

**S2 Table. List of major cross-links found between myotilin and F-actin**

Myotilin constructs used		(A)	250	444	(B)	185	454	(C)	185	498
From Protein	From Residue	To Protein	To Residue	Myotilin region	Myotilin fragment identified			Score		
myotilin	<b>K 474</b>	actin	<b>E 102</b>	C-ter.	C			212.6		
myotilin	<b>K 462</b>	actin	<b>D 27</b>	C-ter.	C			199.5		
myotilin	<b>K 411</b>	actin	<b>D 27*</b>	Ig2	A, B			A) 157.5, B) 175.5		
myotilin	<b>K 469</b>	actin	<b>E 102</b>	C-ter.	C			169.4		
myotilin	<b>D 236</b>	actin	<b>K 330</b>	N-ter.	B, C			B) 138.4, C) 76.2		
myotilin	<b>D 236</b>	actin	<b>K 328*</b>	N-ter.	B			134.9		
myotilin	<b>K 246</b>	actin	<b>E 336</b>	N-ter.	B, C			B) 105.9, C) 111.2		
myotilin	<b>E 245</b>	actin	<b>K 330</b>	N-ter.	B			107.1		
myotilin	<b>K 246</b>	actin	<b>D 26</b>	N-ter.	C			106.3		
myotilin	<b>K 452</b>	actin	<b>D 27*</b>	C-ter.	C			103.9		
myotilin	<b>D 241</b>	actin	<b>K 330*</b>	N-ter.	B			102.4		
myotilin	<b>K 469</b>	actin	<b>D 26*</b>	C-ter.	C			102.0		
myotilin	<b>K 452</b>	actin	<b>D 26</b>	C-ter.	C			100.9		
myotilin	<b>D 239</b>	actin	<b>K 330*</b>	N-ter.	B			97.0		
myotilin	<b>D 239</b>	actin	<b>K 328</b>	N-ter.	B			88.1		
myotilin	<b>K 474</b>	actin	<b>D 27</b>	C-ter.	C			84.6		
myotilin	<b>K 474</b>	actin	<b>E 336*</b>	C-ter.	C			82.7		
myotilin	<b>D 241</b>	actin	<b>K 328*</b>	N-ter.	B			78.2		
myotilin	<b>K 462</b>	actin	<b>D 26*</b>	C-ter.	C			77.7		
myotilin	<b>K 354</b>	actin	<b>D 27*</b>	Ig2	C			76.7		
myotilin	<b>K 246</b>	actin	<b>D 27*</b>	N-ter.	B, C			B) 54.5, C) 73.9		
myotilin	<b>K 415</b>	actin	<b>D 27</b>	Ig2	A, B			A) 66.1, B) 57.6		
myotilin	<b>K 303</b>	actin	<b>D 27*</b>	Ig1	A			65.9		
myotilin	<b>K 367</b>	actin	<b>D 365</b>	Ig2	B			63.6		
myotilin	<b>K 367</b>	actin	<b>E 366</b>	Ig2	B			60.2		
myotilin	<b>K 452</b>	actin	<b>E 363</b>	C-ter.	C			48.2		
myotilin	<b>K 411</b>	actin	<b>D 26</b>	Ig2	A			47.8		
myotilin	<b>K 474</b>	actin	<b>D 26</b>	C-ter.	C			35.4		

\* , cross-links shown on Fig 3; N-ter., region flanking Ig1Ig2 N-terminally; C-ter., region flanking Ig1Ig2 C-terminally; Score, computed as -10 log10 (E-value) representing best identification for a crosslink pair. The higher values of the score indicate more reliable identifications.