

Additional File 2

A)

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EmIR1 LBD SCTVIEGNLLIVMTRLP-----VNASIPNIREITGFLVIYDLMGLDGLATLFPNLTVIR-----GRSLISNFA 63
EmIR2 LBD NCTVINGNLLISGLSNT-QCIQNGLSLPRLFQIFGSLIVEHSSCSGDLSHFLPNLIAIHGILPFSAQIPIEGKVITIPPYS 79
HsIGF1R LBD NCTVIEGYLHLLLSKA--EDYRSYRFPKLTIVITEYLLLRVAGLESGLDLPNLTVIR-----GWKLFYNYA 66
HsINSR LBD NCSVIEGHLQILLMFKTRPEDFRDLSFPKLTIMITDYLLLRVYGLLESKDLFPNLTVIR-----GSRLFFNYA 68

EmIR1 LBD LVIRSTS-LKITGLPSLRVIRGGVRVDLNTNLCYVRTVMNSYILGDQTA---APVRLLTNRILCPDTCQPECAAST 138
EmIR2 LBD LLIHHTA-LSGIGLRCLRVLRGLVLLIDNPQMCYTDITIGVHLLTPSAYPSKPISNDSVASRNGGVFGQDLLRKEGLFD 158
HsIGF1R LBD LVIFEMTNLKDITGLYNLRNITRGATRIEKNAIDLCTYSTVDWSLITDAVSN-----NYIVGNKPP-KECGDLC 132
HsINSR LBD LVIFEMVHLKELGLYNLMNITRGSVRIEKNELCYLATIDWSRI LDSVED-----NYITVLNKDDNEECGDIC 135

EmIR1 LBD PEAISLTELEGTGREKDAKLGHCSLSYCSQISCSANCTSRGIACRMNTQLCCHKECLAGCYGP-GPEACVACKGALHRG 217
EmIR2 LBD LKANACPSGCEWVTVNNLPRSFCSWRDHQHVCAAKCRDASLSCSIHNISECCHANCLGGCTGP-TAGDCLICRDFHHND 237
HsIGF1R LBD PGTMECKPMCKEKTINNEYNYRCWITNRCQKMCPSCTGKRACTE----NNECCHPECLGSCAPDNDTACVACRHYYYAG 208
HsINSR LBD PGTAGKTNCPATVINGQFVERCWTSHHCQKVCPTICKSHGCTA----EGLCCHSECLGNCSPDDPTKCVACRNFYLDG 211
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EmIR1 LBD VCVSQCPPSAYLHFGRRCVTAACFNMSSTYRLPHVAGSSGSSSIGFAASVIVNTTAAVATTAIROFAIHQGRCPDPCPS 297
EmIR2 LBD NCLSSCPDGLYELYGRCVTRNACLSPKIPRDLFSWVFQSR-----HPSGFSIQGRECVPVCDR 298
HsIGF1R LBD VCVPAAPPNTYRFEGRCVDRDFCANILS-AESSDSEG-----FVIHDGECMQECPS 259
HsINSR LBD RCVETCPPPYHFQDWRVCNFSFCQDLHHKCKNSRRQGC-----HQYVIHNNKCTPECPS 266
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EmIR1 LBD GHQRD-EVSGQVPCGDECPRI---CHHMLTSSLSKSLKDKCFSVT-DLYISTHEGDTVLIQQQFDEAFSSLREVES- 371
EmIR2 LBD SFRRS--PSGECRPCVDCEEVKR-DCGDIVTYQQADLASVKDCLSR-SVLISIRAGQD-DLSTSLAEAFSSLRVIYRS 373
HsIGF1R LBD GFIRNGSQSMYCIPCEGPCPVCEEEKTKTIDSVTSAQMLQGCTIFKGNLLINIRGN--NIASELENFMGLIEVVTGY 337
HsINSR LBD GYTMN-SSNLLCTPCLGPCPVCHLLEGEKTIIDSVTSAQELRGCTVINGSLTINIRGN--NLAALEANLGLIETISGY 343

EmIR1 LBD TKVVRATALTSLAFLRHVKRINTIPNSSPN-----VTVIEIRGNDNLELWPPPTRNQTGGQLQVSEGLVHFI 439
EmIR2 LBD LRVIRSDALLSLSFLHHLRTIHGTEPIVKDGLVTPVELSHSGITALEITWNGNLEDLWLLPPGSPK---LETLSGSEVFS 450
HsIGF1R LBD VKIRHSHALVLSFLKNLRLLTGEEQLEGN-----YSFYVD-NQNLQQLWDWDHRNLT----IKACKMYFA 399
HsINSR LBD LKIRRSYALVLSFFRKLRLIRGETEIGN-----YSFYALD-NQNLRLWDWSKHNLIT----ITQGLFFH 405

EmIR1 LBD LNRYLCPPKKITDLVRTGALTLPGGRNFRIEEL 471
EmIR2 LBD VNNRLCPDKIQSFLSN----- 466
HsIGF1R LBD FNPKLQVSEYRMEEVT----- 416
HsINSR LBD YNPKLQVSEYHKMEEVS----- 422

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Additional File 2: (A) Amino acid sequence comparison between the ligand binding domains (LBD) of *Echinococcus* and human insulin receptor tyrosine kinases. Displayed is a sequence pileup of the LBDs of *E. multilocularis* EmIR1 (AJ458426) and EmIR2 (HG326255; this study) as well as the human insulin receptor (HsINSR; P06213) and the insulin-like growth factor receptor (HsIGF1R; P08069). Amino acid residues that are conserved in at least three of the sequences are shown in white on black background. Biochemically related amino acid residues are marked by a grey background. The specificity determining region for the binding of human insulin-like peptides to the receptors is marked by asterisks below the pileup.

B)

	# # ###	
EmIR1 TKD	LNFRHPLGRGNFGMVYRGFVKSLR-----TPAHCFYTEPHNIP-----	38
EmIR2 TKD	YNVEDTLGQGSFGLVCRGRLTCLTTPAAEYLHLATTFANGDSASPGGGGGIRSPSTHSALKSKKWLTSILPKRLRRGSVA	80
HsIGF1R TKD	ITMSRELGQGSFGMVYEG-----VAKGVVKDEPETR-----	31
HsINSR TKD	ITLLRELGQGSFGMVYEG-----NARDIIKGEATR-----	31
	## # #	
EmIR1 TKD	-----AALKTLSSACTVFDRRDFTTEACYMKQFQSFHIVRLFGIVSKCSPSSAVPAAARTFLSGSGSGSGDGGGGF	110
EmIR2 TKD	SGDAQGMDVAVKILSPGSTYEDVREFLGEASHMKQFNCNHIVRLFGIVSKQV-----	132
HsIGF1R TKD	-----VALKTVNEAASMRERIEFLNEASVMKEFNCHIVVRLLGIVSQ-----	73
HsINSR TKD	-----VAVKTVNESASLRERIEFLNEASVMKEFTCHIVVRLLGIVSK-----	73
EmIR1 TKD	SSAQTKFRFSLFRLFGGGGFWRHRPKRQAVVPVPIKKKLFSLSAEEAMTGNTGNGGSLTRTARTPSNEGFNTSRGPDGSN	190
EmIR2 TKD	-----	132
HsIGF1R TKD	-----	73
HsINSR TKD	-----	73
	# #	
EmIR1 TKD	GTTDASPTKRVTGSGRLGRGSFSRLLMKNQKDFRSTLTQDETGVATVQRCSSDSIRPFSQYGLFVVMELMESGDLAS	270
EmIR2 TKD	-----LFRRQPTVVMELMQHGDLAT	152
HsIGF1R TKD	-----GQPTLVVMELMTRGDLKS	91
HsINSR TKD	-----GQPTLVVMELMAHGDLS	91
	## ##### # ### #	
EmIR1 TKD	YLRLKLG---DSGIGFVKP--AQAYLWAVQIADGMAYLERKKYVHRDLAARNCLVDGRGVVKVGDGFLCRDIYERNYYHKV	345
EmIR2 TKD	YLRRHMAQEDYSQGSVSP--EYATKWAEEVADGMAYLEYKGFVHRDLAARNCLVGVGTLVKIGDFGLTRDYSGHLYYRKE	230
HsIGF1R TKD	YLRSLRPEMENNPNVLAPPSLSKMIQMAEIAIDGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMLTRDIYETDYRKG	171
HsINSR TKD	YLRSLRPEAENNPGRPPPTLQEMIQMAEIAIDGMAYLNANKFVHRDLAARNCMVAHDFTVKIGDFGMLTRDIYETDYRKG	171
	# # # ##### # # #	
EmIR1 TKD	GAGKLPVRWMAPESLQSAFTSRSDVWSFGVVLWEIATMACLPYQGMSHNEVISYLDGNTLVSGGAPINCPLLQSVML	425
EmIR2 TKD	GRARLPVRWMAPEALNEAYFTFKSDVWSYGVVLWEIATFAALPESGLSHEVIALVNGGHLGKQGWPPKFPDILLDVMQ	310
HsIGF1R TKD	GKGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRVMEGGLLDK---PDNCPDMLFELMR	248
HsINSR TKD	GKGLLPVRWMAPESLKDGVFTTSSDWSFGVVLWEITSLAEQPYQGLSNEQVLRVMDGGYLDQ---PDNCPERVTDLMR	248
	## ## #	
EmIR1 TKD	YCWSYRFAQRPTFLHLLYLL	445
EmIR2 TKD	ACWHSDECRPSFGTIIISML	330
HsIGF1R TKD	MCWQYNPKMRPSFLEIISSI	268
HsINSR TKD	MCWQFNPKMRPTFLEIVNLL	268

Additional File 2: (B) Amino acid sequence comparison between the tyrosine kinase domains (TKD) of *Echinococcus* and human insulin receptor tyrosine kinases. Displayed is a sequence pileup of the TKDs of *E. multilocularis* EmIR1 (AJ458426) and EmIR2 (HG326255; this study) as well as the human insulin receptor (HsINSR; P06213) and the insulin-like growth factor receptor (HsIGF1R; P08069). Amino acid residues that are conserved in at least three of the sequences are shown in white on black background. Biochemically related amino acid residues are marked by a grey background. Residues that are highly conserved in eukaryotic tyrosine kinases are indicated by number signs (#) above the alignment.