

Figure S4. Alignment of the amino acid sequences included in clade AQP7/AQP9/AQP3. The amino acids conserved in all the sequences are labelled with asterisks (*); the conservative and semi-conservative substitutions are labelled with colons (:) and periods (.), respectively. The NPA motifs are highlighted in yellow, the residues within the ar/R constriction are highlighted in green, and the aspartic acid downstream the second NPA motif is highlighted in gray. The predicted immunogenic peptides from OmAQP97 are highlighted in underlined red letters and their homologous regions in the remaining clade members are highlighted in plain red letters.

OmAQP97	---MANPPFPFMKRFVIKSPVLREFLAEEFFGTFLYIFGGASFAHYIFSGQKDVLAVTFC	57
A0A293N0E3_ORNER	---MANPPYPFLKRFVIRSPAVREFLAEEFFGTFLYIFGGASFAHYIFGNQKDVLAVTFC	57
A0A2R5L6Q7_9ACAR	---MANPPYPFLKRFVIKSPALREFLAEEFFGTFLYIFGGASFAHYIFGNQKDVLAVTFC	57
XP_029845129.1	---MGNPPPPFFKKFVTTNQAVREFLAEEFFGTFLYIFGGASFAHYLFTDNKDVFAVTFC	57
XP_037563616.1	MASAGNPPFPFLRKLVTKNEAVKEFLAEFFGTFLYIFGGASFAHFLFTDSKDVFAVTFC	60
XP_037292097.1	MASAGNPPFPFLRKVFTKNEAVKEFLAEFLGTFLYIFGGASFAHFLFTDQKDVFAVTFC	60
XP_037292096.1	MASAGNPPFPFLRKVFTKNEAVKEFLAEFLGTFLYIFGGASFAHFLFTDQKDVFAVTFC	60
XP_037509276.1	-----MEVKMFGGASFAHFLFTDQKDVFAVTFC	28
XP_037510820.1	MASAGNPPFPFLRKVFTKNEAVKEFLAEFLGTFLYIFGGASFAHFLFTDQKDVFAVTFC	60
XP_037510819.1	MASAGNPPFPFLRKVFTKNEAVKEFLAEFLGTFLYIFGGASFAHFLFTDQKDVFAVTFC	60
CAX48963.1	MASAGNPPFPFLRKVFTKNEAVKEFLAEFLGTFLYIFGGASFAHYLFTAQKDVFAATFC	60
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OmAQP97	WGMGVMLGIQTGAGVSGGHVNPVVTTFASVGRLPWKVPVHYLLGQHLGAFLASAILYFN	117
A0A293N0E3_ORNER	WGMGVMLGIQTGAGVSGGHVNPVVTTSFASVGRLPWRKVPHYILGQHLGAFLASAILYFN	117
A0A2R5L6Q7_9ACAR	WGMGVMLGIQTGAGVSGGHVNPVVTTSFASVGRLPWRKVPHYILGQHLGAFVASAILYFN	117
XP_029845129.1	WGIGVMLGIQTGAGVSGGHVNPIVTTSFASVGKLPWRKVPHYLLGQHLGAFLAAILYFN	117
XP_037563616.1	WGIGVMLGIQTGAGVSGGHVNPVVTTSFASIGKLPWRKVPHYMLGQHLGAFLASAILYFN	120
XP_037292097.1	WGIGVMLGIQTGAGVSGGHVNPIVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	120
XP_037292096.1	WGIGVMLGIQTGAGVSGGHVNPVVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	120
XP_037509276.1	WGIGVMLGIQTGAGVSGGHVNPIVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	88
XP_037510820.1	WGIGVMLGIQTGAGVSGGHVNPVVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	120
XP_037510819.1	WGIGVMLGIQTGAGVSGGHVNPIVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	120
CAX48963.1	WGIGVMLGIQTGAGVSGGHVNPVVTTSFASVGKLPWRKVPHYILGQHLGAFLASAILYFN	120
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OmAQP97	YIDALDHYDGGGERQIFGDRGTGILLTTFPNEHVHLSICIFDITIICSGLLMFTIMVIIDNK	177
A0A293N0E3_ORNER	YVDVLDDHYDGGTRQIFGVNGTGILLTTFPNEHVHLSICIFDITIICSGLLMFTIMVIIDNK	177
A0A2R5L6Q7_9ACAR	YIDVLDHYDGGGERQIFGNKGTGILLTTFPNEHVHLSICIFDITIICSGLLMFTIMVIIDNK	177
XP_029845129.1	YIDLLDKFDGGARQIFGTNGTGILLSTYPHPDVHLSVCVFDTIICSGLLMFTIMVILDDR	177
XP_037563616.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
XP_037292097.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
XP_037292096.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
XP_037509276.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	148
XP_037510820.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
XP_037510819.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
CAX48963.1	YIDLLDSVDGGERQIFGNKGTGILLTTPNDNVHLSVCVFDTIICSGLLMFTIMVILDDR	180
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OmAQP97	NANTTSGMHAFLIGIMVVALCWAFTGNCMAAVNPADFPPRVLASIVGYGPEVFTYRHF	237
A0A293N0E3_ORNER	NANTTAGMHAFLIGIMVIALCWAFTGNCMAAINPADFPPRVLASIVGYGPEVFTYRHF	237
A0A2R5L6Q7_9ACAR	NANTTAGMHAFLIGIMVIALCWAFTGNCMAAINPADFPPRVLASIVGYGPEVFTYRHF	237
XP_029845129.1	NANTTKGMHAFLIGIMVVALCWAFTGNCMAAVNPADFPPRVLSALVGYGAETFSYRQFW	237
XP_037563616.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAETFTFRNFW	240
XP_037292097.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFTFRNFW	240
XP_037292096.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFTFRNFW	240
XP_037509276.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFMFRNFW	208
XP_037510820.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFTFRNFW	240
XP_037510819.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFTFRNFW	240
CAX48963.1	NANTTKGMHAFLIGIMVVALCWAYGANCMAAVNPADFPPRVLSALVGYGAESFMFRNFW	240
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OmAQP97	WIPMFIPHVGGGLIGTWLYVLAIEMHIVPERVRDDRTEREMTNLLPLPPRTEKTGV----	292
A0A293N0E3_ORNER	WIPMFIPHVGGGLIGTWLYVLAIEMHIVPERARDDRTEREMTNLLPLPPRTEKPAI----	292
A0A2R5L6Q7_9ACAR	WIPMFIPHVGGGLIGTWLYVLAIEMHIRPERLHDDRAEREMTNLLPLPPRTEKSAA----	292
XP_029845129.1	WIPLFVPHLGGFLIGTWLYVLFVGMHIKPKRRDGD--EKEVVNLLPLAPRADKTS-----	290
XP_037563616.1	WIPMFVPHLGGGLIGTWLYVLGVGMHISKQSK-D--GPEGVNLLPLAPRADKTV-----	292
XP_037292097.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSR-D--GPEGVNLLPLAPRADKTA-----	292
XP_037292096.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSR-D--GPEGVNLLPLAPRAGESTGNTGVY	297
XP_037509276.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSK-D--GPEGVNLLPLAPRADKVA-----	260
XP_037510820.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSK-D--GPEGVNLLPLAPRADKVA-----	292
XP_037510819.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSK-D--GPEGVNLLPLAPRAGESTGNTGVY	297
CAX48963.1	WIPMFVPHLGGGLIGTWLYVLCIGMHISKQSK-D--GPEGVNLLPLAPRAGESTGNTGVY	297
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OmAQP97	-----	292
A0A293N0E3_ORNER	-----	292
A0A2R5L6Q7_9ACAR	-----	292
XP_029845129.1	-----	290
XP_037563616.1	-----	292
XP_037292097.1	-----	292
XP_037292096.1	TVGLHSAVYHIADNKGTNANIASPGVPAGNVSEEKVK	334
XP_037509276.1	-----	260
XP_037510820.1	-----	292
XP_037510819.1	TVGLRSAVYHITDDRGTHAIVASPGVPAANIEEKIK	334
CAX48963.1	TVGLRSAVYHITDDRGTHANVASPGVPAANIEEKIK	334