

Table 1

Assessment of published endoplasmic reticulum proteomics datasets

Organelle	Tissue/cells	Species	ER purification	Mass spectrometry	Proteins detected	Reference
NE	Neuroblastoma N2a cells	Mouse	NE preparation (Triton-X-100 treatment)	2D-BAC gels, MALDI MS	148	Dreger et al. (2001)
NE	Liver	Mouse	Subtractive proteomics (NE fraction-MM fraction)	MudPIT, LCQ-Deca ion-trap MS, Tandem MS	566	Schirmer et al. (2003)
NE	Liver	Rat	Nuclear pore complex fraction (enriched in nucleoporins)	1D gels, MALDI-QqTOF MS, Tandem MS	94	Cronshaw et al. (2002)
NE	<i>Saccharomyces cerevisiae</i>	Yeast	Purified nuclear pore complex	HPLC, 1D gels, MALDI-TOF MS, Tandem MS	174	Rout et al. (2000)
ER ^a	Liver	Rat ^b	Membrane proteins	1D and 2D gels, MALDI-TOF MS	68 (1D) 39 (2D)	Galeva and Altermann (2002)
ER ^a	Liver	Hamster ^c	Tenfold enrichment ^j (calnexin marker, IB)	2D gels, MALDI-Q-TOF MS	39	Morand et al. (2005)
ER ^d	Liver	Mouse	PCP-fraction co-sedimenting with calnexin	LC, linear ion-trap Fourier transform MS, Tandem MS	229	Foster et al. (2006)
RER	<i>Saccharomyces cerevisiae</i>	Yeast	Purified ribosomes	Multidimensional LC, LCQ ion-trap MS, Tandem MS	95	Link et al. (1999)
RER	Liver	Mouse	75% RM ^e , luminal proteins	2D gels, MALDI-TOF MS, Tandem MS	141	Knoblach et al. (2003)
RER	Pancreas	Dog	Ribosome-associated membrane protein	Blue Native gels, LCQ ion-trap MS, Tandem MS	30	Shibatani et al. (2005)
RER	Liver	Rat	4.0-fold enrichment ^j (G6Pase enzyme assay) 77%	1D gels, LC, QTOF-2 MS, Tandem MS	787	Gilchrist et al. (2006)

SER	Liver	Rat	RM ^{e, f} 4.5-fold enrichment ^j (G6Pase enzyme assay) 58% SM ^e , 39% RM ^{e, g}	1D gels, LC, QTOF-2 MS, Tandem MS	998	Gilchrist et al. (2006)
ERGIC ^h	HepG2 cells ⁱ	Human	110-fold enrichment ^j (ERGIC-53 marker, IB)	1D gels, LC, Tandem MS	24	Breuzza et al. (2004)
ER-Golgi derived vesicles ^d	Liver	Mouse	PCP-fraction co-sedimenting with p115	LC, linear ion-trap Fourier transform MS, Tandem MS	220	Foster et al. (2006)

BAC 16-benzyltrimethyl-*n*-hexadecyl ammonium chloride, *ERGIC* ER-golgi intermediate compartment, *G6Pase* glucose-6-phosphatase, *HPLC* high pressure liquid chromatography, *IB* immuno-blot, *LC* liquid chromatography, *MALDI* matrix-assisted laser desorbition ionization, *MM* microsomal membrane, *MS* mass spectrometry, *MudPIT* Multidimensional protein identification technology, *PCP* protein correlation profiling, *RM* rough microsomes, *SM* smooth microsomes, *TOF* time of flight

^aTotal microsomes (containing both rough and smooth ER membrane derivatives)

^bUntreated and phenobarbital treated rats

^cModel of insulin resistance and metabolic dislipidemia fructose-fed animal

^dFractions obtained by rate-zonal centrifugation of the postnuclear supernatant

^eMorphometric characterization by electron microscopy

^fPresence of ≥ 11 ribosomal particles/vesicle

^gPresence of 1–4 ribosomal particles/vesicle

^hImmuno-affinity purified ERGIC membranes

ⁱCells were treated with brefeldinA to accumulate cycling proteins in the ERGIC

^jEnrichment over homogenate