

**Table 1 The differentially expressed proteins in mandibular chondrocytes undercompressive mechanical stress loading**

<sup>a</sup> Mowse score, for a significant ( $p < 0.05$ ) positive protein identification, cut-off threshold was 59.

Spot	Accession NO	Protein name	Score <sup>a</sup>	MW/PI	Sequence coverage	Peptides <sup>b</sup>	Control/ Stress Ratio <sup>c</sup>	p-value
Endoplasmic reticulum molecular chaperones								
P1	IPI00198887	Protein disulfide-isomerase precursor	222	57315/4.82	37%	24	1:3.924	3.39E-05
P4	IPI00191728	Calreticulin precursor	113	48137/4.33	30%	13	1:4.718	2.01E-05
P5	IPI00192912	Reticulocalbin-1 precursor	81	38067/4.67	33%	14	1:2.010	8.22E-05
Stress-related protein								
7	IPI00201586	Heat shock protein beta-1	92	22936/6.1	31%	20	1:2.171	7.13E-05
Cytoskeleton-related proteins								
2	IPI00214905	Tropomyosin alpha-4 chain	113	28549/4.66	47%	16	1:0.141	2.96E-07
3	IPI00214905	Tropomyosin alpha-4 chain	121	28549/4.66	39%	19	1:0.194	1.39E-06
P8	IPI00656387	Capping protein (actin filament) muscle Z-line, alpha 3	76	34981/6.11	40%	20	1:0.461	2.46E-04
P7	IPI00765011	Actin cytoplasmic 2	95	59163/5.67	31%	16	1:0.245	8.17E-04
Cell cycle protein								
P12	IPI00208306	Translationally-controlled tumor protein	79	19564/4.76	34%	10	1:0.105	5.05E-05
11	IPI00187707	Peptidyl-prolyl cis-trans isomerase	287	23052/7.85	62%	27	1:0.107	2.85E-05
P14	IPI00560544	Retinoblastoma binding protein 6 isoform 1	62	196422/9.62	15%	27	1:0.219	3.49E-05
Signal transduction protein								
4	IPI00231615	Anxa1 44 kDa protein	150	43907/6.97	50%	20	1:2.944	2.15E-04
P3	IPI00360030	G protein-regulated inducer of neurite outgrowth	246	94055/6.20	22%	28	1:0.382	8.63E-05
Glycolytic enzymes								
1	IPI00764301	Isoform M2 of Pyruvate kinase isozymes	289	58472/7.15	58%	36	1:0.267	2.24E-04
5	IPI00555252	Glyceraldehyde-3-phosphate dehydrogenase	166	36090/8.14	56%	20	1:0.287	8.20E-06
P9	IPI00191707	Pyruvate dehydrogenase E1 component alpha subunit	90	43883/8.49	40%	33	1:0.242	4.33E-05
Oxidant enzymes								
8	IPI00768953	Cytochrome c oxidase	116	14849/8.35	67%	15	1:0.226	1.83E-05
9	IPI00231643	Superoxide dismutase	169	16073/5.88	62%	12	1:2.172	8.54E-06
Antioxidant enzymes								
P2	IPI00231737	Aldose reductase	78	36230/6.26	46%	18	1:0.454	1.17E-03
Membrane protein								
6	IPI00200117	Syndecan binding protein Syntenin-1	73	32631/7.05	28%	12	1:2.160	2.52E-04
DNA combination protein								
P6	IPI00767551	Zinc finger protein 69	102	66981/8.32	23%	16	1:2.137	3.80E-02
Protein degradation								
P10	IPI00191501	Proteasome subunit alpha type 6	104	27838/6.34	50%	14	1:3.916	1.36E-05
P11	IPI00231757	Proteasome subunit alpha type 2	91	26024/6.92	37%	8	1:5.804	6.63E-04
Unclassified								
10	IPI00782427	38 kDa protein	119	37861/4.72	45%	15	1:5.120	2.64E-05
P13	IPI00767397	Sjogren syndrome antigen B	293	46655/9.65	42%	29	1:2.143	1.12E-04

<sup>b</sup> Number of peptides matched to the protein sequence.

<sup>c</sup> Ratio represents fold-change of Stress group relative to the control group.