

Electronic Supplementary Information

**Metallomics Investigations on Potential Binding
Partners of Methylmercury in Tuna Fish Muscle Tissue
Using Complementary Mass Spectrometric Techniques**

Daniel J. Kutscher, Alfredo Sanz-Medel and Jörg Bettmer*

* Department of Physical and Analytical Chemistry; University of Oviedo,
C/ Julian Claveria 8, 33006 Oviedo, Spain.

Fax: 0034 985 10 3125; Tel: 0034 985 103000 Ext. 5366; E-mail:
bettmerjorg@uniovi.es

Table S1 Amino acid sequence of Q91520 (Skeletal myosin heavy chain) following the UniProtKB database (www.uniprot.org). The peptides identified by LC-ESI-MS/MS for the tryptic digest of spot No. 5 are underlined.

10	20	30	40	50	60
<u>EEAGGATAAQ</u>	<u>IEMNKKREAE</u>	<u>FQKLRRDLEE</u>	<u>STLQHEATSA</u>	<u>SLRKKQADSV</u>	<u>AELGEQIDNL</u>
70	80	90	100	110	120
<u>QRVKQKLEKE</u>	<u>KSEYKMEIDD</u>	<u>LSSNMEAVAK</u>	SKGNLEKMCR	TIEDQLSELK	AKNDEHVRQL
130	140	150	160	170	180
NDLNGQRARL	QTENGEFSRQ	IEEKDALVSQ	LTRGKQAYTQ	QIEELKRHIE	EEIKAKNALA
190	200	210	220	230	240
HAVQSARHDC	DLLREQYEEE	QEAKGELQRG	MSKANSEVAQ	WRTKYETDAI	QRTEEELEAK
250	260	270	280	290	300
<u>KKLAQRLQDA</u>	<u>EESIEAVNSK</u>	<u>CASLEKTKQR</u>	<u>LQGEVEDLMI</u>	<u>DVERANSLAA</u>	<u>NLDKKQRNFD</u>
310	320	330	340	350	360
KVLADWKQKY	EEGQSELEGA	QKEARSLSTE	<u>LFKMKNSEYEE</u>	<u>ALDHLETMKR</u>	<u>ENKNLQQEIS</u>
370	380	390	400	410	420
<u>DLTEQIGETG</u>	<u>KSIHELEKAK</u>	<u>KHVETEKTEI</u>	<u>QTALEEAEGT</u>	<u>LEHEEAKILR</u>	<u>VQLELNQIKS</u>
430	440	450	460	470	480
<u>EVDRKLAEKD</u>	<u>EEMEQIKRNS</u>	<u>QRVIDSMQST</u>	<u>LDAEVRSRND</u>	<u>ALRIKKKMEG</u>	<u>DLNEMEIQLS</u>
490	500	510	520	530	540
HANRQATESQ	KQLRNVQGQL	KDAQLHLDDA	VRGHEDMKEQ	VAMVERRNGL	MLAEIEELRA
550	560	570	580	590	600
ALEQTERGRK	<u>VAEQELVDAS</u>	<u>ERVGLLHSQN</u>	<u>TSLINTKKKL</u>	<u>EADLVHIQGE</u>	<u>VDDSIQEARN</u>
610	620	630	640	650	660
<u>AEDKAKKAIT</u>	<u>DAAMMAEELK</u>	<u>KEQDTSAHLE</u>	<u>RMKKNLEVS</u>	<u>KDLQHRLDEA</u>	<u>EALAMKGGKK</u>
670	680	690	700	710	720
<u>QLQKLESVR</u>	<u>ELESEVDAES</u>	<u>RRGADAIKGV</u>	<u>RKYERRVKEL</u>	<u>TYQTEEDKKN</u>	<u>VHRLQDLVDK</u>
730	740	750	760	770	780
<u>LQLKVKS</u> YKR	QAEEAEEQAN	THLSRYRKVQ	HEMEEAQERA	DIAESQVNKL	RAKSRDHHHG
786					
KGEHAE					

Sequence coverage of 29 % could be obtained (226 identified of 786 known amino acids).

Table S2 Identified peptides by LC-ESI-MS/MS from the tryptic digest of spot No. 5, unmatched to Q91520, but matched to myosin proteins from other organisms.

Identified peptide	Protein
¹⁷¹ ENQSILITGESGAGK ¹⁸⁵ ²⁶¹ LASADIETYLLEK ²⁷³ ⁴¹⁷ GQTVQQVYNAVGALAK ⁴³² ⁶⁴⁵ GSSFQTVSALFR ⁶⁵⁶ ⁷⁴⁹ LLGSIDVDHTQYK ⁷⁶¹ ¹⁰⁰² ALQEAHQQTLLDDLQAEEDKVNTLTk ¹⁰²⁶ ¹¹¹⁹ IEEELEEEIEAER ¹¹³⁰	Q076A6 (Myosin-1, <i>Canis familiaris</i>)
⁵⁸⁶ AGTVDYNISGWLEK ⁵⁹⁹ ¹⁰²⁸ TKLEQQVDDLEGSLEQEKK ¹⁰⁴⁶	P13538 (Myosin heavy chain, skeletal muscle, adult, <i>Gallus gallus</i>)
²¹⁶ GTLEDQIIQANPLLEAFGNAK ²³⁶ ⁷²⁸ ILNASAIPEGQFIDSK ⁷⁴³	Q9UKX3 (Myosin-13, <i>Homo sapiens</i>)
¹⁴³ NLTEEMATLDENISK ¹⁵⁷	P29616 (Myosin heavy chain, cardiac muscle isoforms, <i>Gallus gallus</i>)