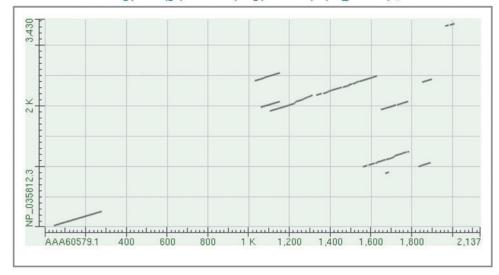
Plot of gi|338441|gb|AAA60579.1| vs gi|110431378|ref|NP\_035812.3| @



Summary of the most significant hits between human beta-spectrin and mouse utrophin:

Hits	% identity	% pos	align length	mismatches	gap opens	q. start	q.end	s.start	s.end	E value	bit score
1	45.76	65.25	236	126	2	45	279	22	256	2.00E-62	226
2	25.76	50.76	132	89	3	1031	1153	2410	2541	3.00E-07	44.3
3	26.6	44.68	94	69	0	1060	1153	1975	2068	4.00E-06	40.4
4	21.57	39.05	612	360	23	1105	1630	1912	2489	6.00E-04	33.5

## Alignment statistics for match #1 Method Identities

			,	Alignment stat	istics I	or match #1			
Sc	core	Expect		Method		Identities	Posit	ives	Gaps
226 bi	its(57	5) 2e-62	Compositio	nal matrix a	adjust.	108/236(46%)	154/23	6(65%)	2/236(0%)
hSpec	45					DGRMLIKLLEVLS		103	
mUtro	26	IK+ +DE IKSRSDEHNI	VQKKTFTKW+N VQKKTFTKWIN			DGR L+ LLE L+0 DGRKLLDLLEGLTO		84	
hSpec	104					RLVLGLIWTIILRE +L LGL+W+IIL 4		163	
mUtro	85					KLTLGLLWSIILHV		144	
hSpec	164					DGLAFNALIHKHRF DGLAFNA++H+H+F		223	
mUtro	145					DGLAFNAVLHRHKE		204	
hSpec	224					KSIITYVVAFYHYE	SK 279		
mUtro	205	++ + RVVKMSPIEF		LGI LLDPED		KSII Y+ + + KSIIMYLTSLFEVI	PQ 260		
mUtro	205	RVVKMSPIEF	LEHAFSKAHTY	LGIEKLLDPED	/AVHLPDK	KSIIMYLTSLFEVI	PQ 260		

SUPPLEMENTARY FIG. S3. Summary of similarity hits between human  $\beta$ -spectrin and mouse utrophin. The two-protein BLAST comparison search was performed according to the Position-Specific Iterative Basic Local Alignment Search Tool (PSI-BLAST) method from the NCBI website. Top: A dot matrix view. Alignment analysis of human  $\beta$ -spectrin and mouse utrophin showed several hits. Middle: The best four hits. Bottom: The two-sequence alignment of the most significant hit is also shown.