

Predicted protein sequence for MtRDR1

MVKS^UKTIELYGFPHYVTVPDVKRFVEQYTGEGSVVAIKIREGKARIRTAFAIIQFTTKD^UHV
TDMMALPSRSL^UPLQYGSSYLKVREMERDIVRRPREILH^USLNDVKLYFCCQISEERL^USV
LWREVDVRVDFGIGMRKWPFTLCHDNKTFKLEL^USYENIWKIELHQPRSKTTKYLLIQLIG
APRVFELYSPTSDDA^UYNVYEDLS^UKNYFSDPPDDQWIRAVDFTPCSCIGQSSALCLELPS^U
NRDFPNFRENFAQYEEESAGPYMLESGSPFSCNLDVVPMSPPQGIQIPFDILFKVNSLV
QHGCL^USG^USELDNAFYHLVDPTRVNVELIENALEKMYYSNDFCYEPVRWLKDQYKMYH
SSNNLPRSPTISLDNGLVYVRAQIT^UPCKVYFCGPEINVSNRVLRKYKKHMDNFLRV^USF
VDEELD^UKLYSSDL^USRIS^UVGGRTDIYRILSILRNGIVIGDKKFEFLAFSSSQLRES^USLWM
FARTPTGDTAG^USIREWMGDFSRIKNVAKYAARLGQSF^USS^UTETT^UTV^USS^UTEIEIILDVHNK
TK^UYVFSDGIGKISLELARRVAQKCG^UYDSMPSAFQIRYGGYKGVVAVDPTSSVKL^USLRMS^U
MLK^UYDSDNTDL^UDLACSKFRPCYLN^URQLITLLSTLDVED^USVFEKKQKEAVDQLNTIL^UTDS^U
TKAHEVLDLMSSGEVTNLIKEMLICGYKPNVEPFLSMMLQTFRASKLLELRQKTRIFIPK
GRAMMGVLDETRTLEYGEV^UFVQYSNNREDSLSHV^UVNGKV^UVVAKNPCLYPGDV^URVLKA
VDVPALRHMVDCV^UVFPQK^UGHRPH^UNECSG^USDLGDIYFVCWDSELIPPKTIDPMEYDS^U
AK^UPIVLDHDVEIEEVQKYFTDYILNDCLGIIANAHTVFAD^UKEPGKAMADPCVELAKLFSTA
VDFPKTGIPAEIPRGLFPTEYPDFMEKPKPI^UYKSKNVIGKLFREIQG^USTKDGSITSFTLE
VA^UKES^UYDS^UDMEFEGFMDYVDDAFYHKTNYDYKLG^UNLMDYYG^UIKTEAEILSGNIMKMSK
SFTKKRDADAITMAVR^USLRKEARS^UWFTDSGAGVDS^UGSDDA^UYAKASAWYYV^UTYHHSY^U
GLYNEGMQRDHFLSFPWC^UVYHLLV^UQIKKEKARMKMHS^URMEQSFSHRLRLD

Additional File 7: Predicted ubiquitination and phosphorylation sites in the MtRDR1 amino acid sequence. Potential ubiquitination sites are back-shaded in black (medium confidence prediction) or high-lighted in green (low confidence prediction). Amino acid residues predicted to be potential phosphorylation sites in the translated MtRDR1 protein sequence are underlined and highlighted in blue. Phosphorylation sites were predicted using NetPhos 2.0 software [64]. Only residues with a potential phosphorylation score > 0.850 (high confidence prediction) have been marked above. Ubiquitination sites were predicted using UbPred software [65].