

Table SI. List of the androgen-enhanced palmitoylated proteins in LNCaP cells by palmitoylome analysis. The 96 androgen-enhanced candidates are listed, including the uniprot ID, gene name, protein function, categories by GO analysis and molecular weight.

Uniprot ID	Gene name	Protein function	Categories	Mol. weight [kDa]
P68363	<i>TUBA1B</i>	Tubulin alpha-1B chain	Cytoskeleton	50.151
P68366	<i>TUBA4A</i>	Tubulin alpha-4A chain	Cytoskeleton	49.924
Q8IZ29	<i>TUBB2C</i>	Tubulin beta chain	Cytoskeleton	49.839
Q5JP53	<i>TUBB</i>	Tubulin beta chain	Cytoskeleton	47.766
A0A024R1N1	<i>MYH9</i>	Myosin, heavy polypeptide 9	Cytoskeleton	226.53
P07737	<i>PFN1</i>	Profilin-1	Cytoskeleton	15.054
A0A0S2Z3G9	<i>ACTN4</i>	Actinin alpha 4	Cytoskeleton	104.85
O75369	<i>FLNB</i>	Filamin-B	Cytoskeleton	278.16
C9J8S3	<i>RAB7A</i>	Ras-related protein Rab-7a	Vesicle trafficking	18.026
A0A024R1U4	<i>RAB5C</i>	RAB5C, member RAS oncogene family	Vesicle trafficking	23.482
Q6IPT9	<i>EEF1A1</i>	Elongation factor 1-alpha	Protein <i>de novo</i> biosynthesis	50.184
P13639	<i>EEF2</i>	Elongation factor 2	Protein <i>de novo</i> biosynthesis	95.337
Q96IR1	<i>RPS4X</i>	40S ribosomal protein S4	Protein <i>de novo</i> biosynthesis	27.259
P30050	<i>RPL12</i>	60S ribosomal protein L12	Protein <i>de novo</i> biosynthesis	17.818
P07814	<i>EPRS</i>	Bifunctional glutamate/proline-tRNA ligase	Protein <i>de novo</i> biosynthesis	170.59
Q9Y262	<i>EIF3L</i>	Eukaryotic translation initiation factor 3 subunit L	Protein <i>de novo</i> biosynthesis	66.726
Q24JU4	<i>EIF3A</i>	Eukaryotic translation initiation factor 3 subunit A	Protein <i>de novo</i> biosynthesis	166.47
P49327	<i>FASN</i>	Fatty acid synthase	Lipid metabolism	273.42
Q13011	<i>ECH1</i>	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Lipid metabolism	35.816
A0A024R1Y2	<i>ACLY</i>	ATP-citrate synthase	Lipid metabolism	119.77
A0A024R6G4	<i>ALDH6A1</i>	Aldehyde dehydrogenase 6 family, member A1	Lipid metabolism	57.839
P49748	<i>ACADVL</i>	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Lipid metabolism	70.389
S4R3V8	<i>LSR</i>	Lipolysis-stimulated lipoprotein receptor	Lipid metabolism	66.175
V9HWB8	<i>HEL-S-30</i>	Pyruvate kinase	Glycometabolism	57.936
V9HVZ4	<i>GAPDH</i>	Glyceraldehyde-3-phosphate dehydrogenase	Glycometabolism	36.053
V9HWJ0	<i>HEL-S-164nA</i>	Epididymis secretory sperm binding protein Li 164nA	Glycometabolism	106.87
A0A024R4F1	<i>ENO1</i>	Enolase 1	Glycometabolism	47.168
A0A0S2Z430	<i>PCK2</i>	Phosphoenolpyruvate carboxykinase 2	Glycometabolism	70.729
P52209	<i>PGD</i>	6-phosphogluconate dehydrogenase, decarboxylating	Glycometabolism	53.139
V9HWK1	<i>HEL-S-49</i>	Triosephosphate isomerase	Glycometabolism	26.669
O43175	<i>PHGDH</i>	D-3-phosphoglycerate dehydrogenase	Amino acid metabolism	56.65
P23526	<i>AHCY</i>	Adenosylhomocysteinase	Amino acid metabolism	47.716
P22695	<i>UQCRC2</i>	Cytochrome b-c1 complex subunit 2, mitochondrial	Respiratory electron-transport chain	48.442
B4DL14	<i>ATP5F1C</i>	ATP synthase subunit gamma	Respiratory electron-transport chain	27.512
E5KRK5	<i>NDUFS1</i>	Mitochondrial NADH-ubiquinone oxidoreductase 75 kDa subunit	Respiratory electron-transport chain	79.467
E9PH64	<i>NDUFB9</i>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Respiratory electron-transport chain	20.383
P31930	<i>UQCRC1</i>	Cytochrome b-c1 complex subunit 1, mitochondrial	Respiratory electron-transport chain	52.645
V9HW26	<i>ATP5F1A</i>	ATP synthase subunit alpha	Respiratory electron-transport chain	59.75

Table SI. Continued.

Uniprot ID	Gene name	Protein function	Categories	Mol. weight [kDa]
Q0QEN7	<i>ATP5B</i>	ATP synthase subunit beta	Respiratory electron-transport chain	48.113
A0A024QZ30	<i>SDHA</i>	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Tricarboxylic acid cycle	72.691
Q53YE7	<i>MAOA</i>	Amine oxidase	Other metabolism-related process	59.681
V9HW89	<i>HEL-S-95n</i>	Epididymis secretory sperm binding protein Li 95n	Other metabolism-related process	38.311
Q6IBT3	<i>CCT7</i>	CCT7 protein	Protein folding	59.328
A0A024QZV0	<i>hCG_1811539</i>	HCG1811539	Protein folding	36.177
P17987	<i>TCP1</i>	T-complex protein 1 subunit alpha	Protein folding	60.343
B3KX11	<i>CCT3</i>	T-complex protein 1 subunit gamma	Protein folding	57.945
V9HWF5	<i>HEL-S-69p</i>	Peptidyl-prolyl cis-trans isomerase	Protein folding	18.012
V9HW22	<i>HEL-S-72p</i>	Epididymis luminal protein 33	Protein folding	70.897
B3KQT9	<i>PDIA3</i>	Protein disulfide-isomerase	Protein folding	54.102
A0A024RD80	<i>HSP90AB1</i>	Heat shock protein 90kDa alpha (Cytosolic), class B member 1	Protein folding	83.263
A0A024R3X4	<i>HSPD1</i>	Heat shock 60kDa protein 1	Protein folding	61.054
K9JA46	<i>EL52</i>	Epididymis luminal secretory protein 52	Protein folding	84.659
Q5CAQ5	<i>TRA1</i>	Tumor rejection antigen (Gp96) 1	Protein folding	92.339
A0A024R8S5	<i>P4HB</i>	Protein disulfide-isomerase	Protein folding	57.116
Q9Y6C9	<i>MTCH2</i>	Mitochondrial carrier homolog 2	Transporter	33.331
Q9H9B4	<i>SFXN1</i>	Sideroflexin-1	Transporter	35.619
Q9NZB2	<i>FAM120A</i>	Constitutive activator of PPAR-gamma-like protein 1	Transporter	121.89
Q92945	<i>KHSRP</i>	Far upstream element-binding protein 2	Transporter	73.114
Q6IBR0	<i>DPN1</i>	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1	Protein modification	68.606
A0A0S2Z5Q3	<i>SUMF2</i>	Sulfatase modifying factor 2 isoform 2	Protein modification	30.833
A0A024R258	<i>UBQLN1</i>	Ubiquilin 1	Protein modification	59.219
A0A024R1A3	<i>UBE1</i>	Testicular secretory protein Li 63	Protein modification	117.85
P05023	<i>ATP1A1</i>	Sodium/potassium-transporting ATPase subunit alpha-1	Ion channel	112.89
A0A0A0MR02	<i>VDAC2</i>	Voltage-dependent anion-selective channel protein 2	Ion channel	30.348
K7EJC8	<i>GOSR1</i>	Golgi SNAP receptor complex member 1	Receptor related	26.989
Q6RW13	<i>AGTRAP</i>	Type-1 angiotensin II receptor-associated protein	Receptor related	17.419
P27824	<i>CANX</i>	Calnexin	Other	67.567
H0Y512	<i>APMAP</i>	Adipocyte plasma membrane-associated protein	Other	45.294
V9HWH2	<i>HEL-S-29</i>	Creatine kinase brain isoform 1	Other	42.644
D9IAI1	<i>HEL-S-34</i>	Epididymis secretory protein Li 34	Other	21.057
J3KPX7	<i>PHB2</i>	Prohibitin-2	Other	33.239
B5BUB1	<i>RUVBL1</i>	RuvB-like helicase	Other	50.215
Q9Y230	<i>RUVBL2</i>	RuvB-like 2	Other	51.156
E5KNY5	<i>LRPPRC</i>	Leucine-rich PPR-motif containing	Other	157.9
P04040	<i>CAT</i>	Catalase	Other	59.755
F8W6I7	<i>HNRNPA1</i>	Heterogeneous nuclear ribonucleoprotein A1	Other	33.155
A8K401	<i>PHB</i>	Prohibitin	Other	29.804
B4DMG8	<i>N/A</i>	Glutamate dehydrogenase	Unkown	55.7
Q53GK6	<i>N/A</i>	Beta actin variant	Unkown	41.722
Q53GR7	<i>N/A</i>	Solute carrier family 25, member 13 (Citrin) variant	Unkown	74.116
H7C2Y5	<i>N/A</i>	Uncharacterized protein	Unkown	19.149
B4DJL0	<i>N/A</i>	cDNA FLJ60278, highly similar to Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 63 kDa subunit	Unkown	31.363

Table SI. Continued.

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A8K9U6	N/A	cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1	Unkown	101.46
A8K6Q8	N/A	cDNA FLJ75881, highly similar to Homo sapiens transferrin receptor (p90, CD71) (TFRC)	Unkown	84.872
Q53FS4	N/A	Lectin, mannose-binding, 1 variant	Unkown	57.557
B2R8R5	N/A	cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28	Unkown	88.559
B4DRH6	N/A	cDNA FLJ54509, highly similar to Trifunctional enzyme subunit alpha, mitochondrial	Unkown	78.314
B4DY09	N/A	cDNA FLJ51660, highly similar to Interleukin enhancer-binding factor 2	Unkown	38.91
B4DG62	N/A	cDNA FLJ56506, highly similar to Hexokinase-1	Unkown	102.31
B3KN05	N/A	cDNA FLJ13129 fis, clone NT2RP3002969, highly similar to Long-chain-fatty-acid-CoA ligase 3	Unkown	79.222
B4DV28	N/A	cDNA FLJ54170, highly similar to Cytosolic nonspecific dipeptidase	Unkown	51.501
B4E0X8	N/A	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1	Unkown	66.231
B4DUQ1	N/A	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K	Unkown	48.51
Q53G71	N/A	Calreticulin variant	Unkown	46.918
B4DU00	N/A	cDNA FLJ54547, highly similar to Alpha-1 catenin (Cadherin-associated protein)	Unkown	88.702
B4DZ87	N/A	cDNA FLJ57240, highly similar to Mitochondrial proteins import receptor	Unkown	56.93