# Supplementary Data\_9\_Alignment H+-ATPases plasma membrane.

This alignment was done using ClustalW on the Lyon PBIL web server :

(<https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_clustalw.html>)

Important residues in the extended C-terminal sequence regulating the enzymatic function of these proton pumps are shown by color overlay : S and T for phosphorylation sites, L for the two leucine residues controlling this phosphorylation.

The C-termini of the two H+-ATPase proteins from Alismatales lacking the canonical auto-regulatory sequence (Zosma16g01420 & Sp4g0034200) are shown in yellow overlay. See **Supplementary Fig. S9.1** for the tree.

10 20 30 40 50 60 70 80 90 100

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Zosma404g00040 ---MEYEKPEMLDAVLREAVDLENIPIDEVFQNLRCSSDGLSTESAKERLIIFGHNKLEEKKESKIFMFLGFMWNPLSWVMEAAAIMAIALANGG----G

Sp2g0059700 ----MAEKPEVLDAVLKETVDLENIPLEEVFENLRCSREGLTTAAAEERLAIFGHNKLEEKKESKVLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

AHA4\_ARATH MTTTVEDNREVLEAVLKEAVDLENVPIEEVFENLRCSKEGLTTQAADERLALFGHNKLEEKKESKFLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

AHA11\_ARATH ----MGDKEEVLEAVLKETVDLENVPIEEVFESLRCSREGLTTEAADERLALFGHNKLEEKKESKFLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

OSA3xx29 ----MAEKEGNLDAVLKEAVDLENIPLEEVFENLRCSREGLTTQQAQQRLEIFGPNKLEEKEESKFLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

OSA1xx31 ----MAEDKGGLDAVLKESVDLENIPIEEVFQNLKCCRQGLTSEEAQLRLQLFGPNKLEEKEESKFLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

OSA2xx30 ----MAEKGDNLEAVLNESVDLENIPLEEVFEHLRCNREGLTSANAEQRLNLFGPNRLEEKKESKFLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

OSA8xx9 ---MLMEVANAMDAITKETVDLEHIPVEEVLDHLKCTREGLTSEVAQQRIHSFGYNKLEEKQESKLLKFLGFMWNPLSWVMEAAAIMAIALAHGGRDARG

AHA7\_ARATH -----MTDIEALKAITTESIDLENVPVEEVFQHLKCTKEGLTSNEVQERLTLFGYNKLEEKKESKILKFLGFMWNPLSWVMEAAALMAIGLAHGG----G

Zosma220g00220 ---MGD-SDGCLDDVKNENIDLETIPLQKVFDKLKCTSGGLSDEEGAKRLLIFGRNKLEEKHESKLLKFLGFMWNPLSWVMEIAAIMAIVLANGG----G

Zosma10g01680 ---MGD-SDGCLDDVKNENIDLETIPLQKVFDKLKCTSGGLSDEEGAKRLLIFGRNKLEEKHESKLLKFLGFMWNPLSWVMEIAAIMAIVLANGG----G

Zosma10g01670 ---MVDGNVAGLDDIKNENIDLESIPIEDVFENLKCSRGGLSDEEGAKRLQVFGPNKLEEKHESKLLKFLGFMWNPLSWVMEMAAIMAIALANGG----G

Zosma16g01420 ---MLN----------MLPFDQEKVSIDEVFIHLKCSRKGLSNDEGGRRLQTFGPNKLEEKKESKILKFLGFMWNPLSWVMEIAAIMAILLANGG----G

Sp4g0034200 --------------------------------------DGLTAEEGEQRLQIFGPNKLEEKEESKILKFLGFMWNPLSWVMESAALMAIVLANGQ----G

OSA6xx8 ---MAS---ISLEDVRNETVDLETIPVEEVFQHLKCSKQGLSAAEGQNRLNIFGPNKLEEKTESKLLKFLGFMWNPLSWVMEAAAIMAIVLANGG----G

OSA4xx32 ----MS---VSLEDLKKENVDLESIPIQEVFAVLKSSPQGLTSADGNGRLEIFGRNKLEEKKESKLLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

AHA6\_ARATH ---MAA--DISWDEIKKENVDLEKIPVDEVFQQLKCSREGLSSEEGRNRLQIFGANKLEEKVENKFLKFLGFMWNPLSWVMEAAAIMAIVLANGG----G

AHA8\_ARATH ---MAT--EFSWDEIKKENVDLERIPVEEVFEQLKCSKEGLSSDEGAKRLEIFGANKLEEKSENKFLKFLGFMWNPLSWVMESAAIMAIVLANGG----G

AHA9\_ARATH ---MAGNKDSSWDDIKNEGIDLEKIPIEEVLTQLRCTREGLTSDEGQTRLEIFGPNKLEEKKENKVLKFLGFMWNPLSWVMELAAIMAIALANGG----G

Sp12g0056200 ---MKGNNAMSLEDIKNETVDLEQIPIEEVFQQLKCSREGLSQEEGENRLQLFGPNKLEEKKESKILKFLGFMWNPLSWVMEMAALMAIVLANGD----G

Sp10g0009400 ---MAGDKAISLEEIRNENVDLERIPIEEVFAQLKCTKEGLSEEEGRSRIEIFGPNKLEEKKESKILKFLGFMWNPLSWVMEMAALMAIVLANGD----G

OSA7xx28 ---MGG-----LEEIKNEAVDLENIPIEEVFEQLKCTREGLSSEEGNRRIEMFGPNKLEEKKESKILKFLGFMWNPLSWVMEMAAIMAIALANGG----G

Zosma25g00380 ---MEN-KGINLEEIKNETVDLERIPVEEVFEQLKCSREGLSGEEGASRLQIFGPNKLEEKKESKFLKFLGFMWNPLSWVMEMAAIMAIALANGD----G

Zosma294g00130 ---MAG---KGLDDIKNETVDLEKIPIEEVFEQLKCTRQGLSTTEGESRLAIFGANKLEEKKENKILKFLGFMWNPLSWVMEAAALMAIVLANGD----G

AHA5\_ARATH ---MSE-----LDHIKNESVDLVRIPMEEVFEELKCTKQGLTANEASHRLDVFGPNKLEEKKESKLLKFLGFMWNPLSWVMEVAALMAIALANGG----G

AHA1\_ARATH ---MSG-----LEDIKNETVDLEKIPIEEVFQQLKCTREGLTTQEGEDRIVIFGPNKLEEKKESKILKFLGFMWNPLSWVMEAAALMAIALANGD----N

AHA2\_ARATH ---MSS-----LEDIKNETVDLEKIPIEEVFQQLKCSREGLTTQEGEDRIQIFGPNKLEEKKESKLLKFLGFMWNPLSWVMEMAAIMAIALANGD----G

AHA3\_ARATH --MASG-----LEDIVNENVDLEKIPIEEVFQQLKCSREGLSGAEGENRLQIFGPNKLEEKKESKLLKFLGFMWNPLSWVMEAAAIMAIALANGG----G

OSA5xx10 MAATASSTADALEQIKNEAVDLEHIPLEEVFQHLKCTREGLTNAEGDARTQVFGPNKLEEKKESKILKFLGFMWNPLSWVMEVAAIMAIALANGG----G

Zosma169g00540 ---MSIS----LEEIKKENVDLESIPVEEVFEQLKCSKNGLSSDEGAKRLQIFGQNKLEENKDSQVLKFLGFMWNPLSWVMELAAIMAIALTNGD----G

OS9xxx11 -MDEPGEPLLGLENFFDEDVDLENLPLEDVFEQLNTSQSGLSSADAAERLKLFGANRLEEKRENKIIKFLSFMWNPLSWVMEAAAVMALVLANGG----S

AHA10\_ARATH MAEDLDKPLLDPDTFNRKGIDLGILPLEEVFEYLRTSPQGLLSGDAEERLKIFGPNRLEEKQENRFVKFLGFMWNPLSWVMEAAALMAIALANSQ----S

Sp2g0033700 ----------------------ERLPLEEVFEQLRTSKEGLSSEDAEARLVLFGPNKLEEKPENKFLKFLGFMWNPLSWVMEAAAVMAIVLANGG----G

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Prim.cons. MA5MAGEK2ESLEDIKNE2VDLENIPIEEVFEQLKCSREGLSSEEGEERLQIFGPNKLEEKKESKILKFLGFMWNPLSWVMEAAAIMAIALANGGRDARG

110 120 130 140 150 160 170 180 190 200

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Zosma404g00040 K--PPDWQDFMGIITLLMINSTISFIEENNAGNAAAALMARLAPKAKVLRDGHWNEDDASILVPGDIISIKLGDIIPADARLLDGDPLKIDQSALTGESL

Sp2g0059700 K--PPDWQDFVGIITLLMINSTISFIEENNAGNAAAALMARLAPKAKVLRDGRWSEEEAAILVPGDIISIKLGDIIPADARLLDGDPLKIDQSALTGESL

AHA4\_ARATH K--PPDWQDFVGIITLLVINSTISFIEENNAGNAAAALMARLAPKAKVLRDGRWGEQDAAILVPGDIISIKLGDIVPADARLLEGDPLKIDQSALTGESL

AHA11\_ARATH K--PPDWQDFVGIITLLVINSTISFIEENNAGNAAAALMARLAPKAKVLRDGRWGEQDAAILVPGDIISIKLGDIVPADARLLEGDPLKIDQSSLTGESL

OSA3xx29 K--PPDWQDFVGIITLLVINSTISFIEENNAGNAAAALMARLAPKAKVLRDGRWTEEEAAILVPGDIVSIKLGDIIPADARLLEGDPLKIDQSALTGESL

OSA1xx31 K--PPDWQDFVGIITLLLINSTISFIEENNAGNAAAALMARLAPKAKVLRNGSWTEEEAAILVPGDIISIKLGDIIPADARLLEGDPLKIDQSALTGESL

OSA2xx30 K--PPDWQDFVGIITLLIINSTISFIEENNAGNAAAALMARLAPKAKVLRNGRWSEEEAAILVPGDIISVKLGDIIPADARLLEGDPLKIDQSALTGESL

OSA8xx9 KRMRIDYHDFVGIVLLLFINSTISFMEENNAGNAAAALMARLAPKAKVLRDGTWDELDASLLVPGDIISVKLGDIIPADARLLEGDPLKIDQSALTGESL

AHA7\_ARATH K--PADYHDFVGIVVLLLINSTISFVEENNAGNAAAALMAQLAPKAKAVRDGKWNEIDAAELVPGDIVSIKLGDIIPADARLLEGDPLKIDQATLTGESL

Zosma220g00220 Q--PPDWQDFVGIVVLLLINSVISFLEENNAGNAAAALMAGLAPRSKILRQGKWVDEEAEILVPGDIISIKLGDIVPADCRLLEGDPLKIDQSALTGESL

Zosma10g01680 Q--PPDWQDFVGIVVLLLINSVISFLEENNAGNAAAALMAGLAPRSKILRQGKWVDEEAEILVPGDIISIKLGDIVPADCRLLEGDPLKIDQSALTGESL

Zosma10g01670 K--PPDWQDFVGIIVLLLINSTISFLEENNAGNAAAALMAGLAPRSKILRQGKWVDEEAEILVPGDIISIKLGDIVPADCRLLEGDPLKIDQSALTGESL

Zosma16g01420 K--GPDWQDFVGIVTLLIINSTISFIEENNAGNAASALMAGLAPKTKVLREGKWSEQEAEILVPGDIISIKLGDIVPADARLLEGDPLKIDQAALTGESL

Sp4g0034200 K--PPDWPDFVGIVTLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDSKWSEQDAAILVPGDIISVKLGDIIPADARLLEGDPLKIDQSALTGESL

OSA6xx8 R--PPDWQDFVGIVVLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGKWQEQDASILVPGDIISIKLGDIIPADARLLEGDPLKVDQAALTGESM

OSA4xx32 R--PPDWQDFVGIVTLLFINSTISFIEENNAGNAAAALMASLAPQTKLLRDGKWSEQDAAILVPGDIISIKLGDIIPADARLMEGDPLKIDQSALTGESL

AHA6\_ARATH R--PPDWQDFVGITCLLIINSTISFIEENNAGNAAAALMANLAPKTKVLRDGRWGEQEAAILVPGDLISIKLGDIVPADARLLEGDPLKIDQSALTGESL

AHA8\_ARATH K--APDWQDFIGIMVLLIINSTISFIEENNAGNAAAALMANLAPKTKVLRDGKWGEQEASILVPGDLISIKLGDIVPADARLLEGDPLKIDQSALTGESL

AHA9\_ARATH R--PPDWQDFVGITVLLIINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGKWSEQEAAILVPGDIISIKLGDIVPADGRLLDGDPLKIDQSALTGESL

Sp12g0056200 R--PPDWQDFVGIVVLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGRWSEQDASILVPGDIISIKLGDIVPADARLLEGDPLKIDQSALTGESL

Sp10g0009400 R--PPDWQDFVGIVVLLVINSTISFIEENNAGNAAAALMANLAPKTKVLRDGRWTEQDASILVPGDIISIKLGDIVPADARLLEGDPLKIDQSALTGESI

OSA7xx28 K--PPDWEDFVGIIVLLVINSTISFIEENNAGNAAAALMANLAPKTKVLRDGRWGEQEAAILVPGDIISIKLGDIVPADARLLEGDPLKIDQSALTGESL

Zosma25g00380 K--PPDWQDFVGIIVLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGQWSEEEAAILVPGDIVSIKLGDIVPADARLLEGDPLKIDQSALTGESL

Zosma294g00130 N--PPDWQDFLGIVVLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGSWSEQEASILVPGDIVSIKLGDIVPADARLLEGDPLKIDQSALTGESL

AHA5\_ARATH R--PPDWQDFVGIVCLLLINSTISFIEENNAGNAAAALMAGLAPKTKVLRDNQWSEQEASILVPGDVISIKLGDIIPADARLLDGDPLKIDQSSLTGESI

AHA1\_ARATH R--PPDWQDFVGIICLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGKWSEQEAAILVPGDIVSIKLGDIIPADARLLEGDPLKVDQSALTGESL

AHA2\_ARATH R--PPDWQDFVGIICLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGKWSEQEAAILVPGDIVSIKLGDIIPADARLLEGDPLKVDQSALTGESL

AHA3\_ARATH K--PPDWQDFVGIVCLLVINSTISFVEENNAGNAAAALMAGLAPKTKVLRDGKWSEQEASILVPGDIVSIKLGDIIPADARLLEGDPLKVDQSALTGESL

OSA5xx10 R--PPDWQDFVGIIALLLINSTISYWEESNAGSAAAALMKNLAPKTKVLRDGRWSETDAFVLVPGDVINVKLGDIVPADARLLDGDPLKIDQSALTGESL

Zosma169g00540 KGKPPDWQDFVGILVLLMLNSTISFWEENNAGNAAAALMAGLAPRTRVLRDRYWSEQDAAILVPGDIISIKLGDIVPADARLLEGDLLKIDQSVLTGESM

OS9xxx11 Q--GTDWEDFLGIVCLLIINSTISFIEENNAGDAAAALMARLALKTKVLRDEQWQELDASTLVPGDIISIRLGDIVPADARLLEGDPLKIDQSALTGESL

AHA10\_ARATH L--GPDWEDFTGIVCLLLINATISFFEENNAGNAAAALMARLALKTRVLRDGQWQEQDASILVPGDIISIKLGDIIPADARLLEGDPLKIDQSVLTGESL

Sp2g0033700 Q--GPDWQDFVGIICLLIINSTISFIEENNAGNAASALMARLAPKTKVLRDGQWQERDAAILVPGDIISIKLGDIIPADARLLEGDPLKIDQSALTGESL

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Prim.cons. K22PPDWQDFVGIVVLLVINSTISFIEENNAGNAAAALMAGLAPKTKVLRDGKWSEQEAAILVPGDIISIKLGDIVPADARLLEGDPLKIDQSALTGESL

210 220 230 240 250 260 270 280 290 300

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Zosma404g00040 PVNKHPGEGIYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNHVGHFQKVLTSIGNFCICSIAVGMIIEIIVMYPIQHRDYRPGIDNLLVLLIGGIP

Sp2g0059700 PVTKGPGDGVYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDTTNQVGHFQKVLTSIGNFCICSIAVGMIIEIIVMYPIQDRAYRPGIDNLLVLLIGGIP

AHA4\_ARATH PVTKSSGDGVYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDTTNQIGHFQQVLTAIGNFCICSIAVGMLIEIVVMYPIQHRAYRPGIDNLLVLLIGGIP

AHA11\_ARATH PVTKGPGDGVYSGSTCKQGELEAVVIATGVHTFFGKAAHLVDTTNHVGHFQQVLTAIGNFCICSIAVGMIIEIVVMYPIQHRAYRPGIDNLLVLLIGGIP

OSA3xx29 PVTKGPGDGVYSGSTVKQGEIEAIVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAVGMFVEIIVMYPIQHRAYRPGIDNLLVLLIGGIP

OSA1xx31 PATKGPGDGVYSGSTVKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAVGMFVEIIVMYPIQHRPYRPGIDNLLVLLIGGIP

OSA2xx30 PVTKGPGDGVYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAIGMVVEIIVMYPIQHRDYRPGIDNLLVLLIGGIP

OSA8xx9 PVTKHPGDGIYSGSTCKQGEIEAVVIATGIHTFFGKAAHLVESTTHVGHFQKVLTSIGNFCICSIAAGMVIELLVMYAVHERKYRQIVDNLLVLLIGGIP

AHA7\_ARATH PVTKNPGASVYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTTHVGHFQKVLTAIGNFCICSIAVGMAIEIVVIYGLQKRGYRVGIDNLLVLLIGGIP

Zosma220g00220 PVTKYPGEGVYSGSTCKQGEIDAVVIATGVRTFFGKAAHLVDSTNNIGHFQMVLTSIGNFCIFTIALGMVVEIIVMYPIQNRKYRDGIDNLLVLLIGGIP

Zosma10g01680 PVTKYPGEGVYSGSTCKQGEIDAVVIATGVRTFFGKAAHLVDSTNNIGHFQMVLTSIGNFCIFTIALGMVVEIIVMYPIQNRKYRDGIDNLLVLLIGGIP

Zosma10g01670 PVTKYPGEGVYSGSTCKQGEIDAVVIATGVRTFFGKAAHLVDSTNNVGHFQTVLTSIGNFCILTIALGMVVEIIVMYPIQNRKYRDGIDNLLVLLIGGIP

Zosma16g01420 PVTKHPGQQVYSGSTCKQGELEAVVIATGIRTFFGKAAHLVDSTNNVGHFQKVLTSIGNFCICSIAVGMVVEIIFMYLIQHRNYREGIDNLLVLLIGGIP

Sp4g0034200 PVTKHPGDEIFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNNVGHFQKVLTAIGNFCICSIALGMLVEIVVMYPVQHRRYRDGIDNLLVLLIGGIP

OSA6xx8 PVNKHAGQGVFSGSTVKQGEIEAVVIATGVHTFFGKAAHLVDSTNNIGHFQLVLTAIGNFCIISIGVGMIIEIIVMYPIQHRAYRDGIDNLLVLLIGGIP

OSA4xx32 PVNKMPGDSIYSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNNVGHFQKVLTAIGNFCICSIAAGMLIEIIVMYPIQHRQYRDGIDNLLVLLIGGIP

AHA6\_ARATH PATKHQGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNNVGHFQKVLTAIGNFCICSIGIGMLIEIIIMYPIQHRKYRDGIDNLLVLLIGGIP

AHA8\_ARATH PTTKHPGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNNVGHFQKVLTSIGNFCICSIGLGMLIEILIMYPIQHRTYRDGIDNLLVLLIGGIP

AHA9\_ARATH PVTKHPGQEVYSGSTCKQGELEAVVIATGVHTFFGKAAHLVDSTNQEGHFQKVLTAIGNFCICSIAIGMLIEIVVMYPIQKRAYRDGIDNLLVLLIGGIP

Sp12g0056200 PVTKNPGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAVGMVVEIIVMYPIQRRKYRDGIDNLLVLLIGGIP

Sp10g0009400 PVTKNPGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAIGMVVEIIVMYPIQKRKYRDGIDNLLVLLIGGIP

OSA7xx28 PVTKNPGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQTVLTAIGNFCICSIAVGIVIEIIVMFPIQHRAYRSGIENLLVLLIGGIP

Zosma25g00380 PVTKHPGDEVFSGSTCKQGEIDAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAIGMVIEIIVMYPIQGRKYRDGIDNLLVLLIGGIP

Zosma294g00130 PVTRNPGSEVFSGSTCKQGEIDAVVIATGVHTFFGKAAHLVDSTNNVGHFQKVLTAIGNFCIVSIAIGIVIEIIVMWPIQRRKYRDGIDNLLVLLIGGIP

AHA5\_ARATH PVTKNPSDEVFSGSICKQGEIEAIVIATGVHTFFGKAAHLVDNTNQIGHFQKVLTSIGNFCICSIALGIIVELLVMYPIQRRRYRDGIDNLLVLLIGGIP

AHA1\_ARATH PVTKHPGQEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTSIGNFCICSIAIGIAIEIVVMYPIQHRKYRDGIDNLLVLLIGGIP

AHA2\_ARATH PVTKHPGQEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAIGMVIEIIVMYPIQRRKYRDGIDNLLVLLIGGIP

AHA3\_ARATH PATKGPGEEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAVGIAIEIVVMYPIQRRHYRDGIDNLLVLLIGGIP

OSA5xx10 PVTKLPGDCVYSGSTCKQGEIDAVVIATGVHTFFGKAAHLVDTTNQVGHFQKVLRAIGNFCIGAIAIGMAVEVIVMYLIQHRLYRDGIDNLLVLLIGGIP

Zosma169g00540 PVTKVSGDEVFSGSTCKQGEIEAVVIATGVRTFFGKAAYLVDSTKQVGHFQNVLTAIGNFCICSIAIGMLIEIIVMYPIQKRKYRDGIDNLLVLLIGGIP

OS9xxx11 PVTKRTGDIVFTGSTCKHGEIEAVVIATGIHSFFGKAAHLVDSTEVVGHFQKVLTSIGNFCICSIAIGAIVEVIIMFPIQHRSYRDGINNVLVLLIGGIP

AHA10\_ARATH PVTKKKGEQVFSGSTCKQGEIEAVVIATGSTTFFGKTARLVDSTDVTGHFQQVLTSIGNFCICSIAVGMVLEIIIMFPVQHRSYRIGINNLLVLLIGGIP

Sp2g0033700 PVTKRTGDQVFSGSTCKQGEIEAIVIATGINSFFGRAAHLVDSTEVIGHFQKVLTSIGNFCICSIAIGMLLEIIVMFPVQRRTYRDGINNLLVLLIGGIP

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Prim.cons. PVTKHPGDEVFSGSTCKQGEIEAVVIATGVHTFFGKAAHLVDSTNQVGHFQKVLTAIGNFCICSIAVGMVIEIIVMYPIQHRKYRDGIDNLLVLLIGGIP

310 320 330 340 350 360 370 380 390 400

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Zosma404g00040 IAMPTVLSVTMAIGSHRLSQHGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFQKG-INQDEVIRMAARASRIENQDAIDCAIVNMLADP

Sp2g0059700 IAMPTVLSVTMAIGSHRLAQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLVEVFAKG-VNQDTVILMAARASRTENQDAIDTAIVGMLADP

AHA4\_ARATH IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFMKG-VDADTVVLMAARASRLENQDAIDAAIVGMLADP

AHA11\_ARATH IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFTKG-VDADTVVLMAAQASRLENQDAIDAAIVGMLADP

OSA3xx29 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIDVFERG-ITQDQVILMAARASRTENQDAIDTAIVGMLADP

OSA1xx31 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEIFERG-VTQDQVILMAARASRTENQDAIDTAIVGMLADP

OSA2xx30 IAMPTVLSVTMAIGSHRLAQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKSLIEVFQRG-VDQDTVILMAARASRTENQDAIDATIVGMLADP

OSA8xx9 IAMPTVLSVTMAIGSHKLAQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFEKG-IEKDDVVLMAARASRLENQDAIDFAIVSMLPDP

AHA7\_ARATH IAMPTVLSVTMAIGAHRLAQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFKRG-IDRDMAVLMAARAARLENQDAIDTAIVSMLSDP

Zosma220g00220 IAMPTVLSVTMAIGSHRLSEQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFDDHHFNKDLVILMAARASRVENQDAIDASIVGMLGDP

Zosma10g01680 IAMPTVLSVTMAIGSHRLSEQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFDDHHFNKDLVILMAARASRVENQDAIDASIVGMLGDP

Zosma10g01670 IAMPTVLSVTMAIGSHRLSEQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFEKD-FNNDLVILMAARASRVENQDAIDASIIGMLNDP

Zosma16g01420 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKKLIEVFSKN-ADDNLVLLTAARASRIENQDAIDTTIVNMLDDP

Sp4g0034200 IAMPTVLSVTMAIGSHRLSEQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKTMIEVFAKD-VEKDTVMLLAARASRTENQDAIDASIVNMLADP

OSA6xx8 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKTLIEVYGRG-LDKDSVLLYAARASRVENQDAIDTCIVGMLADP

OSA4xx32 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNMIEPFVKD-LDKDAIVLYAARASRTENQDAIDASIVGMLADP

AHA6\_ARATH IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFSKD-VDKDYVILLSARASRVENQDAIDTSIVNMLGDP

AHA8\_ARATH IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKSLIEVFPKN-MDSDSVVLMAARASRIENQDAIDASIVGMLGDP

AHA9\_ARATH IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKSMVEVFVKD-LDKDQLLVNAARASRVENQDAIDACIVGMLGDP

Sp12g0056200 IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLSVDKNLIEVFAKG-VEKDHVILLAARASRTENQDAIDAAMVGMLADP

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AHA10\_ARATH IAMPTVLSVTLAIGSHRLSQQGAITKRMTAIEEMAGMDVLCCDKTGTLTLNSLTVDKNLIEVFVDY-MDKDTILLLAGRASRLENQDAIDAAIVSMLADP

Sp2g0033700 IAMPTVLSVTLAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNHLTVERNLIEMFNGD-MDKDMIILLAARASRLENQDAIDTAIVNMLADP

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Prim.cons. IAMPTVLSVTMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKLTVDKNLIEVFAKGHVDKDTVIL2AARASRVENQDAIDAAIVGMLADP

410 420 430 440 450 460 470 480 490 500

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Prim.cons. KEARAGIREVHFLPFNPVDKRTALTYID3SDGNWHRVSKGAPEQILELCNNKEDIERKVHAVIDKFAERGLRSLAVARQEVPEKSKESPGGPWQFVGLLP

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Prim.cons. LFDPPRHDSAETIRRALNLGVNVKMITGDQLAIGKETGRRLGMGTNMYPSSALLGQNGQHKDESIAALPVDELIEKADGFAGVFPEHKYEIVKRLQERKG

610 620 630 640 650 660 670 680 690 700

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Sp2g0033700 HICGMTGDGVNDAPALKKADIGIAVSDSTDAARGAADIVLTEPGLS--------------------IYAVSITIRIVLGFVLLALIWKYDFPPFMVLIIA

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Prim.cons. HICGMTGDGVNDAPALKKADIGIAVADATDAARSASDIVLTEPGLSVIISAVLTSRAIFQRMKNYTIYAVSITIRIVLGFMLIALIWKFDFSPFMVLIIA

710 720 730 740 750 760 770 780 790 800

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OSA1xx31 ILNDGTIMTISKDLVKPSPLPDSWKLAEIFTTGVVLGGYLAMMTVIFFWAAYKTNFFPRIFHVESL---------EKTAQDDYQKLASAVYLQVSTISQA

OSA2xx30 ILNDGTIMTISKDRVKPSPQPDSWKLSEIFATGVVLGSYLAMMTVIFFWVAYKTDFFPRVFHVESL---------EKTAQDDFQKLASAVYLQVSTISQA

OSA8xx9 ILNDGTIMTISKDKVKPSPYPDSWKLTEIFATGVIIGAYLAVTTVLFFWAAYKTQFFVHLFNVDTLNINKVDTTDNELVARNTEKLASAVYLQVSTISQA

AHA7\_ARATH ILNDGTIMTISKDRVKPSPTPDCWKLKEIFATGVVLGAYLAIMTVVFFWAAYETNFFHNIFHVRNFNQHHFKMKDKKVAAHLNEQMASAVYLQVSTISQA

Zosma220g00220 VLNDGTIMTIAKDRVKPSPLPDSWKLKEIFATGVVLGSYLAIMTVIFFWMVHVTDFFTEIFGVHSIR-------------NNKGQLMSALYLQVSIVSQA

Zosma10g01680 VLNDGTIMTIAKDRVKPSPLPDSWKLKEIFATGVVLGSYLAIMTVIFFWMVHVTDFFTEIFGVHSIR-------------NNKGQLMSALYLQVSIVSQA

Zosma10g01670 VLNDGTIMTIAKDRVKPSPLPDSWKLKEIFATGVVLGTYLALMTVIFFWMVHATNVFTEMFGVHSIR-------------NKEEQLMSALYLQVSIISQA

Zosma16g01420 VLNDGTIMTISKDRVKPSPMPDSWKLNEIFATGIVLGTYMAIMTALFFWIAHDTDVFTDVFGVHSLR-------------NNEDEMNAALYLQVSIISQA

Sp4g0034200 ILNDGTIMTISKDRVKPSPLPDSWKLGEIFATGIVLGSYLAVMTVVFFWAAHDTDFFSRVFGVRSIG-------------LESHELNSALYLQVSIVSQA

OSA6xx8 ILNDGTIMTISKDRVKPSPTPDSWKLKEIFATGIVLGTYMALITALFFYLAHDTDFFTETFGVRSIK-------------TNEKEMMAALYLQVSIISQA

OSA4xx32 ILNDGTIMTISKDRVKPSPLPDAWRLQEIFATGIVLGTYLALATVLFFWAVRDTDFFTVTFGVHPIG-------------GSTEELMAAVYLQVSIISQA

AHA6\_ARATH ILNDGTIMTISKDRVKPSPIPDSWKLKEIFATGVVLGTYMALVTVVFFWLAHDTTFFSDKFGVRSLQ-------------GKDEELIAVLYLQVSIISQA

AHA8\_ARATH ILNDGTIMTISKDRVKPSPVPDSWKLNEIFATGVVLGTYMALTTVLFFWLAHDTDFFSKTFGVRSIQ-------------GNEEELMAALYLQVSIISQA

AHA9\_ARATH ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGVVLGTYLAVMTVVFFWAAESTDFFSAKFGVRSIS-------------GNPHELTAAVYLQVSIVSQA

Sp12g0056200 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGIVLGSYLALMTVIFFWGMKDTDFFSKKFSVRSLR-------------NSEDEMMAALYLQVSIVSQA

Sp10g0009400 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGVVLGSYLALMTVIFFWAMKDTDFFSEKFHVRSIR-------------DSEHELMAALYLQVSIVSQA

OSA7xx28 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGIVLGSYLALMTVIFFWAMHKTDFFTDKFGVRSIR-------------NSEHEMMSALYLQVSIVSQA

Zosma25g00380 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGVVLGSYMAIMTVIFFWAMRETDFFSDKFGVRSLRPPTNKN--DPDYNDKRDEMMAALYLQVSIISQA

Zosma294g00130 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGVVLGSYMAVMTVVFFWIMKDTSFFSDKFGVRSIS-------------NSEDEMMGALYLQVSIISQA

AHA5\_ARATH ILNDGTIMTISKDRMKPSPQPDSWKLRDIFSTGVVLGGYQALMTVVFFWVMKDSDFFSNYFGVRPLS-------------QRPEQMMAALYLQVSIISQA

AHA1\_ARATH ILNDGTIMTISKDRVKPSPTPDSWKLKEIFATGIVLGGYQAIMSVIFFWAAHKTDFFSDKFGVRSIR-------------DNNDELMGAVYLQVSIISQA

AHA2\_ARATH ILNDGTIMTISKDRVKPSPTPDSWKLKEIFATGVVLGGYQAIMTVIFFWAAHKTDFFSDTFGVRSIR-------------DNNHELMGAVYLQVSIISQA

AHA3\_ARATH ILNDGTIMTISKDRVKPSPTPDSWKLKEIFATGVVLGGYMAIMTVVFFWAAYKTDFFPRTFHVRDLR-------------GSEHEMMSALYLQVSIVSQA

OSA5xx10 ILNDGTIMTISKDRVKPSPHPDSWKLPEIFITGIVYGTYLAVMTVLFFWAMRSTDFFTSTFHVKPLME-------------K-DEMMSALYLQVSIISQA

Zosma169g00540 ILNDGTIMTISKDRVKPSPLPDSWKLKEIFTTGVILGTYMALVTVVFFWMVKETDFFSDYFRMRSIR-------------ESNDEIMSALYLQVSIISQA

OS9xxx11 ILNDGTIMTISKDRVKPSPSPDSWKLNEIFAAGVVIGTYLALVTVLFYWTVTRTTFFESHFKVRSLK-------------QNSDEISSAMYLQVSIISQA

AHA10\_ARATH ILNDGTIMTISKDRVRPSPTPESWKLNQIFATGIVIGTYLALVTVLFYWIIVSTTFFEKHFHVKSIA-------------NNSEQVSSAMYLQVSIISQA

Sp2g0033700 ILNDGTIMTIAKDYVKPSPMPDSWKLNEIFATGVVIGTYLALVTVLFYWIITETNFFETYFKVKSLS-------------DNDEQISSAIYLQVSIISQA

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Prim.cons. ILNDGTIMTISKDRVKPSPLPDSWKLKEIFATGVVLGSYLALMTVIFFWAAHKTDFFSR2FGVRSLR4333K32DEKTAQDNEEELMSALYLQVSIISQA

810 820 830 840 850 860 870 880 890 900

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Zosma404g00040 LIFVTRSRSWSFVERPGALLLVAFAGAQLIATLIAVYANWGFAAIEGIGWRWAGVVWLYNIICYIPLDFIKFVIRYTLSGKAWDLVIEQRIAFTRQKDFG

Sp2g0059700 LIFVTRSRSWSFVERPGLLLVAAFFVAQLIATLIAVYADWGFSAIKGIGWGWAGVVWLYNIIFYLPLDPIKFMIRYALSGRAWDLVIEQRIAFTRQKDFG

AHA4\_ARATH LIFVTRSRSWSFVERPGIFLMIAFILAQLVATLIAVYANWSFAAIEGIGWGWAGVIWLYNIIFYIPLDFIKFFIRYALSGRAWDLVIEQRVAFTRQKDFG

AHA11\_ARATH LIFVTRSRSWSYVERPGMLLVVAFILAQLVATLIAVYANWSFAAIEGIGWGWAGVIWLYNIVFYIPLDIIKFLIRYALSGRAWDLVIEQRVAFTRQKDFG

OSA3xx29 LIFVTRSRSWSFVERPGFLLVFAFLVAQLIATLIAVYADWAFTSIKGIGWGWAGIVWLYNLIFYFPLDIIKFLIRYALSGKAWDLVIEQRIAFTRKKDFG

OSA1xx31 LIFVTRSRSWSFIERPGFLLVFAFFVAQLIATLIAVYANWAFTSIKGIGWGWAGIVWLYNLVFYFPLDIIKFLIRYALSGKAWDLVIEQRIAFTRKKDFG

OSA2xx30 LIFVTRSRSWSFVERPGFLLVFAFFVAQLIATLIAVYANWGFASIKGIGWGWAGVIWLYNIVFYLPLDIIKFLIRYALSGRAWDLVLEQRIAFTRKKDFG

OSA8xx9 LIFVTRSRGWSFLERPGLLLMAAFVIAQLIATVLAAIATWEVASIRGIGWRWAGAIWVYNIVVYLLLDPMKFAVRYGLSGKAWNLVIDNKVAFTNRKDFG

AHA7\_ARATH LIFVTRSRSWSFVERPGFLLVIAFLIAQLVASVISAMANWPFAGIRSIGWGWTGVIWIFNIVTYMLLDPIKFLVRYALSGKSWDRMVEGRTALTGKKNFG

Zosma220g00220 LIFVTRSRSWSFVERPGLFLVSAFFAAQFIATVIAVYANWQFAKIEGIGWKWAGSIWLYSLVTYIPLDILKFLIRYGLSGRAWDNLFQRRLAFSTRRDYG

Zosma10g01680 LIFVTRSRSWSFVERPGLFLVSAFFAAQFIATVIAVYANWQFAKIEGIGWKWAGSIWLYSLVTYIPLDILKFLIRYGLSGRAWDNLFQRRLAFSTRRDYG

Zosma10g01670 LIFVTRSRSWSFVERPGLFLVSAFFTAQFIATMIAVYGPLHFAKIKGIGWKWAGCIWLYSLVTYIPLDILKFCIRYGLSGRAWDNLFQRRLAFSTRRDYG

Zosma16g01420 LIFVTRSRGWSFLESPSMLLVGAFLAAQFIATIIAVYVDWRFAKVRGIGWRWAGFIWAYSVVTYFPLDLLKFGIRRVLSGKA------------------

Sp4g0034200 LIFVTRSRGWSYAERPGLLLVGAFLIAQLVATLIAVYAKWGFARVHGIGWGWAAVIWLYSFVTYLPLDIIKFVIRYALSGKAWDNLLQNK----------

OSA6xx8 LIFVTRSRSWSFVERPGALLVIAFLAAQLVATCIAVYAEWEFCKMQGIGWGWGGAIWAFSVVTYFPLDVLKFIIRYALSGRAWNN-INNKTAFVNKNDYG

OSA4xx32 LIFVTRARSWFFVERPGLLLVGAFLIAQLMATLIAVYANWPFAKMKGIGWSWGMVIWLFSIVTFFPLDIFKFAIRYFLSGKAWNNAFDNKTAFANELDYG

AHA6\_ARATH LIFVTRSRSWSFVERPGLLLLIAFFVAQLIATLIATYAHWEFARIKGCGWGWCGVIWIYSIVTYIPLDILKFITRYTLSGKAWNNMIENRTAFTTKKDYG

AHA8\_ARATH LIFVTRSRSWSFVERPGFLLLIAFVIAQLVATLIAVYANWGFARIVGCGWGWAGGIWVYSIITYIPLDILKFIIRYALTGKAWDNMINQKTAFTTKKDYG

AHA9\_ARATH LIFVTRSRSWSYVERPGFWLISAFFMAQLIATLIAVYANWNFARIRGIGWGWAGVIWLYSIVFYIPLDILKFIIRYSLSGRAWDNVIENKTAFTSKKDYG

Sp12g0056200 LIFVTRSRSWFFVERPGLLLVTAFAVAQLVATLVAVYADWGFARIKGIGWGWAGVIWLYSIITFFPLDWLKFLIRYVLSGKAWDNLLENRIAFTTKKDYG

Sp10g0009400 LIFVTRSRSWSFVERPGFLLVSAFIIAQLVATAIAVYANWGFARIKGIGWGWAGVIWLYSVVFYFPLDIIKFAVRYILSGKAWDNLLQNKTAFTTKKDYG

OSA7xx28 LIFVTRSRSWSFIERPGLLLVTAFMLAQLVATFLAVYANWGFARIKGIGWGWAGVIWLYSIVFYFPLDIFKFFIRFVLSGRAWDNLLENKIAFTTKKDYG

Zosma25g00380 LIFVTRSRSWSFVERPGFLLLIAFCIAQLVATLIATYANWGFAKIKGIGWGWAGVIWLYSIVTFLPLDVLKFAIRYILSGKAWNNLIDNKTAFTTKKDYG

Zosma294g00130 LIFVTRSRSWSFMERPGLLLVTAFFIAQMCATFIAVYADWGFARVKGVGWGWGGIIWLYSLVTFFPLDILKFITRYVLSGRGWENITENKTAFTSKKDYG

AHA5\_ARATH LIFVTRSRSWSYAECPGLLLLGAFVIAQLVATFIAVYANWSFARIEGAGWGWAGVIWLYSFLTYIPLDLLKFGIRYVLSGKAWLNLLENKTAFTTKKDYG

AHA1\_ARATH LIFVTRSRSWSFVERPGALLMIAFVIAQLVATLIAVYADWTFAKVKGIGWGWAGVIWIYSIVTYFPQDILKFAIRYILSGKAWASLFDNRTAFTTKKDYG

AHA2\_ARATH LIFVTRSRSWSFVERPGALLMIAFLIAQLIATLIAVYANWEFAKIRGIGWGWAGVIWLYSIVTYFPLDVFKFAIRYILSGKAWLNLFENKTAFTMKKDYG

AHA3\_ARATH LIFVTRSRSWSFTERPGYFLLIAFWVAQLIATAIAVYGNWEFARIKGIGWGWAGVIWLYSIVFYFPLDIMKFAIRYILAGTAWKNIIDNRTAFTTKQNYG

OSA5xx10 LIFVTRSRSWCFVERPGMLLCGAFVAAQIIATLVTVYATLGFAHIKGIGWGWAGVIWLYSIVTFLPLDIFKFAVRYALSGRAWDTLIEHKIAFTSKKDYG

Zosma169g00540 LIFVTRSHGWSYMERPGFLLVTAFCCAQLVATFIAVYANIEFAKIKGIGWGWAGVIWLYSIVTFIPLDMIKFVIRYVLSGKAWNNLIENRIAFSTKKDYG

OS9xxx11 LIFVTRSQGLSFLERPGALLICAFILAQLVATLIAVYATISFASISAIGWGWAGVIWLYSLVFYAPLDLIKIAVRYTLSGEAWNLLFDRKAAFASRRDYG

AHA10\_ARATH LIFVTRSRGWSFFERPGTLLIFAFILAQLAATLIAVYANISFAKITGIGWRWAGVIWLYSLIFYIPLDVIKFVFHYALSGEAWNLVLDRKTAFTYKKDYG

Sp2g0033700 LIFVTRSQSWSFTERPGTLLMCAFVVAQLVATLIAVYAHITFAYIHGIGWGWAGVIWLYSLIFYVPLDIIKFTVRYALSGDAWALLFDRKTAFTTKKDYG

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Prim.cons. LIFVTRSRSWSFVERPGLLLVIAFFIAQL2ATLIAVYANWGFAKIKGIGWGWAGVIWLYSIVTY2PLDIIKFAIRYALSGKAWDNLIENRTAFTTKKDYG

910 920 930 940 950 960 970 980

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Zosma404g00040 KEARELKWAHAQRTLHGLQMPD-VKM--FNDRT--AITDLNQMAEEAKRRAEIARLRELHTLKGHVESVVRLKGLDIETIQ-QAYTV

Sp2g0059700 KEARELKWAHAQRTLHGLQPPD-TKM--FGERT--SVTDLNQLAEEAKRRAEIARLRELHTLKGHVESVVRLKGLDIDTIQ-QSYTV

AHA4\_ARATH KEQRELQWAHAQRTLHGLQAPD-TKM--FTDRT--HVSELNQMAEEAKRRAEIARLRELHTLKGHVESVVRLKGLDIETIQ-QAYTV

AHA11\_ARATH KEQRELQWAHAQRTLHGLQAPD-AKM--FPERT--HFNELSQMAEEAKRRAEIARLRELHTLKGHVESVVRLKGLDIETIQ-QAYTV

OSA3xx29 KEERELKWAHAQRTLHGLQPPD-AKM--FSEKA--GYNELNQMAEEAKRRAEIARLRELHTLKGHVESVVKLKGLDIETIQ-QSYTV

OSA1xx31 KEERELKWAHAHRTLHGLQPPD-AKP--FPEKT--GYSELNQMAEEAKRRAEIARLRELHTLKGHVESVVKLKGLDIDTIH-QSYTV

OSA2xx30 TQENQLKWATAQRTIHGLQPAATAAV--FRDMT--SYNDLNQLAEEARRRAEIARLRELTTLKGRMESVVKQKGLDLETIQ-QSYTV

OSA8xx9 REARVVAWAHEQRTLHGLQSAA--S----REKA--ASTELNQMAEEARRRAEITRLRELHTLKGKVESVAKLKGIDLEDVNNQHYTV

AHA7\_ARATH QEERMAAWATEKRTQHGLETGQ--KP--VYERN--SATELNNMAEEAKRRAEIARMRELQTLKGKVESAAKLKGYDLEDPNSNNYTI

Zosma220g00220 RVEREAQWAQEERAKHGLQTTTTEI-NTLLGENTTGYRVLSEIAEQAKKRAEIARMTELRTLKGHVESVVKLKGLEMENIQ-QHYTL

Zosma10g01680 RVEREAQWAQEERAKHGLQTTTTEI-NTLLDENTTGYRVLSEIAEQAKKRAEIARMTELRTLKGHVESVVKLKGLEMENIQ-QHYTL

Zosma10g01670 RAEREAQWVQEERAKRGLQTTTTAM-NTLLDDT-TGYRLLSEIADQAKKRAEIARMIELHTLKGHVESVVRLKGLDIENMQ-QHYTL

Zosma16g01420 --------------SCGGTTDQHKN-ENDLDDH--DLRELSETAELEMRQVEK----------------------------------

Sp4g0034200 -----------------------------LDKH-LSMRIVSPTPDDGGVLC------------------------------------

OSA6xx8 KGEREAQWATAQRTLHGLNQSSTSS-DLFNDKT--GYRELSEIAEQAAKRAEVARLRELHTLKGHVESVVKLKGLDIDTIQ-QSYTV

OSA4xx32 KSKREAQWAIAQRSLHGLQQAETST-ALFDDNK--DYLELSEIAEQAKRRAEIARLRELHTLKGHVESVVKLKGLDIDTIQ-NHYTV

AHA6\_ARATH RGEREAQWALAQRTLHGLKPPE--SM--FEDTA--TYTELSEIAEQAKKRAEVARLREVHTLKGHVESVVKLKGLDIDNLN-QHYTV

AHA8\_ARATH KGEREAQWALAQRTLHGLPPPE--AM--FNDNK----NELSEIAEQAKRRAEVARLRELHTLKGHVESVVKLKGLDIDTIQ-QHYTV

AHA9\_ARATH KGEREAQWAQAQRTLHGLQPAQTSDM--FNDKS--TYRELSEIADQAKRRAEVARLRERHTLKGHVESVVKQKGLDIEAIQ-QHYTL

Sp12g0056200 IEEREAQWATAQRTLHGLQNPQTATL--FSDKS--SYRELSEIAEQAKRRAEIARLRELNTLKGHVESVVKLKGLDIDTIQ-QHYTV

Sp10g0009400 REEREAQWAMAQRTLHGLQPPEATNL--FADKN--SYRELSEIAEQAKRRAEIARLRELHTLKGHVESVVKLKGLDIDTIQ-QHYTV

OSA7xx28 REEREAQWATAQRTLHGLQPPEVASNTLFNDKS--SYRELSEIAEQAKRRAEIARLRELNTLKGHVESVVKLKGLDIDTIQ-QNYTV

Zosma25g00380 REEREAQWATAQRTLHGLQTNESQTL--FADTR--NYRELSEIAEQAKRRAEVARLRELNTLKGHVESVVKLKGLDIDTIQ-QHYTV

Zosma294g00130 REEREAQWATAQRTLHGLQTAESTTN-IFPDKG--GYRELSEIAEQAKRRAEVARLRELNTLKGHVESVVKLKGLDIETIQ-QNYTV

AHA5\_ARATH KEEREAQWAAAQRTLHGLQPAEKNN--IFNEKN--SYSELSQIAEQAKRRAEVVRLREINTLKGHVESVVKLKGLDIDTIQ-QHYTV

AHA1\_ARATH IGEREAQWAQAQRTLHGLQPKEDVN--IFPEKG--SYRELSEIAEQAKRRAEIARLRELHTLKGHVESVAKLKGLDIDTAG-HHYTV

AHA2\_ARATH KEEREAQWALAQRTLHGLQPKEAVN--IFPEKG--SYRELSEIAEQAKRRAEIARLRELHTLKGHVESVVKLKGLDIETP--SHYTV

AHA3\_ARATH IEEREAQWAHAQRTLHGLQNTETAN--VVPERG--GYRELSEIANQAKRRAEIARLRELHTLKGHVESVVKLKGLDIETA--GHYTV

OSA5xx10 RGEREAQWATAQRTLHGLQTPEMGT----TSAA--SYRELSEIAEQAKRRAEVARLRELSTLKGQMESTVRLKGLDMDNVQ-HHYTV

Zosma169g00540 KEEREAQWATAQRTLHGLHTSDEQA--FLAERN--SYRELSEIAEQAKRRAEVARLRELHTLKGHVESVIKLKGLDIGRIN-KHYTV

OS9xxx11 GNERRPETRWPRSHHHHHQQRRALSDHLLSSG-----WRPTRIAERAKRRAEIARLGDAHMLRAHVQSVMRLKRVDSDVIR-SAQTV

AHA10\_ARATH KDDGSPNVTIS--------QRSRSAEELRGSR-----SRASWIAEQTRRRAEIARLLEVHSVSRHLESVIKLKQIDQRMIR-AAHTV

Sp2g0033700 KEDREAKWLRS---Q--KSLEGISSTDLERDA-----RRSSGMAEQARRRAEIARLGELHALRGHVESVVRLKNLDSISIK-TARTV

. .:

Prim.cons. KEEREAQWATAQRTLHGLQPPETAKM2LF2DKTSTGYRELSEIAEQAKRRAEIARLRELHTLKGHVESVVKLKGLDI2TIQ2QHYTV

**Alignment data :**  
Alignment length : 988  
Identity (\*) : 362 is 36.64 %  
Strongly similar (:) : 165 is 16.70 %  
Weakly similar (.) : 56 is 5.67 %  
Different : 405 is 40.99 %  
Sequence 0001 : Zosma404g00040 ( 957 residues).  
Sequence 0002 : Sp2g0059700 ( 956 residues).  
Sequence 0003 : AHA4\_ARATH ( 960 residues).  
Sequence 0004 : AHA11\_ARATH ( 956 residues).  
Sequence 0005 : OSA3xx29 ( 956 residues).  
Sequence 0006 : OSA1xx31 ( 956 residues).  
Sequence 0007 : OSA2xx30 ( 957 residues).  
Sequence 0008 : OSA8xx9 ( 970 residues).  
Sequence 0009 : AHA7\_ARATH ( 961 residues).  
Sequence 0010 : Zosma220g00220 ( 960 residues).  
Sequence 0011 : Zosma10g01680 ( 960 residues).  
Sequence 0012 : Zosma10g01670 ( 959 residues).  
Sequence 0013 : Zosma16g01420 ( 880 residues).  
Sequence 0014 : Sp4g0034200 ( 849 residues).  
Sequence 0015 : OSA6xx8 ( 950 residues).  
Sequence 0016 : OSA4xx32 ( 949 residues).  
Sequence 0017 : AHA6\_ARATH ( 949 residues).  
Sequence 0018 : AHA8\_ARATH ( 948 residues).  
Sequence 0019 : AHA9\_ARATH ( 954 residues).  
Sequence 0020 : Sp12g0056200 ( 954 residues).  
Sequence 0021 : Sp10g0009400 ( 954 residues).  
Sequence 0022 : OSA7xx28 ( 951 residues).  
Sequence 0023 : Zosma25g00380 ( 964 residues).  
Sequence 0024 : Zosma294g00130 ( 952 residues).  
Sequence 0025 : AHA5\_ARATH ( 949 residues).  
Sequence 0026 : AHA1\_ARATH ( 949 residues).  
Sequence 0027 : AHA2\_ARATH ( 948 residues).  
Sequence 0028 : AHA3\_ARATH ( 949 residues).  
Sequence 0029 : OSA5xx10 ( 955 residues).  
Sequence 0030 : Zosma169g00540 ( 951 residues).  
Sequence 0031 : OS9xxx11 ( 956 residues).  
Sequence 0032 : AHA10\_ARATH ( 947 residues).  
Sequence 0033 : Sp2g0033700 ( 908 residues).

Supplementary Fig. S9.1

