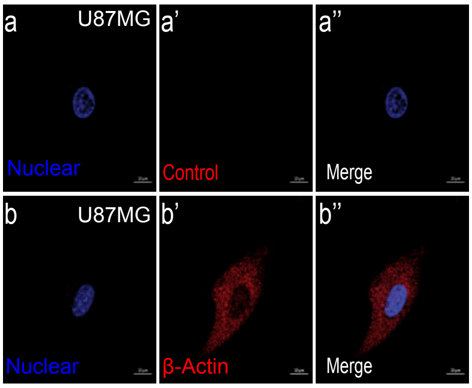
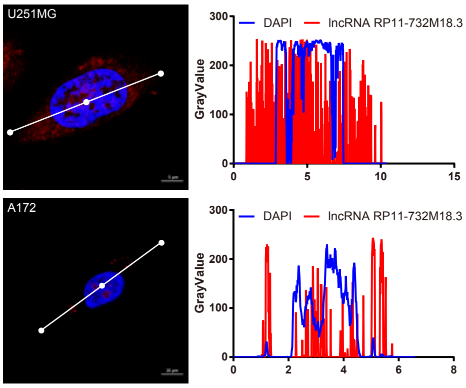
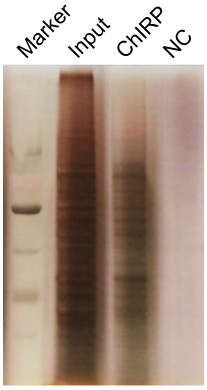
a.



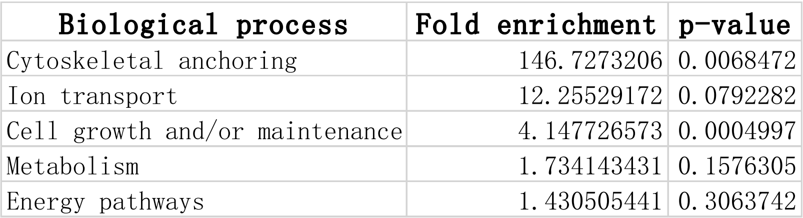
b.



c.

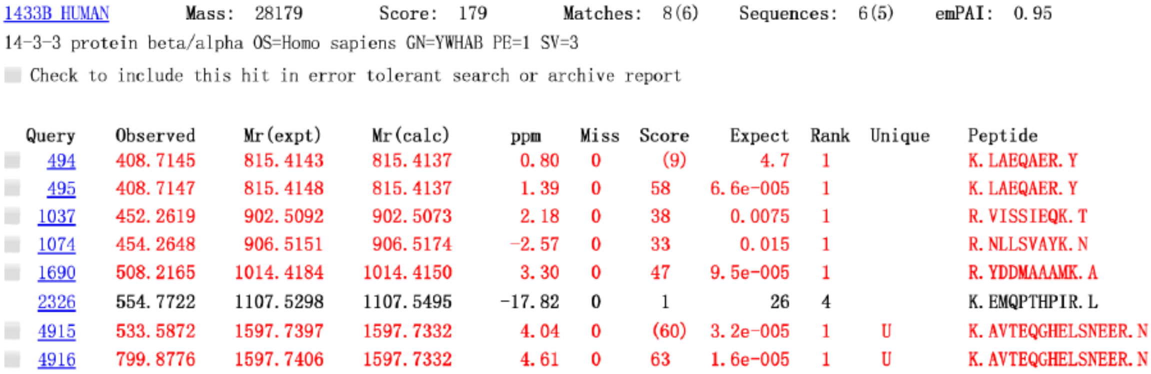


d.



Biological process	Fold enrichment	p-value
Cytoskeletal anchoring	146.7273206	0.0068472
Ion transport	12.25529172	0.0792282
Cell growth and/or maintenance	4.147726573	0.0004997
Metabolism	1.734143431	0.1576305
Energy pathways	1.430505441	0.3063742

e.



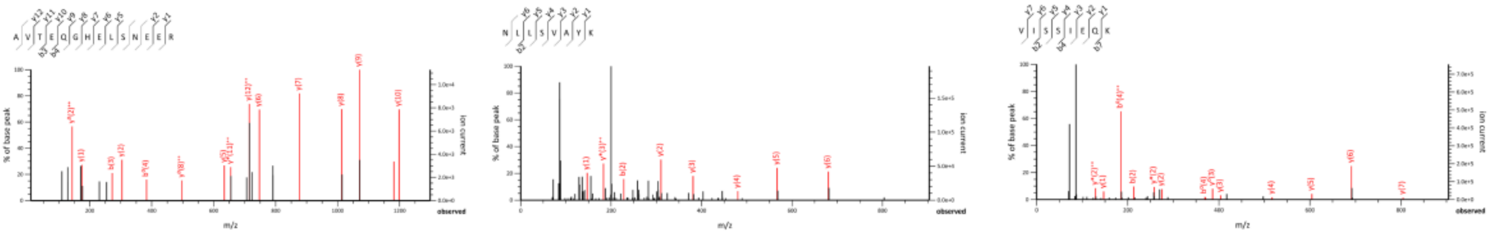
1433B_HUMAN Mass: 28179 Score: 179 Matches: 8(6) Sequences: 6(5) emPAI: 0.95

14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

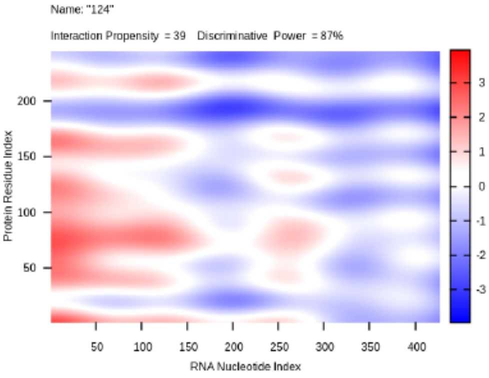
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
☐	494	408.7145	815.4143	815.4137	0.80	0	(9)	4.7	1		K.LAEQAER.Y
☐	495	408.7147	815.4148	815.4137	1.39	0	58	6.6e-005	1		K.LAEQAER.Y
☐	1037	452.2619	902.5092	902.5073	2.18	0	38	0.0075	1		R.VISSIEQK.T
☐	1074	454.2648	906.5151	906.5174	-2.57	0	33	0.015	1		R.NLLSVAYK.N
☐	1690	508.2165	1014.4184	1014.4150	3.30	0	47	9.5e-005	1		R.YDDMAAAMK.A
	2326	554.7722	1107.5298	1107.5495	-17.82	0	1	26	4		K.EMQPTHPIR.L
☐	4915	533.5872	1597.7397	1597.7332	4.04	0	(60)	3.2e-005	1	U	K.AVTEQGHELSNEER.N
☐	4916	799.8776	1597.7406	1597.7332	4.61	0	63	1.6e-005	1	U	K.AVTEQGHELSNEER.N

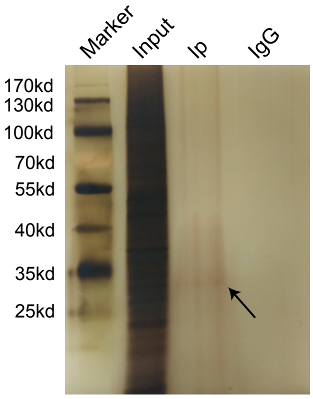
f.



g.



h.



i.