

**Supplementary Data n°2: Summary of the other putative Proteasome Interacting Proteins (PIPs) identified (not listed in Tables I and II)**

Name	# Accession	References	Name	# Accession	References
<b>Nucleotide Excision Repair Pathway</b>			<b>Other proteins</b>		
Histone H2B type 1-B <sup>a,c,d</sup>	P33778	(1)	Nascent polypeptide-associated complex subunit alpha <sup>b,c</sup>	Q13765	/
Histone H4 <sup>b,d</sup>	P62805		14-3-3 protein epsilon1 <sup>d</sup>	P62258	(1)
Purine nucleoside phosphorylase	P00491	/	Programmed cell death protein 6 <sup>a</sup>	O75340	/
<b>Acto-myosin Cytoskeleton Signaling</b>			Activated RNA polymerase II transcription cofactor 4 variant <sup>a,c</sup>	Q59G24	/
Actin, cytoplasmic 1 <sup>b,e</sup>	P60709	(2)	ADP-ribosylation factor 1 <sup>c</sup>	P84077	/
Actin, alpha cardiac muscle 1 <sup>b,e</sup>	P68032		ATP synthase subunit alpha, mitochondrial precursor <sup>b,c</sup>	P25705	/
Myosin, heavy chain 6, cardiac muscle, alpha <sup>a,e</sup>	P13533		ATP synthase subunit beta, mitochondrial precursor <sup>b,c</sup>	P06576	/
Myosin, heavy chain 7, cardiac muscle, beta <sup>e</sup>	A2TDB6		Lysozyme C precursor <sup>a</sup>	P61626	/
			Protein UNQ773/PRO1567 precursor <sup>b,c</sup>	Q96DA0	/
			Deleted in malignant brain tumors 1 <sup>b,c</sup>	Q5JR23	/
			40S ribosomal protein S14 <sup>b,c</sup>	P62263	/
			Importin 9 <sup>a</sup>	Q96P70	/
			UPF0424 protein C1orf128	Q9GZP4	/
			Serpin B6 <sup>a,c</sup>	P35237	/
			Acidic leucine-rich nuclear phosphoprotein 32 family member A <sup>b,c</sup>	P39687	/

Proteins listed in the table were purified as described in the experimental section, separated by SDS-PAGE and identified by nanoLC-ESI-LTQ-Orbitrap, MS/MS analysis and database searching. Non specific interactions could be eliminated by performing a differential analysis with proteins purified with the OX8 antibody and similarly identified.

Criteria for acceptance of proteins identification are described in the experimental part.

<sup>a</sup> : identified only in the non-treated sample

<sup>b</sup> : identified only in the formaldehyde-treated sample

<sup>c</sup> : proteins identified in one experiment only

<sup>d</sup> : reported human PIPs (identical protein or protein from the same family)

<sup>e</sup> : reported PIPs only in other species

#### **References :**

- 1. Wang, X. and Huang, L. (2008) Identifying dynamic interactors of protein complexes by quantitative mass spectrometry. *Mol Cell Proteomics* 7, 46-57**
- 2. Horiguchi, R., Dohra, H. and Tokumoto, T. (2006) Comparative proteome analysis of changes in the 26S proteasome during oocyte maturation in goldfish. *Proteomics* 6, 4195-202**