

**S7 Table. Two blocks/patterns of length 17 aa and 20 aa and their similarity with non-muscle group and muscle group of myosin II.**

Seq. nos.	Similarity (%)	Pattern	Similarity (%)	Pattern
		22128718476518744824		18464837812488338
1	100	381-KRERNTDQATMPDNTAAQKL	94	491-EQLCINYTNEKLQQLFN
2	100	362-KKERNTDQASMPDNTAAQKV	94	472-EQLCINYTNEKLQQLFN
3	100	355-KKERNTDQASMPDNTAAQKV	94	465-EQLCINYTNEKLQQLFN
4	100	362-KKERNTDQASMPENTVAQKL	94	472-EQLCINYTNEKLQQLFN
5	40	201-GKTVNSKHIIQYFATIAAMI	100	486-EQLCINFTNEKLQQFFN
6	40	597-WLEKNKDPLNETVVPIFQKS	100	477-EQLCINFTNEKLQQFFN
7	40	184-GKTVNTRKVIQYFATIAVTG	100	477-EQLCINFTNEKLQQFFN
8	40	184-GKTVNTRKVIQYFATIAVTG	100	477-EQLCINFTNEKLQQFFN
9	40	186-GKTVNTRKVIQYFATIAVTG	100	477-EQLCINFTNEKLQQFFN
10	40	184-GKTVNTRKVIQYFATIAVTG	100	477-EQLCINFTNEKLQQFFN
11	40	184-GKTVNTRKVIQYFATIAATG	100	475-EQLCINFTNEKLQQFFN
12	40	184-GKTVNTRKVIQYFATIAVTG	100	476-EQLCINFTNEKLQQFFN
13	40	206-KKDQSPGKGTLEDQIIQANP	100	474-EQLCINFTNEKLQQFFN
14	40	183-GKTVNTRKVIQYFASIAAIG	100	475-EQLCINFTNEKLQQFFN
<b>Domain</b>		<b>ATP binding site</b>		<b>Nearer to the ending of ATP binding site</b>