

Additional file 3 - Alignment of the fungal transcription factor regulatory middle homology region (FTFRMH region) of Xyr1 and Cep3p and the consensus

Xyr1_dom	359	LPVSLACDLIDLYFSSSSSAQMHPMSPYVLGFVFRKRSFLHPTNPRRCQPALLASMLWVA
Cep3p_dom		-----
Consensus	1	PPREVADRLLDLYFEN-----VHPLFPILHRPTFLRDLESLSYDPSSLSPASLALLLAVL
Xyr1_dom	419	AQTSEASFLTSLPSA-----RSKVCQKLELTVGLLQPLIHTGTNSPSPKTSPPVVGAAA
Cep3p_dom	108	-----KDQSFQLMNFAMEN-----LGALY
Consensus	56	ALAA-----LSLPDSELRGESRRSLAERYEAAARQLLDLALFL---PPSLETQLALLLLA : : * : :
Xyr1_dom	473	LGVLGVAMPGSLNMDSLAGETGAFGAIGSLDDVITYVHLATVVSASEYKGASLRWWGAAW
Cep3p_dom	127	FGSIGDISELYLRVEQYWDRRADKNH--SVDGKYWDALISVFTMCIY----YMPVEKLA
Consensus	108	LYLLGTGDPSS-----AWLLLGLAI : : *
Xyr1_dom	533	SLARELKLGRELPNPPANQEDGEGLSEDVDEHDLNRNNTFRVTEEEEREERRRAWWLIVY
Cep3p_dom	181	EIFSVYPLHEYL-GSNKRLNWEDGMQLVMCQNFARCSLFQLKQCDFMAHPDIRLV--QAY
Consensus	128	RLAQSLGLHRD--PSSLP-----GLSP-----FERELRRRLWWSLY : * . . * : * *
Xyr1_dom	593	IVDRHLALCYNRPLFLLDSECSLDYHPMDDIKWQAGKFRSHDARNSSINIDSSMT-----
Cep3p_dom	238	LILATTFPYDEPL-LANSLLTQCIHTFKN--FHVDDFRPL-LNDDPVESIAKVTLGRI
Consensus	162	ILDRLLSLSLGRPPSISDEDID-----VPLPSNED----- :: : : ..* : : : : :
Xyr1_dom	648	-----DEFGDSPRAARGAHYECRGRSIFGYFLSLMTILGEIVDVHHAKSHPRFGVGFRS
Cep3p_dom	294	YRLCGCDYLQSGPRKPIALHTEVSSLLQHAAYLQDLPN----VDVYREEN-----S
Consensus	192	-----DELSPSSPPPPPPSEEPSLSFFIALIRLARILGRILRLLYS---PRAS-----S * : . . * . . : : *
Xyr1_dom	702	ARDWDEQVAEITRHLDMYEESLKRFAKHLPLSSKDKEQHEMHDSGAVTDMQSPLSVRTN
Cep3p_dom	341	TEVLYWKIISLDRDLQYLNKSSK-----PPLKTLDAIRRELDIFQYKVD-SLEEDFRSN
Consensus	239	PEDSLETILELDAELEEWASL-----PPELRLD .. : : .* : : . . * :
Xyr1_dom	762	ASSRMTESEIQASIVVAYSTHVMHVLH-----ILLADKWDPINLLDDDDDLWISSEGFVT
Cep3p_dom	395	NSRFQKFIALFQISTVSWKLFKMYLIYDADSLKVIHYSKVIISLIVNNFHAKSEFFN
Consensus	268	SSSLESPSLLPQRLLL----HLLY--H-----LLLILLHRPFLLRSLSSSLSPSSSSAES * . : : . : : : * . : . : .
Xyr1_dom	816	ATSHAVSAEAEISQILEF--DPGLEFMPFFYGVYLLQGSFLLLLLIADKLQA-----EAS
Cep3p_dom	455	RHPMVMQITITRVVSFISF-----YQIF-VESA AVKQLLVDLTELTANLPTIFG
Consensus	316	RRA-CLEAAREILELLRLLLSLSSLLLLLWVFLLYYLFSAALVLLLALLLRPSSSELEEAR . : : : : : : : * : .
Xyr1_dom	868	PSVIKACETIVRAHEACVVTLSLEYQRNFSKVMRSAL
Cep3p_dom	502	SKLDKLVYLTTERLSKL-----
Consensus	375	SLLERALELLERLSERWP-RLARRALRLLERLLARAR . : : * :