

QID41594.1	-----MASLSPPATTTTTNISSLQPSPLFHKASQVSLVGKR	37
XP_010647098.3	MSVHYKRKEGPRPFSYPYRLISTMASLSPPAT-TTTTNISSLQPSPLFHKASQVSLVGKR	59
XP_059596123.1	-----MASLPWSLTSTAIANTTNISALPPSPLFHRVSHVPIARNR	41
NP_001268045.1	-----MASLPWSLTSTFTAIANTTNISAFPPSPLFQRASHVPVARNR	41
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QID41594.1	NPRFVRRVVSCLNATNGDERSTSSSKSGESPLGKLDRRNVLGLGGLYGV-SGLGAADPFA	96
XP_010647098.3	NPRFVRRVVSCLNATNGDERSTSSSKSGESPLGKLDRRNVLGLGGLYGV-SGLGAADPFA	118
XP_059596123.1	SRRFAPSKVSCNAANGDPNSDSTSDIRETSPGKLDRRNVLGLGGLYGAAAGLGATKPLA	101
NP_001268045.1	SRRFAPSKVSCNSANGDPNSDSTSDVRETSSGKLDRRNVLGLGGLYGAAAGLGATKPLA	101
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QID41594.1	FAAPISPPDLSECGAADLPAGAQTNCPPVSSKIIDFKLLPKNSPLRIRPAHLASKEY	156
XP_010647098.3	FAAPISPPDLSECGAADLPAGAQTNCPPVSSKIIDFKLLPKNSPLRIRPAHLASKEY	178
XP_059596123.1	FGAPIQAPDISKCGTATVPDGVTPXNCCPPVTTKIIDFQLPSSGSPMRTRPAHLVSKY	161
NP_001268045.1	FGAPIQAPDISKCGTATVPDGVTPXNCCPPVTTKIIDFQLPSSGSPMRTRPAHLVSKY	161
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QID41594.1	IAKYKKAIELMKALPDDDPFSFMQQADVHCAYCNGAYHQVGFDPDLQVHNSWLFLPYHR	216
XP_010647098.3	IAKYKKAIELMKALPDDDPFSFMQQADVHCAYCNGAYHQVGFDPDLQVHNSWLFLPYHR	238
XP_059596123.1	LAKYKKAIELQKALPDDDPFSFQQANVHCTYCQAYDQVGYTDLELQVHASWLFLPFHR	221
NP_001268045.1	LAKYKKAIELQKALPDDDPFSFQQANVHCTYCQAYDQVGYTDLELQVHASWLFLPFHR	221
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QID41594.1	YYLYFYEKILGKLINDPTFALPFWNWADAPAGMQMPAMFADPNSPLYDKLRDAKHQPPKLI	276
XP_010647098.3	YYLYFYEKILGKLINDPTFALPFWNWADAPAGMQMPAMFADPNSPLYDKLRDAKHQPPKLI	298
XP_059596123.1	YYLYFNERILAKLIDDPFALPYAWNDPDGMYMPTIYASSPSSLYDEKRNKHLPTVI	281
NP_001268045.1	YYLYFNERILAKLIDDPFALPYAWNDPDGMYMPTIYASSPSSLYDEKRNKHLPTVI	281
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QID41594.1	DLDYNLTDSNDTNEQQISSNLSIMYRQIVSSAKTTSLFMGAAYRAGDEPDGPQGTLENIP	336
XP_010647098.3	DLDYNLTDSNDTNEQQISSNLSIMYRQIVSSAKTTSLFMGAAYRAGDEPDGPQGTLENIP	358
XP_059596123.1	DLDYDGTSTIPDDELKTDNLAIMYKQIVSGATTPKFLGYPYRAGDAIDPGAGTLEHVP	341
NP_001268045.1	DLDYDGTSTIPDDELKTDNLAIMYKQIVSGATTPKFLGYPYRAGDAIDPGAGTLEHVP	341
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QID41594.1	HGPVHIWCGDRQTQPNIEDMGNFYSAARDPIFFSHHSNVDRMWTVWVGLGGK-RKDFTPDP	395
XP_010647098.3	HGPVHIWCGDRQTQPNIEDMGNFYSAARDPIFFSHHSNVDRMWTVWVGLGGK-RKDFTPDP	417
XP_059596123.1	HNIVHKWTGLADKP-SEDMGNFYTAGRDPIDFFGHANVDRMWNWIKTIGGKNRKDFDTPD	400
NP_001268045.1	HNIVHKWTGLADKP-SEDMGNFYTAGRDPIDFFGHANVDRMWNWIKTIGGKNRKDFDTPD	400
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QID41594.1	WLDAGFVFYDENAQLIRVKVRDCLDPTKLRYAYQEVDIPWLKSRPKPRQILKKVVNKLKH	455
XP_010647098.3	WLDAGFVFYDENAQLVRVKVRDCLDPTKLRYAYQEVDIPWLKSRPKPRQILKKVVNKLKH	477
XP_059596123.1	WLDATFVFYDENKQLVKVKSVCVDTSKLRYQYQDIPWLPKNTKAKAK- ---TTTKSS	456
NP_001268045.1	WLDATFVFYDENKQLVKVKSVCVDTSKLRYQYQDIPWLPKNTKAKAK- ---TTTKSS	456
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QID41594.1	KSGVANAAEIPSS---SSIVFPIKLDSTLRVDVPRPKRSRKEKEDEEEVLVIKIELE	512
XP_010647098.3	KSGVANAAEIPSS---SSIVFPIKLDSTLRVDVPRPKRSRKEKEDEEEVLVIKIELE	534
XP_059596123.1	KSGVAKAAELPKTTISSIGDFPKALNSVIRVEVPRPKRSRKEKEDEEEVLVIKIELE	516
NP_001268045.1	KSGVAKAAELPKTTISSIGDFPKALNSVIRVEVPRPKRSRKEKEDEEEVLVIKIELE	516
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QID41594.1	RDKFVKFDIFINDEDDPVSRPDNTEFAGSFVNVPHQHSHGKKNTILRIGISELLEDLEA	572
XP_010647098.3	RDKFVKFDIFINDEDDPVSRPDNTEFAGSFVNVPHQHSHGKKNTILRIGISELLEDLEA	594
XP_059596123.1	RENFVKFDVYINDEDYSVRPNSEFAGSFVNVPKHMKEMKTKTNLRFAINELLEDLGA	576
NP_001268045.1	RENFVKFDVYINDEDYSVRPNSEFAGSFVNVPKHMKEMKTKTNLRFAINELLEDLGA	576
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QID41594.1	EDDHSVVTLVPRYGADVITIGGIEIELAS- 602	
XP_010647098.3	EDDHSVVTLVPRYGADVITIGGIEIELAS- 624	
XP_059596123.1	EDDESIVTIVPRAGGDDVTIGGIEIEFVSD 607	
NP_001268045.1	EDDESIVTIVPRAGGDDVTIGGIEIEFVSD 607	
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**Figure S1.** Mapping of identified peptides on multiple sequence alignment of grapevine PPOs. The sequence of the peptides identified by LC-MS/MS are marked in red. The thylakoid signal peptide sequence is shaded in black.