ 37 GI NPARSLGAAI I J TVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFWHL/ 36 AGYS KGTGLAAE I I GTFVL VY TVFSA TDPKRSARDSHVPVLAF LP I GFAVFWHL// 37 GI NPARSLGAAI I J TNDQAWDHWI I WG GPF I GAALAALYHOVVL RA I PFKSSAH 37 GI NPARSLGAAI I J TNDQAWDDHWI FWG GPF I GAALAALYHOVVL RA I PFKSSS. 37 GI NPARSLGAAI I J TNDQAWDDHWI FWG GPF I GAALAALAAYHOVVL RA I PFKSSS. 37 GI NPARSLGAAI I J NNCHAWDDHWI FWG GPF I GAALAALAAYHOVVI RA I PFKSSS. 47 GI NPARSLGAAI I J NNCHAWDDHWI FWG GPF I GAALAALAAI YHOVVI I RA I PFKSSS. 47 GI NPARSLGAAI I YNKAAWDDHWI FWG GPF I GAALAALAAYHOVVI RA I PF	GGGANVM 155 GGGANL 166 GGGANEL 164 GGGANEL 164 ATIPITG 236 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 237 ATIPITG 227 ATIPITG
HVPIP2;5 230 TG I NPARS LGAAV I YNKDKAWDDOWI FW GPM I GAA I AA FYHQY I LRAGA I KALGS FRSNA 290 HVPIP2;1 228 TG I NPARS LGAAV I YN TDKAWDDOWI FW GPL I GAA I AAAYHQYVLRASAAK - LGSYRSN 286 HVPIP2;3 229 TG I NPARS FGAAV I YNNEKAWDDHWLFW GPF I GAA I AAAYHQYVLRASATK - LGSSAS FGRS 290	HvPIP2;1 103 HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 171 ZmPIP1;5 171 HvPIP2;1 150 NtPIP2;1 160 HvPIP2;1 160 HvPIP2;1 165 VmPIP1;6 240 HaPIP1;1 233 NtAQP1 233 AtPIP1;2 232 SIPIP1;2 234 OsPIP1;2 234 USPIP1;2 234 USPIP1;2 234 USPIP1;2 234 USPIP1;2 234	5 GISGHINPAVTFGLFLARKVSLVRALLI MVAQCLGAMCGVGLVKAFQSS-YFVRY 3 GVSGHINPAVTFGLFLARKVSLIRALLI YI I AQCLGAICGVGLVKGFQSS-YFVRY 4 GVSGHINPAVTFGLFLARKVSLIRALLI YI I AQCLGAICGVGLVKGFQSS-YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYI I AQCLGAICGVGLVKGFQSS-YFVRY 14 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPALAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 9 AHGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 NPGYTKGDGLGAEI I GTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 2 AGGYSTGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFLVHL/ 2 AGGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 2 AGGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 SAGYSKGTGLAAEI I GTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL// 5 GISPRSLGAAI I YDNPHGWHGHWI FWGPFIGAALAAVYHQVVLRAIPFKSSAH 7 TGINPARSLGAAI I YNDPHGWHGHWI FWGPFIGAALAAVYHQVVLRAIPFKSSAH 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVLRAIPFKSSAH 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSAH 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSAH 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSAH 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSA 7 TGINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSC- 7 GINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSC- 7 GINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSC- 7 GINPARSLGAAI I YNNCHAWDDHWI FWGPFIGAALAALYHQVVI RAIPFKSSC- 7 GINPARSLGAAVYNNNKKAWDDHWI FWGPFIGAALAALA	GGGANVM 155 GGGAN L 166 GGGAN E L 164 GGGAN E L 164 A T I P I TG 233 A T I P I TG 232 A T I P I TG 224 A T I P I TG 225 A T I
HVPIP2;1 228 TG I NPARSLGAAV I YN TDKAWDDQWI FWYGPL I GAA I AAAYHQYVLRASAAK - LGSYRSN 286 HVPIP2;3 229 TG I NPARSFGAAV I YNNEKAWDDHWLFWGPF I GAA I AAAYHQYVLRASATK - LGSSASFGRS 290	HvPIP2;1 103 HvPIP2;1 103 HvPIP2;3 104 ZmPIP1;6 177 HaPIP1;1 174 NtAQP1 170 AtPIP1;2 168 OsPIP1;2 117 OsPIP1;2 168 OsPIP1;5 171 OsPIP1;5 171 OsPIP1;5 171 HvPIP2;1 165 HvPIP2;1 165 HvPIP2;1 165 HvPIP2;3 166 ZmPIP1;6 240 HaPIP1;1 233 AtPIP1;2 233 OsPIP1;2 234 ZmPIP1;5 234 OsPIP1;3 234 HvPIP2;2 225 SiPIP2;7 227 SiPIP2;7 227	5 GISGHINPAVTFGLFLARKVSLVRALLYMVACCLGAMCGVGLVKAFOSA - YFVRY 3 GVSGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 4 GVSGHINPAVTFGLFLARKVSLVRAVLYIIACLGAICGVGLVKGFOSA - YFVRY 7 SPGYTKGDGLGAEIVGTFVLVYTVFSATDAKRTARDSHVPILAFLPIGFAVFLVHL/ 4 ANGYTKGDGLGAEIVGTFVLVYTVFSATDAKRARDSHVPILAFLPIGFAVFLVHL/ 0 NHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 8 AHGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 4 STGYSTGTGLAAEIIGTFVLVYTVFSATDAKRNARDSHVPILAFLPIGFAVFLVHL/ 1 APGYTKGDGLGAEIVGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFLVHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDAKRSARDSHVPLAFLPIGFAVFWHL/ 2 ADGYSTGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 3 ASGFSRGTALGAEIVGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 3 AGGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 3 AGGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 SAGYSKGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISARGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGISAGTGLAAEIIGTFVLVYTVFSATDPKRSARDSHVPVLAFLPIGFAVFWHL/ 5 GGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVVRRAIPFKSSS- 2 TGINPARSLGAAIIFNKDRWDDHWIFWGPFIGAALAALYHVVVRRAIPFKSSS- 2 TGINPARSLGAAIIYNKSKMWDDHWIFWGPFIGAALAALYHVVVRRAIPFKSSS- 2 TGINPARSLGAAIIYNKSKAWDDHWIFWGPFIGAALAALYHVVVRRAIPFKSSS- 2 TGINPARSLGAAIVYNNKKAWDDHWIFWGPFIGAALAALAALYHVVVRRAIFFKSS- 2 TGINPARSLGAA	GGGANVM 155 GGGAN L 164 GGGAN E L 164 GGGAN E L 164 GGGAN E L 164 A T I P I TG 233 A T I P I TG 223 A T I P I TG 224 A T I P I TG 225 A T I P I TG 226 C C C C C C C C C C C C C C C C C C C
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#### FIGURE 1

Sequence alignment of  $CO_2$  permeable aquaporins from plants. Alignment was performed by the online tool Claustral Omega (https://www.ebi.ac. uk/Tools/msa/clustalo/) using default settings (Madeira et al., 2022). Blue shades indicated the percentage of identity. Helical regions were highlighted and denoted H1-H6. The central pore lining region were highlighted in red, including H2, H5 and LoopD. The key residues for  $CO_2$  permeability were highlighted with red rectangles. short linker (Otto et al., 2010). The results demonstrated that the homo-tetrameric assembly of  $CO_2$  permeable NtPIP1;2 was necessary for  $CO_2$  channel activity. However, such a relationship between the oligomeric state and  $CO_2$  permeability was not further investigated in other model plants, except for tobacco.

In 2021, Tyerman et al. gave a systematic review on multifunctional aquaporins, describing the dynamic regulation of the central pore with the high-resolution crystal structures of AQP1 and SoPIP2;1 (Tyerman et al., 2021). Furthermore, the MOLEonline MOLEonline channel radii analysis (Berka et al., 2012) showed a diameter of 3.6 Å at the Leu200 constriction residue, modelled by the closed water channel conformation of SoPIP2;1 (PDB: 1Z98) (Tornroth-Horsefield et al., 2006). According to the analysis, the constriction side would allow the CO<sub>2</sub> to pass when considering a kinetic diameter of 3.3 Å for  $CO_2$ . Additionally, Tyerman et al. (2021) proposed that both post-translational modification and protein-protein interactions could contribute to dynamic regulation of central pore permeability via local conformational changes, allowing a wide range of molecules, including K<sup>+</sup>, Na<sup>+</sup>, as well as CO<sub>2</sub> passing through the central pore. In early studies, aquaporins from the PIP1 family were found to be permeable to CO2. While, later on, members from the PIP2 family were also reported to function as CO<sub>2</sub> channels. Despite the relative conservation of transmembrane helices in all PIP aquaporins, it was difficult to identify the crucial residues creating the selective filter of the central pore, which was not surprising given the very variable pore environment generated by tetrameric assembly. As seen in Figure1, the major part of the central pore lining area is composed of transmembrane helices 2 and 5 and loop D, which were dynamically influenced by other neighboring motifs as well. However, due to the lack of high-resolution structure of PIP1 aquaporin, it remains unresolved how the sequence difference between PIP1s and PIP2s could contribute to CO2 permeability, especially the long N-terminal flexible loop that only exists in PIP1s. Although it is difficult to obtain structural details for the flexible loop region, a detailed biochemical assay might answer this question, such as domain switch or truncated variants in the case of an N-terminal loop. As indicated in Figure 1., conserved residues Leu in helix 5 and Ile at the end of loop E were reported to be essential to allow the passage of a CO<sub>2</sub> molecule based on either simulation or biochemical assays (Mori et al., 2014; Tyerman et al., 2021). However, other residues alone the channel might also be the restriction site, depending on the arrangement of the helixes structures that form the central channel.

## Role of sterols and non-CO<sub>2</sub> permeable proteins and technical challenges in measuring CO<sub>2</sub> permeability

The Singer-Nicolson fluid-mosaic model was widely recognized as the fundamental model for the structure and molecular dynamics of the plasma membrane (Singer and Nicolson, 1972). Many basic properties of biological membranes were characterized on the basis of this two-dimensional fluid model. Among the basic properties, the permeability was also intensively investigated using such a lipid bilayer model both theoretically and experimentally. However, other factors, such as sterols or integrated membrane proteins were not considered, which could influence the overall permeability (Suzuki and Kusumi, 2023). Therefore, lack of such factors could be the potential source for the inconsistency of measured membrane permeability. This inconsistency became non-trivial when determining CO<sub>2</sub> permeability. Due to the higher lipophilic properties of CO<sub>2</sub>, the phospholipid-formed lipid bilayer exhibits very low resistance to  $CO_2$ , while the plasma membrane of X. laevis oocytes, Madin-Darby canine kidney (MDCK) cells, the transformed human embryonal kidney SV40 cell line (tsA201), as well as the apical membrane of the gastric glands, showed extremely low CO<sub>2</sub> permeability (Endeward et al., 2006a; Endeward et al., 2006b; Endeward et al., 2008; Itel et al., 2012). In a recent review, Gros et al. proposed that the cholesterol content in the majority biological membranes dominates its CO<sub>2</sub> permeability, regulating the CO<sub>2</sub> permeability by at least 2 orders of magnitude with a cholesterol content between 0%-70% (Arias-Hidalgo et al., 2018). However, an exception of normal native human red cells showed aquaporin-dependent CO2 permeability instead of cholesterol content, indicating the existence of unidentified factors (Endeward et al., 2008). Kaldenhoff's group suggested a possibility, pointing out the role of non-channel proteins on the CO<sub>2</sub> permeability of the phospholipid bilayer (Kai and Kaldenhoff, 2014). Finally, the existence of lipid rafts, which are rich in both sterols and proteins, could further contribute to the overall permeability [see review by Kai Simons and Elina Ikonen (Simons and Ikonen, 1997)].

One possible reason for the inconsistent permeability of  $\mbox{CO}_2$ reported in many previous reports could be the limitations of different techniques in determining permeability of CO<sub>2</sub>, due to the high permeability of the phospholipid bilayer (Endeward et al., 2014). Both stop flow-based and mass spectrometry-based methods were questioned for their inability to quantify dynamic fast CO<sub>2</sub> across the membrane (Boron et al., 2011; Hannesschlaeger et al., 2019). On the other hand, the scanning pH electrode could provide an alternative that was not limited by the fast dynamics of CO<sub>2</sub> passing through the black lipid membrane. However, the formation of a black lipid membrane with the solvent-containing method was challenged by the presence of organic solvent n-decan, as well as whether aquaporins still survive as a functional form during the formation of the corresponding black lipid membrane (Hannesschlaeger et al., 2019). Therefore, new techniques that can determine the fast transportation of CO2 across the membrane and avoid the influence of solvents may be necessary to improve the accuracy of the CO<sub>2</sub> permeability measurements.

#### Conclusion

Despite the numerous structural and functional studies of aquaporins in the past several decades, our understanding of the detailed mechanism of functional and structural diversity of these relatively conserved channel proteins is still in its infancy. The debate over whether aquaporins are permeable to  $CO_2$  continues, with accumulating both supportive and contradictory evidence. However, the challenges in directly measuring  $CO_2$  permeability across native or artificial membranes make it difficult to fully interpret the results and understand their physiological implications. More attention should be paid to the interpretation of the data and investigating the potential effects of aquaporin overexpression on plant cultivars and photosynthesis-related parameters. Ultimately, a technical breakthrough for the direct measurement of CO<sub>2</sub> transportation through aquaporins would be needed to fully clarify the molecular details and bring an end to the ongoing debate.

#### Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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#### Conflicts of interest

Author KH is employed by Jiangsu Keybio Co. Ltd.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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