

Figure S5. Alignment of the amino acid sequences included in clade AQP_{Ae.a}. 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 and the residues within the ar/R constriction are highlighted in green. The predicted immunogenic peptides from OmAQP91 are highlighted in underlined red letters and their homologous regions in the remaining clade members are highlighted in plain red letters.

OmAQP91	MGRVRQFRSIFGIDELSATSTLWKSMAIEYIGTAMLVFIA	<u>CGTCTNWGRGG</u> ----EPSIA	56
A0A293MYA1_ORNER	MGRVRQFRSVFGIDELSATSTLWKAMIAEYIGTAVLVFIA	<u>CGTCTNWGRPG</u> ----EPSIT	56
XP_029833586.1	MGRVRQFRNLGIDEVSASSTLWKSMAEYIGTAVIVLIG	<u>CGSCINWGSPTKPLGEATMV</u>	60
XP_037582105.1	MGRVRQFRSFCGIDEVSATSSLWKSMAEYIGTAVIVLIG	<u>CGSCINWGSPEKPQGEATMV</u>	60
XP_037502974.1	MGRVRQFRSFCGIDEVSATSSLWKSMAEYIGTAVIVLIG	<u>CGSCINWGSPEKPQGEATMV</u>	60
XP_037283568.1	MGRVRQFRSFCGIDEVSATSSLWKSMAEYIGTAVIVLIG	<u>CGSCINWGSPEKPQGEATMV</u>	60
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OmAQP91	QIALSFAFIVATMAQALGHVSGAHINPAVTMGMLCVGHISILRAFFYICSQLIGGITGAA		116
A0A293MYA1_ORNER	QIALSFAFIVATMAQALGHVSGAHINPAVTMGMLCVGHISILRAFFYICSQLIGGITGAA		116
XP_029833586.1	QIAIGFGITVATMAQAVGHVSGAHLNPAVTMGMLFVGKVSILRSFFYICSQLIGGITGAA		120
XP_037582105.1	QIAIGFGITVATMVQALGHVSGGHLNPAVTIGMLFVGRVSLLRSSFFYLCSQLIGGITGAA		120
XP_037502974.1	QIAIGFGITVASMVQALGHVSGGHLNPAVTIGMLFVGRVSLLRSSFFYLCSQLIGGITGAA		120
XP_037283568.1	QIAIGFGITVASMVQALGHVSGGHLNPAVTIGMLFVGRVSLLRSSFFYLCSQLIGGITGAA		120
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OmAQP91	VLRAVTPEERQGLLGGTALSEGVTFFQGVVVELVITFILVLTTFVAVCDQNRLDVLGSPPL		176
A0A293MYA1_ORNER	ILRAVTPEDRQGLGGLKLDGVTFFQGVVVELMITFILVLTTFVAVCDQNRLDILGSAPL		176
XP_029833586.1	ILRAVTPDARHGALGGTGLAEGVTPLMGLAVEVCITFILVLTTFVAVCDTNRLDVQGSAPL		180
XP_037582105.1	ILRAVTPEARHGALGGTSLAEGVTPLMGLGVEACITFILVLTTFVAVCDTNRLDVQGSAPL		180
XP_037502974.1	ILRAVTPEARHGALGGTSLAEGVTPLMGLGVEACITFILVLTTFVAVCDTNRLDVQGSAPL		180
XP_037283568.1	ILRAVTPEARHGALGGTSLAEGVTPLMGLGVEACITFILVLTTFVAVCDANRLDVQGSAPL		180
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OmAQP91	AIGLAVGAGLMLVIGYTASMNNTATFGPAVISGAFDDHWVYWLGPIGGGILAGFVYQYV		236
A0A293MYA1_ORNER	AIGLSVGAGLMAIGYTASMNNTATFGPAVISGAFDDHWVYWLGPIGGGILAGFVYQYV		236
XP_029833586.1	AIGLSVTTCHVFAVRYTAGMNVASFGPAVMSGIFDDHWVFWVGPILGGIIAAVIYENV		240
XP_037582105.1	AIGLSVTTCHVFAVRYTAGMNVASFGPAVMSGMFDDHWVFWLGPILGGVIAAVVYENV		240
XP_037502974.1	AIGLSVTTCHVFAVRYTAGMNVASFGPAVMSGMFDDHWVFWLGPILGGVIAAVVYENV		240
XP_037283568.1	AIGLSVTTCHVFAVRYTAGMNVASFGPAVMSGMFDDHWVFWLGPILGGVIAAVVYENV		240
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OmAQP91	LSAPPISFEALDKAQLACLARFHNKEAVEDRTTAI	271	
A0A293MYA1_ORNER	FSAPAITSEALDKAQLASLAKFNNKEVVEDRTTSI	271	
XP_029833586.1	FQAPPITTEELDKAQITAMAKLANKEVVADRTTSI	275	
XP_037582105.1	FQAPPITSEDLDKAQITVMAKLANKEVVADRTTSI	275	
XP_037502974.1	FQAPPITTEDLDKAQITVMAKLANKEVVADRTTSI	275	
XP_037283568.1	FQAPPITSEDLDKAQIMAMAKLTNKEVVADRTTSI	275	
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