

Consensus	-----XXGXXXXXKXXXXXXXXFXLLXXGXXXVHGXD-----	
yeast Emp46	MTTRKTASSLQLLGKITGKAGTKQKKNFINGLIWLYMCVWVHGKVTQKDEL-----	54
yeast Emp47	-----MMMLITMKSTVLLSVFTVLATWAGLLEAHPLGDTSDAS-----	38
human ERGIC-53	-----MAGSRQRGLRARVRPLFCALLLSLGRF-VRGDGVGGDPAVALPHR	44
Consensus	KXXXXYSL--PXL---XXKXXXXWXXGXXALEEGRIVLTPX-KNXXKGSLLWKXXXXX	
yeast Emp46	KWNLKGYSL--PNLLEVTDDQKELSQWTLGDKVKLEEGRFVLTGP-KNTKGSLLWKPEYSI	111
yeast Emp47	KLSSDYSL--PDLI---NARKVPNNWQTGEQASLEEGRIVLTSK-QNSKGSLLWKQGFDL	92
human ERGIC-53	RFEYKYSFKGPHLV---QSDGTVPFWAHAGNAIPSSDQIRVAPSLKSQRGSVWTKTKAAF	101
Consensus	KDXXTEWTFRSXGXGXGXTXGGLAFWXXQ-XXNGXXXXLFGGXX-XXNGLXILDXDXL	
yeast Emp46	KDAMTIEWTFRSFGRGSGTKGGLAFWLKQ-GNEGDSLELFGGSSKFFNGLMILLRLLDDKL	170
yeast Emp47	KDSFTMEWTFRSVGYSGQTDGGISFWFVQDSNVPRDKQLYNGPV-NYDGLQLLDVNNGPL	151
human ERGIC-53	EN-WEVEVTFRVTGRGRIGADGLAIWYAE--NQGLEGPVFGSAD-LWNGVGIFFDSFDND	157
Consensus	G----PXXXXLNDGQKXXDXXXXYXQXFAASCLXXYQDSXVPSTXRTYX-----XXD	
yeast Emp46	G----ESVTAYLNDGTDLDIESSPY---FASCLFQYQDSMVPSTLRLTYN-----PLD	217
yeast Emp47	G----PTLRGQLNDGQKPV-DKTKIYDQSFASCLMGYQDSSVPSTIRVTYD-----LED	200
human ERGIC-53	GKKNPAIVIIIGNNGQIHYDHQNDGASQALASCQRDFRNKPYVRAKITYYQNTLTVMIN	217
Consensus	NXXLLKXQXDNXVCFQTRKVXFXSGXFRIGXSAXNGAXXXXXESFEILKMQLXX-GVIED	
yeast Emp46	NHLLKLQMDNRVCFQTRKVKFMGSSPFRIGTSAINDA---SKESFEILKMKLYD-GVIED	273
yeast Emp47	DNLLKQVDNKKVCFQTRKVRFP-SGSYRIGVTAQNGAVNNNAESFEIFKMQFFN-GVIED	258
human ERGIC-53	NGFTPKNDYEFCAKVENMIIPAQGHF--GISAATGGLADDHVDLSLTFQLTEPGKEPP	275
Consensus	SLIPNVNMGQPKXXTKXIXXQTGXEKXXEKX-----PFXXXXESITXXEL---F	
yeast Emp46	SLIPNVNPMGQPRVVTKVINSQTGEESFREKM-----PFSDKEESITSNEL---F	320
yeast Emp47	SLIPNVNAMGQPKLITKYIDQQTGKEKLIKT-----AFDADKDKITNYEL---Y	305
human ERGIC-53	TPDKEISEKEKEKYQEEFEHFQQELDKKKEEFQKGHPDLQGQPAEEIFESVGDRELQVF	335
Consensus	EKXNR--LEGKILANDIDXLL-----XKLNXXVVKX	
yeast Emp46	EKMNK--LEGKIMANDIDPLL-----RKMNKIVEN	348
yeast Emp47	KKLDL--VEGKILANDINALE-----TKLNDVIKV	333
human ERGIC-53	EGQNRIHLEIKQLNRQLDMILDEQRRYVSSLTEEISKRGAGMPGQHGQITQQELDTVVKT	395
Consensus	QXELLXXXXXXXXXX--PXXLXKGXDDSDXXXXEXFQDFLSINXXLXXVXXE----	
yeast Emp46	ERELIQRL-----RPLLDLKKTAISDDS-----FQDFLSMNANLDRLIKE----	388
yeast Emp47	QQELLSFMTTITKQLSSKPPANNEKGTSTDDAIAEDKENFKDFLSINQKLEKVLVE----	389
human ERGIC-53	QHEILRQVNEMKNSM--SETVRLVSGMQHPGSAGGVYETTQHFIDIKEHLHIVKRDIDNL	453
Consensus	-QEKXRXKXXGXXPXXDEIXSKXXWLXXLIFIMLXXAYMFRIXQEIXXKXKLL	
yeast Emp46	-QEKIRQDAKLYGKQTKGHDEIFSKISVWLALLIFIMITLAYMFRIHQDIKKVKLL	444
yeast Emp47	-QEKYREATKRHGQDGPVQVEIARKLMIWLLPLIFIMLVMAYYTFRIRQEIIKTKLL	445
human ERGIC-53	VQRNMPSEKPKCELPFPFSPCLSTVHFIIFVVVQTVLFIGYIMYRSQQEAAAKFF	510