

Supplementary Figure S2

Alignment of Mrp/NBP35-like proteins in *Saccharomyces cerevisiae* and *Yarrowia lipolytica*

		<u>Walker A</u>	
ScCfd1p		MEEQEIGVPAASLAGIKHIIILISGKGGVGKSS	
YALI0E19074g		MYSTATQSSPSLAGVKNIVLVLSGKGGVGKSS	
ScNbp35p	MTEILPHVNDEVLPAEYELNQPEPEH	CPGPESDMAGKSDA	CGGCANKEICE
YALI0E02354g	MPSLVDPVANKTDEGNRDTLKAPEPEH	CPGTESEEAGKADA	CGGCPNQDICE
YALI0B18590g / Ind1	MGRFRLIAPIQRSIAIISRLQPITANFHSSPALR	SHENPLGIPKSPASAPRIPRKT	TRRPEPIAGVKKTIVVSSAKGGVGKST
			83
			↑
			<u>Walker B</u>
Cfd1p	VTTQTALTLCSMG-FKVGVL	DIDLTGPSLPRMFGLENESIYQGPEGWQPVKVETN	STGSLSVISLGFLLGDRGNSVIWRGPKKTSMIKQF
YALI0E19074g	VTTQLALTLAAQG-KKVGVL	DIDLTGPSIPRFFGMEDKQVYQSSAGWVPVYTDASRN	--LCLMSLGFLLSRGRDSSVWRGPRKTAMIRQF
Nbp35p	FAAMLSWALSADEDLQVGAMLDI	CGPSLPHMLGC	IKETVHESNSGWTPVYVTDN----
YALI0E02354g	FSSLLGWGFASDLDRVGLMDIDI	CGPSLPKMMGSEGEQIHTSLSGWSP	IYVSDN----LGMMSVGFM
YALI0B18590g	VSVNTALSLAKRG-LRVGLLDVD	IFGPSIPTMFGLSGEP	RMTHGKLI
			PMSKFG-----IQVMSMGFLVDP-NKAVAWRGLLVQKALEQL
			166
			<u>Mrp signature</u>
Cfd1p	ISDVAWGELDYLLIDTPPGTS	DEHISIAEELRYS-KPDGGIVV	TTPQSVATADV
YALI0E19074g	IRDVVWGELDYLLIDTPPGTS	DEHISIAEELRFCDQILGAVIV	TTPQGVALADVRKELSF
Nbp35p	LKDVDWDKLDYLVIDTPPGTS	DEHISINKYMRES-GIDGALV	VVTPQEVALLDVRKEIDF
YALI0E02354g	LKDVDWGNLDYLVVDTPPGTS	DEHLSVTQYLKES-GVDGAVV	ITTPQEVALLDVRKELDF
YALI0B18590g	LQDVDWGTLDVLVMDLPPGT	GDVQLTIAQT	VKID---GAIIVSTPQDVALVDVVRGLDL
			FEKTYTKVLGLVQNMSVFVCPN
			CNHETHIF
			252
			242 245
Cfd1p	S--SGGGKRLSEQFSVPYLG	NVPIDPKFVEMIENQVSSK	TLVEMYRESSLCPIFEEIMK
YALI0E19074g	S--KGGGENLAKQYECKFL	GTVPIDPKFVLMVENAKGGL	QEIYGETDMAKIFAGICDKAFSE
Nbp35p	KATTGGGEALCKELGIKFL	GSVPLDPRIGKSC	DMGESFLDNYPD
YALI0E02354g	APTTGGGKALAEFNI	PFLGSVPLDPRIGKSC	DHGESFVEEYPDSPATTA
YALI0B18590g	G-VDGAVSKAKSRGLG	VLGNVPLDPQICSQSDK	GVPAVSGGVQAKYYDKIAEGVAEQLGV
			312
			279

Common motifs are in grey: Walker A or P-loop, Gx(4)GK[ST], Walker B, DxxG and the Mrp family signature, Wxx[LIVM]D[VFY][LIVM](3)DxPPGT[GS]D (ProSite PS01215). The arrow marks the cleavage site predicted by TargetP, as confirmed by N-terminal sequencing. Conserved cysteines are in yellow. The amino acid numbering corresponds to YALI0B18590/Ind1.