

Query	42	EAYLEAEIKXXXXXXXXXXXXXXXXXXTVVVKEGDIQQMNPPKXXXXXDMAMLTHLNEXXXXX	101
		EAYLEAEIK TVVVKEGDIQQMNPPK DMAMLTHLNE	
Sbjct	42	EAYLEAEIKENGGGKVTVEVADGKTVVVKEGDIQQMNPPKFDMIEDMAMLTHLNEASVLS	101
Query	102	XXXGKRRSEAPPHIFXXXXXXXX	161
		GKRRSEAPPHIF	
Sbjct	102	NLRKRYANWMIYTYSGLFCVTVNPKSLPVYKTEVVVTAYKGGRRSEAPPHIFSIADNAYH	161
Query	162	XXXXNRENQSMLITGESGAGKTVNTRKVIQYXXXXXXXXXXXXXXXXXXXXXXXXXGGTLEDQI	221
		NRENQSMLITGESGAGKTVNTRKVIQY TGGTLEDQI	
Sbjct	162	DMLRNRENQSMLITGESGAGKTVNTRKVIQYFATVAAIGDPMGKKNQPATKTGGTLEDQI	221
Query	222	IQANPALEAFGNAKXXXXXXXXXXXXFIRIHFGTGKLSADIEIYLLEKSRVIFQQPGE	281
		IQANPALEAFGNAK FIRIHFGTGKLSADIEIYLLEKSRVIFQQPGE	
Sbjct	222	IQANPALEAFGNAKTLRNDNSSRFKGFIRIHFGTGKLSADIEIYLLEKSRVIFQQPGE	281
Query	282	RSYHIFYQITSGKXX	341
		RSYHIFYQITSGK	
Sbjct	282	RSYHIFYQITSGKMSSELQDMLLVSTNPNYDFHFSSQGVVTVDNLDDCEELMATDQAFDILG	341
Query	342	XXXXXXYGAYKLTGAIMHFGNMKXX	401
		YGAYKLTGAIMHFGNMK	
Sbjct	342	FISDEKYGAYKLTGAIMHFGNMKFKQKQREEQAETDGTENTDKAAYLMGISSDLVKGLM	401
Query	402	XXXVKVGNEYVTKXXXXXXXXXXAVGALAKGIYXXXXXXXXXXXXXXXXXLDTKLPRXXXXXX	461
		VKVGNEYVTK AVGALAKGIY LDTKL R	
Sbjct	402	HPRVKVGNEYVTKGQTVAQVVYAVGALAKGIYDRMFKWLVVRINKTLDTKLSRQFFIGVL	461
Query	462	XXXXXXXXXXXXXXXXXXXXXXXXXXLQQFFNHMHFVLEQEEYKXXXXXXXXXXXXXXXXXXXX	521
		LQQFFNHMHFVLEQEEYK	
Sbjct	462	DIAGFEIFDLNSFEQLCINFTNEKLLQQFFNHMHFVLEQEEYKKEGIDWEFIDFGLDLQAC	521
Query	522	XXXDNHLGKSPNFQ 565	
		DNHLGKSPN Q	
Sbjct	522	IDLIEKPLGIMSILEEEMFPAKATDMTFKSKLYDNHLGKSPNLQ 565	
Query	672	VRCIIPNETKTPGAMPFLVLHQLRCNGVLEGIRXXXXXXXXXXVLYADFK 721	
		VRCIIPNETKTPGAMPFLVLHQLRCNGVLEGIR VLYADFK	
Sbjct	672	VRCIIPNETKTPGAMPFLVLHQLRCNGVLEGIRICRKGFPNRVLYADFK 721	
Query	786	ILTLIQARARGKXXXXXXXXXXXXRDALLVIQWNIRXXMTVKNWPWXXXXXXXXXXXXXSA	845
		ILTLIQARARGK RDALLVIQWNIR MTVKNWPW SA	
Sbjct	786	ILTLIQARARGKLMRIEFQKILERRDALLVIQWNIRGFMTVKNWPWMMKLFKIKPLKSA	845
Query	846	ETEKEMANMKEEFLKXXXXXXXXXXXXXXXXXQVTLVQEKXXXXXXXXXXXXXXXXXXXX	905
		ETEKEMANMK+EF K QVTLVQEK	
Sbjct	846	ETEKEMANMKDEFQKLKEALEKSEARRKELEEKQVTLVQEKNDLTLQLQAEQDMFADAE	905
Query	906	RCDLLIKSKIQMEXXXELTERIEDEEEMNSELTSKKRKLEDECSELKKDIDDLEITLAK	965
		RCDLLIK+KIQME +LTERIEDEEEMNSELT+KKRKLEDECSELKKDIDDLEITLAK	
Sbjct	906	RCDLLIKNKIQMESKVKDLTERIEDEEEMNSELTAKKRKLEDECSELKKDIDDLEITLAK	965
Query	966	AEKXXXXXXXXXXNLTEEMASLDDTINKXXXXXKALQEAHQQTLLDLQAEEDKVSTLTKX	1025
		AEK NLTEEMASLDDTINK KALQEAHQQTLLDLQAEEDKV++LTK	
Sbjct	966	AEKEKHATENKVKNLTEEMASLDDTINKLTKKALQEAHQQTLLDLQAEEDKVNSLTKM	1025


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Query  1866  MQDLIDKLQLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMQHELDDAQERADIAESQVNK  1921
        MQDLIDKLQLK                                                    K+QHELDDAQERADIAESQVNK
Sbjct  1866  MQDLIDKLQLKVKSYKHKQAEAESEQANQYLSKYKKLQHELDDAQERADIAESQVNK  1921

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Supplemental figure 1: BLAST alignment between the partial sequence of toad MHC and *Xenopus cardiac* MHC. Blast analysis was performed using the partial sequence of toad MHC derived from LC-MS/MS analyses as query against the non-redundant protein sequences (nr) database. The default settings were used in search parameters. The alignment is shown between the query and the top hit: myosin, heavy polypeptide 15 [*Xenopus laevis*] NP_001085151.1 and GI: 148222862. Because of the long strings of unidentified amino acids, marked as “x”, present in the middle of the query sequence, the alignment was displayed in three segments in Blast result: from amino acid 42-565, 672-721 and 786-1921.