

**Fosfoproteínas identificadas a partir de geles bidimensionales mediante
espectrometría de masas MALDI-TOF**

Spot	Proteína	Num. Acc	Mr	pl	% secuencia	Pèptidos
1	Proteasome sub. beta type 2	Q9R1P3	22888	7	59.20	12
2	Proteasome sub. alpha type 6	Q9QUM9	27354	6.7	47.97	14
3	Proteasome sub. beta type 4	P99026	29098	5.6	39.77	11
4	Proteasome sub. alpha type 3	O70435	28270	5.4	37	14
5	26S protease regulatory sub 8 (p45)	P62196	45608	7.7	83.25	35
6	26S protease regulatory sub 10B (p44)	P62334	44155	7.6	52.70	22
7	26S protease regulatory sub 7	P46471	48498	5.9	69.68	32
8	Transaldolase	Q93092	37369	7	60.5	25
9	Transaldolase	Q93092	37369	7	39.17	16
10	Transaldolase	Q93092	37369	7	60.5	22
11	Transaldolase	Q93092	37369	7	39.47	15
12	Elongation factor 1-delta	P57776	31275	4.9	57.65	17
13	Elongation factor 1-gamma	Q9D8N01	50042	6.7	40.05	18
14	Eukaryotic translation initiation factor 2 sub 1	P05198	35963	5	68.79	23
15	Annexin A3	O35639	36353	5.4	79.57	27
16	Sorting nexin 6	Q9UNH7	46630	6.1	50.49	23
17	Stress induced phosphoprotein 1	Q60864	62592	6.8	66.11	44
18	Proliferation-associated protein 2G4 (p38-2G4)	P50580	43680	6.8	54.57	21
19	T-complex protein 1 alpha subunit B	P11983	60430	6.1	37.05	20
20	Calreticulin precursor	P14211	47976	4.3	57.93	22
21	Protein disulfide isomerase (Erp59)	P09103	57125	4.8	56.19	19
22	Heat shock cognate 71 KDa prot.	P08109	70853	5.4	57.74	39
23	Heat shock protein HSP 90-beta (HSP84)	P11499	83176	5	44.67	42
24	78KDa glucose-regulated protein (GRP78)	P20029	72404	5.1	52.84	37
25	94KDa glucose-regulated protein (GRP94)	P08113	92457	4.8	63.09	52
26	Tropomyosin alpha 1 chain	P58771	32662	4.7	34.51	15
27	Tropomyosin alpha 3 chain	P21107	32844	4.7	63.73	24
28	Tropomyosin alpha 4 chain	P09495	28449	4.7	77.42	19
29	Coronin 1B (Coronin 2)	Q9WUM3	53894	5.7	29.96	21
30	Tubulin tyrosine ligase	P38585	74043	5.3	46.79	23
31	14-3-3 protein zeta/delta (PKC inhibitor 1)	P35215	27753	4.8	68.98	20
32	Glycoprotein gC1qBP	O35658	31013	4.8	12.54	3
33	Proteasome sub. Beta type 4	P99026	28677	5.8	49.61	13
34	Annexin A3	O35639	36353	5.4	52.32	17

**Fosfoproteínas identificadas a partir de un fraccionamiento de un gel
monodimensional mediante nanoLC-ESI-MS/MS**

Proteína	Num acc	Mr	pI	% secuencia	péptidos	Score
Proteasome subunit beta type 5 precursor	O55234	22952.4	8.77	9.1	3	9.2
60S acidic ribosomal protein	P99027	11643.8	4.379	27.0	4	9.2
Nascent polypeptide associated complex alpha sub.	Q60817	23369.7	4.546	13.0	5	9.2
Tropomyosin alpha 3 chain	P21107	32842.7	4.714	8.1	6	9.2
Endoplasmic precursor	P08113	92418.1	4.77	1.5	6	9.2
Heat shock protein HSP90 beta	P11499	83142.1	5.0	6.4	14	9.2
Acidic leucine rich nuclear phosphoprotein 32 (A)	O35381	28520.26	3.98	8.5	4	9.1
Proteasome subunit beta type 2	Q9R1P3	22891.7	6.98	10.4	2	9.0
Small nuclear ribonucleoprotein Sm D3	P62320	13907.30	10.6	7.9	1	8.8
Ubiquitin	P62991	8559.6	7.35	21.1	1	8.8
Proteasome subunit alpha type 4 precursor	Q9R1P0	29452.17	8.04	3.8	1	8.8
Proteasome subunit alpha type 6 precursor	Q9QUM9	27354.8	6.73	5.3	1	8.8
Programmed cell death protein 5	P56812	14135.3	5.64	20.0	2	8.5
High mobility group protein 4	O54879	22864.4	8.74	6.5	1	8.5
Elongation factor 1 beta	O70251	24547.2	4.53	5.8	1	8.3
Annexin A4	P97429	35836.14	5.47	5.0	1	8.3
Proteasome subunit alpha type 7 precursor	Q9Z2U0	27837.62	8.79	5.6	1	8.3
High mobility group protein 2	P30681	24015.8	7.46	5.7	1	7.9
Proteasome subunit beta type 1	O09061	26355.3	8.12	5.8	1	7.9
Splicing factor arginine serine rich 3	P84104	19317.9	11.6	8.5	1	7.5
Acidic leucine rich nuclear phosphoprotein 32 (E)	P97822	29604.4	3.75	5.0	1	6.9
Casein kinase II	Q60737	45132.9	8.2	3.1	4	9.2
Annexin A3	O35639	36217.46	5.41	6.2	6	9.2
tropomyosin 1 alpha chain	P58771	32660.7	4.71	11.3	7	9.2
Nucleophosmin	Q61937	32539.8	4.63	19.5	7	9.2
Elongation factor 1 delta	P57776	31142.8	4.93	13.6	7	9.2
Transaldolase	Q93092	37363.37	7.00	6.5	7	9.2
Hepatoma derived growth factor	P51859	26252.65	4.84	4.6	7	9.2
SET protein phosphatase 2A inhibitor	Q9EQU5	33357.69	4.21	16.6	9	9.2
60S acidic ribosomal protein P0 L10E	P14869	34194.74	6.18	14.5	9	9.2
Heat shock protein HSP90 alpha	P07901	84603.75	4.96	5.1	9	9.2
Nascent polypeptide associated complex alpha sub.	Q60817	23369.7	4.546	19.5	10	9.2
Heat shock protein HSP90 beta	P11499	83142.1	5.0	7.2	15	9.2
Heterogeneous nuclear ribonucleoproteins C1 C2	Q9Z204	34363.8	4.93	8.6	2	9.2
Tropomyosin beta chain	P58774	32816.54	4.68	11.3	4	7.0
Annexin A11	P97384	54076.80	7.95	1.8	1	7.0
Phosducin like protein 3	Q8BVF2	27563.98	4.67	4.2	1	7.0
COP9 signalosome complex subunit 4	O88544	46255.69	5.77	6.4	2	6.5
Methylosome subunit PICIn	Q61189	26004.85	3.97	5.5	1	6.5
Splicing factor U2AF 35KDa subunit	Q9D883	27666.42	9.18	5.5	1	6.5
High mobility group protein 1	P63158	24747.14	5.70	7.0	2	9.2
Ubiquitin	P62991	8559.6	7.35	21.1	3	9.2
CTP synthase	P70698	66668.2	6.5	7.1	5	9.2
Hsc70 interacting protein	Q99L47	41629.5	5.24	6.2	5	9.2
Ras GTPase activating protein	P97855	51796.94	5.53	6.5	5	9.2
Protein disulfide isomerase precursor	P09103	57107.89	4.82	9.0	6	9.2
Elongation factor 1 gamma	Q9D8N0	49898.15	6.67	8.0	7	9.2
Ran GTPase activating protein 1	P46061	63576.57	4.63	8.3	8	9.2

Calreticulin precursor	P14211	47964.9	4.33	12.7	9	9.2
Endoplasmin precursor	P08113	92418.1	4.77	4.0	9	9.2
Eukaryotic translation initiation factor 5	P59325	48937.7	5.46	11.0	12	9.2
Nucleolin protein C23	P09405	76545.8	4.70	8.5	14	9.2
Heat shock protein HSP90 alpha	P07901	84603.75	4.96	14.1	18	9.2
Heat shock protein HSP90 beta	P11499	83142.1	5.0	18.8	27	9.2
Lamin A	P48678	74164.72	6.92	3.6	6	9.2
78KDa glucose regulated protein precursor	P20029	72377.5	5.101	11.1	9	9.2
tubulin beta chain	P68372	49799.02	4.82	13.7	8	9.2
Moesin membrane organizing extension spike prot.	P26041	67593.84	6.53	6.2	4	8.8
Ezrin p81	P26040	69232.64	6.04	3.2	4	7.7
Heterogeneous nuclear ribonucleoprotein K	P61979	50944.4	5.45	2.6	1	7.7
Heat shock cognate 71KDa protein	P63017	70827.29	5.43	6.5	4	6.3
Chromatin assembly factor 1 subunit C	Q60972	51607.19	5.00	2.8	3	5.5
Heat shock related 70KDa protein 2	P17156	69697.84	5.67	4.3	3	5.5
Heat shock protein 75KDa mitochondrial prec.	Q9CQN1	80158.60	6.60	2.0	1	5.5
Hsp90 co chaperone Cdc37	Q61081	44564.97	5.31	4.5	1	4.8
Sorting nexin 1	Q9WV80	58915.71	5.20	5.4	2	4.8
Eukaryotic translation initiation factor 4B	Q8BGD9	68799.15	5.49	5.4	2	4.8
COP9 signalosome complex subunit 2	P61202	51564.13	5.46	2.9	1	4.8
SET protein phosphatase 2A inhibitor	Q9EQU5	33357.69	4.21	8.3	7	9.2
Nucleolin protein C23	P09405	76545.8	4.70	10.1	12	9.2
Endoplasmin precursor	P08113	92418.1	4.77	8.7	15	9.2
Heat shock protein HSP90 alpha	P07901	84603.75	4.96	22.8	43	9.2
Heat shock protein HSP90 beta	P11499	83142.1	5.0	22.7	46	9.2
Cullin associated NEDD8 dissociated protein 1	Q6ZQ38	136244.75	5.69	3.2	3	8.8
heat shock protein 75KDa mitochondrial prec.	Q9CQN1	80158.6	6.60	2.0	1	8.8
E3 ubiquitin protein ligase Nedd4	P46935	102641.6	5.17	2.6	2	8.8
Myb binding protein 1A	Q7TPV4	151941	9.32	0.7	1	8.8
116 KDa U5 small nuclear ribonucleoprotein	Oo8810	109291.4	4.88	1.6	1	8.8

Fosfoproteínas identificadas mediante nanoLC-ESI-MS/MS (gradiente 90 min.)

Proteína	Num. Acc	Mr	pI	% secuencia	péptidos	Score
E3 ubiquitinating protein ligase Nedd4	Q62940	102330.5	5.123	6.2	3	12.1
14-3-3 protein tau 14-3-3 prot. Theta	P68255	27760.7	4.714	11.4	3	12.1
ATP citrate synthase	Q91V92	119651.3	7.536	4.2	3	12.1
Tumor protein D52 mD52	Q62393	20047.1	4.917	13.5	2	12.1
Cofilin 1, non muscle isoform	P18760	18389.6	8.482	18.8	2	12.1
Proteasome subunit alpha type 4	Q91RP0	29479.1	8.044	11.9	2	12.1
T complex protein 1 epsilon subunit	P80316	59648.8	5.653	5.0	1	12.1
Splicing factor U2AF 65KDa sub.	P26369	46625.6	7.63	3.8	1	12.1
Ubiquitinating like 2 activating enzyme E1B	Q9Z1F9	70524.7	5.125	8.0	3	11.4
Septin 2 NEDD5 protein	P42208	41499.2	6.461	12.5	3	11.4
Alpha 1 catenin	P26231	100043.55	6.205	3.2	2	11.4
Proteasome subunit alpha type 1	Q9R1P4	29527.8	6.361	14.1	2	11.4
28KDa heat and acid stable phosphoprotein	Q62785	20592.5	7.49	7.2	1	11.4
Debrin like protein SH3 domain containing prot. 7	Q62418	48669.6	4.93	4.6	1	11.4
Rho GDP dissociation inhibitor 1	Q99PT1	23392.8	5.148	12.3	1	11.4
26S proteasome non ATPase regulatory sub. 11	Q8BG32	47275	6.4	3.1	1	11.4
Nucleosome assembly protein 1	P28656	45316.9	4.36	4.4	1	11.4
Tumor protein D54	Q9CYZ2	24028.1	6.07	4.9	1	11.1
COP9 signalosome complex subunit 6	O88545	35857	5.682	4.0	1	11.0
Proteasome subunit beta type 3	Q9R1P1	22949.4	6.494	7.8	2	11.0
Proteasome subunit alpha type 3	O70435	28256.04	5.371	8.7	2	11.0
26S protease regulatory subunit S10B	P62334	44145.09	7.627	3.6	1	11.0
NSFL1 cofactor p47	Q9UNZ2	40548.3	5.038	3.2	1	11.0
Interleukin enhancer binding factor 2	Q9CXY6	43035.2	5.25	3.6	1	10.7
14-3-3 protein gamma	P61982	28153.8	4.832	11.8	2	10.7
60S ribosomal protein L22	P67984	14618.7	9.49	10.2	1	10.7
COP9 signalosome complex subunit 2	P61202	51564.05	5.46	7.9	2	10.5
14-3-3 protein epsilon	P62259	29155.4	4.65	16.1	3	10.5
Alpha actinin 4 non muscle	P57780	104911.4	5.348	6.5	4	9.9

Fosfoproteínas identificadas mediante nanoLC-ESI-MS/MS (gradiente 240 min.)

Proteína	Num acc	Mr	pl	% secuencia	péptidos	Score
Proteasome beta subunit type 3	Q9R1P1	22949.5	6.5	7.8	1	9.2
Proteasome beta subunit type 2	Q9R1P3	22891.7	6.9	5.5	1	9.2
60S acidic ribosomal protein P1	P47955	11467.7	4.2	14.0	1	9.2
Proteasome beta subunit type 6	Q60692	25362.4	5	4.6	1	9.2
Splicing factor Arg Ser rich 2	Q62093	25330.14	11.86	3.6	1	9.2
60S acidic ribosomal protein P0 L10E	34194.74	34194.74	6.18	3.2	1	9.2
Proteasome beta subunit type 4	P99026	29097.33	5.58	3.8	1	9.2
Glucoside II beta subunit	O08795	58755.8	4.43	1.9	1	9.2
Proteasome subunit alpha type 3	O70435	28256.1	5.37	3.9	1	9.2
Eukariotic translation initiation factor 2 sub 2	Q99L45	38068.23	5.7	3.0	1	9.2
Heterogeneous nuclear ribonucleoprotein K	P61979	50944.4	5.45	2.6	1	9.2
Septin 2 protein NeDD5	P42208	41499.28	6.46	3.3	2	9.2
Histone H1 3 H1 VAR 4 H1d	P43277	21955.1	11.39	5.0	2	9.2
Elongation factor 1 beta	O70251	24547.2	4.53	10.7	2	9.2
Hsc70 interacting protein Hip ST13	Q99L47	41629.52	5.25	6.2	2	9.2
Acidic leucine rich nuclear phosphoprotein 32 E	P97822	29604.4	3.75	10.8	2	9.2
Prostaglandin E synthase 3	Q9R0Q7	18709.42	4.31	15.6	2	9.2
Nucleophosmin NPM Nucleolar phosphoprot. B23	Q61937	32539.83	4.63	9.2	2	9.2
Proteasome subunit alpha type 6	Q9QUM9	27354.8	6.73	9.4	2	9.2
Proteasome subunit alpha type 1	Q9R1P4	29527.83	6.36	4.2	2	9.2
High mobility group protein 4	O54879	22864.4	8.74	6.5	2	9.2
Membrane associated progesterone receptor 1 glycoprotein gC1qBP	O55022	21549.73	4.54	7.2	2	9.2
	O35658	30993.5	4.85	5.0	2	9.2
Histone H1 2 H1 VAR 1 H1c	P15864	21122.68	11.36	5.2	3	9.2
SET protein phosphatase 2A inhibitor	Q9EQU5	33357.7	4.22	12.1	3	9.2
Splicing factor arginine serine rich 1	Q6PDM2	27596.7	10.5	14.6	3	9.2
Nascent polypeptide associated complex alpha sub	Q60817	23369.7	4.54	19.5	3	9.2
Elongation factor 1 gamma	Q9D8N0	49898.1	6.67	4.6	3	9.2
Tropomyosin alpha 4 chain	Q6IRU2	28319.4	4.68	10.9	3	9.2
60S acidic ribosomal protein P2	P99027	11643.8	4.37	24.3	3	9.2
CTP synthase	P70698	66668.2	6.5	3.7	3	9.2
Histone H1 5 H1 VAR 5 H1b	P43276	22431.4	11.3	10.4	3	9.2
Hepatoma derived growth factor HDGF	P51859	26252	4.84	10.5	3	9.2
Type I inositol 3 4 bisphosphatase 4	Q9EPW0	105472.4	7.03	1.0	3	9.2
Niban like protein	Q8R1F1	84765.1	5.87	1.5	3	9.2
Ran GTPase activating protein 1	P46061	63576.57	4.63	2.0	3	9.2
Tropomyosin alpha 3 chain	P21107	32842.8	4.71	11.3	4	9.2
Lamin A	P48678	74192.7	6.92	6.5	4	9.2
High mobility group protein 1	P63158	24747.14	5.7	13.6	4	9.2
Acidic leucine rich nuclear phosphoprotein 32 A	O35381	28520.26	3.98	16.2	4	9.2
Ras GTPase activating protein	P97855	51796.9	5.53	7.3	4	9.2
Src substrate cortactin	Q60598	61222.5	5.32	5.3	4	9.2
Splicing factor arginine serine rich 7	Q8BL97	30798.8	11.89	5.2	4	9.2
Splicing factor arginine serine rich 3	P84104	19317.9	11.6	14.0	4	9.2
Programmed cell death protein 5	P56812	14135.3	5.64	19.2	4	9.2
Transitional endoplasmic reticulum ATPase	Q01853	89120.7	5.2	1.2	4	9.2
elongation factor 1 delta	P57776	31142.8	4.9	16.4	5	9.2
Eukariotic translation initiation factor 4 gamma 1	Q6NZJ6	175966.4	5.37	0.6	5	9.2

Moesin membrane organizing extension spike prot	P26041	67593.84	6.53	10.4	6	9.2
Ezrin p81 cytovillin 2	P26040	69232.64	6.05	8.0	6	9.2
Calreticulin precursor	P14211	47964.9	4.33	17.5	6	9.2
Tubulin alpha 3 alpha 7	P05214	49927.6	5.03	20.2	7	9.2
Transaldolase	Q93092	37363.4	7.00	16.0	7	9.2
Nucleolin protein C23	P09405	76545.85	4.7	12.7	9	9.2
Calnexin precursor	P35564	67235.8	4.5	12.9	9	9.2
Prothymosin alpha	P26350	12116.01	3.67	21.8	11	9.2
Endoplasmin precursor	P08113	92418.11	4.77	15.8	13	9.2
Heat shock protein HSP90 beta	P11499	83142.11	5.00	24.1	25	9.2
Heat shock protein HSP90 alpha	P07901	84603.7	4.96	21.7	25	9.2
Histone H1 4 H1 VAR 2 H1e	P43274	21832.0	11.4	10.6	2	9.2
Proteasome subunit alpha type 7	Q9Z2U0	27837.63	8.8	14.9	3	9.2
Tubulin beta 5 chain	P99024	49638.9	4.81	12.2	6	9.2
Tubulin alpha 2 chain	P05213	50119.6	4.99	28.6	9	9.2
Splicing factor U2AF 65 KDa subunit	P26369	53483.26	9.38	2.1	1	9.2
Histone H2B 291B	P10854	13796.5	10.63	7.2	2	9.2
Tubulin alpha 6 chain	P68373	49877.5	5.01	28.7	9	8.6
Tubulin beta 4 chain	Q9D6F9	49519.9	4.81	8.8	5	8.6
Elongation factor 1 alpha 1	P10126	50082.1	9.34	2.4	1	8.6
Histone H2A type 2 H2A 2	Q6GSS7	13955.8	11.12	7.0	2	8.3
Annexin A3	O35639	36217.46	5.4	2.8	1	8.3
Tubulin alpha 4 chain	P68368	49892.38	4.98	20.1	6	8.3
Tropomyosin 1 alpha	P58771	32660.7	4.7	6.7	2	8.3

Tasas de error obtenidas en los diferentes análisis realizados mediante nanoLC-ESI-MS/MS

Análisis	Nº total de espectros	péptidos observados (p<0.001)	Falsos esperados	% péptidos observados	Verdaderos esperados	Tasa de error (%)
Gradiente 90 min	1219	53	1	4.3	52	2
Gradiente 240 min	6055	173	6	2.86	167	3.4
Gel 1D Fracción 1	1624	58	2	3.77	56	3.45
Gel 1D Fracción 2	3706	109	4	3.54	105	3.66
Gel 1D Fracción 3	3401	179	3	5.26	176	1.67
Gel 1D Fracción 4	2096	131	2	6.25	129	1.52

Contexto biológico e interpretación funcional de las fosfoproteínas identificadas en este estudio

(En negrita aparecen algunas de las fosfoproteínas identificadas)

