Supplementary Information

Effects of weaning on intestinal crypt epithelial cells in piglets

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Figure S1. KEGG pathway enrichment of differentially expressed proteins in jejunal crypt epithelial cells of weaning piglets. Any protein with ≥1.2-fold or ≤0.8-fold difference in values measured from w1d, w3d, w5d, or w7d samples versus w0d level, and *P*-value ≤0.05, was considered differentially expressed.

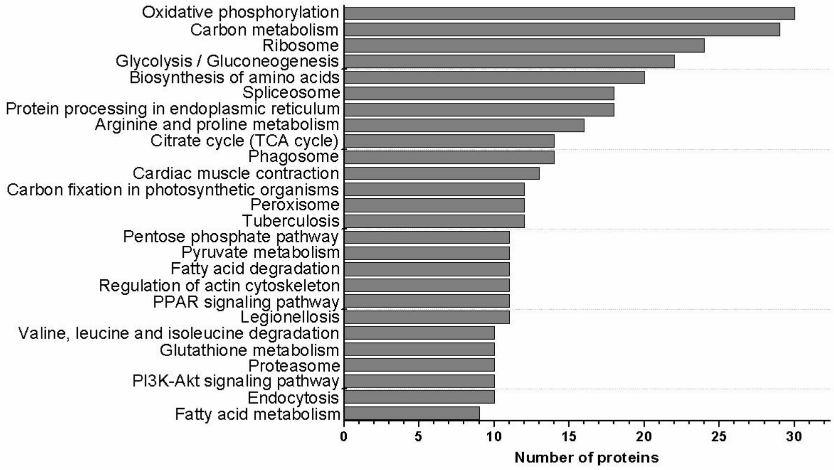

Figure S2. Proteins related to cell cycle in jejunal crypt epithelial cells of weaning piglets. Data are means ± SD; n=5. For each panel, bars not labelled with same superscript indicate values are significantly different at *P* <0.05.

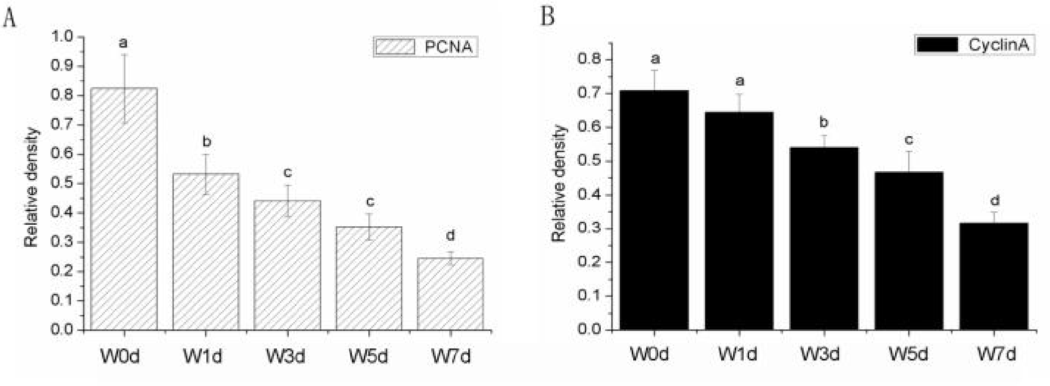

Figure S3. Proteins related to mTOR signaling pathway in jejunal crypt epithelial cells of weaning piglets. Data are means ± SD; n=5. For each panel, bars not labelled with same superscript indicate values are significantly different at P <0.05.

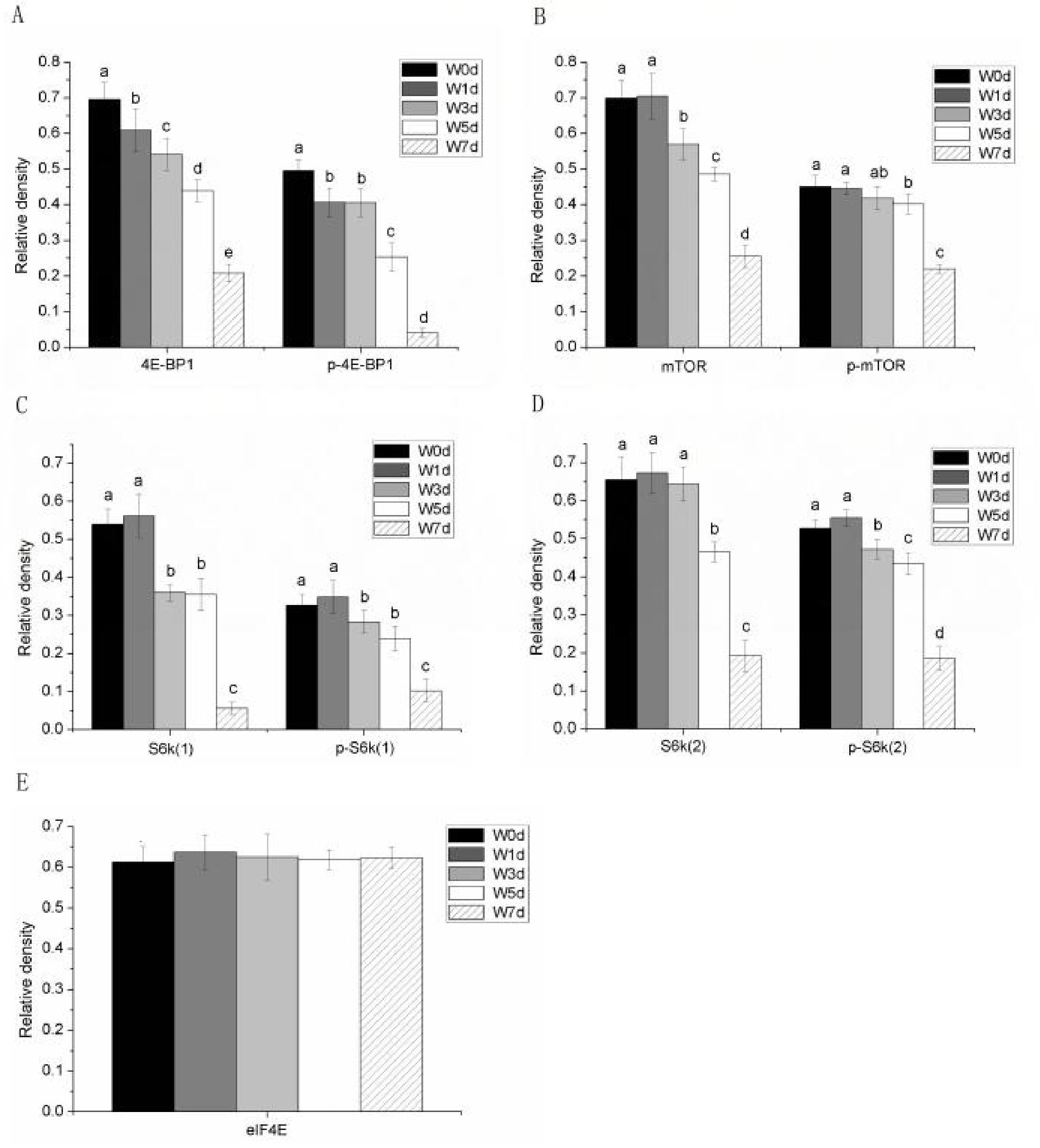

Table S1

Total identified proteins

Accession	Desription	W1d vs W0d	W3d vs W0d	W5d vs W0d	W7d vs W0d
gi|1706761|sp|P49924.1|FABPL_PIG	RecName: Full=Fatty acid-binding protein, liver; AltName: Full=Fatty acid-binding protein 1; AltName: Full=Liver-type fatty acid-binding protein; Short=L-FABP >gi|55742707|ref|NP_001004046.1| fatty acid-binding protein, liver [Sus scrofa] >gi|754910	1.365	1.226	1.187	0.588
gi|71724936|gb|AAZ38898.1|	intestinal fatty acid binding protein [Sus scrofa]	1.479	2.127	2.029	0.869
gi|91206621|sp|Q45KW7.3|FABPI_PIG	RecName: Full=Fatty acid-binding protein, intestinal; AltName: Full=Fatty acid-binding protein 2; AltName: Full=Intestinal-type fatty acid-binding protein; Short=I-FABP >gi|72535172|ref|NP_001026950.1| fatty acid-binding protein, intestinal [Sus scr				
gi|350583843|ref|XP_003126114.3|	PREDICTED: myosin-9 [Sus scrofa]	0.607	0.849	0.925	0.691
gi|1710817|sp|P02632.3|S100G_PIG	RecName: Full=Protein S100-G; AltName: Full=Calbindin-D9k; AltName: Full=S100 calcium-binding protein G; AltName: Full=Vitamin D-dependent calcium-binding protein, intestinal; Short=CABP; Contains: RecName: Full=Protein S100-G, minor isoform >gi|557	1.161	2.371	1.749	1.879
gi|157830532|pdb|1CB1|A	Chain A, Three-Dimensional Solution Structure Of Ca2+-Loaded Porcine Calbindin D9k Determined By Nuclear Magnetic Resonance Spectroscopy				
gi|45269029|gb|AAS55927.1|	cytoskeletal beta actin, partial [Sus scrofa]	1.089	0.585	0.609	0.964
gi|150438831|sp|Q6QAQ1.2|	RecName: Full=Actin, cytoplasmic 1;				

ACTB_PIG	AltName: Full=Beta-actin; Contains: RecName: Full=Actin, cytoplasmic 1, N-terminally processed >gi|311250866|ref|XP_003124328.1| PREDICTED: actin, cytoplasmic 1 [Sus scrofa]				
gi|335297229|ref|XP_003357976.1|	PREDICTED: actin, cytoplasmic 2 [Sus scrofa]				
gi|169139278|gb|ACA48587.1|	liver fatty acid binding protein [Sus scrofa]	0.903	1.628	1.294	0.917
gi|227430407|ref|NP_001153087.1|	keratin, type II cytoskeletal 8 [Sus scrofa]	0.605	0.616	0.767	0.663
gi|194037554|ref|XP_001929445.1|	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	0.748	0.423	0.355	0.607
gi|297591975|ref|NP_001172071.1|	ATP synthase subunit alpha, mitochondrial [Sus scrofa] >gi|187370717|gb|ACD02421.1| cardiac muscle ATP synthase H+ transporting mitochondrial F1 complex alpha subunit 1 [Sus scrofa]	0.768	0.706	0.723	0.799
gi|350585373|ref|XP_003127406.3|	PREDICTED: myosin-14-like [Sus scrofa]	0.667	0.776	0.842	0.605
gi|359811347|ref|NP_001241645.1|	60 kDa heat shock protein, mitochondrial [Sus scrofa] >gi|358009189|gb|AET99216.1| mitochondrial heat shock 60 kDa protein 1 [Sus scrofa]	0.742	0.835	0.735	0.78
gi|358009193|gb|AET99218.1|	prolyl 4-hydroxylase beta polypeptide [Sus scrofa]	0.456	0.471	0.513	0.357
gi|311246557|ref|XP_003122249.1|	PREDICTED: spectrin alpha chain, brain [Sus scrofa]	0.858	1.364	1.308	1.148
gi|47523848|ref|NP_999562.1|	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor [Sus scrofa] >gi|18203301|sp|Q9N0F1.1|ODO2_PIG RecName: Full=Dihydrolipoyllysine-residue succinyltransferase component of 2-ox	0.491	0.642	0.769	0.443
gi|350579657|ref|XP_001927830.3|	PREDICTED: 78 kDa glucose-regulated protein [Sus scrofa]	0.613	0.725	0.723	0.64

gi|350593858|ref|XP_003133682.3|	PREDICTED: carbamoyl-phosphate synthase [ammonia], mitochondrial isoform 1 [Sus scrofa]	1.256	0.64	0.507	0.899
gi|350588218|ref|XP_003129667.3|	PREDICTED: nuclear mitotic apparatus protein 1-like [Sus scrofa]	0.867	0.978	1.042	0.815
gi|48675927|ref|NP_001001632.1|	tropomyosin alpha-3 chain [Sus scrofa] >gi|45272586|gb|AAS57724.1| tropomyosin 3 [Sus scrofa]	0.426	1.649	1.82	1.29
gi|346644743|ref|NP_001231138.1|	calmodulin 3 [Sus scrofa] >gi|346644746|ref|NP_001231139.1| calmodulin 1 [Sus scrofa] >gi|311252670|ref|XP_003125211.1| PREDICTED: calmodulin-like [Sus scrofa]	1.687	2.281	4.172	2.23
gi|335289608|ref|XP_003355931.1|	PREDICTED: alpha-actinin-4-like isoform 2 [Sus scrofa]	1.441	1.12	1.304	1.286
gi|335289612|ref|XP_003127168.2|	PREDICTED: alpha-actinin-4-like isoform 1 [Sus scrofa]				
gi|311273061|ref|XP_001925202.2|	PREDICTED: villin 1 [Sus scrofa]	1.437	1.059	0.998	1.99
gi|85701138|sp|Q3ZD69.1|LMNA_PIG	RecName: Full=Prelamin-A/C; Contains: RecName: Full=Lamin-A/C; Flags: Precursor >gi|162139823|ref|NP_001104727.1| prelamin-A/C [Sus scrofa] >gi|66352014|gb|AAY44741.1| lamin A [Sus scrofa]	0.944	0.905	0.832	0.902
gi|46396062|sp|Q865F1.1|MTP_PIG	RecName: Full=Microsomal triglyceride transfer protein large subunit; Flags: Precursor >gi|47523450|ref|NP_999350.1| microsomal triglyceride transfer protein large subunit precursor [Sus scrofa] >gi|28974486|gb|AAO61497.1| microsomal triglyceride tr	0.965	0.461	0.435	0.601
gi|984249|emb|CAA62352.1|	protein kinase [Sus scrofa]	---	---	---	---
gi|17865698|sp|Q29092.3|ENPL_PIG	RecName: Full=Endoplasmin; AltName: Full=94 kDa glucose-regulated protein; Short=GRP-94; AltName: Full=98 kDa protein kinase; Short=PPK 98; Short=ppk98; AltName: Full=Heat shock protein 90 kDa beta member 1;				

	AltName: Full=gp96 homolog; Flags: Precur				
gi|47523016|ref|NP_999268.1|	endoplasmin precursor [Sus scrofa] >gi|2239253|emb|CAA70347.1| gp96/GRP94 [Sus scrofa]	1.336	0.741	1.314	0.855
gi|343962597|ref|NP_001230636.1|	cytosolic non-specific dipeptidase [Sus scrofa]	1.6	3.758	3.289	2.765
gi|332278130|sp|Q29261.2|VILI_PIG	RecName: Full=Villin-1	1.978	1.393	1.137	1.456
gi|350591286|ref|XP_003132317.3|	PREDICTED: filamin-B-like [Sus scrofa]	1.296	1.839	2.223	1.706
gi|225450|prf||1303334A	valosin precursor	1.408	0.778	0.889	1.181
gi|47523628|ref|NP_999442.1|	aminopeptidase N [Sus scrofa] >gi|1703286|sp|P15145.3|AMPN_PIG RecName: Full=Aminopeptidase N; Short=AP-N; Short=pAPN; AltName: Full=Alanyl aminopeptidase; AltName: Full=Aminopeptidase M; Short=AP-M; AltName: Full=Microsomal aminopeptidase; AltName:	0.377	0.514	0.611	0.898
gi|225735709|ref|NP_001139599.1|	clathrin heavy chain 1 [Sus scrofa] >gi|224492556|emb|CAR65329.1| clathrin heavy chain [Sus scrofa]	1.218	0.807	0.717	1.26
gi|311267276|ref|XP_003131485.1|	PREDICTED: keratin, type I cytoskeletal 19-like [Sus scrofa]	0.627	0.634	0.765	0.792
gi|311264042|ref|XP_003129970.1|	PREDICTED: hypoxia up-regulated protein 1 [Sus scrofa]	0.691	0.661	0.727	0.648
gi|164382|gb|AAA31002.1|	Na+, K+-ATPase alpha-subunit precursor [Sus scrofa]	0.797	0.422	0.473	0.725
gi|283443670|gb|ADB19852.1|	Na+/K+ transporting alpha 1 polypeptide [Sus scrofa]				
gi|225173|prf||1210234A	ATPase alpha,Na/K				
gi|393714792|dbj|BAM28740.1|	sodium/potassium-transporting ATPase subunit alpha-1, partial [Sus scrofa]				
gi|194038728|ref|XP_001929104.1|	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 1 [Sus scrofa]	2.09	1.004	1.201	2.004
gi|345441750|ref|NP_001230836.1|	heat shock 70kDa protein 8 [Sus scrofa]	1.383	0.961	0.98	1.398

gi|311273928|ref|XP_003134106.1|	PREDICTED: nucleophosmin-like isoform 2 [Sus scrofa]	0.919	1.022	1.439	0.668
gi|311273930|ref|XP_003134105.1|	PREDICTED: nucleophosmin-like isoform 1 [Sus scrofa]				
gi|350585579|ref|XP_003481996.1|	PREDICTED: alpha-enolase-like, partial [Sus scrofa]	1.597	1.466	1.565	1.341
gi|54873401|gb|AAV40980.1|	heat shock 60 kDa protein 1 [Sus scrofa]	1.229	0.463	0.45	0.587
gi|311252615|ref|XP_003125184.1|	PREDICTED: ubiquitin-40S ribosomal protein S27a-like [Sus scrofa] >gi|311252617|ref|XP_003125185.1| PREDICTED: ubiquitin-40S ribosomal protein S27a-like [Sus scrofa]	1.316	3.017	2.609	1.82
gi|164414678|emb|CAO81735.1|	Alternative Pig Liver Esterase [Sus scrofa]	0.927	1.243	1.579	1.871
gi|47522754|ref|NP_999127.1|	trifunctional enzyme subunit alpha, mitochondrial [Sus scrofa] >gi|7387634|sp|Q29554.1|ECHA_PIG RecName: Full=Trifunctional enzyme subunit alpha, mitochondrial; AltName: Full=78 kDa gastrin-binding protein; AltName: Full=TP-alpha; Includes: RecName:	---	---	---	---
gi|304365428|ref|NP_001182041.1|	protein disulfide-isomerase A3 precursor [Sus scrofa] >gi|301016769|dbj|BAJ11757.1| glucose regulated protein 58 [Sus scrofa]	0.492	1.192	1.152	0.772
gi|187370723|gb|ACD02424.1|	hydroxyacyl-coenzyme A dehydrogenase/3-ketoacyl-coenzyme A thiolase/enoyl-coenzyme A hydratase alpha subunit [Sus scrofa]	---	---	---	---
gi|350593231|ref|XP_003359478.2|	PREDICTED: lactase-phlorizin hydrolase-like [Sus scrofa]	0.691	0.999	0.733	0.7
gi|47522774|ref|NP_999138.1|	heat shock protein HSP 90-alpha [Sus scrofa] >gi|6016267|sp|O02705.3|HS90A_PIG RecName: Full=Heat shock protein HSP 90-alpha >gi|1945447|gb|AAC48718.1| 90-kDa heat shock protein [Sus scrofa]	1.901	1.11	1.112	1.877

<table>
<tr><th></th><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td>gi|297591979|ref|NP_001172070.1|</td><td>ornithine aminotransferase, mitochondrial [Sus scrofa] >gi|166244455|gb|ABY86572.1| mitochondrial ornithine aminotransferase [Sus scrofa]</td><td>1.701</td><td>1.067</td><td>0.856</td><td>1.434</td></tr>
<tr><td>gi|335287713|ref|XP_003355423.1|</td><td>PREDICTED: tubulin alpha-1C chain isoform 1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311267326|ref|XP_003131510.1|</td><td>PREDICTED: keratin, type I cytoskeletal 20-like [Sus scrofa]</td><td>0.64</td><td>0.647</td><td>0.745</td><td>0.864</td></tr>
<tr><td>gi|350594669|ref|XP_001926037.4|</td><td>PREDICTED: ribosome-binding protein 1 [Sus scrofa]</td><td>0.571</td><td>1.008</td><td>0.992</td><td>0.8</td></tr>
<tr><td>gi|356460899|ref|NP_999466.2|</td><td>catalase [Sus scrofa]</td><td>0.83</td><td>1.677</td><td>1.644</td><td>1.541</td></tr>
<tr><td>gi|2494384|sp|Q29550.1|EST1_PIG</td><td>RecName: Full=Liver carboxylesterase; AltName: Full=Proline-beta-naphthylamidase; AltName: Full=Retinyl ester hydrolase; Short=REH; Flags: Precursor >gi|363817363|emb|CCF23015.1| unnamed protein product [Sus scrofa] >gi|1931|emb|CAA44929.1| carboxyl</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|218314621|emb|CAV28734.1|</td><td>unnamed protein product [Sus sp.]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|297747302|ref|NP_001172115.1|</td><td>aspartyl aminopeptidase [Sus scrofa]</td><td>0.913</td><td>2.217</td><td>1.765</td><td>0.631</td></tr>
<tr><td>gi|335283403|ref|XP_003123930.2|</td><td>PREDICTED: lamin-B1 [Sus scrofa]</td><td>0.698</td><td>0.956</td><td>0.966</td><td>0.827</td></tr>
<tr><td>gi|47522618|ref|NP_999099.1|</td><td>vinculin [Sus scrofa] >gi|17979613|gb|AAL50327.1| vinculin [Sus scrofa]</td><td>1.921</td><td>1.133</td><td>1.151</td><td>1.468</td></tr>
<tr><td>gi|50403675|sp|P26234.4|VINC_PIG</td><td>RecName: Full=Vinculin; AltName: Full=Metavinculin</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|194043861|ref|XP_001928233.1|</td><td>PREDICTED: tubulin alpha-1D chain [Sus scrofa]</td><td>0.839</td><td>0.202</td><td>0.171</td><td>0.878</td></tr>
<tr><td>gi|401871556|pdb|4F5C|A</td><td>Chain A, Crystal Structure Of The Spike Receptor Binding Domain Of A Porcine Respiratory Coronavirus In Complex With The Pig Aminopeptidase N Ectodomain >gi|401871557|pdb|4F5C|B Chain B, Crystal Structure Of The Spike Receptor Binding Domain Of</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
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	A Po				
gi|343790893|ref|NP_001230504.1|	creatine kinase, brain [Sus scrofa]	1.616	0.641	0.774	0.917
gi|47523572|ref|NP_999411.1|	liver carboxylesterase precursor [Sus scrofa] >gi|3831588|gb|AAC70013.1| carboxylesterase [Sus scrofa]	1.484	1.46	2.039	2.172
gi|311250237|ref|XP_003124024.1|	PREDICTED: stress-70 protein, mitochondrial [Sus scrofa]	0.877	0.886	0.721	0.961
gi|350591288|ref|XP_003483241.1|	PREDICTED: filamin-B [Sus scrofa]	1.059	1.552	1.546	1.5
gi|346986466|ref|NP_001231384.1|	proteasome (prosome, macropain) subunit, beta type, 4 [Sus scrofa]	1.495	2.265	3.011	1.72
gi|347300207|ref|NP_001231417.1|	nucleobindin-1 precursor [Sus scrofa]	0.672	1.095	1.007	0.739
gi|47522738|ref|NP_999119.1|	aconitate hydratase, mitochondrial precursor [Sus scrofa] >gi|113159|sp|P16276.1|ACON_PIG RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor >gi|164315|gb|AAA30987.1| heart aconitas	1.77	1.054	1.058	1.686
gi|157837131|pdb|7ACN|A	Chain A, Crystal Structures Of Aconitase With Isocitrate And Nitroisocitrate Bound >gi|157837084|pdb|6ACN|A Chain A, Structure Of Activated Aconitase. Formation Of The (4fe-4s) Cluster In The Crystal >gi|157837014|pdb|5ACN|A Chain A, Structure Of Ac				
gi|335303414|ref|XP_001928370.3|	PREDICTED: tubulin alpha-4A chain [Sus scrofa]	1.239	0.76	0.683	1.233
gi|350591605|ref|XP_003483304.1|	PREDICTED: plastin-1-like [Sus scrofa]	1.46	1.001	0.985	1.418
gi|349501107|ref|NP_001231795.1|	ribosomal protein, large, P2 [Sus scrofa]	0.63	1.484	1.372	0.685
gi|350579435|ref|XP_003122094.3|	PREDICTED: fructose-bisphosphate aldolase B-like, partial [Sus scrofa]	1.468	1.198	1.169	1.175
gi|392513715|ref|NP_001254774.1|	heterogeneous nuclear ribonucleoprotein K [Sus scrofa]	1.038	1.824	1.233	1.272

gi|47523730|ref|NP_999500.1|	tropomyosin alpha-4 chain [Sus scrofa] >gi|54039746|sp|P67937.3|TPM4_PIG RecName: Full=Tropomyosin alpha-4 chain; AltName: Full=Tropomyosin-4 >gi|3661527|gb|AAC61744.1| tropomyosin 4 [Sus scrofa] >gi|262263207|dbj|BAI48106.1| tropomyosin 4 [Sus scro	0.496	0.857	0.634	0.489
gi|311259005|ref|XP_003127890.1|	PREDICTED: myosin regulatory light chain 12B isoform 2 [Sus scrofa] >gi|311259003|ref|XP_003127889.1| PREDICTED: myosin regulatory light chain 12B isoform 1 [Sus scrofa]	0.262	0.4	0.545	0.347
gi|346716324|ref|NP_001231180.1|	myosin regulatory light chain 2 protein isoform 2 [Sus scrofa]				
gi|999620|pdb|1MLD|D	Chain D, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases >gi|999618|pdb|1MLD|B Chain B, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine	2.014	1.057	0.879	1.832
gi|2506849|sp|P00346.2|MDHM_PIG	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor				
gi|350581138|ref|XP_003124036.3|	PREDICTED: catenin alpha-1 isoform 1 [Sus scrofa]	1.094	0.881	0.907	0.976
gi|335306989|ref|XP_003130411.2|	PREDICTED: ATP-dependent RNA helicase A-like [Sus scrofa]	1.146	0.78	0.777	0.994
gi|350593236|ref|XP_003359477.2|	PREDICTED: lactase-phlorizin hydrolase-like, partial [Sus scrofa]	---	---	---	---
gi|311247536|ref|XP_003122689.1|	PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)-like [Sus scrofa]	1.863	0.874	0.935	1.222
gi|335280610|ref|XP_003353615.1|	PREDICTED: LOW QUALITY PROTEIN: talin-1 [Sus scrofa]	1.338	1.018	1.273	1.171
gi|268607671|ref|NP_001161267.1|	actin, alpha skeletal muscle [Sus scrofa] >gi|62287931|sp|P68137.1|AC	1.216	0.517	0.418	1.334

	TS_PIG RecName: Full=Actin, alpha skeletal muscle; AltName: Full=Alpha-actin-1; Flags: Precursor >gi|790202|gb|AAC48692.1| skeletal alpha actin [Sus scrofa]				
gi|281427360|ref|NP_001163988.1|	actin, alpha cardiac muscle 1 [Sus scrofa] >gi|210077998|emb|CAR82077.1| cardiac muscle alpha actin 1 [Sus scrofa] >gi|210077994|emb|CAR82075.1| cardiac muscle alpha actin 1 [Sus scrofa] >gi|210077996|emb|CAR82076.1| cardiac muscle alpha actin 1 [Su				
gi|56748897|sp|Q6S4N2.1|HS71B_PIG	RecName: Full=Heat shock 70 kDa protein 1B; AltName: Full=Heat shock 70 kDa protein 2; Short=HSP70.2 >gi|47523308|ref|NP_998931.1| heat shock 70 kDa protein 1B [Sus scrofa] >gi|39777368|gb|AAR30953.1| heat shock protein 70.2 [Sus scrofa] >gi|1487249	1.002	1.197	1.071	0.58
gi|346986428|ref|NP_001231362.1|	heat shock 90kD protein 1, beta [Sus scrofa]	1.86	1.323	0.967	2.418
gi|346986249|ref|NP_001231282.1|	proteasome subunit beta type-1 [Sus scrofa]	1.43	2.595	2.883	1.853
gi|392513702|ref|NP_001254763.1|	protein disulfide isomerase family A, member 4 precursor [Sus scrofa]	0.946	1.025	1.023	1.005
gi|255683394|ref|NP_001157474.1|	ornithine carbamoyltransferase, mitochondrial [Sus scrofa]	0.91	1.058	1.682	1.552
gi|304365440|ref|NP_001182048.1|	protein disulfide-isomerase A6 precursor [Sus scrofa] >gi|301016767|dbj|BAJ11758.1| protein disulfide isomerase P5 [Sus scrofa]	1.046	0.969	0.942	1.025
gi|164318|gb|AAA30988.1|	albumin, partial [Sus scrofa]	1.129	0.611	0.569	0.712
gi|833798|emb|CAA30970.1|	albumin [Sus scrofa]				
gi|47522844|ref|NP_999174.1|	complement C3 precursor [Sus scrofa] >gi|11869931|gb|AAG40565.1|AF154933_1 complement component C3 [Sus scrofa] >gi|27801787|emb|CAD38823.2| complement C3 precursor [Sus scrofa]	0.64	0.917	0.806	1.028

gi|311259466|ref|XP_003128111.1|	PREDICTED: putative hydroxypyruvate isomerase-like isoform 1 [Sus scrofa]	1.019	2.107	1.793	1.053
gi|112980811|gb|ABI29187.1|	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]	2.033	1.297	0.982	2.414
gi|329744642|ref|NP_001193288.1|	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa] >gi|2506441|sp|P00355.4|G3P_PIG RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH; AltName: Full=Peptidyl-cysteine S-nitrosylase GAPDH				
gi|47522864|ref|NP_999186.1|	unconventional myosin-VI [Sus scrofa] >gi|75039721|sp|Q29122.1|MYO6_PIG RecName: Full=Unconventional myosin-VI; AltName: Full=Unconventional myosin-6 >gi|516155|emb|CAA84559.1| unconventional myosin [Sus scrofa]	0.847	0.744	0.911	0.63
gi|230506|pdb|2FBP|A	Chain A, Structure Refinement Of Fructose-1,6-Bisphosphatase And Its Fructose 2,6-Bisphosphate Complex At 2.8 Angstroms Resolution >gi|230507|pdb|2FBP|B Chain B, Structure Refinement Of Fructose-1,6-Bisphosphatase And Its Fructose 2,6-Bisphosphate C	1.622	1.109	0.814	0.793
gi|99032141|pdb|2F3H|A	Chain A, Mechanism Of Displacement Of A Catalytically Essential Loop From The Active Site Of Fructose-1,6-Bisphosphatase >gi|99032142|pdb|2F3H|B Chain B, Mechanism Of Displacement Of A Catalytically Essential Loop From The Active Site Of Fructose-1,				
gi|24987483|pdb|1KZ8|A	Chain A, Crystal Structure Of Porcine Fructose-1,6-Bisphosphatase Complexed With A Novel Allosteric-Site Inhibitor >gi|24987484|pdb|1KZ8|F				

	Chain F, Crystal Structure Of Porcine Fructose-1,6-Bisphosphatase Complexed With A Novel Allosteric-Site Inhib				
gi|47522784|ref|NP_999144.1|	fructose-1,6-bisphosphatase 1 [Sus scrofa] >gi|1706735|sp|P00636.4|F16P1_PIG RecName: Full=Fructose-1,6-bisphosphatase 1; Short=FBPase 1; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase 1 >gi|300654514|emb|CBV02317.1| unnamed protein pr				
gi|33357497|pdb|1NV1|A	Chain A, Fructose-1,6-Bisphosphatase Complex With Magnesium, Fructose-6- Phosphate, Phosphate And Thallium (5 Mm) >gi|159795376|pdb|2QVV|A Chain A, Porcine Liver Fructose-1,6-Bisphosphatase Cocrystallized With Fru-2,6-P2 And Zn2+, I(T)-State >gi|159				
gi|24987566|pdb|1LEV|F	Chain F, Porcine Kidney Fructose-1,6-Bisphosphatase Complexed With An Amp-Site Inhibitor >gi|24987565|pdb|1LEV|A Chain A, Porcine Kidney Fructose-1,6-Bisphosphatase Complexed With An Amp-Site Inhibitor				
gi|3288991|gb|AAC25597.1|	fructose-1,6-bisphosphatase [Sus scrofa]				
gi|387912908|sp|P28491.3|CALR_PIG	RecName: Full=Calreticulin; AltName: Full=CRP55; AltName: Full=Calregulin; AltName: Full=Endoplasmic reticulum resident protein 60; Short=ERp60; AltName: Full=HACBP; Flags: Precursor >gi|291622246|ref|NP_001167604.1| calreticulin precursor [Sus scro	0.91	0.589	0.581	0.836
gi|343887360|ref|NP_001230	proteasome (prosome, macropain)	1.076	1.677	1.637	1.449

581.1|	subunit, alpha type [Sus scrofa]				
gi|350276134|ref|NP_001231877.1|	LETM1 and EF-hand domain-containing protein 1, mitochondrial [Sus scrofa]	0.568	0.701	0.726	0.558
gi|51701269|sp|Q95334.1|AMPE_PIG	RecName: Full=Glutamyl aminopeptidase; Short=EAP; AltName: Full=Aminopeptidase A; Short=AP-A; AltName: CD_antigen=CD249 >gi|47522856|ref|NP_999182.1| glutamyl aminopeptidase [Sus scrofa] >gi|1518865|gb|AAB07141.1| aminopeptidase A [Sus scrofa]	0.519	0.634	0.513	0.467
gi|347446687|ref|NP_001231527.1|	glucosidase 2 subunit beta precursor [Sus scrofa]	0.456	0.593	0.593	0.549
gi|194037005|ref|XP_001928988.1|	PREDICTED: ribonuclease UK114-like isoform 1 [Sus scrofa]	1.117	2.581	2.299	1.141
gi|335281715|ref|XP_003122673.2|	PREDICTED: L-asparaginase-like [Sus scrofa]	1.844	2.26	2.082	1.32
gi|223046|prf||0410468A	aminotransferase,Asp	1.169	1.787	1.918	1.829
gi|113205892|ref|NP_001038077.1|	tubulin beta chain [Sus scrofa] >gi|75045190|sp|Q767L7.1|TBB5_PIG RecName: Full=Tubulin beta chain; AltName: Full=Tubulin beta-5 chain >gi|81174748|gb|ABB58916.1| beta 5-tubulin [Sus scrofa] >gi|41529175|dbj|BAD08435.1| beta 5-tubulin [Sus scrofa]	0.788	0.442	0.456	0.987
gi|335282386|ref|XP_003354050.1|	PREDICTED: elongation factor 2 [Sus scrofa]	1.833	1.1	0.974	1.955
gi|311254317|ref|XP_001927973.2|	PREDICTED: cingulin-like [Sus scrofa]	0.549	0.991	0.92	0.625
gi|219522018|ref|NP_001137196.1|	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 [Sus scrofa] >gi|217031226|gb|ACJ74160.1| solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	1.571	2.608	2.407	1.557
gi|194018702|ref|NP_001123419.1|	tropomyosin beta chain [Sus scrofa] >gi|83778524|gb|ABC47143.1| beta-tropomyosin [Sus scrofa]	---	---	---	---
gi|350595475|ref|XP_003360	PREDICTED: proteasome subunit	0.713	2.004	2.133	1.102

255.2|	alpha type-2-like [Sus scrofa]				
gi|335281298|ref|XP_003122400.2|	PREDICTED: tubulin beta-2C chain-like [Sus scrofa]	---	---	---	---
gi|330417958|ref|NP_001155225.1|	phosphoenolpyruvate carboxykinase [GTP], mitochondrial [Sus scrofa] >gi|238863892|gb|ACR66222.1| phosphoenolpyruvate carboxykinase 2 [Sus scrofa]	2.689	1.25	0.996	1.532
gi|4033507|sp|P08132.2|ANXA4_PIG	RecName: Full=Annexin A4; AltName: Full=35-beta calcimedin; AltName: Full=Annexin IV; AltName: Full=Annexin-4; AltName: Full=Chromobindin-4; AltName: Full=Endonexin I; AltName: Full=Lipocortin IV; AltName: Full=P32.5; AltName: Full=PP4-X; AltName: F	0.597	0.527	0.325	0.539
gi|311252000|ref|XP_003124873.1|	PREDICTED: fumarylacetoacetate hydrolase domain-containing protein 2-like isoform 2 [Sus scrofa]	1.049	1.282	1.147	0.795
gi|194018698|ref|NP_001123442.1|	cytochrome c [Sus scrofa] >gi|119388070|sp|P62895.2|CYC_PIG RecName: Full=Cytochrome c >gi|62208258|gb|AAX77008.1| cytochrome c-like protein [Sus scrofa]	1.081	2.968	2.164	1.501
gi|194039882|ref|XP_001928584.1|	PREDICTED: histone H2B type 1-H-like [Sus scrofa]	---	---	---	---
gi|335291884|ref|XP_003356615.1|	PREDICTED: histone H2B type 1-like [Sus scrofa] >gi|194039814|ref|XP_001927752.1| PREDICTED: histone H2B type 1-like [Sus scrofa]				
gi|335287029|ref|XP_003355256.1|	PREDICTED: histone H2B type 2-F-like isoform 1 [Sus scrofa]				
gi|335287031|ref|XP_003355257.1|	PREDICTED: histone H2B type 2-F-like isoform 2 [Sus scrofa]				
gi|335291890|ref|XP_003356617.1|	PREDICTED: histone H2B type 1-N-like [Sus scrofa]				
gi|343887370|ref|NP_001230585.1|	histone H2B type 1-D [Sus scrofa] >gi|194039822|ref|XP_001927974.1| PREDICTED: histone H2B				

	type 1-M-like [Sus scrofa]				
gi|311259875|ref|XP_003128266.1|	PREDICTED: histone H2B type 1-K-like [Sus scrofa]				
gi|544445|sp|P80031.2|GSTP1_PIG	RecName: Full=Glutathione S-transferase P; AltName: Full=GST P1-1; AltName: Full=GST class-pi	1.283	1.047	1.337	1.24
gi|1943419|pdb|2GSR|B	Chain B, Structure Of Porcine Class Pi Glutathione S-Transferase >gi|1943418|pdb|2GSR|A Chain A, Structure Of Porcine Class Pi Glutathione S-Transferase				
gi|253577|gb|AAB22893.1|	myosin light chain isoform LC17a [swine, aorta smooth muscle, Peptide, 150 aa]	0.258	0.611	0.537	0.407
gi|255683363|ref|NP_001157469.1|	myosin light polypeptide 6 [Sus scrofa] >gi|47606435|sp|P60662.2|MYL6_PIG RecName: Full=Myosin light polypeptide 6; AltName: Full=17 kDa myosin light chain; Short=LC17; AltName: Full=Myosin light chain 3; Short=MLC-3; AltName: Full=Myosin light chai				
gi|253578|gb|AAB22894.1|	myosin light chain isoform LC17b [swine, aorta smooth muscle, Peptide, 150 aa]				
gi|335287046|ref|XP_003355261.1|	PREDICTED: histone H2B type 1-N-like [Sus scrofa]	---	---	---	---
gi|350583430|ref|XP_003481516.1|	PREDICTED: histone H2B type 2-E-like [Sus scrofa] >gi|350583421|ref|XP_003355262.2| PREDICTED: histone H2B type 2-E-like [Sus scrofa] >gi|350583436|ref|XP_003481518.1| PREDICTED: histone H2B type 2-E-like [Sus scrofa] >gi|335287018|ref|XP_003355253.				
gi|335310903|ref|XP_003123670.2|	PREDICTED: histone H2B type 1-L-like [Sus scrofa]				
gi|350585077|ref|XP_003481871.1|	PREDICTED: hypothetical protein LOC100739300 [Sus scrofa]	0.914	1.823	1.807	2.044
gi|350585079|ref|XP_003127070.3|	PREDICTED: xaa-Pro dipeptidase [Sus scrofa]				

gi|281500757|pdb|3FX4|A	Chain A, Porcine Aldehyde Reductase In Ternary Complex With Inhibitor >gi|229597975|pdb|3H4G|A Chain A, Structure Of Aldehyde Reductase Holoenzyme In Complex With Potent Aldose Reductase Inhibitor Fidarestat: Implications For Inhibitor Binding And S	3.159	1.61	1.18	2.261
gi|114689|sp|P13618.1|ATP5J_PIG	RecName: Full=ATP synthase-coupling factor 6, mitochondrial; Short=ATPase subunit F6	0.351	0.632	0.768	0.496
gi|335309281|ref|XP_003361573.1|	PREDICTED: ATP synthase-coupling factor 6, mitochondrial-like isoform 1 [Sus scrofa] >gi|335300559|ref|XP_003358937.1| PREDICTED: ATP synthase-coupling factor 6, mitochondrial-like [Sus scrofa]				
gi|335309283|ref|XP_003361574.1|	PREDICTED: ATP synthase-coupling factor 6, mitochondrial-like isoform 2 [Sus scrofa]				
gi|229001074|emb|CAX20316.1|	mannose-6-phosphate receptor binding protein 1 [Sus scrofa]	1.122	1.017	0.952	1.056
gi|350591696|ref|XP_003483317.1|	PREDICTED: sucrase-isomaltase, intestinal-like [Sus scrofa]	0.913	1	0.975	0.943
gi|148222268|ref|NP_001090952.1|	tropomyosin alpha-1 chain [Sus scrofa] >gi|158931149|sp|P42639.2|TPM1_PIG RecName: Full=Tropomyosin alpha-1 chain; AltName: Full=Alpha-tropomyosin; AltName: Full=Tropomyosin-1 >gi|117661180|gb|ABK55659.1| TPM1 [Sus scrofa]	0.641	1.115	1.002	0.688
gi|54020966|ref|NP_001005726.1|	annexin A2 [Sus scrofa] >gi|148876771|sp|P19620.4|ANXA2_PIG RecName: Full=Annexin A2; AltName: Full=Annexin II; AltName: Full=Annexin-2; AltName: Full=Calpactin I heavy chain; AltName: Full=Calpactin-1 heavy chain; AltName:	0.905	0.473	0.453	0.667

	Full=Chromobindin-8; AltN				
gi|350587379|ref|XP_003482398.1|	PREDICTED: putative aminopeptidase C13A11.05-like [Sus scrofa]	2.105	2.722	3.623	0.835
gi|1710093|sp|P50121.2|RET2_PIG	RecName: Full=Retinol-binding protein 2; AltName: Full=Cellular retinol-binding protein II; Short=CRBP-II >gi|55741711|ref|NP_999616.1| retinol-binding protein 2 [Sus scrofa] >gi|455523|emb|CAA54729.1| cellular retinol binding protein II [Sus scrofa	1.386	0.766	0.8	0.777
gi|335284397|ref|XP_003354597.1|	PREDICTED: major vault protein isoform 1 [Sus scrofa]	1.404	1.073	1.002	1.37
gi|335305925|ref|XP_003135119.2|	PREDICTED: LOW QUALITY PROTEIN: ubiquitin-like modifier activating enzyme 1 [Sus scrofa]	1.971	0.991	0.967	1.697
gi|51592135|ref|NP_001004043.1|	cofilin-1 [Sus scrofa] >gi|116850|sp|P10668.3|COF1_PIG RecName: Full=Cofilin-1; AltName: Full=Cofilin, non-muscle isoform >gi|164425|gb|AAA31020.1| cofilin [Sus scrofa]	1.814	1.452	0.952	1.469
gi|340007404|ref|NP_001229990.1|	alpha-actinin-1 [Sus scrofa]	1.027	0.914	0.831	0.877
gi|311251248|ref|XP_003124516.1|	PREDICTED: apoptosis-associated speck-like protein containing a CARD-like isoform 1 [Sus scrofa]	3.139	6.012	6.925	3.814
gi|335284318|ref|XP_003354571.1|	PREDICTED: apoptosis-associated speck-like protein containing a CARD-like isoform 2 [Sus scrofa]				
gi|335299026|ref|XP_003132223.2|	PREDICTED: microtubule-associated protein 4-like [Sus scrofa]	0.901	1.857	1.532	1.377
gi|350583970|ref|XP_003126216.3|	PREDICTED: keratin, type II cytoskeletal 75-like [Sus scrofa]	0.448	0.68	0.76	0.546
gi|51317314|sp|P62802.2|H4_PIG	RecName: Full=Histone H4 >gi|350583428|ref|XP_003481515.1| PREDICTED: histone H4-like [Sus scrofa] >gi|335291880|ref|XP_003356614.1| PREDICTED: histone H4-like [Sus	0.435	0.532	0.445	0.417

	scrofa] >gi|335287016|ref|XP_003355252.1| PREDICTED: histone H4-like [Sus scrofa] >g				
gi|218664491|ref|NP_001136314.1|	galectin-3 [Sus scrofa] >gi|215254098|gb|ACJ64061.1| lectin galactoside-binding soluble 2 protein [Sus scrofa]	1.047	1.249	0.849	0.939
gi|346986388|ref|NP_001231345.1|	profilin-1 [Sus scrofa]	2.107	1.375	1.305	2.004
gi|112976|sp|P00503.3|AATC_PIG	RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Glutamate oxaloacetate transaminase 1; AltName: Full=Transaminase A >gi|47522636|ref|NP_999092.1| aspartate aminotransferase, cytoplasmic [Sus scrofa] >gi|300557343|emb|CBV09643.1|	1.113	2.697	3.518	2.144
gi|350584176|ref|XP_003481686.1|	PREDICTED: myosin-Ia-like [Sus scrofa]	0.968	0.862	0.644	1.164
gi|350582932|ref|XP_003125549.2|	PREDICTED: annexin A13 isoform 2 [Sus scrofa]	0.38	0.322	0.384	0.386
gi|350585375|ref|XP_003127408.3|	PREDICTED: myosin-14 [Sus scrofa]	0.739	0.612	0.67	0.696
gi|347300325|ref|NP_001231461.1|	dehydrogenase/reductase SDR family member 11 [Sus scrofa]	2.52	1.354	1.392	1.907
gi|335281609|ref|XP_003353842.1|	PREDICTED: stress-induced-phosphoprotein 1-like [Sus scrofa]	1.48	1.786	1.834	1.491
gi|194044822|ref|XP_001927404.1|	PREDICTED: peroxiredoxin-4 [Sus scrofa]	0.45	1.472	1.707	1.213
gi|311252459|ref|XP_003125105.1|	PREDICTED: poly(rC)-binding protein 1-like [Sus scrofa]	1.293	1.231	1.286	1.261
gi|290463427|sp|Q0QF01.2|DHSA_PIG	RecName: Full=Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial; AltName: Full=Flavoprotein subunit of complex II; Short=Fp; Flags: Precursor	0.678	0.605	0.674	0.695
gi|322812294|pdb|3AE8|A	Chain A, Crystal Structure Of Porcine Heart Mitochondrial Complex Ii Bound With				

	N-(3-Isopropoxy-Phenyl)-2-Trifluoromethylbenzamide >gi|345531796|pdb|3SFE|A Chain A, Crystal Structure Of Porcine Mitochondrial Respiratory Complex Ii Bound With Oxaloac				
gi|47523768|ref|NP_999520.1|	epoxide hydrolase 1 precursor [Sus scrofa] >gi|75069447|sp|P79381.1|HYEP_PIG RecName: Full=Epoxide hydrolase 1; AltName: Full=Epoxide hydratase; AltName: Full=Microsomal epoxide hydrolase >gi|1840391|dbj|BAA19200.1| epoxide hydrolase [Sus scrofa]	0.733	0.492	0.311	0.608
gi|194037042|ref|XP_001927136.1|	PREDICTED: cadherin-17 [Sus scrofa]	0.516	0.558	0.827	0.472
gi|350593820|ref|XP_003483769.1|	PREDICTED: isocitrate dehydrogenase [NADP] cytoplasmic isoform 3 [Sus scrofa] >gi|350593816|ref|XP_003483767.1| PREDICTED: isocitrate dehydrogenase [NADP] cytoplasmic isoform 1 [Sus scrofa] >gi|350593818|ref|XP_003483768.1| PREDICTED: isocitrate deh	2.425	1.236	1.05	1.383
gi|350583022|ref|XP_001927263.3|	PREDICTED: 14-3-3 protein zeta/delta [Sus scrofa]	3.308	1.517	1.086	2.726
gi|3913046|sp|O46409.1|APOA4_PIG	RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor >gi|47523830|ref|NP_999553.1| apolipoprotein A-IV precursor [Sus scrofa] >gi|2695742|emb|CAA11020.1| apolipoprotein A-IV [Sus scrofa]	0.558	0.39	0.478	0.451
gi|350585075|ref|XP_003481870.1|	PREDICTED: xaa-Pro dipeptidase-like [Sus scrofa]	1.176	1.013	1.704	1.131
gi|146741296|dbj|BAF62303.1|	keratin 1 [Sus scrofa]	0.933	1.375	0.846	0.856
gi|350583977|ref|XP_003481635.1|	PREDICTED: keratin, type II cytoskeletal 1 [Sus scrofa]				
gi|311255413|ref|XP_001927240.2|	PREDICTED: keratin, type II cytoskeletal 79 [Sus scrofa]	0.422	0.675	0.754	0.534

gi|83921635|ref|NP_001033089.1|	FKBP1A-like [Sus scrofa] >gi|61098747|gb|AAX37547.1| FKBP1A-like [Sus scrofa]	1.011	1.849	1.72	1.154
gi|112985|sp|P00506.2|AATM_PIG	RecName: Full=Aspartate aminotransferase, mitochondrial; Short=mAspAT; AltName: Full=Fatty acid-binding protein; Short=FABP-1; AltName: Full=Glutamate oxaloacetate transaminase 2; AltName: Full=Plasma membrane-associated fatty acid-binding protein;	1.009	1.728	2.191	1.62
gi|347658971|ref|NP_001231613.1|	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d [Sus scrofa]	0.489	0.543	0.446	0.473
gi|311250151|ref|XP_003123979.1|	PREDICTED: heat shock 70 kDa protein 4 [Sus scrofa]	1.453	2.216	1.688	1.224
gi|55583761|sp|Q64L94.1|PSME1_PIG	RecName: Full=Proteasome activator complex subunit 1; AltName: Full=Proteasome activator 28 subunit alpha; Short=PA28a; Short=PA28alpha >gi|34978646|gb|AAQ83574.1| proteasome activator 28 alpha subunit [Sus scrofa]	1.531	1.257	1.253	1.363
gi|350592528|ref|XP_003483480.1|	PREDICTED: endoplasmic reticulum resident protein 29 [Sus scrofa]	0.787	1.304	1.172	0.982
gi|118403904|ref|NP_001072131.1|	protein DJ-1 [Sus scrofa] >gi|67038668|gb|AAY63803.1| DJ-1 protein [Sus scrofa]	1.06	2.156	1.948	1.543
gi|113205888|ref|NP_001038076.1|	aldehyde dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|122138098|sp|Q2XQV4.1|ALDH2_PIG RecName: Full=Aldehyde dehydrogenase, mitochondrial; AltName: Full=ALDH class 2; AltName: Full=ALDH-E2; Flags: Precursor >gi|81295909|gb|ABB70228.1| mit	1.732	0.778	0.734	1.475
gi|187370719|gb|ACD02422.1|	mitochondrial aldehyde dehydrogenase 2 [Sus scrofa]				
gi|350584145|ref|XP_001929467.3|	PREDICTED: nascent polypeptide-associated complex	0.879	1.852	1.608	1.283

	subunit alpha isoform 1 [Sus scrofa]				
gi|350584147|ref|XP_003481679.1|	PREDICTED: nascent polypeptide-associated complex subunit alpha [Sus scrofa]				
gi|350594035|ref|XP_003483822.1|	PREDICTED: UDP-glucuronosyltransferase 1-10 isoform 3 [Sus scrofa]	0.561	0.348	0.404	0.378
gi|213958609|gb|ACJ54701.1|	glutamine:fructose-6-phosphate amidotransferase 1 variant 2 [Sus scrofa]	1.388	0.576	0.609	1.45
gi|303228252|ref|NP_001181908.1|	glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 [Sus scrofa] >gi|213958607|gb|ACJ54700.1| glutamine:fructose-6-phosphate amidotransferase 1 variant 1 [Sus scrofa]				
gi|75051712|sp|Q9TUB5.1|CLCA1_PIG	RecName: Full=Calcium-activated chloride channel regulator 1; AltName: Full=Calcium-activated chloride channel family member 1; AltName: Full=pCLCA1; Flags: Precursor >gi|47523388|ref|NP_999313.1| calcium-activated chloride channel regulator 1 precu	1.042	1.503	1.076	1.117
gi|162951821|ref|NP_001106165.1|	heterogeneous nuclear ribonucleoprotein A/B [Sus scrofa] >gi|160858224|dbj|BAF93845.1| CArG-binding factor A [Sus scrofa]	0.998	2.227	1.941	1.736
gi|350276234|ref|NP_001231897.1|	anterior gradient protein 2 homolog precursor [Sus scrofa]	1.123	1.229	1.016	1.215
gi|1364248|emb|CAA82246.1|	glucosephosphate isomerase [Sus scrofa]	2.652	1.874	1.372	2.71
gi|21730305|pdb|1GZD|A	Chain A, Crystal Structure Of Pig Phosphoglucose Isomerase >gi|24987288|pdb|1GZV|A Chain A, The Crystal Structure Of Phosphoglucose Isomerase From Pig Muscle Complexed With 5-Phosphoarabinonate				
gi|47523720|ref|NP_999495.1|	glucose-6-phosphate isomerase [Sus scrofa] >gi|120742|sp|P08059.3|G6PI_PIG RecName:				

	Full=Glucose-6-phosphate isomerase; Short=GPI; AltName: Full=Autocrine motility factor; Short=AMF; AltName: Full=Neuroleukin; Short=NLK; AltName: Full=Phosphoglucose				
gi|350593430|ref|XP_003483683.1|	PREDICTED: glutathione reductase, mitochondrial isoform 1 [Sus scrofa]	0.713	1.184	1.473	1.349
gi|350580243|ref|XP_003123005.3|	PREDICTED: harmonin-like [Sus scrofa]	0.886	2.1	1.767	1.414
gi|194039884|ref|XP_001928592.1|	PREDICTED: histone H2A type 1-like [Sus scrofa]	0.354	0.344	0.267	0.246
gi|335291888|ref|XP_001928674.3|	PREDICTED: histone H2A type 1-F-like [Sus scrofa]				
gi|335291892|ref|XP_003356618.1|	PREDICTED: histone H2A type 1-like [Sus scrofa] >gi|311259877|ref|XP_003128263.1| PREDICTED: histone H2A type 1-like [Sus scrofa] >gi|194039812|ref|XP_001927727.1| PREDICTED: histone H2A type 1-like [Sus scrofa]				
gi|335291882|ref|XP_001928646.3|	PREDICTED: histone H2A type 1-F-like [Sus scrofa]				
gi|335308465|ref|XP_003361239.1|	PREDICTED: histone H2A type 1-like [Sus scrofa] >gi|194039816|ref|XP_001927762.1| PREDICTED: histone H2A type 1-like [Sus scrofa]				
gi|350583438|ref|XP_003481519.1|	PREDICTED: histone H2A type 2-C-like [Sus scrofa]				
gi|350583432|ref|XP_003355263.2|	PREDICTED: histone H2A type 2-A-like [Sus scrofa]				
gi|47523692|ref|NP_999478.1|	thioredoxin [Sus scrofa] >gi|20141821|sp|P82460.3|THIO_PIG RecName: Full=Thioredoxin; Short=Trx >gi|332368598|gb|AEE61373.1| thioredoxin [Sus scrofa] >gi|14326453|gb|AAK60272.1|AF382821_1 thioredoxin [Sus scrofa]	1.007	2.615	2.229	1.258
gi|281427374|ref|NP_001163991.1|	T-complex protein 1 subunit beta [Sus	1.265	0.945	0.666	1.224

	scrofa] >gi|262036935|dbj|BAI47602.1| chaperonin containing TCP1, subunit 2 (beta) [Sus scrofa]				
gi|350596362|ref|XP_003361090.2|	PREDICTED: CD2-associated protein-like [Sus scrofa]	1.357	5.83	3.915	2.031
gi|222136590|ref|NP_001138373.1|	proteasome subunit alpha type-5 [Sus scrofa]	1.041	2.413	2.229	1.879
gi|335285948|ref|XP_003131991.2|	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like isoform 1 [Sus scrofa]	1.314	0.725	0.661	0.646
gi|335285950|ref|XP_003354989.1|	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like isoform 2 [Sus scrofa]				
gi|2500586|sp|Q29099.1|PTBP1_PIG	RecName: Full=Polypyrimidine tract-binding protein 1; Short=PTB; AltName: Full=Heterogeneous nuclear ribonucleoprotein I; Short=hnRNP I >gi|47523538|ref|NP_999396.1| polypyrimidine tract-binding protein 1 [Sus scrofa] >gi|1122433|emb|CAA63597.1| pol	1.078	2.503	2.591	3.405
gi|350592201|ref|XP_003359029.2|	PREDICTED: hypothetical protein LOC100620809 isoform 1, partial [Sus scrofa]	0.604	0.664	0.798	0.503
gi|335305558|ref|XP_003134901.2|	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform 1 [Sus scrofa]	1.127	0.765	0.745	1.284
gi|346986324|ref|NP_001231316.1|	tumor protein D52 [Sus scrofa]	0.72	0.882	1.075	1.124
gi|47522692|ref|NP_999062.1|	long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|2829676|sp|P79274.1|ACADL_PIG RecName: Full=Long-chain specific acyl-CoA dehydrogenase, mitochondrial; Short=LCAD; Flags: Precursor >gi|1695729|dbj|BAA13965.1| long	0.734	0.971	0.828	0.632

gi|148747594|ref|NP_001092068.1|	60S acidic ribosomal protein P0 [Sus scrofa] >gi|182705234|sp|Q29214.2|RLA0_PIG RecName: Full=60S acidic ribosomal protein P0; AltName: Full=60S ribosomal protein L10E >gi|83854099|gb|ABC47963.1| ribosomal phosphoprotein large PO subunit [Sus scrofa	0.785	0.612	0.651	0.807
gi|297591965|ref|NP_001172061.1|	leukotriene A-4 hydrolase [Sus scrofa] >gi|262204898|dbj|BAI48029.1| leukotriene A4 hydrolase [Sus scrofa]	1.816	0.956	0.872	1.682
gi|303304923|dbj|BAJ14788.1|	aminopeptidase T [Sus scrofa]				
gi|350586352|ref|XP_003482167.1|	PREDICTED: serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Sus scrofa]	1.608	0.798	0.757	1.136
gi|194033860|ref|XP_001927901.1|	PREDICTED: UV excision repair protein RAD23 homolog B [Sus scrofa]	1.642	2.407	2.937	1.236
gi|347300165|ref|NP_001231397.1|	proteasome subunit alpha type-4 [Sus scrofa]	0.938	1.904	1.898	1.546
gi|299611|gb|AAB26236.1|	cerebroside sulfate activator, CS-Act [swine, kidneys, Peptide, 79 aa]	0.957	0.947	1.163	0.607
gi|17380295|sp|P81405.2|SAP_PIG	RecName: Full=Saposin-B-Val; Contains: RecName: Full=Saposin-B; AltName: Full=Cerebroside sulfate activator; Short=CS-ACT; AltName: Full=Non-specific activator; AltName: Full=Sphingolipid activator protein 1; Short=SAP-1				
gi|311246990|ref|XP_003122442.1|	PREDICTED: mucin-2, partial [Sus scrofa]	1.835	0.865	0.677	1.098
gi|222136592|ref|NP_001138374.1|	proteasome subunit beta type-3 [Sus scrofa]	1.162	1.55	1.872	1.409
gi|68532157|gb|AAY98813.1|	proteasome subunit 10 [Sus scrofa] >gi|68532159|gb|AAY98814.1| proteasome subunit 10 [Sus scrofa]	1.961	1.767	3.009	1.305
gi|113205704|ref|NP_001038030.1|	proteasome subunit beta type-10 [Sus scrofa] >gi|90823108|gb|ABE01081.1| proteasome beta 10 subunit [Sus scrofa]				
gi|194042318|ref|XP_001928	PREDICTED: putative hexokinase	0.716	0.557	0.679	0.825

917.1|	HKDC1 [Sus scrofa]				
gi|350583750|ref|XP_003481579.1|	PREDICTED: hsc70-interacting protein-like isoform 1 [Sus scrofa]	1.648	1.355	1.322	1.35
gi|350583752|ref|XP_003481580.1|	PREDICTED: hsc70-interacting protein-like isoform 2 [Sus scrofa]				
gi|47523764|ref|NP_999518.1|	peptidyl-prolyl cis-trans isomerase A [Sus scrofa] >gi|51702768|sp|P62936.2|PPIA_PIG RecName: Full=Peptidyl-prolyl cis-trans isomerase A; Short=PPIase A; AltName: Full=Cyclophilin A; AltName: Full=Cyclosporin A-binding protein; AltName: Full=Rotamas	2.721	1.273	0.985	2.422
gi|350589126|ref|XP_003482792.1|	PREDICTED: nucleoprotein TPR [Sus scrofa]	0.863	0.852	0.757	0.883
gi|350586779|ref|XP_003482273.1|	PREDICTED: LOW QUALITY PROTEIN: IQ motif containing GTPase activating protein 1 [Sus scrofa]	1.126	0.971	0.793	1.146
gi|311244872|ref|XP_003121596.1|	PREDICTED: creatine kinase U-type, mitochondrial-like isoform 2 [Sus scrofa] >gi|311244870|ref|XP_003121595.1| PREDICTED: creatine kinase U-type, mitochondrial-like isoform 1 [Sus scrofa]	1.676	1.552	1.153	1.306
gi|343791015|ref|NP_001230554.1|	carboxylesterase 3 precursor [Sus scrofa]	0.942	0.662	0.829	0.924
gi|194040624|ref|XP_001929173.1|	PREDICTED: plastin-2 isoform 1 [Sus scrofa]	1.786	1.252	1.164	1.583
gi|162952052|ref|NP_001106151.1|	transketolase [Sus scrofa] >gi|159502444|gb|ABW97521.1| transketolase [Sus scrofa]	1.819	2.627	3.235	3.514
gi|311272935|ref|XP_003133651.1|	PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 1 [Sus scrofa]	0.699	0.592	0.38	0.592
gi|335303281|ref|XP_003359671.1|	PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 2 [Sus scrofa]				
gi|335302040|ref|XP_001927564.2|	PREDICTED: delta-1-pyrroline-5-carboxylate synthase isoform 1 [Sus scrofa]	0.834	0.466	0.373	0.665

gi|346644799|ref|NP_001231157.1|	thymopoietin [Sus scrofa]	0.723	0.984	0.854	0.716
gi|311252403|ref|XP_003125080.1|	PREDICTED: sepiapterin reductase-like [Sus scrofa]	1.394	1.35	1.971	1.837
gi|1170740|sp|P00339.3|LDHA_PIG	RecName: Full=L-lactate dehydrogenase A chain; Short=LDH-A; AltName: Full=LDH muscle subunit; Short=LDH-M >gi|473571|gb|AAA50436.1| lactate dehydrogenase-A [Sus scrofa domesticus]	1.799	0.825	0.705	1.44
gi|48675953|ref|NP_001001643.1|	rab GDP dissociation inhibitor beta [Sus scrofa] >gi|75043802|sp|Q6Q7J2.1|GDIB_PIG RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2 >gi|45758488|gb|AAS76	2.866	1.102	0.916	1.781
gi|335297609|ref|XP_003358079.1|	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Sus scrofa]	0.788	0.386	0.515	0.459
gi|350578484|ref|XP_003121491.3|	PREDICTED: NAD-dependent malic enzyme, mitochondrial [Sus scrofa]	1.031	0.947	1.075	1.163
gi|345441771|ref|NP_001230857.1|	aldolase C, fructose-bisphosphate [Sus scrofa]	1.123	0.698	1.148	0.868
gi|71042645|pdb|2BKI|A	Chain A, Myosin Vi Nucleotide-Free (Mdinsert2-Iq) Crystal Structure	---	---	---	---
gi|320089676|pdb|2X51|A	Chain A, M6 Delta Insert1				
gi|73536335|pdb|2BKH|A	Chain A, Myosin Vi Nucleotide-Free (Mdinsert2) Crystal Structure				
gi|162330177|pdb|2VAS|A	Chain A, Myosin Vi (Md-Insert2-Cam, Delta-Insert1) Post-Rigor State >gi|162330179|pdb|2VB6|A Chain A, Myosin Vi (Md-Insert2-Cam, Delta Insert1) Post-Rigor State (Crystal Form 2)				
gi|160877818|pdb|2V26|A	Chain A, Myosin Vi (Md) Pre-Powerstroke State (Mg.Adp.Vo4)				
gi|313754272|pdb|3L9I|A	Chain A, Myosin Vi Nucleotide-Free (Mdinsert2) L310g Mutant Crystal				

	Structure				
gi|122064583|sp|P04178.2|SODC_PIG	RecName: Full=Superoxide dismutase [Cu-Zn] >gi|298677090|ref|NP_001177351.1| superoxide dismutase [Cu-Zn] [Sus scrofa] >gi|297593564|gb|ADI47520.1| superoxide dismutase 1 [Sus scrofa]	0.935	1.54	1.45	1.125
gi|350589456|ref|XP_003357762.2|	PREDICTED: ubiquilin-1 [Sus scrofa]	0.873	1.238	1.248	1.101
gi|47523420|ref|NP_999331.1|	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase [Sus scrofa] >gi|75051805|sp|Q9TV69.1|DHDH_PIG RecName: Full=Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase; AltName: Full=D-xylose 1-dehydrogenase; AltName: Full=D-xylose-NADP dehydrogenase; AltName:	1.382	1.448	1.126	1.422
gi|47522608|ref|NP_999106.1|	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor [Sus scrofa] >gi|75056105|sp|Q9GL01.1|RPN2_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosph	0.966	0.55	0.412	0.788
gi|350589336|ref|XP_003130615.3|	PREDICTED: heterogeneous nuclear ribonucleoprotein U [Sus scrofa]	0.796	1.037	0.907	0.885
gi|380509273|gb|AFD64639.1|	peroxisomal acyl-coenzyme A oxidase 1 isoform 1 [Sus scrofa]	1.069	0.86	1.61	0.514
gi|380509275|gb|AFD64640.1|	peroxisomal acyl-coenzyme A oxidase 1 isoform 2 [Sus scrofa]				
gi|350592730|ref|XP_003483523.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein F [Sus scrofa] >gi|335301642|ref|XP_003359253.1| PREDICTED: heterogeneous nuclear ribonucleoprotein F [Sus scrofa] >gi|194042674|ref|XP_001929089.1| PREDICTED: heterogeneous nuclear ribonucleoprotei	1.215	1.29	1.078	1.133

gi|311254039|ref|XP_003125724.1|	PREDICTED: mucosal pentraxin-like [Sus scrofa]	0.42	0.286	0.227	0.291
gi|311248177|ref|XP_003123013.1|	PREDICTED: proteasome subunit alpha type-1-like [Sus scrofa]	0.627	1.485	1.428	1.467
gi|347300163|ref|NP_001231396.1|	succinate-semialdehyde dehydrogenase, mitochondrial [Sus scrofa]	1.038	0.391	0.419	0.599
gi|347300243|ref|NP_001231430.1|	glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	0.826	0.563	0.527	0.727
gi|335309939|ref|XP_003133770.2|	PREDICTED: nucleolin-like [Sus scrofa]	1.089	1.648	1.607	1.599
gi|283993079|gb|ADB57036.1|	L-gulonate 3-dehydrogenase [Sus scrofa]	2.065	0.888	1.278	1.51
gi|350582175|ref|XP_003481218.1|	PREDICTED: mitochondrial inner membrane protein, partial [Sus scrofa]	0.546	0.513	0.778	0.61
gi|1702996|sp|P54612.2|2AAA_PIG	RecName: Full=Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform; AltName: Full=PP2A subunit A isoform PR65-alpha; AltName: Full=PP2A subunit A isoform R1-alpha >gi|47522870|ref|NP_999189.1| serine/threonine-protein ph	2.623	1.146	1.059	2.451
gi|311270597|ref|XP_003132922.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 9-like [Sus scrofa]	0.599	1.217	1.425	0.755
gi|47169449|pdb|1VJD|A	Chain A, Structure Of Pig Muscle Pgk Complexed With Atp >gi|47169448|pdb|1VJC|A Chain A, Structure Of Pig Muscle Pgk Complexed With Mgatp	1.879	0.606	0.764	1.515
gi|153792027|ref|NP_001093402.1|	phosphoglycerate kinase 1 [Sus scrofa] >gi|56757507|sp|Q7SIB7.3|PGK1_PIG RecName: Full=Phosphoglycerate kinase 1 >gi|50513041|gb|AAT77773.1| phosphoglycerate kinase 1 [Sus scrofa]				
gi|335281047|ref|XP_003353724.1|	PREDICTED: LOW QUALITY PROTEIN: long-chain fatty acid transport protein 4 [Sus scrofa]	0.817	0.381	0.401	0.431

gi|219521964|ref|NP_001137170.1|	long-chain-fatty-acid--CoA ligase 3 [Sus scrofa] >gi|217314893|gb|ACK36981.1| acyl-CoA synthetase long-chain family member 3 [Sus scrofa]	0.559	0.389	0.335	0.432
gi|47523158|ref|NP_999015.1|	glutathione S-transferase A2 [Sus scrofa] >gi|1185280|emb|CAA93434.1| glutathione S-transferase [Sus scrofa]	2.229	1.726	1.798	3.489
gi|83921643|ref|NP_001033096.1|	serine/arginine-rich splicing factor 1 [Sus scrofa] >gi|114152157|sp|Q3YLA6.3|SRSF1_PIG RecName: Full=Serine/arginine-rich splicing factor 1; AltName: Full=Splicing factor, arginine/serine-rich 1 >gi|73810231|gb|AAZ86089.1| splicing factor arginine/	0.658	0.758	0.713	0.711
gi|311270878|ref|XP_003132994.1|	PREDICTED: AP-1 complex subunit beta-1 isoform 3 [Sus scrofa]	1.174	0.863	0.845	1.105
gi|335301395|ref|XP_003359198.1|	PREDICTED: AP-1 complex subunit beta-1 [Sus scrofa]				
gi|164669|gb|AAA31120.1|	succinyl-CoA synthetase beta-subunit, partial [Sus scrofa]	1.758	0.974	0.824	1.244
gi|90109583|pdb|2FPP|B	Chain B, Crystal Structure Of Pig Gtp-Specific Succinyl-Coa Synthetase From Polyethylene Glycol With Chloride Ions >gi|90109575|pdb|2FPI|B Chain B, Crystal Structure Of Pig Gtp-Specific Succinyl-Coa Synthetase From Polyethylene Glycol >gi|90109573|p				
gi|350591336|ref|XP_003132357.3|	PREDICTED: succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial isoform 1 [Sus scrofa]				
gi|21264506|sp|P53590.2|SUCB2_PIG	RecName: Full=Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial; AltName: Full=GTP-specific succinyl-CoA synthetase subunit beta; AltName: Full=Succinyl-CoA synthetase beta-G chain; Short=SCS-betaG; Flags:				

	Precursor				
gi|9955020|pdb|1EUC|B	Chain B, Crystal Structure Of Dephosphorylated Pig Heart, Gtp-Specific Succinyl-Coa Synthetase				
gi|9955022|pdb|1EUD|B	Chain B, Crystal Structure Of Phosphorylated Pig Heart, Gtp-Specific Succinyl-Coa Synthetase				
gi|120968|sp|P80147.2|GABT_PIG	RecName: Full=4-aminobutyrate aminotransferase, mitochondrial; AltName: Full=(S)-3-amino-2-methylpropionate transaminase; AltName: Full=GABA aminotransferase; Short=GABA-AT; AltName: Full=Gamma-amino-N-butyrate transaminase; Short=GABA transaminase;	1.695	0.783	0.717	1.39
gi|284559|pir||A42481	4-aminobutyrate transaminase (EC 2.6.1.19) precursor - pig				
gi|47523600|ref|NP_999428.1|	4-aminobutyrate aminotransferase, mitochondrial [Sus scrofa] >gi|531154|gb|AAA96981.1| 4-aminobutyrate aminotransferase [Sus scrofa]				
gi|255327|gb|AAB23231.1|	4-aminobutyrate aminotransferase {EC 2.6.1.19} [swine, liver, Peptide, 472 aa] >gi|38492644|pdb|1OHY|C Chain C, 4-Aminobutyrate-Aminotransferase Inactivated By Gamma- Ethynyl Gaba >gi|38492642|pdb|1OHY|A Chain A, 4-Aminobutyrate-Aminotransferase Ina				
gi|346644699|ref|NP_001231019.1|	protein SET [Sus scrofa]	1.404	4.301	2.967	2.469
gi|47522760|ref|NP_999131.1|	long-chain 3-ketoacyl-CoA thiolase [Sus scrofa] >gi|6165556|gb|AAF04612.1| AF028007_1 long-chain 3-ketoacyl-CoA thiolase [Sus scrofa]	0.787	0.43	0.44	0.542
gi|155369760|ref|NP_001094	peroxisomal acyl-coenzyme A	1.021	0.945	1.126	1.452

498.1|	oxidase 1 [Sus scrofa] >gi|112292673|gb|ABI14815.1| palmitoyl acyl-CoA oxidase 1 [Sus scrofa]				
gi|350595285|ref|XP_003484077.1|	PREDICTED: N-alpha-acetyltransferase 38, NatC auxiliary subunit-like [Sus scrofa] >gi|311275562|ref|XP_003134801.1| PREDICTED: N-alpha-acetyltransferase 38, NatC auxiliary subunit-like [Sus scrofa]	2.056	2.91	2.97	2.266
gi|335299041|ref|XP_001926664.3|	PREDICTED: cytochrome b-c1 complex subunit 1, mitochondrial [Sus scrofa]	0.764	0.572	0.812	0.72
gi|61744020|gb|AAX55638.1|	fatty acid synthase [Sus scrofa]	1.431	0.884	0.92	1.488
gi|198443141|pdb|2VZ8|A	Chain A, Crystal Structure Of Mammalian Fatty Acid Synthase >gi|198443142|pdb|2VZ8|B Chain B, Crystal Structure Of Mammalian Fatty Acid Synthase >gi|198443144|pdb|2VZ9|B Chain B, Crystal Structure Of Mammalian Fatty Acid Synthase In Complex With Nad	---	---	---	---
gi|153792600|ref|NP_001093400.1|	fatty acid synthase [Sus scrofa] >gi|148733529|gb|ABR09275.1| fatty acid synthase [Sus scrofa]				
gi|335309408|ref|XP_003361627.1|	PREDICTED: myosin-11-like, partial [Sus scrofa]				
gi|350582036|ref|XP_003481179.1|	PREDICTED: U5 small nuclear ribonucleoprotein 200 kDa helicase [Sus scrofa]	0.686	0.793	0.968	0.662
gi|347800709|ref|NP_001231660.1|	scinderin [Sus scrofa]	1.556	1.156	1.037	1.955
gi|335281857|ref|XP_003122760.2|	PREDICTED: catenin delta-1 [Sus scrofa]	0.533	0.586	0.496	0.613
gi|178056532|ref|NP_001116688.1|	Z-DNA-binding protein 1 [Sus scrofa] >gi|147223427|emb|CAN13344.1| Z-DNA binding protein 1 [Sus scrofa]	0.703	0.731	1.318	1.195
gi|215882147|gb|ACJ70709.1|	DNA-dependent activator of IFN-regulatory factor [Sus scrofa]				
gi|350587231|ref|XP_003482	PREDICTED: LOW QUALITY	1.192	0.769	0.69	0.967

373.1|	PROTEIN: cytoplasmic dynein 1 heavy chain 1 [Sus scrofa]				
gi|311251336|ref|XP_003124563.1|	PREDICTED: elongation factor Tu, mitochondrial-like [Sus scrofa]	0.973	0.501	0.508	0.696
gi|47523726|ref|NP_999498.1|	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Sus scrofa] >gi|75056164|sp|Q9GMB0.1|RPN1_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1; AltName: Full=Dolichyl-diphosph	0.625	0.627	0.547	0.709
gi|350593062|ref|XP_003133228.3|	PREDICTED: xaa-Pro aminopeptidase 1 isoform 2 [Sus scrofa]	1.117	0.832	0.607	1.023
gi|297591969|ref|NP_001172062.1|	ubiquitin-conjugating enzyme E2 L3 [Sus scrofa] >gi|219563058|gb|ACL27888.1| ubiquitin-conjugating enzyme E2L3 [Sus scrofa]	0.729	1.377	1.106	1.111
gi|311265664|ref|XP_003130763.1|	PREDICTED: LOW QUALITY PROTEIN: kinesin-1 heavy chain [Sus scrofa]	0.823	0.71	1.111	0.887
gi|148234672|ref|NP_001090881.1|	porphobilinogen deaminase [Sus scrofa] >gi|112980813|gb|ABI29188.1| hydroxymethylbilane synthase [Sus scrofa]	0.86	2.163	1.615	1.225
gi|350591926|ref|XP_003358845.2|	PREDICTED: golgin subfamily B member 1 [Sus scrofa]	0.766	0.971	0.959	0.915
gi|113205886|ref|NP_001038075.1|	nucleoside diphosphate kinase B [Sus scrofa] >gi|115311824|sp|Q2EN76.1|NDKB_PIG RecName: Full=Nucleoside diphosphate kinase B; Short=NDK B; Short=NDP kinase B; AltName: Full=Histidine protein kinase NDKB >gi|87047646|gb|ABD18456.1| nm23-H2 [Sus scro	0.829	1.823	1.107	0.757
gi|311249165|ref|XP_003123479.1|	PREDICTED: A-kinase anchor protein 8 [Sus scrofa]	---	---	---	---
gi|47522814|ref|NP_999159.1|	dihydrolipoyllysine-residue acetyltransferase component of	1.069	0.753	0.7	0.863

<table>
<tr><td></td><td>pyruvate dehydrogenase complex, mitochondrial precursor [Sus scrofa] >gi|14587786|dbj|BAB61720.1| dihydrolipoamide acetyltransferase [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|47523086|ref|NP_999309.1|</td><td>peroxiredoxin-5, mitochondrial [Sus scrofa] >gi|10305336|gb|AAG13452.2|AF110735_1 peroxiredoxin 5 [Sus scrofa]</td><td>1.866</td><td>0.912</td><td>0.881</td><td>1.432</td></tr>
<tr><td>gi|312062797|ref|NP_001185848.1|</td><td>proactivator polypeptide precursor [Sus scrofa] >gi|310789269|gb|ADP24688.1| prosaposin variant 2 [Sus scrofa]</td><td>0.731</td><td>2.233</td><td>2.259</td><td>1.324</td></tr>
<tr><td>gi|194036975|ref|XP_001927782.1|</td><td>PREDICTED: polyadenylate-binding protein 1 [Sus scrofa]</td><td>0.878</td><td>1.445</td><td>1.228</td><td>1.255</td></tr>
<tr><td>gi|1332717|gb|AAB36056.1|</td><td>acylamino acid-releasing enzyme, AARE {EC 3.4.19.1} [swine, liver, Peptide, 732 aa] >gi|1583737|prf||2121361A acyl-AA releasing enzyme</td><td>1.103</td><td>0.791</td><td>0.977</td><td>0.93</td></tr>
<tr><td>gi|47522644|ref|NP_999088.1|</td><td>acylamino-acid-releasing enzyme [Sus scrofa] >gi|1351862|sp|P19205.2|ACPH_PIG RecName: Full=Acylamino-acid-releasing enzyme; Short=AARE; AltName: Full=Acyl-peptide hydrolase; Short=APH; AltName: Full=Acylaminoacyl-peptidase >gi|217672|dbj|BAA00411.1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|47523548|ref|NP_999398.1|</td><td>glutaredoxin-1 [Sus scrofa] >gi|121442|sp|P12309.2|GLRX1_PIG RecName: Full=Glutaredoxin-1; AltName: Full=Thioltransferase-1; Short=TTase-1 >gi|332368592|gb|AEE61370.1| glutaredoxin [Sus scrofa] >gi|326632057|gb|ADZ99031.1| glutaredoxin [Sus scrofa]</td><td>0.25</td><td>0.475</td><td>0.406</td><td>0.527</td></tr>
<tr><td>gi|157831627|pdb|1KTE|A</td><td>Chain A, Crystal Structure Of Thioltransferase At 2.2 Angstrom Resolution</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|164359|gb|AAA30992.1|</td><td>apolipoprotein A-I [Sus scrofa]</td><td>1.067</td><td>0.411</td><td>0.499</td><td>0.666</td></tr>
</table>

gi|37787313|gb|AAP69607.1|	nicotinate phosphoribosyltransferase-like protein [Sus scrofa]	1.437	0.862	0.804	1.205
gi|311252547|ref|XP_003125148.1|	PREDICTED: T-complex protein 1 subunit delta-like [Sus scrofa]	2.114	0.936	1.142	1.491
gi|298160970|ref|NP_999423.2|	cAMP-dependent protein kinase type II-alpha regulatory subunit [Sus scrofa] >gi|228008282|dbj|BAH57697.1| cAMP-dependent protein kinase regulatory subunit type II alpha [Sus scrofa]	1.181	0.8	0.707	0.754
gi|325652138|ref|NP_001191702.1|	A-kinase anchor protein 1, mitochondrial [Sus scrofa] >gi|321267428|dbj|BAJ72691.1| A kinase anchor protein 1 [Sus scrofa]	0.686	1.18	1.032	1.126
gi|90200404|gb|ABD92704.1|	triosephosphate isomerase 1 [Sus scrofa]	2.706	1.493	1.114	3.048
gi|262263205|dbj|BAI48105.1|	triosephosphate isomerase 1 [Sus scrofa]				
gi|35384836|gb|AAQ84564.1|	electron transfer flavoprotein alpha subunit precursor [Sus scrofa]	2.734	1.242	1.16	2.173
gi|346986361|ref|NP_001231332.1|	electron-transfer-flavoprotein, alpha polypeptide [Sus scrofa]				
gi|385137156|ref|NP_001245232.1|	kinectin 1 (kinesin receptor) [Sus scrofa]	1.035	1.311	1.263	0.932
gi|350597130|ref|XP_003484362.1|	PREDICTED: V-type proton ATPase subunit B, brain isoform-like [Sus scrofa] >gi|350592249|ref|XP_003483427.1| PREDICTED: V-type proton ATPase subunit B, brain isoform [Sus scrofa]	0.718	0.671	0.6	0.752
gi|350591034|ref|XP_003483187.1|	PREDICTED: glycerol-3-phosphate dehydrogenase 1-like protein-like [Sus scrofa]	1.304	0.697	0.704	0.941
gi|353819|prf||1106188C	cytochrome b5	0.588	0.84	0.666	0.833
gi|48976129|ref|NP_001001770.1|	cytochrome b5 [Sus scrofa] >gi|6166051|sp|P00172.3|CYB5_PIG RecName: Full=Cytochrome b5 >gi|2642486|gb|AAC48779.1| cytochrome b5 [Sus scrofa]				
gi|311277231|ref|XP_003135	PREDICTED: trimethyllysine	1.143	5.553	3.922	1.817

559.1|	dioxygenase, mitochondrial-like [Sus scrofa]				
gi|154147698|ref|NP_001093665.1|	eukaryotic initiation factor 4A-II [Sus scrofa] >gi|85792276|gb|ABC84195.1| eukaryotic translation initiation factor 4A isoform 2 [Sus scrofa]	0.841	0.769	0.49	1.06
gi|311270662|ref|XP_003132938.1|	PREDICTED: phosphatidylethanolamine-binding protein 1-like [Sus scrofa]	1.826	3.013	2.036	1.876
gi|178056588|ref|NP_001116645.1|	ras-related protein Rab-1B [Sus scrofa] >gi|122064946|sp|Q06AU7.1|RAB1B_PIG RecName: Full=Ras-related protein Rab-1B >gi|115394758|gb|ABI97173.1| RAB1B [Sus scrofa]	0.951	0.817	1.011	1.055
gi|62511144|sp|Q764M5.1|STAT1_PIG	RecName: Full=Signal transducer and activator of transcription 1 >gi|47523306|ref|NP_998934.1| signal transducer and activator of transcription 1 [Sus scrofa] >gi|40363629|dbj|BAD06318.1| signal transducer and activator of transcription 1 [Sus scrof	1.669	1.216	1.57	1.391
gi|353468887|gb|AER08620.1|	signal transducer and activator of transcription 1 [Sus scrofa]				
gi|353468891|gb|AER08622.1|	signal transducer and activator of transcription 1 transcript variant 2 [Sus scrofa]				
gi|353468889|gb|AER08621.1|	signal transducer and activator of transcription 1 transcript variant 1 [Sus scrofa]				
gi|194044626|ref|XP_001927289.1|	PREDICTED: 14-3-3 protein beta/alpha isoform 1 [Sus scrofa]	2.234	1.272	0.948	1.724
gi|2947100|gb|AAC39170.1|	15-oxoprostaglandin 13-reductase [Sus scrofa]	1.605	1.793	2.825	3.912
gi|47523824|ref|NP_999550.1|	prostaglandin reductase 1 [Sus scrofa] >gi|2498509|sp|Q29073.1|PTGR1_PIG RecName: Full=Prostaglandin reductase 1; Short=PRG-1; AltName: Full=15-oxoprostaglandin 13-reductase; AltName: Full=NADP-dependent leukotriene				

	B4 12-hydroxydehydrogenase >gi|11				
gi|1845|emb|CAA48565.1|	aminoacylase I [Sus scrofa]	1.855	2.955	3.909	2.438
gi|47522690|ref|NP_999061.1|	aminoacylase-1 [Sus scrofa] >gi|584724|sp|P37111.2|ACY1_PIG RecName: Full=Aminoacylase-1; Short=ACY-1; AltName: Full=N-acyl-L-amino-acid amidohydrolase >gi|533335|dbj|BAA02731.1| N-acylamino acid aminohydrolase (Aminoacylase 1) [Sus scrofa] >gi|4586				
gi|350538593|ref|NP_001233247.1|	phosphoglucomutase-1 [Sus scrofa] >gi|321574209|gb|ADW94631.1| phosphoglucomutase 1 [Sus scrofa]	1.17	0.359	0.319	0.381
gi|194036835|ref|XP_001924895.1|	PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase [Sus scrofa]	1.684	0.809	0.783	1.223
gi|264681460|ref|NP_001161124.1|	acyl carrier protein, mitochondrial [Sus scrofa] >gi|262204908|dbj|BAI48034.1| NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa [Sus scrofa]	0.35	0.688	0.513	0.468
gi|311258000|ref|XP_003127386.1|	PREDICTED: AP-2 complex subunit alpha-1 isoform 1 [Sus scrofa]	1.207	0.648	0.815	1.052
gi|311258002|ref|XP_003127387.1|	PREDICTED: AP-2 complex subunit alpha-1 isoform 2 [Sus scrofa]				
gi|311258004|ref|XP_003127388.1|	PREDICTED: AP-2 complex subunit alpha-1 isoform 3 [Sus scrofa]				
gi|311247353|ref|XP_003122594.1|	PREDICTED: N-acetylated alpha-linked acidic dipeptidase-like 1 [Sus scrofa]	1.445	1.262	2.702	0.96
gi|118675|sp|P09623.1|DLDH_PIG	RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial; AltName: Full=Dihydrolipoamide dehydrogenase; Flags: Precursor >gi|47522940|ref|NP_999227.1| dihydrolipoyl dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|164539|gb|AAA31069.1| lipoam	0.665	0.684	0.543	0.589
gi|122220|sp|P17630.1|TCO1	RecName: Full=Transcobalamin-1;	1.622	1.801	1.275	2.573

_PIG	Short=TC-1; AltName: Full=Cobalophilin; AltName: Full=Haptocorrin; AltName: Full=Protein R; AltName: Full=Transcobalamin I; Short=TC I; Short=TCI; Flags: Precursor >gi|1964|emb|CAA36800.1| unnamed protein product [Sus				
gi|335306899|ref|XP_003360619.1|	PREDICTED: transcobalamin-1 isoform 1 [Sus scrofa]				
gi|47522620|ref|NP_999100.1|	proteasome subunit beta type-8 [Sus scrofa] >gi|4545092|gb|AAD22390.1|AF059493_1 proteasome subunit LMP7 [Sus scrofa]				
gi|335282599|ref|XP_003123290.2|	PREDICTED: interleukin enhancer-binding factor 3 [Sus scrofa]	1.011	1.226	1.104	1.319
gi|335284501|ref|XP_003124603.2|	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial-like [Sus scrofa]	0.886	0.408	0.423	0.451
gi|145559663|gb|ABP73657.1|	MHC class I antigen [Sus scrofa]	0.936	0.687	0.802	1.355
gi|350529387|ref|NP_001231927.1|	basic transcription factor 3 [Sus scrofa]	1.132	3.045	1.918	0.87
gi|264681436|ref|NP_001161113.1|	copper transport protein ATOX1 [Sus scrofa] >gi|262036932|dbj|BAI47601.1| antioxidant protein 1 homolog (yeast) [Sus scrofa]	1.28	2.727	3.209	3.307
gi|350596533|ref|XP_003484288.1|	PREDICTED: copper transport protein ATOX1-like, partial [Sus scrofa]				
gi|335294829|ref|XP_003357324.1|	PREDICTED: acetyl-CoA acetyltransferase, mitochondrial [Sus scrofa]	1.112	0.989	0.72	1.428
gi|350594033|ref|XP_003483821.1|	PREDICTED: UDP-glucuronosyltransferase 1-10 isoform 2 [Sus scrofa]	0.806	0.583	0.609	1.105
gi|350581149|ref|XP_003480971.1|	PREDICTED: matrin-3 [Sus scrofa] >gi|350581147|ref|XP_003480970.1| PREDICTED: matrin-3 [Sus scrofa] >gi|335283551|ref|XP_003354341.1| PREDICTED: matrin-3 [Sus scrofa] >gi|311250254|ref|XP_00312	0.329	0.595	0.655	0.656

	4025.1| PREDICTED: matrin-3 isoform 1 [Sus scrofa]				
gi|350582222|ref|XP_003481226.1|	PREDICTED: LOW QUALITY PROTEIN: dynactin subunit 1 [Sus scrofa]	1.234	2.422	2.124	1.903
gi|47523650|ref|NP_999459.1|	tropomodulin-3 [Sus scrofa] >gi|7288863|gb|AAF45300.1|AF237632_1 ubiquitous tropomodulin U-Tmod [Sus scrofa]	1.732	1.748	1.283	1.247
gi|335292272|ref|XP_003356696.1|	PREDICTED: fumarylacetoacetase-like [Sus scrofa]	1.473	3.38	2.688	1.629
gi|335297524|ref|XP_003358060.1|	PREDICTED: 116 kDa U5 small nuclear ribonucleoprotein component [Sus scrofa] >gi|311267074|ref|XP_003131380.1| PREDICTED: 116 kDa U5 small nuclear ribonucleoprotein component isoform 1 [Sus scrofa]	1.432	1.101	1.086	1.3
gi|335297526|ref|XP_003131381.2|	PREDICTED: 116 kDa U5 small nuclear ribonucleoprotein component isoform 2 [Sus scrofa]				
gi|55977740|sp|Q29387.2|EF1G_PIG	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma >gi|19111049|gb|AAL85414.1|AF480162_1 eukaryotic elongation factor 1 gamma-like protein [Sus scrofa]	1.33	0.435	0.704	1.36
gi|350580027|ref|XP_003480738.1|	PREDICTED: elongation factor 1-gamma [Sus scrofa]				
gi|113196863|gb|ABI31729.1|	low molecular mass protein 7 [Sus scrofa]	1.128	1.616	1.651	1.131
gi|147225186|emb|CAN13318.1|	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) [Sus scrofa]				
gi|311260174|ref|XP_001924154.2|	PREDICTED: proteasome subunit beta type-8 [Sus scrofa] >gi|147225184|emb|CAN13316.1| proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) [Sus scrofa]				

<table>
<tr><td>gi|72535190|ref|NP_001026957.1|</td><td>ras-related protein Rab-1A [Sus scrofa] >gi|75056559|sp|Q52NJ2.3|RAB1A_PIG RecName: Full=Ras-related protein Rab-1A >gi|62868642|gb|AAY17509.1| Ras-related protein Rab-1A [Sus scrofa]</td><td>0.891</td><td>0.85</td><td>0.853</td><td>0.998</td></tr>
<tr><td>gi|178056596|ref|NP_001116608.1|</td><td>U6 snRNA-associated Sm-like protein LSm2 [Sus scrofa] >gi|147225158|emb|CAN13335.1| LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Sus scrofa]</td><td>0.96</td><td>2.495</td><td>1.884</td><td>1.641</td></tr>
<tr><td>gi|311276332|ref|XP_003135175.1|</td><td>PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2-like isoform 2 [Sus scrofa]</td><td>1.185</td><td>0.75</td><td>0.745</td><td>1.037</td></tr>
<tr><td>gi|311276336|ref|XP_003135176.1|</td><td>PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2-like isoform 3 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311276334|ref|XP_003135174.1|</td><td>PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2-like isoform 1 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|346986418|ref|NP_001231359.1|</td><td>DnaJ (Hsp40) homolog, subfamily B, member 1 [Sus scrofa]</td><td>1.162</td><td>1.428</td><td>1.22</td><td>1.139</td></tr>
<tr><td>gi|47522680|ref|NP_999069.1|</td><td>neutral alpha-glucosidase AB precursor [Sus scrofa] >gi|54037147|sp|P79403.1|GANAB_PIG RecName: Full=Neutral alpha-glucosidase AB; AltName: Full=Alpha-glucosidase 2; AltName: Full=Glucosidase II subunit alpha; Flags: Precursor >gi|1890664|gb|AAB4975</td><td>0.917</td><td>0.548</td><td>0.547</td><td>0.771</td></tr>
<tr><td>gi|349585085|ref|NP_001231804.1|</td><td>RAB11B, member RAS oncogene family [Sus scrofa]</td><td>1.031</td><td>0.664</td><td>0.52</td><td>0.848</td></tr>
<tr><td>gi|335296459|ref|XP_003130769.2|</td><td>PREDICTED: vimentin-like [Sus scrofa]</td><td>0.816</td><td>1.537</td><td>1.283</td><td>1.234</td></tr>
<tr><td>gi|47523888|ref|NP_999583.1|</td><td>ADP/ATP translocase 3 [Sus scrofa] >gi|52000613|sp|Q6QRN9.3|ADT3_PIG RecName: Full=ADP/ATP translocase 3; AltName: Full=ADP,ATP carrier protein 3; AltName: Full=Adenine</td><td>0.649</td><td>0.471</td><td>0.325</td><td>0.687</td></tr>
</table>

	nucleotide translocator 3; Short=ANT 3; AltName: Full=Solute carrier family 25 m				
gi|1827464|dbj|BAA19181.1|	metallothionein isoform [Sus scrofa]	576.898	5099.604	2186.181	949.007
gi|18202369|sp|P79431.1|MT1E_PIG	RecName: Full=Metallothionein-1E; Short=MT-1E; AltName: Full=Metallothionein-IE; Short=MT-IE >gi|1827462|dbj|BAA19180.1| metallothionein isoform [Sus scrofa]				
gi|335281589|ref|XP_003353840.1|	PREDICTED: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3 isoform 2 [Sus scrofa]	1.089	1.046	1.031	1.203
gi|335281591|ref|XP_003122641.2|	PREDICTED: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3 isoform 1 [Sus scrofa]				
gi|311259696|ref|XP_003128216.1|	PREDICTED: LOW QUALITY PROTEIN: desmoplakin-like [Sus scrofa]	1.077	0.805	1.083	1
gi|350596559|ref|XP_003361362.2|	PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 3-like, partial [Sus scrofa]	0.727	0.735	0.828	0.662
gi|350580256|ref|XP_003480773.1|	PREDICTED: nucleobindin-2 [Sus scrofa]	0.608	1.207	1.564	1.02
gi|350580258|ref|XP_003122998.3|	PREDICTED: nucleobindin-2 isoform 2 [Sus scrofa]				
gi|311261483|ref|XP_003128742.1|	PREDICTED: LOW QUALITY PROTEIN: golgin subfamily A member 5-like [Sus scrofa]	1.092	1.63	1.604	1.104
gi|342187276|ref|NP_001230112.1|	AP-2 complex subunit beta [Sus scrofa]	0.861	0.815	0.909	1.118
gi|47522662|ref|NP_999076.1|	membrane-associated progesterone receptor component 1 [Sus scrofa] >gi|6647580|sp|Q95250.3|PGRC1_PIG RecName: Full=Membrane-associated progesterone receptor component 1 >gi|1657409|emb|CAA68050.1| steroid membrane binding protein	0.562	0.373	0.608	0.603

	[Sus scrofa]				
gi|335286672|ref|XP_003125720.2|	PREDICTED: transgelin-2-like isoform 1 [Sus scrofa] >gi|335286674|ref|XP_003355153.1| PREDICTED: transgelin-2-like isoform 2 [Sus scrofa]	1.501	0.95	0.996	1.143
gi|311259388|ref|XP_003128071.1|	PREDICTED: cytochrome b-c1 complex subunit 6, mitochondrial-like [Sus scrofa]	0.606	0.434	0.581	0.418
gi|194042189|ref|XP_001924213.1|	PREDICTED: annexin A11 [Sus scrofa]	1.218	0.642	0.78	0.835
gi|346421435|ref|NP_001231091.1|	sorbitol dehydrogenase [Sus scrofa]	1.724	1.163	0.884	1.309
gi|544074|sp|Q99028.1|COMT_PIG	RecName: Full=Catechol O-methyltransferase	1.179	0.618	0.878	1.088
gi|305855180|ref|NP_001182259.1|	catechol O-methyltransferase [Sus scrofa] >gi|285818436|gb|ADC38891.1| catechol-O-methyltransferase [Sus scrofa]				
gi|350586831|ref|XP_003482287.1|	PREDICTED: cytochrome c oxidase subunit 5A, mitochondrial-like isoform 1 [Sus scrofa] >gi|350586833|ref|XP_003482288.1| PREDICTED: cytochrome c oxidase subunit 5A, mitochondrial-like isoform 2 [Sus scrofa]	0.26	0.519	0.473	0.375
gi|350579447|ref|XP_003480607.1|	PREDICTED: protein NipSnap homolog 3A [Sus scrofa]	0.815	1.531	1.298	1.206
gi|335280113|ref|XP_003121789.2|	PREDICTED: LOW QUALITY PROTEIN: 60S ribosomal protein L4 [Sus scrofa]	0.772	0.477	0.419	1.1
gi|311249564|ref|XP_003123691.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein H [Sus scrofa]	0.699	0.928	0.779	0.843
gi|343790906|ref|NP_001230510.1|	calcineurin-like phosphoesterase domain containing 1 [Sus scrofa]	0.755	2.436	1.559	1.194
gi|113205878|ref|NP_001038072.1|	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial [Sus scrofa] >gi|90024980|gb|AAZ82038.2| peroxisomal enoyl coenzyme A hydratase 1 [Sus scrofa]	1.299	1.408	0.971	1.065

gi|120564445|gb|ABM30148.1|	peroxisomal enoyl coenzyme A hydratase 1 [Sus scrofa]				
gi|311268173|ref|XP_003131919.1|	PREDICTED: myb-binding protein 1A [Sus scrofa]	0.608	2.053	1.081	1.739
gi|47523406|ref|NP_999324.1|	polymeric immunoglobulin receptor precursor [Sus scrofa] >gi|6863080|dbj|BAA84283.2| poly-Ig receptor [Sus scrofa]	0.825	0.854	0.69	1.094
gi|312283580|ref|NP_999292.2|	superoxide dismutase [Mn], mitochondrial [Sus scrofa]	0.97	1.8	0.677	0.974
gi|335296662|ref|XP_003130891.2|	PREDICTED: 6-phosphofructokinase type C [Sus scrofa]	1.462	0.995	1.326	1.464
gi|335281560|ref|XP_003353830.1|	PREDICTED: splicing factor 1 isoform 2 [Sus scrofa]	1.14	1.611	1.992	0.968
gi|335281562|ref|XP_003353831.1|	PREDICTED: splicing factor 1 isoform 3 [Sus scrofa]				
gi|335281564|ref|XP_003122635.2|	PREDICTED: splicing factor 1 isoform 1 [Sus scrofa]				
gi|346986445|ref|NP_001231372.1|	NSFL1 (p97) cofactor (p47) [Sus scrofa]	1.188	1.88	1.872	1.52
gi|154147660|ref|NP_001093666.1|	eukaryotic initiation factor 4A-I [Sus scrofa] >gi|85792232|gb|ABC84193.1| eukaryotic translation initiation factor 4A isoform 1 [Sus scrofa]	1.139	0.781	0.373	1.323
gi|335308568|ref|XP_003361283.1|	PREDICTED: eukaryotic initiation factor 4A-I-like [Sus scrofa]				
gi|148225750|ref|NP_001090973.1|	heat shock protein 105 kDa [Sus scrofa] >gi|141521428|gb|ABO88027.1| heat shock 105kDa/110kDa protein 1 [Sus scrofa]	0.908	1.023	0.959	1.296
gi|311274155|ref|XP_003134215.1|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial-like [Sus scrofa]	0.891	0.494	1.079	0.589
gi|3746946|gb|AAC64131.1|	phosphoglucomutase 1 [Sus scrofa] >gi|3746944|gb|AAC64130.1| phosphoglucomutase 1 [Sus scrofa]	0.855	0.665	0.452	0.453
gi|350578005|ref|XP_001924268.4|	PREDICTED: ezrin [Sus scrofa]	1.43	1.542	1.413	1.084
gi|343790977|ref|NP_001230537.1|	phospholysine phosphohistidine inorganic pyrophosphate phosphatase [Sus scrofa]	2.963	1.89	1.485	1.259
gi|350577999|ref|XP_001928	PREDICTED: ezrin-like [Sus scrofa]	1.848	0.828	1.314	1.341

755.4|					
gi|350580184|ref|XP_003353965.2|	PREDICTED: reticulocalbin-1-like isoform 2 [Sus scrofa]	0.631	0.986	1.263	0.758
gi|311259408|ref|XP_003128090.1|	PREDICTED: peroxiredoxin-1 isoform 5 [Sus scrofa]	2.943	1.704	1.309	3.046
gi|311259416|ref|XP_003128087.1|	PREDICTED: peroxiredoxin-1 isoform 2 [Sus scrofa] >gi|311259412|ref|XP_003128089.1| PREDICTED: peroxiredoxin-1 isoform 4 [Sus scrofa] >gi|311259414|ref|XP_003128088.1| PREDICTED: peroxiredoxin-1 isoform 3 [Sus scrofa] >gi|311259410|ref|XP_003128086.				
gi|1236646|gb|AAC48775.1|	ch4 and secrete domains of swine IgM [Sus scrofa]	0.779	0.684	0.478	0.807
gi|291202695|dbj|BAI82566.1|	IgM heavy chain constant region [Sus scrofa]				
gi|113205854|ref|NP_001038066.1|	40S ribosomal protein S3 [Sus scrofa] >gi|115502828|sp|Q0Z8U2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|110006645|gb|ABG48767.1| ribosomal protein S3 [Sus scrofa]	0.59	0.43	0.367	0.585
gi|47523792|ref|NP_999532.1|	catenin beta-1 [Sus scrofa] >gi|167834655|gb|ACA03158.1| beta-catenin [Sus scrofa] >gi|18146999|dbj|BAB82984.1| beta-catenin [Sus scrofa]	0.615	0.612	0.533	0.625
gi|335302729|ref|XP_003359534.1|	PREDICTED: catenin beta-1-like [Sus scrofa]				
gi|311275253|ref|XP_003134650.1|	PREDICTED: single-stranded DNA-binding protein, mitochondrial-like isoform 1 [Sus scrofa]	0.973	1.943	1.71	1.215
gi|47523618|ref|NP_999441.1|	citrate synthase, mitochondrial precursor [Sus scrofa] >gi|116470|sp|P00889.2|CISY_PIG RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor >gi|164419|gb|AAA31017.1| citrate synthase precursor (EC	2.016	0.966	1.408	2.124

	4.1.3.7) [Sus scrofa]				
gi|157834775|pdb|2CTS|A	Chain A, Crystallographic Refinement And Atomic Models Of Two Different Forms Of Citrate Synthase At 2.7 And 1.7 Angstroms Resolution				
gi|253723327|pdb|3ENJ|A	Chain A, Structure Of Pig Heart Citrate Synthase At 1.78 A Resolution >gi|157830720|pdb|1CTS|A Chain A, Crystallographic Refinement And Atomic Models Of Two Different Forms Of Citrate Synthase At 2.7 And 1.7 Angstroms Resolution >gi|230994|pdb|4CTS|				
gi|311247022|ref|XP_003122449.1|	PREDICTED: cadherin-related family member 5 [Sus scrofa]	0.425	0.525	0.89	0.481
gi|335310692|ref|XP_003362151.1|	PREDICTED: protein LZIC-like [Sus scrofa]	1.219	2.177	2.93	1.599
gi|55583765|sp|Q863Z0.3|PSME2_PIG	RecName: Full=Proteasome activator complex subunit 2; AltName: Full=Proteasome activator 28 subunit beta; Short=PA28b; Short=PA28beta >gi|47523632|ref|NP_999444.1| proteasome activator complex subunit 2 [Sus scrofa] >gi|34978648|gb|AAQ83575.1| prote	1.436	0.64	1.096	1.422
gi|342349319|ref|NP_001230139.1|	calnexin precursor [Sus scrofa]	0.685	0.549	0.7	0.759
gi|350590415|ref|XP_003131608.3|	PREDICTED: prohibitin-like [Sus scrofa]	1.62	0.765	0.723	1.186
gi|311258421|ref|XP_003127605.1|	PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating [Sus scrofa]	1.967	1.556	1.349	1.821
gi|71361861|gb|AAZ30034.1|	Mx1 [Sus scrofa]	0.967	1.069	0.893	1.743
gi|156720190|dbj|BAF76736.1|	Mx1 [Sus scrofa]				
gi|343488474|ref|NP_001230453.1|	elongation factor 1-beta [Sus scrofa]	0.927	1.277	2.426	1.258
gi|347300276|ref|NP_001231441.1|	poly(rC) binding protein 2 [Sus scrofa]	1.094	0.854	0.85	1.302
gi|345090969|ref|NP_001230	septin 2 [Sus scrofa]	1.57	1.505	1.305	1.276

722.1|					
gi|448581|prf||1917268B	pyruvate dehydrogenase:SUBUNIT=beta	1.03	0.518	0.699	0.734
gi|346986351|ref|NP_001231327.1|	pyruvate dehydrogenase E1 component subunit beta, mitochondrial [Sus scrofa]				
gi|311268663|ref|XP_003132151.1|	PREDICTED: 3-ketoacyl-CoA thiolase A, peroxisomal isoform 1 [Sus scrofa]	2.147	1.584	1.713	1.641
gi|349732238|ref|NP_001231864.1|	transaldolase [Sus scrofa]	1.195	2.121	1.642	1.788
gi|213021241|ref|NP_001132944.1|	proteasome subunit alpha type-6 [Sus scrofa] >gi|210062872|gb|ACJ06406.1| proteasome subunit alpha type 6 [Sus scrofa]	1.055	1.229	1.076	1.231
gi|335296435|ref|XP_003357777.1|	PREDICTED: cytoplasmic aconitate hydratase [Sus scrofa]	2.956	1.061	1.068	1.935
gi|350587882|ref|XP_003129304.3|	PREDICTED: caspase-6-like [Sus scrofa]	0.925	2.035	1.475	1.488
gi|335296241|ref|XP_003357722.1|	PREDICTED: ladinin-1-like [Sus scrofa]	0.587	0.68	0.71	0.87
gi|311254260|ref|XP_001929592.2|	PREDICTED: interleukin enhancer-binding factor 2 [Sus scrofa]	1.471	1.176	0.872	1.452
gi|343887442|ref|NP_001230623.1|	heterogeneous nuclear ribonucleoprotein C (C1/C2) 2 [Sus scrofa]	0.738	0.645	0.614	0.827
gi|311261988|ref|XP_003128958.1|	PREDICTED: phosphoglucomutase-2 [Sus scrofa]	1.677	1.345	1.583	2.313
gi|2833353|sp|Q29058.1|LEG4_PIG	RecName: Full=Galectin-4; Short=Gal-4; AltName: Full=L-36 lactose-binding protein; Short=L36LBP; AltName: Full=Lactose-binding lectin 4 >gi|47522788|ref|NP_999146.1| galectin-4 [Sus scrofa] >gi|623346|emb|CAA55884.1| L-36 lactose binding protein [Su	0.835	1.744	1.568	1.613
gi|350594031|ref|XP_003483820.1|	PREDICTED: UDP-glucuronosyltransferase 1-10 isoform 1 [Sus scrofa]	0.773	0.689	0.694	0.597
gi|350591042|ref|XP_003132	PREDICTED: programmed cell death	1.284	0.954	1.22	1.59

145.3|	6-interacting protein [Sus scrofa]				
gi|343478174|ref|NP_001230356.1|	T-complex protein 1 subunit alpha [Sus scrofa]	1.601	0.881	1.189	1.637
gi|335282824|ref|XP_003123501.2|	PREDICTED: ilvB (bacterial acetolactate synthase)-like [Sus scrofa]	0.942	0.825	0.694	0.805
gi|345507389|gb|AEO00192.1|	mucin 13A [Sus scrofa]	0.3	0.499	0.463	0.521
gi|345507392|gb|AEO00194.1|	mucin 13A [Sus scrofa] >gi|345507386|gb|AEO00190.1| mucin 13A [Sus scrofa]				
gi|163310773|ref|NP_001090990.2|	membrane-associated progesterone receptor component 2 [Sus scrofa] >gi|160688702|gb|ABX45133.1| progesterone receptor membrane component 2 [Sus scrofa] >gi|160688700|gb|ABX45132.1| progesterone receptor membrane component 2 [Sus scrofa]	0.546	0.683	0.9	0.82
gi|350586183|ref|XP_003128050.3|	PREDICTED: enoyl-CoA hydratase domain-containing protein 2, mitochondrial-like isoform 1 [Sus scrofa]	1.14	0.512	0.439	0.738
gi|281427370|ref|NP_001163993.1|	T-complex protein 1 subunit eta [Sus scrofa] >gi|262036937|dbj|BAI47603.1| chaperonin containing TCP1, subunit 7 (eta) [Sus scrofa]	1.904	0.901	0.911	1.878
gi|194037681|ref|XP_001926390.1|	PREDICTED: early endosome antigen 1 [Sus scrofa]	0.749	1.226	1.334	0.818
gi|349732201|ref|NP_001231854.1|	dpy-30 homolog [Sus scrofa]	0.546	1.038	2.141	2.438
gi|47523892|ref|NP_999584.1|	epithelial cell adhesion molecule precursor [Sus scrofa] >gi|75045149|sp|Q75QW1.1|EPCAM_PIG RecName: Full=Epithelial cell adhesion molecule; Short=Ep-CAM; AltName: Full=Tumor-associated calcium signal transducer 1; AltName: CD_antigen=CD326; Flags:	0.935	0.504	0.553	0.642
gi|311248247|ref|XP_003123039.1|	PREDICTED: ATP synthase subunit delta, mitochondrial-like isoform 1 [Sus scrofa]	0.28	0.385	0.346	0.274

gi|350580769|ref|XP_003480894.1|	PREDICTED: ATP synthase subunit delta, mitochondrial-like [Sus scrofa]				
gi|350591788|ref|XP_003358782.2|	PREDICTED: hypothetical protein LOC448846 [Sus scrofa]	1.439	0.714	0.869	0.874
gi|311250071|ref|XP_003123947.1|	PREDICTED: solute carrier family 12 member 2 [Sus scrofa]	---	---	---	---
gi|132574|sp|P10775.1|RINI_PIG	RecName: Full=Ribonuclease inhibitor; AltName: Full=Ribonuclease/angiogenin inhibitor 1	1.696	1.691	0.941	1.56
gi|313507173|pdb|1DFJ|I	Chain I, Ribonuclease Inhibitor Complexed With Ribonuclease A >gi|253723219|pdb|2BNH|A Chain A, Porcine Ribonuclease Inhibitor				
gi|48675943|ref|NP_001001640.1|	amine oxidase [flavin-containing] A [Sus scrofa] >gi|62899648|sp|Q6Q2J0.1|AOFA_PIG RecName: Full=Amine oxidase [flavin-containing] A; AltName: Full=Monoamine oxidase type A; Short=MAO-A >gi|45551418|gb|AAS68020.1| monoamine oxidase A [Sus scrofa]	0.908	0.565	0.663	1.069
gi|350592964|ref|XP_003483582.1|	PREDICTED: PDZ and LIM domain protein 1 [Sus scrofa]	1.389	2.467	2.281	1.529
gi|62529273|gb|AAX84942.1|	type III calpastatin [Sus scrofa]	0.743	1.941	2.387	1.443
gi|160425376|gb|ABX39530.1|	calpastatin [Sus scrofa]				
gi|160425375|gb|ABX39529.1|	calpastatin [Sus scrofa]				
gi|47522950|ref|NP_999232.1|	calpastatin [Sus scrofa] >gi|44990121|gb|AAS50179.1| calpastatin [Sus scrofa]				
gi|160425379|gb|ABX39533.1|	calpastatin [Sus scrofa]				
gi|124109|sp|P12675.1|ICAL_PIG	RecName: Full=Calpastatin; AltName: Full=Calpain inhibitor >gi|39545760|gb|AAR27961.1| calpastatin [Sus scrofa] >gi|164407|gb|AAA31012.1| heart calpastatin [Sus scrofa]				

gi|160425377|gb|ABX39531.1|	calpastatin [Sus scrofa]				
gi|160425378|gb|ABX39532.1|	calpastatin [Sus scrofa]				
gi|345091067|ref|NP_001230751.1|	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) [Sus scrofa]	1.684	1.225	1.113	1.685
gi|350590384|ref|XP_003131576.3|	PREDICTED: importin subunit beta-1-like isoform 1 [Sus scrofa]	1.133	0.693	0.653	0.91
gi|148232214|ref|NP_001090964.1|	ribose-5-phosphate isomerase [Sus scrofa] >gi|158512830|sp|A2TLM1.1|RPIA_PIG RecName: Full=Ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase >gi|124265188|gb|ABM98101.1| ribose 5-phosphate isomerase-like protein [Sus scrofa]	0.938	3.291	3.682	1.253
gi|311275469|ref|XP_003134753.1|	PREDICTED: calumenin isoform 2 [Sus scrofa]	0.129	1.092	0.556	0.512
gi|1346670|sp|P04175.2|NCPR_PIG	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	0.722	0.432	0.709	0.752
gi|194018678|ref|NP_001123431.1|	NADPH--cytochrome P450 reductase [Sus scrofa] >gi|499862|gb|AAA85368.1| NADPH-cytochrome P-450 oxidoreductase [Sus scrofa]				
gi|194035831|ref|XP_001928742.1|	PREDICTED: coatomer subunit alpha isoform 2 [Sus scrofa]	1.561	1.003	0.878	1.562
gi|194035835|ref|XP_001928732.1|	PREDICTED: coatomer subunit alpha isoform 1 [Sus scrofa]				
gi|350579323|ref|XP_003122006.3|	PREDICTED: retinal dehydrogenase 1-like, partial [Sus scrofa]	1.35	1.241	1.953	1.515
gi|194044922|ref|XP_001927475.1|	PREDICTED: ADP/ATP translocase 2 [Sus scrofa]	0.806	0.269	0.464	0.69
gi|350579921|ref|XP_003353801.2|	PREDICTED: dipeptidyl peptidase 3-like isoform 1 [Sus scrofa] >gi|335281448|ref|XP_003353806.1| PREDICTED: dipeptidyl peptidase 3-like [Sus scrofa]	1.859	1.16	1.027	2.216
gi|350579923|ref|XP_003480	PREDICTED: dipeptidyl peptidase				

715.1|	3-like isoform 2 [Sus scrofa]				
gi|18699303|gb|AAL78518.1|AF464056_1	MHC class I antigen [Sus scrofa]	---	---	---	---
gi|29027455|gb|AAO62097.1|	MHC class I antigen [Sus scrofa]				
gi|168208432|gb|ACA21801.1|	MHC class I antigen [Sus scrofa]				
gi|347300323|ref|NP_001231460.1|	thioredoxin-dependent peroxide reductase, mitochondrial [Sus scrofa]	0.606	0.676	0.513	0.331
gi|350588020|ref|XP_003357153.2|	PREDICTED: protein transport protein Sec31A [Sus scrofa]	1.508	0.744	0.93	1.055
gi|194595733|gb|ACF77144.1|	clathrin light chain (CLTA) protein [Sus scrofa]	2.514	2.008	3.157	1.538
gi|47523670|ref|NP_999471.1|	peroxisomal multifunctional enzyme type 2 [Sus scrofa] >gi|499340|emb|CAA55037.1| 17beta-estradiol dehydrogenase [Sus scrofa]	1.407	1.131	1.217	1.501
gi|1702997|sp|P54613.1|2AAB_PIG	RecName: Full=Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform; AltName: Full=PP2A subunit A isoform PR65-beta; AltName: Full=PP2A subunit A isoform R1-beta >gi|510347|emb|CAA84403.1| protein phosphatase 2A 65 kDa reg	---	---	---	---
gi|335294859|ref|XP_003357335.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform 3 [Sus scrofa]				
gi|335294855|ref|XP_003357333.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform 1 [Sus scrofa]				
gi|335294861|ref|XP_003357336.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform 4 [Sus scrofa]				
gi|335294857|ref|XP_003357334.1|	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform 2 [Sus scrofa]				

gi|80971504|ref|NP_001032223.1|	40S ribosomal protein SA [Sus scrofa] >gi|122069666|sp|Q4GWZ2.3|RSSA_PIG RecName: Full=40S ribosomal protein SA; AltName: Full=37 kDa laminin receptor precursor; Short=37LRP; AltName: Full=37/67 kDa laminin receptor; Short=LRP/LR; AltName: Full=67 k	2.076	1.036	0.727	1.462
gi|335302965|ref|XP_001925033.2|	PREDICTED: lupus La protein homolog [Sus scrofa]	1.032	0.677	0.571	1.326
gi|319401915|ref|NP_001188313.1|	rho GDP-dissociation inhibitor 1 [Sus scrofa] >gi|315321426|gb|ADU04840.1| Rho GDP dissociation inhibitor alpha [Sus scrofa]	2.584	0.973	1.127	1.81
gi|350580873|ref|XP_003123770.3|	PREDICTED: ras GTPase-activating-like protein IQGAP2-like [Sus scrofa]	0.937	0.761	0.636	0.979
gi|343780950|ref|NP_001230488.1|	39S ribosomal protein L40, mitochondrial isoform 1 [Sus scrofa]	0.573	0.577	0.466	0.63
gi|343780952|ref|NP_001230489.1|	39S ribosomal protein L40, mitochondrial [Sus scrofa]				
gi|350595262|ref|XP_003484071.1|	PREDICTED: calumenin [Sus scrofa]	0.635	0.71	0.802	0.56
gi|305855176|ref|NP_001182260.1|	cleavage and polyadenylation specificity factor subunit 6 [Sus scrofa] >gi|285818464|gb|ADC38905.1| cleavage and polyadenylation specific factor 6 [Sus scrofa]	0.757	1.403	1.44	0.672
gi|311254645|ref|XP_003125912.1|	PREDICTED: EPS8-like 3 [Sus scrofa]	0.87	0.538	0.696	0.824
gi|311273235|ref|XP_003133777.1|	PREDICTED: intestinal-type alkaline phosphatase-like isoform 2 [Sus scrofa]	0.879	1.307	2.392	0.652
gi|311257294|ref|XP_003127050.1|	PREDICTED: cytochrome b-c1 complex subunit Rieske, mitochondrial-like [Sus scrofa]	0.723	0.545	0.722	0.632
gi|335304027|ref|XP_003134070.2|	PREDICTED: 28S ribosomal protein S36, mitochondrial-like [Sus scrofa]	0.469	0.658	0.771	0.704
gi|350587377|ref|XP_003356918.2|	PREDICTED: cytosol aminopeptidase-like [Sus scrofa]	1.687	2.747	3.579	1.011
gi|335284301|ref|XP_003354567.1|	PREDICTED: T-complex protein 1 subunit zeta-like isoform 2 [Sus	2.957	1.74	1.338	2.699

	scrofa]				
gi|335284299|ref|XP_003124509.2|	PREDICTED: T-complex protein 1 subunit zeta-like isoform 1 [Sus scrofa]				
gi|335281222|ref|XP_003353764.1|	PREDICTED: probable 2-ketogluconate reductase-like isoform 2 [Sus scrofa]	2.964	2.138	1.42	2.895
gi|335281224|ref|XP_001924750.3|	PREDICTED: probable 2-ketogluconate reductase-like isoform 1 [Sus scrofa]				
gi|164543|gb|AAA31072.1|	malate dehydrogenase (EC 1.1.1.37), partial [Sus scrofa]	0.973	0.715	0.601	0.988
gi|6226874|sp|P11708.4|MDHC_PIG	RecName: Full=Malate dehydrogenase, cytoplasmic; AltName: Full=Cytosolic malate dehydrogenase >gi|47523114|ref|NP_999039.1| malate dehydrogenase, cytoplasmic [Sus scrofa] >gi|1469402|gb|AAC48610.1| cytosolic malate dehydrogenase [Sus scrofa]				
gi|5107783|pdb|5MDH|A	Chain A, Crystal Structure Of Ternary Complex Of Porcine Cytoplasmic Malate Dehydrogenase Alpha-Ketomalonate And Tnad At 2.4 Angstroms Resolution >gi|5107784|pdb|5MDH|B Chain B, Crystal Structure Of Ternary Complex Of Porcine Cytoplasmic Malate Dehy				
gi|350596594|ref|XP_003484293.1|	PREDICTED: malate dehydrogenase, cytoplasmic-like [Sus scrofa]				
gi|311247012|ref|XP_003122436.1|	PREDICTED: epidermal growth factor receptor kinase substrate 8-like protein 2-like [Sus scrofa]	0.712	1.308	1.067	0.98
gi|83816981|ref|NP_001033050.1|	proteasome subunit beta type-9 [Sus scrofa] >gi|311260176|ref|XP_003128374.1| PREDICTED: proteasome subunit beta type-9-like [Sus scrofa] >gi|110276961|gb|ABG57117.1| proteasome beta 9 subunit [Sus scrofa] >gi|83320492|gb|ABC02872.1| proteasome beta	1.175	1.396	1.46	1.491

<table>
<tr><td>gi|147225181|emb|CAN13313.1|</td><td>proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|116175259|ref|NP_001070686.1|</td><td>heterogeneous nuclear ribonucleoprotein A1 [Sus scrofa] >gi|115371763|gb|ABI96206.1| ROA1 [Sus scrofa]</td><td>1.325</td><td>0.865</td><td>0.712</td><td>1.539</td></tr>
<tr><td>gi|45479848|gb|AAS66766.1|</td><td>histone H1.3-like protein [Sus scrofa]</td><td>0.519</td><td>1.101</td><td>0.872</td><td>1.21</td></tr>
<tr><td>gi|72535198|ref|NP_001026962.1|</td><td>histone H1.3-like protein [Sus scrofa] >gi|45479846|gb|AAS66765.1| histone H1.3-like protein [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|47522712|ref|NP_999108.1|</td><td>pyridoxal kinase [Sus scrofa] >gi|67470293|sp|O46560.1|PDXK_PIG RecName: Full=Pyridoxal kinase; AltName: Full=Pyridoxine kinase >gi|2773404|gb|AAB96794.1| pyridoxal kinase [Sus scrofa]</td><td>0.708</td><td>0.261</td><td>0.275</td><td>0.245</td></tr>
<tr><td>gi|194036227|ref|XP_001929678.1|</td><td>PREDICTED: selenium-binding protein 1 [Sus scrofa]</td><td>1.132</td><td>1.756</td><td>2.005</td><td>1.465</td></tr>
<tr><td>gi|350529411|ref|NP_001231937.1|</td><td>proteasome (prosome, macropain) 26S subunit, ATPase, 2 [Sus scrofa]</td><td>0.795</td><td>0.859</td><td>1.186</td><td>1.024</td></tr>
<tr><td>gi|462384|sp|P33198.1|IDHP_PIG</td><td>RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=ICD-M; AltName: Full=IDP; AltName: Full=NADP(+)-specific ICDH; AltName: Full=Oxalosuccinate decarboxylase; Flags: Precursor >gi|294223|gb|AAA31089.1| NADPH-specif</td><td>1.284</td><td>0.588</td><td>0.64</td><td>0.99</td></tr>
<tr><td>gi|27065481|pdb|1LWD|B</td><td>Chain B, Crystal Structure Of Nadp-Dependent Isocitrate Dehydrogenase From Porcine Heart Mitochondria >gi|27065480|pdb|1LWD|A Chain A, Crystal Structure Of Nadp-Dependent Isocitrate Dehydrogenase From Porcine Heart Mitochondria</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|255683404|ref|NP_001157479.1|</td><td>isocitrate dehydrogenase [NADP], mitochondrial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
</table>

gi|311268489|ref|XP_003132080.1|	PREDICTED: fatty aldehyde dehydrogenase-like [Sus scrofa]	0.804	0.424	0.401	0.695
gi|346644882|ref|NP_001231113.1|	reticulocalbin 2, EF-hand calcium binding domain precursor [Sus scrofa]	0.68	0.644	0.763	0.748
gi|350593970|ref|XP_001925937.3|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 1 [Sus scrofa]	0.88	1.075	1.463	1.26
gi|297307133|ref|NP_001171997.1|	protein canopy homolog 2 precursor [Sus scrofa]	0.75	1.048	1.338	0.943
gi|349732227|ref|NP_001231859.1|	heterogeneous nuclear ribonucleoprotein M [Sus scrofa]	0.574	0.507	0.477	0.618
gi|350587641|ref|XP_003129114.3|	PREDICTED: UDP-glucuronosyltransferase 2C1-like [Sus scrofa]	0.934	0.43	0.67	0.942
gi|335282758|ref|XP_003123386.2|	PREDICTED: UV excision repair protein RAD23 homolog A-like [Sus scrofa]	0.577	1.518	1.899	0.832
gi|51493747|gb|AAU04861.1|	enoyl-Coenzyme A hydratase/3-hydroxyacyl Coenzyme A [Sus scrofa]	1.749	1.377	1.622	1.487
gi|351738777|gb|AEQ61487.1|	ribokinase [Sus scrofa]	1.083	1.493	1.603	1.019
gi|311260951|ref|XP_003128591.1|	PREDICTED: dehydrogenase/reductase SDR family member 1-like [Sus scrofa]	0.695	0.789	0.682	1.04
gi|194038973|ref|XP_001929258.1|	PREDICTED: purine nucleoside phosphorylase [Sus scrofa]	1.05	0.89	0.952	0.937
gi|350595461|ref|XP_003134939.3|	PREDICTED: LOW QUALITY PROTEIN: 2-oxoglutarate dehydrogenase, mitochondrial-like [Sus scrofa]	0.912	0.602	0.409	0.891
gi|178056556|ref|NP_001116620.1|	probable aminopeptidase NPEPL1 [Sus scrofa] >gi|147223400|emb|CAN13197.1| aminopeptidase-like 1 [Sus scrofa]	1.378	2.15	2.596	0.755
gi|311253799|ref|XP_001926739.2|	PREDICTED: ras-related protein Rab-2A [Sus scrofa]	1.027	0.39	0.427	0.617
gi|350596433|ref|XP_003484271.1|	PREDICTED: PDZ and LIM domain protein 1-like [Sus scrofa]	0.669	0.927	1.06	0.662
gi|335290692|ref|XP_003356	PREDICTED: UDP-glucose	0.766	0.24	0.268	0.393

250.1|	4-epimerase [Sus scrofa]				
gi|350589440|ref|XP_003130687.3|	PREDICTED: Golgi membrane protein 1-like [Sus scrofa]	0.268	0.679	0.831	0.666
gi|343098455|ref|NP_001230202.1|	ras-related protein Rab-6A [Sus scrofa]	1.156	0.719	0.616	0.97
gi|343488534|ref|NP_001230423.1|	homeobox prox 1 [Sus scrofa]	1.246	1.094	1.062	0.853
gi|335285943|ref|XP_003354987.1|	PREDICTED: eukaryotic translation initiation factor 5A-1-like [Sus scrofa] >gi|311268294|ref|XP_003131981.1| PREDICTED: eukaryotic translation initiation factor 5A-1-like isoform 4 [Sus scrofa] >gi|311268290|ref|XP_003131978.1| PREDICTED: eukaryotic	1.099	1.491	1.183	0.938
gi|335283574|ref|XP_003354345.1|	PREDICTED: transcriptional activator protein Pur-alpha isoform 2 [Sus scrofa] >gi|335283572|ref|XP_003354344.1| PREDICTED: transcriptional activator protein Pur-alpha isoform 1 [Sus scrofa]	0.921	1.144	1.289	0.939
gi|350579350|ref|XP_003353611.2|	PREDICTED: stomatin-like protein 2-like [Sus scrofa]	0.571	0.404	0.611	0.539
gi|350592614|ref|XP_003483500.1|	PREDICTED: splicing factor 3A subunit 1 isoform 1 [Sus scrofa]	0.967	1.291	0.815	1.114
gi|350591864|ref|XP_001926353.4|	PREDICTED: LOW QUALITY PROTEIN: melanotransferrin [Sus scrofa]	0.828	0.796	1.07	0.643
gi|311254575|ref|XP_003125894.1|	PREDICTED: rho-related GTP-binding protein RhoC-like [Sus scrofa]	0.832	0.891	0.934	0.864
gi|346986432|ref|NP_001231366.1|	ras homolog gene family, member A [Sus scrofa]				
gi|75053043|sp|Q6UAQ8.3|ETFB_PIG	RecName: Full=Electron transfer flavoprotein subunit beta; Short=Beta-ETF >gi|328550534|ref|NP_001192208.1| electron transfer flavoprotein subunit beta [Sus scrofa] >gi|35384838|gb|AAQ84565.1| electron transfer flavoprotein beta subunit precursor [S	1.237	0.867	1.028	1.205
gi|350580630|ref|XP_003123	PREDICTED: far upstream	0.981	1.596	1.271	1.194

158.3|	element-binding protein 2-like [Sus scrofa]				
gi|343478210|ref|NP_001230371.1|	syntaxin 12 [Sus scrofa]	0.949	1.837	2.884	1.001
gi|350591495|ref|XP_003132454.3|	PREDICTED: coatomer subunit gamma [Sus scrofa]	1.377	0.929	0.721	1.045
gi|350582722|ref|XP_003481338.1|	PREDICTED: 14-3-3 protein theta isoform 1 [Sus scrofa]	1.696	1.369	1.297	1.659
gi|350582724|ref|XP_003481339.1|	PREDICTED: 14-3-3 protein theta isoform 2 [Sus scrofa]				
gi|217039113|gb|ACJ76845.1|	HDL binding protein [Sus scrofa]	0.968	0.866	0.691	0.902
gi|345090979|ref|NP_001230725.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) [Sus scrofa]	0.51	0.285	0.248	0.434
gi|335310868|ref|XP_003362230.1|	PREDICTED: T-complex protein 1 subunit epsilon, partial [Sus scrofa]	1.491	0.598	0.472	1.125
gi|334305778|sp|D2SW95.1|COPB_PIG	RecName: Full=Coatomer subunit beta; AltName: Full=Beta-coat protein; Short=Beta-COP >gi|288860138|ref|NP_001165837.1| coatomer subunit beta [Sus scrofa] >gi|268633765|gb|ACZ15983.1| coatomer protein subunit beta 1 [Sus scrofa]	1.192	0.661	0.623	0.916
gi|12231040|sp|Q29048.2|VATA_PIG	RecName: Full=V-type proton ATPase catalytic subunit A; Short=V-ATPase subunit A; AltName: Full=V-ATPase 69 kDa subunit; AltName: Full=Vacuolar proton pump subunit alpha	0.868	0.558	0.642	0.755
gi|51592133|ref|NP_001004042.1|	V-type proton ATPase catalytic subunit A [Sus scrofa] >gi|1968|emb|CAA44213.1| H+ ATPase [Sus scrofa]				
gi|116047849|gb|ABJ53147.1|	glutathione S-transferase mu 2 [Sus scrofa]	2.29	1.598	1.589	3.519
gi|118403788|ref|NP_001072152.1|	glutathione S-transferase mu 2 [Sus scrofa] >gi|116047847|gb|ABJ53146.1| glutathione S-transferase mu 2 [Sus scrofa]				

gi|350584479|ref|XP_003126643.3|	PREDICTED: bcl-2-like protein 13 [Sus scrofa]	0.678	1.003	0.721	0.739
gi|345100481|pdb|1C9P|A	Chain A, Complex Of Bdellastasin With Porcine Trypsin >gi|3318722|pdb|1AN1|E Chain E, Leech-Derived Tryptase InhibitorTRYPSIN COMPLEX	0.612	0.894	0.765	0.701
gi|311259162|ref|XP_003127965.1|	PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	0.59	0.988	0.965	0.846
gi|350586216|ref|XP_003128039.3|	PREDICTED: thioredoxin domain-containing protein 12-like [Sus scrofa]	0.456	1.098	1.272	1.059
gi|197251946|ref|NP_001127815.1|	actin-related protein 3 [Sus scrofa] >gi|195562215|gb|ACG50179.1| actin-related protein 3-like protein [Sus scrofa]	1.498	1.237	1.031	1.763
gi|136192|sp|P09571.2|TRFE_PIG	RecName: Full=Serotransferrin; Short=Transferrin; AltName: Full=Beta-1 metal-binding globulin; AltName: Full=Siderophilin >gi|18655907|pdb|1H76|A Chain A, The Crystal Structure Of Diferric Porcine Serum Transferrin	0.803	0.46	0.442	0.476
gi|350591529|ref|XP_003483289.1|	PREDICTED: serotransferrin isoform 1 [Sus scrofa]				
gi|347582654|ref|NP_001231582.1|	serotransferrin precursor [Sus scrofa] >gi|350591531|ref|XP_003483290.1| PREDICTED: serotransferrin isoform 2 [Sus scrofa] >gi|189232884|emb|CAQ34904.1| transferrin [Sus scrofa]				
gi|833800|emb|CAA30943.1|	transferrin [Sus scrofa]				
gi|335281104|ref|XP_003353734.1|	PREDICTED: argininosuccinate synthase [Sus scrofa]	1.671	2.308	2.587	1.797
gi|47523456|ref|NP_999349.1|	serine/threonine-protein phosphatase PP1-beta catalytic subunit [Sus scrofa] >gi|47116968|sp|P61292.3|PP1B_PIG RecName: Full=Serine/threonine-protein phosphatase PP1-beta catalytic subunit;	1.843	1.251	1.257	1.937

	Short=PP-1B >gi|89257972|gb|ABD65256.1| protein phosphatase				
gi|113205690|ref|NP_001038024.1|	protein phosphatase 1 catalytic subunit alpha isoform [Sus scrofa] >gi|87621715|gb|ABD38708.1| protein phosphatase 1 catalytic subunit alpha isoform [Sus scrofa]				
gi|113205694|ref|NP_001038025.1|	protein phosphatase 1 catalytic subunit gamma isoform [Sus scrofa] >gi|87621736|gb|ABD38709.1| protein phosphatase 1 catalytic subunit gamma isoform [Sus scrofa]				
gi|335300836|ref|XP_003359054.1|	PREDICTED: ES1 protein homolog, mitochondrial-like [Sus scrofa]	0.485	1.208	0.769	1.133
gi|335280672|ref|XP_003353634.1|	PREDICTED: aldehyde dehydrogenase X, mitochondrial [Sus scrofa]	1.944	0.802	0.591	1.353
gi|311258550|ref|XP_003127676.1|	PREDICTED: EF-hand domain-containing protein D2-like [Sus scrofa]	0.429	0.804	0.768	0.614
gi|335300581|ref|XP_003358947.1|	PREDICTED: T-complex protein 1 subunit theta-like isoform 1 [Sus scrofa]	1.545	0.974	0.794	1.863
gi|335300583|ref|XP_003358948.1|	PREDICTED: T-complex protein 1 subunit theta-like isoform 2 [Sus scrofa]				
gi|335300585|ref|XP_003358949.1|	PREDICTED: T-complex protein 1 subunit theta-like isoform 3 [Sus scrofa]				
gi|47523680|ref|NP_999472.1|	10 kDa heat shock protein, mitochondrial [Sus scrofa] >gi|30525868|gb|AAP32465.1| heat shock 10kD protein [Sus scrofa]	0.739	2.1	0.843	0.766
gi|305855170|ref|NP_001182250.1|	long-chain-fatty-acid--CoA ligase 5 [Sus scrofa] >gi|285818418|gb|ADC38882.1| acyl-CoA synthetase long-chain family member 5 [Sus scrofa]	0.82	0.53	0.574	0.782
gi|350581487|ref|XP_003124444.3|	PREDICTED: 14-3-3 protein gamma-like [Sus scrofa]	2.892	1.76	1.578	2.189
gi|350587966|ref|XP_003482525.1|	PREDICTED: PDZ and LIM domain protein 5 isoform 3 [Sus scrofa]	0.779	1.597	1.479	1.14

gi|311257850|ref|XP_003127328.1|	PREDICTED: 17-beta-hydroxysteroid dehydrogenase 14-like [Sus scrofa]	1.285	0.541	0.462	0.492
gi|194043292|ref|XP_001928111.1|	PREDICTED: 14-3-3 protein eta [Sus scrofa]	3.227	1.275	1.172	2.33
gi|164507|gb|AAA51295.1|	immunoglobulin gamma-chain [Sus scrofa]	0.635	0.488	0.566	0.442
gi|122131841|sp|Q06A98.1|SRSF2_PIG	RecName: Full=Serine/arginine-rich splicing factor 2; AltName: Full=Splicing component, 35 kDa; AltName: Full=Splicing factor SC35; Short=SC-35; AltName: Full=Splicing factor, arginine/serine-rich 2 >gi|116175283|ref|NP_001070697.1| serine/arginine-	1.196	1.38	1.786	1.313
gi|1921|emb|CAA33169.1|	unnamed protein product [Sus scrofa]	0.735	0.558	0.573	0.786
gi|114313|sp|P11607.1|AT2A2_PIG	RecName: Full=Sarcoplasmic/endoplasmic reticulum calcium ATPase 2; Short=SERCA2; Short=SR Ca(2+)-ATPase 2; AltName: Full=Calcium pump 2; AltName: Full=Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform; AltN				
gi|47522682|ref|NP_999066.1|	propionyl-CoA carboxylase beta chain, mitochondrial precursor [Sus scrofa] >gi|6093657|sp|P79384.1|PCCB_PIG RecName: Full=Propionyl-CoA carboxylase beta chain, mitochondrial; Short=PCCase subunit beta; AltName: Full=Propanoyl-CoA:carbon dioxide liga	0.717	0.681	1.051	0.758
gi|311272700|ref|XP_003133549.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein A3-like isoform 1 [Sus scrofa]	1.347	0.704	0.642	1.203
gi|335303045|ref|XP_003359613.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein A3-like isoform 2 [Sus scrofa]				
gi|335291231|ref|XP_003356440.1|	PREDICTED: desmoglein-2 [Sus scrofa]	0.805	0.477	0.561	0.564

gi|116551|sp|P04404.2|CMGA_PIG	RecName: Full=Chromogranin-A; Short=CgA; Contains: RecName: Full=Pancreastatin; Contains: RecName: Full=Parastatin; Contains: RecName: Full=WE-14; Flags: Precursor >gi|164417|gb|AAA31016.1| chromogranin A precursor, partial [Sus scrofa]	0.486	0.982	0.552	0.599
gi|341823654|ref|NP_001157477.2|	chromogranin-A precursor [Sus scrofa]				
gi|335298834|ref|XP_003358406.1|	PREDICTED: leucine-rich repeat flightless-interacting protein 2 [Sus scrofa]	0.894	1.546	1.044	1.027
gi|50916342|gb|AAT88086.1|	heat shock protein 27kDa, partial [Sus scrofa]	0.746	1.031	1.13	1.143
gi|55926209|ref|NP_001007519.1|	heat shock protein beta-1 [Sus scrofa] >gi|75062102|sp|Q5S1U1.1|HSPB1_PIG RecName: Full=Heat shock protein beta-1; Short=HspB1; AltName: Full=Heat shock 27 kDa protein; Short=HSP 27 >gi|335284212|ref|XP_003354542.1| PREDICTED: heat shock protein bet				
gi|335284210|ref|XP_003354541.1|	PREDICTED: heat shock protein beta-1-like isoform 1 [Sus scrofa]				
gi|311272309|ref|XP_003133393.1|	PREDICTED: ADP/ATP translocase 1-like isoform 2 [Sus scrofa]	---	---	---	---
gi|251823933|ref|NP_001156532.1|	cadherin-1 precursor [Sus scrofa] >gi|209875157|gb|ACI94878.1| E-cadherin [Sus scrofa]	0.515	1.117	1.208	0.636
gi|350579011|ref|XP_003121807.3|	PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member A-like [Sus scrofa]	0.519	0.577	0.573	0.629
gi|45479844|gb|AAS66764.1|	histone H1.3-like protein [Sus scrofa]	---	---	---	---
gi|68534962|ref|NP_001020387.1|	histone H1.2-like protein [Sus scrofa] >gi|66775665|gb|AAY56388.1| histone H1.2-like protein [Sus scrofa]				
gi|45268981|gb|AAS55903.1|	60S ribosomal protein L12, partial [Sus scrofa]	0.878	0.609	0.594	0.987
gi|350579668|ref|XP_003480657.1|	PREDICTED: hypothetical protein LOC414416 [Sus scrofa]				

gi|350590640|ref|XP_003131788.3|	PREDICTED: myosin-Id [Sus scrofa]	0.75	0.444	0.53	0.597
gi|264681430|ref|NP_001161110.1|	3-ketoacyl-CoA thiolase, mitochondrial [Sus scrofa] >gi|262036903|dbj|BAI47587.1| acetyl-Coenzyme A acyltransferase 2 [Sus scrofa]	1.383	0.591	0.719	0.56
gi|335297068|ref|XP_001927259.3|	PREDICTED: CLYBL protein [Sus scrofa]	0.888	1.271	1.636	1.036
gi|350593495|ref|XP_003483700.1|	PREDICTED: LOW QUALITY PROTEIN: glycerol-3-phosphate dehydrogenase, mitochondrial [Sus scrofa]	0.709	0.479	0.534	0.518
gi|350588026|ref|XP_003129409.3|	PREDICTED: heterogeneous nuclear ribonucleoprotein D-like, partial [Sus scrofa]	0.889	1.523	0.997	1.46
gi|47523870|ref|NP_999573.1|	peroxiredoxin-6 [Sus scrofa] >gi|75074817|sp|Q9TSX9.3|PRDX6_PIG RecName: Full=Peroxiredoxin-6; AltName: Full=Non-selenium glutathione peroxidase; Short=NSGPx >gi|6689393|emb|CAB65456.1| non-selenium glutathione phospholipid hydroperoxide peroxidase	1.132	2.008	1.577	1.343
gi|190360593|ref|NP_001121945.1|	interferon-induced guanylate-binding protein 1 [Sus scrofa] >gi|166202346|gb|ABY84597.1| guanylate binding protein 1 [Sus scrofa]	0.933	0.844	0.731	1.258
gi|2500494|sp|Q29308.3|RS19_PIG	RecName: Full=40S ribosomal protein S19	0.747	0.585	0.525	0.846
gi|350585266|ref|XP_003127229.3|	PREDICTED: 40S ribosomal protein S19-like isoform 1 [Sus scrofa] >gi|350585268|ref|XP_003481921.1| PREDICTED: 40S ribosomal protein S19-like [Sus scrofa]				
gi|311267406|ref|XP_003131549.1|	PREDICTED: gasdermin-B-like [Sus scrofa]	1.558	1.337	1.747	2.213
gi|47523724|ref|NP_999497.1|	guanine nucleotide-binding protein subunit beta-2-like 1 [Sus scrofa] >gi|54037165|sp|P63246.3|GB	1.197	0.934	1.038	1.506

	LP_PIG RecName: Full=Guanine nucleotide-binding protein subunit beta-2-like 1; AltName: Full=Receptor for activated C kinase; AltName: Full=Receptor of				
gi|187373263|gb|ACD03295.1|	ISG15 ubiquitin-like modifier [Sus scrofa]	1.661	1.719	3.82	1.158
gi|298104082|ref|NP_001177109.1|	dynein light chain roadblock-type 1 [Sus scrofa]	0.847	2.213	3.05	1.09
gi|311266781|ref|XP_003131241.1|	PREDICTED: galactokinase-like [Sus scrofa]	1.426	0.926	0.906	1.083
gi|350585425|ref|XP_003127517.3|	PREDICTED: isochorismatase domain-containing protein 2, mitochondrial-like isoform 1, partial [Sus scrofa]	0.409	1.462	1.207	0.534
gi|346716265|ref|NP_001231271.1|	omega-amidase NIT2 [Sus scrofa]	1.536	1.113	0.832	1.558
gi|311260243|ref|XP_001927987.2|	PREDICTED: protein CutA isoform 1 [Sus scrofa]	0.621	2.449	1.975	0.951
gi|335292054|ref|XP_003356656.1|	PREDICTED: protein CutA [Sus scrofa]				
gi|335292058|ref|XP_003356658.1|	PREDICTED: protein CutA [Sus scrofa]				
gi|335292056|ref|XP_003356657.1|	PREDICTED: protein CutA [Sus scrofa]				
gi|37962872|gb|AAR05785.1|	cytochrome c oxidase subunit 2 [Sus scrofa] >gi|162423271|gb|ABX89412.1| cytochrome c oxidase subunit 2 [Sus scrofa]	0.868	0.423	0.338	0.684
gi|342316093|gb|ABF56563.2|	cytochrome c oxidase subunit II [Sus scrofa]				
gi|347802433|gb|AEP22017.1|	cytochrome c oxidase subunit II (mitochondrion) [Potamochoerus porcus]				
gi|306485877|gb|ABF49552.2|	cytochrome c oxidase subunit II [Sus scrofa]				
gi|312233367|ref|YP_004021578.1|	cytochrome c oxidase subunit II [Sus scrofa taiwanensis] >gi|317054710|ref|YP_002600780.2| cytochrome c oxidase subunit II [Sus scrofa domesticus] >gi|124358980|ref|YP_0				

	01023766.1| cytochrome c oxidase subunit II [Phacochoerus africanus] >gi|5835866				
gi|157056539|gb|ABV02170.1|	cytochrome c oxidase subunit 2 [Sus scrofa]				
gi|145315754|gb|ABP63291.1|	cytochrome c oxidase subunit II [Sus scrofa]				
gi|157056524|gb|ABV02156.1|	cytochrome c oxidase subunit 2 [Sus scrofa]				
gi|45826173|gb|AAS77694.1|	cytochrome c oxidase subunit 2 [Sus scrofa]				
gi|311252952|ref|XP_003125350.1|	PREDICTED: ketohexokinase-like isoform 3 [Sus scrofa]	0.538	0.556	0.633	0.506
gi|311252954|ref|XP_003125348.1|	PREDICTED: ketohexokinase-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350592835|ref|XP_003483550.1|	PREDICTED: protein transport protein Sec24C isoform 2 [Sus scrofa]				
gi|2497487|sp|Q29561.1|KCY_PIG	RecName: Full=UMP-CMP kinase; AltName: Full=Cytidine monophosphate kinase; AltName: Full=Cytidylate kinase; AltName: Full=Deoxycytidylate kinase; AltName: Full=Uridine monophosphate kinase; AltName: Full=Uridine monophosphate/cytidine monophosphate	0.913	1.002	0.698	0.736
gi|350586231|ref|XP_003128059.3|	PREDICTED: UMP-CMP kinase-like [Sus scrofa]				
gi|335309657|ref|XP_003361720.1|	PREDICTED: 14-3-3 protein epsilon-like [Sus scrofa]	1.488	0.899	0.78	1.393
gi|350579445|ref|XP_003480606.1|	PREDICTED: protein NipSnap homolog 3A-like [Sus scrofa]	0.842	1.427	1.801	0.984
gi|640352|pdb|3MDE|A	Chain A, Crystal Structures Of Medium Chain Acyl-Coa Dehydrogenase From Pig Liver Mitochondria With And Without Substrate >gi|640350|pdb|3MDD|A Chain A, Crystal Structures Of Medium Chain Acyl-Coa Dehydrogenase From Pig Liver Mitochondria With And W	1.391	0.684	0.685	0.883

gi|148872486|sp|P41367.3|ACADM_PIG	RecName: Full=Medium-chain specific acyl-CoA dehydrogenase, mitochondrial; Short=MCAD; Flags: Precursor >gi|56791886|gb|AAW30430.1| medium-chain acyl-coA dehydrogenase [Sus scrofa]				
gi|40889737|pdb|1UDY|D	Chain D, Medium-Chain Acyl-Coa Dehydrogenase With 3-Thiaoctanoyl-Coa >gi|40889735|pdb|1UDY|B Chain B, Medium-Chain Acyl-Coa Dehydrogenase With 3-Thiaoctanoyl-Coa >gi|40889736|pdb|1UDY|C Chain C, Medium-Chain Acyl-Coa Dehydrogenase With 3-Thiaoctanoy				
gi|47522898|ref|NP_999204.1|	medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|1127798|gb|AAA83759.1| medium-chain acyl-CoA dehydrogenase [Sus scrofa]				
gi|325652098|ref|NP_001191688.1|	nucleoside diphosphate kinase A [Sus scrofa]	0.73	1.65	1.102	0.703
gi|194037373|ref|XP_001927584.1|	PREDICTED: coatomer subunit zeta-1 isoform 1 [Sus scrofa]	1.781	1.371	1.598	1.578
gi|311244862|ref|XP_001925828.2|	PREDICTED: huntingtin-interacting protein K-like [Sus scrofa]	0.776	1.342	1.28	0.902
gi|311277261|ref|XP_003135572.1|	PREDICTED: 55 kDa erythrocyte membrane protein-like isoform 1 [Sus scrofa]	0.801	0.558	0.535	0.811
gi|47523516|ref|NP_999381.1|	inositol monophosphatase 1 [Sus scrofa] >gi|68568737|sp|O77591.1|IMPA1_PIG RecName: Full=Inositol monophosphatase 1; Short=IMP 1; Short=IMPase 1; AltName: Full=Inositol-1(or 4)-monophosphatase 1; AltName: Full=Lithium-sensitive myo-inositol monophos	1.006	2.592	2.528	1.676
gi|194038734|ref|XP_001929226.1|	PREDICTED: protein transport protein Sec23A isoform 2 [Sus scrofa]	1.655	0.875	0.634	1.202
gi|6435805|pdb|3HDH|B	Chain B, Pig Heart Short Chain	0.962	0.465	0.228	0.846

	L-3-Hydroxyacyl Coa Dehydrogenase Revisited: Sequence Analysis And Crystal Structure Determination >gi|6435806|pdb|3HDH|C Chain C, Pig Heart Short Chain L-3-Hydroxyacyl Coa Dehydrogenase Revisited: Sequence Analysis An				
gi|47523722|ref|NP_999496.1|	hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|7404364|sp|P00348.2|HCDH_PIG RecName: Full=Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial; Short=HCDH; AltName: Full=Medium and short-chain L-3-hydroxyacyl-coenzyme				
gi|311275164|ref|XP_003134601.1|	PREDICTED: amiloride-sensitive amine oxidase [copper-containing] [Sus scrofa]	0.807	0.699	0.984	0.858
gi|164557|gb|AAA31078.1|	MHC PD14 transplantation antigen [Sus scrofa]	2.698	1.722	3.598	1.878
gi|164558|gb|AAA31079.1|	MHC PD14a transplantation antigen [Sus scrofa]				
gi|47523822|ref|NP_999549.1|	glutamate carboxypeptidase 2 [Sus scrofa] >gi|20138100|sp|O77564.1|FOLH1_PIG RecName: Full=Glutamate carboxypeptidase 2; AltName: Full=Folate hydrolase 1; AltName: Full=Folylpoly-gamma-glutamate carboxypeptidase; Short=FGCP; AltName: Full=Glutamate	1.112	2.071	2.577	1.21
gi|116175265|ref|NP_001070688.1|	regucalcin [Sus scrofa] >gi|122131846|sp|Q06AA3.1|RGN_PIG RecName: Full=Regucalcin; Short=RC; AltName: Full=Gluconolactonase; Short=GNL; AltName: Full=Senescence marker protein 30; Short=SMP-30 >gi|115371745|gb|ABI96197.1| SMP-30 [Sus scrofa]	1.624	1.934	2.09	1.639
gi|335305927|ref|XP_003360	PREDICTED: regucalcin-like				

333.1|	isoform 2 [Sus scrofa] >gi|335305929|ref|XP_003135107.2| PREDICTED: regucalcin-like isoform 1 [Sus scrofa]				
gi|311248380|ref|XP_003123108.1|	PREDICTED: cyclic AMP-responsive element-binding protein 3-like protein 3-like isoform 1 [Sus scrofa]	1.073	0.511	0.489	0.485
gi|311248382|ref|XP_003123109.1|	PREDICTED: cyclic AMP-responsive element-binding protein 3-like protein 3-like isoform 2 [Sus scrofa]				
gi|335299760|ref|XP_003358667.1|	PREDICTED: neprilysin isoform 2 [Sus scrofa] >gi|311269573|ref|XP_003132549.1| PREDICTED: neprilysin isoform 1 [Sus scrofa]	0.571	0.385	0.373	0.435
gi|311258794|ref|XP_003127785.1|	PREDICTED: sphingomyelin phosphodiesterase, acid-like 3B [Sus scrofa]	0.849	1.649	1.632	0.918
gi|11641132|gb|AAG38247.1|	cyclophilin [Sus scrofa]	---	---	---	---
gi|335282345|ref|XP_003354038.1|	PREDICTED: mitochondrial import inner membrane translocase subunit Tim13-like [Sus scrofa]	1.78	2.187	2.239	1.616
gi|345441801|ref|NP_001230874.1|	TNF receptor-associated protein 1 [Sus scrofa]	1.932	0.894	0.943	1.689
gi|350539097|ref|NP_001233144.1|	ubiquitin/ISG15-conjugating enzyme E2 L6 [Sus scrofa] >gi|332113317|gb|AEE02035.1| ubiquitin-conjugating enzyme E2L 6 [Sus scrofa]	1.621	1.36	2.399	1.698
gi|194036918|ref|XP_001928194.1|	PREDICTED: thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1-like [Sus scrofa]	0.678	2.719	2.204	1.842
gi|350584866|ref|XP_003355801.2|	PREDICTED: Golgi apparatus protein 1-like isoform 1 [Sus scrofa]	0.976	0.826	1.083	0.867
gi|350584868|ref|XP_003481837.1|	PREDICTED: Golgi apparatus protein 1-like isoform 2 [Sus scrofa]				
gi|194042126|ref|XP_001928377.1|	PREDICTED: eukaryotic translation initiation factor 3 subunit A [Sus scrofa]	0.9	1.082	0.968	1.434

gi|194034199|ref|XP_001928042.1|	PREDICTED: proteasome subunit alpha type-3 isoform 2 [Sus scrofa]	1.08	2.055	1.906	1.477
gi|194034201|ref|XP_001928025.1|	PREDICTED: proteasome subunit alpha type-3 isoform 1 [Sus scrofa]				
gi|21954744|gb|AAM83105.1|AF525487_1	Ran [Sus scrofa]	1.757	0.822	0.618	1.618
gi|194043605|ref|XP_001925468.1|	PREDICTED: GTP-binding nuclear protein Ran [Sus scrofa]				
gi|194038542|ref|XP_001929208.1|	PREDICTED: methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial [Sus scrofa]	1.593	0.928	0.929	1.458
gi|322510017|sp|Q007T2.2|CDC42_PIG	RecName: Full=Cell division control protein 42 homolog; Flags: Precursor >gi|269994011|dbj|BAI50642.1| Cell division control protein 42 homolog [Sus scrofa]	1.125	0.764	0.921	1.172
gi|346421347|ref|NP_001231022.1|	glucosamine-6-phosphate isomerase 1 [Sus scrofa]	0.958	1.649	1.438	1.064
gi|335310032|ref|XP_003126353.2|	PREDICTED: dynactin subunit 2-like isoform 3 [Sus scrofa]	1.748	1.035	0.915	1.093
gi|350584186|ref|XP_003126370.2|	PREDICTED: dynactin subunit 2-like [Sus scrofa]				
gi|311247963|ref|XP_003122904.1|	PREDICTED: apoptosis inhibitor 5 isoform 1 [Sus scrofa]	0.895	0.634	0.736	0.863
gi|350594828|ref|XP_003134450.3|	PREDICTED: charged multivesicular body protein 4b-like [Sus scrofa]	1.599	0.904	1.138	0.787
gi|85542092|sp|Q2YGT9.3|RL6_PIG	RecName: Full=60S ribosomal protein L6 >gi|113205608|ref|NP_001038007.1| 60S ribosomal protein L6 [Sus scrofa] >gi|56384243|gb|AAV85770.1| ribosomal protein L6 [Sus scrofa]	0.806	0.295	0.432	0.89
gi|335300802|ref|XP_003359038.1|	PREDICTED: 6-phosphofructokinase, liver type-like [Sus scrofa]	1.026	0.859	0.933	1.51
gi|239977642|sp|Q29183.1|TFF3_PIG	RecName: Full=Trefoil factor 3; AltName: Full=Intestinal trefoil factor; Flags: Precursor	0.853	4.328	3.069	1.667
gi|343478295|ref|NP_001230412.1|	trefoil factor 3 (intestinal) precursor [Sus scrofa]				
gi|350592195|ref|XP_003483	PREDICTED: trefoil factor 3-like,				

<table>
<tr><td>413.1|</td><td>partial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|262072939|dbj|BAI47777.1|</td><td>CCHC-type zinc finger, nucleic acid binding protein [Sus scrofa]</td><td>1.38</td><td>2.221</td><td>1.925</td><td>2.168</td></tr>
<tr><td>gi|47523464|ref|NP_999353.1|</td><td>dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor [Sus scrofa] >gi|218511750|sp|Q29381.2|OST48_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit; Short=DDOST 48 kDa</td><td>0.753</td><td>0.525</td><td>1.151</td><td>0.715</td></tr>
<tr><td>gi|113205874|ref|NP_001038071.1|</td><td>ATP synthase subunit O, mitochondrial precursor [Sus scrofa] >gi|122145941|sp|Q2EN81.1|ATPO_PIG RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor >gi|87047636|gb</td><td>1.062</td><td>0.495</td><td>0.536</td><td>0.661</td></tr>
<tr><td>gi|311265228|ref|XP_003130565.1|</td><td>PREDICTED: LOW QUALITY PROTEIN: bifunctional aminoacyl-tRNA synthetase [Sus scrofa]</td><td>0.783</td><td>0.898</td><td>0.846</td><td>1.048</td></tr>
<tr><td>gi|350591601|ref|XP_003132498.3|</td><td>PREDICTED: sodium/potassium-transporting ATPase subunit beta-3-like [Sus scrofa]</td><td>0.747</td><td>0.364</td><td>0.396</td><td>0.531</td></tr>
<tr><td>gi|335309396|ref|XP_003361623.1|</td><td>PREDICTED: adenylate kinase 2, mitochondrial-like isoform 1 [Sus scrofa]</td><td>2.203</td><td>1.887</td><td>1.877</td><td>1.706</td></tr>
<tr><td>gi|385862179|ref|NP_001245364.1|</td><td>protein diaphanous homolog 1 [Sus scrofa]</td><td>0.625</td><td>0.552</td><td>0.764</td><td>0.564</td></tr>
<tr><td>gi|350587405|ref|XP_003482406.1|</td><td>PREDICTED: cytosolic beta-glucosidase-like, partial [Sus scrofa]</td><td>1.402</td><td>0.973</td><td>0.831</td><td>1.198</td></tr>
<tr><td>gi|350597193|ref|XP_003484383.1|</td><td>PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase B [Sus scrofa]</td><td>0.394</td><td>1.723</td><td>0.922</td><td>0.958</td></tr>
<tr><td>gi|47523762|ref|NP_999517.1|</td><td>plasma membrane calcium-transporting ATPase 1 [Sus scrofa] >gi|114319|sp|P23220.1|AT2B1_PIG RecName: Full=Plasma</td><td>0.673</td><td>0.627</td><td>0.775</td><td>0.857</td></tr>
</table>

	membrane calcium-transporting ATPase 1; Short=PMCA1; AltName: Full=Plasma membrane calcium pump isoform 1 >gi|2061|emb|CAA37536.1| plasm				
gi|194038540|ref|XP_001929175.1|	PREDICTED: ectonucleoside triphosphate diphosphohydrolase 5 [Sus scrofa]	0.769	0.948	0.509	1.118
gi|350579385|ref|XP_001925894.4|	PREDICTED: glyoxylate reductase/hydroxypyruvate reductase [Sus scrofa]	0.895	0.493	0.623	0.64
gi|343780941|ref|NP_001230485.1|	prohibitin 2 [Sus scrofa]	1.815	0.803	0.787	1.352
gi|311275457|ref|XP_003134747.1|	PREDICTED: filamin-C isoform 1 [Sus scrofa]	---	---	---	---
gi|311275463|ref|XP_003134750.1|	PREDICTED: filamin-C isoform 4 [Sus scrofa]				
gi|335305357|ref|XP_003360191.1|	PREDICTED: filamin-C [Sus scrofa]				
gi|311275461|ref|XP_003134749.1|	PREDICTED: filamin-C isoform 3 [Sus scrofa]				
gi|311275459|ref|XP_003134748.1|	PREDICTED: filamin-C isoform 2 [Sus scrofa]				
gi|164505|gb|AAA51294.1|	immunoglobulin gamma-chain, partial [Sus scrofa]	0.237	0.099	0.217	0.183
gi|433128|gb|AAA52219.1|	Ig gamma 1a chain constant region [Sus scrofa] >gi|2136515|pir||I47161 Ig gamma 3 chain constant region - pig (fragment)				
gi|47523192|ref|NP_998993.1|	IgG heavy chain precursor [Sus scrofa] >gi|5052050|gb|AAD38418.1|AF062384_1 IgG heavy chain precursor [Sus scrofa]				
gi|159138024|gb|ABW89018.1|	immunoglobulin heavy chain gamma constant region [Sus scrofa]				
gi|433122|gb|AAA52216.1|	Ig gamma 1b chain constant region [Sus scrofa] >gi|2136512|pir||I47158 Ig gamma 1 chain constant region - pig (fragment)				
gi|227130|prf||1614425A	chymodenin	0.452	0.325	0.286	0.294
gi|311262177|ref|XP_003129051.1|	PREDICTED: electron transfer flavoprotein-ubiquinone	0.626	0.679	0.626	0.498

	oxidoreductase, mitochondrial-like [Sus scrofa]				
gi|197251934|ref|NP_001127826.1|	actin-related protein 2 [Sus scrofa] >gi|195562213|gb|ACG50178.1| actin-related protein 2-like protein [Sus scrofa]	1.397	0.5	0.574	1.417
gi|78172717|gb|ABB29449.1|	transporter associated with antigen processing 1 [Sus scrofa]	0.541	0.382	0.447	0.711
gi|350586535|ref|XP_003128377.3|	PREDICTED: antigen peptide transporter 1 isoform 1 [Sus scrofa]				
gi|147225183|emb|CAN13315.1|	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Sus scrofa]				
gi|113205778|ref|NP_001038046.1|	antigen peptide transporter 1 [Sus scrofa] >gi|78172715|gb|ABB29448.1| transporter associated with antigen processing 1 [Sus scrofa]				
gi|311252239|ref|XP_003124992.1|	PREDICTED: all-trans-retinol 13,14-reductase [Sus scrofa]	0.52	0.2	0.307	0.231
gi|335293373|ref|XP_003356947.1|	PREDICTED: UDP-glucose 6-dehydrogenase-like isoform 1 [Sus scrofa]	1.734	1.612	1.136	1.981
gi|350580651|ref|XP_003480867.1|	PREDICTED: scaffold attachment factor B1-like isoform 2 [Sus scrofa]	0.687	1.076	0.762	0.763
gi|350580653|ref|XP_003354065.2|	PREDICTED: scaffold attachment factor B1-like isoform 1 [Sus scrofa]				
gi|194041736|ref|XP_001927852.1|	PREDICTED: fucose mutarotase isoform 1 [Sus scrofa]	2.396	1.735	1.948	1.845
gi|311272085|ref|XP_003133293.1|	PREDICTED: fucose mutarotase isoform 2 [Sus scrofa]				
gi|194038586|ref|XP_001926746.1|	PREDICTED: transmembrane emp24 domain-containing protein 10 [Sus scrofa]	0.582	0.399	0.461	0.628
gi|72535208|ref|NP_001026966.1|	2~-5~-oligoadenylate synthase 2 [Sus scrofa] >gi|45594389|gb|AAQ22351.1| 2~-5~ oligoadenylate synthetase 2 [Sus scrofa]	1.025	0.661	0.815	0.993
gi|85687558|sp|Q4A3R3.1|DMBT1_PIG	RecName: Full=Deleted in malignant brain tumors 1 protein; AltName: Full=Hensin; Flags: Precursor >gi|73531021|emb|CAJ27171.1| DMBT1 protein [Sus scrofa]	0.397	0.523	0.555	0.462

gi|114703738|ref|NP_001041653.1|	deleted in malignant brain tumors 1 protein precursor [Sus scrofa] >gi|110431268|emb|CAJ14977.1| deleted in malignant brain tumors 1 protein [Sus scrofa]				
gi|311246094|ref|XP_001924927.2|	PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member B [Sus scrofa]	0.936	0.598	0.775	1.029
gi|298104076|ref|NP_001177104.1|	enoyl-CoA hydratase, mitochondrial [Sus scrofa]	1.176	0.473	0.43	0.891
gi|350596379|ref|XP_003484266.1|	PREDICTED: vesicle-trafficking protein SEC22b-like [Sus scrofa] >gi|350583458|ref|XP_003481524.1| PREDICTED: vesicle-trafficking protein SEC22b [Sus scrofa]	0.749	0.447	0.474	0.538
gi|350582129|ref|XP_003354780.2|	PREDICTED: ig kappa chain V-II region RPMI 6410-like [Sus scrofa]	0.919	1.388	1.364	0.923
gi|350592539|ref|XP_003483482.1|	PREDICTED: translational activator GCN1, partial [Sus scrofa]	---	---	---	---
gi|17432930|sp|Q9N2I1.1|CASP1_PIG	RecName: Full=Caspase-1; Short=CASP-1; AltName: Full=Interleukin-1 beta convertase; Short=IL-1BC; AltName: Full=Interleukin-1 beta-converting enzyme; Short=ICE; Short=IL-1 beta-converting enzyme; AltName: Full=p45; Contains: RecName: Full=Caspase-1	2.442	1.382	1.594	1.486
gi|340007402|ref|NP_001229989.1|	RAB10, member RAS oncogene family [Sus scrofa]	0.916	0.388	0.456	0.797
gi|212549623|ref|NP_001131101.1|	endoplasmic reticulum resident protein 44 precursor [Sus scrofa] >gi|187480160|gb|ACD13000.1| thioredoxin domain-containing 4 [Sus scrofa]	1.194	0.716	0.968	1.059
gi|229620|prf||770227A	dehydrogenase H4,lactate	2.789	2.491	1.866	3.254
gi|56792866|gb|AAW30628.1|	unknown [Sus scrofa]				
gi|282403837|pdb|5LDH|A	Chain A, Structure Of The Active Ternary Complex Of Pig Heart Lactate Dehydrogenase With S-Lac-Nad At 2.7 Angstroms				

	Resolution >gi|282403838|pdb|5LDH|B Chain B, Structure Of The Active Ternary Complex Of Pig Heart Lactate Dehydrogenase With S-Lac-Na				
gi|56792857|gb|AAW30625.1|	unknown, partial [Sus scrofa] >gi|56792872|gb|AAW30630.1| unknown [Sus scrofa]				
gi|164518958|ref|NP_001106758.1|	L-lactate dehydrogenase B chain [Sus scrofa] >gi|1170738|sp|P00336.3|LDHB_PIG RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B; AltName: Full=LDH heart subunit; Short=LDH-H >gi|473575|gb|AAA50438.1| lactate dehydrogenase-B [Sus scrofa dome				
gi|194044035|ref|XP_001928829.1|	PREDICTED: splicing factor 3B subunit 1 isoform 1 [Sus scrofa]	0.537	0.939	0.99	1.072
gi|350582773|ref|XP_003481353.1|	PREDICTED: 40S ribosomal protein S7-like isoform 2 [Sus scrofa] >gi|350582771|ref|XP_003481352.1| PREDICTED: 40S ribosomal protein S7-like isoform 1 [Sus scrofa]	0.624	0.404	0.255	0.765
gi|335309199|ref|XP_003361534.1|	PREDICTED: AP-1 complex subunit sigma-1A-like [Sus scrofa]	0.824	0.539	0.476	0.893
gi|298160923|ref|NP_001177141.1|	DDRGK domain-containing protein 1 [Sus scrofa]	0.358	0.749	0.594	0.461
gi|2498311|sp|Q28943.1|DPYD_PIG	RecName: Full=Dihydropyrimidine dehydrogenase [NADP(+)]; Short=DHPDHase; Short=DPD; AltName: Full=Dihydrothymine dehydrogenase; AltName: Full=Dihydrouracil dehydrogenase; Flags: Precursor >gi|47522904|ref|NP_999209.1| dihydropyrimidine dehydrogenase	1.144	1.171	1.04	1.431
gi|20663678|pdb|1GTH|D	Chain D, Dihydropyrimidine Dehydrogenase (Dpd) From Pig, Ternary Complex With Nadph And 5-Iodouracil >gi|20663676|pdb|1GTH|B Chain B, Dihydropyrimidine				

	Dehydrogenase (Dpd) From Pig, Ternary Complex With Nadph And 5-Iodouracil >gi|20663644|pdb|1GTE|D				
gi|13399653|pdb|1H7X|C	Chain C, Dihydropyrimidine Dehydrogenase (Dpd) From Pig, Ternary Complex Of A Mutant Enzyme (C671a), Nadph And 5-Fluorouracil >gi|13399651|pdb|1H7X|A Chain A, Dihydropyrimidine Dehydrogenase (Dpd) From Pig, Ternary Complex Of A Mutant Enzyme (C671a				
gi|350591497|ref|XP_003483284.1|	PREDICTED: ras-related protein Rab-7a-like [Sus scrofa]	0.731	0.453	0.527	0.729
gi|190360663|ref|NP_001121949.1|	FYVE and coiled-coil domain-containing protein 1 [Sus scrofa] >gi|41688293|dbj|BAD08647.1| FYVE and coiled-coil domain containing 1 [Sus scrofa]	0.991	0.625	1.214	0.925
gi|194042806|ref|XP_001927837.1|	PREDICTED: annexin A7 isoform 1 [Sus scrofa]	0.478	1.169	1.679	1.453
gi|335301795|ref|XP_003359285.1|	PREDICTED: annexin A7 [Sus scrofa]				
gi|194038359|ref|XP_001929028.1|	PREDICTED: glutaredoxin-related protein 5, mitochondrial-like [Sus scrofa]	1.169	0.703	0.919	0.677
gi|148235351|ref|NP_001090944.1|	NADH dehydrogenase ubiquinone flavoprotein 2 [Sus scrofa] >gi|117660947|gb|ABK55646.1| NDUFV2 [Sus scrofa]	0.501	0.531	0.567	0.591
gi|335287837|ref|XP_001926233.3|	PREDICTED: prefoldin subunit 5-like isoform 1 [Sus scrofa]	1.066	2.467	2.792	1.805
gi|343790920|ref|NP_001230517.1|	fumarate hydratase [Sus scrofa]	1.509	0.966	0.89	1.303
gi|297747368|ref|NP_001172101.1|	ubiquinol-cytochrome c reductase binding protein [Sus scrofa]	0.352	0.887	1.053	0.506
gi|350591701|ref|XP_003132571.3|	PREDICTED: Golgi integral membrane protein 4 [Sus scrofa]	---	---	---	---
gi|350583385|ref|XP_001927905.3|	PREDICTED: tuftelin, partial [Sus scrofa]	0.927	0.974	1.298	0.546
gi|350589959|ref|XP_003482	PREDICTED: LIM domain only	0.679	1.532	1.067	0.786

961.1|	protein 7-like [Sus scrofa]				
gi|350585977|ref|XP_003127887.3|	PREDICTED: erythrocyte membrane protein band 4.1-like 3 [Sus scrofa]	0.659	0.795	0.953	0.92
gi|335281676|ref|XP_003353867.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein U-like 2 [Sus scrofa]	1.432	0.889	1.03	1.367
gi|350578507|ref|XP_003121503.3|	PREDICTED: asparaginyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]	1.923	1.266	1.484	1.92
gi|335281552|ref|XP_003122601.2|	PREDICTED: EH domain-containing protein 1 [Sus scrofa]	1.348	2.254	2.244	1.547
gi|312062805|ref|NP_001185852.1|	chloride intracellular channel protein 5 [Sus scrofa] >gi|197361201|gb|ACH70136.1| chloride intracellular channel 5 [Sus scrofa]	2.034	0.871	1	1.572
gi|346716348|ref|NP_001231189.1|	arginine--tRNA ligase, cytoplasmic [Sus scrofa]	1.61	0.986	0.841	1.429
gi|335309827|ref|XP_003361787.1|	PREDICTED: nuclear autoantigenic sperm protein, partial [Sus scrofa]	1.435	2.468	1.368	2.088
gi|335288150|ref|XP_003126347.2|	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus scrofa]	0.776	0.558	0.53	0.707
gi|335294978|ref|XP_003357366.1|	PREDICTED: coatomer subunit delta isoform 1 [Sus scrofa]	0.933	0.878	0.796	1.047
gi|47523744|ref|NP_999507.1|	serine/threonine-protein kinase OSR1 [Sus scrofa] >gi|73621342|sp|Q863I2.1|OXSR1_PIG RecName: Full=Serine/threonine-protein kinase OSR1; AltName: Full=Oxidative stress-responsive 1 protein >gi|30525874|gb|AAP32466.1| oxidative-stress responsive 1 [S	0.723	0.654	0.991	0.473
gi|113205586|ref|NP_001038000.1|	26S proteasome non-ATPase regulatory subunit 4 [Sus scrofa] >gi|55983054|gb|AAV69969.1| proteasome 26S subunit non-ATPase 4 [Sus scrofa]	0.572	0.843	1.19	0.746
gi|158514030|sp|A1XQU3.1|RL14_PIG	RecName: Full=60S ribosomal protein L14 >gi|148237282|ref|NP_001090947.1| 60S ribosomal protein L14 [Sus	1.034	0.626	0.479	0.855

	scrofa] >gi|117661006|gb|ABK55649.1| RPL14 [Sus scrofa]				
gi|350586418|ref|XP_001929155.3|	PREDICTED: GMP reductase 1 [Sus scrofa]	---	---	---	---
gi|350587731|ref|XP_003357047.2|	PREDICTED: LPS-responsive vesicle trafficking, beach and anchor containing, partial [Sus scrofa]	0.695	0.477	0.325	0.352
gi|350595424|ref|XP_003484107.1|	PREDICTED: chromobox protein homolog 3-like isoform 2 [Sus scrofa] >gi|350595422|ref|XP_003360239.2| PREDICTED: chromobox protein homolog 3-like isoform 1 [Sus scrofa]	1.138	2.126	2.251	1.606
gi|311255888|ref|XP_003126410.1|	PREDICTED: cullin-associated NEDD8-dissociated protein 1-like [Sus scrofa]	1.43	0.839	0.627	0.959
gi|350584746|ref|XP_003481817.1|	PREDICTED: cullin-associated NEDD8-dissociated protein 1 [Sus scrofa]				
gi|330688410|ref|NP_001193464.1|	actin related protein 2/3 complex, subunit 4 [Sus scrofa] >gi|195562233|gb|ACG50184.1| actin related protein 2/3 complex subunit 4 [Sus scrofa]	1.832	0.682	0.707	1.312
gi|350581241|ref|XP_003124117.3|	PREDICTED: leucyl-tRNA synthetase, cytoplasmic [Sus scrofa]	46.169	0.722	1.086	1.314
gi|335310669|ref|XP_003362140.1|	PREDICTED: hypothetical protein LOC100622909 [Sus scrofa]	0.605	0.902	0.685	0.684
gi|350590115|ref|XP_003131204.3|	PREDICTED: RING finger protein 213-like, partial [Sus scrofa]	1.242	0.866	0.787	1.607
gi|89573899|gb|ABD77175.1|	ribosomal protein L18 [Sus scrofa]	0.92	0.907	0.779	1.498
gi|335289913|ref|XP_003356019.1|	PREDICTED: 60S ribosomal protein L18 isoform 2 [Sus scrofa] >gi|335289911|ref|XP_003356018.1| PREDICTED: 60S ribosomal protein L18 isoform 1 [Sus scrofa]				
gi|335289915|ref|XP_003356020.1|	PREDICTED: 60S ribosomal protein L18 isoform 3 [Sus scrofa]				
gi|22770997|gb|AAN06824.1|	thioredoxin reductase [Sus scrofa]	2.086	1.864	1.576	2.294
gi|255918208|ref|NP_999319.2|	thioredoxin reductase 1, cytoplasmic [Sus scrofa]				
gi|194036302|ref|XP_001926	PREDICTED: histone H2A type	0.779	1.057	1.179	0.893

704.1|	2-B-like [Sus scrofa]				
gi|194039746|ref|XP_001925399.1|	PREDICTED: histone H2A type 1-A-like [Sus scrofa]				
gi|335294990|ref|XP_003129998.2|	PREDICTED: histone H2A.x-like [Sus scrofa]				
gi|350595677|ref|XP_003360362.2|	PREDICTED: GRIP1-associated protein 1 [Sus scrofa]	0.784	1.938	1.963	0.87
gi|311258910|ref|XP_003127843.1|	PREDICTED: splicing factor 3A subunit 3 isoform 1 [Sus scrofa]	0.817	0.532	0.761	1.035
gi|335291009|ref|XP_003356364.1|	PREDICTED: splicing factor 3A subunit 3 isoform 2 [Sus scrofa]				
gi|350594057|ref|XP_003359743.2|	PREDICTED: leucine-rich repeat flightless-interacting protein 2-like [Sus scrofa]	0.725	0.781	1.048	0.688
gi|350596308|ref|XP_003361027.2|	PREDICTED: leucine-rich repeat flightless-interacting protein 2-like [Sus scrofa]				
gi|58801555|ref|NP_001011727.1|	adenosylhomocysteinase [Sus scrofa] >gi|61216107|sp|Q710C4.3|SAHH_PIG RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase >gi|40644231|emb|CAD20603.1| S-adenosylhomocysteine hydrolase [Sus scrofa]	1.846	1.077	1.022	1.112
gi|262036923|dbj|BAI47597.1|	adenosylhomocysteinase [Sus scrofa] >gi|67513973|dbj|BAD99576.1| S-adenosylhomocysteine hydrolase [Sus scrofa]				
gi|347300360|ref|NP_001231474.1|	serine/arginine repetitive matrix protein 2 [Sus scrofa]	0.351	0.966	0.517	0.477
gi|335279750|ref|XP_003353424.1|	PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 2 [Sus scrofa] >gi|194034801|ref|XP_001925712.1| PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 1 [Sus scrofa]	0.512	0.43	0.425	0.466
gi|335282347|ref|XP_003354039.1|	PREDICTED: lamin-B2 [Sus scrofa]	0.704	0.775	0.682	0.731
gi|75054313|sp|Q8WNW3.1|	RecName: Full=Junction	1.027	1.124	0.855	1.047

PLAK_PIG	plakoglobin >gi|47523712|ref|NP_999488.1| junction plakoglobin [Sus scrofa] >gi|218103017|emb|CAT82339.1| unnamed protein product [Sus scrofa] >gi|211637711|emb|CAR97094.1| unnamed protein product [Sus scrofa] >gi|158065996|em				
gi|335294095|ref|XP_003357133.1|	PREDICTED: phosphatidylinositol N-acetylglucosaminyltransferase subunit Y-like isoform 2 [Sus scrofa]	0.198	1.244	0.789	0.539
gi|346644830|ref|NP_001231167.1|	sulfide:quinone oxidoreductase, mitochondrial [Sus scrofa]	0.889	0.519	0.467	0.803
gi|350578685|ref|XP_003480424.1|	PREDICTED: sulfide:quinone oxidoreductase, mitochondrial-like [Sus scrofa]				
gi|311275515|ref|XP_003134775.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5-like [Sus scrofa]	0.491	0.657	0.595	0.425
gi|91208342|sp|Q4FAT7.1|BGLR_PIG	RecName: Full=Beta-glucuronidase; Flags: Precursor >gi|178056516|ref|NP_001116593.1| beta-glucuronidase precursor [Sus scrofa] >gi|69146955|gb|AAZ03639.1| beta-glucuronidase [Sus scrofa]	1.038	1.395	1.756	1.38
gi|147899784|ref|NP_001090887.1|	elongation factor 1-alpha 1 [Sus scrofa] >gi|223019599|emb|CAX36487.1| eukaryotic translation elongation factor 1 alpha 1 [Sus scrofa] >gi|223019597|emb|CAX36486.1| eukaryotic translation elongation factor 1 alpha 1 [Sus scrofa] >gi|110287842|gb|ABG	0.764	0.57	0.438	0.68
gi|350582040|ref|XP_003481180.1|	PREDICTED: U5 small nuclear ribonucleoprotein 200 kDa helicase-like [Sus scrofa]	1.299	0.968	0.982	0.974
gi|311255145|ref|XP_001926338.2|	PREDICTED: thiosulfate sulfurtransferase [Sus scrofa]	1.947	0.819	1.357	1.494
gi|122143720|sp|Q19QT7.1|CGL_PIG	RecName: Full=Cystathionine gamma-lyase; AltName: Full=Cysteine-protein sulfhydrase; AltName: Full=Gamma-cystathionase >gi|1132	1.277	1.871	0.771	1.408

	05776|ref|NP_001038050.1| cystathionine gamma-lyase [Sus scrofa] >gi|104295139|gb|ABF72039.1| cystathionase [Sus scrofa]				
gi|335307937|ref|XP_003361036.1|	PREDICTED: golgin subfamily A member 2, partial [Sus scrofa]	0.688	0.535	1.047	0.64
gi|335281280|ref|XP_003122383.2|	PREDICTED: apical endosomal glycoprotein [Sus scrofa]	0.502	0.431	0.468	0.419
gi|350535040|ref|NP_001233182.1|	eukaryotic translation initiation factor 4 gamma 1 [Sus scrofa] >gi|338784423|gb|AEI98874.1| eukaryotic translation initiation factor 4 gamma 1 [Sus scrofa]	0.75	1.018	0.881	1.059
gi|335285985|ref|XP_003125470.2|	PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]	0.952	0.469	0.543	0.886
gi|346716222|ref|NP_001231254.1|	histidine triad nucleotide-binding protein 2, mitochondrial isoform 1 precursor [Sus scrofa]	2.84	1.204	1.571	1.916
gi|350586921|ref|XP_003482304.1|	PREDICTED: LOW QUALITY PROTEIN: apoptotic chromatin condensation inducer in the nucleus-like [Sus scrofa]	0.842	1.424	0.894	1.102
gi|54036319|sp|Q6QAP7.3|RS17_PIG	RecName: Full=40S ribosomal protein S17 >gi|48675931|ref|NP_001001634.1| 40S ribosomal protein S17 [Sus scrofa] >gi|45269037|gb|AAS55931.1| 40S ribosomal protein S17 [Sus scrofa]	0.7	0.663	0.859	0.552
gi|389618965|gb|AFK92990.1|	U2 small nuclear RNA auxiliary factor 2 [Sus scrofa]	1.303	1.058	1.085	1.315
gi|166796061|ref|NP_001107756.1|	60S ribosomal protein L5 [Sus scrofa] >gi|164598076|gb|ABY61325.1| ribosomal protein L5 [Sus scrofa]	1.091	1.397	1.374	1.602
gi|350584106|ref|XP_003481667.1|	PREDICTED: SWI/SNF complex subunit SMARCC2 [Sus scrofa]	0.755	0.898	0.717	0.863
gi|350584110|ref|XP_003481668.1|	PREDICTED: SWI/SNF complex subunit SMARCC2 [Sus scrofa]				
gi|350584134|ref|XP_003355513.2|	PREDICTED: SWI/SNF complex subunit SMARCC2-like [Sus scrofa]				
gi|350584108|ref|XP_001929203.4|	PREDICTED: SWI/SNF complex subunit SMARCC2 isoform 2 [Sus				

	scrofa]				
gi|350582612|ref|XP_003481312.1|	PREDICTED: protein phosphatase 1G-like [Sus scrofa]	1.641	2.347	2.165	1.949
gi|335287568|ref|XP_003126098.2|	PREDICTED: probable ATP-dependent RNA helicase DDX17-like [Sus scrofa]	1.312	0.99	0.748	1.883
gi|350539515|ref|NP_001233132.1|	ATP-dependent RNA helicase DDX3X [Sus scrofa] >gi|332113313|gb|AEE02033.1| X-linked DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 [Sus scrofa]	1.197	0.674	1.417	1.242
gi|47522800|ref|NP_999152.1|	60S ribosomal protein L22 [Sus scrofa] >gi|54039123|sp|P67985.2|RL22_PIG RecName: Full=60S ribosomal protein L22; AltName: Full=Heparin-binding protein HBp15 >gi|409074|dbj|BAA04547.1| heparin binding protein [Sus scrofa]	0.815	0.549	0.479	0.997
gi|122114359|gb|AAY42145.2|	cathepsin D [Sus scrofa]	1.729	1.191	1.125	1.992
gi|311271975|ref|XP_001926332.2|	PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial [Sus scrofa]	1.307	0.714	0.94	1.408
gi|297632426|ref|NP_001172096.1|	signal sequence receptor, alpha [Sus scrofa]	0.756	0.387	0.391	0.624
gi|335293128|ref|XP_003128866.2|	PREDICTED: alpha-adducin [Sus scrofa]	1.111	2.272	1.557	1.839
gi|343790870|ref|NP_001230573.1|	adaptor-related protein complex 2, mu 1 subunit [Sus scrofa]	---	---	---	---
gi|70986480|gb|AAZ16514.1|	hepatic nuclear factor 1 [Sus scrofa]	0.768	1.128	1.78	0.882
gi|239836872|gb|ACS29489.1|	HNF1A, partial [Sus scrofa]				
gi|74024901|ref|NP_001027560.1|	hepatocyte nuclear factor 1-alpha [Sus scrofa] >gi|67866955|gb|AAY82454.1| hepatic nuclear factor 1 [Sus scrofa]				
gi|350592969|ref|XP_003483583.1|	PREDICTED: phosphoglycerate mutase 1-like [Sus scrofa]	1.569	0.987	1.19	1.621
gi|350587465|ref|XP_003128987.3|	PREDICTED: RNA-binding protein 47-like isoform 1 [Sus scrofa]	0.543	0.435	0.259	0.65

gi|350587467|ref|XP_003482419.1|	PREDICTED: RNA-binding protein 47-like [Sus scrofa]				
gi|335302082|ref|XP_001926734.3|	PREDICTED: pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2-like, partial [Sus scrofa]	0.426	0.287	0.465	0.295
gi|146741316|dbj|BAF62313.1|	adaptor-related protein complex 3, delta-1 subunit [Sus scrofa]				
gi|335282242|ref|XP_003354004.1|	PREDICTED: AT-rich interactive domain-containing protein 3A [Sus scrofa]	1.469	1.101	1.576	1.164
gi|345110571|ref|NP_001230773.1|	coproporphyrinogen oxidase [Sus scrofa]	1.109	1.074	1.359	1.315
gi|350529438|ref|NP_001231909.1|	prefoldin subunit 3 [Sus scrofa]	0.853	1.619	1.339	1.117
gi|347582591|ref|NP_001231560.1|	cytoskeleton-associated protein 4 [Sus scrofa]	0.93	1.457	1.466	0.995
gi|350583879|ref|XP_003481608.1|	PREDICTED: LOW QUALITY PROTEIN: cytoskeleton-associated protein 4 [Sus scrofa]				
gi|311247240|ref|XP_003122553.1|	PREDICTED: splicing factor 3B subunit 2 [Sus scrofa]	0.716	1.012	0.897	0.818
gi|347543782|ref|NP_001231554.1|	glutathione synthetase [Sus scrofa]	1.749	1.676	2.554	1.735
gi|335293186|ref|XP_003356895.1|	PREDICTED: grpE protein homolog 1, mitochondrial-like isoform 1 [Sus scrofa]	0.674	0.743	0.608	0.791
gi|350587324|ref|XP_003482387.1|	PREDICTED: grpE protein homolog 1, mitochondrial-like isoform 2 [Sus scrofa]				
gi|194039403|ref|XP_001929632.1|	PREDICTED: CDC5 cell division cycle 5-like [Sus scrofa]	0.541	0.668	0.72	0.847
gi|311247879|ref|XP_003122857.1|	PREDICTED: 26S protease regulatory subunit 6A [Sus scrofa]	1.082	0.958	0.856	1.058
gi|72535182|ref|NP_001026953.1|	ras-related protein Rab-14 [Sus scrofa] >gi|75060237|sp|Q52NJ6.3|RAB14_PIG RecName: Full=Ras-related protein Rab-14 >gi|62868634|gb|AAY17505.1| Ras-related protein Rab-14 [Sus scrofa]	1.13	0.664	0.654	1.221
gi|346421343|ref|NP_001231	ribosomal protein S10 [Sus scrofa]	0.558	0.991	0.938	0.682

035.1|					
gi|311245734|ref|XP_003121939.1|	PREDICTED: hypothetical protein LOC100038023 [Sus scrofa] >gi|311245732|ref|XP_003121938.1| PREDICTED: hypothetical protein LOC100038023 [Sus scrofa]	0.464	0.315	0.345	0.559
gi|311275226|ref|XP_003134622.1|	PREDICTED: glutathione S-transferase kappa 1-like isoform 2 [Sus scrofa]	0.864	0.619	0.577	1.072
gi|311275228|ref|XP_003134621.1|	PREDICTED: glutathione S-transferase kappa 1-like isoform 1 [Sus scrofa]				
gi|47523672|ref|NP_999468.1|	2~-5~-oligoadenylate synthase 1 [Sus scrofa] >gi|6226834|sp|Q29599.3|OAS1_PIG RecName: Full=2~-5~-oligoadenylate synthase 1; Short=(2-5~)oligo(A) synthase 1; Short=2-5A synthase 1; AltName: Full=p42 OAS >gi|3451331|emb|CAA12397.1| 2~-5~ oligoadenyla	0.885	0.462	0.342	0.831
gi|39654572|pdb|1PX5|A	Chain A, Crystal Structure Of The 2~-Specific And Double-Stranded Rna-Activated Interferon-Induced Antiviral Protein 2~-5~-Oligoadenylate Synthetase >gi|39654573|pdb|1PX5|B Chain B, Crystal Structure Of The 2~-Specific And Double-Stranded Rna-Activ				
gi|311247106|ref|XP_003122482.1|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial-like isoform 1 [Sus scrofa]	0.729	0.793	0.549	0.59
gi|311247108|ref|XP_003122483.1|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial-like isoform 2 [Sus scrofa]				
gi|335310373|ref|XP_003362002.1|	PREDICTED: hypothetical protein LOC100628225, partial [Sus scrofa]	0.441	0.79	0.879	0.607
gi|311252247|ref|XP_003124998.1|	PREDICTED: macrophage-capping protein-like isoform 4 [Sus scrofa] >gi|311252243|ref|XP_00312	1.498	2.4	4.476	1.818

	4996.1| PREDICTED: macrophage-capping protein-like isoform 2 [Sus scrofa] >gi|311252249|ref|XP_003124997.1| PREDICTED: macrophage-capping protein-like isofor				
gi|311254554|ref|XP_003125887.1|	PREDICTED: bcl-2-like protein 15-like [Sus scrofa]	0.924	0.644	0.797	0.933
gi|342349346|ref|NP_001230149.1|	lon peptidase 1, mitochondrial [Sus scrofa]	0.825	0.398	0.342	0.849
gi|350529356|ref|NP_001231917.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) [Sus scrofa]	0.217	0.436	0.519	0.262
gi|347582660|ref|NP_001231584.1|	mesencephalic astrocyte-derived neurotrophic factor precursor [Sus scrofa] >gi|350591263|ref|XP_003483237.1| PREDICTED: mesencephalic astrocyte-derived neurotrophic factor [Sus scrofa] >gi|306563669|gb|ADN03186.1| mesencephalic astrocyte-derived neu	0.557	0.812	0.705	0.639
gi|311252948|ref|XP_003125347.1|	PREDICTED: cell growth regulator with EF hand domain protein 1-like isoform 2 [Sus scrofa]	0.317	0.344	0.421	0.354
gi|311252950|ref|XP_003125346.1|	PREDICTED: cell growth regulator with EF hand domain protein 1-like isoform 1 [Sus scrofa]				
gi|212549619|ref|NP_001131099.1|	ERO1-like protein alpha precursor [Sus scrofa] >gi|226741411|sp|B6CVD7.1|ERO1A_PIG RecName: Full=ERO1-like protein alpha; Short=ERO1-L; Short=ERO1-L-alpha; AltName: Full=Endoplasmic oxidoreductin-1-like protein; AltName: Full=Oxidoreductin-1-L-alpha	1.314	1.946	1.577	1.857
gi|335288894|ref|XP_003126772.2|	PREDICTED: ubiquitin-conjugating enzyme E2 N-like [Sus scrofa]	1.78	2.226	1.835	1.902

gi|350587106|ref|XP_003128729.2|	PREDICTED: protein sel-1 homolog 1-like [Sus scrofa]	---	---	---	---
gi|260593713|ref|NP_001157119.1|	occludin [Sus scrofa] >gi|239934655|emb|CAZ64276.1| occludin [Sus scrofa domesticus]	1.191	---	---	1.157
gi|329744588|ref|NP_001193269.1|	p30 DBC protein [Sus scrofa]	1.715	1.761	0.955	1.182
gi|311245701|ref|XP_003121927.1|	PREDICTED: S-methyl-5~-thioadenosine phosphorylase-like [Sus scrofa]	2.559	2.314	1.457	1.57
gi|84028320|sp|Q9GKX6.1|GALM_PIG	RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase >gi|47523866|ref|NP_999571.1| aldose 1-epimerase [Sus scrofa] >gi|11611545|dbj|BAB18973.1| aldose 1-epimerase [Sus scrofa]	1.501	0.864	0.931	1.695
gi|350584800|ref|XP_003355778.2|	PREDICTED: cytochrome c oxidase subunit 4 isoform 1, mitochondrial-like [Sus scrofa]	0.5	0.278	0.305	0.408
gi|335278800|ref|XP_003121142.2|	PREDICTED: afadin [Sus scrofa]	0.568	1.225	1.062	0.765
gi|167908791|ref|NP_001108148.1|	EPLIN-b [Sus scrofa] >gi|86450155|gb|ABC96266.1| EPLIN-b [Sus scrofa]	0.656	0.97	0.799	0.801
gi|335291962|ref|XP_001928015.3|	PREDICTED: E3 ubiquitin-protein ligase TRIM31 [Sus scrofa] >gi|211926941|dbj|BAG82682.1| tripartite motif-containing protein 31 [Sus scrofa]	0.99	0.644	1.319	1.179
gi|350584162|ref|XP_003481682.1|	PREDICTED: serine hydroxymethyltransferase, mitochondrial-like isoform 2 [Sus scrofa]	1.205	0.748	0.778	0.894
gi|350584170|ref|XP_003355531.2|	PREDICTED: serine hydroxymethyltransferase, mitochondrial-like [Sus scrofa] >gi|311255743|ref|XP_003126345.1| PREDICTED: serine hydroxymethyltransferase, mitochondrial-like isoform 1 [Sus scrofa]				
gi|346716298|ref|NP_001231025.1|	heterogeneous nuclear ribonucleoprotein G [Sus scrofa]	0.958	1.657	1.159	1.09

gi|335287882|ref|XP_003126232.2|	PREDICTED: LOW QUALITY PROTEIN: sterol O-acyltransferase 2-like [Sus scrofa]	1.336	0.918	1.402	0.942
gi|335282871|ref|XP_003123529.2|	PREDICTED: epidermal growth factor receptor pathway substrate 15-like 1 [Sus scrofa]	1.048	1.619	1.354	1.24
gi|343478283|ref|NP_001230406.1|	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 [Sus scrofa]	0.871	1.141	0.897	1.024
gi|311277195|ref|XP_003135533.1|	PREDICTED: host cell factor 1 [Sus scrofa]	0.794	0.801	1.1	0.752
gi|75059260|sp|Q29041.1|FCN2_PIG	RecName: Full=Ficolin-2; AltName: Full=Collagen/fibrinogen domain-containing protein 2; AltName: Full=Ficolin-B; AltName: Full=Ficolin-beta; AltName: Full=L-ficolin; Flags: Precursor >gi|47523126|ref|NP_999033.1| ficolin-2 precursor [Sus scrofa] >gi	0.555	0.353	0.303	0.509
gi|350584750|ref|XP_003126831.3|	PREDICTED: cysteine-rich with EGF-like domain protein 2-like isoform 1 [Sus scrofa]	0.813	1.265	1.285	1.047
gi|350584752|ref|XP_003481818.1|	PREDICTED: cysteine-rich with EGF-like domain protein 2-like [Sus scrofa]				
gi|346986456|ref|NP_001231378.1|	nucleoside diphosphate kinase 3 isoform 1 precursor [Sus scrofa]	0.489	0.953	0.592	0.467
gi|346986458|ref|NP_001231379.1|	nucleoside diphosphate kinase 3 isoform 2 precursor [Sus scrofa]				
gi|238018148|ref|NP_001153899.1|	ADP-ribosylation factor 1 [Sus scrofa] >gi|212725657|gb|ACJ38117.1| ADP-ribosylation factor 1 [Sus scrofa] >gi|237638742|gb|ACR07973.1| ADP-ribosylation factor 1 [Sus scrofa]	0.779	0.435	0.407	0.868
gi|335280985|ref|XP_003122213.2|	PREDICTED: golgin subfamily A member 1 [Sus scrofa]	1.837	1.582	2.493	1.315
gi|350594464|ref|XP_003483904.1|	PREDICTED: LOW QUALITY PROTEIN: clathrin interactor 1 [Sus scrofa]	1.167	0.847	1.137	1.276
gi|2493048|sp|Q95312.1|ATPD_PIG	RecName: Full=ATP synthase subunit delta, mitochondrial;	0.313	0.434	0.45	0.302

	AltName: Full=F-ATPase delta subunit; Flags: Precursor				
gi|356461003|ref|NP_001238977.1|	RNA-binding protein EWS [Sus scrofa] >gi|351738726|gb|AEQ61463.1| EWS [Sus scrofa]	1	1.531	1.38	1.45
gi|350585922|ref|XP_003127872.3|	PREDICTED: adenylyl cyclase-associated protein 1, partial [Sus scrofa]	3.624	2.043	1.696	4.525
gi|350585924|ref|XP_003356378.2|	PREDICTED: adenylyl cyclase-associated protein 1-like [Sus scrofa]				
gi|311249270|ref|XP_003123549.1|	PREDICTED: coiled-coil domain-containing protein 124-like [Sus scrofa]	---	---	---	---
gi|346421386|ref|NP_001231066.1|	ATP synthase subunit g, mitochondrial [Sus scrofa]	0.905	0.362	0.382	0.946
gi|356614808|gb|AET25525.1|	mitochondrial NADH dehydrogenase Fe-S protein 4 [Sus scrofa]	0.432	0.564	0.552	0.513
gi|190360639|ref|NP_001121941.1|	interferon-induced 17 kDa protein [Sus scrofa] >gi|182406743|gb|ACB87600.1| interferon stimulated gene 15 [Sus scrofa]	0.78	2.3	4.581	2.706
gi|335299628|ref|XP_001926139.3|	PREDICTED: coatomer subunit beta~ [Sus scrofa]	0.808	0.654	0.856	0.817
gi|311245810|ref|XP_001924714.2|	PREDICTED: GTP:AMP phosphotransferase, mitochondrial isoform 1 [Sus scrofa]	1.66	0.785	1.152	1.897
gi|345090993|ref|NP_001230731.1|	RAB8A, member RAS oncogene family [Sus scrofa]	0.701	0.514	0.564	0.856
gi|335296120|ref|XP_003357690.1|	PREDICTED: Golgi resident protein GCP60-like [Sus scrofa]	0.636	0.595	0.763	0.857
gi|335292526|ref|XP_001927459.2|	PREDICTED: receptor-interacting serine/threonine-protein kinase 3-like [Sus scrofa]	---	---	---	---
gi|350593418|ref|XP_003359535.2|	PREDICTED: hypothetical protein LOC100627320 [Sus scrofa]	1.522	1.994	2.167	1.535
gi|47522860|ref|NP_999184.1|	dehydrogenase/reductase SDR family member 4 [Sus scrofa] >gi|186972939|pdb|2ZAT|D Chain D, Crystal Structure Of A Mammalian	1.41	1.015	0.948	0.791

	Reductase >gi|186972937|pdb|2ZAT|B Chain B, Crystal Structure Of A Mammalian Reductase >gi|186972938|pdb|2ZAT|C Chain C, Crys				
gi|308153436|sp|Q8WNV7.2|DHRS4_PIG	RecName: Full=Dehydrogenase/reductase SDR family member 4; AltName: Full=NADPH-dependent carbonyl reductase/NADP-retinol dehydrogenase; Short=CR; Short=PHCR; AltName: Full=NADPH-dependent retinol dehydrogenase/reductase; Short=NDRD; AltName: Full=Pe				
gi|305855148|ref|NP_001182266.1|	peptidyl-prolyl cis-trans isomerase FKBP4 [Sus scrofa] >gi|285818414|gb|ADC38880.1| FK506 binding protein 4 [Sus scrofa]	0.978	0.691	0.784	1.009
gi|346644874|ref|NP_001231109.1|	T-complex protein 1 subunit gamma [Sus scrofa]	1.406	0.959	0.898	1.328
gi|350590014|ref|XP_003357929.2|	PREDICTED: serine/threonine-protein kinase 24 [Sus scrofa]	1.139	0.962	1.02	1.073
gi|335289671|ref|XP_003355951.1|	PREDICTED: transcription elongation factor SPT5 isoform 3 [Sus scrofa] >gi|335289667|ref|XP_003355949.1| PREDICTED: transcription elongation factor SPT5 isoform 1 [Sus scrofa] >gi|335289669|ref|XP_003355950.1| PREDICTED: transcription elongation fac	0.921	1.108	1.49	0.892
gi|311249625|ref|XP_003123708.1|	PREDICTED: FAS-associated factor 2 [Sus scrofa]	0.689	0.734	1.36	0.551
gi|350581449|ref|XP_003481037.1|	PREDICTED: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2-like [Sus scrofa] >gi|311251041|ref|XP_003124417.1| PREDICTED: guanine	1.102	0.709	0.749	0.867

	nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2-like isoform 2 [Sus scrofa]				
gi|311259100|ref|XP_003127931.1|	PREDICTED: meprin A subunit beta [Sus scrofa]	0.371	0.316	0.293	0.284
gi|350579827|ref|XP_003480692.1|	PREDICTED: LOW QUALITY PROTEIN: nucleosome assembly protein 1-like 4-like [Sus scrofa]	1.236	1.033	1.196	1.168
gi|356650697|gb|AET34758.1|	nucleosome assembly protein 1-like 4 [Sus scrofa]				
gi|343887420|ref|NP_001230609.1|	transcription elongation factor A protein 1 [Sus scrofa]	0.935	1.433	1.33	0.857
gi|343780936|ref|NP_001230484.1|	heterogeneous nuclear ribonucleoprotein H3 [Sus scrofa]	0.699	0.934	1.088	0.843
gi|194042010|ref|XP_001924773.1|	PREDICTED: gamma-adducin isoform 1 [Sus scrofa]	0.896	0.415	0.659	1.128
gi|194042012|ref|XP_001924864.1|	PREDICTED: gamma-adducin isoform 3 [Sus scrofa] >gi|335302227|ref|XP_003359413.1| PREDICTED: gamma-adducin [Sus scrofa]				
gi|335306217|ref|XP_003360420.1|	PREDICTED: 60S ribosomal protein L9-like [Sus scrofa]	1.077	0.628	0.964	1.517
gi|343478291|ref|NP_001230410.1|	ribosomal protein L9 [Sus scrofa]				
gi|350594715|ref|XP_001927122.3|	PREDICTED: adipocyte plasma membrane-associated protein-like [Sus scrofa]	0.721	0.215	0.2	0.678
gi|335293615|ref|XP_003357006.1|	PREDICTED: UDP-glucuronosyltransferase 2A1 [Sus scrofa]	0.731	0.513	0.642	0.911
gi|127804|sp|P26429.1|SC5A1_PIG	RecName: Full=Sodium/glucose cotransporter 1; Short=Na(+)/glucose cotransporter 1; AltName: Full=High affinity sodium-glucose cotransporter; AltName: Full=Solute carrier family 5 member 1 >gi|164675|gb|AAA31122.1| Na+/glucose cotransporter (SGLT1),	1.227	0.435	0.562	0.89
gi|255683521|ref|NP_001157493.1|	sodium/glucose cotransporter 1 [Sus scrofa]				
gi|335297787|ref|XP_003131	PREDICTED: puromycin-sensitive	1.467	0.977	0.697	1.664

575.2|	aminopeptidase isoform 1 [Sus scrofa]				
gi|350593466|ref|XP_003359556.2|	PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 [Sus scrofa]	1.622	0.511	0.758	1.28
gi|1165145|emb|CAA64477.1|	annexin I [Sus scrofa]	0.423	0.578	0.912	0.848
gi|13399613|pdb|1HM6|A	Chain A, X-Ray Structure Of Full-Length Annexin 1 >gi|28948618|pdb|1MCX|A Chain A, Structure Of Full-Length Annexin A1 In The Presence Of Calcium >gi|13399614|pdb|1HM6|B Chain B, X-Ray Structure Of Full-Length Annexin 1				
gi|255683368|ref|NP_001157470.1|	annexin A1 [Sus scrofa] >gi|20141168|sp|P19619.3|ANXA1_PIG RecName: Full=Annexin A1; AltName: Full=Annexin I; AltName: Full=Annexin-1; AltName: Full=Calpactin II; AltName: Full=Calpactin-2; AltName: Full=Chromobindin-9; AltName: Full=Lipocortin I; A				
gi|343183313|ref|NP_001230231.1|	gephyrin [Sus scrofa]	1.148	1.148	1.4	1.115
gi|350584292|ref|XP_003481715.1|	PREDICTED: dynamin 1-like [Sus scrofa]	---	---	---	---
gi|350597090|ref|XP_003484356.1|	PREDICTED: dynamin-1-like protein-like, partial [Sus scrofa]				
gi|194038067|ref|XP_001927944.1|	PREDICTED: protein DEK isoform 1 [Sus scrofa]	0.564	0.737	1.077	0.544
gi|335291757|ref|XP_003356581.1|	PREDICTED: protein DEK [Sus scrofa]				
gi|335291759|ref|XP_003356582.1|	PREDICTED: protein DEK [Sus scrofa]				
gi|350587196|ref|XP_003482363.1|	PREDICTED: tryptophanyl-tRNA synthetase, cytoplasmic-like isoform 2 [Sus scrofa] >gi|350587194|ref|XP_003128776.3| PREDICTED: tryptophanyl-tRNA synthetase, cytoplasmic-like isoform 1 [Sus	1.241	0.79	0.815	0.894

	scrofa]				
gi|350578528|ref|XP_003480383.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase B-like, partial [Sus scrofa]	---	---	---	---
gi|2494023|sp|Q29290.1|CYTB_PIG	RecName: Full=Cystatin-B; AltName: Full=Stefin-B	0.968	1.922	2.05	1.433
gi|311259195|ref|XP_003127983.1|	PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like isoform 2 [Sus scrofa]	1.114	1.411	1.334	1.164
gi|311259199|ref|XP_003127984.1|	PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like isoform 3 [Sus scrofa]				
gi|311259197|ref|XP_003127982.1|	PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like isoform 1 [Sus scrofa]				
gi|335291374|ref|XP_003356484.1|	PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like [Sus scrofa]				
gi|72535210|ref|NP_001026967.1|	protein FADD [Sus scrofa] >gi|46397561|gb|AAS91711.1| Fas-associating death domain-containing protein [Sus scrofa]	1.231	0.704	1.654	0.722
gi|350584002|ref|XP_003126228.3|	PREDICTED: keratin, type I cytoskeletal 18 [Sus scrofa]	0.903	0.753	0.534	0.611
gi|335309807|ref|XP_003361778.1|	PREDICTED: delta-aminolevulinic acid dehydratase-like, partial [Sus scrofa]	0.853	1.284	1.316	0.803
gi|194044992|ref|XP_001928105.1|	PREDICTED: sorting nexin-12 [Sus scrofa]	1.055	1.04	1.066	1.481
gi|350586335|ref|XP_003356548.2|	PREDICTED: nuclease-sensitive element-binding protein 1-like [Sus scrofa]	0.357	1.959	0.998	0.852
gi|354549569|gb|AER27829.1|	Y box binding protein 1 [Sus scrofa]				
gi|47523784|ref|NP_999528.1|	40S ribosomal protein S12 [Sus scrofa] >gi|1173191|sp|P46405.2|RS12_PIG RecName: Full=40S ribosomal protein S12 >gi|872315|emb|CAA55946.1| 40S ribosomal protein S12 [Sus scrofa]	0.974	1.068	0.878	1.607

gi|311260817|ref|XP_001925607.2|	PREDICTED: protein PML isoform 1 [Sus scrofa]	0.605	0.668	0.609	0.849
gi|335292411|ref|XP_003356725.1|	PREDICTED: protein PML isoform 2 [Sus scrofa]				
gi|350596898|ref|XP_003361788.2|	PREDICTED: GTP cyclohydrolase 1-like [Sus scrofa]	---	---	---	---
gi|311247118|ref|XP_003122486.1|	PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial-like isoform 1 [Sus scrofa]	1.053	0.587	0.656	0.836
gi|311247120|ref|XP_003122487.1|	PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial-like isoform 2 [Sus scrofa]				
gi|311262725|ref|XP_003129324.1|	PREDICTED: inorganic pyrophosphatase 2, mitochondrial-like [Sus scrofa]	1.016	1.01	0.817	0.985
gi|335287403|ref|XP_001927013.3|	PREDICTED: calcium-activated chloride channel regulator 4 [Sus scrofa]	1.181	0.665	0.95	0.821
gi|311253255|ref|XP_003125488.1|	PREDICTED: alanine aminotransferase 1-like [Sus scrofa]	1.108	1.782	2.46	1.848
gi|326633214|ref|NP_001192023.1|	ubiquitin-conjugating enzyme E2 variant 1 [Sus scrofa]	---	---	---	---
gi|335298430|ref|XP_003131953.2|	PREDICTED: LOW QUALITY PROTEIN: mitochondrial 2-oxoglutarate/malate carrier protein [Sus scrofa]	0.922	0.612	0.416	0.502
gi|311250943|ref|XP_003124353.1|	PREDICTED: 28 kDa heat- and acid-stable phosphoprotein-like [Sus scrofa]	0.855	1.997	1.66	1.733
gi|47522750|ref|NP_999125.1|	voltage-dependent anion-selective channel protein 1 [Sus scrofa] >gi|75050406|sp|Q9MZ16.3|VDAC1_PIG RecName: Full=Voltage-dependent anion-selective channel protein 1; Short=VDAC-1 >gi|8745552|gb|AAF78963.1|AF268461_1 voltage-dependent anion channel	0.661	0.45	0.434	0.729
gi|24987656|pdb|1LXE|A	Chain A, Crystal Structure Of The Cathelicidin Motif Of Protegrins >gi|24987482|pdb|1KWI|A	0.329	1.16	0.826	2.176

	Chain A, Crystal Structure Analysis Of The Cathelicidin Motif Of Protegrins				
gi|159162733|pdb|1N5P|A	Chain A, Solution Structure Of The Cathelin-Like Domain Of Protegrins (All Amide Bonds Involving Proline Residues Are In Trans Conformation) >gi|159162732|pdb|1N5H|A Chain A, Solution Structure Of The Cathelin-Like Domain Of Protegrins (The R87-P88				
gi|52000924|sp|Q29238.2|CLIC1_PIG	RecName: Full=Chloride intracellular channel protein 1; AltName: Full=Nuclear chloride ion channel 27	1.73	0.733	0.748	1.761
gi|194036322|ref|XP_001928206.1|	PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF3 isoform 1 [Sus scrofa] >gi|194036324|ref|XP_001928212.1| PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF3 isoform 2 [Sus scrofa]	1.081	1.545	1.68	1.125
gi|156120152|ref|NP_001095294.1|	complement factor B precursor [Sus scrofa] >gi|148724909|emb|CAN87697.1| B-factor, properdin [Sus scrofa]	1.303	0.829	0.753	1.237
gi|162138242|gb|ABX82825.1|	complement factor B [Sus scrofa]				
gi|335290029|ref|XP_003356052.1|	PREDICTED: nuclear pore glycoprotein p62 [Sus scrofa]	0.611	0.516	0.685	0.524
gi|335294212|ref|XP_003129427.2|	PREDICTED: 60S ribosomal protein L27a-like isoform 1 [Sus scrofa]	1.376	0.517	0.659	0.736
gi|350588060|ref|XP_003482544.1|	PREDICTED: 60S ribosomal protein L27a-like [Sus scrofa]				
gi|56404320|sp|Q6PWT7.1|CCS_PIG	RecName: Full=Copper chaperone for superoxide dismutase; AltName: Full=Superoxide dismutase copper chaperone >gi|49274647|ref|NP_001001866.1| copper chaperone for superoxide dismutase [Sus scrofa] >gi|46395042|gb|AAS91658.1| superoxide dismutase cop	1.032	1.247	1.516	1.198
gi|262399411|ref|NP_001161062.1|	uncharacterized protein C14orf142 homolog [Sus scrofa] >gi|212288175|sp|P0C8B5.1|	1.721	2.291	2.179	1.65

	CN142_PIG RecName: Full=Uncharacterized protein C14orf142 homolog				
gi|335293826|ref|XP_003357065.1|	PREDICTED: LOW QUALITY PROTEIN: short coiled-coil protein-like [Sus scrofa]	0.372	3.119	1.888	0.975
gi|329663948|ref|NP_001192334.1|	ras GTPase-activating protein-binding protein 1 [Sus scrofa]	0.664	0.971	1.069	0.932
gi|350587586|ref|XP_003129077.3|	PREDICTED: hypothetical protein LOC100522154 [Sus scrofa]	1.027	1.932	2.369	1.379
gi|350586208|ref|XP_003128041.3|	PREDICTED: epidermal growth factor receptor substrate 15 [Sus scrofa]	0.871	1.063	0.837	0.912
gi|555827|gb|AAA65943.1|	immunoglobulin alpha heavy chain constant region, partial [Sus scrofa] >gi|2136551|pir||I47175 Ig alpha chain C region - pig (fragment)	0.72	0.817	1.044	1.378
gi|290578621|gb|ADD51207.1|	immunoglobulin IgA heavy chain constant region [Sus scrofa]				
gi|311250752|ref|XP_003124284.1|	PREDICTED: NACHT, LRR and PYD domains-containing protein 6 [Sus scrofa]	1	2.178	1.782	1.213
gi|311249251|ref|XP_003123542.1|	PREDICTED: 6-phosphogluconolactonase-like [Sus scrofa]	1.405	0.796	0.756	1.009
gi|197251940|ref|NP_001127829.1|	actin-related protein 2/3 complex subunit 5 [Sus scrofa] >gi|195562237|gb|ACG50185.1| actin related protein 2/3 complex subunit 5 [Sus scrofa]	0.9	1.278	0.982	1.803
gi|311260144|ref|XP_003128362.1|	PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]	---	---	---	---
gi|350586520|ref|XP_003128365.3|	PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]				
gi|350586522|ref|XP_003482204.1|	PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]				
gi|350581286|ref|XP_003124146.3|	PREDICTED: hypothetical protein LOC100516425 [Sus scrofa]	1.102	1.883	1.285	1.111
gi|350580953|ref|XP_003354274.2|	PREDICTED: 60S acidic ribosomal protein P1-like [Sus scrofa]	0.421	1.608	1.595	0.92
gi|47522916|ref|NP_999215.1|	glutathione S-transferase omega-1 [Sus	1.41	0.791	0.625	1.755

	scrofa] >gi|20141290|sp|Q9N1F5.2|GSTO1_PIG RecName: Full=Glutathione S-transferase omega-1; Short=GSTO-1; AltName: Full=Glutathione S-transferase omega 1-1; Short=GSTO 1-1; AltName: Full=Glutathione-dependent d				
gi|335293690|ref|XP_003129163.2|	PREDICTED: general vesicular transport factor p115-like [Sus scrofa]	0.836	2.522	2.176	1.516
gi|47523794|ref|NP_999534.1|	voltage-dependent anion-selective channel protein 2 [Sus scrofa] >gi|75050405|sp|Q9MZ15.1|VDAC2_PIG RecName: Full=Voltage-dependent anion-selective channel protein 2; Short=VDAC-2 >gi|8745554|gb|AAF78964.1|AF268462_1 voltage-dependent anion channel	0.872	0.478	0.433	0.922
gi|343432604|ref|NP_001230320.1|	ubiquitin-conjugating enzyme E2 variant 2 [Sus scrofa]	---	---	---	---
gi|335291035|ref|XP_003127861.2|	PREDICTED: polyadenylate-binding protein 4 isoform 1 [Sus scrofa]	---	---	---	---
gi|350585908|ref|XP_003482078.1|	PREDICTED: polyadenylate-binding protein 4 isoform 2 [Sus scrofa]				
gi|350586828|ref|XP_003482286.1|	PREDICTED: paired amphipathic helix protein Sin3a-like isoform 2 [Sus scrofa] >gi|335292401|ref|XP_003356722.1| PREDICTED: paired amphipathic helix protein Sin3a-like isoform 1 [Sus scrofa]	1.135	1.157	2.238	1.077
gi|5542425|pdb|1QPW|D	Chain D, Crystal Structure Determination Of Porcine Hemoglobin At 1.8a Resolution >gi|5542423|pdb|1QPW|B Chain B, Crystal Structure Determination Of Porcine Hemoglobin At 1.8a Resolution >gi|809285|pdb|2PGH|D Chain D, Structure Determination Of Aquo	0.842	0.728	0.606	0.619
gi|402550453|pdb|4F4O|H	Chain H, Structure Of The Haptoglobin-Haemoglobin				

	Complex >gi|402550447|pdb|4F4O|B Chain B, Structure Of The Haptoglobin-Haemoglobin Complex >gi|402550456|pdb|4F4O|K Chain K, Structure Of The Haptoglobin-Haemoglobin Complex >gi|402550450|pdb|4F4O|E				
gi|261245058|ref|NP_001138313.1|	hemoglobin subunit beta [Sus scrofa] >gi|3041678|sp|P02067.3|HBB_PIG RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain >gi|806381|emb|CAA60490.1| beta-globin [Sus scrofa]				
gi|120564455|gb|ABM30153.1|	beta-globin [Sus scrofa]				
gi|1900|emb|CAA27575.1|	unnamed protein product [Sus scrofa]	1.005	0.503	0.769	1.152
gi|335892232|pdb|3N2F|B	Chain B, Crystal Structure Of The Sodium-Potassium Pump >gi|335892235|pdb|3N2F|D Chain D, Crystal Structure Of The Sodium-Potassium Pump >gi|319443575|pdb|3N23|D Chain D, Crystal Structure Of The High Affinity Complex Between Ouabain And The E2p For				
gi|48374077|ref|NP_001001542.1|	sodium/potassium-transporting ATPase subunit beta-1 [Sus scrofa] >gi|164380|gb|AAA31001.1| Na+, K+-ATPase [Sus scrofa]				
gi|1703469|sp|P05027.2|AT1B1_PIG	RecName: Full=Sodium/potassium-transporting ATPase subunit beta-1; AltName: Full=Sodium/potassium-dependent ATPase subunit beta-1 >gi|225192|prf||1211232A ATPase beta,Na/K >gi|1902|emb|CAA28301.1| unnamed protein product [Sus scrofa]				
gi|288965538|pdb|3KDP|D	Chain D, Crystal Structure Of The Sodium-Potassium				

	Pump >gi|288965535|pdb|3KDP|B Chain B, Crystal Structure Of The Sodium-Potassium Pump				
gi|114326183|ref|NP_001041537.1|	ADP-ribosylation factor 4 [Sus scrofa] >gi|221327932|gb|ACM17702.1| ADP-ribosylation factor 4 [Sus scrofa] >gi|203283175|gb|ACH96700.1| ADP-ribosylation factor 4 [Sus scrofa] >gi|62208269|gb|AAX77012.1| ADP-ribosylation factor family-like protein [S	0.686	0.442	0.301	0.822
gi|350582454|ref|XP_003125231.3|	PREDICTED: LOW QUALITY PROTEIN: leucine-rich PPR motif-containing protein, mitochondrial [Sus scrofa]	1.183	0.968	0.808	1.206
gi|311248919|ref|XP_003123379.1|	PREDICTED: protein Hook homolog 2 [Sus scrofa]	---	---	---	---
gi|311259611|ref|XP_003128182.1|	PREDICTED: 40S ribosomal protein S5-like isoform 2 [Sus scrofa] >gi|311259613|ref|XP_003128181.1| PREDICTED: 40S ribosomal protein S5-like isoform 1 [Sus scrofa]	1.156	0.55	0.608	1.144
gi|335290571|ref|XP_003356212.1|	PREDICTED: UPF0485 protein C1orf144 homolog isoform 2 [Sus scrofa]	0.702	1.491	1.375	0.757
gi|47522846|ref|NP_999175.1|	ATP-binding cassette sub-family G member 2 [Sus scrofa] >gi|68051987|sp|Q8MIB3.1|ABCG2_PIG RecName: Full=ATP-binding cassette sub-family G member 2; AltName: Full=Brain multidrug resistance protein; AltName: CD_antigen=CD338 >gi|21530795|emb|CAD1278	1.247	0.674	0.582	0.785
gi|350592328|ref|XP_001926837.4|	PREDICTED: kinesin family member 13B [Sus scrofa]	1.331	1.467	1.406	1.294
gi|103472127|ref|NP_001033715.2|	aldo-keto reductase family 1, member C-like 1 [Sus scrofa] >gi|94421332|gb|ABF18834.1| putative aldo-keto reductase family 1 member C4 [Sus scrofa]	1.037	1.744	2.546	3.783
gi|158148957|dbj|BAF82012.	aldo-keto reductase [Sus				

1|	scrofa] >gi|61741954|gb|AAX54862.1| prostaglandin F synthase [Sus scrofa]				
gi|178056496|ref|NP_001116547.1|	aldo-keto reductase family 1 member C4 [Sus scrofa] >gi|94962086|gb|ABF48390.1| aldo-keto reductase family 1 member C4 [Sus scrofa]				
gi|350586674|ref|XP_001929500.4|	PREDICTED: exportin-5 [Sus scrofa]	0.936	0.699	0.653	1.018
gi|335292368|ref|XP_001926489.3|	PREDICTED: calcium and integrin-binding protein 1 [Sus scrofa]	0.454	0.7	0.817	0.648
gi|38569723|gb|AAR24382.1|	GDP dissociation inhibitor 2 [Sus scrofa]	---	---	---	---
gi|350276172|ref|NP_001231880.1|	leucine-rich repeat-containing protein 59 [Sus scrofa]	0.495	0.761	0.604	0.665
gi|89573851|gb|ABD77151.1|	succinate dehydrogenase complex subunit B [Sus scrofa]	0.734	0.37	0.483	0.563
gi|322812295|pdb|3AE8|B	Chain B, Crystal Structure Of Porcine Heart Mitochondrial Complex Ii Bound With N-(3-Isopropoxy-Phenyl)-2-Trifluoromethylbenzamide >gi|322812327|pdb|3AEG|B Chain B, Crystal Structure Of Porcine Heart Mitochondrial Complex Ii Bound With N-Biphenyl-3-				
gi|345531797|pdb|3SFE|B	Chain B, Crystal Structure Of Porcine Mitochondrial Respiratory Complex Ii Bound With Oxaloacetate And Thiabendazole >gi|345531793|pdb|3SFD|B Chain B, Crystal Structure Of Porcine Mitochondrial Respiratory Complex Ii Bound With Oxaloacetate And Pent				
gi|157279735|ref|NP_001098423.1|	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor [Sus scrofa] >gi|122131481|sp|Q007T0.1|DHSB_PIG RecName: Full=Succinate dehydrogenase [ubiquinone] iron-sulfur subunit,				

	mitochondrial; AltName: Full=Iron-sulfur subuni				
gi|50262041|gb|AAT72764.1|	fatty acid binding protein 3, partial [Sus scrofa]	1.966	1.67	1.37	2.192
gi|374637318|gb|AEZ54788.1|	heart fatty acid-binding protein [Sus scrofa]				
gi|198250386|gb|ACH85195.1|	fatty acid binding protein 3 [Sus scrofa]				
gi|148792972|gb|ABR12603.1|	heart fatty acid-binding protein [Sus scrofa]				
gi|172073181|ref|NP_001093401.1|	fatty acid-binding protein, heart [Sus scrofa] >gi|2811020|sp|O02772.3|FABPH_PIG RecName: Full=Fatty acid-binding protein, heart; AltName: Full=Fatty acid-binding protein 3; AltName: Full=Heart-type fatty acid-binding protein; Short=H-FABP >gi|30237				
gi|224994935|gb|ACN76574.1|	fatty acid-binding protein 3 [Sus scrofa]				
gi|266018|gb|AAB25484.1|	calmodulin=low affinity vasoactive intestinal polypeptide binding protein [swine, liver, Peptide Partial, 34 aa]	1.397	2.473	2.726	4.203
gi|343790897|ref|NP_001230506.1|	eukaryotic translation initiation factor [Sus scrofa]	---	---	---	---
gi|335284027|ref|XP_003354495.1|	PREDICTED: LOW QUALITY PROTEIN: brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1-like [Sus scrofa]	---	---	---	---
gi|311259030|ref|XP_003127902.1|	PREDICTED: small nuclear ribonucleoprotein Sm D1-like [Sus scrofa]	1.41	1.528	1.301	0.682
gi|47522948|ref|NP_999231.1|	D-amino-acid oxidase [Sus scrofa] >gi|129305|sp|P00371.2|OXDA_PIG RecName: Full=D-amino-acid oxidase; Short=DAAO; Short=DAMOX; Short=DAO >gi|164306|gb|AAA30985.1| D-amino acid oxidase [Sus scrofa] >gi|48425898|pdb|1VE9|A Chain A, Porcine Kidney D-Am	1.109	0.677	0.555	0.816
gi|335310745|ref|XP_003125	PREDICTED: hypothetical protein	1.353	1.643	1.34	1.558

987.2|	LOC100515435, partial [Sus scrofa]				
gi|350582854|ref|XP_003481372.1|	PREDICTED: elongation factor 1-delta-like isoform 1 [Sus scrofa]				
gi|350582856|ref|XP_003481373.1|	PREDICTED: elongation factor 1-delta-like isoform 2 [Sus scrofa]				
gi|335279372|ref|XP_003121421.2|	PREDICTED: LOW QUALITY PROTEIN: myristoylated alanine-rich C-kinase substrate-like [Sus scrofa]	0.352	0.423	0.313	0.457
gi|356582293|ref|NP_001239141.1|	DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Sus scrofa]	0.875	0.801	0.869	1.207
gi|335286637|ref|XP_001927783.3|	PREDICTED: nitrilase homolog 1 isoform 2 [Sus scrofa]	1.142	1.595	1.118	0.932
gi|335290948|ref|XP_003356342.1|	PREDICTED: uncharacterized protein KIAA1522-like [Sus scrofa]				
gi|335293906|ref|XP_003129266.2|	PREDICTED: annexin A5-like [Sus scrofa]	0.335	0.364	0.348	0.325
gi|350586356|ref|XP_003482168.1|	PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone]-like [Sus scrofa]	1.234	0.977	1.294	0.558
gi|311246132|ref|XP_003122091.1|	PREDICTED: 39S ribosomal protein L50, mitochondrial-like [Sus scrofa]	0.428	0.347	0.475	0.429
gi|350536531|ref|NP_001233199.1|	phosphatidylinositol-binding clathrin assembly protein [Sus scrofa] >gi|338784421|gb|AEI98873.1| phosphatidylinositol-binding clathrin assembly protein [Sus scrofa]	1.507	2.488	4.681	1.808
gi|350596835|ref|XP_003361703.2|	PREDICTED: phosphatidylinositol-binding clathrin assembly protein-like [Sus scrofa]				
gi|335310931|ref|XP_003362256.1|	PREDICTED: vacuolar protein sorting-associated protein 35 [Sus scrofa]	2.403	0.722	1.158	1.45
gi|335307273|ref|XP_003360776.1|	PREDICTED: mitogen-activated protein kinase 3, partial [Sus scrofa]	4.06	0.684	0.408	0.44
gi|164664456|ref|NP_001106915.1|	F-actin-capping protein subunit beta [Sus scrofa] >gi|148613359|gb|ABQ96223.1| F-actin capping protein beta subunit [Sus scrofa] >gi|148613353|gb|ABQ96220.1| F-actin capping protein beta	2.198	0.855	0.819	1.465

	subunit [Sus scrofa]				
gi|270000214|gb|ACZ57956.1|	F-actin capping protein beta subunit variant I [Sus scrofa]				
gi|270000216|gb|ACZ57957.1|	F-actin capping protein beta subunit variant II [Sus scrofa]				
gi|148222609|ref|NP_001090925.1|	F-actin-capping protein subunit beta [Sus scrofa] >gi|134035396|sp|A0PFK7.1|CAPZB_PIG RecName: Full=F-actin-capping protein subunit beta; AltName: Full=CapZ beta >gi|118627576|emb|CAL69437.1| F-actin capping protein subunit beta 1 [Sus scrofa]				
gi|346986241|ref|NP_001231394.1|	neurocalcin delta [Sus scrofa] >gi|346986243|ref|NP_001231395.1| neurocalcin delta [Sus scrofa]	1.329	2.765	2.675	1.757
gi|335294002|ref|XP_003357106.1|	PREDICTED: 3-hydroxybutyrate dehydrogenase type 2-like isoform 2 [Sus scrofa] >gi|335294000|ref|XP_003129333.2| PREDICTED: 3-hydroxybutyrate dehydrogenase type 2-like isoform 1 [Sus scrofa]	2.36	0.622	0.791	1.663
gi|335300663|ref|XP_003358983.1|	PREDICTED: trifunctional purine biosynthetic protein adenosine-3-like [Sus scrofa]	1.521	1.571	0.85	1.601
gi|335289705|ref|XP_003355965.1|	PREDICTED: flavin reductase-like [Sus scrofa]	1.05	1.11	1.107	1.542
gi|311261216|ref|XP_001924364.2|	PREDICTED: c-1-tetrahydrofolate synthase, cytoplasmic [Sus scrofa]	1.698	0.908	0.953	1.733
gi|311271203|ref|XP_001925518.2|	PREDICTED: ras-related protein Rab-4A-like [Sus scrofa]	---	---	---	---
gi|350585214|ref|XP_003481903.1|	PREDICTED: ras-related protein Rab-4B-like [Sus scrofa] >gi|311257582|ref|XP_003127192.1| PREDICTED: ras-related protein Rab-4B-like isoform 2 [Sus scrofa]				
gi|106073274|gb|ABF81975.1|	hypothetical protein [Sus scrofa]	1.521	1.032	1.234	1.545
gi|172072661|ref|NP_001116458.1|	tRNA-splicing ligase RtcB homolog [Sus				

	scrofa] >gi|118573909|sp|Q19PY3.1|RTCB_PIG RecName: Full=tRNA-splicing ligase RtcB homolog >gi|106073298|gb|ABF81976.1| hypothetical protein [Sus scrofa]				
gi|335289428|ref|XP_003127055.2|	PREDICTED: hypothetical protein LOC100523791 [Sus scrofa]	1.451	1.827	2.253	1.323
gi|347349312|gb|AEO80316.1|	programmed cell death protein 5 [Sus scrofa]				
gi|329663924|ref|NP_001192332.1|	tubulin-folding cofactor B-like [Sus scrofa] >gi|24528346|emb|CAD56044.1| cytoskeleton-associated protein 1 [Sus scrofa]	1.001	1.31	1.194	1.124
gi|350584424|ref|XP_003126577.3|	PREDICTED: chromodomain-helicase-DNA-binding protein 4 [Sus scrofa]	0.602	0.885	0.588	0.978
gi|178056560|ref|NP_001116630.1|	phosphoenolpyruvate carboxykinase, cytosolic [Sus scrofa] >gi|238863890|gb|ACR66221.1| phosphoenolpyruvate carboxykinase 1 [Sus scrofa] >gi|147223435|emb|CAN13128.1| phosphoenolpyruvate carboxykinase 1 (soluble) [Sus scrofa]	2.378	0.556	0.615	0.866
gi|350595271|ref|XP_003134762.3|	PREDICTED: hypothetical protein LOC100521760 [Sus scrofa]	1.787	1.246	1.2	1.484
gi|335310107|ref|XP_003361890.1|	PREDICTED: non-POU domain-containing octamer-binding protein [Sus scrofa]	1.266	0.594	0.636	0.877
gi|194043017|ref|XP_001928354.1|	PREDICTED: MGC159817 protein isoform 1 [Sus scrofa]	2.079	1.832	2.726	2.978
gi|350591430|ref|XP_003483266.1|	PREDICTED: protein SEC13 homolog [Sus scrofa]	0.852	0.702	0.715	0.613
gi|311270318|ref|XP_001925732.2|	PREDICTED: zinc transporter ZIP14 [Sus scrofa]	1.034	0.639	0.68	0.687
gi|311271598|ref|XP_001925392.2|	PREDICTED: bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 2-like [Sus scrofa]	1.47	1.492	1.161	2.034
gi|47522660|ref|NP_999079.1|	fatty-acid amide hydrolase 1 [Sus scrofa] >gi|21542039|sp|Q9TUI8.1|FAAH1_PIG RecName:	1.107	0.598	1.183	0.743

	Full=Fatty-acid amide hydrolase 1; AltName: Full=Anandamide amidohydrolase 1; AltName: Full=Oleamide hydrolase 1 >gi|6451573|dbj|BAA86917.1| fatty acid amide hydro				
gi|350581741|ref|XP_003124660.3|	PREDICTED: phosphomannomutase 2-like, partial [Sus scrofa]	1.863	1.052	1.59	1.141
gi|311267482|ref|XP_003131586.1|	PREDICTED: chromobox protein homolog 1-like [Sus scrofa]	---	---	---	---
gi|130759|sp|P23687.1|PPCE_PIG	RecName: Full=Prolyl endopeptidase; Short=PE; AltName: Full=Post-proline cleaving enzyme >gi|51592147|ref|NP_001004050.1| prolyl endopeptidase [Sus scrofa] >gi|387766256|pdb|4AN1|A Chain A, Prolyl Oligopeptidase From Porcine Brain With A Covalently	2.184	0.997	1.054	1.385
gi|5107662|pdb|1QFM|A	Chain A, Prolyl Oligopeptidase From Porcine Muscle				
gi|50514023|pdb|1VZ3|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, T597c Mutant				
gi|157879457|pdb|1O6F|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, D641a Mutant With Bound Peptide Ligand Suc-Gly-Pro				
gi|334878488|pdb|1H2Z|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, S554a Mutant With Bound Peptide Ligand Suc-Gly-Pro >gi|13096640|pdb|1E8M|A Chain A, Prolyl Oligopeptidase From Porcine Brain, Mutant, Complexed With Inhibitor >gi|37928243|pdb|1UOQ|A Chain A, Prolyl				
gi|157879458|pdb|1O6G|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, D641n Mutant With Bound Peptide Ligand Suc-Gly-Pro				
gi|10835490|pdb|1E5T|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, Mutant				
gi|27065054|pdb|1H2X|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, Y473f Mutant >gi|27065055|pdb|1H2Y|A Chain A, Prolyl Oligopeptidase From				

	Porcine Brain, Y473f Mutant With Covalently Bound Inhibitor Z-Pro-Prolinal				
gi|50514022|pdb|1VZ2|A	Chain A, Prolyl Oligopeptidase From Porcine Brain, Y73cV427CC255T Mutant				
gi|350584879|ref|XP_003126924.3|	PREDICTED: alanyl-tRNA synthetase, cytoplasmic [Sus scrofa]	1.61	0.915	1.097	1.114
gi|56711362|ref|NP_001008689.1|	GTP-binding protein SAR1b [Sus scrofa] >gi|75061519|sp|Q5PYH3.1|SAR1B_PIG RecName: Full=GTP-binding protein SAR1b >gi|55977172|gb|AAV68380.1| Sar1b protein [Sus scrofa]	0.806	0.515	0.613	0.785
gi|62948008|gb|AAY23007.1|	GTP-binding protein SAR1b [Sus scrofa]				
gi|122058965|gb|ABM66369.1|	Sara2 protein [Sus scrofa]				
gi|350581244|ref|XP_003354387.2|	PREDICTED: transcription elongation regulator 1-like [Sus scrofa]	1.157	0.827	1.12	0.839
gi|311256485|ref|XP_003126672.1|	PREDICTED: protein SCAF11 [Sus scrofa]	0.564	0.884	0.534	0.89
gi|335301749|ref|XP_001925115.3|	PREDICTED: inorganic pyrophosphatase [Sus scrofa]	0.845	1.353	0.98	1.4
gi|311257919|ref|XP_003127356.1|	PREDICTED: aldehyde dehydrogenase family 16 member A1-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311257921|ref|XP_003127357.1|	PREDICTED: aldehyde dehydrogenase family 16 member A1-like isoform 2 [Sus scrofa]				
gi|350590070|ref|XP_003131163.3|	PREDICTED: paraspeckle component 1 [Sus scrofa]	1.256	0.892	0.844	1.179
gi|343791007|ref|NP_001230549.1|	dynein, cytoplasmic 1, light intermediate chain 2 [Sus scrofa]	0.937	0.602	0.787	0.595
gi|194044484|ref|XP_001929185.1|	PREDICTED: eukaryotic translation initiation factor 2 subunit 2 [Sus scrofa]	0.878	0.871	0.883	0.824
gi|350583407|ref|XP_003481511.1|	PREDICTED: cathepsin S [Sus scrofa]	0.807	3.109	2.841	1.171
gi|298104126|ref|NP_001177126.1|	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 [Sus	0.475	0.386	0.242	0.436

	scrofa]				
gi|350582355|ref|XP_003354851.2|	PREDICTED: exportin-1 [Sus scrofa]	2.597	2.292	1.444	1.821
gi|148237564|ref|NP_001090977.1|	adenylosuccinate synthetase isozyme 2 [Sus scrofa] >gi|189031715|sp|A4Z6H1.1|PURA2_PIG RecName: Full=Adenylosuccinate synthetase isozyme 2; Short=AMPSase 2; Short=AdSS 2; AltName: Full=Adenylosuccinate synthetase, acidic isozyme; AltName: Full=Adeny	2.151	1.756	2.876	1.842
gi|147225159|emb|CAN13336.1|	valyl-tRNA synthetase 2 [Sus scrofa]	0.936	0.861	1.053	1.209
gi|305855130|ref|NP_001182307.1|	valyl-tRNA synthetase [Sus scrofa] >gi|162138236|gb|ABX82822.1| valyl-tRNA synthetase [Sus scrofa]				
gi|347300500|ref|NP_001231502.1|	pre-mRNA-processing factor 40 homolog A [Sus scrofa]	0.486	0.417	0.497	0.543
gi|350592272|ref|XP_003483433.1|	PREDICTED: LOW QUALITY PROTEIN: PDZ and LIM domain protein 2-like [Sus scrofa]	0.472	0.971	1.074	0.77
gi|343887450|ref|NP_001230627.1|	acireductone dioxygenase 1 [Sus scrofa]	---	---	---	---
gi|335310208|ref|XP_003361930.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4-like [Sus scrofa]	1.201	0.436	0.449	0.822
gi|297307137|ref|NP_001171999.1|	ran-specific GTPase-activating protein [Sus scrofa]	1.286	1.053	1.001	1.898
gi|237681312|ref|NP_001153744.1|	protein S100-A12 [Sus scrofa] >gi|126302600|sp|P80310.2|S10AC_PIG RecName: Full=Protein S100-A12; AltName: Full=Calgranulin-C; Short=CAGC; AltName: Full=Extracellular newly identified RAGE-binding protein; Short=EN-RAGE; AltName: Full=S100 calcium-b	0.787	1.875	1.494	2.476
gi|311275455|ref|XP_003134746.1|	PREDICTED: V-type proton ATPase subunit F-like [Sus scrofa]	1.032	1.05	1.458	1.027
gi|270047494|ref|NP_001161	fructose-1,6-bisphosphatase isozyme	1.007	0.651	0.666	0.64

104.2|	2 [Sus scrofa]				
gi|335300686|ref|XP_003358992.1|	PREDICTED: carbonyl reductase [NADPH] 1-like [Sus scrofa]	3.339	1.314	1.332	3.405
gi|350588305|ref|XP_003482618.1|	PREDICTED: methylosome subunit pICln-like [Sus scrofa]	---	---	---	---
gi|311245238|ref|XP_003121750.1|	PREDICTED: lisH domain and HEAT repeat-containing protein KIAA1468-like [Sus scrofa]	---	---	---	---
gi|219522002|ref|NP_001137188.1|	dual specificity mitogen-activated protein kinase kinase 1 [Sus scrofa] >gi|217314899|gb|ACK36984.1| mitogen-activated protein kinase kinase 1 [Sus scrofa]	---	---	---	---
gi|350580571|ref|XP_003480850.1|	PREDICTED: dual specificity mitogen-activated protein kinase kinase 2-like [Sus scrofa]				
gi|347300370|ref|NP_001231479.1|	mitogen-activated protein kinase kinase 2 [Sus scrofa]				
gi|350579773|ref|XP_001925384.4|	PREDICTED: U2 small nuclear ribonucleoprotein A~ [Sus scrofa]	0.703	0.733	0.655	0.683
gi|178056212|ref|NP_001116678.1|	tubulin polymerization-promoting protein [Sus scrofa] >gi|170178280|gb|ACB10579.1| tubulin polymerization promoting protein p25 alpha [Sus scrofa]	---	---	---	---
gi|350584885|ref|XP_003126937.3|	PREDICTED: splicing factor 3B subunit 3-like [Sus scrofa]	1.029	0.697	0.616	1.068
gi|62082662|gb|AAX62160.1|	glycogen synthase 1 [Sus scrofa]	---	---	---	---
gi|306029976|gb|ADM83431.1|	glycogen synthase 1 [Sus scrofa] >gi|306782595|ref|NP_001182437.1| glycogen [starch] synthase, muscle [Sus scrofa]				
gi|178056623|ref|NP_001116685.1|	vesicle-associated membrane protein-associated protein B [Sus scrofa] >gi|160210890|sp|A5GFS8.1|VAPB_PIG RecName: Full=Vesicle-associated membrane protein-associated protein B; Short=VAMP-B; Short=VAMP-associated protein B; Short=VAP-B >gi|147223393	0.473	0.849	0.623	0.782
gi|132566481|gb|ABO34136.	bactericidal permeability increasing	1.007	0.321	0.341	0.863

1|	protein [Sus scrofa]				
gi|226533693|ref|NP_001152779.1|	bactericidal permeability-increasing protein precursor [Sus scrofa] >gi|225922170|gb|ACO37155.1| bactericidal/permeability increasing protein [Sus scrofa]				
gi|347543763|ref|NP_001231548.1|	calmodulin-like 4 [Sus scrofa]	0.596	0.478	0.608	0.471
gi|240851536|ref|NP_001155875.1|	ubiquitin thioesterase OTUB1 [Sus scrofa] >gi|167888450|gb|ACA09613.1| OTUB1 [Sus scrofa]	1.916	1.458	1.235	1.685
gi|298231139|ref|NP_001177220.1|	pancreatic lipase-related protein 2 precursor [Sus scrofa] >gi|204307484|gb|ACI00231.1| pancreatic lipase-related protein 2 [Sus scrofa] >gi|204307482|gb|ACI00230.1| pancreatic lipase-related protein 2 [Sus scrofa]	1.485	1.001	0.449	0.797
gi|350580438|ref|XP_003480823.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7-like [Sus scrofa]	0.407	0.396	0.258	0.394
gi|335310428|ref|XP_003362028.1|	PREDICTED: surfeit locus protein 4-like, partial [Sus scrofa]	0.968	0.242	0.24	0.501
gi|311259825|ref|XP_001924399.2|	PREDICTED: leucine-rich repeat-containing protein 16A [Sus scrofa]	1.062	1.41	1.161	1.191
gi|346986364|ref|NP_001231333.1|	serine/threonine-protein phosphatase 6 catalytic subunit [Sus scrofa]	---	---	---	---
gi|148887343|sp|Q9MYT8.4|ATP5I_PIG	RecName: Full=ATP synthase subunit e, mitochondrial; Short=ATPase subunit e	0.728	0.624	0.575	0.535
gi|311268019|ref|XP_003131834.1|	PREDICTED: carboxypeptidase D [Sus scrofa]	0.829	0.626	0.85	0.993
gi|148230268|ref|NP_001090970.1|	galectin-3 [Sus scrofa] >gi|124830340|gb|ABN15099.1| lectin galactoside-binding soluble 3 [Sus scrofa]	0.987	0.842	0.859	0.77
gi|157427728|ref|NP_001098772.1|	ATP-citrate synthase isoform 2 [Sus scrofa] >gi|380509279|gb|AFD64642.1| ATP citrate lyase short isoform [Sus scrofa] >gi|156140098|gb|ABU51323	0.96	0.574	0.853	0.991

<table>
<tr><td></td><td>.1| ATP citrate lyase [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|381140346|ref|NP_001244205.1|</td><td>ATP-citrate synthase isoform 1 [Sus scrofa] >gi|380509277|gb|AFD64641.1| ATP citrate lyase long isoform [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|341942463|gb|AEL12455.1|</td><td>ATP citrate lyase [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|335289328|ref|XP_003355850.1|</td><td>PREDICTED: ubiquinone biosynthesis protein COQ9, mitochondrial-like [Sus scrofa]</td><td>0.95</td><td>0.625</td><td>0.737</td><td>0.889</td></tr>
<tr><td>gi|335307327|ref|XP_003127745.2|</td><td>PREDICTED: heterogeneous nuclear ribonucleoprotein R [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|343488538|ref|NP_001230424.1|</td><td>cytoplasmic dynein 1 intermediate chain 2 [Sus scrofa]</td><td>0.686</td><td>1.581</td><td>1.663</td><td>1.087</td></tr>
<tr><td>gi|343790888|ref|NP_001230502.1|</td><td>uncharacterized protein LOC100627352 [Sus scrofa]</td><td>0.852</td><td>0.333</td><td>0.465</td><td>0.797</td></tr>
<tr><td>gi|311265230|ref|XP_003130552.1|</td><td>PREDICTED: 3~(2~),5~-bisphosphate nucleotidase 1-like isoform 2 [Sus scrofa]</td><td>1.739</td><td>1.093</td><td>0.851</td><td>2.146</td></tr>
<tr><td>gi|311265232|ref|XP_003130551.1|</td><td>PREDICTED: 3~(2~),5~-bisphosphate nucleotidase 1-like isoform 1 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350597093|ref|XP_003362096.2|</td><td>PREDICTED: pyruvate kinase isozymes R/L-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311269055|ref|XP_003132321.1|</td><td>PREDICTED: monoacylglycerol lipase ABHD6 [Sus scrofa]</td><td>0.846</td><td>0.276</td><td>0.256</td><td>0.585</td></tr>
<tr><td>gi|346421372|ref|NP_001231060.1|</td><td>ferritin, light polypeptide [Sus scrofa]</td><td>0.84</td><td>1.455</td><td>2.659</td><td>1.513</td></tr>
<tr><td>gi|311261863|ref|XP_003128900.1|</td><td>PREDICTED: cell growth-regulating nucleolar protein [Sus scrofa]</td><td>1.193</td><td>1.164</td><td>1.529</td><td>1.079</td></tr>
<tr><td>gi|346644844|ref|NP_001231177.1|</td><td>phosphotriesterase-related protein [Sus scrofa]</td><td>1.138</td><td>2.16</td><td>2.467</td><td>1.396</td></tr>
<tr><td>gi|7288152|dbj|BAA92850.1|</td><td>esterase D [Sus scrofa]</td><td>3.122</td><td>1.562</td><td>2.008</td><td>3.194</td></tr>
<tr><td>gi|47522936|ref|NP_999225.1|</td><td>S-formylglutathione hydrolase [Sus scrofa] >gi|62900112|sp|Q9GJT2.1|ESTD_PIG RecName: Full=S-formylglutathione hydrolase; Short=FGH; AltName: Full=Esterase D >gi|10443892|gb|AAG17630.1|AF254785_1 esterase D [Sus scrofa] >gi|9857260|dbj|BAB11922.1|e</td><td></td><td></td><td></td><td></td></tr>
</table>

gi|348605151|ref|NP_001231720.1|	hydroxysteroid (17-beta) dehydrogenase 3 [Sus scrofa]	---	---	---	---
gi|350589482|ref|XP_003357775.2|	PREDICTED: BAG family molecular chaperone regulator 1-like isoform 1 [Sus scrofa]				
gi|347300398|ref|NP_001231491.1|	core histone macro-H2A.1 isoform 1 [Sus scrofa]	1.416	0.411	0.92	1.318
gi|347300400|ref|NP_001231492.1|	core histone macro-H2A.1 isoform 2 [Sus scrofa]				
gi|350588303|ref|XP_003129732.3|	PREDICTED: serine/threonine-protein kinase PAK 1-like [Sus scrofa]	1.086	0.799	0.761	0.84
gi|45268967|gb|AAS55896.1|	40S ribosomal protein S28, partial [Sus scrofa]	0.812	1.156	1.082	1.173
gi|48597082|ref|NP_001001587.1|	40S ribosomal protein S28 [Sus scrofa] >gi|51316555|sp|Q6QAT1.2|RS28_PIG RecName: Full=40S ribosomal protein S28				
gi|13878316|sp|P79273.1|ACADS_PIG	RecName: Full=Short-chain specific acyl-CoA dehydrogenase, mitochondrial; Short=SCAD; AltName: Full=Butyryl-CoA dehydrogenase; Flags: Precursor >gi|47522686|ref|NP_999063.1| short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Sus s	1.815	0.506	0.361	0.938
gi|311252326|ref|XP_003125038.1|	PREDICTED: mannosyl-oligosaccharide glucosidase [Sus scrofa]	---	---	---	---
gi|166796059|ref|NP_001107755.1|	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 [Sus scrofa] >gi|164598078|gb|ABY61326.1| small inducible cytokine subfamily E member 1 [Sus scrofa]	1.039	0.894	0.937	1.423
gi|297747346|ref|NP_001177097.1|	S100 calcium binding protein A14 [Sus scrofa]	0.868	1.211	1.289	0.925
gi|346716331|ref|NP_001231183.1|	ras-related protein Rab-5C [Sus scrofa]	0.994	1.048	0.475	0.811
gi|122142619|sp|Q19S50.1|STAT3_PIG	RecName: Full=Signal transducer and activator of transcription 3 >gi|113205774|ref|NP_001038045.	0.697	0.816	0.729	0.586

	1| signal transducer and activator of transcription 3 [Sus scrofa] >gi|315273320|gb|ADU03227.1| signal transducer and activator of transcription 3 isofor				
gi|315273324|gb|ADU03228.1|	signal transducer and activator of transcription 3 isoform 2 [Sus scrofa]				
gi|335284676|ref|XP_003124691.2|	PREDICTED: coronin-7-like [Sus scrofa]	2.172	1.572	1.581	1.798
gi|350582437|ref|XP_003481270.1|	PREDICTED: multiple coagulation factor deficiency protein 2-like [Sus scrofa]	---	---	---	---
gi|56788496|gb|AAW29969.1|	unknown [Sus scrofa] >gi|56792880|gb|AAW30632.1| unknown [Sus scrofa]	0.647	1.212	0.768	1.437
gi|311268139|ref|XP_003131895.1|	PREDICTED: sedoheptulokinase [Sus scrofa]	---	---	---	---
gi|335310769|ref|XP_003362184.1|	PREDICTED: THO complex subunit 4-like, partial [Sus scrofa]	0.639	0.688	0.742	0.587
gi|350589921|ref|XP_003482951.1|	PREDICTED: olfactomedin-4-like [Sus scrofa]				
gi|335284655|ref|XP_003124675.2|	PREDICTED: putative oxidoreductase GLYR1 isoform 1 [Sus scrofa]				
gi|335284657|ref|XP_003354668.1|	PREDICTED: putative oxidoreductase GLYR1 isoform 2 [Sus scrofa]				
gi|335284659|ref|XP_003354669.1|	PREDICTED: putative oxidoreductase GLYR1 isoform 3 [Sus scrofa]				
gi|319738636|ref|NP_001188360.1|	selenoprotein O [Sus scrofa]	---	---	---	---
gi|311256987|ref|XP_003126905.1|	PREDICTED: telomeric repeat-binding factor 2-interacting protein 1 [Sus scrofa]	1.368	2.792	2.63	1.525
gi|350591252|ref|XP_003132269.3|	PREDICTED: RNA-binding protein 5 [Sus scrofa]	---	---	---	---
gi|335281184|ref|XP_003353752.1|	PREDICTED: WD repeat-containing protein 5 [Sus scrofa]	0.726	1.433	1.209	1.175
gi|345199288|ref|NP_001230831.1|	protein phosphatase 1, regulatory (inhibitor) subunit 7 [Sus scrofa]	1.888	1.653	0.854	2.001
gi|311276634|ref|XP_003135	PREDICTED: mitochondrial import	0.885	1.602	1.803	0.802

287.1|	inner membrane translocase subunit Tim8 A-like [Sus scrofa]				
gi|350584903|ref|XP_003126945.3|	PREDICTED: AP-1 complex subunit gamma-1 isoform 1 [Sus scrofa]	1.115	0.685	0.787	1.059
gi|350584905|ref|XP_003481845.1|	PREDICTED: AP-1 complex subunit gamma-1 isoform 2 [Sus scrofa]				
gi|178056464|ref|NP_001116693.1|	beta-hexosaminidase subunit alpha precursor [Sus scrofa] >gi|169117926|gb|ACA43012.1| hexosaminidase A alpha polypeptide [Sus scrofa]	0.957	0.757	0.809	0.847
gi|385648284|ref|NP_001245315.1|	topoisomerase (DNA) II beta 180kDa [Sus scrofa]	0.719	0.554	0.635	0.674
gi|311260926|ref|XP_001924849.2|	PREDICTED: sec1 family domain-containing protein 1 [Sus scrofa]	1.944	0.808	1.404	1.612
gi|311248720|ref|XP_003123296.1|	PREDICTED: eukaryotic translation initiation factor 3 subunit G-like [Sus scrofa]	0.707	1.429	1.503	1.273
gi|335285938|ref|XP_003131986.2|	PREDICTED: Y-box-binding protein 2-like [Sus scrofa]	---	---	---	---
gi|350590843|ref|XP_003483149.1|	PREDICTED: Y-box-binding protein 2-like [Sus scrofa]				
gi|57528035|ref|NP_001009582.1|	stathmin [Sus scrofa] >gi|75043336|sp|Q6DUB7.3|STMN1_PIG RecName: Full=Stathmin >gi|49615355|gb|AAT66936.1| stathmin-1 [Sus scrofa]	0.699	1.231	1.255	1.081
gi|350578790|ref|XP_003121632.3|	PREDICTED: calcium-binding protein p22-like [Sus scrofa]	0.862	0.931	1.199	0.729
gi|350596649|ref|XP_003361456.2|	PREDICTED: calcium-binding protein p22-like [Sus scrofa]				
gi|350578792|ref|XP_003480452.1|	PREDICTED: calcium-binding protein p22-like isoform 1 [Sus scrofa]				
gi|4432942|dbj|BAA21081.1|	ribosomal protein S4 [Sus scrofa]	1.354	1.001	0.784	1.355
gi|324021713|ref|NP_001191212.1|	ribosomal protein S4 [Sus scrofa]				
gi|350590315|ref|XP_003483030.1|	PREDICTED: eukaryotic translation initiation factor 1-like [Sus scrofa]	0.736	1.146	1.26	1.239
gi|194043083|ref|XP_001928729.1|	PREDICTED: malectin-like [Sus scrofa]	0.792	0.388	0.53	0.878

<table>
<tr><td>gi|335309994|ref|XP_003130977.2|</td><td>PREDICTED: hypothetical protein LOC100522509, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|89216|pir||PT0220</td><td>Ig lambda chain V-C region PLC3 - pig (fragment)</td><td>0.534</td><td>0.84</td><td>0.664</td><td>0.541</td></tr>
<tr><td>gi|164511|gb|AAA03572.1|</td><td>immunoglobulin lambda-chain, partial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|343183368|ref|NP_001230248.1|</td><td>immunoglobulin lambda-like polypeptide 5 precursor [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|125947|sp|P01846.1|LAC_PIG</td><td>RecName: Full=Ig lambda chain C region</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350592642|ref|XP_003483508.1|</td><td>PREDICTED: T-cell receptor beta chain T17T-22-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311271023|ref|XP_003133034.1|</td><td>PREDICTED: immunoglobulin lambda-like polypeptide 5-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350584919|ref|XP_003481848.1|</td><td>PREDICTED: IST1 homolog [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335290688|ref|XP_003356248.1|</td><td>PREDICTED: hydroxymethylglutaryl-CoA lyase, mitochondrial-like isoform 1 [Sus scrofa]</td><td>0.92</td><td>1.174</td><td>0.679</td><td>0.763</td></tr>
<tr><td>gi|335310870|ref|XP_003362231.1|</td><td>PREDICTED: tumor protein D54-like, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|19883961|sp|P35750.3|CAN1_PIG</td><td>RecName: Full=Calpain-1 catalytic subunit; AltName: Full=Calcium-activated neutral proteinase 1; Short=CANP 1; AltName: Full=Calpain mu-type; AltName: Full=Calpain-1 large subunit; AltName: Full=Micromolar-calpain; Short=muCANP >gi|8132993|gb|AAF734</td><td>1.292</td><td>1.074</td><td>1.2</td><td>1.214</td></tr>
<tr><td>gi|47522772|ref|NP_999137.1|</td><td>calpain-1 catalytic subunit [Sus scrofa] >gi|8132991|gb|AAF73443.1|AF263609_1 micromolar calcium-activated neutral protease 1 isoform B [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|335282905|ref|XP_003354187.1|</td><td>PREDICTED: 60S ribosomal protein L18a-like isoform 4 [Sus scrofa] >gi|335282901|ref|XP_003354185.1| PREDICTED: 60S ribosomal protein L18a-like isoform 2 [Sus</td><td>0.673</td><td>0.483</td><td>0.4</td><td>0.83</td></tr>
</table>

	scrofa] >gi|335282903|ref|XP_003354186.1| PREDICTED: 60S ribosomal protein L18a-like isofor				
gi|2275401|gb|AAB63894.1|	ovarian sterol carrier protein 2, partial [Sus scrofa]	1.491	0.833	1.117	1.32
gi|350586177|ref|XP_003482126.1|	PREDICTED: non-specific lipid-transfer protein-like [Sus scrofa]				
gi|350587510|ref|XP_003482430.1|	PREDICTED: pre-mRNA 3~-end-processing factor FIP1-like [Sus scrofa]	0.645	0.841	1.135	1.033
gi|113205600|ref|NP_001038003.1|	guanine nucleotide-binding protein subunit alpha-11 [Sus scrofa] >gi|122142902|sp|Q2XSV9.2|GNA11_PIG RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G alpha-11; Short=G-protein subunit alpha-11 >gi|84688557|gb|ABB71823.2| gu	1.305	0.455	0.502	0.734
gi|146741292|dbj|BAF62301.1|	guanine nucleotide-binding protein, alpha-11 [Sus scrofa]				
gi|350587233|ref|XP_003482374.1|	PREDICTED: cytoplasmic dynein 1 heavy chain 1-like [Sus scrofa]	---	---	---	---
gi|335310309|ref|XP_003361972.1|	PREDICTED: 39S ribosomal protein L12, mitochondrial-like, partial [Sus scrofa]	---	---	---	---
gi|121149|sp|P20735.1|GGT1_PIG	RecName: Full=Gamma-glutamyltranspeptidase 1; Short=GGT 1; AltName: Full=Gamma-glutamyltransferase 1; AltName: Full=Glutathione hydrolase 1; AltName: Full=Leukotriene-C4 hydrolase; AltName: CD_antigen=CD224; Contains: RecName: Full=Gamma-glutamyltra	0.92	0.941	1.029	0.802
gi|146741348|dbj|BAF62329.1|	gamma-glutamyltranspeptidase 1 [Sus scrofa]				
gi|193788671|ref|NP_001123277.1|	carnitine O-palmitoyltransferase 1, liver isoform [Sus scrofa] >gi|14579225|gb|AAK69171.1|AF288789_1 carnitine palmitoyltransferase I [Sus scrofa] >gi|222090415|gb|ACM42415	1.518	0.619	1.096	0.742

	.1| liver type carnitine palmitoyltransferase I [Sus scrofa]				
gi|312062795|ref|NP_001185851.1|	mitogen-activated protein kinase 1 [Sus scrofa] >gi|310789265|gb|ADP24686.1| extracellular signal-regulated kinase-2 [Sus scrofa]	---	---	---	---
gi|335310941|ref|XP_003362261.1|	PREDICTED: 40S ribosomal protein S2-like [Sus scrofa]	0.619	0.566	0.74	0.944
gi|124857|sp|P00998.1|ISK1_PIG	RecName: Full=Pancreatic secretory trypsin inhibitor; AltName: Full=Serine protease inhibitor Kazal-type 1 >gi|230351|pdb|1TGS|I Chain I, Three-Dimensional Structure Of The Complex Between Pancreatic Secretory Inhibitor (Kazal Type) And Trypsinogen	0.546	1.059	0.297	0.98
gi|229311|prf||700704A	inhibitor II,trypsin				
gi|335283733|ref|XP_003354394.1|	PREDICTED: pancreatic secretory trypsin inhibitor-like isoform 1 [Sus scrofa]				
gi|343432640|ref|NP_001230334.1|	39S ribosomal protein L44, mitochondrial [Sus scrofa]	1.053	0.959	0.789	0.981
gi|311252785|ref|XP_003125258.1|	PREDICTED: serine/arginine-rich splicing factor 7-like isoform 1 [Sus scrofa]	0.925	1.059	1.163	1.091
gi|350586583|ref|XP_003482220.1|	PREDICTED: serine/arginine-rich splicing factor 3-like [Sus scrofa]				
gi|350596827|ref|XP_003128414.2|	PREDICTED: serine/arginine-rich splicing factor 3-like [Sus scrofa]				
gi|311252787|ref|XP_003125259.1|	PREDICTED: serine/arginine-rich splicing factor 7-like isoform 2 [Sus scrofa]				
gi|311264036|ref|XP_003129968.1|	PREDICTED: 40S ribosomal protein S25-like isoform 2 [Sus scrofa] >gi|311264034|ref|XP_003129967.1| PREDICTED: 40S ribosomal protein S25-like isoform 1 [Sus scrofa]	0.408	0.174	0.194	0.439
gi|75054309|sp|Q8WNQ7.1|GALNS_PIG	RecName: Full=N-acetylgalactosamine-6-sulfatase; AltName: Full=Chondroitinsulfatase;	1.114	1.206	1.362	0.958

	Short=Chondroitinase; AltName: Full=Galactose-6-sulfate sulfatase; AltName: Full=N-acetylgalactosamine-6-sulfate sulfatase; Short=GalNAc6S sulfatase; Flags: Precurs				
gi|298160993|ref|NP_001177169.1|	glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic [Sus scrofa]	0.658	0.354	0.279	0.313
gi|350583346|ref|XP_003125776.3|	PREDICTED: ubiquitin associated protein 2-like isoform 3 [Sus scrofa]	0.946	1.471	1.696	1.033
gi|350596813|ref|XP_003484323.1|	PREDICTED: ubiquitin-associated protein 2-like [Sus scrofa]				
gi|347922148|ref|NP_001231673.1|	charged multivesicular body protein 5 [Sus scrofa]	0.442	0.792	1.053	0.549
gi|335289683|ref|XP_003355956.1|	PREDICTED: LOW QUALITY PROTEIN: mitochondrial import inner membrane translocase subunit TIM50-like [Sus scrofa]	0.891	1.032	0.715	0.748
gi|114326218|ref|NP_001041535.1|	hematological and neurological expressed 1-like protein [Sus scrofa] >gi|54114954|tpg|DAA01824.1| TPA_inf: HN1-like protein [Sus scrofa]	0.682	1.098	0.968	1.471
gi|346986315|ref|NP_001231313.1|	alpha-soluble NSF attachment protein [Sus scrofa]	1.129	0.696	0.769	0.769
gi|350592026|ref|XP_003132761.3|	PREDICTED: TBC1 domain family member 23-like [Sus scrofa]	0.957	0.835	1.06	0.95
gi|311255134|ref|XP_003126086.1|	PREDICTED: 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial-like isoform 1 [Sus scrofa] >gi|311255118|ref|XP_003126081.1| PREDICTED: 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial-like isoform 1 [Sus scrofa]	0.922	0.418	---	0.493
gi|350589397|ref|XP_003357727.2|	PREDICTED: aminopeptidase B-like [Sus scrofa]	1.773	1.562	1.107	1.839
gi|47716872|gb|AAT37622.1|	galectin-1 [Sus scrofa]	0.635	0.693	0.67	0.513
gi|311259452|ref|XP_003128108.1|	PREDICTED: 40S ribosomal protein S8-like [Sus scrofa]	1.064	0.634	0.671	1.375
gi|189043876|sp|A1XQU9.1|	RecName: Full=40S ribosomal	0.872	0.66	0.567	0.93

RS20_PIG	protein S20 >gi|194018718|ref|NP_001123426.1| 40S ribosomal protein S20 [Sus scrofa] >gi|117661119|gb|ABK55655.1| RPS20 [Sus scrofa]				
gi|113205666|ref|NP_001038019.1|	NADH dehydrogenase 1 beta subcomplex 6 [Sus scrofa] >gi|87047638|gb|ABD18452.1| NADH dehydrogenase 1 beta subcomplex 6 [Sus scrofa]	---	---	---	---
gi|311270922|ref|XP_003133013.1|	PREDICTED: up-regulated during skeletal muscle growth protein 5-like [Sus scrofa] >gi|311271791|ref|XP_003133221.1| PREDICTED: up-regulated during skeletal muscle growth protein 5-like [Sus scrofa]	---	---	---	---
gi|256838109|ref|NP_001157984.1|	phosphate carrier protein, mitochondrial [Sus scrofa] >gi|255964672|gb|ACU44653.1| solute carrier family 25 member 3 [Sus scrofa]	0.704	0.387	0.381	0.659
gi|343790856|ref|NP_001230567.1|	glutathione transferase zeta 1 [Sus scrofa]	1.644	0.741	0.595	1.333
gi|195972993|ref|NP_001124446.1|	stromal interaction molecule 1 precursor [Sus scrofa] >gi|157929328|gb|ABW03922.1| stromal interaction molecule 1 [Sus scrofa]				
gi|178056753|ref|NP_001116644.1|	glycogen phosphorylase, liver form [Sus scrofa] >gi|167834153|gb|ACA02827.1| glycogen storage disease type VI-related protein [Sus scrofa]	---	---	---	---
gi|350589278|ref|XP_003130571.3|	PREDICTED: melanoma inhibitory activity protein 3-like, partial [Sus scrofa]	0.752	1.073	0.757	0.72
gi|335287593|ref|XP_003355390.1|	PREDICTED: ras-related C3 botulinum toxin substrate 2-like [Sus scrofa]	---	---	---	---
gi|342672022|ref|NP_001230144.1|	exportin-2 [Sus scrofa]	1.359	0.529	0.497	1.03
gi|311274576|ref|XP_003134	PREDICTED: small nuclear	---	---	---	---

384.1|	ribonucleoprotein-associated protein B~-like [Sus scrofa]				
gi|343887452|ref|NP_001230628.1|	small nuclear ribonucleoprotein polypeptide N [Sus scrofa]				
gi|381352839|gb|AFG25597.1|	SNRPN [Sus scrofa]				
gi|335292262|ref|XP_001927373.3|	PREDICTED: isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial [Sus scrofa]	0.941	0.61	1.02	0.702
gi|335281115|ref|XP_001926630.3|	PREDICTED: nuclear pore complex protein Nup214 [Sus scrofa]	0.588	1.43	0.797	0.893
gi|350587460|ref|XP_003128981.3|	PREDICTED: sister chromatid cohesion protein PDS5 homolog A-like [Sus scrofa]	---	---	---	---
gi|219521990|ref|NP_001137182.1|	granzyme B precursor [Sus scrofa] >gi|216408333|gb|ACJ72857.1| granzyme B [Sus scrofa]	1.167	3.528	4.173	3.057
gi|335299970|ref|XP_003358743.1|	PREDICTED: DCN1-like protein 1-like [Sus scrofa]	---	---	---	---
gi|194040450|ref|XP_001927992.1|	PREDICTED: lactoylglutathione lyase isoform 1 [Sus scrofa]	1.245	1.591	3.199	2.25
gi|350586543|ref|XP_003482212.1|	PREDICTED: glutamate--cysteine ligase catalytic subunit isoform 2 [Sus scrofa]	2.588	1.351	1.762	2.034
gi|51702802|sp|P62901.1|RL31_PIG	RecName: Full=60S ribosomal protein L31 >gi|350582083|ref|XP_003481192.1| PREDICTED: 60S ribosomal protein L31-like isoform 4 [Sus scrofa] >gi|350582079|ref|XP_003481190.1| PREDICTED: 60S ribosomal protein L31-like isoform 2 [Sus scrofa] >gi|3505820	0.573	0.991	0.69	0.994
gi|349585075|ref|NP_001231802.1|	small acidic protein [Sus scrofa]	---	---	---	---
gi|47524464|gb|AAT34965.1|	2~-5~ oligoadenylate synthetase 1 [Sus scrofa]	---	---	---	---
gi|740987|prf||2006263A	Arg Gly amidinotransferase	0.768	0.399	0.54	0.432
gi|190360601|ref|NP_001121914.1|	glycine amidinotransferase, mitochondrial [Sus scrofa] >gi|308153447|sp|P50441.2|GATM_PIG RecName: Full=Glycine				

	amidinotransferase, mitochondrial; AltName: Full=L-arginine:glycine amidinotransferase; AltName: Full=Transamidinase; Flags: Precursor >g				
gi|350594954|ref|XP_003360054.2|	PREDICTED: adenosine deaminase [Sus scrofa]	0.473	0.933	0.854	1.307
gi|350582315|ref|XP_003481243.1|	PREDICTED: NFU1 iron-sulfur cluster scaffold homolog, mitochondrial-like [Sus scrofa]	0.809	1.818	1.689	1.055
gi|311276040|ref|XP_003135024.1|	PREDICTED: LOW QUALITY PROTEIN: acyl-coenzyme A thioesterase 9, mitochondrial-like [Sus scrofa]	1.339	0.598	0.958	0.858
gi|75074354|sp|Q9GL51.3|LIS1_PIG	RecName: Full=Platelet-activating factor acetylhydrolase IB subunit alpha; AltName: Full=Lissencephaly-1 protein; Short=LIS-1; AltName: Full=PAF acetylhydrolase 45 kDa subunit; Short=PAF-AH 45 kDa subunit; AltName: Full=PAF-AH alpha; Short=PAFAH alp	0.992	0.695	0.644	0.883
gi|350590470|ref|XP_003131623.3|	PREDICTED: canalicular multispecific organic anion transporter 2 [Sus scrofa]	0.962	0.719	0.732	0.732
gi|47522764|ref|NP_999133.1|	integrin beta-1 precursor [Sus scrofa] >gi|75050024|sp|Q9GLP0.1|ITB1_PIG RecName: Full=Integrin beta-1; AltName: Full=Fibronectin receptor subunit beta; AltName: Full=VLA-4 subunit beta; AltName: CD_antigen=CD29; Flags: Precursor >gi|10336839|gb|AAG	---	---	---	---
gi|335281543|ref|XP_003122613.2|	PREDICTED: protein fat-free homolog [Sus scrofa]	---	---	---	---
gi|350587133|ref|XP_001926860.4|	PREDICTED: thyroid receptor-interacting protein 11 [Sus scrofa]	0.712	1.283	0.892	1.203
gi|350595681|ref|XP_003135172.3|	PREDICTED: structural maintenance of chromosomes protein 1A-like [Sus scrofa]	---	---	---	---
gi|346716326|ref|NP_001231	SWI/SNF-related matrix-associated	0.627	0.547	0.905	0.991

<table>
<tr><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>181.1|</td><td>actin-dependent regulator of chromatin subfamily D member 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|145279215|ref|NP_001077410.1|</td><td>angiotensin-converting enzyme isoform 2 precursor [Sus scrofa] >gi|119381511|gb|ABL73884.1| angiotensin I converting enzyme [Sus scrofa]</td><td>1.814</td><td>1.096</td><td>2.012</td><td>1.498</td></tr>
<tr><td>gi|311273877|ref|XP_003134081.1|</td><td>PREDICTED: 28S ribosomal protein S27, mitochondrial-like [Sus scrofa]</td><td>1.338</td><td>0.635</td><td>0.986</td><td>1.095</td></tr>
<tr><td>gi|350587174|ref|XP_003356842.2|</td><td>PREDICTED: serpin A3-6 [Sus scrofa]</td><td>1.228</td><td>0.874</td><td>1.477</td><td>0.914</td></tr>
<tr><td>gi|335295413|ref|XP_003130208.2|</td><td>PREDICTED: calcium-binding mitochondrial carrier protein Aralar2 [Sus scrofa]</td><td>0.922</td><td>0.459</td><td>0.572</td><td>0.493</td></tr>
<tr><td>gi|400294561|gb|AFP81702.1|</td><td>solute carrier family 27 member 4, partial [Sus scrofa]</td><td>0.627</td><td>0.518</td><td>0.399</td><td>0.655</td></tr>
<tr><td>gi|183228163|gb|ACC59785.1|</td><td>PRP19/PSO4 pre-mRNA processing factor 19-like protien [Sus scrofa]</td><td>1.04</td><td>1.003</td><td>0.467</td><td>0.837</td></tr>
<tr><td>gi|190360605|ref|NP_001121929.1|</td><td>pre-mRNA-processing factor 19 [Sus scrofa] >gi|356995561|dbj|BAL14717.1| nuclear matrix protein 200 [Sus scrofa] >gi|171920012|gb|ACB59178.1| pre-mRNA processing factor 19 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|55926217|ref|NP_001007518.1|</td><td>cytochrome c oxidase subunit 5B, mitochondrial precursor [Sus scrofa] >gi|75042739|sp|Q5S3G4.1|COX5B_PIG RecName: Full=Cytochrome c oxidase subunit 5B, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide Vb; Flags: Precursor >gi|55583747|g</td><td>0.467</td><td>0.331</td><td>0.397</td><td>0.379</td></tr>
<tr><td>gi|350580071|ref|XP_003122734.3|</td><td>PREDICTED: oxysterol-binding protein 1 [Sus scrofa]</td><td>0.815</td><td>1.016</td><td>0.753</td><td>0.838</td></tr>
<tr><td>gi|148226851|ref|NP_001090933.1|</td><td>ATP synthase subunit f, mitochondrial [Sus scrofa] >gi|117660512|gb|ABK55624.1| mitochondrial Atp5j2 [Sus scrofa]</td><td>0.81</td><td>0.22</td><td>0.278</td><td>0.434</td></tr>
<tr><td>gi|158518654|sp|Q95339.4|ATPK_PIG</td><td>RecName: Full=ATP synthase subunit f, mitochondrial</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|251764755|sp|A6M931.1|I</td><td>RecName: Full=Eukaryotic initiation</td><td>1.469</td><td>0.813</td><td>0.904</td><td>1.401</td></tr>
</table>

F4A3_PIG	factor 4A-III; Short=eIF-4A-III; Short=eIF4A-III; AltName: Full=ATP-dependent RNA helicase DDX48; AltName: Full=ATP-dependent RNA helicase eIF4A-3; AltName: Full=DEAD box protein 48; AltName: Full=Eukaryotic trans				
gi|350586361|ref|XP_003356557.2|	PREDICTED: serine/threonine-protein kinase PRP4 homolog [Sus scrofa]	0.523	0.604	0.573	0.522
gi|335290248|ref|XP_003127516.2|	PREDICTED: hsp70-binding protein 1-like [Sus scrofa]	---	---	---	---
gi|342349338|ref|NP_001230145.1|	elaC homolog 2 [Sus scrofa]	---	---	---	---
gi|350590206|ref|XP_003131326.3|	PREDICTED: protein kinase C alpha type, partial [Sus scrofa]	---	---	---	---
gi|49274643|ref|NP_001001864.1|	amine oxidase [flavin-containing] B [Sus scrofa] >gi|62899647|sp|Q6PLK3.3|AOFB_PIG RecName: Full=Amine oxidase [flavin-containing] B; AltName: Full=Monoamine oxidase type B; Short=MAO-B >gi|46909483|gb|AAT06259.1| monoamine oxidase B [Sus scrofa]	0.901	0.405	0.432	0.776
gi|335280279|ref|XP_001928782.2|	PREDICTED: 26S protease regulatory subunit 10B [Sus scrofa]	1.174	0.812	0.717	1.112
gi|350583020|ref|XP_003481419.1|	PREDICTED: zinc finger protein 706-like [Sus scrofa]	1.271	1.945	2.395	1.9
gi|195539476|ref|NP_001124208.1|	bifunctional purine biosynthesis protein PURH [Sus scrofa] >gi|192383834|gb|ACF04802.1| 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Sus scrofa]	1.674	0.855	1.284	1.949
gi|113205898|ref|NP_001038078.1|	microtubule-associated protein RP/EB family member 1 [Sus scrofa] >gi|81174752|gb|ABB58918.1| microtubule-associated protein RP/EB family member 1 [Sus scrofa]	---	---	---	---
gi|335308271|ref|XP_003361	PREDICTED: pre-mRNA-processing	---	---	---	---

162.1|	factor 6-like [Sus scrofa]				
gi|60394813|sp|Q29201.4|RS16_PIG	RecName: Full=40S ribosomal protein S16 >gi|212549659|ref|NP_001131092.1| 40S ribosomal protein S16 [Sus scrofa] >gi|335289675|ref|XP_003355953.1| PREDICTED: 40S ribosomal protein S16-like isoform 2 [Sus scrofa] >gi|335289677|ref|XP_003355954.1| PRE	1.01	0.711	0.563	1.304
gi|350588052|ref|XP_003357166.2|	PREDICTED: importin-7, partial [Sus scrofa]	1.07	1.011	0.855	0.961
gi|222090420|gb|ACM42418.1|	carnitine palmitoyltransferase II [Sus scrofa]	1.253	0.307	0.223	0.492
gi|229358270|gb|ACQ57802.1|	mitochondrial carnitine palmitoyltransferase II [Sus scrofa]				
gi|350536125|ref|NP_001233172.1|	carnitine O-palmitoyltransferase 2, mitochondrial precursor [Sus scrofa] >gi|294805368|gb|ADF42518.1| mitochondrial carnitine palmitoyltransferase II [Sus scrofa]				
gi|113205668|ref|NP_001038021.1|	microsomal glutathione S-transferase 3 [Sus scrofa] >gi|120564453|gb|ABM30152.1| microsomal glutathione S-transferase 3 [Sus scrofa] >gi|87047644|gb|ABD18455.1| microsomal glutathione S-transferase 3 [Sus scrofa]	1.689	0.87	0.986	0.95
gi|335309593|ref|XP_003361696.1|	PREDICTED: 39S ribosomal protein L12, mitochondrial-like, partial [Sus scrofa]	0.419	0.93	0.562	0.587
gi|346716090|ref|NP_001231205.1|	thioredoxin-like protein 1 [Sus scrofa]	1.061	0.842	0.83	0.965
gi|12055551|emb|CAC21172.1|	diazepam binding inhibitor [Sus scrofa]	1.667	2.489	2.516	1.486
gi|110825776|sp|P12026.2|ACBP_PIG	RecName: Full=Acyl-CoA-binding protein; Short=ACBP; AltName: Full=Diazepam-binding inhibitor; Short=DBI; AltName: Full=Endozepine; Short=EP; Contains: RecName: Full=DBI(32-86) >gi|47523046|ref|N				

	P_999284.1| acyl-CoA-binding protein [Sus scrofa] >gi|1				
gi|281427368|ref|NP_001163992.1|	steroid hormone receptor ERR1 [Sus scrofa] >gi|229609707|gb|ACQ83469.1| ERRa [Sus scrofa]	---	---	---	---
gi|297632416|ref|NP_001172092.1|	enhancer of rudimentary homolog [Sus scrofa]	0.36	0.948	1.154	0.569
gi|118403852|ref|NP_001072139.1|	UBC1 [Sus scrofa] >gi|115371727|gb|ABI96188.1| UBC1 [Sus scrofa]	1.67	1.155	1.259	1.448
gi|343887409|ref|NP_001230603.1|	deoxynucleotidyltransferase terminal-interacting protein 2 [Sus scrofa]	---	---	---	---
gi|347300356|ref|NP_001231473.1|	uncharacterized protein LOC100689297 [Sus scrofa]	1.224	1.686	1.919	1.106
gi|311247993|ref|XP_003122918.1|	PREDICTED: probable methylthioribulose-1-phosphate dehydratase-like [Sus scrofa]	1.308	1.874	2.593	1.715
gi|349732262|ref|NP_001231870.1|	3-hydroxyanthranilate 3,4-dioxygenase [Sus scrofa]	0.477	0.418	0.343	0.525
gi|311252389|ref|XP_003125056.1|	PREDICTED: STAM-binding protein [Sus scrofa]	---	---	---	---
gi|343790890|ref|NP_001230503.1|	acyl-CoA dehydrogenase family, member 8 [Sus scrofa]	1.868	1.044	1.462	1.699
gi|343780946|ref|NP_001230486.1|	D-dopachrome decarboxylase [Sus scrofa]	1.248	1.873	1.422	1.566
gi|335289112|ref|XP_003126904.2|	PREDICTED: lysyl-tRNA synthetase isoform 1 [Sus scrofa]	1.504	0.655	0.639	1.189
gi|335289114|ref|XP_003355791.1|	PREDICTED: lysyl-tRNA synthetase isoform 2 [Sus scrofa]				
gi|350587855|ref|XP_003129278.3|	PREDICTED: protein transport protein Sec24D [Sus scrofa]	---	---	---	---
gi|335309819|ref|XP_003361783.1|	PREDICTED: charged multivesicular body protein 2a-like, partial [Sus scrofa]	---	---	---	---
gi|113205716|ref|NP_001038033.1|	1,5-anhydro-D-fructose reductase [Sus scrofa] >gi|94421324|gb|ABF18830.1| putative aldo-keto reductase family 1 member CL2 [Sus scrofa]	1.44	1.224	0.906	1.522
gi|239938601|sp|P82125.2|AKCL2_PIG	RecName: Full=1,5-anhydro-D-fructose				

<table>
<tr><td></td><td>reductase; Short=AF reductase; AltName: Full=Aldo-keto reductase family 1 member C-like protein 2; Short=Aldo-keto reductase family 1 member CL2; AltName: Full=Aldo-keto reductase family 1 member E2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350589668|ref|XP_003482894.1|</td><td>PREDICTED: 1,5-anhydro-D-fructose reductase-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311258972|ref|XP_003127870.1|</td><td>PREDICTED: adenylyl cyclase-associated protein 1-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|266686|sp|P29804.1|ODPA_PIG</td><td>RecName: Full=Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial; AltName: Full=PDHE1-A type I; Flags: Precursor >gi|1851|emb|CAA37180.1| pyruvate dehydrogenase (lipoamide) [Sus scrofa domesticus]</td><td>1.493</td><td>0.329</td><td>0.515</td><td>0.96</td></tr>
<tr><td>gi|448580|prf||1917268A</td><td>pyruvate dehydrogenase:SUBUNIT=alpha</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350595555|ref|XP_003360292.2|</td><td>PREDICTED: pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform 1 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350595557|ref|XP_003484129.1|</td><td>PREDICTED: pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350539577|ref|NP_001233167.1|</td><td>coatomer subunit gamma-2 [Sus scrofa] >gi|301087607|gb|ADK56184.1| coatomer protein complex subunit gamma 2 [Sus scrofa]</td><td>1.059</td><td>0.472</td><td>0.381</td><td>0.867</td></tr>
<tr><td>gi|1262435|emb|CAA61864.1|</td><td>put. 26S protease subunit [Sus scrofa]</td><td>0.765</td><td>0.82</td><td>0.599</td><td>0.929</td></tr>
<tr><td>gi|47522792|ref|NP_999148.1|</td><td>26S protease regulatory subunit 8 [Sus scrofa] >gi|49065781|sp|P62197.1|PRS8_PIG RecName: Full=26S protease regulatory subunit 8; AltName: Full=26S proteasome AAA-ATPase</td><td></td><td></td><td></td><td></td></tr>
</table>

	subunit RPT6; AltName: Full=Proteasome 26S subunit ATPase 5; AltName: Full=Prot				
gi|311252444|ref|XP_003125100.1|	PREDICTED: small nuclear ribonucleoprotein G-like [Sus scrofa]	0.638	0.44	0.527	0.508
gi|194036463|ref|XP_001928684.1|	PREDICTED: ras-related protein Rap-1A isoform 1 [Sus scrofa] >gi|335287176|ref|XP_003355289.1| PREDICTED: ras-related protein Rap-1A isoform 2 [Sus scrofa]	0.726	0.228	0.197	0.487
gi|350584241|ref|XP_003481702.1|	PREDICTED: ras-related protein Rap-1b [Sus scrofa] >gi|350596871|ref|XP_003484329.1| PREDICTED: ras-related protein Rap-1b-like [Sus scrofa]				
gi|51512143|gb|AAU05316.1|	hepatitis B virus x interacting protein [Sus scrofa]	---	---	---	---
gi|187471167|sp|Q66X52.2|HBXIP_PIG	RecName: Full=Hepatitis B virus X-interacting protein homolog; Short=HBV X-interacting protein homolog; Short=HBX-interacting protein homolog				
gi|335307770|ref|XP_003360968.1|	PREDICTED: hepatitis B virus X-interacting protein homolog, partial [Sus scrofa]				
gi|350595155|ref|XP_003360146.2|	PREDICTED: maltase-glucoamylase, intestinal-like, partial [Sus scrofa]	0.458	0.608	0.571	0.338
gi|350597052|ref|XP_003361964.2|	PREDICTED: maltase-glucoamylase, intestinal-like, partial [Sus scrofa]				
gi|350580871|ref|XP_003123769.3|	PREDICTED: ras GTPase-activating-like protein IQGAP2-like [Sus scrofa]	0.962	0.63	0.649	1.002
gi|345199274|ref|NP_001230825.1|	glutaredoxin 3 [Sus scrofa]	1.323	0.863	0.929	1.587
gi|335283420|ref|XP_003123942.2|	PREDICTED: protein PRRC1-like, partial [Sus scrofa]	1.596	1.527	0.935	1.343
gi|335301657|ref|XP_001929317.3|	PREDICTED: coiled-coil domain-containing protein 6 [Sus scrofa]	---	---	---	---
gi|335308509|ref|XP_003361258.1|	PREDICTED: microsomal glutathione S-transferase 2-like,	0.711	0.282	0.335	0.585

<table>
<tr><td></td><td>partial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|346421419|ref|NP_001231084.1|</td><td>lysosome membrane protein 2 precursor [Sus scrofa]</td><td>0.696</td><td>0.52</td><td>0.332</td><td>0.768</td></tr>
<tr><td>gi|163915141|ref|NP_001106518.1|</td><td>carnitine O-acetyltransferase [Sus scrofa] >gi|162852671|emb|CAP49176.1| carnitine acetyl transferase [Sus scrofa]</td><td>1.806</td><td>1.038</td><td>1.109</td><td>1.343</td></tr>
<tr><td>gi|239504558|ref|NP_001155112.1|</td><td>caspase-10 [Sus scrofa] >gi|229365449|dbj|BAH57972.1| caspase 10 [Sus scrofa]</td><td>1.116</td><td>0.668</td><td>0.738</td><td>0.988</td></tr>
<tr><td>gi|350590094|ref|XP_003357986.2|</td><td>PREDICTED: putative sodium-coupled neutral amino acid transporter 10 isoform 1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350590096|ref|XP_003482987.1|</td><td>PREDICTED: putative sodium-coupled neutral amino acid transporter 10 isoform 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|62510530|sp|Q8MJ30.1|DHPR_PIG</td><td>RecName: Full=Dihydropteridine reductase; AltName: Full=HDHPR; AltName: Full=Quinoid dihydropteridine reductase >gi|47523746|ref|NP_999508.1| dihydropteridine reductase [Sus scrofa] >gi|22094813|gb|AAM91996.1|AF526879_1 quinoid dihydropteridine redu</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|164023822|ref|NP_001106688.1|</td><td>60S ribosomal protein L7 [Sus scrofa] >gi|56384247|gb|AAV85772.1| ribosomal protein L7 [Sus scrofa]</td><td>0.808</td><td>0.736</td><td>0.535</td><td>1.166</td></tr>
<tr><td>gi|47522730|ref|NP_999115.1|</td><td>60S ribosomal protein L29 [Sus scrofa] >gi|51704218|sp|Q95281.4|RL29_PIG RecName: Full=60S ribosomal protein L29 >gi|4586439|dbj|BAA76404.1| ribosomal protein L29/heparin/heparan sulfate interacting protein [Sus scrofa] >gi|4586433|dbj|BAA76401.1|r</td><td>0.323</td><td>0.44</td><td>0.287</td><td>0.306</td></tr>
<tr><td>gi|350591380|ref|XP_003358554.2|</td><td>PREDICTED: ADP-ribosylation factor-like protein 8B-like, partial [Sus scrofa]</td><td>1.719</td><td>1.334</td><td>---</td><td>1.377</td></tr>
<tr><td>gi|356582297|ref|NP_001239143.1|</td><td>ADP-ribosylation factor-like 8B [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
</table>

gi|194474046|ref|NP_001124006.1|	1-acyl-sn-glycerol-3-phosphate acyltransferase beta precursor [Sus scrofa] >gi|262036915|dbj|BAI47593.1| 1-acylglycerol-3-phosphate O-acyltransferase 2 [Sus scrofa] >gi|216408319|gb|ACJ72850.1| 1-acylglycerol-3-phosphate O-acyltransferase 2 [Sus scr	0.835	0.385	0.563	0.422
gi|311256096|ref|XP_003126504.1|	PREDICTED: epidermal growth factor receptor kinase substrate 8 [Sus scrofa]	1.005	1.468	1.663	1.18
gi|350578257|ref|XP_001927626.3|	PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform 1 [Sus scrofa]	---	---	---	---
gi|319401911|ref|NP_001188310.1|	adenosylhomocysteinase-like protein 1 [Sus scrofa] >gi|315321422|gb|ADU04838.1| adenosylhomocysteinase-like protein 1 [Sus scrofa]	---	---	---	---
gi|335293809|ref|XP_003129222.2|	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [Sus scrofa]	---	---	---	---
gi|21263966|sp|O97580.1|SUCB1_PIG	RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial; AltName: Full=ATP-specific succinyl-CoA synthetase subunit beta; AltName: Full=Succinyl-CoA synthetase beta-A chain; Short=SCS-betaA; Flags: Precursor >gi|3808237|gb|AAC697	1.603	0.886	0.685	1.279
gi|311266259|ref|XP_003131022.1|	PREDICTED: succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial [Sus scrofa]				
gi|350584784|ref|XP_003481823.1|	PREDICTED: acyl-CoA synthetase family member 3, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|311272155|ref|XP_003133324.1|	PREDICTED: activated RNA polymerase II transcriptional coactivator p15-like [Sus scrofa]	1.272	0.887	1.028	0.92
gi|164664444|ref|NP_001106907.1|	alpha-2-macroglobulin receptor-associated protein precursor [Sus	0.444	0.486	0.435	0.456

	scrofa] >gi|162946612|gb|ABY21262.1| alpha-2-macroglobulin receptor-associated protein [Sus scrofa]				
gi|1709973|sp|P53027.3|RL10A_PIG	RecName: Full=60S ribosomal protein L10a	1.019	0.786	0.75	1.14
gi|350584352|ref|XP_001926213.3|	PREDICTED: putative deoxyribose-phosphate aldolase-like [Sus scrofa]	1.499	0.84	1.311	1.266
gi|345091011|ref|NP_001230734.1|	PCTP-like protein [Sus scrofa]	1.458	0.724	0.904	1.656
gi|335286933|ref|XP_003355223.1|	PREDICTED: 39S ribosomal protein L9, mitochondrial-like isoform 1 [Sus scrofa]	---	---	---	---
gi|335286935|ref|XP_003355224.1|	PREDICTED: 39S ribosomal protein L9, mitochondrial-like isoform 2 [Sus scrofa]				
gi|335286937|ref|XP_003355225.1|	PREDICTED: 39S ribosomal protein L9, mitochondrial-like isoform 3 [Sus scrofa]				
gi|335285324|ref|XP_003354827.1|	PREDICTED: prenylcysteine oxidase-like [Sus scrofa]	1.016	0.403	0.147	0.77
gi|350580104|ref|XP_003353925.2|	PREDICTED: mitochondrial carrier homolog 2 [Sus scrofa]	0.732	---	0.78	1.032
gi|335297415|ref|XP_003358038.1|	PREDICTED: 60S ribosomal protein L38-like isoform 2 [Sus scrofa] >gi|311266862|ref|XP_003131289.1| PREDICTED: 60S ribosomal protein L38-like isoform 1 [Sus scrofa]	0.659	0.354	0.29	0.677
gi|350589263|ref|XP_003130553.2|	PREDICTED: isoleucyl-tRNA synthetase, mitochondrial [Sus scrofa]	---	---	---	---
gi|350589265|ref|XP_003482824.1|	PREDICTED: isoleucyl-tRNA synthetase, mitochondrial-like [Sus scrofa]				
gi|311258593|ref|XP_003127690.1|	PREDICTED: adaptin ear-binding coat-associated protein 2-like [Sus scrofa]	---	---	---	---
gi|350590733|ref|XP_003131874.3|	PREDICTED: pre-mRNA-processing-splicing factor 8, partial [Sus scrofa]	1.245	0.745	0.327	1.182

<table>
<tr><td>gi|171465894|gb|ACB46190.1|</td><td>solute carrier family 3 member 2 [Sus scrofa]</td><td>1.19</td><td>1.317</td><td>1.335</td><td>1.619</td></tr>
<tr><td>gi|335281655|ref|XP_003353857.1|</td><td>PREDICTED: 4F2 cell-surface antigen heavy chain [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|335290721|ref|XP_003356259.1|</td><td>PREDICTED: platelet-activating factor acetylhydrolase 2, cytoplasmic-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350589961|ref|XP_003482962.1|</td><td>PREDICTED: LIM domain only protein 7-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350594202|ref|XP_003133916.3|</td><td>PREDICTED: threonyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]</td><td>1.321</td><td>1.138</td><td>1.101</td><td>1.8</td></tr>
<tr><td>gi|121118|sp|P20305.1|GELS_PIG</td><td>RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor >gi|164472|gb|AAA31042.1| plasma gelsolin precursor, partial [Sus scrofa] >gi|758306|emb|CAA32077.1| gelsolin [Sus scrofa]</td><td>0.313</td><td>0.654</td><td>0.571</td><td>0.497</td></tr>
<tr><td>gi|350587978|ref|XP_003129373.3|</td><td>PREDICTED: protein FAM13A-like [Sus scrofa]</td><td>0.659</td><td>0.866</td><td>0.618</td><td>0.781</td></tr>
<tr><td>gi|311260959|ref|XP_003128594.1|</td><td>PREDICTED: magnesium-dependent phosphatase 1-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335308200|ref|XP_003361139.1|</td><td>PREDICTED: ADP-sugar pyrophosphatase-like [Sus scrofa]</td><td>0.954</td><td>0.904</td><td>0.3</td><td>0.59</td></tr>
<tr><td>gi|350589627|ref|XP_003482885.1|</td><td>PREDICTED: ADP-sugar pyrophosphatase-like isoform 2 [Sus scrofa] >gi|350589625|ref|XP_003482884.1| PREDICTED: ADP-sugar pyrophosphatase-like isoform 1 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|147832425|emb|CAN59677.1|</td><td>HLA-B associated transcript 3 [Sus scrofa]</td><td>0.548</td><td>0.744</td><td>0.786</td><td>0.679</td></tr>
<tr><td>gi|147832426|emb|CAN59678.1|</td><td>HLA-B associated transcript 3 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|162138209|gb|ABX82810.1|</td><td>HLA-B-associated protein 3 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|223950621|ref|NP_001138854.1|</td><td>large proline-rich protein BAG6 [Sus scrofa] >gi|317374853|sp|A5D9M6.1|BAG6_PIG RecName: Full=Large</td><td></td><td></td><td></td><td></td></tr>
</table>

	proline-rich protein BAG6; AltName: Full=BCL2-associated athanogene 6; AltName: Full=HLA-B-associated transcript 3 >gi|147832424|emb|CAN59676.1| HLA-				
gi|350580973|ref|XP_003123871.3|	PREDICTED: alpha-mannosidase 2 [Sus scrofa]	1.133	0.658	0.917	0.809
gi|350583728|ref|XP_003126027.3|	PREDICTED: protein kinase C and casein kinase substrate in neurons protein 2-like [Sus scrofa]	---	---	---	---
gi|350588987|ref|XP_003130351.3|	PREDICTED: protein PRRC2C [Sus scrofa]	---	---	---	---
gi|359465576|ref|NP_001240753.1|	A-kinase anchor protein 9 [Sus scrofa]	0.772	1.137	0.982	0.663
gi|311254196|ref|XP_003125793.1|	PREDICTED: double-stranded RNA-specific adenosine deaminase, partial [Sus scrofa]	0.75	1.18	1.736	1.162
gi|311270046|ref|XP_003132745.1|	PREDICTED: 60S ribosomal protein L24-like isoform 1 [Sus scrofa]	0.42	0.371	0.263	0.418
gi|57527982|ref|NP_001009576.1|	radixin [Sus scrofa] >gi|131821|sp|P26044.1|RADI_PIG RecName: Full=Radixin; AltName: Full=Moesin-B >gi|164586|gb|AAB02865.1| moesin B [Sus scrofa]	---	---	---	---
gi|335292025|ref|XP_003128369.2|	PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]	0.82	0.746	0.935	0.779
gi|350586526|ref|XP_003482206.1|	PREDICTED: butyrophilin-like protein 1-like [Sus scrofa]				
gi|311248954|ref|XP_003123394.1|	PREDICTED: methylthioribose-1-phosphate isomerase [Sus scrofa]	1.08	0.841	0.697	1.123
gi|335290012|ref|XP_003356047.1|	PREDICTED: protein arginine N-methyltransferase 1 isoform 1 [Sus scrofa]	1.589	0.772	0.747	1.434
gi|335290016|ref|XP_003356049.1|	PREDICTED: protein arginine N-methyltransferase 1 isoform 3 [Sus scrofa]				
gi|350581874|ref|XP_003124716.3|	PREDICTED: rab11 family-interacting protein 3-like [Sus scrofa]	0.509	0.444	0.527	0.474

gi|47523066|ref|NP_999296.1|	caspase-3 [Sus scrofa] >gi|54035961|sp|Q95ND5.1|CASP3_PIG RecName: Full=Caspase-3; Short=CASP-3; Contains: RecName: Full=Caspase-3 subunit p17; Contains: RecName: Full=Caspase-3 subunit p12; Flags: Precursor >gi|14090240|dbj|BAB55544.1| caspase-3 [S	1.672	1.439	1.284	1.702
gi|335290940|ref|XP_003356338.1|	PREDICTED: histone-binding protein RBBP4-like [Sus scrofa]	---	---	---	---
gi|346986460|ref|NP_001231381.1|	AP-2 complex subunit sigma isoform 1 [Sus scrofa]	---	---	---	---
gi|194038455|ref|XP_001928714.1|	PREDICTED: arginase-2, mitochondrial [Sus scrofa]	1.045	1.8	1.849	1.528
gi|350579579|ref|XP_001925536.4|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 5 [Sus scrofa]	2.285	0.861	0.75	1.323
gi|346421378|ref|NP_001231061.1|	serpin H1 precursor [Sus scrofa]	0.667	0.74	0.49	0.32
gi|347543818|ref|NP_001231565.1|	cytochrome P450, family 4, subfamily F, polypeptide 55 precursor [Sus scrofa]	0.959	0.472	0.472	0.986
gi|349585046|ref|NP_001231798.1|	uncharacterized protein LOC100513647 [Sus scrofa]	1.129	1.102	1.159	1.01
gi|346421403|ref|NP_001231076.1|	translocon-associated protein subunit gamma [Sus scrofa]	---	---	---	---
gi|350580262|ref|XP_003123007.3|	PREDICTED: pleckstrin homology domain-containing family A member 7 [Sus scrofa]	0.79	0.737	0.979	0.755
gi|350596440|ref|XP_003484272.1|	PREDICTED: elongation factor Tu GTP-binding domain-containing protein 1 [Sus scrofa]	---	---	---	---
gi|335288532|ref|XP_001925819.3|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 5 isoform 1 [Sus scrofa]	0.985	1.005	1.02	1.252
gi|335288534|ref|XP_003355644.1|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 5 isoform 2 [Sus scrofa]				
gi|350593631|ref|XP_003359617.2|	PREDICTED: LOW QUALITY PROTEIN: alkyldihydroxyacetonephosphate	1.415	1.103	1.169	1.625

	synthase, peroxisomal [Sus scrofa]				
gi|311274849|ref|XP_001925742.2|	PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 1B [Sus scrofa]	0.672	1.313	0.928	0.755
gi|311247401|ref|XP_003122628.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP2-like isoform 1 [Sus scrofa]	0.659	0.769	0.771	0.931
gi|335281587|ref|XP_003353839.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP2-like isoform 4 [Sus scrofa] >gi|335281583|ref|XP_003353837.1| PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP2-like isoform 2 [Sus scrofa] >gi|335281585|ref|XP_003353838.1| PREDICTED: peptidyl				
gi|335308437|ref|XP_003361229.1|	PREDICTED: nodal modulator 1, partial [Sus scrofa]	---	---	---	---
gi|171986635|gb|ACB59309.1|	intelectin 2 [Sus scrofa]	1.352	0.631	0.358	0.858
gi|350583241|ref|XP_003481467.1|	PREDICTED: intelectin-2-like [Sus scrofa]				
gi|194042631|ref|XP_001925414.1|	PREDICTED: ATP-binding cassette sub-family B member 10, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|346986378|ref|NP_001231341.1|	heme oxygenase 2 [Sus scrofa]	0.834	0.975	0.848	0.916
gi|335305501|ref|XP_003134862.2|	PREDICTED: E3 ubiquitin-protein ligase ZNRF2-like [Sus scrofa]	0.453	1.019	1.358	0.815
gi|164302|gb|AAA30983.1|	alpha-1 acid glycoprotein, partial [Sus scrofa]	0.263	0.696	0.494	0.699
gi|350579533|ref|XP_003480630.1|	PREDICTED: alpha-1-acid glycoprotein-like [Sus scrofa] >gi|194033903|ref|XP_001928762.1| PREDICTED: alpha-1-acid glycoprotein [Sus scrofa]				
gi|297747284|ref|NP_001172109.1|	prefoldin subunit 6 [Sus scrofa] >gi|297747282|ref|NP_001172108.1| prefoldin subunit 6 [Sus scrofa]	1.246	1.047	1.771	1.188
gi|343887362|ref|NP_001230582.1|	small nuclear ribonucleoprotein Sm D2 [Sus scrofa]	0.577	0.588	0.599	0.648

gi|335280302|ref|XP_003353540.1|	PREDICTED: actin-related protein 10-like [Sus scrofa]	---	---	---	---
gi|52001458|sp|P22411.3|DPP4_PIG	RecName: Full=Dipeptidyl peptidase 4; AltName: Full=Dipeptidyl peptidase IV; Short=DPP IV; AltName: Full=T-cell activation antigen CD26; AltName: CD_antigen=CD26; Contains: RecName: Full=Dipeptidyl peptidase 4 membrane form; AltName: Full=Dipeptidyl	0.986	1.192	1.335	1.094
gi|90108717|pdb|2AJC|D	Chain D, Porcine Dipeptidyl Peptidase Iv (Cd26) In Complex With 4-(2- Aminoethyl)-Benzene Sulphonyl Fluoride (Aebsf) >gi|90108715|pdb|2AJC|B Chain B, Porcine Dipeptidyl Peptidase Iv (Cd26) In Complex With 4-(2- Aminoethyl)-Benzene Sulphonyl Fluoride				
gi|350588982|ref|XP_003130335.2|	PREDICTED: thiamin pyrophosphokinase 1-like [Sus scrofa]	---	---	---	---
gi|194035181|ref|XP_001925325.1|	PREDICTED: sphingomyelin phosphodiesterase 2 [Sus scrofa]	---	---	---	---
gi|350593416|ref|XP_003483680.1|	PREDICTED: BAG family molecular chaperone regulator 4-like [Sus scrofa]	0.782	1.77	1.183	0.995
gi|311274558|ref|XP_003134376.1|	PREDICTED: vacuolar protein sorting-associated protein 16 homolog isoform 1 [Sus scrofa]				
gi|311274560|ref|XP_003134377.1|	PREDICTED: vacuolar protein sorting-associated protein 16 homolog isoform 2 [Sus scrofa]				
gi|297632389|ref|NP_001172080.1|	mitochondrial ribosomal protein L52 [Sus scrofa]	0.14	0.446	0.448	0.294
gi|347658999|ref|NP_001231625.1|	uncharacterized protein LOC100512671 [Sus scrofa]	0.634	1.694	2.208	1.089
gi|350588410|ref|XP_003482644.1|	PREDICTED: ester hydrolase C11orf54 homolog [Sus scrofa]				
gi|350582160|ref|XP_003124976.3|	PREDICTED: threonine synthase-like 2-like [Sus scrofa]	---	---	---	---
gi|148234110|ref|NP_001087	selenide, water dikinase 2 [Sus	---	---	---	---

204.1|	scrofa] >gi|171769747|sp|A1YIZ1.2|SPS2_PIG RecName: Full=Selenide, water dikinase 2; AltName: Full=Selenium donor protein 2; AltName: Full=Selenophosphate synthase 2 >gi|120988510|gb|ABM46855.1| selenophosphate synthe				
gi|343432623|ref|NP_001230325.1|	bolA-like protein 1 [Sus scrofa]	1.648	1.679	1.528	1.58
gi|335284508|ref|XP_003124605.2|	PREDICTED: mu-crystallin homolog [Sus scrofa]	---	---	---	---
gi|178057067|ref|NP_001116568.1|	hsp90 co-chaperone Cdc37 [Sus scrofa] >gi|51870491|emb|CAG15149.1| CDC37 cell division cycle 37 protein [Sus scrofa]	0.935	0.666	0.807	0.831
gi|297591959|ref|NP_001172060.1|	farnesyl pyrophosphate synthase precursor [Sus scrofa] >gi|262072800|dbj|BAI47708.1| farnesyl diphosphate synthase [Sus scrofa]	---	---	---	---
gi|2498644|sp|Q29075.1|NKL_PIG	RecName: Full=Antimicrobial peptide NK-lysin; Short=NKL; Flags: Precursor >gi|736317|emb|CAA59720.1| NK-lysin [Sus scrofa]	---	---	---	---
gi|311252221|ref|XP_003124987.1|	PREDICTED: antimicrobial peptide NK-lysin [Sus scrofa]				
gi|1352666|sp|P11493.2|PP2AB_PIG	RecName: Full=Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform; Short=PP2A-beta >gi|164298|gb|AAA30982.1| protein phosphatase 2A beta subunit, partial [Sus scrofa]	2.065	1.224	0.936	1.719
gi|47523790|ref|NP_999531.1|	serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform [Sus scrofa] >gi|54038797|sp|P67776.1|PP2AA_PIG RecName: Full=Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform; Short=PP2A-alpha >gi|164296|gb|AA				

	A30981.1|				
gi|311272409|ref|XP_003133430.1|	PREDICTED: serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform [Sus scrofa]				
gi|194034423|ref|XP_001926853.1|	PREDICTED: l-2-hydroxyglutarate dehydrogenase, mitochondrial [Sus scrofa]	0.722	0.257	0.397	0.518
gi|347658980|ref|NP_001231616.1|	ribosomal protein L36 [Sus scrofa] >gi|350580660|ref|XP_003480870.1| PREDICTED: 60S ribosomal protein L36 isoform 3 [Sus scrofa] >gi|350580656|ref|XP_003480868.1| PREDICTED: 60S ribosomal protein L36 isoform 1 [Sus scrofa] >gi|350580658|ref|XP_00348	0.476	0.379	0.238	0.385
gi|350581899|ref|XP_003124791.3|	PREDICTED: LOW QUALITY PROTEIN: putative N-acetylglucosamine-6-phosphate deacetylase-like [Sus scrofa]	---	---	---	---
gi|60097959|ref|NP_001012408.1|	dystrophin [Sus scrofa] >gi|75052798|sp|Q5GN48.1|DMD_PIG RecName: Full=Dystrophin >gi|58416122|emb|CAI26302.1| dystrophin [Sus scrofa]	1.086	0.933	1.591	0.858
gi|325652134|ref|NP_001191701.1|	bromodomain-containing protein 4 [Sus scrofa] >gi|321172828|gb|ADW77216.1| bromodomain-containing protein 4 [Sus scrofa]	0.575	1.145	0.883	0.932
gi|347300394|ref|NP_001231489.1|	vesicle-fusing ATPase [Sus scrofa]	0.525	0.58	0.503	0.645
gi|350596345|ref|XP_003484261.1|	PREDICTED: vesicle-fusing ATPase-like [Sus scrofa]				
gi|350594565|ref|XP_003134235.3|	PREDICTED: acid ceramidase-like [Sus scrofa]	0.498	1.252	1.005	0.73
gi|160420271|ref|NP_001038047.1|	zinc finger Ran-binding domain-containing protein 2 [Sus scrofa] >gi|118578026|sp|Q19QU3.1|ZRAB2_PIG RecName: Full=Zinc finger Ran-binding domain-containing protein 2; AltName: Full=Zinc finger protein	0.664	1.344	0.97	0.958

	265 >gi|104295127|gb|ABF72033.1| zinc finger pr				
gi|335306763|ref|XP_003360560.1|	PREDICTED: ubiquitin-like protein 4A-like isoform 1 [Sus scrofa]	0.8	0.778	0.894	0.843
gi|335306765|ref|XP_003360561.1|	PREDICTED: ubiquitin-like protein 4A-like isoform 2 [Sus scrofa]				
gi|311255898|ref|XP_003126418.1|	PREDICTED: LOW QUALITY PROTEIN: nuclear pore complex protein Nup107-like [Sus scrofa]	---	---	---	---
gi|335310331|ref|XP_003361983.1|	PREDICTED: poly(U)-binding-splicing factor PUF60-like [Sus scrofa]	1.293	1.065	0.792	1.76
gi|178056703|ref|NP_001116542.1|	angiotensin-converting enzyme 2 precursor [Sus scrofa] >gi|170066580|gb|ACB06678.1| angiotensin converting enzyme 2 [Sus scrofa]	0.613	0.88	0.945	0.81
gi|254546340|gb|ACT66265.1|	angiotensin I converting enzyme 2 [Sus scrofa domesticus]				
gi|335310935|ref|XP_003362258.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-like [Sus scrofa]	0.74	0.563	0.475	0.74
gi|346644697|ref|NP_001231015.1|	eukaryotic translation initiation factor 3 subunit L [Sus scrofa]	2.308	1.055	1.577	1.845
gi|194041975|ref|XP_001929465.1|	PREDICTED: STE20-like kinase isoform 2 [Sus scrofa]	---	---	---	---
gi|346227222|ref|NP_001230997.1|	ribosomal protein L13a isoform 1 [Sus scrofa]	0.802	0.636	0.5	0.943
gi|346227224|ref|NP_001230998.1|	ribosomal protein L13a isoform 2 [Sus scrofa]				
gi|58618083|gb|AAW80612.1|	P2X7 receptor [Sus scrofa]	0.605	0.439	0.663	0.308
gi|311270616|ref|XP_001926839.2|	PREDICTED: P2X purinoceptor 7 [Sus scrofa]				
gi|58826311|gb|AAW82880.1|	P2X7 purinergic receptor [Sus scrofa]				
gi|122064241|sp|Q06AT0.3|HPCL1_PIG	RecName: Full=Hippocalcin-like protein 1 >gi|178056468|ref|NP_001116598.1| hippocalcin-like protein 1 [Sus scrofa] >gi|115394792|gb|ABI97190.1| HPCL1 [Sus scrofa]	1.122	1.907	2.156	1.642

gi|343478230|ref|NP_001230382.1|	enhancer of yellow 2 transcription factor homolog isoform 1 [Sus scrofa] >gi|350582977|ref|XP_003481405.1| PREDICTED: enhancer of yellow 2 transcription factor homolog isoform 1 [Sus scrofa]	---	---	---	---
gi|343478234|ref|NP_001230383.1|	enhancer of yellow 2 transcription factor homolog isoform 2 [Sus scrofa] >gi|350582979|ref|XP_003481406.1| PREDICTED: enhancer of yellow 2 transcription factor homolog isoform 2 [Sus scrofa]				
gi|585657|sp|P37109.1|ISK4_PIG	RecName: Full=Serine protease inhibitor Kazal-type 4; AltName: Full=Peptide PEC-60; Flags: Precursor >gi|47523134|ref|NP_999029.1| serine protease inhibitor Kazal-type 4 precursor [Sus scrofa] >gi|5705936|gb|AAB23691.2| PEC-60 [Sus scrofa] >gi|2034|	---	---	---	---
gi|159162822|pdb|1PCE|A	Chain A, Solution Structure And Dynamics Of Pec-60, A Protein Of The Kazal Type Inhibitor Family, Determined By Nuclear Magnetic Resonance Spectroscopy				
gi|350595064|ref|XP_003134565.3|	PREDICTED: dnaJ homolog subfamily B member 6-like [Sus scrofa]	1.018	1.082	1.298	1.144
gi|54039304|sp|P62279.2|RS13_PIG	RecName: Full=40S ribosomal protein S13	0.681	0.401	0.457	0.918
gi|348605266|ref|NP_001231758.1|	ribosomal protein S13 [Sus scrofa]				
gi|164525|gb|AAA31059.1|	lactoferrin [Sus scrofa]	---	1.107	---	0.8
gi|17467354|gb|AAL40161.1|L77887_1	lactoferrin, partial [Sus scrofa]				
gi|3915882|sp|P14632.3|TRFL_PIG	RecName: Full=Lactotransferrin; Short=Lactoferrin; Flags: Precursor				
gi|47523782|ref|NP_999527.1|	lactotransferrin precursor [Sus scrofa] >gi|164614|gb|AAA31102.1| lactoferrin [Sus scrofa]				
gi|116488296|gb|ABJ98718.1|	lactoferrin [Sus scrofa]				
gi|41688298|dbj|BAD08651.1	lactotransferrin [Sus scrofa]				

|					
gi|32130549|gb|AAP70487.1|	lactoferrin [Sus scrofa]				
gi|194043274|ref|XP_001927288.1|	PREDICTED: developmentally-regulated GTP-binding protein 1 isoform 1 [Sus scrofa]	---	---	---	---
gi|311257796|ref|XP_003127291.1|	PREDICTED: SUMO-activating enzyme subunit 1-like isoform 1 [Sus scrofa]	---	---	---	---
gi|335289862|ref|XP_003356004.1|	PREDICTED: SUMO-activating enzyme subunit 1-like isoform 2 [Sus scrofa]				
gi|2258465|gb|AAB94003.1|	succinyl-CoA synthetase alpha subunit [Sus scrofa]	0.61	0.582	0.448	0.616
gi|12621910|gb|AAB94002.2|	succinyl-CoA synthetase [Sus scrofa]				
gi|9955019|pdb|1EUC|A	Chain A, Crystal Structure Of Dephosphorylated Pig Heart, Gtp-Specific Succinyl-Coa Synthetase				
gi|90109582|pdb|2FPP|A	Chain A, Crystal Structure Of Pig Gtp-Specific Succinyl-Coa Synthetase From Polyethylene Glycol With Chloride Ions >gi|90109574|pdb|2FPI|A Chain A, Crystal Structure Of Pig Gtp-Specific Succinyl-Coa Synthetase From Polyethylene Glycol >gi|90109554|p				
gi|90109572|pdb|2FPG|A	Chain A, Crystal Structure Of Pig Gtp-Specific Succinyl-Coa Synthetase In Complex With Gdp				
gi|223634702|sp|O19069.2|SUCA_PIG	RecName: Full=Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha; Flags: Precursor				
gi|9955021|pdb|1EUD|A	Chain A, Crystal Structure Of Phosphorylated Pig Heart, Gtp-Specific Succinyl-Coa Synthetase				
gi|311263942|ref|XP_003129926.1|	PREDICTED: oligoribonuclease, mitochondrial-like [Sus scrofa]	---	---	---	---

<table>
<tr><td>gi|194035009|ref|XP_001925846.1|</td><td>PREDICTED: ras-related protein Rab-27B-like [Sus scrofa]</td><td>0.921</td><td>0.767</td><td>0.639</td><td>0.911</td></tr>
<tr><td>gi|17933431|gb|AAL48289.1|AF452448_1</td><td>beta-2-microglobulin protein [Sus scrofa]</td><td>0.551</td><td>1.527</td><td>1.177</td><td>1.363</td></tr>
<tr><td>gi|47522782|ref|NP_999143.1|</td><td>beta-2-microglobulin precursor [Sus scrofa] >gi|1168611|sp|Q07717.1|B2MG_PIG RecName: Full=Beta-2-microglobulin; AltName: Full=Lactollin; Flags: Precursor >gi|350578710|ref|XP_003480435.1| PREDICTED: beta-2-microglobulin-like [Sus scrofa] >gi|350578</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|365813031|pdb|3QQ3|E</td><td>Chain E, Crystal Structure Of Swine Major Histocompatibility Complex Class I Sla-1 0401 And Identification Of 2009 Pandemic Swine-Origin Influenza A H1n1 Virus Cytotoxic T Lymphocyte Epitope Peptides >gi|365813034|pdb|3QQ4|B Chain B, Crystal Structu</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|77176666|gb|ABA64451.1|</td><td>beta-2-microglobulin protein, partial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350578712|ref|XP_003480436.1|</td><td>PREDICTED: beta-2-microglobulin-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311248023|ref|XP_003122934.1|</td><td>PREDICTED: eukaryotic translation initiation factor 3 subunit M [Sus scrofa]</td><td>1.029</td><td>0.97</td><td>1.863</td><td>1.341</td></tr>
<tr><td>gi|346986292|ref|NP_001231303.1|</td><td>uncharacterized protein LOC100155717 isoform 1 [Sus scrofa] >gi|346986290|ref|NP_001231302.1| uncharacterized protein LOC100155717 isoform 1 [Sus scrofa]</td><td>1.313</td><td>0.813</td><td>0.747</td><td>0.706</td></tr>
<tr><td>gi|346986294|ref|NP_001231304.1|</td><td>uncharacterized protein LOC100155717 isoform 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350589017|ref|XP_003482769.1|</td><td>PREDICTED: 28S ribosomal protein S14, mitochondrial-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|45268975|gb|AAS55900.1|</td><td>60S ribosomal protein L11, partial [Sus scrofa]</td><td>2.079</td><td>1.202</td><td>2.07</td><td>1.478</td></tr>
<tr><td>gi|51704216|sp|Q29205.3|RL</td><td>RecName: Full=60S ribosomal</td><td></td><td></td><td></td><td></td></tr>
</table>

11_PIG	protein L11 >gi|48675939|ref|NP_001001638.1| 60S ribosomal protein L11 [Sus scrofa] >gi|45239006|gb|AAS55632.1| ribosomal protein L11 [Sus scrofa]				
gi|433126|gb|AAA52218.1|	Ig gamma 2b chain constant region, partial [Sus scrofa] >gi|2136514|pir||I47160 Ig gamma 2b chain constant region - pig (fragment)	---	---	---	---
gi|350591483|ref|XP_003358588.2|	PREDICTED: acyl-CoA dehydrogenase family member 9, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|311253264|ref|XP_001925395.2|	PREDICTED: zinc transporter ZIP4-like [Sus scrofa]	---	---	---	---
gi|311260258|ref|XP_003128394.1|	PREDICTED: LEM domain-containing protein 2 [Sus scrofa]	---	---	---	---
gi|335288032|ref|XP_001929448.3|	PREDICTED: prostaglandin E synthase 3 isoform 1 [Sus scrofa]	---	---	---	---
gi|335288038|ref|XP_003355506.1|	PREDICTED: prostaglandin E synthase 3 isoform 4 [Sus scrofa]				
gi|335288034|ref|XP_003355504.1|	PREDICTED: prostaglandin E synthase 3 isoform 2 [Sus scrofa]				
gi|47522718|ref|NP_999109.1|	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 [Sus scrofa] >gi|3023621|sp|Q29036.3|DAD1_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1; Short=Oligosaccharyltransferase sub	0.875	0.615	0.56	0.973
gi|350585844|ref|XP_003356353.2|	PREDICTED: histone deacetylase 1-like, partial [Sus scrofa]	---	---	---	---
gi|350585862|ref|XP_003127820.3|	PREDICTED: histone deacetylase 1-like [Sus scrofa]				
gi|311247551|ref|XP_003122699.1|	PREDICTED: DNA damage-binding protein 1-like isoform 1 [Sus scrofa]	1.254	0.422	0.742	0.802
gi|335281341|ref|XP_003122446.2|	PREDICTED: mitochondrial glutamate carrier 1-like [Sus scrofa]	---	---	---	---
gi|194042439|ref|XP_001928	PREDICTED: ATPase family AAA	0.481	1.189	1.064	0.8

012.1|	domain-containing protein 1 isoform 1 [Sus scrofa]				
gi|335301975|ref|XP_003359338.1|	PREDICTED: ATPase family AAA domain-containing protein 1 isoform 2 [Sus scrofa]				
gi|194033654|ref|XP_001928369.1|	PREDICTED: ubiquinone biosynthesis protein COQ4 homolog, mitochondrial [Sus scrofa]	---	---	---	---
gi|47117721|sp|P83884.2|RL36A_PIG	RecName: Full=60S ribosomal protein L36a; AltName: Full=60S ribosomal protein L44 >gi|47522650|ref|NP_999082.1| 60S ribosomal protein L36a [Sus scrofa] >gi|335303998|ref|XP_003134062.2| PREDICTED: 60S ribosomal protein L36a-like [Sus scrofa] >gi|335	1.132	0.672	0.743	1.439
gi|194035409|ref|XP_001926511.1|	PREDICTED: syntaxin-7 [Sus scrofa]	0.461	0.897	0.68	0.715
gi|365796119|dbj|BAL43002.1|	toll-interacting protein [Sus scrofa]	0.769	1.115	1.202	0.594
gi|194033405|ref|XP_001928380.1|	PREDICTED: acetyl-CoA acetyltransferase, cytosolic [Sus scrofa]	0.884	0.927	0.657	0.802
gi|311248940|ref|XP_003123387.1|	PREDICTED: growth arrest and DNA damage-inducible proteins-interacting protein 1-like [Sus scrofa]	0.625	1.146	1.178	0.724
gi|335289143|ref|XP_003126912.2|	PREDICTED: probable D-lactate dehydrogenase, mitochondrial [Sus scrofa]	1.998	1.083	2.112	1.394
gi|311246098|ref|XP_003122082.1|	PREDICTED: coronin-2A-like [Sus scrofa]	0.864	0.93	0.766	1.106
gi|178056567|ref|NP_001116632.1|	prefoldin subunit 4 [Sus scrofa] >gi|147225098|emb|CAN13185.1| prefoldin 4 [Sus scrofa]	1.299	2.181	1.298	1.388
gi|148232463|ref|NP_001090940.1|	methylmalonyl-CoA epimerase, mitochondrial [Sus scrofa] >gi|117660706|gb|ABK55633.1| MCEE [Sus scrofa]	---	---	---	---
gi|359807141|ref|NP_001240850.1|	mannose-6-phosphate isomerase [Sus scrofa]	---	---	---	---
gi|350536495|ref|NP_001233	probable ATP-dependent RNA	1.051	1.216	1.219	1.395

197.1|	helicase DDX46 [Sus scrofa] >gi|336092215|gb|AEI00731.1| DEAD box polypeptide 46 [Sus scrofa]				
gi|298228972|ref|NP_001177201.1|	autophagy-related protein 16-1 isoform 1 [Sus scrofa] >gi|296874478|gb|ADH81744.1| autophagy related 16-like protein 1 transcript variant 1 [Sus scrofa]	---	---	---	---
gi|298231102|ref|NP_001177202.1|	autophagy-related protein 16-1 isoform 2 [Sus scrofa] >gi|296874480|gb|ADH81745.1| autophagy related 16-like protein 1 transcript variant 2 [Sus scrofa]				
gi|343403779|ref|NP_001230274.1|	ribosomal protein L13 [Sus scrofa]	1.041	0.385	0.387	1.096
gi|335298292|ref|XP_003358241.1|	PREDICTED: phosphatidylinositol transfer protein alpha isoform-like [Sus scrofa]	---	---	---	---
gi|350579520|ref|XP_003353667.2|	PREDICTED: U4/U6 small nuclear ribonucleoprotein Prp4-like [Sus scrofa]	1.08	0.968	1.519	0.658
gi|350582982|ref|XP_003481407.1|	PREDICTED: tetratricopeptide repeat protein 35-like [Sus scrofa]	---	---	---	---
gi|311252708|ref|XP_003125227.1|	PREDICTED: LOW QUALITY PROTEIN: protein phosphatase 1B-like [Sus scrofa]	1.755	0.953	0.884	0.89
gi|343790912|ref|NP_001230514.1|	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) [Sus scrofa]	---	---	---	---
gi|213021237|ref|NP_001132943.1|	DNA-(apurinic or apyrimidinic site) lyase [Sus scrofa] >gi|210062866|gb|ACJ06403.1| APEX nuclease 1 [Sus scrofa]	1.59	0.705	0.937	0.827
gi|47523060|ref|NP_999293.1|	serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform [Sus scrofa] >gi|14209665|gb|AAK56844.1|AF193515_1 calcineurin catalytic subunit delta isoform [Sus scrofa]	---	---	---	---
gi|311250082|ref|XP_003123949.1|	PREDICTED: isochorismatase domain-containing protein 1-like [Sus scrofa]	0.95	0.901	1.01	0.792

gi|350529419|ref|NP_001231941.1|	inositol polyphosphate-1-phosphatase [Sus scrofa]	---	---	---	---
gi|350593719|ref|XP_003483752.1|	PREDICTED: inositol polyphosphate 1-phosphatase-like, partial [Sus scrofa]				
gi|347543777|ref|NP_001231552.1|	protein LYRIC [Sus scrofa]	0.777	1.226	1.046	1.089
gi|350590001|ref|XP_003357925.2|	PREDICTED: multidrug resistance-associated protein 4-like, partial [Sus scrofa]	0.814	0.461	0.545	0.631
gi|350580632|ref|XP_003123159.3|	PREDICTED: general transcription factor IIF subunit 1-like [Sus scrofa]	---	---	---	---
gi|350585533|ref|XP_003356179.2|	PREDICTED: leucine-rich repeat-containing protein 47-like [Sus scrofa]	---	0.923	1.23	0.852
gi|335290197|ref|XP_003356098.1|	PREDICTED: LOW QUALITY PROTEIN: 40S ribosomal protein S9-like, partial [Sus scrofa]	0.594	0.672	0.735	0.801
gi|311273092|ref|XP_001925601.2|	PREDICTED: protein FAM134A [Sus scrofa]	---	---	---	---
gi|335293289|ref|XP_003356924.1|	PREDICTED: O-phosphoseryl-tRNA(Sec) selenium transferase-like [Sus scrofa]	---	---	---	---
gi|350596387|ref|XP_003361109.2|	PREDICTED: O-phosphoseryl-tRNA(Sec) selenium transferase-like [Sus scrofa]				
gi|47523704|ref|NP_999484.1|	double stranded RNA-dependent protein kinase [Sus scrofa] >gi|29292936|dbj|BAC66439.1| double stranded RNA-dependent protein kinase [Sus scrofa]	0.76	1.035	1.042	1.077
gi|311252821|ref|XP_003125284.1|	PREDICTED: interferon-induced, double-stranded RNA-activated protein kinase-like [Sus scrofa]				
gi|219521982|ref|NP_001137178.1|	erlin-2 precursor [Sus scrofa] >gi|217314887|gb|ACK36978.1| ER lipid raft-associated 2 isoform 2 [Sus scrofa]	---	---	---	---
gi|239504580|ref|NP_001155120.1|	selenoprotein M precursor [Sus scrofa] >gi|237930353|gb|ACR33808.1| selenoprotein M [Sus scrofa]	---	---	---	---
gi|311257625|ref|XP_003127	PREDICTED: platelet-activating	---	---	---	---

213.1|	factor acetylhydrolase IB subunit gamma-like [Sus scrofa] >gi|311257641|ref|XP_003127220.1| PREDICTED: platelet-activating factor acetylhydrolase IB subunit gamma-like [Sus scrofa]				
gi|350592333|ref|XP_003359097.2|	PREDICTED: mitochondrial peptide methionine sulfoxide reductase [Sus scrofa]	---	---	---	---
gi|335295539|ref|XP_003130253.2|	PREDICTED: multidrug resistance protein 1 isoform 2 [Sus scrofa]	---	---	---	---
gi|350588870|ref|XP_003130261.3|	PREDICTED: multidrug resistance protein 1-like, partial [Sus scrofa]				
gi|350582950|ref|XP_003481396.1|	PREDICTED: double-strand-break repair protein rad21 homolog [Sus scrofa]	0.699	0.672	1.136	0.806
gi|350597023|ref|XP_003361918.2|	PREDICTED: double-strand-break repair protein rad21 homolog [Sus scrofa]				
gi|93359412|gb|ABF13285.1|	proliferating cell nuclear antigen [Sus scrofa]	---	---	---	---
gi|335304393|ref|XP_003359931.1|	PREDICTED: proliferating cell nuclear antigen [Sus scrofa]				
gi|60389430|sp|Q8MIZ3.1|DCPS_PIG	RecName: Full=m7GpppX diphosphatase; AltName: Full=DCS-1; AltName: Full=Hint-related 7meGMP-directed hydrolase; AltName: Full=Histidine triad protein member 5; Short=HINT-5; AltName: Full=Scavenger mRNA-decapping enzyme DcpS >gi|47523260|ref|NP_9989	---	---	---	---
gi|194042142|ref|XP_001929035.1|	PREDICTED: BAG family molecular chaperone regulator 3 [Sus scrofa]	0.803	0.732	0.843	0.588
gi|326632513|gb|ADZ99177.1|	BCL2-associated athanogene 3, partial [Sus scrofa]				
gi|335282832|ref|XP_003354166.1|	PREDICTED: protein Wiz isoform 2 [Sus scrofa]	---	---	---	---
gi|335282838|ref|XP_003354168.1|	PREDICTED: protein Wiz isoform 4 [Sus scrofa]				

gi|335282836|ref|XP_003123504.2|	PREDICTED: protein Wiz isoform 1 [Sus scrofa]				
gi|335282840|ref|XP_003354169.1|	PREDICTED: protein Wiz isoform 5 [Sus scrofa]				
gi|350595384|ref|XP_003134854.3|	PREDICTED: glycyl-tRNA synthetase-like [Sus scrofa]	---	---	---	---
gi|350585317|ref|XP_003127269.3|	PREDICTED: poliovirus receptor-like [Sus scrofa]	---	---	---	---
gi|349732213|ref|NP_001231857.1|	LSM3 homolog, U6 small nuclear RNA associated [Sus scrofa]	1.066	1.554	1.348	1.109
gi|350582471|ref|XP_003125244.3|	PREDICTED: echinoderm microtubule associated protein like 4 [Sus scrofa]	0.952	1.303	1.407	1.152
gi|350593526|ref|XP_003359584.2|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 14 [Sus scrofa]	---	---	---	---
gi|51338616|sp|P62831.1|RL23_PIG	RecName: Full=60S ribosomal protein L23; AltName: Full=Ribosomal protein L17 >gi|194018720|ref|NP_001123427.1| 60S ribosomal protein L23 [Sus scrofa] >gi|117661026|gb|ABK55650.1| RPL23 [Sus scrofa]	0.6	0.498	0.522	0.903
gi|350589072|ref|XP_003357606.2|	PREDICTED: sulfhydryl oxidase 1-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350589074|ref|XP_003357607.2|	PREDICTED: sulfhydryl oxidase 1-like isoform 2 [Sus scrofa]				
gi|335304552|ref|XP_001927148.2|	PREDICTED: acetyl-coenzyme A synthetase 2-like, mitochondrial-like [Sus scrofa]	1.29	0.748	0.638	1.105
gi|285818412|gb|ADC38879.1|	periostin, osteoblast specific factor [Sus scrofa]	0.836	1.196		1.034
gi|329744611|ref|NP_001193280.1|	periostin, osteoblast specific factor isoform 2 precursor [Sus scrofa]				
gi|329744601|ref|NP_001193276.1|	periostin, osteoblast specific factor isoform 1 precursor [Sus scrofa]				
gi|350579947|ref|XP_003122565.3|	PREDICTED: U4/U6.U5 tri-snRNP-associated protein 1 [Sus scrofa]	---	---	---	---
gi|194037097|ref|XP_001927840.1|	PREDICTED: carbonic anhydrase 2 [Sus scrofa]	0.798	1.38	1.495	0.798
gi|350582678|ref|XP_003354	PREDICTED: HCLS1-binding	---	---	---	---

961.2|	protein 3-like [Sus scrofa]				
gi|350590394|ref|XP_003131590.3|	PREDICTED: pyridoxine-5~-phosphate oxidase-like [Sus scrofa]	1.599	2.451	2.121	1.531
gi|335285134|ref|XP_003354782.1|	PREDICTED: charged multivesicular body protein 3-like isoform 2 [Sus scrofa]	0.402	0.867	0.704	0.463
gi|335285138|ref|XP_003125011.2|	PREDICTED: charged multivesicular body protein 3-like isoform 1 [Sus scrofa]				
gi|335285136|ref|XP_003354783.1|	PREDICTED: charged multivesicular body protein 3-like isoform 3 [Sus scrofa]				
gi|335290686|ref|XP_003356247.1|	PREDICTED: tissue alpha-L-fucosidase-like [Sus scrofa]	1.253	0.498	0.564	0.97
gi|336455302|gb|AEI59128.1|	fucosidase alpha-L-1 [Sus scrofa]				
gi|347543811|ref|NP_001231562.1|	cytochrome P450, family 2, subfamily J, polypeptide 34 [Sus scrofa]	0.682	0.669	0.73	0.888
gi|194041937|ref|XP_001928912.1|	PREDICTED: alpha-centractin [Sus scrofa]	1.787	1.406	1.284	1.802
gi|335286356|ref|XP_001927203.3|	PREDICTED: copine-3 [Sus scrofa]	0.525	0.444	0.348	0.456
gi|346716148|ref|NP_001231230.1|	importin-5 [Sus scrofa]	1.188	1.243	1.296	1.211
gi|311271339|ref|XP_003133112.1|	PREDICTED: sphingosine-1-phosphate lyase 1 isoform 2 [Sus scrofa]	0.583	0.569	0.74	0.661
gi|311271341|ref|XP_003133111.1|	PREDICTED: sphingosine-1-phosphate lyase 1 isoform 1 [Sus scrofa]				
gi|345091002|ref|NP_001230732.1|	nuclear distribution gene C homolog [Sus scrofa]	---	---	---	---
gi|194042094|ref|XP_001925670.1|	PREDICTED: shootin-1-like isoform 1 [Sus scrofa]	0.813	0.553	0.594	0.553
gi|113205762|ref|NP_001038043.1|	granulins precursor [Sus scrofa] >gi|55247591|gb|AAV48633.1| granulin precursor [Sus scrofa]	1.234	1.344	1.056	0.679
gi|350585670|ref|XP_003127678.3|	PREDICTED: filamin-binding LIM protein 1-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350585672|ref|XP_003482022.1|	PREDICTED: filamin-binding LIM protein 1-like isoform 2 [Sus scrofa]				

gi|350594224|ref|XP_003359804.2|	PREDICTED: LOW QUALITY PROTEIN: nipped-B-like protein [Sus scrofa]	---	---	---	---
gi|335302969|ref|XP_001925494.2|	PREDICTED: Golgi reassembly-stacking protein 2 isoform 1 [Sus scrofa]	1.023	1.281	0.907	1.224
gi|335302971|ref|XP_003359599.1|	PREDICTED: Golgi reassembly-stacking protein 2 isoform 2 [Sus scrofa]				
gi|311258558|ref|XP_003127668.1|	PREDICTED: protein DDI1 homolog 2 [Sus scrofa]	---	---	---	---
gi|346716195|ref|NP_001231246.1|	nucleosome assembly protein 1-like 1 [Sus scrofa] >gi|346716193|ref|NP_001231245.1| nucleosome assembly protein 1-like 1 [Sus scrofa]	---	---	---	---
gi|335310655|ref|XP_003362133.1|	PREDICTED: hypothetical protein LOC100621842 [Sus scrofa]	---	---	---	---
gi|335283905|ref|XP_003354455.1|	PREDICTED: BET1-like protein-like isoform 2 [Sus scrofa] >gi|311250744|ref|XP_003124272.1| PREDICTED: BET1-like protein-like isoform 1 [Sus scrofa]	---	---	---	---
gi|178056852|ref|NP_001116541.1|	ATP-binding cassette sub-family F member 1 [Sus scrofa] >gi|56404330|sp|Q767L0.1|ABCF1_PIG RecName: Full=ATP-binding cassette sub-family F member 1 >gi|41529180|dbj|BAD08439.1| ATP-binding cassette, sub-family F (GCN20), member 1 [Sus scrofa]	---	---	---	---
gi|350579945|ref|XP_003480721.1|	PREDICTED: barrier-to-autointegration factor-like [Sus scrofa] >gi|335281491|ref|XP_003353819.1| PREDICTED: barrier-to-autointegration factor-like [Sus scrofa] >gi|335281487|ref|XP_003353817.1| PREDICTED: barrier-to-autointegration factor-like [Sus	0.942	1.351	1.123	0.909

gi|335298830|ref|XP_001925616.3|	PREDICTED: golgin subfamily A member 4 [Sus scrofa]	0.735	1.062	1.363	0.765
gi|347300222|ref|NP_001231422.1|	basic leucine zipper and W2 domain-containing protein 1 [Sus scrofa]	---	---	---	---
gi|350590801|ref|XP_003483139.1|	PREDICTED: phospholipase D2-like [Sus scrofa]	---	---	---	---
gi|350595116|ref|XP_003360118.2|	PREDICTED: NEDD8 ultimate buster 1 [Sus scrofa]	---	---	---	---
gi|116175275|ref|NP_001070689.1|	transformer-2 protein homolog beta [Sus scrofa] >gi|115371737|gb|ABI96193.1| TRA2B [Sus scrofa]	0.879	1.049	1.069	1.067
gi|6094365|sp|O02799.1|STAT2_PIG	RecName: Full=Signal transducer and activator of transcription 2 >gi|47522708|ref|NP_999054.1| signal transducer and activator of transcription 2 [Sus scrofa] >gi|315273316|gb|ADU03225.1| signal transducer and activator of transcription 2 [Sus scrof	---	---	---	---
gi|346644866|ref|NP_001231105.1|	coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial [Sus scrofa]	---	---	---	---
gi|311273314|ref|XP_003133809.1|	PREDICTED: COP9 signalosome complex subunit 8-like isoform 1 [Sus scrofa]	---	---	---	---
gi|4538854|emb|CAB39532.1|	54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa]	---	---	---	---
gi|47523554|ref|NP_999405.1|	V-type proton ATPase subunit H [Sus scrofa] >gi|4538856|emb|CAB39533.1| 54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa]				
gi|18206257|sp|Q9TVC1.1|VATH_PIG	RecName: Full=V-type proton ATPase subunit H; Short=V-ATPase subunit H; AltName: Full=V-ATPase 50/57 kDa subunits; AltName: Full=Vacuolar proton pump subunit H; AltName: Full=Vacuolar proton pump subunit SFD >gi|23956412|emb|CAB39537.1| 54 kDa vacuo				
gi|311263676|ref|XP_003129	PREDICTED: dipeptidyl peptidase	---	---	---	---

789.1|	1-like [Sus scrofa]				
gi|350586576|ref|XP_001929450.4|	PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase FKBP5 [Sus scrofa]	0.774	0.52	0.632	0.547
gi|194035744|ref|XP_001928514.1|	PREDICTED: protein Dr1-like [Sus scrofa]	---	---	---	---
gi|346986339|ref|NP_001231321.1|	small glutamine-rich tetratricopeptide repeat-containing protein alpha [Sus scrofa]	1.912	1.27	2.541	2.032
gi|3023862|sp|P81140.1|GCDH_PIG	RecName: Full=Glutaryl-CoA dehydrogenase, mitochondrial; Short=GCD; Flags: Precursor >gi|260168|gb|AAB24225.1| glutaryl-CoA dehydrogenase, GCDH [swine, liver, Peptide Partial, 408 aa]	---	---	---	---
gi|311248913|ref|XP_003123376.1|	PREDICTED: glutaryl-CoA dehydrogenase, mitochondrial-like isoform 1 [Sus scrofa]				
gi|311248915|ref|XP_003123377.1|	PREDICTED: glutaryl-CoA dehydrogenase, mitochondrial-like isoform 2 [Sus scrofa]				
gi|385648282|ref|NP_001245314.1|	glucosidase, beta (bile acid) 2 [Sus scrofa]	0.636	0.76	0.737	0.977
gi|210062464|gb|ABY85807.2|	immunoglobulin gamma chain 6a [Sus scrofa]	---	---	---	---
gi|311275995|ref|XP_003135004.1|	PREDICTED: histone-binding protein RBBP7-like isoform 1 [Sus scrofa]	1.042	0.65	0.931	1.266
gi|350585895|ref|XP_003127841.3|	PREDICTED: MAP7 domain-containing protein 1 [Sus scrofa]	0.378	0.548	0.646	0.417
gi|350592486|ref|XP_001929589.3|	PREDICTED: acyl-CoA dehydrogenase family member 10 [Sus scrofa]	---	---	---	---
gi|350587337|ref|XP_003128893.2|	PREDICTED: peroxisomal acyl-coenzyme A oxidase 3 [Sus scrofa]	---	---	---	---
gi|47116966|sp|P61288.1|TCTP_PIG	RecName: Full=Translationally-controlled tumor protein; Short=TCTP >gi|47523802|ref|NP_99	0.76	0.917	0.893	0.853

	9538.1| translationally-controlled tumor protein [Sus scrofa] >gi|18482460|gb|AAL68965.1| translationally controlled tumor protein [Sus scrofa]				
gi|335281686|ref|XP_003353872.1|	PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	0.843	1.119	0.973	0.796
gi|75053356|sp|Q764M6.1|IRF3_PIG	RecName: Full=Interferon regulatory factor 3; Short=IRF-3 >gi|47523300|ref|NP_998935.1| interferon regulatory factor 3 [Sus scrofa] >gi|40363627|dbj|BAD06317.1| interferon regulatory factor 3 [Sus scrofa]	---	---	---	---
gi|317016904|gb|ADU85980.1|	interferon regulatory factor 3 [Sus scrofa] >gi|163141076|gb|ABY26589.1| interferon regulatory factor 3 [Sus scrofa]				
gi|261490800|ref|NP_001159781.1|	survival of motor neuron-related-splicing factor 30 [Sus scrofa] >gi|190333253|gb|ACE73645.1| survival motor neuron domain-containing protein 1 [Sus scrofa] >gi|190576653|gb|ACE73646.1| survival motor neuron domain-containing protein 1 [Sus scrofa]	0.834	1.322	1.148	1.092
gi|335282050|ref|XP_003122930.2|	PREDICTED: caprin-1 isoform 1 [Sus scrofa]	---	---	---	---
gi|335282052|ref|XP_003353957.1|	PREDICTED: caprin-1 isoform 2 [Sus scrofa]				
gi|148235477|ref|NP_001090932.1|	protein QIL1 precursor [Sus scrofa] >gi|148839601|sp|A1XQR7.1|QIL1_PIG RecName: Full=Protein QIL1 >gi|117660492|gb|ABK55623.1| QIL1 [Sus scrofa]	---	---	---	---
gi|335301140|ref|XP_003359135.1|	PREDICTED: transmembrane emp24 domain-containing protein 2-like isoform 1 [Sus scrofa]	1.466	1.188	1.206	1.585
gi|335301142|ref|XP_003359136.1|	PREDICTED: transmembrane emp24 domain-containing protein 2-like				

	isoform 2 [Sus scrofa]				
gi|148231223|ref|NP_001090898.1|	mitochondrial antiviral-signaling protein [Sus scrofa] >gi|156144883|gb|ABU53000.1| virus-induced signaling adapter [Sus scrofa] >gi|119507309|dbj|BAF42542.1| mitochondrial antiviral signaling protein [Sus scrofa]	0.771	1.333	1.416	1.219
gi|238176|gb|AAB20199.1|	3,4-dihydroxyphenylalanine (Dopa) decarboxylase [swine, kidney, Peptide, 485 aa]	---	---	---	---
gi|126513274|gb|ABO15741.1|	L-aromatic dopa decarboxylase [Sus scrofa]				
gi|47523148|ref|NP_999019.1|	aromatic-L-amino-acid decarboxylase [Sus scrofa] >gi|2829681|sp|P80041.2|DDC_PIG RecName: Full=Aromatic-L-amino-acid decarboxylase; Short=AADC; AltName: Full=DOPA decarboxylase; Short=DDC >gi|1839555|gb|AAB47157.1| dopa decarboxylase [Sus scrofa] >g				
gi|126513279|gb|ABO15742.1|	L-aromatic dopa decarboxylase splice variant 1 [Sus scrofa]				
gi|350580560|ref|XP_003123249.3|	PREDICTED: transcription activator BRG1 [Sus scrofa]	1.009	0.858	1.256	0.901
gi|311262372|ref|XP_003129135.1|	PREDICTED: N-acylethanolamine-hydrolyzing acid amidase-like [Sus scrofa]	---	---	---	---
gi|335292565|ref|XP_003128593.2|	PREDICTED: charged multivesicular body protein 4a-like [Sus scrofa]	---	---	---	---
gi|343403828|ref|NP_001230291.1|	serine beta-lactamase-like protein LACTB, mitochondrial [Sus scrofa]	0.703			0.932
gi|194036296|ref|XP_001926524.1|	PREDICTED: splicing factor 3B subunit 4 [Sus scrofa]	0.863	1.231	1.161	0.76
gi|297632428|ref|NP_001172097.1|	28S ribosomal protein S28, mitochondrial [Sus scrofa]	0.837	0.477	0.428	0.701
gi|350582501|ref|XP_003481284.1|	PREDICTED: atlastin-2-like isoform 2 [Sus scrofa]	1.596	1.146	0.929	1.273

gi|350582505|ref|XP_003125271.2|	PREDICTED: atlastin-2-like isoform 1 [Sus scrofa]				
gi|350582503|ref|XP_003481285.1|	PREDICTED: atlastin-2-like isoform 3 [Sus scrofa]				
gi|298104120|ref|NP_001177123.1|	V-type proton ATPase subunit G 1 [Sus scrofa]	0.329	0.557	0.485	0.429
gi|118403868|ref|NP_001072136.1|	N-acetylglucosaminyltransferase I [Sus scrofa] >gi|112821182|dbj|BAF03221.1| N-acetylglucosaminyltransferase I [Sus scrofa]	---	---	---	---
gi|194045136|ref|XP_001927417.1|	PREDICTED: immunoglobulin-binding protein 1 isoform 2 [Sus scrofa]	0.871	0.641	0.531	0.896
gi|194045138|ref|XP_001927405.1|	PREDICTED: immunoglobulin-binding protein 1 isoform 1 [Sus scrofa]				
gi|311264357|ref|XP_003130126.1|	PREDICTED: suppressor of tumorigenicity 14 protein homolog [Sus scrofa]	---	---	---	---
gi|147899011|ref|NP_001090950.1|	40S ribosomal protein S26 [Sus scrofa] >gi|187606917|sp|P49171.4|RS26_PIG RecName: Full=40S ribosomal protein S26 >gi|117661156|gb|ABK55657.1| RPS26 [Sus scrofa]	---	---	---	---
gi|335307625|ref|XP_003360911.1|	PREDICTED: 40S ribosomal protein S26-like [Sus scrofa]				
gi|350588024|ref|XP_003482537.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein D0-like [Sus scrofa]	---	---	---	---
gi|311254587|ref|XP_003125898.1|	PREDICTED: CTTNBP2 N-terminal like [Sus scrofa]	---	---	---	---
gi|147899312|ref|NP_001090923.1|	F-actin capping protein subunit alpha 1 [Sus scrofa] >gi|148613357|gb|ABQ96222.1| F-actin capping protein alpha 1 subunit [Sus scrofa] >gi|118627572|emb|CAL69435.1| F-actin capping protein subunit alpha 1 [Sus scrofa]	---	---	---	---
gi|350583525|ref|XP_003481537.1|	PREDICTED: hypothetical protein LOC100737138 [Sus scrofa]				

gi|311268984|ref|XP_003132296.1|	PREDICTED: glycerate kinase-like [Sus scrofa]	1.015	0.491	0.604	0.683
gi|350592016|ref|XP_003358886.2|	PREDICTED: LOW QUALITY PROTEIN: protein TFG [Sus scrofa]	---	---	---	---
gi|229626|prf||770504A	hemoglobin alpha	---	---	---	---
gi|402550455|pdb|4F4O|J	Chain J, Structure Of The Haptoglobin-Haemoglobin Complex >gi|402550449|pdb|4F4O|D Chain D, Structure Of The Haptoglobin-Haemoglobin Complex >gi|402550452|pdb|4F4O|G Chain G, Structure Of The Haptoglobin-Haemoglobin Complex >gi|402550446|pdb|4F4O|A				
gi|350581852|ref|XP_003481137.1|	PREDICTED: hemoglobin subunit alpha-like isoform 6 [Sus scrofa] >gi|350581848|ref|XP_003481135.1| PREDICTED: hemoglobin subunit alpha-like isoform 4 [Sus scrofa] >gi|350581844|ref|XP_003481133.1| PREDICTED: hemoglobin subunit alpha-like isoform 2 [S				
gi|178056781|ref|NP_001116594.1|	histone H2A.Z [Sus scrofa] >gi|166407422|gb|ABY87518.1| H2A histone family member Z [Sus scrofa]	---	---	---	---
gi|350595451|ref|XP_003134922.3|	PREDICTED: histone H2A.V-like [Sus scrofa]				
gi|348605274|ref|NP_001231762.1|	alcohol dehydrogenase 5 (class III), chi polypeptide [Sus scrofa]	1.887	0.872	0.792	1.618
gi|335310819|ref|XP_003362206.1|	PREDICTED: ankyrin repeat and LEM domain-containing protein 2, partial [Sus scrofa]	---	---	---	---
gi|335296651|ref|XP_003130877.2|	PREDICTED: tubulin alpha chain-like 3-like [Sus scrofa]	---	---	---	---
gi|350589654|ref|XP_003357831.2|	PREDICTED: tubulin alpha chain-like 3, partial [Sus scrofa]				
gi|311245655|ref|XP_003121912.1|	PREDICTED: nesprin-2-like [Sus scrofa]	---	---	---	---
gi|330340461|ref|NP_001193383.1|	2-hydroxyacyl-CoA lyase 1 [Sus scrofa]	---	---	---	---
gi|335278852|ref|XP_003353	PREDICTED: sorting nexin-9 [Sus	1.186	0.908	0.906	0.666

219.1|	scrofa]				
gi|308081427|ref|NP_001183950.1|	hydroxysteroid dehydrogenase-like protein 2 [Sus scrofa]	0.789	0.489	0.551	0.593
gi|160333766|ref|NP_001103898.1|	protein canopy homolog 3 precursor [Sus scrofa] >gi|166216082|sp|A5GFQ5.1|CNPY3_PIG RecName: Full=Protein canopy homolog 3; AltName: Full=Trinucleotide repeat-containing gene 5 protein; Flags: Precursor >gi|147223347|emb|CAN13167.1| trinucleotide re	0.942	0.367	0.762	0.836
gi|346986322|ref|NP_001231315.1|	peptidyl-prolyl cis-trans isomerase D [Sus scrofa]	0.891	1.065	0.833	1.246
gi|350583831|ref|XP_003355400.2|	PREDICTED: pyridoxal phosphate phosphatase-like, partial [Sus scrofa]	---	---	---	---
gi|335284421|ref|XP_003354609.1|	PREDICTED: ataxin 2-like [Sus scrofa]	---	---	---	---
gi|335284425|ref|XP_003354611.1|	PREDICTED: ataxin 2-like [Sus scrofa]				
gi|335284427|ref|XP_003354612.1|	PREDICTED: ataxin 2-like [Sus scrofa]				
gi|335284423|ref|XP_003354610.1|	PREDICTED: ataxin 2-like [Sus scrofa]				
gi|335284429|ref|XP_003124559.2|	PREDICTED: ataxin 2-like isoform 1 [Sus scrofa]				
gi|350585179|ref|XP_003481897.1|	PREDICTED: seryl-tRNA synthetase, mitochondrial-like [Sus scrofa]	1.123	0.969	1.234	1.477
gi|311266963|ref|XP_003131335.1|	PREDICTED: putative rRNA methyltransferase 3 [Sus scrofa]	---	---	---	---
gi|350586678|ref|XP_003482243.1|	PREDICTED: DNA-directed RNA polymerases I and III subunit RPAC1 [Sus scrofa]	---	---	---	---
gi|311247599|ref|XP_003122720.1|	PREDICTED: vacuolar protein sorting-associated protein 37C-like [Sus scrofa]	---	---	---	---
gi|311262785|ref|XP_003129351.1|	PREDICTED: ragulator complex protein LAMTOR3-like isoform 3 [Sus scrofa] >gi|311262781|ref|XP_003129349.1| PREDICTED: ragulator	0.677	0.447	0.638	0.591

	complex protein LAMTOR3-like isoform 1 [Sus scrofa] >gi|311262783|ref|XP_003129350.1| PREDICTED: ragulator complex protei				
gi|342349340|ref|NP_001230146.1|	carnitine O-octanoyltransferase [Sus scrofa]	---	---	---	---
gi|311253960|ref|XP_001927701.2|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial [Sus scrofa]	---	---	---	---
gi|343790970|ref|NP_001230536.1|	translin-associated protein X [Sus scrofa]	---	---	1.122	---
gi|335303755|ref|XP_003359787.1|	PREDICTED: Golgi phosphoprotein 3-like [Sus scrofa]	---	---	---	---
gi|311272290|ref|XP_003133380.1|	PREDICTED: CDKN2A-interacting protein isoform 1 [Sus scrofa]	---	---	---	---
gi|335302635|ref|XP_003359511.1|	PREDICTED: CDKN2A-interacting protein isoform 2 [Sus scrofa]				
gi|47522786|ref|NP_999145.1|	UTP--glucose-1-phosphate uridylyltransferase [Sus scrofa] >gi|6136110|sp|P79303.3|UGPA_PIG RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphorylase; Short=UDPGP; Short=UGPase >gi|1752677|emb|CAA67690.1|	1.821	1.319	1.126	2.247
gi|298104080|ref|NP_001177107.1|	ribosomal protein L30 [Sus scrofa]	---	---	---	---
gi|47522710|ref|NP_999050.1|	mannosyl-oligosaccharide 1,2-alpha-mannosidase IA [Sus scrofa] >gi|41017248|sp|O02773.1|MA1A1_PIG RecName: Full=Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA; AltName: Full=Man(9)-alpha-mannosidase; Short=Man9-mannosidase; AltName: Full=Mannosid	---	---	---	---
gi|156120140|ref|NP_001095287.1|	helicase SKI2W [Sus scrofa] >gi|148724903|emb|CAN87691.1| superkiller viralicidic activity 2-like (S. cerevisiae) [Sus scrofa]	0.943	1.061	1.13	0.702

gi|162138264|gb|ABX82836.1|	putative superkiller viralicidic activity 2 protein [Sus scrofa]				
gi|335284313|ref|XP_003124517.2|	PREDICTED: RNA-binding protein FUS-like isoform 1 [Sus scrofa]	0.713	0.899	0.633	1.032
gi|335284315|ref|XP_003354570.1|	PREDICTED: RNA-binding protein FUS-like isoform 2 [Sus scrofa]				
gi|351738724|gb|AEQ61462.1|	FUS [Sus scrofa]				
gi|311260957|ref|XP_003128592.1|	PREDICTED: NEDD8-like [Sus scrofa]	1.32	2.052	1.478	1.848
gi|335292563|ref|XP_003356757.1|	PREDICTED: NEDD8-like [Sus scrofa]				
gi|194038855|ref|XP_001928049.1|	PREDICTED: hypothetical protein LOC100154068 [Sus scrofa]	---	---	---	---
gi|350591669|ref|XP_003483310.1|	PREDICTED: GMP synthase [glutamine-hydrolyzing]-like [Sus scrofa]	---	---	---	---
gi|335299136|ref|XP_003358504.1|	PREDICTED: poly [ADP-ribose] polymerase 3 [Sus scrofa]	0.853	0.943		0.951
gi|116175255|ref|NP_001070683.1|	regulator of differentiation 1 [Sus scrofa] >gi|115371761|gb|ABI96205.1| ROD1 [Sus scrofa]	---	---	---	---
gi|47523818|ref|NP_999546.1|	calcium/calmodulin-dependent protein kinase type II subunit delta [Sus scrofa] >gi|75073672|sp|Q95266.1|KCC2D_PIG RecName: Full=Calcium/calmodulin-dependent protein kinase type II subunit delta; Short=CaM kinase II subunit delta; Short=CaMK-II subun	1.253	1.013	0.852	1.523
gi|307078155|ref|NP_001182495.1|	splicing factor, arginine/serine-rich 9 [Sus scrofa]	---	---	---	---
gi|349732254|ref|NP_001231868.1|	glutathione S-transferase Mu 3-like [Sus scrofa]	---	---	---	---
gi|335293678|ref|XP_003357027.1|	PREDICTED: ras GTPase-activating protein-binding protein 2 isoform 1 [Sus scrofa]	---	---	---	---
gi|335293682|ref|XP_003357029.1|	PREDICTED: ras GTPase-activating protein-binding protein 2 isoform 3 [Sus scrofa] >gi|335293680|ref|XP_00335				

	7028.1| PREDICTED: ras GTPase-activating protein-binding protein 2 isoform 2 [Sus scrofa]				
gi|335293613|ref|XP_003357005.1|	PREDICTED: UDP-glucuronosyltransferase 2C1-like [Sus scrofa]	---	---	---	---
gi|335308671|ref|XP_003361329.1|	PREDICTED: 60S ribosomal protein L23a-like [Sus scrofa] >gi|311267953|ref|XP_003131820.1| PREDICTED: 60S ribosomal protein L23a-like [Sus scrofa]	0.436	0.214	0.141	0.499
gi|350593534|ref|XP_003483707.1|	PREDICTED: grancalcin-like [Sus scrofa]	1.5	0.974	1.667	1.364
gi|350593538|ref|XP_003483709.1|	PREDICTED: grancalcin-like [Sus scrofa]				
gi|311271760|ref|XP_003133218.1|	PREDICTED: nucleolar and coiled-body phosphoprotein 1 [Sus scrofa]	---	---	---	---
gi|350587063|ref|XP_001924746.3|	PREDICTED: YLP motif-containing protein 1 [Sus scrofa]	0.939	1.091	1.197	0.542
gi|311258899|ref|XP_003127836.1|	PREDICTED: poly(ADP-ribose) glycohydrolase ARH3-like [Sus scrofa]	---	---	---	---
gi|350585235|ref|XP_003481909.1|	PREDICTED: coiled-coil domain-containing protein 97-like [Sus scrofa] >gi|350585231|ref|XP_003127200.3| PREDICTED: coiled-coil domain-containing protein 97-like [Sus scrofa]	0.869	1.668	0.938	0.981
gi|335286349|ref|XP_001927382.3|	PREDICTED: regulator of microtubule dynamics protein 1 [Sus scrofa]	---	---	---	---
gi|350590765|ref|XP_003358260.2|	PREDICTED: zinc finger ZZ-type and EF-hand domain-containing protein 1-like, partial [Sus scrofa]	---	---	---	---
gi|346227226|ref|NP_001230999.1|	40S ribosomal protein S11 [Sus scrofa]	0.559	0.52	0.403	1.019
gi|346644805|ref|NP_001231160.1|	pinin [Sus scrofa]	0.459	0.95	0.861	0.838
gi|350589580|ref|XP_003130823.3|	PREDICTED: dnaJ homolog subfamily C member 1 [Sus scrofa]	---	---	---	---

gi|350580945|ref|XP_003480928.1|	PREDICTED: endoplasmic reticulum aminopeptidase 2-like [Sus scrofa]	0.852	0.642	0.618	0.901
gi|297632397|ref|NP_001172084.1|	high mobility group protein HMG-I/HMG-Y isoform 2 [Sus scrofa] >gi|294494645|gb|ADE93010.1| high mobility group AT-hook protein 1 [Sus scrofa]	---	---	---	---
gi|75050051|sp|Q9GLV6.1|DDX58_PIG	RecName: Full=Probable ATP-dependent RNA helicase DDX58; AltName: Full=DEAD box protein 58; AltName: Full=RHIV-1; AltName: Full=RIG-I-like receptor 1; Short=RLR-1; AltName: Full=RNA helicase induced by virus; AltName: Full=Retinoic acid-inducible ge	---	---	---	---
gi|350596885|ref|XP_003484332.1|	PREDICTED: probable ATP-dependent RNA helicase DDX58-like, partial [Sus scrofa]				
gi|157272171|gb|ABV26717.1|	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide [Sus scrofa]				
gi|356460981|ref|NP_998969.2|	probable ATP-dependent RNA helicase DDX58 [Sus scrofa] >gi|224176124|dbj|BAH23574.1| DEAD box polypeptide 58 [Sus scrofa]				
gi|349732258|ref|NP_001231869.1|	uroporphyrinogen decarboxylase [Sus scrofa]	---	---	---	---
gi|350579853|ref|XP_003480698.1|	PREDICTED: liprin-alpha-1-like [Sus scrofa]	1.347	1.462	1.395	0.919
gi|350596914|ref|XP_003361801.2|	PREDICTED: dihydroorotate dehydrogenase (quinone), mitochondrial-like [Sus scrofa]	---	---	---	---
gi|350582270|ref|XP_003125088.3|	PREDICTED: zinc finger protein 638-like [Sus scrofa]	0.733	0.873	1.286	0.906
gi|346716375|ref|NP_001231201.1|	integrin alpha-2 precursor [Sus scrofa]	0.908	0.498	0.769	0.679
gi|335297522|ref|XP_003131393.2|	PREDICTED: LOW QUALITY PROTEIN: glycylpeptide N-tetradecanoyltransferase 1 [Sus scrofa]	---	---	---	---
gi|350590362|ref|XP_003483042.1|	PREDICTED: protein phosphatase 1 regulatory subunit 1B-like [Sus scrofa]	0.988	0.887	0.978	1.135

gi|47522648|ref|NP_999086.1|	beta-hexosaminidase subunit beta precursor [Sus scrofa] >gi|1041667|emb|CAA63123.1| 65 kDa epididymal boar protein [Sus scrofa]	---	---	---	---
gi|262072808|dbj|BAI47712.1|	hexosaminidase B (beta polypeptide) [Sus scrofa]				
gi|78100037|sp|Q29548.2|HEXB_PIG	RecName: Full=Beta-hexosaminidase subunit beta; AltName: Full=65 kDa epididymal boar protein; AltName: Full=Beta-N-acetylhexosaminidase subunit beta; Short=Hexosaminidase subunit B; AltName: Full=N-acetyl-beta-glucosaminidase subunit beta; Flags: Pr				
gi|311248396|ref|XP_003123114.1|	PREDICTED: endophilin-A2-like [Sus scrofa]	---	---	---	---
gi|113205798|ref|NP_001038052.1|	serine/arginine-rich splicing factor 11 [Sus scrofa] >gi|104295153|gb|ABF72046.1| splicing factor, arginine/serine-rich 11 [Sus scrofa]	---	---	---	---
gi|311276941|ref|XP_003135418.1|	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform 1 [Sus scrofa]	0.848	0.56	0.777	0.636
gi|311276943|ref|XP_003135419.1|	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform 2 [Sus scrofa]				
gi|335306508|ref|XP_003360488.1|	PREDICTED: apoptosis-inducing factor 1, mitochondrial [Sus scrofa]				
gi|335299816|ref|XP_003358692.1|	PREDICTED: latexin-like [Sus scrofa]	---	---	---	---
gi|335289036|ref|XP_003355772.1|	PREDICTED: adenine phosphoribosyltransferase-like [Sus scrofa] >gi|311256890|ref|XP_003126852.1| PREDICTED: adenine phosphoribosyltransferase-like [Sus scrofa]	1.231	1.138	1.085	0.799
gi|343072|gb|AAA32030.1|	ATPase 8, partial (mitochondrion) [Sus scrofa]	0.683	0.285	0.431	0.745
gi|223976083|ref|YP_002600781.1|	ATP synthase F0 subunit 8 [Sus scrofa domesticus] >gi|5835867|ref|NP_008				

	638.1|ATP8_15069 ATP synthase F0 subunit 8 [Sus scrofa] >gi|347448714|gb|AEO93028.1| ATP synthase F0 subunit 8 (mitochondrion) [Sus scrofa] >gi|347448658|gb|AEO92976.1| ATP synt				
gi|209166273|gb|ACI41640.1|	ATP synthase F0 subunit 8 [Sus scrofa]				
gi|262072813|dbj|BAI47714.1|	hydroxysteroid (17-beta) dehydrogenase 12 [Sus scrofa]	0.728	0.376	0.498	0.648
gi|335281993|ref|XP_003353940.1|	PREDICTED: estradiol 17-beta-dehydrogenase 12 [Sus scrofa]				
gi|8569334|pdb|1EIO|A	Chain A, Ileal Lipid Binding Protein In Complex With Glycocholate	1.497	1.823	0.959	0.734
gi|356460931|ref|NP_999380.2|	gastrotropin [Sus scrofa]				
gi|157830915|pdb|1EAL|A	Chain A, Nmr Study Of Ileal Lipid Binding Protein				
gi|125151|sp|P00571.1|KAD1_PIG	RecName: Full=Adenylate kinase isoenzyme 1; Short=AK 1; AltName: Full=ATP-AMP transphosphorylase 1; AltName: Full=Myokinase >gi|350579686|ref|XP_003122225.3| PREDICTED: adenylate kinase isoenzyme 1 isoform 1 [Sus scrofa] >gi|229498|prf||742496A kina	---	---	---	---
gi|313507265|pdb|3ADK|A	Chain A, Refined Structure Of Porcine Cytosolic Adenylate Kinase At 2.1 Angstroms Resolution				
gi|350579688|ref|XP_003480663.1|	PREDICTED: adenylate kinase isoenzyme 1 [Sus scrofa]				
gi|194035478|ref|XP_001924964.1|	PREDICTED: 60S ribosomal protein L8 [Sus scrofa]	---	---	---	---
gi|87133208|gb|ABD24291.1|	Tax1 binding protein 3 [Sus scrofa]	---	---	---	---
gi|311268143|ref|XP_003131896.1|	PREDICTED: tax1-binding protein 3-like [Sus scrofa]				
gi|350589935|ref|XP_003131063.3|	PREDICTED: tax1-binding protein 3-like, partial [Sus scrofa]				
gi|194036902|ref|XP_001927	PREDICTED: prefoldin subunit	---	---	---	---

358.1|	2-like [Sus scrofa]				
gi|350595023|ref|XP_003484029.1|	PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 2 [Sus scrofa]	---	---	---	---
gi|194044826|ref|XP_001927474.1|	PREDICTED: [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial isoform 1 [Sus scrofa]	---	---	---	---
gi|335305794|ref|XP_003360296.1|	PREDICTED: [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial isoform 2 [Sus scrofa]				
gi|311263751|ref|XP_003129801.1|	PREDICTED: protein CWC15 homolog isoform 2 [Sus scrofa]	---	---	---	---
gi|335294720|ref|XP_003129800.2|	PREDICTED: protein CWC15 homolog isoform 1 [Sus scrofa]				
gi|90903287|gb|ABE02211.1|	MX2 [Sus scrofa]	---	---	---	---
gi|206557741|sp|A7VK00.1| MX2_PIG	RecName: Full=Interferon-induced GTP-binding protein Mx2; AltName: Full=Myxovirus resistance protein 2 >gi|210050415|dbj|BAG80705.1| Mx2 protein [Sus scrofa] >gi|156720189|dbj|BAF76735.1| Mx2 [Sus scrofa]				
gi|148235632|ref|NP_001090885.1|	interferon-induced GTP-binding protein Mx2 [Sus scrofa] >gi|58701898|gb|AAW81693.1| MX2 [Sus scrofa]				
gi|311253020|ref|XP_003125380.1|	PREDICTED: putative peptidyl-tRNA hydrolase PTRHD1-like [Sus scrofa]	0.406	0.392	0.647	0.521
gi|311258562|ref|XP_003127670.1|	PREDICTED: agmatinase, mitochondrial-like [Sus scrofa]	1.979	0.893	1.312	1.357
gi|1016321|gb|AAA79108.1|	cytochrome P450 2C35, partial [Sus scrofa]	---	---	---	---
gi|47523894|ref|NP_999585.1|	cytochrome P450 2C49 precursor [Sus scrofa] >gi|19071840|dbj|BAB85664.1| cytochrome P450 2C49 [Sus scrofa]				
gi|311248306|ref|XP_003123072.1|	PREDICTED: U6 snRNA-associated Sm-like protein LSm7-like [Sus	0.751	0.974	1.158	1.071

	scrofa]				
gi|335288048|ref|XP_001927642.3|	PREDICTED: partner of Y14 and mago-like [Sus scrofa]	---	---	---	---
gi|37934198|gb|AAP68768.1|	2,4-dienoyl-CoA reductase [Sus scrofa]	1.33	0.905	0.922	0.844
gi|346421316|ref|NP_001177161.2|	2,4-dienoyl-CoA reductase, mitochondrial [Sus scrofa]				
gi|295442674|gb|ADG21261.1|	2,4-dienoyl-CoA reductase 1 [Sus scrofa]				
gi|350582325|ref|XP_003354840.2|	PREDICTED: calcineurin subunit B type 1-like [Sus scrofa] >gi|335306878|ref|XP_003125129.2| PREDICTED: calcineurin subunit B type 1-like [Sus scrofa]	0.823	0.982	0.989	1.117
gi|311259157|ref|XP_003127967.1|	PREDICTED: interferon-induced protein 44-like [Sus scrofa]	0.829	0.924	0.904	1.383
gi|350586528|ref|XP_003482207.1|	PREDICTED: butyrophilin-like protein 2 [Sus scrofa] >gi|350586524|ref|XP_003482205.1| PREDICTED: butyrophilin-like protein 2-like [Sus scrofa]	---	---	---	---
gi|1346657|sp|P48762.1|SL9A1_PIG	RecName: Full=Sodium/hydrogen exchanger 1; AltName: Full=Na(+)/H(+) exchanger 1; Short=NHE-1; AltName: Full=Solute carrier family 9 member 1 >gi|164596|gb|AAA31092.1| Na+-H+ exchanger [Sus scrofa]	---	---	---	---
gi|55741758|ref|NP_001007104.1|	sodium/hydrogen exchanger 1 [Sus scrofa] >gi|240707|gb|AAB20633.1| Na(+)-H+ exchanger [Sus scrofa]				
gi|311264699|ref|XP_003130289.1|	PREDICTED: mitochondrial-processing peptidase subunit beta [Sus scrofa]	---	---	---	---
gi|335308134|ref|XP_003361114.1|	PREDICTED: mitochondrial-processing peptidase subunit beta-like [Sus scrofa]				
gi|350583174|ref|XP_001927278.4|	PREDICTED: acyl-protein thioesterase 1 [Sus scrofa]	2.18	0.982	0.968	1.35
gi|110832818|sp|Q29221.3|CAZA2_PIG	RecName: Full=F-actin-capping protein subunit alpha-2; AltName:	---	---	---	---

	Full=CapZ alpha-2 >gi|148613355|gb|ABQ96221.1| F-actin capping protein alpha 2 subunit [Sus scrofa] >gi|38322751|gb|AAR16302.1| capping protein (actin filament) muscle Z-line, alpha 2 [				
gi|350596747|ref|XP_003484313.1|	PREDICTED: F-actin-capping protein subunit alpha-2-like [Sus scrofa]				
gi|147903595|ref|NP_001090924.1|	F-actin-capping protein subunit alpha-2 [Sus scrofa] >gi|118627574|emb|CAL69436.1| F-actin capping protein subunit alpha 2 [Sus scrofa]				
gi|350595294|ref|XP_003134809.3|	PREDICTED: F-actin-capping protein subunit alpha-2-like [Sus scrofa]				
gi|350591814|ref|XP_003483340.1|	PREDICTED: lipoma-preferred partner-like [Sus scrofa]	0.669	0.732	0.815	0.863
gi|335290435|ref|XP_003356182.1|	PREDICTED: rho guanine nucleotide exchange factor 16 [Sus scrofa]	1.187	0.883	0.642	1.232
gi|311250341|ref|XP_003124106.1|	PREDICTED: transcription initiation factor TFIID subunit 7 [Sus scrofa]	1.001	1.809	1.608	1.345
gi|113205780|ref|NP_001038049.1|	quinone oxidoreductase [Sus scrofa] >gi|104295137|gb|ABF72038.1| zeta-crystallin [Sus scrofa]	---	---	---	---
gi|115502567|sp|Q0MVN8.1|QOR_PIG	RecName: Full=Quinone oxidoreductase; AltName: Full=NADPH:quinone reductase; AltName: Full=Zeta-crystallin >gi|111434264|gb|ABH10011.1| zeta-crystallin [Sus scrofa]				
gi|311249297|ref|XP_003123564.1|	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 [Sus scrofa]	---	---	---	---
gi|339895863|ref|NP_001229960.1|	coiled-coil and C2 domain-containing 1A [Sus scrofa]	---	---	---	---
gi|311247589|ref|XP_003122716.1|	PREDICTED: coiled-coil domain-containing protein 86-like [Sus scrofa]	---	---	---	---
gi|350594682|ref|XP_003134	PREDICTED: D-tyrosyl-tRNA(Tyr)	---	---	---	---

325.3|	deacylase 1-like [Sus scrofa]				
gi|5739517|gb|AAD50507.1|AF176246_1	macrophage migration inhibitory factor, partial [Sus scrofa]	0.505	0.499	0.353	0.26
gi|262204902|dbj|BAI48031.1|	macrophage migration inhibitory factor [Sus scrofa]				
gi|116175251|ref|NP_001070681.1|	macrophage migration inhibitory factor [Sus scrofa] >gi|124075357|sp|P80928.3|MIF_PIG RecName: Full=Macrophage migration inhibitory factor; Short=MIF; AltName: Full=Glycosylation-inhibiting factor; Short=GIF; AltName: Full=L-dopachrome isomerase; Al				
gi|350594292|ref|XP_003134012.3|	PREDICTED: superkiller viralicidic activity 2-like 2 isoform 1 [Sus scrofa]	---	---	---	---
gi|350580668|ref|XP_003123154.3|	PREDICTED: scaffold attachment factor B2 [Sus scrofa]	---	---	---	---
gi|335310888|ref|XP_003362240.1|	PREDICTED: importin subunit alpha-4-like, partial [Sus scrofa]	---	---	---	---
gi|345199331|ref|NP_001230852.1|	CWC27 spliceosome-associated protein homolog [Sus scrofa]	---	---	---	---
gi|350592457|ref|XP_001929016.4|	PREDICTED: CAP-Gly domain-containing linker protein 1 [Sus scrofa]	1.419	1.214	1.321	1.129
gi|350579992|ref|XP_003122608.3|	PREDICTED: EH domain binding protein 1-like 1 [Sus scrofa]	---	---	---	---
gi|356582360|ref|NP_001239162.1|	ADP-ribosylation factor interacting protein 1 [Sus scrofa]	---	---	---	---
gi|194043071|ref|XP_001928539.1|	PREDICTED: gatC-like protein-like [Sus scrofa]	---	---	---	---
gi|227121291|gb|ACP19336.1|	claudin 3 variant 1 [Sus scrofa]	---	---	---	---
gi|229892832|ref|NP_001153547.1|	claudin-3 [Sus scrofa] >gi|227121293|gb|ACP19337.1| claudin 3 variant 2 [Sus scrofa]				
gi|346986400|ref|NP_001231351.1|	kunitz-type protease inhibitor 1 precursor [Sus scrofa]	0.573	0.736	0.762	0.681
gi|350581652|ref|XP_003354625.2|	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial-like [Sus scrofa]	---	---	---	---

gi|350593477|ref|XP_003483694.1|	PREDICTED: myosin-VIIb [Sus scrofa]	0.821	0.831	1.173	0.709
gi|335287187|ref|XP_003355292.1|	PREDICTED: ATP synthase subunit b, mitochondrial [Sus scrofa]	---	---	---	---
gi|311275507|ref|XP_003134773.1|	PREDICTED: neural Wiskott-Aldrich syndrome protein-like [Sus scrofa]	0.716	0.861	0.847	0.958
gi|350589312|ref|XP_003130599.3|	PREDICTED: LOW QUALITY PROTEIN: protein ELYS-like [Sus scrofa]	---	---	---	---
gi|344259276|gb|AEN03335.1|	proteasome subunit beta type 6 [Sus scrofa] >gi|344259274|gb|AEN03334.1| proteasome subunit beta type 6 [Sus scrofa]	2.594	0.743	1.107	0.517
gi|346716138|ref|NP_001138398.2|	proteasome subunit beta type-6 [Sus scrofa]				
gi|350592919|ref|XP_001924466.4|	PREDICTED: neutral ceramidase [Sus scrofa]	0.821	1.269	1.808	1.064
gi|311246780|ref|XP_003122339.1|	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2-like [Sus scrofa]	0.868	1.466	1.718	1.043
gi|350596685|ref|XP_003361498.2|	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2-like isoform 1 [Sus scrofa]				
gi|311273575|ref|XP_003133933.1|	PREDICTED: NAD kinase domain-containing protein 1 isoform 1 [Sus scrofa]	---	---	---	---
gi|335303800|ref|XP_003359802.1|	PREDICTED: NAD kinase domain-containing protein 1 isoform 2 [Sus scrofa]				
gi|335286747|ref|XP_001924678.3|	PREDICTED: hepatoma-derived growth factor-like [Sus scrofa]	1.35	1.402	1.013	1.412
gi|350594009|ref|XP_003483813.1|	PREDICTED: PERQ amino acid-rich with GYF domain-containing protein 2-like, partial [Sus scrofa]	0.465	0.784	0.856	0.665
gi|311267458|ref|XP_003131579.1|	PREDICTED: 39S ribosomal protein L10, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|335310432|ref|XP_003362030.1|	PREDICTED: splicing factor 3B subunit 3-like [Sus scrofa]	0.927	1.004	0.927	1.065
gi|311269853|ref|XP_003132	PREDICTED: choline-phosphate	0.689	0.563	0.584	0.844

661.1|	cytidylyltransferase A [Sus scrofa]				
gi|311262619|ref|XP_003129271.1|	PREDICTED: mitotic spindle assembly checkpoint protein MAD2A-like [Sus scrofa]	---	---	---	---
gi|335307137|ref|XP_003360720.1|	PREDICTED: BRISC and BRCA1-A complex member 1-like [Sus scrofa]	---	---	---	---
gi|335286799|ref|XP_003355186.1|	PREDICTED: FAD synthase [Sus scrofa] >gi|335286797|ref|XP_001929410.3| PREDICTED: FAD synthase isoform 1 [Sus scrofa]	---	---	---	---
gi|264681454|ref|NP_001161122.1|	S-adenosylmethionine synthase isoform type-2 [Sus scrofa] >gi|262204900|dbj|BAI48030.1| methionine adenosyltransferase II alpha [Sus scrofa]	---	---	---	---
gi|335297289|ref|XP_003357996.1|	PREDICTED: septin-9-like [Sus scrofa]	---	---	---	---
gi|311276184|ref|XP_003135086.1|	PREDICTED: FUN14 domain-containing protein 1-like [Sus scrofa]	0.718	1.337	1.354	1.308
gi|297307135|ref|NP_001171998.1|	protein unc-45 homolog A [Sus scrofa]	---	---	---	---
gi|350582906|ref|XP_001925367.4|	PREDICTED: gasdermin-C-like [Sus scrofa]	---	---	---	---
gi|298160958|ref|NP_001177156.1|	NHP2 non-histone chromosome protein 2-like 1 [Sus scrofa] >gi|298160960|ref|NP_001177155.1| NHP2 non-histone chromosome protein 2-like 1 [Sus scrofa]	---	---	---	---
gi|335306662|ref|XP_003360532.1|	PREDICTED: NHP2-like protein 1-like [Sus scrofa]				
gi|349732194|ref|NP_001231852.1|	armadillo repeat containing 10 [Sus scrofa] >gi|350588904|ref|XP_003482738.1| PREDICTED: armadillo repeat-containing protein 10-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350588908|ref|XP_003482740.1|	PREDICTED: armadillo repeat-containing protein 10-like isoform 3 [Sus scrofa]				
gi|350588906|ref|XP_003482739.1|	PREDICTED: armadillo repeat-containing protein 10-like				

	isoform 2 [Sus scrofa]				
gi|350588910|ref|XP_003482741.1|	PREDICTED: armadillo repeat-containing protein 10-like isoform 4 [Sus scrofa]				
gi|347300383|ref|NP_001231485.1|	aminoacyl tRNA synthase complex-interacting multifunctional protein 2 isoform 1 [Sus scrofa]	---	---	---	---
gi|347300385|ref|NP_001231486.1|	aminoacyl tRNA synthase complex-interacting multifunctional protein 2 isoform 2 [Sus scrofa]				
gi|311272660|ref|XP_003133533.1|	PREDICTED: secernin-3-like [Sus scrofa]	---	---	---	---
gi|343478220|ref|NP_001230376.1|	eukaryotic translation initiation factor 4H 1 [Sus scrofa]	---	---	---	---
gi|343478222|ref|NP_001230377.1|	eukaryotic translation initiation factor 4H 2 [Sus scrofa]				
gi|350597032|ref|XP_001925921.4|	PREDICTED: aldehyde dehydrogenase family 1 member A3, partial [Sus scrofa]	2.31	4.2	3.338	3.713
gi|21703165|gb|AAM76080.1|AF334742_1	immunoglobulin kappa light chain VJ region [Sus scrofa]	---	---	---	---
gi|41323521|gb|AAR99918.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323519|gb|AAR99917.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323567|gb|AAR99941.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323635|gb|AAR99975.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323673|gb|AAR99994.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323593|gb|AAR99954.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323525|gb|AAR99920.1| immunoglobulin kappa variable region [Sus scrofa]				
gi|41323677|gb|AAR99996.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323583|gb|AAR99949.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323535|gb|AAR99925.1|	immunoglobulin kappa variable region [Sus scrofa]				

gi|41323653|gb|AAR99984.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323645|gb|AAR99980.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323561|gb|AAR99938.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323557|gb|AAR99936.1| immunoglobulin				
gi|41323671|gb|AAR99993.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323661|gb|AAR99988.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323597|gb|AAR99956.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323553|gb|AAR99934.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323541|gb|AAR99928.1| immunoglobulin				
gi|41323619|gb|AAR99967.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323539|gb|AAR99927.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323643|gb|AAR99979.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323633|gb|AAR99974.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323563|gb|AAR99939.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323627|gb|AAR99971.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323509|gb|AAR99912.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323551|gb|AAR99933.1| immunoglobulin kappa variable region [Sus scrofa]				
gi|41323665|gb|AAR99990.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323629|gb|AAR99972.1|	immunoglobulin kappa variable region [Sus scrofa]				

gi|41323579|gb|AAR99947.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323569|gb|AAR99942.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323581|gb|AAR99948.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323639|gb|AAR99977.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323681|gb|AAR99998.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323685|gb|AAS00001.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323641|gb|AAR99978.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323683|gb|AAR99999.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323547|gb|AAR99931.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323523|gb|AAR99919.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323623|gb|AAR99969.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323675|gb|AAR99995.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323617|gb|AAR99966.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323533|gb|AAR99924.1| immunoglobulin kappa variable region [Sus scrofa]				
gi|41323621|gb|AAR99968.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323589|gb|AAR99952.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323573|gb|AAR99944.1| immunoglobulin kappa variable region [Sus scrofa] >gi|41323611|gb|AAR99963.1| immunoglobulin				
gi|41323655|gb|AAR99985.1|	immunoglobulin kappa variable region [Sus scrofa] >gi|41323651|gb|AAR99983.				

	1| immunoglobulin kappa variable region [Sus scrofa]				
gi|41323565|gb|AAR99940.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323667|gb|AAR99991.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|350580067|ref|XP_003122733.3|	PREDICTED: protein PAT1 homolog 1 [Sus scrofa]	---	---	---	---
gi|147906270|ref|NP_001090905.1|	E3 ubiquitin-protein ligase XIAP [Sus scrofa] >gi|119567669|gb|ABL84299.1| X-linked inhibitor of apoptosis [Sus scrofa]	---	---	---	---
gi|311249593|ref|XP_003123724.1|	PREDICTED: vesicular integral-membrane protein VIP36 [Sus scrofa]	0.559	0.214	0.214	0.626
gi|270289750|ref|NP_001161887.1|	non-specific lipid-transfer protein [Sus scrofa] >gi|262263195|dbj|BAI48100.1| sterol carrier protein 2 [Sus scrofa]	---	---	---	---
gi|335298382|ref|XP_003358265.1|	PREDICTED: thioredoxin domain-containing protein 17-like isoform 2 [Sus scrofa] >gi|311268187|ref|XP_003131925.1| PREDICTED: thioredoxin domain-containing protein 17-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350584189|ref|XP_003481688.1|	PREDICTED: phosphatidylinositol-5-phosphate 4-kinase type-2 gamma-like [Sus scrofa]	---	---	---	---
gi|194042810|ref|XP_001928060.1|	PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform 2 [Sus scrofa]	---	---	---	---
gi|326368169|emb|CAZ65757.1|	protein phosphatase 3, catalytic subunit, beta isoform [Phacochoerus africanus]				
gi|311271387|ref|XP_001928050.2|	PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform 1 [Sus scrofa]				
gi|326368171|emb|CAZ6575	protein phosphatase 3, catalytic				

<table>
<tr><td>8.1|</td><td>subunit, beta isoform [Babyrousa babyrussa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|326368167|emb|CAZ65756.1|</td><td>protein phosphatase 3, catalytic subunit, beta isoform [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|147225127|emb|CAN13255.1|</td><td>novel protein similar to butyrophilin family proteins [Sus scrofa]</td><td>0.673</td><td>0.418</td><td>0.595</td><td>0.502</td></tr>
<tr><td>gi|350586516|ref|XP_003128364.3|</td><td>PREDICTED: butyrophilin subfamily 1 member A1-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|147225163|emb|CAN13303.1|</td><td>novel protein similar to butyrophilin family proteins [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|194035115|ref|XP_001925615.1|</td><td>PREDICTED: ubiquitin carboxyl-terminal hydrolase 45 [Sus scrofa]</td><td>1.763</td><td>---</td><td>---</td><td>0.168</td></tr>
<tr><td>gi|350591061|ref|XP_003132153.3|</td><td>PREDICTED: nuclease EXOG, mitochondrial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|194035837|ref|XP_001928904.1|</td><td>PREDICTED: peroxisomal biogenesis factor 19 isoform 1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311254007|ref|XP_003125714.1|</td><td>PREDICTED: peroxisomal biogenesis factor 19 isoform 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|148747288|ref|NP_001092072.1|</td><td>sideroflexin-1 [Sus scrofa] >gi|166977631|sp|A5A761.1|SFXN1_PIG RecName: Full=Sideroflexin-1 >gi|146741302|dbj|BAF62306.1| sideroflexin 1 [Sus scrofa]</td><td>0.951</td><td>0.642</td><td>0.587</td><td>0.663</td></tr>
<tr><td>gi|166796069|ref|NP_001107760.1|</td><td>signal peptidase complex subunit 1 [Sus scrofa] >gi|187611464|sp|B0FWK4.1|SPCS1_PIG RecName: Full=Signal peptidase complex subunit 1; AltName: Full=Microsomal signal peptidase 12 kDa subunit; Short=SPase 12 kDa subunit >gi|164598074|gb|ABY61324.1| s</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311274550|ref|XP_001924843.2|</td><td>PREDICTED: 28S ribosomal protein S26, mitochondrial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350585199|ref|XP_003355972.2|</td><td>PREDICTED: rRNA 2~-O-methyltransferase fibrillarin-like isoform 1 [Sus scrofa]</td><td>0.703</td><td>0.823</td><td>0.753</td><td>1.083</td></tr>
</table>

gi|350585201|ref|XP_003481901.1|	PREDICTED: rRNA 2~-O-methyltransferase fibrillarin-like isoform 2 [Sus scrofa]				
gi|47522616|ref|NP_999102.1|	ubiquitin-like protein FUBI precursor [Sus scrofa] >gi|1628628|gb|AAB52915.1| ubiquitin-like/S30 ribosomal fusion protein [Sus scrofa]	0.111	0.123	0.101	0.111
gi|51338624|sp|P62863.1|RS30_PIG	RecName: Full=40S ribosomal protein S30				
gi|350589515|ref|XP_003482862.1|	PREDICTED: hypothetical protein LOC100738725 [Sus scrofa]				
gi|75056777|sp|Q8HZV3.1|TFR1_PIG	RecName: Full=Transferrin receptor protein 1; Short=TR; Short=TfR; Short=TfR1; Short=Trfr; AltName: CD_antigen=CD71 >gi|47522828|ref|NP_999166.1| transferrin receptor protein 1 [Sus scrofa] >gi|22854661|gb|AAN09749.1|AF416763_1 transferrin receptor	0.648	0.447	0.379	0.547
gi|298162731|gb|ADI59732.1|	transferrin receptor protein [Sus scrofa]				
gi|311259609|ref|XP_003128180.1|	PREDICTED: alpha-1B-glycoprotein-like [Sus scrofa]	---	---	---	---
gi|350585516|ref|XP_003356167.2|	PREDICTED: cyclin-dependent kinase 11 [Sus scrofa]	---	---	---	---
gi|194042021|ref|XP_001927084.1|	PREDICTED: programmed cell death protein 4 isoform 1 [Sus scrofa]	2.4	0.92	0.975	1.571
gi|335302236|ref|XP_003359415.1|	PREDICTED: programmed cell death protein 4 isoform 2 [Sus scrofa]				
gi|350586098|ref|XP_003482113.1|	PREDICTED: PDZ domain-containing protein GIPC2-like isoform 2 [Sus scrofa]	---	---	---	---
gi|350586100|ref|XP_003356469.2|	PREDICTED: PDZ domain-containing protein GIPC2-like isoform 1 [Sus scrofa]				
gi|335297132|ref|XP_003131142.2|	PREDICTED: cysteinyl-tRNA synthetase, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|148724904|emb|CAN87692.1|	RD RNA binding protein [Sus scrofa]	---	---	---	---

gi|156120154|ref|NP_001095295.1|	negative elongation factor E [Sus scrofa] >gi|148724907|emb|CAN87695.1| RD RNA binding protein [Sus scrofa]				
gi|148724908|emb|CAN87696.1|	RD RNA binding protein [Sus scrofa]				
gi|148724905|emb|CAN87693.1|	RD RNA binding protein [Sus scrofa]				
gi|148724906|emb|CAN87694.1|	RD RNA binding protein [Sus scrofa]				
gi|350579603|ref|XP_003480647.1|	PREDICTED: ribosome-recycling factor, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|350579605|ref|XP_003122165.3|	PREDICTED: ribosome-recycling factor, mitochondrial-like isoform 2 [Sus scrofa]				
gi|345199333|ref|NP_001230853.1|	SEC24 family, member A [Sus scrofa]	---	---	---	---
gi|194038534|ref|XP_001929109.1|	PREDICTED: prostaglandin reductase 2 isoform 1 [Sus scrofa] >gi|311261328|ref|XP_003128705.1| PREDICTED: prostaglandin reductase 2 isoform 2 [Sus scrofa]	---	---	---	---
gi|335288570|ref|XP_003126608.2|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial-like [Sus scrofa]	1.076	0.863	0.648	0.825
gi|305855162|ref|NP_001182263.1|	ELAV-like protein 1 [Sus scrofa] >gi|285818484|gb|ADC38915.1| ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 [Sus scrofa]	0.766	0.611	0.609	0.783
gi|346716187|ref|NP_001231241.1|	WAS/WASL-interacting protein family member 2 [Sus scrofa]	---	---	---	---
gi|47522624|ref|NP_999098.1|	arylsulfatase A precursor [Sus scrofa] >gi|45686371|gb|AAL58668.2|AF316108_1 arylsulfatase A [Sus scrofa]	---	---	---	---
gi|335281873|ref|XP_003353914.1|	PREDICTED: 182 kDa tankyrase-1-binding protein [Sus scrofa]	0.975	0.921	1.108	0.694
gi|350586715|ref|XP_001925	PREDICTED: CD2-associated	---	---	---	---

766.4|	protein-like, partial [Sus scrofa]				
gi|343790936|ref|NP_001230525.1|	KH domain containing, RNA binding, signal transduction associated 1 [Sus scrofa]	---	---	---	---
gi|264681474|ref|NP_001161108.1|	sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating [Sus scrofa] >gi|262204910|dbj|BAI48035.1| NAD(P) dependent steroid dehydrogenase-like [Sus scrofa]	---	---	---	---
gi|194042179|ref|XP_001929427.1|	PREDICTED: 40S ribosomal protein S24 isoform 4 [Sus scrofa]	---	---	---	---
gi|335301826|ref|XP_003359293.1|	PREDICTED: 40S ribosomal protein S24 [Sus scrofa] >gi|335301828|ref|XP_003359294.1| PREDICTED: 40S ribosomal protein S24 [Sus scrofa] >gi|335301824|ref|XP_003359292.1| PREDICTED: 40S ribosomal protein S24 [Sus scrofa]				
gi|311271421|ref|XP_001929422.2|	PREDICTED: 40S ribosomal protein S24 isoform 3 [Sus scrofa] >gi|194042181|ref|XP_001929415.1| PREDICTED: 40S ribosomal protein S24 isoform 1 [Sus scrofa]				
gi|335306028|ref|XP_003360371.1|	PREDICTED: 40S ribosomal protein S24-like [Sus scrofa]				
gi|335301836|ref|XP_003359297.1|	PREDICTED: 40S ribosomal protein S24 [Sus scrofa] >gi|311271423|ref|XP_001929420.2| PREDICTED: 40S ribosomal protein S24 isoform 2 [Sus scrofa]				
gi|335301831|ref|XP_003359295.1|	PREDICTED: 40S ribosomal protein S24 [Sus scrofa]				
gi|311273577|ref|XP_003133934.1|	PREDICTED: 40S ribosomal protein S24-like [Sus scrofa]				
gi|227430316|ref|NP_001153064.1|	cytochrome b5 type B [Sus scrofa]	---	---	---	---
gi|311266655|ref|XP_003131200.1|	PREDICTED: charged multivesicular body protein 6-like [Sus scrofa]	---	---	---	---
gi|335299053|ref|XP_003132249.2|	PREDICTED: inosine-5~-monophosphate dehydrogenase 2-like isoform 1 [Sus	2.258	1.474	1.885	1.826

	scrofa]				
gi|335299055|ref|XP_003358476.1|	PREDICTED: inosine-5~-monophosphate dehydrogenase 2-like isoform 2 [Sus scrofa]				
gi|335297344|ref|XP_003131243.2|	PREDICTED: integrin beta-4-like [Sus scrofa]	0.73	1.151	1.519	1.199
gi|335282293|ref|XP_003354026.1|	PREDICTED: UPF0449 protein C19orf25 homolog [Sus scrofa]	---	---	---	---
gi|346421411|ref|NP_001231080.1|	proteasome (prosome, macropain) 26S subunit, ATPase, 1 [Sus scrofa]	---	---	---	---
gi|335290010|ref|XP_003127394.2|	PREDICTED: splicing factor, arginine/serine-rich 19 [Sus scrofa]	0.441	0.39	0.467	0.395
gi|350579829|ref|XP_003480693.1|	PREDICTED: LOW QUALITY PROTEIN: cysteinyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]	---	---	---	---
gi|350592384|ref|XP_001927025.4|	PREDICTED: golgin subfamily A member 3 [Sus scrofa]	---	---	---	---
gi|350597062|ref|XP_003362000.2|	PREDICTED: golgin subfamily A member 3-like, partial [Sus scrofa]				
gi|335300274|ref|XP_003132696.2|	PREDICTED: hematopoietic lineage cell-specific protein [Sus scrofa]	---	---	---	---
gi|311256155|ref|XP_003126523.1|	PREDICTED: DNA-binding protein A-like isoform 1 [Sus scrofa]	---	---	---	---
gi|335288453|ref|XP_003355623.1|	PREDICTED: DNA-binding protein A-like isoform 2 [Sus scrofa]				
gi|350578568|ref|XP_003480395.1|	PREDICTED: beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 3-like [Sus scrofa] >gi|350578566|ref|XP_003121521.3| PREDICTED: beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 3-l	---	---	---	---
gi|343403767|ref|NP_001230312.1|	solute carrier family 46, member 1 [Sus scrofa]	---	---	---	---
gi|350590667|ref|XP_003483116.1|	PREDICTED: proton-coupled folate transporter-like [Sus scrofa]				

gi|116175263|ref|NP_001070687.1|	ubiquitin-conjugating enzyme E2 J1 [Sus scrofa] >gi|115371729|gb|ABI96189.1| UB2J1 [Sus scrofa]	---	---	---	---
gi|350579496|ref|XP_003353657.2|	PREDICTED: proteasome-associated protein ECM29 homolog [Sus scrofa]	1.214	1.076	1.216	1.332
gi|194474050|ref|NP_001124003.1|	disintegrin and metalloproteinase domain-containing protein 10 precursor [Sus scrofa] >gi|190610714|gb|ACE80208.1| disintegrin and metallopeptidase domain 10 [Sus scrofa]	---	---	---	---
gi|350581743|ref|XP_003481100.1|	PREDICTED: phosphomannomutase 2-like, partial [Sus scrofa]	---	---	---	---
gi|3023900|sp|P79382.3|MGST1_PIG	RecName: Full=Microsomal glutathione S-transferase 1; Short=Microsomal GST-1; AltName: Full=Microsomal GST-I >gi|47523668|ref|NP_999465.1| microsomal glutathione S-transferase 1 [Sus scrofa] >gi|1840393|dbj|BAA19201.1| glutathione S-transferase [Sus	---	---	---	---
gi|350583937|ref|XP_003355432.2|	PREDICTED: LIM domain and actin-binding protein 1-like [Sus scrofa]	---	---	---	---
gi|350584488|ref|XP_003126654.3|	PREDICTED: kinesin family member 21A [Sus scrofa]	---	---	---	---
gi|350595170|ref|XP_003484054.1|	PREDICTED: UPF0562 protein C7orf55 homolog [Sus scrofa]	---	---	---	---
gi|350595172|ref|XP_003484055.1|	PREDICTED: UPF0562 protein C7orf55 homolog [Sus scrofa]				
gi|350595174|ref|XP_003484056.1|	PREDICTED: UPF0562 protein C7orf55 homolog [Sus scrofa]				
gi|335310367|ref|XP_003361999.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein H2-like [Sus scrofa]	0.699	0.928	0.744	0.843
gi|194036098|ref|XP_001929432.1|	PREDICTED: SHC-transforming protein 1 isoform 1 [Sus scrofa]	---	---	---	---
gi|335286795|ref|XP_003355185.1|	PREDICTED: SHC-transforming protein 1 [Sus scrofa]				
gi|3913338|sp|O46658.3|CP2	RecName: Full=Vitamin D(3)	---	---	---	---

DP_PIG	25-hydroxylase; AltName: Full=CYPIID25; AltName: Full=Cytochrome P450 2D25 >gi|47523842|ref|NP_999559.1| vitamin D(3) 25-hydroxylase [Sus scrofa] >gi|2956688|emb|CAA76205.1| vitamin D3 25-Hydroxylase (CYP2D25) [Sus scrofa]				
gi|94490432|gb|ABF29435.1|	cytochrome P450 family 2 subfamily D polypeptide 6 [Sus scrofa]				
gi|10179958|gb|AAG13962.1|	vitamin D-25-hydroxylase [Sus scrofa]				
gi|47523696|ref|NP_999480.1|	hormone-sensitive lipase [Sus scrofa] >gi|2764520|emb|CAA04121.1| Hormone-sensitive lipase [Sus scrofa] >gi|3169109|emb|CAA04122.1| hormone-sensitive lipase [Sus scrofa]	---	---	---	---
gi|302372518|gb|ADL28431.1|	hormone-sensitive lipase [Sus scrofa]				
gi|75071455|sp|Q68J42.1|LIPS_PIG	RecName: Full=Hormone-sensitive lipase; Short=HSL >gi|51101229|gb|AAT95417.1| hormone-sensitive lipase [Sus scrofa]				
gi|51101227|gb|AAT95416.1|	hormone-sensitive lipase [Sus scrofa]				
gi|345110630|ref|NP_001230796.1|	RuvB-like 2 [Sus scrofa]	1.554	0.962	0.722	1.409
gi|335296521|ref|XP_003130802.2|	PREDICTED: acyl-CoA-binding domain-containing protein 5 [Sus scrofa]	---	---	---	---
gi|350586271|ref|XP_003482146.1|	PREDICTED: E3 ubiquitin-protein ligase HECTD3-like, partial [Sus scrofa]	---	---	---	---
gi|343478171|ref|NP_001230355.1|	small nuclear ribonucleoprotein Sm D3 [Sus scrofa]	0.583	0.802	0.423	0.689
gi|16798651|gb|AAL29467.1|AF435591_1	ribosomal protein L19 [Sus scrofa]	---	---	---	---
gi|311267438|ref|XP_003131557.1|	PREDICTED: 60S ribosomal protein L19 [Sus scrofa]				
gi|347300387|ref|NP_001231487.1|	60S ribosomal protein L17 [Sus scrofa]	0.669	0.697	0.429	0.549

<table>
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<tr><td>gi|1839536|gb|AAB47145.1|</td><td>dipeptidyl peptidase II, DPP II, dipeptidyl aminopeptidase II {N-terminal} [swine, seminal plasma, Peptide Partial, 41 aa] >gi|1881845|gb|AAB49532.1| dipeptidyl-peptidase II, DPP II {N-terminal} {EC 3.4.14.2} [swine, seminal plasma, Peptide Partial,</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|157427709|ref|NP_001098761.1|</td><td>leucyl-cystinyl aminopeptidase [Sus scrofa] >gi|156763828|emb|CAC84519.1| insulin-regulated aminopeptidase [Sus scrofa] >gi|156778063|emb|CAC88117.1| insulin-regulated aminopeptidase [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|195562223|gb|ACG50182.1|</td><td>actin related protein 2/3 complex subunit 2 [Sus scrofa]</td><td>1.277</td><td>0.509</td><td>0.891</td><td>1.037</td></tr>
<tr><td>gi|298160991|ref|NP_001177168.1|</td><td>actin-related protein 2/3 complex subunit 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350582201|ref|XP_003125018.3|</td><td>PREDICTED: hypothetical protein LOC100524080 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350579136|ref|XP_003480530.1|</td><td>PREDICTED: protein phosphatase 1A-like [Sus scrofa]</td><td>0.838</td><td>0.943</td><td>1.301</td><td>0.886</td></tr>
<tr><td>gi|335284548|ref|XP_003354635.1|</td><td>PREDICTED: transmembrane channel-like 5 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311248055|ref|XP_003122952.1|</td><td>PREDICTED: protein lin-7 homolog C-like [Sus scrofa]</td><td>0.802</td><td>0.753</td><td>0.669</td><td>0.898</td></tr>
<tr><td>gi|350584725|ref|XP_003126793.3|</td><td>PREDICTED: protein lin-7 homolog A-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|346644810|ref|NP_001231161.1|</td><td>protein lin-7 homolog B [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350578494|ref|XP_003480379.1|</td><td>PREDICTED: methyl-CpG-binding domain protein 2-like, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|343478269|ref|NP_001230399.1|</td><td>RNA 3~-terminal phosphate cyclase [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|223509|prf||0810207A</td><td>glucagon 37</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|279613|pir||GCPG</td><td>glucagon precursor - pig (fragment)</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|46397418|sp|P01274.4|GLUC_PIG</td><td>RecName: Full=Glucagon; Contains: RecName: Full=Glicentin; Contains: RecName: Full=Glicentin-related polypeptide; Short=GRPP; Contains:</td><td></td><td></td><td></td><td></td></tr>
</table>

	RecName: Full=Oxyntomodulin; Short=OXM; Short=OXY; Contains: RecName: Full=Glucagon; Contains: RecName: Full=Gluc				
gi|509403|emb|CAA84355.1|	BAT1 [Sus scrofa]	---	---	---	---
gi|55742824|ref|NP_001005157.1|	spliceosome RNA helicase DDX39B [Sus scrofa] >gi|47117788|sp|Q29024.2|DX39B_PIG RecName: Full=Spliceosome RNA helicase DDX39B; AltName: Full=56 kDa U2AF65-associated protein; AltName: Full=DEAD box protein UAP56 >gi|162138207|gb|ABX82809.1| HLA-B-as				
gi|350582986|ref|XP_001925424.4|	PREDICTED: eukaryotic translation initiation factor 3 subunit E [Sus scrofa]	---	---	---	---
gi|350529421|ref|NP_001231942.1|	mitochondrial ribosomal protein L49 [Sus scrofa]	---	---	---	---
gi|311250199|ref|XP_003124018.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein A0-like [Sus scrofa]	---	---	---	---
gi|335298275|ref|XP_003131863.2|	PREDICTED: glyoxalase domain-containing protein 4-like [Sus scrofa]	1.799	1.22	1.084	1.553
gi|335310707|ref|XP_003362158.1|	PREDICTED: 39S ribosomal protein L37, mitochondrial-like, partial [Sus scrofa]	---	---	---	---
gi|335286179|ref|XP_003125563.2|	PREDICTED: eukaryotic translation initiation factor 3 subunit H-like isoform 1 [Sus scrofa] >gi|335286181|ref|XP_003355036.1| PREDICTED: eukaryotic translation initiation factor 3 subunit H-like isoform 2 [Sus scrofa]	---	---	---	---
gi|311251198|ref|XP_003124496.1|	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|311273437|ref|XP_003133863.1|	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 2,				

	mitochondrial-like [Sus scrofa]				
gi|311262316|ref|XP_003129121.1|	PREDICTED: mps one binder kinase activator-like 1A-like [Sus scrofa]	---	---	---	---
gi|350582248|ref|XP_003481231.1|	PREDICTED: mps one binder kinase activator-like 1B-like [Sus scrofa]				
gi|350581864|ref|XP_003481142.1|	PREDICTED: protein disulfide-isomerase A2-like [Sus scrofa]	0.828	0.529	0.616	0.75
gi|194042794|ref|XP_001925861.1|	PREDICTED: calcium uniporter protein, mitochondrial [Sus scrofa]	---	---	---	---
gi|311245746|ref|XP_001925192.2|	PREDICTED: endophilin-A1-like [Sus scrofa]	---	---	---	---
gi|350583507|ref|XP_003481532.1|	PREDICTED: cold shock domain-containing protein E1-like [Sus scrofa]	---	---	---	---
gi|75065380|sp|Q8MJ49.1|OSTF1_PIG	RecName: Full=Osteoclast-stimulating factor 1 >gi|47522836|ref|NP_999170.1| osteoclast-stimulating factor 1 [Sus scrofa] >gi|21930129|gb|AAM82161.1|AF523268_1 osteoclast stimulating factor [Sus scrofa]	---	---	---	---
gi|350590012|ref|XP_003482975.1|	PREDICTED: FERM, RhoGEF and pleckstrin domain-containing protein 1 [Sus scrofa]	---	---	---	---
gi|350596332|ref|XP_003361056.2|	PREDICTED: FERM, RhoGEF and pleckstrin domain-containing protein 1-like, partial [Sus scrofa]				
gi|350580442|ref|XP_003123420.3|	PREDICTED: trans-2,3-enoyl-CoA reductase-like [Sus scrofa]	---	---	---	---
gi|349732216|ref|NP_001231858.1|	maspardin [Sus scrofa]	---	---	---	---
gi|350578512|ref|XP_003353370.2|	PREDICTED: maspardin-like [Sus scrofa]				
gi|350581893|ref|XP_003481146.1|	PREDICTED: RNA-binding protein with serine-rich domain 1-like isoform 1 [Sus scrofa] >gi|350581895|ref|XP_003481147.1| PREDICTED: RNA-binding protein with serine-rich domain 1-like isoform 2 [Sus scrofa]	---	---	---	---
gi|220900279|gb|ACL82340.	galectin-related protein [Sus scrofa]	---	---	---	---

1|					
gi|350582342|ref|XP_003481250.1|	PREDICTED: galectin-related protein A [Sus scrofa]				
gi|350596839|ref|XP_003484324.1|	PREDICTED: galectin-related protein A-like [Sus scrofa]				
gi|350582694|ref|XP_003481333.1|	PREDICTED: ATP-dependent RNA helicase DDX1-like [Sus scrofa]	---	---	---	---
gi|311248402|ref|XP_003123126.1|	PREDICTED: hepatoma-derived growth factor-related protein 2-like [Sus scrofa]	---	---	---	---
gi|54039371|sp|P62272.3|RS18_PIG	RecName: Full=40S ribosomal protein S18 >gi|47522714|ref|NP_999105.1| 40S ribosomal protein S18 [Sus scrofa] >gi|1841304|dbj|BAA19211.1| ribosomal protein [Sus scrofa]	0.629	0.226	0.178	0.7
gi|194038457|ref|XP_001928802.1|	PREDICTED: retinol dehydrogenase 11 [Sus scrofa]	---	---	---	---
gi|350581931|ref|XP_003354725.2|	PREDICTED: isoleucyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]	---	---	---	---
gi|350581941|ref|XP_003354723.2|	PREDICTED: isoleucyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]				
gi|147832430|emb|CAN59682.1|	HLA-B associated transcript 2 [Sus scrofa]	---	---	---	---
gi|167908789|ref|NP_001108147.1|	HLA-B associated transcript 2 [Sus scrofa] >gi|158537754|gb|ABW73319.1| HLA-B associated transcript 2 [Sus scrofa]				
gi|311250094|ref|XP_003123955.1|	PREDICTED: histidine triad nucleotide-binding protein 1-like [Sus scrofa]	0.766	1.029	0.941	0.7
gi|119416776|emb|CAL92193.1|	elongation initiation factor 4E [Sus scrofa]	---	---	---	---
gi|311262801|ref|XP_003129362.1|	PREDICTED: eukaryotic translation initiation factor 4E [Sus scrofa]				
gi|21703161|gb|AAM76078.1|AF334740_1	immunoglobulin kappa light chain VJ region [Sus scrofa]	---	---	---	---
gi|41323513|gb|AAR99914.1|	immunoglobulin kappa variable region [Sus scrofa]				
gi|41323531|gb|AAR99923.1|	immunoglobulin kappa variable				

	region [Sus scrofa]				
gi|345199326|ref|NP_001230850.1|	sperm associated antigen 7 [Sus scrofa]	---	---	---	---
gi|343432672|ref|NP_001230350.1|	carbohydrate kinase domain-containing protein isoform 1 [Sus scrofa]	1.276	1.35	0.875	0.768
gi|343432674|ref|NP_001230351.1|	carbohydrate kinase domain-containing protein isoform 2 [Sus scrofa]				
gi|350578316|ref|XP_003121377.3|	PREDICTED: absent in melanoma 1 protein [Sus scrofa]	1.747	1.189	1.311	1.295
gi|223950631|ref|NP_001138859.1|	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 [Sus scrofa] >gi|166915512|gb|ABZ03970.1| guanine nucleotide-binding protein gamma 12 subunit [Sus scrofa]	0.982	0.646	1.014	0.841
gi|194039313|ref|XP_001929257.1|	PREDICTED: kinesin light chain 4 [Sus scrofa]	0.607	0.471	0.544	0.599
gi|311255064|ref|XP_003126064.1|	PREDICTED: mitochondrial import receptor subunit TOM22 homolog [Sus scrofa]	0.746	0.648	0.642	0.877
gi|171948776|gb|ACB59245.1|	cathepsin B [Sus scrofa]	6.941	11.882	9.941	13.412
gi|187470655|sp|A1E295.1|CATB_PIG	RecName: Full=Cathepsin B; Contains: RecName: Full=Cathepsin B light chain; Contains: RecName: Full=Cathepsin B heavy chain; Flags: Precursor >gi|147906534|ref|NP_001090927.1| cathepsin B precursor [Sus scrofa] >gi|118490058|gb|ABK96810.1| cathepsin				
gi|350591026|ref|XP_003132136.3|	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B [Sus scrofa]	---	---	---	---
gi|335299677|ref|XP_003358644.1|	PREDICTED: U2 snRNP-associated SURP motif-containing protein [Sus scrofa]	---	---	---	---
gi|194018716|ref|NP_001123450.1|	cytochrome b-c1 complex subunit 9 [Sus scrofa] >gi|87047640|gb|ABD18453.1| ubiquinol-cytochrome c reductase	---	---	---	---

	complex [Sus scrofa]				
gi|47575891|ref|NP_001001260.1|	peptidoglycan recognition protein 1 precursor [Sus scrofa] >gi|47028067|gb|AAT09052.1| peptidoglycan recognition protein short isoform 1 [Sus scrofa]	---	---	---	---
gi|350585327|ref|XP_003356027.2|	PREDICTED: peptidoglycan recognition protein 1-like [Sus scrofa]				
gi|343432658|ref|NP_001230343.1|	protein phosphatase 1, regulatory (inhibitor) subunit 8 [Sus scrofa]	---	---	---	---
gi|350591508|ref|XP_003483287.1|	PREDICTED: DNA replication licensing factor MCM2 [Sus scrofa]	---	---	---	---
gi|194035343|ref|XP_001928597.1|	PREDICTED: heme-binding protein 2 [Sus scrofa]	---	---	---	---
gi|350580713|ref|XP_003480884.1|	PREDICTED: hypothetical protein LOC100737370 [Sus scrofa]	---	---	---	---
gi|311275781|ref|XP_003134908.1|	PREDICTED: drebrin-like protein-like [Sus scrofa]	---	---	---	---
gi|264681458|ref|NP_001161123.1|	2-acylglycerol O-acyltransferase 2 [Sus scrofa] >gi|262204904|dbj|BAI48032.1| monoacylglycerol O-acyltransferase 2 [Sus scrofa]	0.608	0.314	0.222	0.311
gi|223950623|ref|NP_001138857.1|	dynein light chain Tctex-type 1 [Sus scrofa] >gi|219563062|gb|ACL27890.1| Tctex-type 1 dynein light chain [Sus scrofa]	---	---	---	---
gi|350591965|ref|XP_003132730.3|	PREDICTED: autophagy-related 3 isoform 2 [Sus scrofa]	---	---	---	---
gi|335283921|ref|XP_003354461.1|	PREDICTED: single Ig IL-1-related receptor [Sus scrofa]	---	---	---	---
gi|335307722|ref|XP_003360950.1|	PREDICTED: single Ig IL-1-related receptor-like [Sus scrofa]				
gi|365796117|dbj|BAL43001.1|	single immunoglobulin IL-1R-related molecule [Sus scrofa]				
gi|350588343|ref|XP_003129759.3|	PREDICTED: disks large homolog 2-like [Sus scrofa]	---	---	---	---
gi|350591860|ref|XP_003358811.2|	PREDICTED: disks large homolog 1, partial [Sus scrofa]				
gi|335289860|ref|XP_003127290.2|	PREDICTED: LOW QUALITY PROTEIN: zinc finger CCCH domain-containing protein 4-like [Sus	---	---	---	---

	scrofa]				
gi|350579966|ref|XP_003122620.3|	PREDICTED: tRNA methyltransferase 112 homolog [Sus scrofa]	---	---	---	---
gi|335282788|ref|XP_003123414.2|	PREDICTED: PDZ domain-containing protein GIPC1-like, partial [Sus scrofa]	---	---	---	---
gi|311271301|ref|XP_001926034.2|	PREDICTED: vacuolar protein sorting-associated protein 26A isoform 1 [Sus scrofa]	1.278	0.537	0.55	1.032
gi|350591121|ref|XP_003358453.2|	PREDICTED: phosphatidylinositide phosphatase SAC1-like [Sus scrofa]	---	---	---	---
gi|350591135|ref|XP_003483215.1|	PREDICTED: phosphatidylinositide phosphatase SAC1-like [Sus scrofa]				
gi|1399282|gb|AAB03248.1|	hypoxanthine phosphoribosyltransferase, partial [Sus scrofa]	1.786	0.932	1.113	1.596
gi|4809241|gb|AAD30159.1|	hypoxanthine phosphoribosyltransferase [Sus scrofa]				
gi|74024903|ref|NP_001027548.1|	hypoxanthine-guanine phosphoribosyltransferase [Sus scrofa] >gi|85542050|sp|Q45FY6.3|HPRT_PIG RecName: Full=Hypoxanthine-guanine phosphoribosyltransferase; Short=HGPRT; Short=HGPRTase >gi|71842219|gb|AAZ43258.1| hypoxanthine phosphoribosyltransferas				
gi|1661110|gb|AAB18389.1|	hypoxanthine phosphoribosyltransferase [Sus scrofa]				
gi|264681434|ref|NP_001161112.1|	asparagine synthetase [Sus scrofa] >gi|262036930|dbj|BAI47600.1| asparagine synthetase [Sus scrofa]	---	---	---	---
gi|350579892|ref|XP_003122508.3|	PREDICTED: coronin-1B-like [Sus scrofa]	1.087	1.264	1.046	1.222
gi|147225114|emb|CAN13231.1|	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit [Sus scrofa] >gi|147223388|emb|CAN13123.1| dolichyl-phosphate	---	---	---	---

	mannosyltransferase polypeptide 1, catalytic subunit [Sus scrofa]				
gi|167001855|ref|NP_001095290.1|	dolichol-phosphate mannosyltransferase [Sus scrofa] >gi|158513309|sp|A5GFZ5.1|DPM1_PIG RecName: Full=Dolichol-phosphate mannosyltransferase; AltName: Full=Dolichol-phosphate mannose synthase; Short=DPM synthase; AltName: Full=Dolichyl-phosphate beta				
gi|262072949|dbj|BAI47782.1|	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit [Sus scrofa]				
gi|350593701|ref|XP_003483747.1|	PREDICTED: hypothetical protein LOC100737189 [Sus scrofa]	---	---	---	---
gi|350580832|ref|XP_003123718.3|	PREDICTED: clathrin light chain B-like isoform 1 [Sus scrofa]	0.561	1.155	0.995	0.586
gi|311275636|ref|XP_003134838.1|	PREDICTED: septin-7-like isoform 1 [Sus scrofa]	1.268	0.852	0.765	1.169
gi|350595354|ref|XP_003134840.2|	PREDICTED: septin-7-like isoform 3 [Sus scrofa]				
gi|335305478|ref|XP_003360219.1|	PREDICTED: septin-7-like [Sus scrofa]				
gi|311251345|ref|XP_003124567.1|	PREDICTED: rab GTPase-binding effector protein 2-like [Sus scrofa]	---	---	---	---
gi|350583690|ref|XP_003125999.3|	PREDICTED: tetratricopeptide repeat protein 38-like [Sus scrofa]	2.899	1.326	1.043	1.622
gi|350593076|ref|XP_001925759.4|	PREDICTED: vesicle transport through interaction with t-SNAREs homolog 1A-like, partial [Sus scrofa]	---	---	---	---
gi|350593078|ref|XP_001926059.4|	PREDICTED: vesicle transport through interaction with t-SNAREs homolog 1A-like, partial [Sus scrofa]				
gi|311253520|ref|XP_003125581.1|	PREDICTED: 60S ribosomal protein L35a-like [Sus scrofa]	---	---	---	---
gi|335300197|ref|XP_003358821.1|	PREDICTED: 60S ribosomal protein L35a-like isoform 1 [Sus scrofa] >gi|335294628|ref|XP_003357274.1| PREDICTED: 60S ribosomal protein L35a-like [Sus				

	scrofa] >gi|335300199|ref|XP_003358822.1| PREDICTED: 60S ribosomal protein L35a-like isoform 2 [Sus s				
gi|350580587|ref|XP_003123193.3|	PREDICTED: neuropathy target esterase isoform 1 [Sus scrofa]	---	---	---	---
gi|350580589|ref|XP_003480855.1|	PREDICTED: neuropathy target esterase [Sus scrofa]				
gi|311269349|ref|XP_003132451.1|	PREDICTED: histone H1x-like [Sus scrofa]	---	---	---	---
gi|350584300|ref|XP_003355577.2|	PREDICTED: FYVE, RhoGEF and PH domain-containing protein 4-like [Sus scrofa]	---	---	---	---
gi|178056175|ref|NP_001116558.1|	basigin precursor [Sus scrofa] >gi|166244451|gb|ABY86570.1| CD147 [Sus scrofa]	0.412	0.438	0.408	0.371
gi|194033639|ref|XP_001927971.1|	PREDICTED: prostaglandin E synthase 2 [Sus scrofa]	---	---	---	---
gi|246580|gb|AAB21636.1|	zona pellucida-binding protein, AWN-1=C12 fragment [swine, sperm, Peptide Partial, 22 aa]	0.19		0.186	0.22
gi|335309560|ref|XP_003361682.1|	PREDICTED: DNA-directed RNA polymerase I subunit RPA34-like [Sus scrofa]	---	---	---	---
gi|311275477|ref|XP_003134759.1|	PREDICTED: staphylococcal nuclease domain-containing protein 1-like [Sus scrofa]	---	---	---	---
gi|61214649|sp|Q767K9.1|PP1RA_PIG	RecName: Full=Serine/threonine-protein phosphatase 1 regulatory subunit 10; AltName: Full=MHC class I region proline-rich protein CAT53; AltName: Full=Protein FB19 >gi|178056844|ref|NP_001116637.1| serine/threonine-protein phosphatase 1 regulatory s	0.821	0.933	1.391	0.92
gi|311271051|ref|XP_003133041.1|	PREDICTED: synaptosomal-associated protein 29-like [Sus scrofa]	---	---	---	---
gi|350594395|ref|XP_003359859.2|	PREDICTED: transportin-1 [Sus scrofa]	0.539	0.288	1.011	0.628
gi|195539480|ref|NP_001124203.1|	bystin [Sus scrofa] >gi|155964243|gb|ABU40181	---	---	---	---

	.1| bystin-like [Sus scrofa]				
gi|350595768|ref|XP_003135230.3|	PREDICTED: phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform-like, partial [Sus scrofa]	---	---	---	---
gi|296531513|ref|NP_001171875.1|	lymphocyte antigen 75 precursor [Sus scrofa] >gi|283854885|gb|ACV89989.1| CD205 [Sus scrofa]	---	---	---	---
gi|50657386|ref|NP_001002801.1|	apolipoprotein C-III precursor [Sus scrofa] >gi|416627|sp|P27917.2|APOC3_PIG RecName: Full=Apolipoprotein C-III; Short=Apo-CIII; Short=ApoC-III; AltName: Full=Apolipoprotein C3; Flags: Precursor >gi|164361|gb|AAA30993.1| apolipoprotein C-III [Sus sc	0.204	0.24	0.217	0.237
gi|311249451|ref|XP_003123641.1|	PREDICTED: uncharacterized protein UNQ511/PRO1026 homolog isoform 1 [Sus scrofa]	---	---	---	---
gi|335282983|ref|XP_003354207.1|	PREDICTED: uncharacterized protein UNQ511/PRO1026 homolog isoform 2 [Sus scrofa]				
gi|350582720|ref|XP_003481337.1|	PREDICTED: isoamyl acetate-hydrolyzing esterase 1 homolog [Sus scrofa]	---	---	---	---
gi|951375|gb|AAA74655.1|	apolipoprotein B [Sus scrofa]	---	---	---	---
gi|350597081|ref|XP_003484354.1|	PREDICTED: LOW QUALITY PROTEIN: apolipoprotein B-100 [Sus scrofa]				
gi|6013139|gb|AAF01257.1|AF109646_1	coxsackie-adenovirus-receptor homolog [Sus scrofa]	---	---	---	---
gi|350592092|ref|XP_001924589.4|	PREDICTED: coxsackievirus and adenovirus receptor homolog isoform 1 [Sus scrofa]				
gi|350586377|ref|XP_003128223.3|	PREDICTED: thioredoxin domain-containing protein 5-like, partial [Sus scrofa]	---	---	---	---
gi|190360629|ref|NP_001121936.1|	stromal membrane-associated protein 2 [Sus scrofa] >gi|183223973|dbj|BAG24503.1| stromal membrane-associated protein 1-like [Sus scrofa]	---	---	---	---

gi|335300981|ref|XP_001926354.2|	PREDICTED: 60S acidic ribosomal protein P1-like [Sus scrofa]	---	---	---	---
gi|311248936|ref|XP_003123385.1|	PREDICTED: phenylalanyl-tRNA synthetase alpha chain-like [Sus scrofa]	---	---	---	---
gi|335308639|ref|XP_003361313.1|	PREDICTED: probable hydrolase PNKD-like, partial [Sus scrofa]	0.744	0.459	0.519	0.559
gi|350587090|ref|XP_001926625.4|	PREDICTED: serine palmitoyltransferase 2 [Sus scrofa]	---	---	---	---
gi|350589269|ref|XP_003357681.2|	PREDICTED: LOW QUALITY PROTEIN: MOSC domain-containing protein 1, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|350589272|ref|XP_003482825.1|	PREDICTED: MOSC domain-containing protein 1, mitochondrial-like [Sus scrofa]				
gi|335296836|ref|XP_003357876.1|	PREDICTED: hypothetical protein LOC100624456 [Sus scrofa]	---	---	---	---
gi|335301996|ref|XP_001925416.3|	PREDICTED: insulin-degrading enzyme isoform 1 [Sus scrofa]	---	---	---	---
gi|335301998|ref|XP_003359343.1|	PREDICTED: insulin-degrading enzyme isoform 2 [Sus scrofa]				
gi|350581169|ref|XP_003124100.2|	PREDICTED: UPF0467 protein C5orf32 homolog [Sus scrofa]	---	---	---	---
gi|227336237|gb|ACP20834.1|	selenocysteine lyase [Sus scrofa]	---	---	---	---
gi|311273333|ref|XP_003133817.1|	PREDICTED: selenocysteine lyase [Sus scrofa]				
gi|311267394|ref|XP_003131544.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 3-like [Sus scrofa]	---	---	---	---
gi|335307890|ref|XP_003131560.2|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 3-like, partial [Sus scrofa]				
gi|50401716|sp|Q6J1I8.1|RN114_PIG	RecName: Full=RING finger protein 114; AltName: Full=Zinc finger protein 313 >gi|49274651|ref|NP_001001869.1| RING finger protein 114 [Sus scrofa] >gi|47607447|gb|AAT36620.1| zinc finger protein 313 [Sus scrofa]	---	---	---	---
gi|335298143|ref|XP_003131	PREDICTED: zinc finger protein 207	---	---	---	---

778.2|	isoform 1 [Sus scrofa]				
gi|335298147|ref|XP_003131780.2|	PREDICTED: zinc finger protein 207 isoform 3 [Sus scrofa]				
gi|335298145|ref|XP_003131779.2|	PREDICTED: zinc finger protein 207 isoform 2 [Sus scrofa]				
gi|335307509|ref|XP_003360867.1|	PREDICTED: lipoma-preferred partner-like, partial [Sus scrofa]	0.795	1.317	1.276	1.036
gi|350591812|ref|XP_003483339.1|	PREDICTED: lipoma-preferred partner-like [Sus scrofa]				
gi|335294600|ref|XP_003129756.2|	PREDICTED: pre-mRNA cleavage complex 2 protein Pcf11 [Sus scrofa]	0.728	1.004	1.125	0.759
gi|28373591|pdb|1M3E|C	Chain C, Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart (Selenomethionine) >gi|28373589|pdb|1M3E|A Chain A, Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart (Selenomethionine) >gi|28373592|pdb|1M3E|D Chain D, Succinyl-Coa:3-Ketoacid Co	---	---	---	---
gi|300193176|pdb|3K6M|B	Chain B, Dynamic Domains Of Succinyl-Coa:3-Ketoacid-Coenzyme A Transferase From Pig Heart. >gi|300193174|pdb|3K6M|D Chain D, Dynamic Domains Of Succinyl-Coa:3-Ketoacid-Coenzyme A Transferase From Pig Heart. >gi|300193175|pdb|3K6M|C Chain C, Dynamic				
gi|395398464|sp|Q29551.2|SCOT1_PIG	RecName: Full=Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial; AltName: Full=3-oxoacid CoA-transferase 1; AltName: Full=Somatic-type succinyl-CoA:3-oxoacid CoA-transferase; Short=SCOT-s; Flags: Precursor				
gi|47522610|ref|NP_999103.1|	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial precursor [Sus scrofa] >gi|164423|gb|AAA31019.1| succinyl-CoA:alpha-ketoacid				

<table>
<tr><td></td><td>coenzyme A transferase [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|158429140|pdb|2NRC|D</td><td>Chain D, C28a Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|158429138|pdb|2NRC|B Chain B, C28a Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|158429139|pdb|2NRC|C Chain C, C28a Mutant Of Succinyl-Coa:3-Ke</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|48425138|pdb|1OPE|A</td><td>Chain A, Deletion Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|48425136|pdb|1OOZ|A Chain A, Deletion Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|48425139|pdb|1OPE|B Chain B, Deletion Mutant Of Succiny</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|158429135|pdb|2NRB|C</td><td>Chain C, C28s Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|158429133|pdb|2NRB|A Chain A, C28s Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart >gi|158429136|pdb|2NRB|D Chain D, C28s Mutant Of Succinyl-Coa:3-Ke</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350591891|ref|XP_003132672.3|</td><td>PREDICTED: uridine 5~-monophosphate synthase-like [Sus scrofa]</td><td>1.043</td><td>0.583</td><td>0.734</td><td>0.766</td></tr>
<tr><td>gi|311243865|ref|XP_003121220.1|</td><td>PREDICTED: costars family protein C6orf115-like isoform 2 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335278956|ref|XP_003353243.1|</td><td>PREDICTED: costars family protein C6orf115-like [Sus scrofa] >gi|335278958|ref|XP_003353244.1| PREDICTED: costars family protein C6orf115-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350596336|ref|XP_003361058.2|</td><td>PREDICTED: desmocollin-2 [Sus scrofa]</td><td>1.338</td><td>1.363</td><td>1.878</td><td>1.045</td></tr>
<tr><td>gi|350579705|ref|XP_003122</td><td>PREDICTED: TBC1 domain family</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
</table>

274.3|	member 13 [Sus scrofa]				
gi|311254945|ref|XP_003126007.1|	PREDICTED: nuclear pore complex protein Nup50 [Sus scrofa]	---	---	---	---
gi|350596555|ref|XP_003484289.1|	PREDICTED: nuclear pore complex protein Nup50-like [Sus scrofa]				
gi|350591479|ref|XP_003483280.1|	PREDICTED: acyl-CoA dehydrogenase family member 9, mitochondrial-like, partial [Sus scrofa]	---	---	---	---
gi|335289868|ref|XP_003127303.2|	PREDICTED: coiled-coil domain-containing protein 9 [Sus scrofa]	---	---	---	---
gi|350593239|ref|XP_003483642.1|	PREDICTED: UBX domain-containing protein 4-like [Sus scrofa]	---	---	---	---
gi|350587143|ref|XP_001927117.4|	PREDICTED: legumain [Sus scrofa]	---	---	---	---
gi|350589300|ref|XP_003130593.3|	PREDICTED: hypothetical protein LOC100525245 [Sus scrofa]	0.586	0.804	0.667	0.852
gi|335300577|ref|XP_003358945.1|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 16-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311270664|ref|XP_001924462.2|	PREDICTED: V-set and immunoglobulin domain-containing protein 10 [Sus scrofa]	---	---	---	---
gi|335307295|ref|XP_003360785.1|	PREDICTED: tetraspanin-31-like [Sus scrofa]	0.264	0.17		0.255
gi|350588836|ref|XP_003357506.2|	PREDICTED: tetraspanin-13-like [Sus scrofa]				
gi|194044687|ref|XP_001928924.1|	PREDICTED: acyl-coenzyme A thioesterase 8 [Sus scrofa]	---	---	---	---
gi|335284373|ref|XP_003354586.1|	PREDICTED: LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase BRE1B-like [Sus scrofa]	---	---	---	---
gi|126302599|sp|P04163.2|S10AA_PIG	RecName: Full=Protein S100-A10; AltName: Full=Calpactin I light chain; AltName: Full=Calpactin-1 light chain; AltName: Full=Cellular ligand of annexin II; AltName: Full=S100 calcium-binding protein A10; AltName: Full=p10 protein; AltName: Full=p11	0.619	1.123	1.869	1.304

<table>
<tr><td>gi|335286919|ref|XP_003355216.1|</td><td>PREDICTED: protein S100-A10-like isoform 4 [Sus scrofa] >gi|335286915|ref|XP_003355214.1| PREDICTED: protein S100-A10-like isoform 2 [Sus scrofa] >gi|335286917|ref|XP_003355215.1| PREDICTED: protein S100-A10-like isoform 3 [Sus scrofa] >gi|311254303</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|335288415|ref|XP_003355612.1|</td><td>PREDICTED: serine-threonine kinase receptor-associated protein-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350591920|ref|XP_003483358.1|</td><td>PREDICTED: poly [ADP-ribose] polymerase 14 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|158514031|sp|A1XQU5.1|RL27_PIG</td><td>RecName: Full=60S ribosomal protein L27 >gi|148226949|ref|NP_001090948.1| 60S ribosomal protein L27 [Sus scrofa] >gi|117661046|gb|ABK55651.1| RPL27 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|47523714|ref|NP_999490.1|</td><td>mitochondrial Rho GTPase 2 [Sus scrofa] >gi|75072868|sp|Q864R5.1|MIRO2_PIG RecName: Full=Mitochondrial Rho GTPase 2; Short=MIRO-2; AltName: Full=Ras homolog gene family member T2 >gi|30025664|gb|AAP04408.1| rho GTPase [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|342187294|ref|NP_001230119.1|</td><td>syndecan-1 precursor [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|194042152|ref|XP_001924391.1|</td><td>PREDICTED: WD repeat-containing protein 11 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|5915886|sp|O46427.1|CATH_PIG</td><td>RecName: Full=Pro-cathepsin H; Contains: RecName: Full=Cathepsin H mini chain; Contains: RecName: Full=Cathepsin H; Contains: RecName: Full=Cathepsin H heavy chain; Contains: RecName: Full=Cathepsin H light chain; Flags: Precursor >gi|47522632|ref|N</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|156046107|gb|ABU42573.1|</td><td>cathepsin H variant 2 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|172050735|gb|ACB70169.</td><td>cathepsin H transcript variant 3 [Sus</td><td></td><td></td><td></td><td></td></tr>
</table>

1|	scrofa]				
gi|28948787|pdb|1NB3|C	Chain C, Crystal Structure Of Stefin A In Complex With Cathepsin H: N-Terminal Residues Of Inhibitors Can Adapt To The Active Sites Of Endo-And Exopeptidases >gi|28948781|pdb|1NB3|A Chain A, Crystal Structure Of Stefin A In Complex With Cathepsin H:				
gi|171948778|gb|ACB59246.1|	cathepsin H [Sus scrofa]				
gi|350588133|ref|XP_003482569.1|	PREDICTED: LOW QUALITY PROTEIN: interferon-induced very large GTPase 1, partial [Sus scrofa]	---	---	---	---
gi|194041277|ref|XP_001924306.1|	PREDICTED: TATA element modulatory factor [Sus scrofa]	---	---	---	---
gi|350590398|ref|XP_003131591.3|	PREDICTED: CDK5 regulatory subunit-associated protein 3-like [Sus scrofa]	---	---	---	---
gi|350582111|ref|XP_003124939.2|	PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 5B [Sus scrofa]	---	---	---	---
gi|335309033|ref|XP_003121764.2|	PREDICTED: organic solute transporter subunit beta-like [Sus scrofa]	---	---	---	---
gi|335310602|ref|XP_003362108.1|	PREDICTED: echinoderm microtubule-associated protein-like 2-like, partial [Sus scrofa]	---	---	---	---
gi|350594364|ref|XP_003134050.3|	PREDICTED: protein LAP2 [Sus scrofa]	---	---	---	---
gi|343488514|ref|NP_001230416.1|	ubiquitin-related modifier 1 homolog [Sus scrofa]	---	---	---	---
gi|350582717|ref|XP_003125434.3|	PREDICTED: rho-associated protein kinase 2, partial [Sus scrofa]	---	---	---	---
gi|350580947|ref|XP_003123849.3|	PREDICTED: endoplasmic reticulum aminopeptidase 2-like, partial [Sus scrofa]	0.801	0.635	0.615	0.908
gi|212549621|ref|NP_001131100.1|	growth factor receptor-bound protein 2 [Sus scrofa] >gi|208612619|gb|ACI29749.1| growth factor receptor bound	---	---	---	---

	protein 2 [Sus scrofa]				
gi|311248892|ref|XP_003123362.1|	PREDICTED: lysosomal alpha-mannosidase-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311275439|ref|XP_003134730.1|	PREDICTED: transportin-3 isoform 1 [Sus scrofa]	---	---	---	---
gi|335305352|ref|XP_003360189.1|	PREDICTED: transportin-3 isoform 2 [Sus scrofa]				
gi|335305354|ref|XP_003360190.1|	PREDICTED: transportin-3 isoform 3 [Sus scrofa]				
gi|116175267|ref|NP_001070690.1|	U1 small nuclear ribonucleoprotein A [Sus scrofa] >gi|122131847|sp|Q06AA4.1|SNRPA_PIG RecName: Full=U1 small nuclear ribonucleoprotein A; Short=U1 snRNP A; Short=U1-A; Short=U1A >gi|115371743|gb|ABI96196.1| SNRPA [Sus scrofa]	---	---	---	---
gi|116175273|ref|NP_001070696.1|	uncharacterized protein LOC768116 [Sus scrofa] >gi|115371759|gb|ABI96204.1| RU2B [Sus scrofa]				
gi|311248398|ref|XP_003123116.1|	PREDICTED: chromatin assembly factor 1 subunit A-like [Sus scrofa]	---	---	---	---
gi|350578878|ref|XP_003353487.2|	PREDICTED: tight junction protein ZO-1 [Sus scrofa]	---	---	---	---
gi|194042423|ref|XP_001926989.1|	PREDICTED: cleavage stimulation factor subunit 2 tau variant isoform 1 [Sus scrofa]	---	---	---	---
gi|311276614|ref|XP_003135279.1|	PREDICTED: cleavage stimulation factor subunit 2-like isoform 1 [Sus scrofa]				
gi|335306285|ref|XP_003360436.1|	PREDICTED: cleavage stimulation factor subunit 2-like isoform 2 [Sus scrofa]				
gi|350593080|ref|XP_001927062.4|	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein C10orf118 [Sus scrofa]	---	---	---	---
gi|311249343|ref|XP_003123584.1|	PREDICTED: coatomer subunit epsilon-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311249345|ref|XP_003123586.1|	PREDICTED: coatomer subunit epsilon-like isoform 3 [Sus scrofa]				

gi|350595741|ref|XP_003484170.1|	PREDICTED: disks large homolog 3 isoform 2 [Sus scrofa]	---	---	---	---
gi|350595743|ref|XP_003135199.3|	PREDICTED: disks large homolog 3 isoform 1 [Sus scrofa]				
gi|350595745|ref|XP_003484171.1|	PREDICTED: disks large homolog 3 isoform 3 [Sus scrofa]				
gi|311276931|ref|XP_003135414.1|	PREDICTED: U3 small nucleolar RNA-associated protein 14 homolog A-like isoform 1 [Sus scrofa]	0.44	0.533	0.443	0.578
gi|311276933|ref|XP_003135415.1|	PREDICTED: U3 small nucleolar RNA-associated protein 14 homolog A-like isoform 2 [Sus scrofa]				
gi|350582038|ref|XP_003124891.3|	PREDICTED: U5 small nuclear ribonucleoprotein 200 kDa helicase-like [Sus scrofa]	---	---	---	---
gi|311257842|ref|XP_003127319.1|	PREDICTED: glutamate-rich WD repeat-containing protein 1-like [Sus scrofa]	---	---	---	---
gi|335291465|ref|XP_003128033.2|	PREDICTED: UPF0587 protein C1orf123 homolog [Sus scrofa]	---	---	---	---
gi|1717797|sp|P52552.1|PRDX2_PIG	RecName: Full=Peroxiredoxin-2; AltName: Full=Thiol-specific antioxidant protein; Short=TSA; AltName: Full=Thioredoxin peroxidase 1; AltName: Full=Thioredoxin-dependent peroxide reductase 1	2.762	1.141	0.737	1.769
gi|347300176|ref|NP_001231403.1|	peroxiredoxin-2 [Sus scrofa]				
gi|264681442|ref|NP_001161116.1|	dynactin subunit 6 [Sus scrofa] >gi|262072943|dbj|BAI47779.1| dynactin 6 [Sus scrofa]	---	---	---	---
gi|31074212|gb|AAP37947.1|	cell cycle progression 2 protein [Sus scrofa]	---	---	---	---
gi|178056484|ref|NP_001116573.1|	protein TBRG4 [Sus scrofa] >gi|31074402|gb|AAP37946.1| cell cycle progression 2 protein [Sus scrofa]				
gi|124053394|sp|Q7YS91.2|TBRG4_PIG	RecName: Full=Protein TBRG4; AltName: Full=Cell cycle progression protein 2; AltName: Full=Transforming growth factor beta				

	regulator 4				
gi|335310523|ref|XP_003362072.1|	PREDICTED: protein TBRG4-like, partial [Sus scrofa]				
gi|350593043|ref|XP_001929355.3|	PREDICTED: alpha-internexin [Sus scrofa]	0.589	0.71	0.753	0.56
gi|350583051|ref|XP_003125610.3|	PREDICTED: protein virilizer homolog [Sus scrofa]	---	---	---	---
gi|311277128|ref|XP_003135516.1|	PREDICTED: high mobility group protein B3-like [Sus scrofa]	---	---	---	---
gi|350588037|ref|XP_003482541.1|	PREDICTED: high mobility group protein B3-like [Sus scrofa] >gi|350588033|ref|XP_003482539.1| PREDICTED: high mobility group protein B3-like [Sus scrofa]				
gi|350594590|ref|XP_003483925.1|	PREDICTED: golgin subfamily A member 7-like isoform 1 [Sus scrofa] >gi|350594586|ref|XP_003483923.1| PREDICTED: golgin subfamily A member 7 [Sus scrofa] >gi|350594592|ref|XP_003483926.1| PREDICTED: golgin subfamily A member 7-like isoform 2 [Sus scr	---	---	---	---
gi|350583523|ref|XP_003481536.1|	PREDICTED: putative helicase MOV-10 [Sus scrofa]	---	---	---	---
gi|350580612|ref|XP_003123174.3|	PREDICTED: cdc42-interacting protein 4-like isoform 1 [Sus scrofa]	---	---	---	---
gi|343478257|ref|NP_001230394.1|	peptidase M20 domain containing 1 [Sus scrofa]	---	---	---	---
gi|335307003|ref|XP_001926406.3|	PREDICTED: LanC lantibiotic synthetase component C-like 1 [Sus scrofa]	2.656	0.591	0.618	1.642
gi|298160936|ref|NP_001177146.1|	transmembrane protein C9orf46 [Sus scrofa]	0.545	0.35	0.364	0.601
gi|350595661|ref|XP_003360337.2|	PREDICTED: RNA-binding protein 10-like, partial [Sus scrofa]	---	---	---	---
gi|350590442|ref|XP_003483060.1|	PREDICTED: epsin-3-like [Sus scrofa] >gi|311267546|ref|XP_003131620.1| PREDICTED: epsin-3 [Sus scrofa]	---	---	---	---
gi|350578717|ref|XP_003121581.3|	PREDICTED: eukaryotic translation initiation factor 3 subunit J-like	---	---	---	---

	isoform 1 [Sus scrofa]				
gi|350592596|ref|XP_003133009.3|	PREDICTED: merlin isoform 1 [Sus scrofa]	---	---	---	---
gi|350592600|ref|XP_003483495.1|	PREDICTED: merlin [Sus scrofa]				
gi|350592602|ref|XP_003483496.1|	PREDICTED: merlin [Sus scrofa]				
gi|350592606|ref|XP_003483497.1|	PREDICTED: merlin [Sus scrofa]				
gi|350592598|ref|XP_003483494.1|	PREDICTED: merlin [Sus scrofa]				
gi|350592604|ref|XP_003133012.3|	PREDICTED: merlin isoform 4 [Sus scrofa]				
gi|311251005|ref|XP_003124395.1|	PREDICTED: TSC22 domain family protein 4-like [Sus scrofa] >gi|311251027|ref|XP_003124405.1| PREDICTED: TSC22 domain family protein 4-like [Sus scrofa]	---	---	---	---
gi|350529368|ref|NP_001231920.1|	synaptojanin 2 binding protein [Sus scrofa]	---	---	---	---
gi|350584802|ref|XP_003481825.1|	PREDICTED: neighbor of COX4-like [Sus scrofa]	---	---	---	---
gi|350584804|ref|XP_003355777.2|	PREDICTED: neighbor of COX4-like, partial [Sus scrofa]				
gi|350591308|ref|XP_003132335.3|	PREDICTED: bis(5~-adenosyl)-triphosphatase-like [Sus scrofa]	---	---	---	---
gi|34978340|sp|P36887.4|KAPCA_PIG	RecName: Full=cAMP-dependent protein kinase catalytic subunit alpha; Short=PKA C-alpha	---	---	---	---
gi|190589912|gb|ACE79215.1|	cyclic AMP-dependent protein kinase A catalytic subunit [Sus scrofa]				
gi|334878385|pdb|1CDK|A	Chain A, Camp-Dependent Protein Kinase Catalytic Subunit (E.C.2.7.1.37) (Protein Kinase A) Complexed With Protein Kinase Inhibitor Peptide Fragment 5-24 (Pki(5-24) Isoelectric Variant Ca) And Mn2+ Adenylyl Imidodiphosphate (Mnamp-Pnp) At Ph 5.6 And				
gi|305677665|pdb|3AGM|A	Chain A, Complex Of Pka With The				

	Bisubstrate Protein Kinase Inhibitor Arc-670				
gi|334878402|pdb|1CTP|E	Chain E, Structure Of The Mammalian Catalytic Subunit Of Camp-Dependent Protein Kinase And An Inhibitor Peptide Displays An Open Conformation				
gi|157838448|pdb|1CMK|E	Chain E, Crystal Structures Of The Myristylated Catalytic Subunit Of Camp- Dependent Protein Kinase Reveal Open And Closed Conformations				
gi|311248983|ref|XP_003123401.1|	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha isoform 1 [Sus scrofa]				
gi|335282773|ref|XP_003354151.1|	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha [Sus scrofa]				
gi|311250750|ref|XP_003124275.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 13-like [Sus scrofa]	---	---	---	---
gi|194039474|ref|XP_001924848.1|	PREDICTED: DNA replication licensing factor MCM3 [Sus scrofa]	---	---	---	---
gi|350534920|ref|NP_001233134.1|	interferon-induced protein 44 [Sus scrofa] >gi|332113311|gb|AEE02032.1| interferon-inducible microtubular aggregate protein 44 [Sus scrofa]	---	---	---	---
gi|346716263|ref|NP_001231270.1|	protein tyrosine phosphatase type IVA 2 [Sus scrofa]	---	---	---	---
gi|335308977|ref|XP_003361445.1|	PREDICTED: cytoplasmic FMR1-interacting protein 1-like, partial [Sus scrofa]	---	---	---	---
gi|350594468|ref|XP_003134162.3|	PREDICTED: cytoplasmic FMR1-interacting protein 2-like [Sus scrofa]				
gi|38569755|gb|AAR24396.1|	vimentin [Sus scrofa]	---	---	---	---
gi|346716275|ref|NP_001231275.1|	dnaJ homolog subfamily B member 11 precursor [Sus scrofa]	---	---	---	---
gi|350594138|ref|XP_001927044.4|	PREDICTED: signal transducing adapter molecule 2 [Sus scrofa]	---	---	---	---
gi|231467|sp|P29700.1|FETUA_PIG	RecName: Full=Alpha-2-HS-glycoprotein;	---	---	---	---

	AltName: Full=Fetuin-A; Flags: Precursor >gi|3980229|emb|CAA39498.1| fetuin [Sus scrofa]				
gi|311269753|ref|XP_003132624.1|	PREDICTED: alpha-2-HS-glycoprotein [Sus scrofa]				
gi|122131855|sp|Q06AB3.1|UCHL3_PIG	RecName: Full=Ubiquitin carboxyl-terminal hydrolase isozyme L3; Short=UCH-L3; AltName: Full=Ubiquitin thioesterase L3 >gi|116175277|ref|NP_001070695.1| ubiquitin carboxyl-terminal hydrolase isozyme L3 [Sus scrofa] >gi|115371725|gb|ABI96187.1| UCHL3	---	---	---	---
gi|350583835|ref|XP_003355399.2|	PREDICTED: ADP-ribosylation factor-binding protein GGA1 [Sus scrofa]	---	---	---	---
gi|350578554|ref|XP_003480390.1|	PREDICTED: talin-2 [Sus scrofa]	---	---	---	---
gi|343403848|ref|NP_001230297.1|	phosphopantothenoylcysteine decarboxylase [Sus scrofa]	---	---	---	---
gi|311265237|ref|XP_003130554.1|	PREDICTED: LOW QUALITY PROTEIN: rab3 GTPase-activating protein non-catalytic subunit-like [Sus scrofa]	---	---	---	---
gi|350587371|ref|XP_003482396.1|	PREDICTED: cytosol aminopeptidase-like [Sus scrofa]	2.89	2.142	2.61	1.252
gi|350596353|ref|XP_003361080.2|	PREDICTED: gamma-soluble NSF attachment protein-like [Sus scrofa]	0.767	0.636	0.846	0.758
gi|38569721|gb|AAR24381.1|	isopentyl-diphosphate delta isomerase [Sus scrofa]	---	---	---	---
gi|350589674|ref|XP_003482895.1|	PREDICTED: isopentenyl-diphosphate Delta-isomerase 1-like [Sus scrofa] >gi|335296666|ref|XP_003357836.1| PREDICTED: isopentenyl-diphosphate Delta-isomerase 1-like [Sus scrofa]				
gi|350587135|ref|XP_003482353.1|	PREDICTED: cleavage and polyadenylation specificity factor subunit 2-like [Sus scrofa]	---	---	---	---
gi|194034586|ref|XP_001925948.1|	PREDICTED: 3-ketodihydrosphingosine	---	---	---	---

	reductase-like [Sus scrofa]				
gi|297591981|ref|NP_001172068.1|	sialic acid synthase [Sus scrofa] >gi|262204906|dbj|BAI48033.1| N-acetylneuraminic acid synthase [Sus scrofa]	---	---	---	---
gi|311276241|ref|XP_003135104.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311276243|ref|XP_003135105.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial-like isoform 2 [Sus scrofa]				
gi|335284154|ref|XP_003354525.1|	PREDICTED: solute carrier family 12 member 9-like [Sus scrofa]	---	---	---	---
gi|335298303|ref|XP_003131887.2|	PREDICTED: protein KIAA0664-like [Sus scrofa]	0.999	1.392	1.554	1.051
gi|311276865|ref|XP_003135390.1|	PREDICTED: 60S ribosomal protein L39-like [Sus scrofa] >gi|335306463|ref|XP_003360477.1| PREDICTED: 60S ribosomal protein L39-like [Sus scrofa] >gi|335284542|ref|XP_003354632.1| PREDICTED: 60S ribosomal protein L39-like [Sus scrofa] >gi|311247842|re	0.308	0.286	0.279	0.265
gi|335306465|ref|XP_003360478.1|	PREDICTED: 60S ribosomal protein L39-like [Sus scrofa]				
gi|357580498|sp|C5HGF3.1|TMCO1_PIG	RecName: Full=Transmembrane and coiled-coil domains protein 1 >gi|262399400|ref|NP_001161057.1| transmembrane and coiled-coil domains protein 1 precursor [Sus scrofa] >gi|225200247|gb|ACN82430.1| transmembrane and coiled-coil domains 1 [Sus scrofa]	---	---	---	---
gi|350585688|ref|XP_003482025.1|	PREDICTED: LOW QUALITY PROTEIN: protein RCC2 [Sus scrofa]	---	---	---	---
gi|270289756|ref|NP_001161893.1|	endophilin-B1 [Sus scrofa] >gi|262263199|dbj|BAI48102.1| SH3-domain GRB2-like endophilin B1 [Sus scrofa]	---	---	---	---

gi|346986269|ref|NP_001231292.1|	interferon-induced protein with tetratricopeptide repeats 1 [Sus scrofa]	---	---	---	---
gi|311274743|ref|XP_003134451.1|	PREDICTED: RNA-binding protein Raly isoform 2 [Sus scrofa]	0.735	0.569	0.566	0.682
gi|335304688|ref|XP_003359995.1|	PREDICTED: RNA-binding protein Raly [Sus scrofa] >gi|311274741|ref|XP_001929139.2| PREDICTED: RNA-binding protein Raly isoform 1 [Sus scrofa]				
gi|66866411|gb|AAY57853.1|	DJ-1 protein, partial [Sus scrofa]	---	---	---	---
gi|194043105|ref|XP_001929229.1|	PREDICTED: cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial isoform 1 [Sus scrofa]	---	---	---	---
gi|311270785|ref|XP_003132971.1|	PREDICTED: cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial isoform 2 [Sus scrofa]				
gi|350596216|ref|XP_003360918.2|	PREDICTED: sorting nexin-2, partial [Sus scrofa]	---	---	---	---
gi|311272760|ref|XP_001926651.2|	PREDICTED: zinc finger CCCH domain-containing protein 15 [Sus scrofa]	---	---	---	---
gi|11055649|gb|AAG28195.1|AF304201_6	ATPase 6 [Sus scrofa]	---	---	---	---
gi|45826189|gb|AAS77709.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|209166162|gb|ACI41537.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|118135679|gb|ABK62690.1|	ATPase subunit 6 [Sus scrofa]				
gi|223976084|ref|YP_002600782.1|	ATP synthase F0 subunit 6 [Sus scrofa domesticus] >gi|5835868|ref|NP_008639.1|ATP6_15069 ATP synthase F0 subunit 6 [Sus scrofa] >gi|347448701|gb|AEO93016.1| ATP synthase F0 subunit 6 (mitochondrion) [Sus scrofa] >gi|347448645|gb|AEO92964.1| ATP synt				
gi|251829655|gb|ACT21208.1|	ATP synthase F0 subunit 6 [Sus scrofa]				

gi|33320871|gb|AAQ06154.1|	ATPase subunit 6 [Sus scrofa]				
gi|33320927|gb|AAQ06206.1|	ATPase subunit 6 [Sus scrofa] >gi|33320689|gb|AAQ05985.1| ATPase subunit 6 [Sus scrofa]				
gi|145315588|gb|ABP63137.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|145315644|gb|ABP63189.1|	ATP synthase F0 subunit 6 [Sus scrofa] >gi|145315630|gb|ABP63176.1| ATP synthase F0 subunit 6 [Sus scrofa]				
gi|157056526|gb|ABV02158.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|11055677|gb|AAG28221.1|AF304203_6	ATPase 6 [Sus scrofa]				
gi|145315686|gb|ABP63228.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|290750183|gb|ADD52030.1|	ATP synthase subunit 6 [Sus scrofa]				
gi|145315658|gb|ABP63202.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|342316094|gb|ABF56565.2|	ATPase subunit 6 [Sus scrofa]				
gi|312233369|ref|YP_004021580.1|	ATP synthase F0 subunit 6 [Sus scrofa taiwanensis] >gi|347448729|gb|AEO93042.1| ATP synthase F0 subunit 6 (mitochondrion) [Sus scrofa] >gi|347448673|gb|AEO92990.1| ATP synthase F0 subunit 6 (mitochondrion) [Sus scrofa] >gi|347448743|gb|AEO93055.1| A				
gi|145315448|gb|ABP63007.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|37719398|gb|AAR01785.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|209166176|gb|ACI41550.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|80972998|gb|ABB53229.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|209166246|gb|ACI41615.1|	ATP synthase F0 subunit 6 [Sus scrofa] >gi|209166218|gb|ACI41589.				

	1| ATP synthase F0 subunit 6 [Sus scrofa] >gi|209166134|gb|ACI41511.1| ATP synthase F0 subunit 6 [Sus scrofa] >gi|209166106|gb|ACI41485.1| ATP synthase F0 subunit 6 [Sus scrofa] >gi|20				
gi|76262555|gb|ABA41441.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|157056541|gb|ABV02172.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|45826217|gb|AAS77735.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|315057191|gb|ADT71729.1|	ATP synthase subunit 6 [Sus scrofa]				
gi|94981326|gb|ABF49554.1|	ATPase subunit 6 [Sus scrofa] >gi|124249813|gb|ABM92886.1| ATPase subunit 6 [Sus scrofa]				
gi|83779137|gb|ABC47381.1|	ATP synthase F0 subunit 6 [Sus scrofa]				
gi|311257281|ref|XP_003127042.1|	PREDICTED: dnaJ homolog subfamily A member 2-like [Sus scrofa]	---	---	---	---
gi|350587021|ref|XP_003356786.2|	PREDICTED: MAGUK p55 subfamily member 5 [Sus scrofa]	---	---	---	---
gi|350591244|ref|XP_003483235.1|	PREDICTED: RNA-binding protein 6 isoform 2 [Sus scrofa]	---	---	---	---
gi|350591246|ref|XP_003132268.3|	PREDICTED: RNA-binding protein 6 isoform 1 [Sus scrofa]				
gi|350592445|ref|XP_003483465.1|	PREDICTED: hypothetical protein LOC100154492 [Sus scrofa]	---	---	---	---
gi|350592447|ref|XP_003483466.1|	PREDICTED: hypothetical protein LOC100154492 [Sus scrofa]				
gi|335304534|ref|XP_003134355.2|	PREDICTED: 5~-3~ exoribonuclease 2 [Sus scrofa]	---	---	---	---
gi|194034833|ref|XP_001928153.1|	PREDICTED: microfibrillar-associated protein 1 [Sus scrofa]	0.905	1.801	1.48	1.208
gi|350578774|ref|XP_003480447.1|	PREDICTED: EH domain-containing protein 4, partial [Sus scrofa]	---	---	---	---
gi|350585748|ref|XP_003127751.3|	PREDICTED: hypothetical protein LOC100521629 isoform 1 [Sus scrofa]	0.638	0.605	0.671	0.624

gi|350585750|ref|XP_003482044.1|	PREDICTED: hypothetical protein LOC100521629 isoform 2 [Sus scrofa]				
gi|350585912|ref|XP_003127855.3|	PREDICTED: microtubule-actin cross-linking factor 1 isoform 1, partial [Sus scrofa]	---	---	---	---
gi|6166237|sp|O19175.1|KC1A_PIG	RecName: Full=Casein kinase I isoform alpha; Short=CKI-alpha; AltName: Full=CK1	---	---	---	---
gi|311250475|ref|XP_003124136.1|	PREDICTED: casein kinase I isoform alpha isoform 1 [Sus scrofa]				
gi|350582213|ref|XP_003481224.1|	PREDICTED: 60S ribosomal protein L7a-like [Sus scrofa] >gi|350582215|ref|XP_003481225.1| PREDICTED: 60S ribosomal protein L7a-like [Sus scrofa] >gi|335285208|ref|XP_003125024.2| PREDICTED: 60S ribosomal protein L7a-like isoform 1 [Sus scrofa]	---	---	---	---
gi|311266801|ref|XP_003131259.1|	PREDICTED: nuclear pore complex protein Nup85-like [Sus scrofa]	---	---	---	---
gi|350592132|ref|XP_003358973.2|	PREDICTED: splicing factor, arginine/serine-rich 15 [Sus scrofa]	---	---	---	---
gi|350578880|ref|XP_003480471.1|	PREDICTED: tight junction protein ZO-1-like, partial [Sus scrofa]	---	---	---	---
gi|16506695|gb|AAL23907.1|AF339885_1	mannose-6-phosphate/insulin-like growth factor II receptor [Sus scrofa]	---	---	---	---
gi|350577990|ref|XP_003480266.1|	PREDICTED: cation-independent mannose-6-phosphate receptor-like [Sus scrofa]				
gi|347300273|ref|NP_001231402.1|	cation-independent mannose-6-phosphate receptor precursor [Sus scrofa] >gi|334853107|gb|AEH05671.1| insulin-like growth factor 2 receptor precursor [Sus scrofa]				
gi|374305556|gb|AEZ06359.1|	insulin-like growth factor II receptor [Sus scrofa]				
gi|350588656|ref|XP_003357409.2|	PREDICTED: amyloid beta (A4) precursor-like protein 2 [Sus scrofa]	---	---	---	---
gi|311259534|ref|XP_003128	PREDICTED:	---	---	---	---

<table>
<tr><td>149.1|</td><td>phosphopantothenate--cysteine ligase-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|194038370|ref|XP_001929110.1|</td><td>PREDICTED: poly(A) polymerase alpha isoform 1 [Sus scrofa]</td><td>0.607</td><td>1.121</td><td>0.874</td><td>0.836</td></tr>
<tr><td>gi|343403833|ref|NP_001230293.1|</td><td>coiled-coil domain containing 167 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350586346|ref|XP_003482166.1|</td><td>PREDICTED: transmembrane and coiled-coil domain-containing protein C6orf129-like, partial [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350594977|ref|XP_001929182.3|</td><td>PREDICTED: nuclear receptor coactivator 5 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350596467|ref|XP_003129178.3|</td><td>PREDICTED: fibrinogen alpha chain, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|346716281|ref|NP_001231278.1|</td><td>eukaryotic translation initiation factor 1A, Y-linked [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350586900|ref|XP_003128597.3|</td><td>PREDICTED: transmembrane 9 superfamily member 1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|305855210|ref|NP_001182286.1|</td><td>DNA mismatch repair protein Msh2 [Sus scrofa] >gi|285818416|gb|ADC38881.1| MutS-like protein 2 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335299797|ref|XP_003358684.1|</td><td>PREDICTED: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350587061|ref|XP_003482336.1|</td><td>PREDICTED: iron-sulfur cluster assembly 2 homolog, mitochondrial-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|217314881|gb|ACK36975.1|</td><td>phosphatidic acid phosphatase type 2C isoform 3 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|219522016|ref|NP_001137195.1|</td><td>lipid phosphate phosphohydrolase 2 [Sus scrofa] >gi|217314877|gb|ACK36973.1| phosphatidic acid phosphatase type 2C isoform 1 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|346421308|ref|NP_001231011.1|</td><td>trans-2-enoyl-CoA reductase, mitochondrial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|113205616|ref|NP_001038008.1|</td><td>60S ribosomal protein L10 [Sus scrofa] >gi|85681889|sp|Q29195.3|RL10_PIG RecName: Full=60S ribosomal protein L10; AltName: Full=Protein QM</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
</table>

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<tr><td></td><td>homolog >gi|56384249|gb|AAV85773.1| ribosomal protein L10 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311245451|ref|XP_003121835.1|</td><td>PREDICTED: 60S ribosomal protein L10-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350579589|ref|XP_003353682.2|</td><td>PREDICTED: erythrocyte band 7 integral membrane protein-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350578478|ref|XP_003121483.3|</td><td>PREDICTED: myosin-Vb-like, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335282227|ref|XP_003123029.2|</td><td>PREDICTED: switch-associated protein 70-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|147901025|ref|NP_001090949.1|</td><td>40S ribosomal protein S21 [Sus scrofa] >gi|52783791|sp|P63221.1|RS21_PIG RecName: Full=40S ribosomal protein S21 >gi|311261595|ref|XP_003128784.1| PREDICTED: 40S ribosomal protein S21-like isoform 1 [Sus scrofa] >gi|117661139|gb|ABK55656.1| RPS21 [S</td><td>1.084</td><td>1.406</td><td>0.892</td><td>1.171</td></tr>
<tr><td>gi|335281869|ref|XP_003353912.1|</td><td>PREDICTED: FACT complex subunit SSRP1 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|2833354|sp|Q29223.2|RL34_PIG</td><td>RecName: Full=60S ribosomal protein L34</td><td>0.879</td><td>0.523</td><td>0.566</td><td>0.941</td></tr>
<tr><td>gi|311262701|ref|XP_003129308.1|</td><td>PREDICTED: 60S ribosomal protein L34-like isoform 2 [Sus scrofa] >gi|311262697|ref|XP_003129307.1| PREDICTED: 60S ribosomal protein L34-like isoform 1 [Sus scrofa] >gi|311262699|ref|XP_003129309.1| PREDICTED: 60S ribosomal protein L34-like isoform 3</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|350592681|ref|XP_003483514.1|</td><td>PREDICTED: ubiquitin fusion degradation protein 1 homolog, partial [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|297632410|ref|NP_001172089.1|</td><td>ADP-ribosylation-like factor 6 interacting protein 4 isoform a [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|297632413|ref|NP_001172090.1|</td><td>ADP-ribosylation-like factor 6 interacting protein 4 isoform b [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|335298923|ref|XP_003132</td><td>PREDICTED: anoctamin-10 [Sus</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
</table>

196.2|	scrofa]				
gi|350591798|ref|XP_003483335.1|	PREDICTED: replication factor C (activator 1) 4, 37kDa [Sus scrofa]	---	---	---	---
gi|335308196|ref|XP_003361137.1|	PREDICTED: cell division cycle protein 123 homolog [Sus scrofa]	---	---	---	---
gi|345091069|ref|NP_001230752.1|	cell division cycle 123 homolog [Sus scrofa]				
gi|350592375|ref|XP_001927668.3|	PREDICTED: LOW QUALITY PROTEIN: probable ATP-dependent RNA helicase DDX60 [Sus scrofa]	---	---	---	---
gi|335293236|ref|XP_003356909.1|	PREDICTED: ADP-ribosyl cyclase 2-like [Sus scrofa]	---	---	---	---
gi|311273371|ref|XP_003133833.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial-like [Sus scrofa]	0.942	0.553	0.566	0.856
gi|350594832|ref|XP_003134443.3|	PREDICTED: uncharacterized protein C20orf112 homolog [Sus scrofa]	0.779	0.697	0.945	0.869
gi|343780920|ref|NP_001230477.1|	polyadenylate-binding protein 2 [Sus scrofa]	---	---	---	---
gi|335293623|ref|XP_003357010.1|	PREDICTED: immunoglobulin J chain-like isoform 2 [Sus scrofa] >gi|335293621|ref|XP_003357009.1| PREDICTED: immunoglobulin J chain-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350579839|ref|XP_003353781.2|	PREDICTED: 7-dehydrocholesterol reductase-like [Sus scrofa]	---	---	---	---
gi|194044529|ref|XP_001925282.1|	PREDICTED: RNA-binding protein 39 isoform 2 [Sus scrofa]	---	---	---	---
gi|335304749|ref|XP_003360015.1|	PREDICTED: RNA-binding protein 39 [Sus scrofa]				
gi|335304742|ref|XP_003360012.1|	PREDICTED: RNA-binding protein 39 [Sus scrofa]				
gi|335304745|ref|XP_003360013.1|	PREDICTED: RNA-binding protein 39 [Sus scrofa]				
gi|335280058|ref|XP_003121747.2|	PREDICTED: vacuolar protein sorting-associated protein 4B-like [Sus scrofa]	---	---	---	---
gi|335303022|ref|XP_003359611.1|	PREDICTED: LOW QUALITY PROTEIN: WAS/WASL-interacting	---	---	---	---

	protein family member 1-like [Sus scrofa]				
gi|311262216|ref|XP_003129070.1|	PREDICTED: LOW QUALITY PROTEIN: signal recognition particle 72 kDa protein-like [Sus scrofa]	1.184	1.064	1.23	1.278
gi|311270305|ref|XP_001926790.2|	PREDICTED: exportin-7 [Sus scrofa]	---	---	---	---
gi|335308535|ref|XP_003361271.1|	PREDICTED: N(2),N(2)-dimethylguanosine tRNA methyltransferase-like, partial [Sus scrofa]	0.874	1.076	1.253	1.203
gi|415463|gb|AAB28132.1|	cytochrome c oxidase subunit VIIc {N-terminal} [swine, intestine, Peptide, 47 aa]	---	---	---	---
gi|91694325|gb|ABE41807.1|	cytochrome c oxidase subunit VIIc [Sus scrofa] >gi|90819632|gb|ABD98461.1| cytochrome c oxidase subunit VIIc [Sus scrofa]				
gi|110278917|sp|Q1W0Y2.1|COX7C_PIG	RecName: Full=Cytochrome c oxidase subunit 7C, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIc; Flags: Precursor >gi|147900047|ref|NP_001090943.1| cytochrome c oxidase subunit 7C, mitochondrial precursor [Sus scrofa] >gi|117660817				
gi|335309123|ref|XP_003361503.1|	PREDICTED: cytochrome c oxidase subunit 7C, mitochondrial-like [Sus scrofa]				
gi|350578030|ref|XP_003121180.3|	PREDICTED: cytochrome c oxidase subunit 7C, mitochondrial-like [Sus scrofa]				
gi|194039547|ref|XP_001928898.1|	PREDICTED: LDLR chaperone MESD [Sus scrofa]	---	---	---	---
gi|350593111|ref|XP_001927517.4|	PREDICTED: SEC23-interacting protein [Sus scrofa]	---	---	---	---
gi|350581370|ref|XP_003124307.3|	PREDICTED: MICAL-like protein 2 [Sus scrofa]	0.502	1.128	1.227	0.912
gi|350592753|ref|XP_001929357.4|	PREDICTED: ankyrin-3 isoform 1 [Sus scrofa]	---	---	---	---
gi|350592755|ref|XP_003483	PREDICTED: ankyrin-3 isoform 2				

<table>
<tr><td>528.1|</td><td>[Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|198282001|ref|NP_001123683.1|</td><td>transcription factor A, mitochondrial precursor [Sus scrofa] >gi|75052621|sp|Q5D144.1|TFAM_PIG RecName: Full=Transcription factor A, mitochondrial; Short=mtTFA; Flags: Precursor >gi|60326706|gb|AAX18878.1| mitochondrial transcription factor A [Sus s</td><td>0.487</td><td>0.264</td><td>0.384</td><td>0.359</td></tr>
<tr><td>gi|194042017|ref|XP_001926614.1|</td><td>PREDICTED: structural maintenance of chromosomes protein 3 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350584221|ref|XP_003126398.3|</td><td>PREDICTED: exportin-T [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|5835872|ref|NP_008643.1|ND4_15069</td><td>NADH dehydrogenase subunit 4 [Sus scrofa] >gi|20455496|sp|O79881.2|NU4M_PIG RecName: Full=NADH-ubiquinone oxidoreductase chain 4; AltName: Full=NADH dehydrogenase subunit 4 >gi|4958961|gb|AAD34194.1|AF034253_10 NADH dehydrogenase subunit 4 [Sus scro</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|76262531|gb|ABA41419.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|251829659|gb|ACT21212.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|45826193|gb|AAS77713.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|145315786|gb|ABP63321.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|118135683|gb|ABK62694.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|95116714|gb|ABF56569.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|312233373|ref|YP_004021584.1|</td><td>NADH dehydrogenase subunit 4 [Sus scrofa taiwanensis] >gi|347448733|gb|AEO93046.1| NADH dehydrogenase subunit 4 (mitochondrion) [Sus scrofa] >gi|347448677|gb|AEO92994.1| NADH dehydrogenase subunit 4</td><td></td><td></td><td></td><td></td></tr>
</table>

	(mitochondrion) [Sus scrofa] >gi|347448747|gb|AEO9				
gi|223976088|ref|YP_002600786.1|	NADH dehydrogenase subunit 4 [Sus scrofa domesticus] >gi|347448705|gb|AEO93020.1| NADH dehydrogenase subunit 4 (mitochondrion) [Sus scrofa] >gi|347448649|gb|AEO92968.1| NADH dehydrogenase subunit 4 (mitochondrion) [Sus scrofa] >gi|347448621|gb|AEO92				
gi|45826179|gb|AAS77700.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|94981330|gb|ABF49558.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|76262559|gb|ABA41445.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|162279942|ref|YP_001023772.2|	NADH dehydrogenase subunit 4 [Phacochoerus africanus]				
gi|157056530|gb|ABV02162.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|145315774|gb|ABP63310.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|162423277|gb|ABX89418.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|76262545|gb|ABA41432.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|37962878|gb|AAR05791.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|80973002|gb|ABB53233.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|238625892|gb|ACR48218.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|159162014|gb|ABM92890.2|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|45826207|gb|AAS77726.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|37719402|gb|AAR01789.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|83779155|gb|ABC47398.1|	NADH dehydrogenase subunit 4 [Sus scrofa]				
gi|45826221|gb|AAS77739.1|	NADH dehydrogenase subunit 4 [Sus				

	scrofa]				
gi|161777647|gb|ABX79190.1|	N-acetylneuraminic acid hydroxylase variant 3 [Sus scrofa]	---	---	---	---
gi|73918051|sp|O19074.1|CMAH_PIG	RecName: Full=Cytidine monophosphate-N-acetylneuraminic acid hydroxylase; Short=CMP-N-acetylneuraminic acid hydroxylase; AltName: Full=CMP-N-acetylneuraminate monooxygenase; AltName: Full=CMP-Neu5Ac hydroxylase; AltName: Full=CMP-NeuAc hydroxylase >				
gi|163915137|ref|NP_001106486.1|	cytidine monophosphate-N-acetylneuraminic acid hydroxylase [Sus scrofa] >gi|158726707|gb|ABW80749.1| CMP-N-acetylneuraminic acid hydroxylase [Sus scrofa]				
gi|350585957|ref|XP_003482084.1|	PREDICTED: LOW QUALITY PROTEIN: AFG3-like protein 2, partial [Sus scrofa]	---	---	---	---
gi|47522752|ref|NP_999126.1|	optineurin [Sus scrofa] >gi|62286962|sp|Q7YS99.1|OPTN_PIG RecName: Full=Optineurin >gi|31324103|gb|AAP47176.1|AF513722_1 optineurin [Sus scrofa]	---	---	---	---
gi|350584686|ref|XP_003481803.1|	PREDICTED: polypeptide N-acetylgalactosaminyltransferase 4 isoform 2 [Sus scrofa]	---	---	---	---
gi|350596113|ref|XP_003360781.2|	PREDICTED: polypeptide N-acetylgalactosaminyltransferase 4-like [Sus scrofa] >gi|350584684|ref|XP_003481802.1| PREDICTED: polypeptide N-acetylgalactosaminyltransferase 4 isoform 1 [Sus scrofa]				
gi|346421398|ref|NP_001231071.1|	sorcin isoform 1 [Sus scrofa]	---	---	---	---
gi|346644814|ref|NP_001231072.1|	sorcin isoform 2 [Sus scrofa]				
gi|68534998|ref|NP_0010203	nuclear receptor coactivator 1 [Sus	---	---	---	---

99.1|	scrofa] >gi|75075065|sp|Q4PJW2.1|NCOA1_PIG RecName: Full=Nuclear receptor coactivator 1; Short=NCoA-1; AltName: Full=Steroid receptor coactivator 1; Short=SRC-1 >gi|67866953|gb|AAY82453.1| nuclear receptor coactiv				
gi|164523392|gb|ABY60786.1|	steroid receptor coactivator 1 isoform 2 [Sus scrofa]				
gi|164523390|gb|ABY60785.1|	steroid receptor coactivator 1 isoform 1 [Sus scrofa]				
gi|350578786|ref|XP_003121657.3|	PREDICTED: RNA polymerase-associated protein RTF1 homolog [Sus scrofa]	---	---	---	---
gi|350581632|ref|XP_003124588.3|	PREDICTED: hypothetical protein LOC100521783 isoform 1 [Sus scrofa]	---	---	---	---
gi|311276906|ref|XP_001924366.2|	PREDICTED: THO complex subunit 2 [Sus scrofa]	---	---	---	---
gi|350587373|ref|XP_003128918.3|	PREDICTED: condensin complex subunit 3 [Sus scrofa]	---	---	---	---
gi|194041854|ref|XP_001929564.1|	PREDICTED: biogenesis of lysosome-related organelles complex-1 subunit 2 [Sus scrofa]	---	---	---	---
gi|350595685|ref|XP_003135150.3|	PREDICTED: E3 ubiquitin-protein ligase HUWE1-like [Sus scrofa]	---	---	---	---
gi|311269675|ref|XP_003132593.1|	PREDICTED: actin-like 6A isoform 1 [Sus scrofa]	---	---	---	---
gi|343962595|ref|NP_001230634.1|	thioredoxin, mitochondrial [Sus scrofa]	1.024	1.646	1.288	1.379
gi|350591320|ref|XP_003132344.3|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 [Sus scrofa]	1.844	1.187	0.979	1.468
gi|298160941|ref|NP_001177148.1|	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha [Sus scrofa]	1.246	1.287	1.274	1.312
gi|350585782|ref|XP_003127781.3|	PREDICTED: AT-rich interactive domain-containing protein 1A, partial [Sus scrofa]	---	---	---	---
gi|38488989|tpg|DAA01973.1|	TPA_inf: RTN4-Aw [Sus scrofa]	---	---	---	---

gi|194018686|ref|NP_001123435.1|	reticulon-4 [Sus scrofa] >gi|38327590|tpg|DAA01967.1| TPA_inf: RTN4-C [Sus scrofa]				
gi|219521986|ref|NP_001137180.1|	glycerol kinase [Sus scrofa] >gi|217314913|gb|ACK36991.1| glycerol kinase [Sus scrofa]	---	---	---	---
gi|311273120|ref|XP_003133723.1|	PREDICTED: glycerol kinase-like [Sus scrofa]				
gi|311264064|ref|XP_003129981.1|	PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF4 isoform 1 [Sus scrofa]	---	---	---	---
gi|311264066|ref|XP_003129982.1|	PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF4 isoform 2 [Sus scrofa]				
gi|3288634|emb|CAA04598.1|	Bak protein [Sus scrofa]	---	---	---	---
gi|194040311|ref|XP_001928182.1|	PREDICTED: putative Bcl-2 homologous antagonist/killer 2 [Sus scrofa]				
gi|335294984|ref|XP_003357369.1|	PREDICTED: trehalase [Sus scrofa]	---	---	---	---
gi|221325626|ref|NP_001138314.1|	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial [Sus scrofa] >gi|219563064|gb|ACL27891.1| NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Sus scrofa]	---	---	---	---
gi|335283923|ref|XP_003354462.1|	PREDICTED: plakophilin-3-like [Sus scrofa]	---	---	---	---
gi|311268067|ref|XP_003131870.1|	PREDICTED: replication protein A 70 kDa DNA-binding subunit [Sus scrofa]	---	---	---	---
gi|335293447|ref|XP_003129021.2|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 46 [Sus scrofa]	---	---	---	---
gi|335296741|ref|XP_003130951.2|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 12 [Sus scrofa]				
gi|335295199|ref|XP_003357427.1|	PREDICTED: zinc finger CCCH domain-containing protein 11A isoform 2 [Sus	---	---	---	---

	scrofa] >gi|335295197|ref|XP_003357426.1| PREDICTED: zinc finger CCCH domain-containing protein 11A isoform 1 [Sus scrofa]				
gi|222136636|ref|NP_001138402.1|	nuclear transcription factor Y subunit beta [Sus scrofa]	---	---	---	---
gi|335310220|ref|XP_003361935.1|	PREDICTED: elongation factor Ts, mitochondrial-like, partial [Sus scrofa]	---	---	---	---
gi|311258370|ref|XP_003127581.1|	PREDICTED: pleckstrin homology domain-containing family G member 5 [Sus scrofa]	---	---	---	---
gi|343790928|ref|NP_001230520.1|	mini-chromosome maintenance complex-binding protein [Sus scrofa]	---	---	---	---
gi|311266774|ref|XP_003131239.1|	PREDICTED: WW domain-binding protein 2-like [Sus scrofa]	---	---	---	---
gi|345091084|ref|NP_001230758.1|	RNA binding motif protein 25 [Sus scrofa]	---	---	---	---
gi|350596600|ref|XP_003128714.3|	PREDICTED: RNA-binding protein 25, partial [Sus scrofa]				
gi|229892828|ref|NP_001153565.1|	protein arginine N-methyltransferase 5 [Sus scrofa] >gi|197692948|gb|ACH71262.1| protein arginine methyltransferase 5 [Sus scrofa]	---	---	---	---
gi|194036657|ref|XP_001928045.1|	PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 1 [Sus scrofa]	---	---	---	---
gi|55741851|ref|NP_001001264.1|	Wilms tumor protein homolog [Sus scrofa] >gi|3915298|sp|O62651.1|WT1_PIG RecName: Full=Wilms tumor protein homolog >gi|3132272|dbj|BAA28147.1| unnamed protein product [Sus scrofa]	---	---	---	---
gi|98283612|gb|ABF58000.1|	mitochondrial NAD+isocitrate dehydrogenase 3 beta variant 1 [Sus scrofa]	---	---	---	---
gi|98283616|gb|ABF58003.1|	mitochondrial NAD+isocitrate dehydrogenase 3 beta variant 1 [Sus scrofa]				
gi|98283613|gb|ABF58001.1|	mitochondrial NAD+isocitrate				

	dehydrogenase 3 beta variant 2 [Sus scrofa] >gi|98283614|gb|ABF58002.1| mitochondrial NAD+isocitrate dehydrogenase 3 beta variant 3 [Sus scrofa]				
gi|113205754|ref|NP_001038040.1|	isocitrate dehydrogenase [NAD] subunit beta, mitochondrial [Sus scrofa] >gi|98283620|gb|ABF58005.1| mitochondrial NAD+isocitrate dehydrogenase 3 beta variant 3 [Sus scrofa] >gi|98283618|gb|ABF58004.1| mitochondrial NAD+isocitrate dehydrogenase 3 bet				
gi|335309458|ref|XP_003361645.1|	PREDICTED: isocitrate dehydrogenase [NAD] subunit beta, mitochondrial-like [Sus scrofa]				
gi|350583819|ref|XP_003126103.3|	PREDICTED: brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 2-like, partial [Sus scrofa]	---	---	---	---
gi|350584473|ref|XP_003126641.3|	PREDICTED: V-type proton ATPase subunit E 1 isoform 2 [Sus scrofa]	---	---	---	---
gi|350584475|ref|XP_003481754.1|	PREDICTED: V-type proton ATPase subunit E 1 [Sus scrofa]				
gi|39646090|emb|CAE83881.1|	unnamed protein product [Sus scrofa]	---	---	---	---
gi|47523636|ref|NP_999446.1|	complement factor H precursor [Sus scrofa] >gi|21464594|emb|CAC81999.1| complement regulator factor H [Sus scrofa]				
gi|346644842|ref|NP_001231175.1|	NOP2 nucleolar protein homolog [Sus scrofa]	---	---	---	---
gi|347922122|ref|NP_001231672.1|	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa [Sus scrofa] >gi|350588320|ref|XP_003482623.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 subunit C2-like isoform 1 [Sus scrofa]	---	---	---	---
gi|350588322|ref|XP_003482624.1|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 subunit C2-like isoform 2 [Sus scrofa]				

gi|187470928|sp|A5A779.1|PGTA_PIG	RecName: Full=Geranylgeranyl transferase type-2 subunit alpha; AltName: Full=Geranylgeranyl transferase type II subunit alpha; AltName: Full=Rab geranyl-geranyltransferase subunit alpha; Short=Rab GG transferase alpha; Short=Rab GGTase alpha; AltNam	---	---	---	---
gi|297747277|ref|NP_001172107.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa [Sus scrofa] >gi|350583744|ref|XP_003481577.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6-like [Sus scrofa]	---	---	---	---
gi|335310969|ref|XP_001928237.3|	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6-like, partial [Sus scrofa]				
gi|346986447|ref|NP_001231373.1|	ribonuclease H2 subunit A [Sus scrofa]	0.934	1.495	0.612	0.901
gi|335282567|ref|XP_003123239.2|	PREDICTED: evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|311267157|ref|XP_003131429.1|	PREDICTED: coiled-coil domain-containing protein 56-like [Sus scrofa]	---	---	---	---
gi|350583671|ref|XP_003125970.3|	PREDICTED: interferon-induced guanylate-binding protein 2-like isoform 2, partial [Sus scrofa]	---	---	---	---
gi|311264070|ref|XP_003129980.1|	PREDICTED: E3 ubiquitin-protein ligase CBL [Sus scrofa]	---	---	---	---
gi|335296877|ref|XP_003357884.1|	PREDICTED: cytidine and dCMP deaminase domain-containing protein 1-like [Sus scrofa]	---	---	---	---
gi|335292471|ref|XP_001927834.3|	PREDICTED: signal recognition particle 54 kDa protein isoform 1 [Sus scrofa]	---	---	---	---
gi|335292473|ref|XP_003356739.1|	PREDICTED: signal recognition particle 54 kDa protein [Sus scrofa]				
gi|350589889|ref|XP_003482942.1|	PREDICTED: TSC22 domain family protein 1-like [Sus scrofa]	---	---	---	---

gi|311260236|ref|XP_001925503.2|	PREDICTED: tapasin-like [Sus scrofa]	---	---	---	---
gi|350589164|ref|XP_003357646.2|	PREDICTED: acyl-CoA:lysophosphatidylglycerol acyltransferase 1-like [Sus scrofa]	---	---	---	---
gi|311246039|ref|XP_003122046.1|	PREDICTED: golgi-associated plant pathogenesis-related protein 1-like [Sus scrofa]	---	---	---	---
gi|350579373|ref|XP_003480598.1|	PREDICTED: golgi-associated plant pathogenesis-related protein 1-like, partial [Sus scrofa]				
gi|148222591|ref|NP_001090955.1|	ATPase inhibitor, mitochondrial precursor [Sus scrofa] >gi|148887342|sp|Q29307.2|ATIF1_PIG RecName: Full=ATPase inhibitor, mitochondrial; AltName: Full=Inhibitor of F(1)F(o)-ATPase; Short=IF(1); Short=IF1; Flags: Precursor >gi|117661240|gb|ABK55664.	---	---	---	---
gi|350590642|ref|XP_003131789.3|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 11-like [Sus scrofa]	---	---	---	---
gi|335310105|ref|XP_003361889.1|	PREDICTED: acyl-CoA dehydrogenase family member 10-like, partial [Sus scrofa]	---	---	---	---
gi|148233298|ref|NP_001090954.1|	heat shock factor-binding protein 1 [Sus scrofa] >gi|117661226|gb|ABK55663.1| HSBP1 [Sus scrofa]	---	---	---	---
gi|311247522|ref|XP_003122684.1|	PREDICTED: succinate dehydrogenase assembly factor 2, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|335289736|ref|XP_003127196.2|	PREDICTED: inositol-trisphosphate 3-kinase C [Sus scrofa]	---	---	---	---
gi|335280193|ref|XP_003121819.2|	PREDICTED: cutaneous T-cell lymphoma-associated antigen 5-like isoform 1 [Sus scrofa] >gi|335280187|ref|XP_003353518.1| PREDICTED: cutaneous T-cell lymphoma-associated antigen 5 isoform 2 [Sus scrofa]	0.991	0.752	0.959	0.889
gi|335280195|ref|XP_003353	PREDICTED: cutaneous T-cell				

520.1|	lymphoma-associated antigen 5-like isoform 2 [Sus scrofa] >gi|335280191|ref|XP_003353519.1| PREDICTED: cutaneous T-cell lymphoma-associated antigen 5 isoform 3 [Sus scrofa]				
gi|211578376|ref|NP_001129984.1|	beta,beta-carotene 15,15~-monooxygenase [Sus scrofa] >gi|209571749|gb|ACI62530.1| beta-carotene 15,15~-monooxygenase 1 [Sus scrofa]	1.281	1.155	1.164	1.667
gi|311247444|ref|XP_003122650.1|	PREDICTED: reticulon-3 isoform 1 [Sus scrofa]	---	---	---	---
gi|47523756|ref|NP_999514.1|	pyruvate carboxylase, mitochondrial [Sus scrofa] >gi|300632138|emb|CBU89073.1| unnamed protein product [Sus scrofa] >gi|300628626|emb|CBU85988.1| unnamed protein product [Sus scrofa] >gi|300641281|emb|CBU93285.1| unnamed protein product [Sus scrofa]	---	---	---	---
gi|335292522|ref|XP_001924480.2|	PREDICTED: proteasome subunit beta type-5 [Sus scrofa]	---	---	---	---
gi|335310829|ref|XP_003362211.1|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 14-like [Sus scrofa]	1.053	0.697	1.262	0.778
gi|311244988|ref|XP_003121641.1|	PREDICTED: regulator of microtubule dynamics protein 3-like [Sus scrofa]	---	---	---	---
gi|311260254|ref|XP_003128393.1|	PREDICTED: inositol 1,4,5-trisphosphate receptor type 3 [Sus scrofa]	---	---	---	---
gi|163915153|ref|NP_001106524.1|	NF-kappa-B essential modulator [Sus scrofa] >gi|161137769|gb|ABX57883.1| inhibitor of kappa light polypeptide gene enhancer in B-cells kinase gamma [Sus scrofa]	---	---	---	---
gi|166079195|gb|ABY81299.1|	inhibitor of kappa light polypeptide gene enhancer in B-cells kinase gamma transcript variant 1 [Sus scrofa]				

gi|34810486|pdb|1NX2|A	Chain A, Calpain Domain Vi >gi|34810482|pdb|1NX1|A Chain A, Calpain Domain Vi Complexed With Calpastatin Inhibitory Domain C (Dic) >gi|34810478|pdb|1NX0|B Chain B, Structure Of Calpain Domain 6 In Complex With Calpastatin Dic >gi|3319069|pdb|1ALV|B	0.843	0.93	1.21	1.038
gi|47523694|ref|NP_999483.1|	calpain small subunit 1 [Sus scrofa] >gi|115613|sp|P04574.1|CPNS1_PIG RecName: Full=Calpain small subunit 1; Short=CSS1; AltName: Full=Calcium-activated neutral proteinase small subunit; Short=CANP small subunit; AltName: Full=Calcium-dependent prot				
gi|219521950|ref|NP_001137167.1|	acetyl-coenzyme A synthetase, cytoplasmic [Sus scrofa] >gi|217039101|gb|ACJ76839.1| acyl-CoA synthetase short-chain family member 2 [Sus scrofa]	---	---	---	---
gi|350583332|ref|XP_001927031.4|	PREDICTED: pre-B-cell leukemia transcription factor-interacting protein 1-like [Sus scrofa]	---	---	---	---
gi|6174950|sp|P79324.1|RL15_PIG	RecName: Full=60S ribosomal protein L15	---	---	---	---
gi|346227216|ref|NP_001230994.1|	ribosomal protein L15 [Sus scrofa] >gi|335298742|ref|XP_003358383.1| PREDICTED: 60S ribosomal protein L15-like isoform 1 [Sus scrofa] >gi|335298744|ref|XP_003358384.1| PREDICTED: 60S ribosomal protein L15-like isoform 2 [Sus scrofa]				
gi|311252561|ref|XP_003125153.1|	PREDICTED: prefoldin subunit 1-like [Sus scrofa]	---	---	---	---
gi|350581165|ref|XP_003480975.1|	PREDICTED: prefoldin subunit 1-like [Sus scrofa]				
gi|350584178|ref|XP_003481687.1|	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus scrofa]	---	---	---	---

gi|7716549|gb|AAF68430.1|AF239165_1	serine hydroxymethyltransferase, partial [Sus scrofa]	---	---	---	---
gi|47523070|ref|NP_999298.1|	pantetheinase precursor [Sus scrofa] >gi|46577140|sp|Q9BDJ5.1|VNN1_PIG RecName: Full=Pantetheinase; AltName: Full=Pantetheine hydrolase; AltName: Full=Vascular non-inflammatory molecule 1; Short=Vanin-1; Flags: Precursor >gi|13655618|gb|AAK29437.2|A	---	---	---	---
gi|194035771|ref|XP_001927964.1|	PREDICTED: guanylate-binding protein 4 [Sus scrofa]	1.152	1.559	1.072	0.948
gi|311256822|ref|XP_003126824.1|	PREDICTED: histone deacetylase 10-like [Sus scrofa]	---	---	---	---
gi|335310624|ref|XP_003362118.1|	PREDICTED: histone deacetylase 10-like [Sus scrofa]				
gi|164414802|pdb|2RME|A	Chain A, Stressin	---	---	---	---
gi|311248590|ref|XP_003123248.1|	PREDICTED: mitochondrial import inner membrane translocase subunit TIM44 [Sus scrofa]	---	---	---	---
gi|335298785|ref|XP_003132130.2|	PREDICTED: COX assembly mitochondrial protein homolog [Sus scrofa]	---	---	---	---
gi|335308716|ref|XP_003361344.1|	PREDICTED: selenide, water dikinase 1, partial [Sus scrofa]	---	---	---	---
gi|335281875|ref|XP_003353915.1|	PREDICTED: proteoglycan 3-like [Sus scrofa]	---	---	---	---
gi|311272131|ref|XP_003133314.1|	PREDICTED: aspartyl-tRNA synthetase, cytoplasmic-like isoform 1 [Sus scrofa]	0.967	0.599	0.349	0.865
gi|335302484|ref|XP_003359474.1|	PREDICTED: aspartyl-tRNA synthetase, cytoplasmic-like isoform 2 [Sus scrofa]				
gi|350587769|ref|XP_003129218.3|	PREDICTED: ATP-binding cassette sub-family E member 1 [Sus scrofa]	---	---	---	---
gi|311275848|ref|XP_003134937.1|	PREDICTED: biliverdin reductase A-like [Sus scrofa]	---	---	---	---
gi|311271149|ref|XP_003133065.1|	PREDICTED: uncharacterized protein C1orf31 homolog [Sus scrofa]	---	---	---	---
gi|335301594|ref|XP_003359	PREDICTED: uncharacterized				

243.1|	protein C1orf31 homolog [Sus scrofa] >gi|335301592|ref|XP_003359242.1| PREDICTED: uncharacterized protein C1orf31 homolog [Sus scrofa]				
gi|346716287|ref|NP_001231279.1|	carboxymethylenebutenolidase homolog [Sus scrofa]	---	---	---	---
gi|47522956|ref|NP_999236.1|	N-acetylneuraminate lyase [Sus scrofa] >gi|75049298|sp|Q9BEC7.1|NPL_PIG RecName: Full=N-acetylneuraminate lyase; Short=NALase; AltName: Full=N-acetylneuraminate pyruvate-lyase; AltName: Full=N-acetylneuraminic acid aldolase; AltName: Full=Sialate ly	---	---	---	---
gi|335292737|ref|XP_001927469.2|	PREDICTED: serine/arginine-rich splicing factor 5 isoform 2 [Sus scrofa] >gi|335292735|ref|XP_001927454.2| PREDICTED: serine/arginine-rich splicing factor 5 isoform 1 [Sus scrofa]	---	---	---	---
gi|335307313|ref|XP_003360793.1|	PREDICTED: serine/arginine-rich splicing factor 5-like [Sus scrofa]				
gi|346421328|ref|NP_001231038.1|	synapse-associated protein 1 isoform 2 [Sus scrofa]	---	---	---	---
gi|346421345|ref|NP_001231036.1|	synapse-associated protein 1 isoform 1 [Sus scrofa]				
gi|350580558|ref|XP_003354114.2|	PREDICTED: dynamin-2-like [Sus scrofa]	---	---	---	---
gi|178057329|ref|NP_001116638.1|	protein phosphatase 1 regulatory subunit 11 [Sus scrofa] >gi|194039988|ref|XP_001929404.1| PREDICTED: protein phosphatase 1 regulatory subunit 11-like [Sus scrofa] >gi|211926939|dbj|BAG82680.1| protein phosphatase 1, regulatory subunit 11 [Sus scrof	---	---	---	---
gi|350584858|ref|XP_003126900.3|	PREDICTED: craniofacial development protein 1, partial [Sus scrofa]	---	---	---	---
gi|347800629|ref|NP_001231	synaptosomal-associated protein,	---	---	---	---

648.1|	23kDa [Sus scrofa]				
gi|298104112|ref|NP_001177119.1|	charged multivesicular body protein 4c [Sus scrofa]	---	---	---	---
gi|311264732|ref|XP_003130306.1|	PREDICTED: synaptophysin-like protein 1-like [Sus scrofa]	---	---	---	---
gi|148230691|ref|NP_001090958.1|	Krueppel-like factor 5 [Sus scrofa] >gi|110007347|gb|ABG49105.1| kruppel-like factor 5 [Sus scrofa]	---	---	---	---
gi|335282891|ref|XP_003123558.2|	PREDICTED: myosin-IXb-like [Sus scrofa]	---	---	---	---
gi|194044882|ref|XP_001926942.1|	PREDICTED: 26S proteasome non-ATPase regulatory subunit 10 isoform 1 [Sus scrofa] >gi|335309762|ref|XP_003361757.1| PREDICTED: 26S proteasome non-ATPase regulatory subunit 10-like isoform 1 [Sus scrofa]	---	---	---	---
gi|343887438|ref|NP_001230620.1|	plasma glutamate carboxypeptidase precursor [Sus scrofa]	0.432	0.694	0.732	0.475
gi|350579791|ref|XP_003480684.1|	PREDICTED: endothelial differentiation-related factor 1-like isoform 2 [Sus scrofa] >gi|350579789|ref|XP_003480683.1| PREDICTED: endothelial differentiation-related factor 1-like isoform 1 [Sus scrofa] >gi|149132072|gb|ABR20898.1| multiprotein bridg	---	---	---	---
gi|350586171|ref|XP_003356500.2|	PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 [Sus scrofa]	---	---	---	---
gi|232142|sp|P29797.1|GNAS_PIG	RecName: Full=Guanine nucleotide-binding protein G(s) subunit alpha; AltName: Full=Adenylate cyclase-stimulating G alpha protein >gi|1958|emb|CAA45355.1| alpha-stimulatory subunit of GTP-binding protein [Sus scrofa]	---	---	---	---
gi|147223308|emb|CAN13201.1|	GNAS complex locus [Sus scrofa] >gi|147223420|emb|CAN13152.1| GNAS complex locus [Sus scrofa]				

gi|147223417|emb|CAN13149.1|	GNAS complex locus [Sus scrofa] >gi|147223306|emb|CAN13199.1| GNAS complex locus [Sus scrofa]				
gi|285002235|ref|NP_999477.2|	guanine nucleotide-binding protein G(s) subunit alpha GNASL [Sus scrofa] >gi|147223423|emb|CAN13155.1| GNAS complex locus [Sus scrofa] >gi|147223313|emb|CAN13206.1| GNAS complex locus [Sus scrofa]				
gi|285002237|ref|NP_001165454.1|	guanine nucleotide-binding protein G(s) subunit alpha GNASS [Sus scrofa]				
gi|285002241|ref|NP_001165456.1|	guanine nucleotide-binding protein G(s) subunit alpha isoform g [Sus scrofa] >gi|147223316|emb|CAN13209.1| GNAS complex locus [Sus scrofa] >gi|147223424|emb|CAN13156.1| GNAS complex locus [Sus scrofa]				
gi|138752630|emb|CAM32247.1|	guanine nucleotide-binding protein, alpha-stimulating activity polypeptide 1 [Sus scrofa]				
gi|147223418|emb|CAN13150.1|	GNAS complex locus [Sus scrofa] >gi|147223307|emb|CAN13200.1| GNAS complex locus [Sus scrofa]				
gi|285002239|ref|NP_001165455.1|	guanine nucleotide-binding protein G(s) subunit alpha isoform f [Sus scrofa] >gi|147223425|emb|CAN13157.1| GNAS complex locus [Sus scrofa] >gi|147223315|emb|CAN13208.1| GNAS complex locus [Sus scrofa]				
gi|350585712|ref|XP_003482033.1|	PREDICTED: eukaryotic translation initiation factor 4 gamma 3-like [Sus scrofa]	---	---	---	---
gi|350579849|ref|XP_003480696.1|	PREDICTED: src substrate cortactin-like [Sus scrofa]	---	---	---	---
gi|343790902|ref|NP_001230508.1|	thymidylate synthetase [Sus scrofa]	---	---	---	---
gi|350596976|ref|XP_003361	PREDICTED: methionyl-tRNA	---	---	---	---

857.2|	synthetase, cytoplasmic-like [Sus scrofa]				
gi|343488509|ref|NP_001230414.1|	valacyclovir hydrolase precursor [Sus scrofa]	---	---	---	---
gi|227430403|ref|NP_001153085.1|	NAD(P)H dehydrogenase [quinone] 1 [Sus scrofa]	---	---	---	---
gi|350586151|ref|XP_003128006.3|	PREDICTED: LOW QUALITY PROTEIN: inaD-like protein [Sus scrofa]	---	---	---	---
gi|335284763|ref|XP_003124756.2|	PREDICTED: E3 ubiquitin-protein ligase CHIP-like [Sus scrofa]	---	---	---	---
gi|335297742|ref|XP_003131565.2|	PREDICTED: protein C17orf37 homolog [Sus scrofa]	---	---	---	---
gi|335300657|ref|XP_003358980.1|	PREDICTED: protein SON isoform 1 [Sus scrofa]	---	---	---	---
gi|335300659|ref|XP_003358981.1|	PREDICTED: protein SON isoform 2 [Sus scrofa]				
gi|311264544|ref|XP_003130216.1|	PREDICTED: replication protein A 14 kDa subunit-like [Sus scrofa]	---	---	---	---
gi|335307995|ref|XP_003361061.1|	PREDICTED: replication protein A 14 kDa subunit-like [Sus scrofa]				
gi|55926205|ref|NP_001007520.1|	interferon-related developmental regulator 1 [Sus scrofa] >gi|68565361|sp|Q5S1U6.1|IFRD1_PIG RecName: Full=Interferon-related developmental regulator 1 >gi|55709896|gb|AAV58829.1| interferon-related developmental regulator 1 [Sus scrofa]	---	---	---	---
gi|350590514|ref|XP_003131675.3|	PREDICTED: retinoid-inducible serine carboxypeptidase [Sus scrofa]	---	---	---	---
gi|335290950|ref|XP_003356343.1|	PREDICTED: tyrosyl-tRNA synthetase, cytoplasmic [Sus scrofa]	---	---	---	---
gi|350592546|ref|XP_001925361.4|	PREDICTED: TP53-regulated inhibitor of apoptosis 1-like, partial [Sus scrofa]	---	---	---	---
gi|350584124|ref|XP_003481674.1|	PREDICTED: melanocyte protein PMEL, partial [Sus scrofa]	---	---	---	---
gi|350584130|ref|XP_003126312.3|	PREDICTED: proliferation-associated protein 2G4 [Sus scrofa]				

gi|311276400|ref|XP_003135190.1|	PREDICTED: LOW QUALITY PROTEIN: hephaestin-like [Sus scrofa]	---	---	---	---
gi|350588022|ref|XP_003482536.1|	PREDICTED: protein transport protein Sec31A-like [Sus scrofa]	---	---	---	---
gi|347300255|ref|NP_001231435.1|	DAZ-associated protein 1 [Sus scrofa]	---	---	---	---
gi|311270533|ref|XP_003132904.1|	PREDICTED: splicing factor, suppressor of white-apricot homolog [Sus scrofa]	---	---	---	---
gi|335297337|ref|XP_003131233.2|	PREDICTED: signal recognition particle 68 kDa protein-like [Sus scrofa]	---	---	---	---
gi|350584672|ref|XP_003126766.2|	PREDICTED: transmembrane and coiled-coil domains protein 3 [Sus scrofa]	---	---	---	---
gi|350585412|ref|XP_003356115.2|	PREDICTED: receptor-type tyrosine-protein phosphatase H, partial [Sus scrofa]	---	---	---	---
gi|311248328|ref|XP_003123084.1|	PREDICTED: nicalin [Sus scrofa]	---	---	---	---
gi|194038528|ref|XP_001929053.1|	PREDICTED: acyl-coenzyme A thioesterase 6-like [Sus scrofa]	---	---	---	---
gi|194042067|ref|XP_001929334.1|	PREDICTED: actin-binding LIM protein 1 isoform 1 [Sus scrofa]	---	---	---	---
gi|311271869|ref|XP_003133239.1|	PREDICTED: actin-binding LIM protein 1 isoform 3 [Sus scrofa]				
gi|311271871|ref|XP_003133238.1|	PREDICTED: actin-binding LIM protein 1 isoform 2 [Sus scrofa]				
gi|311249377|ref|XP_003123620.1|	PREDICTED: transcriptional repressor p66-alpha [Sus scrofa]	---	---	---	---
gi|194043684|ref|XP_001926541.1|	PREDICTED: inward rectifier potassium channel 13 isoform 1 [Sus scrofa]	---	---	---	---
gi|16033755|gb|AAL13316.1|AF424780_1	cytochrome P450 3A [Sus scrofa]	---	---	---	---
gi|19071856|dbj|BAB85672.1|	cytochrome P450 3A46v1 [Sus scrofa]				
gi|19071846|dbj|BAB85667.1|	cytochrome P450 3A29v3 [Sus scrofa]				
gi|196475656|gb|ACG76385.1|	cytochrome P450 CYP3A [Sus scrofa]				

gi|47523900|ref|NP_999588.1|	cytochrome P450 3A29 [Sus scrofa] >gi|5921921|sp|P79401.1|CP3AT_PIG RecName: Full=Cytochrome P450 3A29; AltName: Full=CYPIIIA29 >gi|1903317|emb|CAB07513.1| cytochrome P450 [Sus scrofa]				
gi|19071852|dbj|BAB85670.1|	cytochrome P450 3A39v3 [Sus scrofa]				
gi|19071844|dbj|BAB85666.1|	cytochrome P450 3A29v2 [Sus scrofa]				
gi|19071854|dbj|BAB85671.1|	cytochrome P450 3A39v4 [Sus scrofa]				
gi|198282077|ref|NP_001128296.1|	cytochrome P450 3A46 [Sus scrofa] >gi|197791176|gb|ABS58488.2| cytochrome P450 [Sus scrofa]				
gi|47523898|ref|NP_999587.1|	cytochrome P450 3A39 [Sus scrofa] >gi|4151927|gb|AAD04628.1| cytochrome P450 [Sus scrofa]				
gi|19071848|dbj|BAB85668.1|	cytochrome P450 3A29v4 [Sus scrofa]				
gi|154101336|gb|ABS58494.1|	cytochrome P450 [Sus scrofa]				
gi|19071858|dbj|BAB85673.1|	cytochrome P450 3A46v2 [Sus scrofa]				
gi|343488540|ref|NP_001230425.1|	GSK3-beta interaction protein [Sus scrofa]	1.315	1.569	1.714	0.976
gi|335308872|ref|XP_003361404.1|	PREDICTED: serine hydroxymethyltransferase, cytosolic [Sus scrofa]	---	---	---	---
gi|335309568|ref|XP_003130716.2|	PREDICTED: ubiquitin-associated protein 2-like, partial [Sus scrofa]	---	---	---	---
gi|350589476|ref|XP_003482855.1|	PREDICTED: ubiquitin-associated protein 2-like [Sus scrofa]				
gi|346986410|ref|NP_001231355.1|	glycine cleavage system T-protein [Sus scrofa]	---	---	---	---
gi|350587512|ref|XP_003129026.3|	PREDICTED: pre-mRNA 3~-end-processing factor FIP1-like [Sus scrofa]	---	---	---	---
gi|313570009|ref|NP_001186292.1|	calcium-binding mitochondrial carrier protein SCaMC-1-like [Sus scrofa] >gi|186886352|gb|ACC93575.	---	---	---	---

	1| small calcium-binding mitochondrial carrier 1 [Sus scrofa]				
gi|350591284|ref|XP_003132316.2|	PREDICTED: sarcolemmal membrane-associated protein [Sus scrofa]	---	---	---	---
gi|350580065|ref|XP_003122766.3|	PREDICTED: syntaxin-3-like, partial [Sus scrofa]	0.474	0.757	0.71	0.552
gi|335296874|ref|XP_003131019.2|	PREDICTED: calcium-binding protein 39-like [Sus scrofa]	---	---	---	---
gi|335310350|ref|XP_003361992.1|	PREDICTED: carbonyl reductase [NADPH] 1-like, partial [Sus scrofa]	---	---	---	---
gi|350580387|ref|XP_003480810.1|	PREDICTED: calcium homeostasis endoplasmic reticulum protein-like [Sus scrofa]	---	---	---	---
gi|335296376|ref|XP_003357763.1|	PREDICTED: probable gluconokinase-like [Sus scrofa]	---	---	---	---
gi|335297595|ref|XP_003358072.1|	PREDICTED: interferon-induced 35 kDa protein-like [Sus scrofa]	---	---	---	---
gi|350595403|ref|XP_003134876.3|	PREDICTED: hypothetical protein LOC100516841 [Sus scrofa]	---	---	---	---
gi|350594194|ref|XP_003359791.2|	PREDICTED: hypothetical protein LOC100620294 [Sus scrofa]	---	---	---	---
gi|350582696|ref|XP_003354965.2|	PREDICTED: ATP-dependent RNA helicase DDX1 [Sus scrofa]	---	---	---	---
gi|297747306|ref|NP_001177083.1|	zinc finger, CCHC domain containing 8 [Sus scrofa]	---	---	---	---
gi|350596491|ref|XP_003484281.1|	PREDICTED: zinc finger CCHC domain-containing protein 8-like, partial [Sus scrofa]				
gi|298104144|ref|NP_001177137.1|	S100 calcium binding protein A16 [Sus scrofa] >gi|298104142|ref|NP_001177136.1| S100 calcium binding protein A16 [Sus scrofa]	---	---	---	---
gi|350583616|ref|XP_003481553.1|	PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial isoform 2 [Sus scrofa]	---	---	---	---
gi|350583618|ref|XP_001924875.4|	PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid				

	dehydrogenase complex, mitochondrial isoform 1 [Sus scrofa]				
gi|343488551|ref|NP_001230428.1|	mitochondrial intermembrane space import and assembly protein 40 [Sus scrofa]	---	---	---	---
gi|311272864|ref|XP_003133619.1|	PREDICTED: uncharacterized protein C2orf47 homolog, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|350596869|ref|XP_003361751.2|	PREDICTED: uncharacterized protein C2orf47 homolog, mitochondrial-like [Sus scrofa]				
gi|194043356|ref|XP_001929473.1|	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 isoform 2 [Sus scrofa]	---	---	---	---
gi|194043360|ref|XP_001929472.1|	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 isoform 1 [Sus scrofa]				
gi|350583576|ref|XP_003125920.3|	PREDICTED: sortilin [Sus scrofa]	---	---	---	---
gi|373248672|emb|CCF70742.1|	sortilin 1, partial [Sus scrofa] >gi|373248668|emb|CCF70740.1| sortilin 1, partial [Sus scrofa] >gi|373248674|emb|CCF70743.1| sortilin 1, partial [Sus scrofa] >gi|373248670|emb|CCF70741.1| sortilin 1, partial [Sus scrofa]				
gi|350588230|ref|XP_003129648.3|	PREDICTED: nuclear pore complex protein Nup98-Nup96-like [Sus scrofa]	---	---	---	---
gi|121195|sp|P01281.1|GIP_PIG	RecName: Full=Gastric inhibitory polypeptide; Short=GIP; AltName: Full=Glucose-dependent insulinotropic polypeptide	---	---	---	---
gi|388255283|gb|AFK25156.1|	gastric inhibitory polypeptide precursor [Sus scrofa]				
gi|415514|gb|AAB28179.1|	diazepam-binding inhibitor (32-86), DBI(32-86)=antibacterial peptide [swine, small intestine, Peptide Partial, 36 aa]				
gi|335297830|ref|XP_003358130.1|	PREDICTED: gastric inhibitory polypeptide-like [Sus scrofa]				

gi|350592229|ref|XP_003359063.2|	PREDICTED: lanosterol synthase-like [Sus scrofa]	---	---	---	---
gi|311246600|ref|XP_001926112.2|	PREDICTED: serine/threonine-protein phosphatase 2A activator-like isoform 1 [Sus scrofa]	---	---	---	---
gi|335281070|ref|XP_003353729.1|	PREDICTED: serine/threonine-protein phosphatase 2A activator-like isoform 2 [Sus scrofa]				
gi|147900197|ref|NP_001090953.1|	cytochrome c oxidase subunit 7A2, mitochondrial [Sus scrofa] >gi|117661207|gb|ABK55662.1| COX7A2 [Sus scrofa]	---	---	---	---
gi|311270525|ref|XP_003132902.1|	PREDICTED: tRNA pseudouridine synthase A, mitochondrial [Sus scrofa] >gi|194043580|ref|XP_001928625.1| PREDICTED: tRNA pseudouridine synthase A, mitochondrial isoform 2 [Sus scrofa]	---	---	---	---
gi|311245687|ref|XP_003121922.1|	PREDICTED: uncharacterized protein C9orf82 homolog [Sus scrofa]	---	---	---	---
gi|350587407|ref|XP_003482407.1|	PREDICTED: hypothetical protein LOC100737378 [Sus scrofa]	---	---	---	---
gi|335307979|ref|XP_003361054.1|	PREDICTED: abhydrolase domain-containing protein 10, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|189232885|emb|CAQ34905.1|	signal recognition particle receptor B subunit [Sus scrofa]	---	---	---	---
gi|311269414|ref|XP_003132477.1|	PREDICTED: signal recognition particle receptor subunit beta-like [Sus scrofa]				
gi|350594246|ref|XP_003133954.3|	PREDICTED: disabled homolog 2 [Sus scrofa]	---	---	---	---
gi|147903209|ref|NP_001090934.1|	small nuclear ribonucleoprotein E [Sus scrofa] >gi|166233313|sp|A1XQR9.1| RUXE_PIG RecName: Full=Small nuclear ribonucleoprotein E; Short=snRNP-E; AltName: Full=Sm protein E; Short=Sm-E; Short=SmE >gi|117660560|gb|ABK55626.1| NDUFB2 [Sus scrofa] >gi|	---	---	---	---

gi|350594505|ref|XP_003359894.2|	PREDICTED: annexin A6-like [Sus scrofa]	---	---	---	---
gi|348041218|ref|NP_001231706.1|	Ena-vasodilator stimulated phosphoprotein [Sus scrofa]	---	---	---	---
gi|350587198|ref|XP_003482364.1|	PREDICTED: ena/VASP-like protein-like [Sus scrofa]				
gi|156779005|gb|ABU95648.1|	sirtuin 2 [Sus scrofa]	---	---	---	---
gi|166796035|ref|NP_001107743.1|	NAD-dependent deacetylase sirtuin-2 [Sus scrofa] >gi|164653929|gb|ABY65333.1| sirtuin 2 [Sus scrofa]				
gi|227057425|gb|ACP18879.1|	truncated sirtuin 2 [Sus scrofa]				
gi|227057441|gb|ACP18880.1|	sirtuin 2 [Sus scrofa]				
gi|311258366|ref|XP_003127578.1|	PREDICTED: espin [Sus scrofa]	---	---	---	---
gi|350585555|ref|XP_003481987.1|	PREDICTED: espin-like [Sus scrofa]				
gi|350578468|ref|XP_003121482.3|	PREDICTED: myosin-Vb [Sus scrofa]	---	---	---	---
gi|350581059|ref|XP_003123938.3|	PREDICTED: phosphorylated adapter RNA export protein-like [Sus scrofa]	---	---	---	---
gi|350584132|ref|XP_003481675.1|	PREDICTED: proliferation-associated protein 2G4-like [Sus scrofa]	---	---	---	---
gi|347800675|ref|NP_001231654.1|	molybdenum cofactor synthesis 2 [Sus scrofa]	---	---	---	---
gi|63139103|gb|AAY33861.1|	centrin 2 [Sus scrofa]	---	---	---	---
gi|194044860|ref|XP_001927244.1|	PREDICTED: centrin-2 [Sus scrofa]				
gi|33320702|gb|AAQ05997.1|	ATPase subunit 8 [Sus scrofa]	---	---	---	---
gi|90969048|gb|ABE02601.1|	ATP synthase F0 subunit 8 [Sus scrofa]				
gi|94981325|gb|ABF49553.1|	ATPase subunit 8 [Sus scrofa] >gi|145315685|gb|ABP63227.1| ATP synthase F0 subunit 8 [Sus scrofa] >gi|145315447|gb|ABP63006.1| ATP synthase F0 subunit 8 [Sus scrofa] >gi|124249812|gb|ABM92885				

	.1| ATPase subunit 8 [Sus scrofa]				
gi|124358981|ref|YP_001023767.1|	ATP synthase F0 subunit 8 [Phacochoerus africanus] >gi|88766365|gb|ABD49697.1| ATP synthase F0 subunit 8 [Phacochoerus africanus]				
gi|33320870|gb|AAQ06153.1|	ATPase subunit 8 [Sus scrofa]				
gi|312233368|ref|YP_004021579.1|	ATP synthase F0 subunit 8 [Sus scrofa taiwanensis] >gi|347448742|gb|AEO93054.1| ATP synthase F0 subunit 8 (mitochondrion) [Sus scrofa] >gi|347448686|gb|AEO93002.1| ATP synthase F0 subunit 8 (mitochondrion) [Sus scrofa] >gi|347448728|gb|AEO93041.1| A				
gi|347802434|gb|AEP22018.1|	ATP synthase F0 subunit 8 (mitochondrion) [Potamochoerus porcus]				
gi|45826174|gb|AAS77695.1|	ATP synthase F0 subunit 8 [Sus scrofa]				
gi|335282277|ref|XP_003354019.1|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial-like isoform 1 [Sus scrofa]	---	---	---	---
gi|335282279|ref|XP_003354020.1|	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial-like isoform 2 [Sus scrofa]				
gi|157427724|ref|NP_001098770.1|	COP9 signalosome complex subunit 5 [Sus scrofa] >gi|148800597|gb|ABR13016.1| COP9 constitutive photomorphogenic-like subunit 5 [Sus scrofa]	---	---	---	---
gi|226709210|sp|A1XQT2.1|COX6C_PIG	RecName: Full=Cytochrome c oxidase subunit 6C; AltName: Full=Cytochrome c oxidase polypeptide VIc >gi|148225574|ref|NP_001090942.1| cytochrome c oxidase subunit 6C [Sus	0.532	0.35	0.448	0.376

	scrofa] >gi|117660798|gb|ABK55638.1| COX6C [Sus scrofa]				
gi|335297915|ref|XP_003358154.1|	PREDICTED: ankyrin repeat domain-containing protein 40-like [Sus scrofa]	---	---	---	---
gi|194043190|ref|XP_001928943.1|	PREDICTED: protein NipSnap homolog 1 isoform 1 [Sus scrofa]	---	---	---	---
gi|335301406|ref|XP_003359199.1|	PREDICTED: protein NipSnap homolog 1 isoform 2 [Sus scrofa]				
gi|56404321|sp|Q71LE2.3|H33_PIG	RecName: Full=Histone H3.3 >gi|47522626|ref|NP_999095.1| histone H3.3 [Sus scrofa] >gi|311266778|ref|XP_003131242.1| PREDICTED: histone H3.3-like [Sus scrofa] >gi|18643343|gb|AAL76273.1|AF469469_1 histone H3.3A [Sus scrofa]	---	---	---	---
gi|335291702|ref|XP_003356567.1|	PREDICTED: hypothetical protein LOC100627410 [Sus scrofa]				
gi|311259879|ref|XP_003128260.1|	PREDICTED: histone H3.1-like [Sus scrofa] >gi|194039818|ref|XP_001927801.1| PREDICTED: histone H3.1-like [Sus scrofa] >gi|336092201|gb|AEI00724.1| histone cluster 1 [Sus scrofa]				
gi|194039886|ref|XP_001928622.1|	PREDICTED: histone H3.1-like [Sus scrofa]				
gi|350583434|ref|XP_003481517.1|	PREDICTED: histone H3.2 [Sus scrofa] >gi|350583419|ref|XP_003481513.1| PREDICTED: histone H3.2-like [Sus scrofa] >gi|335287027|ref|XP_003355255.1| PREDICTED: histone H3.2-like [Sus scrofa] >gi|347582608|ref|NP_001231571.1| histone H3.2 [Sus scrofa]				
gi|19919838|gb|AAM08402.1|AF490841_1	glutaminase [Sus scrofa]	---	---	---	---
gi|350593725|ref|XP_003133597.3|	PREDICTED: glutaminase kidney isoform, mitochondrial [Sus scrofa]				
gi|335289253|ref|XP_003126970.2|	PREDICTED: nuclear transport factor 2-like [Sus scrofa]	---	---	---	---

gi|335310392|ref|XP_003362011.1|	PREDICTED: nuclear transport factor 2-like [Sus scrofa]				
gi|311276597|ref|XP_003135272.1|	PREDICTED: hypothetical protein LOC100511612 [Sus scrofa]	---	---	---	---
gi|335301488|ref|XP_003359221.1|	PREDICTED: phosphatidylinositol 4-kinase alpha-like [Sus scrofa]	---	---	---	---
gi|335292819|ref|XP_003356805.1|	PREDICTED: activator of 90 kDa heat shock protein ATPase homolog 1-like [Sus scrofa] >gi|194038625|ref|XP_001928925.1| PREDICTED: activator of 90 kDa heat shock protein ATPase homolog 1 [Sus scrofa]	---	---	---	---
gi|298104110|ref|NP_001177118.1|	tricarboxylate transport protein, mitochondrial [Sus scrofa]	---	---	---	---
gi|343790961|ref|NP_001230534.1|	calcium uptake protein 1, mitochondrial [Sus scrofa]	---	---	---	---
gi|350593895|ref|XP_003483787.1|	PREDICTED: E3 ubiquitin-protein ligase RNF25 [Sus scrofa]	---	---	---	---
gi|350596061|ref|XP_003484224.1|	PREDICTED: E3 ubiquitin-protein ligase RNF25-like [Sus scrofa]				
gi|106073338|gb|ABF81978.1|	muscle glycogen phosphorylase [Sus scrofa]	---	---	---	---
gi|335281566|ref|XP_003122636.2|	PREDICTED: glycogen phosphorylase, muscle form isoform 1 [Sus scrofa]				
gi|335281570|ref|XP_003353833.1|	PREDICTED: glycogen phosphorylase, muscle form isoform 3 [Sus scrofa]				
gi|335281568|ref|XP_003353832.1|	PREDICTED: glycogen phosphorylase, muscle form isoform 2 [Sus scrofa]				
gi|300119711|gb|ABF81977.2|	muscle glycogen phosphorylase [Sus scrofa]				
gi|311254844|ref|XP_001929459.2|	PREDICTED: serine/threonine-protein kinase N2 isoform 1 [Sus scrofa]	---	---	---	---
gi|335305150|ref|XP_003134640.2|	PREDICTED: zyxin [Sus scrofa]	---	---	---	---
gi|350591506|ref|XP_003132459.3|	PREDICTED: ruvB-like 1-like, partial [Sus scrofa]	---	---	---	---
gi|311274870|ref|XP_003134	PREDICTED:	---	---	---	---

<table>
<tr><td>490.1|</td><td>1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1-like [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|311243834|ref|XP_003121200.1|</td><td>PREDICTED: splicing factor 3B subunit 5-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350578376|ref|XP_001924454.2|</td><td>PREDICTED: phosphoacetylglucosamine mutase [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|298104097|ref|NP_001177113.1|</td><td>dnaJ homolog subfamily C member 3 precursor [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|308208140|gb|ADO20319.1|</td><td>P58IPK [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|67468552|gb|AAY67906.1|</td><td>centrin 3 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|311249828|ref|XP_003123825.1|</td><td>PREDICTED: centrin-3 [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|349732208|ref|NP_001231856.1|</td><td>mitochondrial ribosomal protein S35 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350583519|ref|XP_003125889.2|</td><td>PREDICTED: round spermatid basic protein 1-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|12229602|sp|Q9XS72.1|CD1A_PIG</td><td>RecName: Full=T-cell surface glycoprotein CD1a; AltName: CD_antigen=CD1a; Flags: Precursor >gi|47523190|ref|NP_998996.1| T-cell surface glycoprotein CD1a precursor [Sus scrofa] >gi|6822270|gb|AAF28737.1| CD1 antigen [Sus scrofa] >gi|4678984|gb|AAD26983.1|AF059492_1 CD1 antigen [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|118764570|dbj|BAF38758.1|</td><td>CD1A antigen [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|118764597|dbj|BAF38778.1|</td><td>CD1A1 antigen [Sus scrofa]</td><td></td><td></td><td></td><td></td></tr>
<tr><td>gi|47523884|ref|NP_999578.1|</td><td>cytochrome P450 2B22 precursor [Sus scrofa] >gi|19071836|dbj|BAB85662.1| cytochrome P450 2B22 [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|335290417|ref|XP_003356174.1|</td><td>PREDICTED: protein RER1-like [Sus scrofa]</td><td>---</td><td>---</td><td>---</td><td>---</td></tr>
<tr><td>gi|350585528|ref|XP_003481</td><td>PREDICTED: protein RER1-like</td><td></td><td></td><td></td><td></td></tr>
</table>

980.1|	[Sus scrofa]				
gi|311260790|ref|XP_003128538.1|	PREDICTED: serine/threonine-protein kinase ULK3 [Sus scrofa]	---	---	---	---
gi|68565351|sp|Q767L8.1|MDC1_PIG	RecName: Full=Mediator of DNA damage checkpoint protein 1 >gi|178056868|ref|NP_001116610.1| mediator of DNA damage checkpoint protein 1 [Sus scrofa] >gi|41529174|dbj|BAD08434.1| NFBD1 [Sus scrofa]	---	---	---	---
gi|311246626|ref|XP_003122268.1|	PREDICTED: uncharacterized protein C9orf78-like [Sus scrofa]	---	---	---	---
gi|350589666|ref|XP_003482893.1|	PREDICTED: malignant T cell-amplified sequence 1-like [Sus scrofa] >gi|350589658|ref|XP_003482889.1| PREDICTED: malignant T cell-amplified sequence 1-like [Sus scrofa]	---	---	---	---
gi|148747342|ref|NP_001092055.1|	AP-3 complex subunit beta-1 [Sus scrofa] >gi|146741314|dbj|BAF62312.1| adaptor-related protein complex 3, beta-1 subunit [Sus scrofa]	---	---	---	---
gi|335287423|ref|XP_001929441.3|	PREDICTED: transcription initiation factor IIB [Sus scrofa]	---	---	---	---
gi|346716308|ref|NP_001231150.1|	RNA-binding protein 14 [Sus scrofa]	---	---	---	---
gi|335308902|ref|XP_003361415.1|	PREDICTED: heterogeneous nuclear ribonucleoprotein L-like [Sus scrofa]	---	---	---	---
gi|350579679|ref|XP_003480661.1|	PREDICTED: niban-like protein 1-like [Sus scrofa]	---	---	---	---
gi|194034889|ref|XP_001929437.1|	PREDICTED: zinc finger FYVE domain-containing protein 19 [Sus scrofa]	---	---	---	---
gi|350589849|ref|XP_003357888.2|	PREDICTED: fibronectin type-III domain-containing protein 3A-like [Sus scrofa]	---	---	---	---
gi|350585300|ref|XP_003127257.3|	PREDICTED: protein ETHE1, mitochondrial-like isoform 1 [Sus scrofa]	---	---	---	---
gi|47522794|ref|NP_999149.1|	small ubiquitin-related modifier 2 precursor [Sus	---	---	---	---

	scrofa] >gi|48429127|sp|P61958.1|SUMO2_PIG RecName: Full=Small ubiquitin-related modifier 2; Short=SUMO-2; AltName: Full=MIF2 suppressor; AltName: Full=SMT3 homolog 2; AltName: Full=Sentrin-2; AltNam				
gi|335300844|ref|XP_003359058.1|	PREDICTED: small ubiquitin-related modifier 3-like [Sus scrofa]				
gi|194039401|ref|XP_001929628.1|	PREDICTED: alanyl-tRNA synthetase, mitochondrial [Sus scrofa]	---	---	---	---
gi|109675377|gb|ABG37112.1|	ataxia-telangiectasia mutated protein splice variant 7 [Sus scrofa]	---	---	---	---
gi|178056824|ref|NP_001116552.1|	serine-protein kinase ATM [Sus scrofa] >gi|152031564|sp|Q6PQD5.2|ATM_PIG RecName: Full=Serine-protein kinase ATM; AltName: Full=Ataxia telangiectasia mutated homolog; Short=A-T mutated homolog >gi|115433705|gb|AAT01608.2| ataxia-telangiectasia mutat				
gi|335302143|ref|XP_003359391.1|	PREDICTED: nucleoplasmin-3-like [Sus scrofa]	---	---	---	---
gi|118403762|ref|NP_001072156.1|	extracellular superoxide dismutase precursor [Sus scrofa] >gi|115522015|gb|ABJ09397.1| extracellular superoxide dismutase [Sus scrofa]	---	---	---	---
gi|58332866|ref|NP_001011509.1|	heme-binding protein 1 [Sus scrofa] >gi|75040507|sp|Q5ISC6.1|HEBP1_PIG RecName: Full=Heme-binding protein 1 >gi|51847749|gb|AAU10512.1| heme-binding protein [Sus scrofa]	---	---	---	---
gi|350594366|ref|XP_003134051.3|	PREDICTED: splicing regulatory glutamine/lysine-rich protein 1, partial [Sus scrofa]	---	---	---	---
gi|311247104|ref|XP_003122481.1|	PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 3 [Sus scrofa]	---	---	---	---
gi|346986279|ref|NP_001231	serine/arginine-rich splicing factor 10	---	---	---	---

297.1|	isoform 2 [Sus scrofa]				
gi|346986281|ref|NP_001231298.1|	serine/arginine-rich splicing factor 10 isoform 1 [Sus scrofa] >gi|338784425|gb|AEI98875.1| serine/arginine-rich splicing factor 10 isoform 2 [Sus scrofa]				
gi|343183422|ref|NP_001230269.1|	proteasome inhibitor PI31 subunit [Sus scrofa]	---	---	---	---
gi|350594770|ref|XP_003483974.1|	PREDICTED: proteasome inhibitor PI31 subunit-like [Sus scrofa]				
gi|335300014|ref|XP_003358759.1|	PREDICTED: von Willebrand factor A domain-containing protein 5B2 [Sus scrofa]	---	---	---	---
gi|335304240|ref|XP_003359898.1|	PREDICTED: tRNA (cytosine(34)-C(5))-methyltransferase isoform 2 [Sus scrofa]	---	---	---	---
gi|335304242|ref|XP_003134206.2|	PREDICTED: tRNA (cytosine(34)-C(5))-methyltransferase isoform 1 [Sus scrofa]				
gi|350596463|ref|XP_003484278.1|	PREDICTED: high mobility group protein 20A-like [Sus scrofa] >gi|350586820|ref|XP_003482285.1| PREDICTED: high mobility group protein 20A [Sus scrofa]	---	---	---	---
gi|194038051|ref|XP_001926686.1|	PREDICTED: nuclear pore complex protein Nup153 [Sus scrofa]	---	---	---	---
gi|347300376|ref|NP_001231482.1|	28S ribosomal protein S9, mitochondrial [Sus scrofa]	---	---	---	---
gi|350583688|ref|XP_003355353.2|	PREDICTED: TBC1 domain family member 22A-like [Sus scrofa]	---	---	---	---
gi|335290628|ref|XP_003356226.1|	PREDICTED: LOW QUALITY PROTEIN: heterochromatin protein 1-binding protein 3 [Sus scrofa]	---	---	---	---
gi|350582787|ref|XP_003481357.1|	PREDICTED: low molecular weight phosphotyrosine protein phosphatase-like [Sus scrofa]	---	---	---	---
gi|350596121|ref|XP_003125455.3|	PREDICTED: hypothetical protein LOC100516434 [Sus scrofa]				
gi|297747311|ref|NP_001177084.1|	coiled-coil-helix-coiled-coil-helix domain containing 1 [Sus scrofa]	---	---	---	---
gi|311247991|ref|XP_003122917.1|	PREDICTED: pyruvate dehydrogenase protein X	---	---	---	---

	component-like isoform 1 [Sus scrofa]				
gi|335282040|ref|XP_003353955.1|	PREDICTED: pyruvate dehydrogenase protein X component-like isoform 2 [Sus scrofa]				
gi|350595129|ref|XP_003360127.2|	PREDICTED: ATP-binding cassette sub-family B member 8, mitochondrial-like [Sus scrofa]	---	---	---	---
gi|1827456|dbj|BAA19177.1|	metallothionein isoform [Sus scrofa]	---	---	---	---
gi|350596343|ref|XP_003361065.2|	PREDICTED: myomegalin-like, partial [Sus scrofa]	---	---	---	---
gi|55776192|gb|AAV65283.1|	cytochrome P450 2C34 [Sus scrofa]	---	---	---	---
gi|335291123|ref|XP_003356402.1|	PREDICTED: receptor-type tyrosine-protein phosphatase mu-like [Sus scrofa]	---	---	---	---
gi|350580860|ref|XP_003123760.3|	PREDICTED: IQ motif containing GTPase activating protein 2 [Sus scrofa]	---	---	---	---
gi|311246904|ref|XP_003122389.1|	PREDICTED: torsin family protein C9orf167-like [Sus scrofa]	---	---	---	---
gi|14269035|gb|AAK57999.1|	immunoglobulin lambda chain [Sus scrofa]	0.318	0.138	0.11	0.073
gi|335310412|ref|XP_003362020.1|	PREDICTED: centrin-2-like [Sus scrofa]	---	---	---	---
gi|194035504|ref|XP_001927493.1|	PREDICTED: vacuolar protein sorting-associated protein 28 homolog [Sus scrofa]	---	---	---	---
gi|39931643|sp|P83686.1|NB5R3_PIG	RecName: Full=NADH-cytochrome b5 reductase 3; Short=B5R; Short=Cytochrome b5 reductase; AltName: Full=Diaphorase-1 >gi|157832094|pdb|1NDH|A Chain A, Crystal Structure Of Nadh-Cytochrome B5 Reductase From Pig Liver At 2.4 Angstroms Resolution	---	---	---	---
gi|311254975|ref|XP_003126030.1|	PREDICTED: NADH-cytochrome b5 reductase 3-like [Sus scrofa]				
gi|1827460|dbj|BAA19179.1|	metallothionein isoform [Sus scrofa]	---	---	---	---
gi|18202364|sp|P79377.2|MT1D_PIG	RecName: Full=Metallothionein-1D; Short=MT-1D; AltName:				

	Full=Metallothionein-ID; Short=MT-ID				
gi|18202365|sp|P79378.1|MT1F_PIG	RecName: Full=Metallothionein-1F; Short=MT-1F; AltName: Full=Metallothionein-IF; Short=MT-IF >gi|1827466|dbj|BAA19182.1| metallothionein isoform [Sus scrofa]				

Data file 2. Differentially expressed proteins

Gene	W0d vs W0d	W1d vs W0d	W3d vs W0d	W5d vs W0d	W7d vs W0d
gi|14269035|gb|AAK57999.1| immunoglobulin lambda chain [Sus scrofa]	1.000	0.318	0.138	0.110	0.073
gi|47522616|ref|NP_999102.1| ubiquitin-like protein FUBI precursor [Sus scrofa] >gi|1628628|gb|AAB52915.1| ubiquitin-like/S30 ribosomal fusion protein [Sus scrofa]	1.000	0.111	0.123	0.101	0.111
gi|164505|gb|AAA51294.1| immunoglobulin gamma-chain, partial [Sus scrofa]	1.000	0.237	0.099	0.217	0.183
gi|311252239|ref|XP_003124992.1| PREDICTED: all-trans-retinol 13,14-reductase [Sus scrofa]	1.000	0.520	0.200	0.307	0.231
gi|50657386|ref|NP_001002801.1| apolipoprotein C-III precursor [Sus scrofa] >gi|416627|sp|P27917.2|APOC3_PIG RecName: Full=Apolipoprotein C-III; Short=Apo-CIII; Short=ApoC-III; AltName: Full=Apolipoprotein C3; Flags: Precursor >gi|164361|gb|AAA30993.1| apolipoprotein C-III [Sus sc	1.000	0.204	0.240	0.217	0.237
gi|47522712|ref|NP_999108.1| pyridoxal kinase [Sus scrofa] >gi|67470293|sp|O46560.1|PDXK_PIG RecName: Full=Pyridoxal kinase; AltName: Full=Pyridoxine kinase >gi|2773404|gb|AAB96794.1| pyridoxal kinase [Sus scrofa]	1.000	0.708	0.261	0.275	0.245
gi|194039884|ref|XP_001928592.1| PREDICTED: histone H2A type 1-like [Sus scrofa]	1.000	0.354	0.344	0.267	0.246
gi|350529356|ref|NP_001231917.1| NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) [Sus scrofa]	1.000	0.217	0.436	0.519	0.262
gi|311248247|ref|XP_003123039.1| PREDICTED: ATP synthase subunit delta, mitochondrial-like isoform 1 [Sus scrofa]	1.000	0.280	0.385	0.346	0.274

gi|311259100|ref|XP_003127931.1| PREDICTED: meprin A subunit beta [Sus scrofa]	1.000	0.371	0.316	0.293	0.284
gi|311254039|ref|XP_003125724.1| PREDICTED: mucosal pentraxin-like [Sus scrofa]	1.000	0.420	0.286	0.227	0.291
gi|264681458|ref|NP_001161123.1| 2-acylglycerol O-acyltransferase 2 [Sus scrofa] >gi|262204904|dbj|BAI48032.1| monoacylglycerol O-acyltransferase 2 [Sus scrofa]	1.000	0.608	0.314	0.222	0.311
gi|298160993|ref|NP_001177169.1| glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic [Sus scrofa]	1.000	0.658	0.354	0.279	0.313
gi|346421378|ref|NP_001231061.1| serpin H1 precursor [Sus scrofa]	1.000	0.667	0.740	0.490	0.320
gi|347300323|ref|NP_001231460.1| thioredoxin-dependent peroxide reductase, mitochondrial [Sus scrofa]	1.000	0.606	0.676	0.513	0.331
gi|198282001|ref|NP_001123683.1| transcription factor A, mitochondrial precursor [Sus scrofa] >gi|75052621|sp|Q5D144.1|TFAM_PIG RecName: Full=Transcription factor A, mitochondrial; Short=mtTFA; Flags: Precursor >gi|60326706|gb|AAX18878.1| mitochondrial transcription factor A [Sus s	1.000	0.487	0.264	0.384	0.359
gi|350586831|ref|XP_003482287.1| PREDICTED: cytochrome c oxidase subunit 5A, mitochondrial-like isoform 1 [Sus scrofa] >gi|350586833|ref|XP_003482288.1| PREDICTED: cytochrome c oxidase subunit 5A, mitochondrial-like isoform 2 [Sus scrofa]	1.000	0.260	0.519	0.473	0.375
gi|226709210|sp|A1XQT2.1|COX6C_PIG RecName: Full=Cytochrome c oxidase subunit 6C; AltName: Full=Cytochrome c oxidase polypeptide VIc >gi|148225574|ref|NP_001090942.1| cytochrome c oxidase subunit 6C [Sus scrofa] >gi|117660798|gb|ABK55638.1| COX6C [Sus scrofa]	1.000	0.532	0.350	0.448	0.376
gi|350594035|ref|XP_003483822.1| PREDICTED: UDP-glucuronosyltransferase 1-10 isoform 3 [Sus scrofa]	1.000	0.561	0.348	0.404	0.378

gi|55926217|ref|NP_001007518.1| cytochrome c oxidase subunit 5B, mitochondrial precursor [Sus scrofa] >gi|75042739|sp|Q5S3G4.1|COX5B_PIG RecName: Full=Cytochrome c oxidase subunit 5B, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide Vb; Flags: Precursor >gi|55583747|g	1.000	0.467	0.331	0.397	0.379
gi|350538593|ref|NP_001233247.1| phosphoglucomutase-1 [Sus scrofa] >gi|321574209|gb|ADW94631.1| phosphoglucomutase 1 [Sus scrofa]	1.000	1.170	0.359	0.319	0.381
gi|350582932|ref|XP_003125549.2| PREDICTED: annexin A13 isoform 2 [Sus scrofa]	1.000	0.380	0.322	0.384	0.386
gi|335290692|ref|XP_003356250.1| PREDICTED: UDP-glucose 4-epimerase [Sus scrofa]	1.000	0.766	0.240	0.268	0.393
gi|350580438|ref|XP_003480823.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7-like [Sus scrofa]	1.000	0.407	0.396	0.258	0.394
gi|350584800|ref|XP_003355778.2| PREDICTED: cytochrome c oxidase subunit 4 isoform 1, mitochondrial-like [Sus scrofa]	1.000	0.500	0.278	0.305	0.408
gi|51317314|sp|P62802.2|H4_PIG RecName: Full=Histone H4 >gi|350583428|ref|XP_003481515.1| PREDICTED: histone H4-like [Sus scrofa] >gi|335291880|ref|XP_003356614.1| PREDICTED: histone H4-like [Sus scrofa] >gi|335287016|ref|XP_003355252.1| PREDICTED: histone H4-like [Sus scrofa] >g	1.000	0.435	0.532	0.445	0.417
gi|311259388|ref|XP_003128071.1| PREDICTED: cytochrome b-c1 complex subunit 6, mitochondrial-like [Sus scrofa]	1.000	0.606	0.434	0.581	0.418
gi|335281280|ref|XP_003122383.2| PREDICTED: apical endosomal glycoprotein [Sus scrofa]	1.000	0.502	0.431	0.468	0.419
gi|311246132|ref|XP_003122091.1| PREDICTED: 39S ribosomal protein L50, mitochondrial-like [Sus scrofa]	1.000	0.428	0.347	0.475	0.429
gi|335281047|ref|XP_003353724.1| PREDICTED: LOW QUALITY PROTEIN:	1.000	0.817	0.381	0.401	0.431

long-chain fatty acid transport protein 4 [Sus scrofa]					
gi|219521964|ref|NP_001137170.1| long-chain-fatty-acid--CoA ligase 3 [Sus scrofa] >gi|217314893|gb|ACK36981.1| acyl-CoA synthetase long-chain family member 3 [Sus scrofa]	1.000	0.559	0.389	0.335	0.432
gi|345090979|ref|NP_001230725.1| NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) [Sus scrofa]	1.000	0.510	0.285	0.248	0.434
gi|335299760|ref|XP_003358667.1| PREDICTED: neprilysin isoform 2 [Sus scrofa] >gi|311269573|ref|XP_003132549.1| PREDICTED: neprilysin isoform 1 [Sus scrofa]	1.000	0.571	0.385	0.373	0.435
gi|311264036|ref|XP_003129968.1| PREDICTED: 40S ribosomal protein S25-like isoform 2 [Sus scrofa] >gi|311264034|ref|XP_003129967.1| PREDICTED: 40S ribosomal protein S25-like isoform 1 [Sus scrofa]	1.000	0.408	0.174	0.194	0.439
gi|164507|gb|AAA51295.1| immunoglobulin gamma-chain [Sus scrofa]	1.000	0.635	0.488	0.566	0.442
gi|335284501|ref|XP_003124603.2| PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial-like [Sus scrofa]	1.000	0.886	0.408	0.423	0.451
gi|3913046|sp|O46409.1|APOA4_PIG RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor >gi|47523830|ref|NP_999553.1| apolipoprotein A-IV precursor [Sus scrofa] >gi|2695742|emb|CAA11020.1| apolipoprotein A-IV [Sus scrofa]	1.000	0.558	0.390	0.478	0.451
gi|3746946|gb|AAC64131.1| phosphoglucomutase 1 [Sus scrofa] >gi|3746944|gb|AAC64130.1| phosphoglucomutase 1 [Sus scrofa]	1.000	0.855	0.665	0.452	0.453
gi|335297609|ref|XP_003358079.1| PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Sus scrofa]	1.000	0.788	0.386	0.515	0.459
gi|85687558|sp|Q4A3R3.1|DMBT1_PIG RecName: Full=Deleted in malignant brain	1.000	0.397	0.523	0.555	0.462

tumors 1 protein; AltName: Full=Hensin; Flags: Precursor >gi|73531021|emb|CAJ27171.1| DMBT1 protein [Sus scrofa]					
gi|335279750|ref|XP_003353424.1| PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 2 [Sus scrofa] >gi|194034801|ref|XP_001925712.1| PREDICTED: normal mucosa of esophagus-specific gene 1 protein-like isoform 1 [Sus scrofa]	1.000	0.512	0.430	0.425	0.466
gi|346986456|ref|NP_001231378.1| nucleoside diphosphate kinase 3 isoform 1 precursor [Sus scrofa]	1.000	0.489	0.953	0.592	0.467
gi|51701269|sp|Q95334.1|AMPE_PIG RecName: Full=Glutamyl aminopeptidase; Short=EAP; AltName: Full=Aminopeptidase A; Short=AP-A; AltName: CD_antigen=CD249 >gi|47522856|ref|NP_999182.1| glutamyl aminopeptidase [Sus scrofa] >gi|1518865|gb|AAB07141.1| aminopeptidase A [Sus scrofa]	1.000	0.519	0.634	0.513	0.467
gi|264681460|ref|NP_001161124.1| acyl carrier protein, mitochondrial [Sus scrofa] >gi|262204908|dbj|BAI48034.1| NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa [Sus scrofa]	1.000	0.350	0.688	0.513	0.468
gi|347658971|ref|NP_001231613.1| ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d [Sus scrofa]	1.000	0.489	0.543	0.446	0.473
gi|350581874|ref|XP_003124716.3| PREDICTED: rab11 family-interacting protein 3-like [Sus scrofa]	1.000	0.509	0.444	0.527	0.474
gi|136192|sp|P09571.2|TRFE_PIG RecName: Full=Serotransferrin; Short=Transferrin; AltName: Full=Beta-1 metal-binding globulin; AltName: Full=Siderophilin >gi|18655907|pdb|1H76|A Chain A, The Crystal Structure Of Diferric Porcine Serum Transferrin	1.000	0.803	0.460	0.442	0.476
gi|347300360|ref|NP_001231474.1| serine/arginine repetitive matrix protein 2 [Sus scrofa]	1.000	0.351	0.966	0.517	0.477
gi|311247022|ref|XP_003122449.1|	1.000	0.425	0.525	0.890	0.481

PREDICTED: cadherin-related family member 5 [Sus scrofa]					
gi|311248380|ref|XP_003123108.1| PREDICTED: cyclic AMP-responsive element-binding protein 3-like protein 3-like isoform 1 [Sus scrofa]	1.000	1.073	0.511	0.489	0.485
gi|194036463|ref|XP_001928684.1| PREDICTED: ras-related protein Rap-1A isoform 1 [Sus scrofa] >gi|335287176|ref|XP_003355289.1| PREDICTED: ras-related protein Rap-1A isoform 2 [Sus scrofa]	1.000	0.726	0.228	0.197	0.487
gi|47523730|ref|NP_999500.1| tropomyosin alpha-4 chain [Sus scrofa] >gi|54039746|sp|P67937.3|TPM4_PIG RecName: Full=Tropomyosin alpha-4 chain; AltName: Full=Tropomyosin-4 >gi|3661527|gb|AAC61744.1| tropomyosin 4 [Sus scrofa] >gi|262263207|dbj|BAI48106.1| tropomyosin 4 [Sus scro	1.000	0.496	0.857	0.634	0.489
gi|222090420|gb|ACM42418.1| carnitine palmitoyltransferase II [Sus scrofa]	1.000	1.253	0.307	0.223	0.492
gi|311257850|ref|XP_003127328.1| PREDICTED: 17-beta-hydroxysteroid dehydrogenase 14-like [Sus scrofa]	1.000	1.285	0.541	0.462	0.492
gi|114689|sp|P13618.1|ATP5J_PIG RecName: Full=ATP synthase-coupling factor 6, mitochondrial; Short=ATPase subunit F6	1.000	0.351	0.632	0.768	0.496
gi|121118|sp|P20305.1|GELS_PIG RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor >gi|164472|gb|AAA31042.1| plasma gelsolin precursor, partial [Sus scrofa] >gi|758306|emb|CAA32077.1| gelsolin [Sus scrofa]	1.000	0.313	0.654	0.571	0.497
gi|335310428|ref|XP_003362028.1| PREDICTED: surfeit locus protein 4-like, partial [Sus scrofa]	1.000	0.968	0.242	0.240	0.501
gi|147225127|emb|CAN13255.1| novel protein similar to butyrophilin family proteins [Sus scrofa]	1.000	0.673	0.418	0.595	0.502

gi|350592201|ref|XP_003359029.2| PREDICTED: hypothetical protein LOC100620809 isoform 1, partial [Sus scrofa]	1.000	0.604	0.664	0.798	0.503
gi|311252952|ref|XP_003125350.1| PREDICTED: ketohexokinase-like isoform 3 [Sus scrofa]	1.000	0.538	0.556	0.633	0.506
gi|297747368|ref|NP_001172101.1| ubiquinol-cytochrome c reductase binding protein [Sus scrofa]	1.000	0.352	0.887	1.053	0.506
gi|311275469|ref|XP_003134753.1| PREDICTED: calumenin isoform 2 [Sus scrofa]	1.000	0.129	1.092	0.556	0.512
gi|356614808|gb|AET25525.1| mitochondrial NADH dehydrogenase Fe-S protein 4 [Sus scrofa]	1.000	0.432	0.564	0.552	0.513
gi|344259276|gb|AEN03335.1| proteasome subunit beta type 6 [Sus scrofa] >gi|344259274|gb|AEN03334.1| proteasome subunit beta type 6 [Sus scrofa]	1.000	2.594	0.743	1.107	0.517
gi|350593495|ref|XP_003483700.1| PREDICTED: LOW QUALITY PROTEIN: glycerol-3-phosphate dehydrogenase, mitochondrial [Sus scrofa]	1.000	0.709	0.479	0.534	0.518
gi|311253020|ref|XP_003125380.1| PREDICTED: putative peptidyl-tRNA hydrolase PTRHD1-like [Sus scrofa]	1.000	0.406	0.392	0.647	0.521
gi|335290029|ref|XP_003356052.1| PREDICTED: nuclear pore glycoprotein p62 [Sus scrofa]	1.000	0.611	0.516	0.685	0.524
gi|47523548|ref|NP_999398.1| glutaredoxin-1 [Sus scrofa] >gi|121442|sp|P12309.2|GLRX1_PIG RecName: Full=Glutaredoxin-1; AltName: Full=Thioltransferase-1; Short=TTase-1 >gi|332368592|gb|AEE61370.1| glutaredoxin [Sus scrofa] >gi|326632057|gb|ADZ99031.1| glutaredoxin [Sus scrofa]	1.000	0.250	0.475	0.406	0.527
gi|350591601|ref|XP_003132498.3| PREDICTED: sodium/potassium-transporting ATPase subunit beta-3-like [Sus scrofa]	1.000	0.747	0.364	0.396	0.531
gi|350585425|ref|XP_003127517.3| PREDICTED: isochorismatase domain-containing protein 2, mitochondrial-like	1.000	0.409	1.462	1.207	0.534

isoform 1, partial [Sus scrofa]					
gi|311255413|ref|XP_001927240.2| PREDICTED: keratin, type II cytoskeletal 79 [Sus scrofa]	1.000	0.422	0.675	0.754	0.534
gi|148887343|sp|Q9MYT8.4|ATP5I_PIG RecName: Full=ATP synthase subunit e, mitochondrial; Short=ATPase subunit e	1.000	0.728	0.624	0.575	0.535
gi|350596379|ref|XP_003484266.1| PREDICTED: vesicle-trafficking protein SEC22b-like [Sus scrofa] >gi|350583458|ref|XP_003481524.1| PREDICTED: vesicle-trafficking protein SEC22b [Sus scrofa]	1.000	0.749	0.447	0.474	0.538
gi|4033507|sp|P08132.2|ANXA4_PIG RecName: Full=Annexin A4; AltName: Full=35-beta calcimedin; AltName: Full=Annexin IV; AltName: Full=Annexin-4; AltName: Full=Chromobindin-4; AltName: Full=Endonexin I; AltName: Full=Lipocortin IV; AltName: Full=P32.5; AltName: Full=PP4-X; AltName: F	1.000	0.597	0.527	0.325	0.539
gi|89216|pir||PT0220 Ig lambda chain V-C region PLC3 - pig (fragment)	1.000	0.534	0.840	0.664	0.541
gi|47522760|ref|NP_999131.1| long-chain 3-ketoacyl-CoA thiolase [Sus scrofa] >gi|6165556|gb|AAF04612.1|AF028007_1 long-chain 3-ketoacyl-CoA thiolase [Sus scrofa]	1.000	0.787	0.430	0.440	0.542
gi|194038067|ref|XP_001927944.1| PREDICTED: protein DEK isoform 1 [Sus scrofa]	1.000	0.564	0.737	1.077	0.544
gi|350583970|ref|XP_003126216.3| PREDICTED: keratin, type II cytoskeletal 75-like [Sus scrofa]	1.000	0.448	0.680	0.760	0.546
gi|350583385|ref|XP_001927905.3| PREDICTED: tuftelin, partial [Sus scrofa]	1.000	0.927	0.974	1.298	0.546
gi|350586576|ref|XP_001929450.4| PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase FKBP5 [Sus scrofa]	1.000	0.774	0.520	0.632	0.547
gi|347922148|ref|NP_001231673.1| charged multivesicular body protein 5 [Sus scrofa]	1.000	0.442	0.792	1.053	0.549
gi|347446687|ref|NP_001231527.1| glucosidase 2	1.000	0.456	0.593	0.593	0.549

subunit beta precursor [Sus scrofa]					
gi|350276134|ref|NP_001231877.1| LETM1 and EF-hand domain-containing protein 1, mitochondrial [Sus scrofa]	1.000	0.568	0.701	0.726	0.558
gi|350586356|ref|XP_003482168.1| PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone]-like [Sus scrofa]	1.000	1.234	0.977	1.294	0.558
gi|311245734|ref|XP_003121939.1| PREDICTED: hypothetical protein LOC100038023 [Sus scrofa] >gi|311245732|ref|XP_003121938.1| PREDICTED: hypothetical protein LOC100038023 [Sus scrofa]	1.000	0.464	0.315	0.345	0.559
gi|335291231|ref|XP_003356440.1| PREDICTED: desmoglein-2 [Sus scrofa]	1.000	0.805	0.477	0.561	0.564
gi|385862179|ref|NP_001245364.1| protein diaphanous homolog 1 [Sus scrofa]	1.000	0.625	0.552	0.764	0.564
gi|311276931|ref|XP_003135414.1| PREDICTED: U3 small nucleolar RNA-associated protein 14 homolog A-like isoform 1 [Sus scrofa]	1.000	0.440	0.533	0.443	0.578
gi|113205854|ref|NP_001038066.1| 40S ribosomal protein S3 [Sus scrofa] >gi|115502828|sp|Q0Z8U2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|110006645|gb|ABG48767.1| ribosomal protein S3 [Sus scrofa]	1.000	0.590	0.430	0.367	0.585
gi|335308509|ref|XP_003361258.1| PREDICTED: microsomal glutathione S-transferase 2-like, partial [Sus scrofa]	1.000	0.711	0.282	0.335	0.585
gi|122142619|sp|Q19S50.1|STAT3_PIG RecName: Full=Signal transducer and activator of transcription 3 >gi|113205774|ref|NP_001038045.1| signal transducer and activator of transcription 3 [Sus scrofa] >gi|315273320|gb|ADU03227.1| signal transducer and activator of transcription 3 isofor	1.000	0.697	0.816	0.729	0.586
gi|54873401|gb|AAV40980.1| heat shock 60 kDa protein 1 [Sus scrofa]	1.000	1.229	0.463	0.450	0.587
gi|335310769|ref|XP_003362184.1| PREDICTED: THO complex subunit 4-like, partial [Sus scrofa]	1.000	0.639	0.688	0.742	0.587
gi|335309593|ref|XP_003361696.1|	1.000	0.419	0.930	0.562	0.587

PREDICTED: 39S ribosomal protein L12, mitochondrial-like, partial [Sus scrofa]					
gi|118675|sp|P09623.1|DLDH_PIG RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial; AltName: Full=Dihydrolipoamide dehydrogenase; Flags: Precursor >gi|47522940|ref|NP_999227.1| dihydrolipoyl dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|164539|gb|AAA31069.1| lipoam	1.000	0.665	0.684	0.543	0.589
gi|311274155|ref|XP_003134215.1| PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial-like [Sus scrofa]	1.000	0.891	0.494	1.079	0.589
gi|148235351|ref|NP_001090944.1| NADH dehydrogenase ubiquinone flavoprotein 2 [Sus scrofa] >gi|117660947|gb|ABK55646.1| NDUFV2 [Sus scrofa]	1.000	0.501	0.531	0.567	0.591
gi|308081427|ref|NP_001183950.1| hydroxysteroid dehydrogenase-like protein 2 [Sus scrofa]	1.000	0.789	0.489	0.551	0.593
gi|350590640|ref|XP_003131788.3| PREDICTED: myosin-Id [Sus scrofa]	1.000	0.750	0.444	0.530	0.597
gi|116551|sp|P04404.2|CMGA_PIG RecName: Full=Chromogranin-A; Short=CgA; Contains: RecName: Full=Pancreastatin; Contains: RecName: Full=Parastatin; Contains: RecName: Full=WE-14; Flags: Precursor >gi|164417|gb|AAA31016.1| chromogranin A precursor, partial [Sus scrofa]	1.000	0.486	0.982	0.552	0.599
gi|46396062|sp|Q865F1.1|MTP_PIG RecName: Full=Microsomal triglyceride transfer protein large subunit; Flags: Precursor >gi|47523450|ref|NP_999350.1| microsomal triglyceride transfer protein large subunit precursor [Sus scrofa] >gi|28974486|gb|AAO61497.1| microsomal triglyceride tr	1.000	0.965	0.461	0.435	0.601
gi|298160936|ref|NP_001177146.1| transmembrane protein C9orf46 [Sus scrofa]	1.000	0.545	0.350	0.364	0.601
gi|47522662|ref|NP_999076.1| membrane-associated progesterone receptor component 1 [Sus	1.000	0.562	0.373	0.608	0.603

scrofa] >gi|6647580|sp|Q95250.3|PGRC1_PIG RecName: Full=Membrane-associated progesterone receptor component 1 >gi|1657409|emb|CAA68050.1| steroid membrane binding protein [Sus scrofa]					
gi|350585373|ref|XP_003127406.3| PREDICTED: myosin-14-like [Sus scrofa]	1.000	0.667	0.776	0.842	0.605
gi|194037554|ref|XP_001929445.1| PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	1.000	0.748	0.423	0.355	0.607
gi|299611|gb|AAB26236.1| cerebroside sulfate activator, CS-Act [swine, kidneys, Peptide, 79 aa]	1.000	0.957	0.947	1.163	0.607
gi|47523768|ref|NP_999520.1| epoxide hydrolase 1 precursor [Sus scrofa] >gi|75069447|sp|P79381.1|HYEP_PIG RecName: Full=Epoxide hydrolase 1; AltName: Full=Epoxide hydratase; AltName: Full=Microsomal epoxide hydrolase >gi|1840391|dbj|BAA19200.1| epoxide hydrolase [Sus scrofa]	1.000	0.733	0.492	0.311	0.608
gi|350582175|ref|XP_003481218.1| PREDICTED: mitochondrial inner membrane protein, partial [Sus scrofa]	1.000	0.546	0.513	0.778	0.610
gi|350584002|ref|XP_003126228.3| PREDICTED: keratin, type I cytoskeletal 18 [Sus scrofa]	1.000	0.903	0.753	0.534	0.611
gi|311258550|ref|XP_003127676.1| PREDICTED: EF-hand domain-containing protein D2-like [Sus scrofa]	1.000	0.429	0.804	0.768	0.614
gi|2258465|gb|AAB94003.1| succinyl-CoA synthetase alpha subunit [Sus scrofa]	1.000	0.610	0.582	0.448	0.616
gi|311253799|ref|XP_001926739.2| PREDICTED: ras-related protein Rab-2A [Sus scrofa]	1.000	1.027	0.390	0.427	0.617
gi|349732227|ref|NP_001231859.1| heterogeneous nuclear ribonucleoprotein M [Sus scrofa]	1.000	0.574	0.507	0.477	0.618
gi|5542425|pdb|1QPW|D Chain D, Crystal Structure Determination Of Porcine Hemoglobin At 1.8a Resolution >gi|5542423|pdb|1QPW|B Chain B, Crystal Structure Determination Of Porcine Hemoglobin At 1.8a	1.000	0.842	0.728	0.606	0.619

Resolution >gi|809285|pdb|2PGH|D Chain D, Structure Determination Of Aquo					
gi|297632426|ref|NP_001172096.1| signal sequence receptor, alpha [Sus scrofa]	1.000	0.756	0.387	0.391	0.624
gi|47523792|ref|NP_999532.1| catenin beta-1 [Sus scrofa] >gi|167834655|gb|ACA03158.1| beta-catenin [Sus scrofa] >gi|18146999|dbj|BAB82984.1| beta-catenin [Sus scrofa]	1.000	0.615	0.612	0.533	0.625
gi|311254317|ref|XP_001927973.2| PREDICTED: cingulin-like [Sus scrofa]	1.000	0.549	0.991	0.920	0.625
gi|194038586|ref|XP_001926746.1| PREDICTED: transmembrane emp24 domain-containing protein 10 [Sus scrofa]	1.000	0.582	0.399	0.461	0.628
gi|47522864|ref|NP_999186.1| unconventional myosin-VI [Sus scrofa] >gi|75039721|sp|Q29122.1|MYO6_PIG RecName: Full=Unconventional myosin-VI; AltName: Full=Unconventional myosin-6 >gi|516155|emb|CAA84559.1| unconventional myosin [Sus scrofa]	1.000	0.847	0.744	0.911	0.630
gi|343780950|ref|NP_001230488.1| 39S ribosomal protein L40, mitochondrial isoform 1 [Sus scrofa]	1.000	0.573	0.577	0.466	0.630
gi|297747302|ref|NP_001172115.1| aspartyl aminopeptidase [Sus scrofa]	1.000	0.913	2.217	1.765	0.631
gi|311257294|ref|XP_003127050.1| PREDICTED: cytochrome b-c1 complex subunit Rieske, mitochondrial-like [Sus scrofa]	1.000	0.723	0.545	0.722	0.632
gi|347582660|ref|NP_001231584.1| mesencephalic astrocyte-derived neurotrophic factor precursor [Sus scrofa] >gi|350591263|ref|XP_003483237.1| PREDICTED: mesencephalic astrocyte-derived neurotrophic factor [Sus scrofa] >gi|306563669|gb|ADN03186.1| mesencephalic astrocyte-derived neu	1.000	0.557	0.812	0.705	0.639
gi|350579385|ref|XP_001925894.4| PREDICTED: glyoxylate reductase/hydroxypyruvate reductase [Sus scrofa]	1.000	0.895	0.493	0.623	0.640
gi|47523892|ref|NP_999584.1| epithelial cell adhesion molecule precursor [Sus	1.000	0.935	0.504	0.553	0.642

scrofa] >gi|75045149|sp|Q75QW1.1|EPCAM_PIG RecName: Full=Epithelial cell adhesion molecule; Short=Ep-CAM; AltName: Full=Tumor-associated calcium signal transducer 1; AltName: CD_antigen=CD326; Flags:					
gi|350591864|ref|XP_001926353.4| PREDICTED: LOW QUALITY PROTEIN: melanotransferrin [Sus scrofa]	1.000	0.828	0.796	1.070	0.643
gi|335285948|ref|XP_003131991.2| PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like isoform 1 [Sus scrofa]	1.000	1.314	0.725	0.661	0.646
gi|262072813|dbj|BAI47714.1| hydroxysteroid (17-beta) dehydrogenase 12 [Sus scrofa]	1.000	0.728	0.376	0.498	0.648
gi|335292368|ref|XP_001926489.3| PREDICTED: calcium and integrin-binding protein 1 [Sus scrofa]	1.000	0.454	0.700	0.817	0.648
gi|350587465|ref|XP_003128987.3| PREDICTED: RNA-binding protein 47-like isoform 1 [Sus scrofa]	1.000	0.543	0.435	0.259	0.650
gi|311273235|ref|XP_003133777.1| PREDICTED: intestinal-type alkaline phosphatase-like isoform 2 [Sus scrofa]	1.000	0.879	1.307	2.392	0.652
gi|256838109|ref|NP_001157984.1| phosphate carrier protein, mitochondrial [Sus scrofa] >gi|255964672|gb|ACU44653.1| solute carrier family 25 member 3 [Sus scrofa]	1.000	0.704	0.387	0.381	0.659
gi|350596559|ref|XP_003361362.2| PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 3-like, partial [Sus scrofa]	1.000	0.727	0.735	0.828	0.662
gi|350582036|ref|XP_003481179.1| PREDICTED: U5 small nuclear ribonucleoprotein 200 kDa helicase [Sus scrofa]	1.000	0.686	0.793	0.968	0.662
gi|359465576|ref|NP_001240753.1| A-kinase anchor protein 9 [Sus scrofa]	1.000	0.772	1.137	0.982	0.663
gi|350276172|ref|NP_001231880.1| leucine-rich repeat-containing protein 59 [Sus scrofa]	1.000	0.495	0.761	0.604	0.665
gi|335302040|ref|XP_001927564.2| PREDICTED: delta-1-pyrroline-5-carboxylate synthase isoform 1 [Sus scrofa]	1.000	0.834	0.466	0.373	0.665
gi|350589440|ref|XP_003130687.3|	1.000	0.268	0.679	0.831	0.666

PREDICTED: Golgi membrane protein 1-like [Sus scrofa]					
gi|164359|gb|AAA30992.1| apolipoprotein A-I [Sus scrofa]	1.000	1.067	0.411	0.499	0.666
gi|54020966|ref|NP_001005726.1| annexin A2 [Sus scrofa] >gi|148876771|sp|P19620.4|ANXA2_PIG RecName: Full=Annexin A2; AltName: Full=Annexin II; AltName: Full=Annexin-2; AltName: Full=Calpactin I heavy chain; AltName: Full=Calpactin-1 heavy chain; AltName: Full=Chromobindin-8; AltN	1.000	0.905	0.473	0.453	0.667
gi|311273928|ref|XP_003134106.1| PREDICTED: nucleophosmin-like isoform 2 [Sus scrofa]	1.000	0.919	1.022	1.439	0.668
gi|305855176|ref|NP_001182260.1| cleavage and polyadenylation specificity factor subunit 6 [Sus scrofa] >gi|285818464|gb|ADC38905.1| cleavage and polyadenylation specific factor 6 [Sus scrofa]	1.000	0.757	1.403	1.440	0.672
gi|194038359|ref|XP_001929028.1| PREDICTED: glutaredoxin-related protein 5, mitochondrial-like [Sus scrofa]	1.000	1.169	0.703	0.919	0.677
gi|335297415|ref|XP_003358038.1| PREDICTED: 60S ribosomal protein L38-like isoform 2 [Sus scrofa] >gi|311266862|ref|XP_003131289.1| PREDICTED: 60S ribosomal protein L38-like isoform 1 [Sus scrofa]	1.000	0.659	0.354	0.290	0.677
gi|350594715|ref|XP_001927122.3| PREDICTED: adipocyte plasma membrane-associated protein-like [Sus scrofa]	1.000	0.721	0.215	0.200	0.678
gi|147899784|ref|NP_001090887.1| elongation factor 1-alpha 1 [Sus scrofa] >gi|223019599|emb|CAX36487.1| eukaryotic translation elongation factor 1 alpha 1 [Sus scrofa] >gi|223019597|emb|CAX36486.1| eukaryotic translation elongation factor 1 alpha 1 [Sus scrofa] >gi|110287842|gb|ABG	1.000	0.764	0.570	0.438	0.680
gi|346986400|ref|NP_001231351.1| kunitz-type protease inhibitor 1 precursor [Sus scrofa]	1.000	0.573	0.736	0.762	0.681
gi|311259030|ref|XP_003127902.1| PREDICTED: small nuclear ribonucleoprotein Sm D1-like [Sus scrofa]	1.000	1.410	1.528	1.301	0.682

gi|37962872|gb|AAR05785.1| cytochrome c oxidase subunit 2 [Sus scrofa] >gi|162423271|gb|ABX89412.1| cytochrome c oxidase subunit 2 [Sus scrofa]	1.000	0.868	0.423	0.338	0.684
gi|335310669|ref|XP_003362140.1| PREDICTED: hypothetical protein LOC100622909 [Sus scrofa]	1.000	0.605	0.902	0.685	0.684
gi|349501107|ref|NP_001231795.1| ribosomal protein, large, P2 [Sus scrofa]	1.000	0.630	1.484	1.372	0.685
gi|47523888|ref|NP_999583.1| ADP/ATP translocase 3 [Sus scrofa] >gi|52000613|sp|Q6QRN9.3|ADT3_PIG RecName: Full=ADP/ATP translocase 3; AltName: Full=ADP,ATP carrier protein 3; AltName: Full=Adenine nucleotide translocator 3; Short=ANT 3; AltName: Full=Solute carrier family 25 m	1.000	0.649	0.471	0.325	0.687
gi|350594057|ref|XP_003359743.2| PREDICTED: leucine-rich repeat flightless-interacting protein 2-like [Sus scrofa]	1.000	0.725	0.781	1.048	0.688
gi|148222268|ref|NP_001090952.1| tropomyosin alpha-1 chain [Sus scrofa] >gi|158931149|sp|P42639.2|TPM1_PIG RecName: Full=Tropomyosin alpha-1 chain; AltName: Full=Alpha-tropomyosin; AltName: Full=Tropomyosin-1 >gi|117661180|gb|ABK55659.1| TPM1 [Sus scrofa]	1.000	0.641	1.115	1.002	0.688
gi|290463427|sp|Q0QF01.2|DHSA_PIG RecName: Full=Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial; AltName: Full=Flavoprotein subunit of complex II; Short=Fp; Flags: Precursor	1.000	0.678	0.605	0.674	0.695
gi|311268489|ref|XP_003132080.1| PREDICTED: fatty aldehyde dehydrogenase-like [Sus scrofa]	1.000	0.804	0.424	0.401	0.695
gi|311251336|ref|XP_003124563.1| PREDICTED: elongation factor Tu, mitochondrial-like [Sus scrofa]	1.000	0.973	0.501	0.508	0.696
gi|164302|gb|AAA30983.1| alpha-1 acid glycoprotein, partial [Sus scrofa]	1.000	0.263	0.696	0.494	0.699
gi|54039371|sp|P62272.3|RS18_PIG RecName: Full=40S ribosomal protein S18 >gi|47522714|ref|NP_999105.1| 40S	1.000	0.629	0.226	0.178	0.700

ribosomal protein S18 [Sus scrofa] >gi|1841304|dbj|BAA19211.1| ribosomal protein [Sus scrofa]					
gi|350593231|ref|XP_003359478.2| PREDICTED: lactase-phlorizin hydrolase-like [Sus scrofa]	1.000	0.691	0.999	0.733	0.700
gi|345100481|pdb|1C9P|A Chain A, Complex Of Bdellastasin With Porcine Trypsin >gi|3318722|pdb|1AN1|E Chain E, Leech-Derived Tryptase InhibitorTRYPSIN COMPLEX	1.000	0.612	0.894	0.765	0.701
gi|156120140|ref|NP_001095287.1| helicase SKI2W [Sus scrofa] >gi|148724903|emb|CAN87691.1| superkiller viralicidic activity 2-like (S. cerevisiae) [Sus scrofa]	1.000	0.943	1.061	1.130	0.702
gi|335304027|ref|XP_003134070.2| PREDICTED: 28S ribosomal protein S36, mitochondrial-like [Sus scrofa]	1.000	0.469	0.658	0.771	0.704
gi|335288150|ref|XP_003126347.2| PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus scrofa]	1.000	0.776	0.558	0.530	0.707
gi|47523726|ref|NP_999498.1| dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Sus scrofa] >gi|75056164|sp|Q9GMB0.1|RPN1_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1; AltName: Full=Dolichyl-diphosph	1.000	0.625	0.627	0.547	0.709
gi|78172717|gb|ABB29449.1| transporter associated with antigen processing 1 [Sus scrofa]	1.000	0.541	0.382	0.447	0.711
gi|164318|gb|AAA30988.1| albumin, partial [Sus scrofa]	1.000	1.129	0.611	0.569	0.712
gi|346644799|ref|NP_001231157.1| thymopoietin [Sus scrofa]	1.000	0.723	0.984	0.854	0.716
gi|335299041|ref|XP_001926664.3| PREDICTED: cytochrome b-c1 complex subunit 1, mitochondrial [Sus scrofa]	1.000	0.764	0.572	0.812	0.720
gi|350589278|ref|XP_003130571.3| PREDICTED: melanoma inhibitory activity protein 3-like, partial [Sus scrofa]	1.000	0.752	1.073	0.757	0.720
gi|164382|gb|AAA31002.1| Na+, K+-ATPase	1.000	0.797	0.422	0.473	0.725

alpha-subunit precursor [Sus scrofa]					
gi|347300243|ref|NP_001231430.1| glutamate dehydrogenase 1, mitochondrial [Sus scrofa]	1.000	0.826	0.563	0.527	0.727
gi|47522750|ref|NP_999125.1| voltage-dependent anion-selective channel protein 1 [Sus scrofa] >gi|75050406|sp|Q9MZ16.3|VDAC1_PIG RecName: Full=Voltage-dependent anion-selective channel protein 1; Short=VDAC-1 >gi|8745552|gb|AAF78963.1|AF268461_1 voltage-dependent anion channel	1.000	0.661	0.450	0.434	0.729
gi|8569334|pdb|1EIO|A Chain A, Ileal Lipid Binding Protein In Complex With Glycocholate	1.000	1.497	1.823	0.959	0.734
gi|448581|prf||1917268B pyruvate dehydrogenase:SUBUNIT=beta	1.000	1.030	0.518	0.699	0.734
gi|350584479|ref|XP_003126643.3| PREDICTED: bcl-2-like protein 13 [Sus scrofa]	1.000	0.678	1.003	0.721	0.739
gi|347300207|ref|NP_001231417.1| nucleobindin-1 precursor [Sus scrofa]	1.000	0.672	1.095	1.007	0.739
gi|343072|gb|AAA32030.1| ATPase 8, partial (mitochondrion) [Sus scrofa]	1.000	0.683	0.285	0.431	0.745
gi|1346670|sp|P04175.2|NCPR_PIG RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	1.000	0.722	0.432	0.709	0.752
gi|311270597|ref|XP_003132922.1| PREDICTED: 26S proteasome non-ATPase regulatory subunit 9-like [Sus scrofa]	1.000	0.599	1.217	1.425	0.755
gi|178056556|ref|NP_001116620.1| probable aminopeptidase NPEPL1 [Sus scrofa] >gi|147223400|emb|CAN13197.1| aminopeptidase-like 1 [Sus scrofa]	1.000	1.378	2.150	2.596	0.755
gi|12231040|sp|Q29048.2|VATA_PIG RecName: Full=V-type proton ATPase catalytic subunit A; Short=V-ATPase subunit A; AltName: Full=V-ATPase 69 kDa subunit; AltName: Full=Vacuolar proton pump subunit alpha	1.000	0.868	0.558	0.642	0.755
gi|311274849|ref|XP_001925742.2| PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 1B [Sus scrofa]	1.000	0.672	1.313	0.928	0.755
gi|113205886|ref|NP_001038075.1| nucleoside diphosphate kinase B [Sus scrofa] >gi|115311824|sp|Q2EN76.1|NDKB_PIG RecName: Full=Nucleoside diphosphate kinase	1.000	0.829	1.823	1.107	0.757

B; Short=NDK B; Short=NDP kinase B; AltName: Full=Histidine protein kinase NDKB >gi|87047646|gb|ABD18456.1| nm23-H2 [Sus scro					
gi|350580184|ref|XP_003353965.2| PREDICTED: reticulocalbin-1-like isoform 2 [Sus scrofa]	1.000	0.631	0.986	1.263	0.758
gi|350596353|ref|XP_003361080.2| PREDICTED: gamma-soluble NSF attachment protein-like [Sus scrofa]	1.000	0.767	0.636	0.846	0.758
gi|342349319|ref|NP_001230139.1| calnexin precursor [Sus scrofa]	1.000	0.685	0.549	0.700	0.759
gi|194036296|ref|XP_001926524.1| PREDICTED: splicing factor 3B subunit 4 [Sus scrofa]	1.000	0.862	1.231	1.161	0.760
gi|350580651|ref|XP_003480867.1| PREDICTED: scaffold attachment factor B1-like isoform 2 [Sus scrofa]	1.000	0.687	1.076	0.762	0.763
gi|335278800|ref|XP_003121142.2| PREDICTED: afadin [Sus scrofa]	1.000	0.568	1.225	1.062	0.765
gi|350582773|ref|XP_003481353.1| PREDICTED: 40S ribosomal protein S7-like isoform 2 [Sus scrofa] >gi|350582771|ref|XP_003481352.1| PREDICTED: 40S ribosomal protein S7-like isoform 1 [Sus scrofa]	1.000	0.624	0.404	0.255	0.765
gi|346421419|ref|NP_001231084.1| lysosome membrane protein 2 precursor [Sus scrofa]	1.000	0.696	0.520	0.332	0.768
gi|335285324|ref|XP_003354827.1| PREDICTED: prenylcysteine oxidase-like [Sus scrofa]	1.000	1.016	0.403	0.147	0.770
gi|47522680|ref|NP_999069.1| neutral alpha-glucosidase AB precursor [Sus scrofa] >gi|54037147|sp|P79403.1|GANAB_PIG RecName: Full=Neutral alpha-glucosidase AB; AltName: Full=Alpha-glucosidase 2; AltName: Full=Glucosidase II subunit alpha; Flags: Precursor >gi|1890664|gb|AAB4975	1.000	0.917	0.548	0.547	0.771
gi|304365428|ref|NP_001182041.1| protein disulfide-isomerase A3 precursor [Sus scrofa] >gi|301016769|dbj|BAJ11757.1| glucose regulated protein 58 [Sus scrofa]	1.000	0.492	1.192	1.152	0.772
gi|1710093|sp|P50121.2|RET2_PIG RecName:	1.000	1.386	0.766	0.800	0.777

Full=Retinol-binding protein 2; AltName: Full=Cellular retinol-binding protein II; Short=CRBP-II >gi|55741711|ref|NP_999616.1| retinol-binding protein 2 [Sus scrofa] >gi|455523|emb|CAA54729.1| cellular retinol binding protein II [Sus scrofa					
gi|305855170|ref|NP_001182250.1| long-chain-fatty-acid--CoA ligase 5 [Sus scrofa] >gi|285818418|gb|ADC38882.1| acyl-CoA synthetase long-chain family member 5 [Sus scrofa]	1.000	0.820	0.530	0.574	0.782
gi|178056623|ref|NP_001116685.1| vesicle-associated membrane protein-associated protein B [Sus scrofa] >gi|160210890|sp|A5GFS8.1|VAPB_PIG RecName: Full=Vesicle-associated membrane protein-associated protein B; Short=VAMP-B; Short=VAMP-associated protein B; Short=VAP-B >gi|147223393	1.000	0.473	0.849	0.623	0.782
gi|47522846|ref|NP_999175.1| ATP-binding cassette sub-family G member 2 [Sus scrofa] >gi|68051987|sp|Q8MIB3.1|ABCG2_PIG RecName: Full=ATP-binding cassette sub-family G member 2; AltName: Full=Brain multidrug resistance protein; AltName: CD_antigen=CD338 >gi|21530795|emb|CAD1278	1.000	1.247	0.674	0.582	0.785
gi|1921|emb|CAA33169.1| unnamed protein product [Sus scrofa]	1.000	0.735	0.558	0.573	0.786
gi|47522608|ref|NP_999106.1| dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor [Sus scrofa] >gi|75056105|sp|Q9GL01.1|RPN2_PIG RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosph	1.000	0.966	0.550	0.412	0.788
gi|335293186|ref|XP_003356895.1| PREDICTED: grpE protein homolog 1, mitochondrial-like isoform 1 [Sus scrofa]	1.000	0.674	0.743	0.608	0.791
gi|311267276|ref|XP_003131485.1| PREDICTED: keratin, type I cytoskeletal 19-like [Sus scrofa]	1.000	0.627	0.634	0.765	0.792

gi|230506|pdb|2FBP|A Chain A, Structure Refinement Of Fructose-1,6-Bisphosphatase And Its Fructose 2,6-Bisphosphate Complex At 2.8 Angstroms Resolution >gi|230507|pdb|2FBP|B Chain B, Structure Refinement Of Fructose-1,6-Bisphosphatase And Its Fructose 2,6-Bisphosphate C	1.000	1.622	1.109	0.814	0.793
gi|335281686|ref|XP_003353872.1| PREDICTED: UBX domain-containing protein 1-like [Sus scrofa]	1.000	0.843	1.119	0.973	0.796
gi|340007402|ref|NP_001229989.1| RAB10, member RAS oncogene family [Sus scrofa]	1.000	0.916	0.388	0.456	0.797
gi|343790888|ref|NP_001230502.1| uncharacterized protein LOC100627352 [Sus scrofa]	1.000	0.852	0.333	0.465	0.797
gi|194037097|ref|XP_001927840.1| PREDICTED: carbonic anhydrase 2 [Sus scrofa]	1.000	0.798	1.380	1.495	0.798
gi|297591975|ref|NP_001172071.1| ATP synthase subunit alpha, mitochondrial [Sus scrofa] >gi|187370717|gb|ACD02421.1| cardiac muscle ATP synthase H+ transporting mitochondrial F1 complex alpha subunit 1 [Sus scrofa]	1.000	0.768	0.706	0.723	0.799
gi|350594669|ref|XP_001926037.4| PREDICTED: ribosome-binding protein 1 [Sus scrofa]	1.000	0.571	1.008	0.992	0.800
gi|194042439|ref|XP_001928012.1| PREDICTED: ATPase family AAA domain-containing protein 1 isoform 1 [Sus scrofa]	1.000	0.481	1.189	1.064	0.800
gi|346644830|ref|NP_001231167.1| sulfide:quinone oxidoreductase, mitochondrial [Sus scrofa]	1.000	0.889	0.519	0.467	0.803
gi|335309807|ref|XP_003361778.1| PREDICTED: delta-aminolevulinic acid dehydratase-like, partial [Sus scrofa]	1.000	0.853	1.284	1.316	0.803
gi|148747594|ref|NP_001092068.1| 60S acidic ribosomal protein P0 [Sus scrofa] >gi|182705234|sp|Q29214.2|RLA0_PIG RecName: Full=60S acidic ribosomal protein P0; AltName: Full=60S ribosomal protein L10E >gi|83854099|gb|ABC47963.1| ribosomal phosphoprotein large PO subunit [Sus scrofa	1.000	0.785	0.612	0.651	0.807

gi|1236646|gb|AAC48775.1| ch4 and secrete domains of swine IgM [Sus scrofa]	1.000	0.779	0.684	0.478	0.807
gi|311277261|ref|XP_003135572.1| PREDICTED: 55 kDa erythrocyte membrane protein-like isoform 1 [Sus scrofa]	1.000	0.801	0.558	0.535	0.811
gi|47522948|ref|NP_999231.1| D-amino-acid oxidase [Sus scrofa] >gi|129305|sp|P00371.2|OXDA_PIG RecName: Full=D-amino-acid oxidase; Short=DAAO; Short=DAMOX; Short=DAO >gi|164306|gb|AAA30985.1| D-amino acid oxidase [Sus scrofa] >gi|48425898|pdb|1VE9|A Chain A, Porcine Kidney D-Am	1.000	1.109	0.677	0.555	0.816
gi|335299628|ref|XP_001926139.3| PREDICTED: coatomer subunit beta~ [Sus scrofa]	1.000	0.808	0.654	0.856	0.817
gi|311247240|ref|XP_003122553.1| PREDICTED: splicing factor 3B subunit 2 [Sus scrofa]	1.000	0.716	1.012	0.897	0.818
gi|194037681|ref|XP_001926390.1| PREDICTED: early endosome antigen 1 [Sus scrofa]	1.000	0.749	1.226	1.334	0.818
gi|335310208|ref|XP_003361930.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4-like [Sus scrofa]	1.000	1.201	0.436	0.449	0.822
gi|311254645|ref|XP_003125912.1| PREDICTED: EPS8-like 3 [Sus scrofa]	1.000	0.870	0.538	0.696	0.824
gi|194042318|ref|XP_001928917.1| PREDICTED: putative hexokinase HKDC1 [Sus scrofa]	1.000	0.716	0.557	0.679	0.825
gi|335283403|ref|XP_003123930.2| PREDICTED: lamin-B1 [Sus scrofa]	1.000	0.698	0.956	0.966	0.827
gi|343887442|ref|NP_001230623.1| heterogeneous nuclear ribonucleoprotein C (C1/C2) 2 [Sus scrofa]	1.000	0.738	0.645	0.614	0.827
gi|47523672|ref|NP_999468.1| 2~-5~-oligoadenylate synthase 1 [Sus scrofa] >gi|6226834|sp|Q29599.3|OAS1_PIG RecName: Full=2~-5~-oligoadenylate synthase 1; Short=(2-5~)oligo(A) synthase 1; Short=2-5A synthase 1; AltName: Full=p42	1.000	0.885	0.462	0.342	0.831

OAS >gi|3451331|emb|CAA12397.1| 2~-5~ oligoadenyla					
gi|353819|prf||1106188C cytochrome b5	1.000	0.588	0.840	0.666	0.833
gi|350587379|ref|XP_003482398.1| PREDICTED: putative aminopeptidase C13A11.05-like [Sus scrofa]	1.000	2.105	2.722	3.623	0.835
gi|194042189|ref|XP_001924213.1| PREDICTED: annexin A11 [Sus scrofa]	1.000	1.218	0.642	0.780	0.835
gi|311247118|ref|XP_003122486.1| PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial-like isoform 1 [Sus scrofa]	1.000	1.053	0.587	0.656	0.836
gi|387912908|sp|P28491.3|CALR_PIG RecName: Full=Calreticulin; AltName: Full=CRP55; AltName: Full=Calregulin; AltName: Full=Endoplasmic reticulum resident protein 60; Short=ERp60; AltName: Full=HACBP; Flags: Precursor >gi|291622246|ref|NP_001167604.1| calreticulin precursor [Sus scro	1.000	0.910	0.589	0.581	0.836
gi|183228163|gb|ACC59785.1| PRP19/PSO4 pre-mRNA processing factor 19-like protien [Sus scrofa]	1.000	1.040	1.003	0.467	0.837
gi|350588303|ref|XP_003129732.3| PREDICTED: serine/threonine-protein kinase PAK 1-like [Sus scrofa]	1.000	1.086	0.799	0.761	0.840
gi|335306763|ref|XP_003360560.1| PREDICTED: ubiquitin-like protein 4A-like isoform 1 [Sus scrofa]	1.000	0.800	0.778	0.894	0.843
gi|311269853|ref|XP_003132661.1| PREDICTED: choline-phosphate cytidylyltransferase A [Sus scrofa]	1.000	0.689	0.563	0.584	0.844
gi|37934198|gb|AAP68768.1| 2,4-dienoyl-CoA reductase [Sus scrofa]	1.000	1.330	0.905	0.922	0.844
gi|311259162|ref|XP_003127965.1| PREDICTED: far upstream element-binding protein 1 [Sus scrofa]	1.000	0.590	0.988	0.965	0.846
gi|194039403|ref|XP_001929632.1| PREDICTED: CDC5 cell division cycle 5-like [Sus scrofa]	1.000	0.541	0.668	0.720	0.847
gi|1165145|emb|CAA64477.1| annexin I [Sus scrofa]	1.000	0.423	0.578	0.912	0.848

gi|349585085|ref|NP_001231804.1| RAB11B, member RAS oncogene family [Sus scrofa]	1.000	1.031	0.664	0.520	0.848
gi|311260817|ref|XP_001925607.2| PREDICTED: protein PML isoform 1 [Sus scrofa]	1.000	0.605	0.668	0.609	0.849
gi|350586335|ref|XP_003356548.2| PREDICTED: nuclease-sensitive element-binding protein 1-like [Sus scrofa]	1.000	0.357	1.959	0.998	0.852
gi|158514030|sp|A1XQU3.1|RL14_PIG RecName: Full=60S ribosomal protein L14 >gi|148237282|ref|NP_001090947.1| 60S ribosomal protein L14 [Sus scrofa] >gi|117661006|gb|ABK55649.1| RPL14 [Sus scrofa]	1.000	1.034	0.626	0.479	0.855
gi|311273371|ref|XP_003133833.1| PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial-like [Sus scrofa]	1.000	0.942	0.553	0.566	0.856
gi|146741296|dbj|BAF62303.1| keratin 1 [Sus scrofa]	1.000	0.933	1.375	0.846	0.856
gi|345090993|ref|NP_001230731.1| RAB8A, member RAS oncogene family [Sus scrofa]	1.000	0.701	0.514	0.564	0.856
gi|343887420|ref|NP_001230609.1| transcription elongation factor A protein 1 [Sus scrofa]	1.000	0.935	1.433	1.330	0.857
gi|311275164|ref|XP_003134601.1| PREDICTED: amiloride-sensitive amine oxidase [copper-containing] [Sus scrofa]	1.000	0.807	0.699	0.984	0.858
gi|171986635|gb|ACB59309.1| intelectin 2 [Sus scrofa]	1.000	1.352	0.631	0.358	0.858
gi|311276040|ref|XP_003135024.1| PREDICTED: LOW QUALITY PROTEIN: acyl-coenzyme A thioesterase 9, mitochondrial-like [Sus scrofa]	1.000	1.339	0.598	0.958	0.858
gi|350584106|ref|XP_003481667.1| PREDICTED: SWI/SNF complex subunit SMARCC2 [Sus scrofa]	1.000	0.755	0.898	0.717	0.863
gi|132566481|gb|ABO34136.1| bactericidal permeability increasing protein [Sus scrofa]	1.000	1.007	0.321	0.341	0.863
gi|311267326|ref|XP_003131510.1| PREDICTED: keratin, type I cytoskeletal 20-like [Sus scrofa]	1.000	0.640	0.647	0.745	0.864
gi|350581449|ref|XP_003481037.1|	1.000	1.102	0.709	0.749	0.867

PREDICTED: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2-like [Sus scrofa] >gi|311251041|ref|XP_003124417.1| PREDICTED: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2-like isoform 2 [Sus scrofa]					
gi|350539577|ref|NP_001233167.1| coatomer subunit gamma-2 [Sus scrofa] >gi|301087607|gb|ADK56184.1| coatomer protein complex subunit gamma 2 [Sus scrofa]	1.000	1.059	0.472	0.381	0.867
gi|238018148|ref|NP_001153899.1| ADP-ribosylation factor 1 [Sus scrofa] >gi|212725657|gb|ACJ38117.1| ADP-ribosylation factor 1 [Sus scrofa] >gi|237638742|gb|ACR07973.1| ADP-ribosylation factor 1 [Sus scrofa]	1.000	0.779	0.435	0.407	0.868
gi|345441771|ref|NP_001230857.1| aldolase C, fructose-bisphosphate [Sus scrofa]	1.000	1.123	0.698	1.148	0.868
gi|350595677|ref|XP_003360362.2| PREDICTED: GRIP1-associated protein 1 [Sus scrofa]	1.000	0.784	1.938	1.963	0.870
gi|335296241|ref|XP_003357722.1| PREDICTED: ladinin-1-like [Sus scrofa]	1.000	0.587	0.680	0.710	0.870
gi|350591788|ref|XP_003358782.2| PREDICTED: hypothetical protein LOC448846 [Sus scrofa]	1.000	1.439	0.714	0.869	0.874
gi|335310107|ref|XP_003361890.1| PREDICTED: non-POU domain-containing octamer-binding protein [Sus scrofa]	1.000	1.266	0.594	0.636	0.877
gi|194043083|ref|XP_001928729.1| PREDICTED: malectin-like [Sus scrofa]	1.000	0.792	0.388	0.530	0.878
gi|194043861|ref|XP_001928233.1| PREDICTED: tubulin alpha-1D chain [Sus scrofa]	1.000	0.839	0.202	0.171	0.878
gi|70986480|gb|AAZ16514.1| hepatic nuclear factor 1 [Sus scrofa]	1.000	0.768	1.128	1.780	0.882
gi|640352|pdb|3MDE|A Chain A, Crystal Structures Of Medium Chain Acyl-Coa Dehydrogenase From Pig Liver Mitochondria With And Without Substrate >gi|640350|pdb|3MDD|A Chain A, Crystal Structures Of Medium Chain Acyl-Coa	1.000	1.391	0.684	0.685	0.883

Dehydrogenase From Pig Liver Mitochondria With And W					
gi|311265664|ref|XP_003130763.1| PREDICTED: LOW QUALITY PROTEIN: kinesin-1 heavy chain [Sus scrofa]	1.000	0.823	0.710	1.111	0.887
gi|85542092|sp|Q2YGT9.3|RL6_PIG RecName: Full=60S ribosomal protein L6 >gi|113205608|ref|NP_001038007.1| 60S ribosomal protein L6 [Sus scrofa] >gi|56384243|gb|AAV85770.1| ribosomal protein L6 [Sus scrofa]	1.000	0.806	0.295	0.432	0.890
gi|350595461|ref|XP_003134939.3| PREDICTED: LOW QUALITY PROTEIN: 2-oxoglutarate dehydrogenase, mitochondrial-like [Sus scrofa]	1.000	0.912	0.602	0.409	0.891
gi|298104076|ref|NP_001177104.1| enoyl-CoA hydratase, mitochondrial [Sus scrofa]	1.000	1.176	0.473	0.430	0.891
gi|335289671|ref|XP_003355951.1| PREDICTED: transcription elongation factor SPT5 isoform 3 [Sus scrofa] >gi|335289667|ref|XP_003355949.1| PREDICTED: transcription elongation factor SPT5 isoform 1 [Sus scrofa] >gi|335289669|ref|XP_003355950.1| PREDICTED: transcription elongation fac	1.000	0.921	1.108	1.490	0.892
gi|194036302|ref|XP_001926704.1| PREDICTED: histone H2A type 2-B-like [Sus scrofa]	1.000	0.779	1.057	1.179	0.893
gi|335309199|ref|XP_003361534.1| PREDICTED: AP-1 complex subunit sigma-1A-like [Sus scrofa]	1.000	0.824	0.539	0.476	0.893
gi|47523628|ref|NP_999442.1| aminopeptidase N [Sus scrofa] >gi|1703286|sp|P15145.3|AMPN_PIG RecName: Full=Aminopeptidase N; Short=AP-N; Short=pAPN; AltName: Full=Alanyl aminopeptidase; AltName: Full=Aminopeptidase M; Short=AP-M; AltName: Full=Microsomal aminopeptidase; AltName:	1.000	0.377	0.514	0.611	0.898
gi|350593858|ref|XP_003133682.3| PREDICTED: carbamoyl-phosphate synthase [ammonia], mitochondrial isoform 1 [Sus scrofa]	1.000	1.256	0.640	0.507	0.899

gi|346986447|ref|NP_001231373.1| ribonuclease H2 subunit A [Sus scrofa]	1.000	0.934	1.495	0.612	0.901
gi|311244862|ref|XP_001925828.2| PREDICTED: huntingtin-interacting protein K-like [Sus scrofa]	1.000	0.776	1.342	1.280	0.902
gi|335293615|ref|XP_003357006.1| PREDICTED: UDP-glucuronosyltransferase 2A1 [Sus scrofa]	1.000	0.731	0.513	0.642	0.911
gi|350581370|ref|XP_003124307.3| PREDICTED: MICAL-like protein 2 [Sus scrofa]	1.000	0.502	1.128	1.227	0.912
gi|350591926|ref|XP_003358845.2| PREDICTED: golgin subfamily B member 1 [Sus scrofa]	1.000	0.766	0.971	0.959	0.915
gi|334305778|sp|D2SW95.1|COPB_PIG RecName: Full=Coatomer subunit beta; AltName: Full=Beta-coat protein; Short=Beta-COP >gi|288860138|ref|NP_001165837.1| coatomer subunit beta [Sus scrofa] >gi|268633765|gb|ACZ15983.1| coatomer protein subunit beta 1 [Sus scrofa]	1.000	1.192	0.661	0.623	0.916
gi|169139278|gb|ACA48587.1| liver fatty acid binding protein [Sus scrofa]	1.000	0.903	1.628	1.294	0.917
gi|343790893|ref|NP_001230504.1| creatine kinase, brain [Sus scrofa]	1.000	1.616	0.641	0.774	0.917
gi|311258794|ref|XP_003127785.1| PREDICTED: sphingomyelin phosphodiesterase, acid-like 3B [Sus scrofa]	1.000	0.849	1.649	1.632	0.918
gi|350579853|ref|XP_003480698.1| PREDICTED: liprin-alpha-1-like [Sus scrofa]	1.000	1.347	1.462	1.395	0.919
gi|350580953|ref|XP_003354274.2| PREDICTED: 60S acidic ribosomal protein P1-like [Sus scrofa]	1.000	0.421	1.608	1.595	0.920
gi|47523794|ref|NP_999534.1| voltage-dependent anion-selective channel protein 2 [Sus scrofa] >gi|75050405|sp|Q9MZ15.1|VDAC2_PIG RecName: Full=Voltage-dependent anion-selective channel protein 2; Short=VDAC-2 >gi|8745554|gb|AAF78964.1|AF268462_1 voltage-dependent anion channel	1.000	0.872	0.478	0.433	0.922
gi|350582129|ref|XP_003354780.2| PREDICTED: ig kappa chain V-II region RPMI 6410-like [Sus scrofa]	1.000	0.919	1.388	1.364	0.923

gi|343791015|ref|NP_001230554.1| carboxylesterase 3 precursor [Sus scrofa]	1.000	0.942	0.662	0.829	0.924
gi|297747346|ref|NP_001177097.1| S100 calcium binding protein A14 [Sus scrofa]	1.000	0.868	1.211	1.289	0.925
gi|190360663|ref|NP_001121949.1| FYVE and coiled-coil domain-containing protein 1 [Sus scrofa] >gi|41688293|dbj|BAD08647.1| FYVE and coiled-coil domain containing 1 [Sus scrofa]	1.000	0.991	0.625	1.214	0.925
gi|1262435|emb|CAA61864.1| put. 26S protease subunit [Sus scrofa]	1.000	0.765	0.820	0.599	0.929
gi|1332717|gb|AAB36056.1| acylamino acid-releasing enzyme, AARE {EC 3.4.19.1} [swine, liver, Peptide, 732 aa] >gi|1583737|prf||2121361A acyl-AA releasing enzyme	1.000	1.103	0.791	0.977	0.930
gi|335286637|ref|XP_001927783.3| PREDICTED: nitrilase homolog 1 isoform 2 [Sus scrofa]	1.000	1.142	1.595	1.118	0.932
gi|325652134|ref|NP_001191701.1| bromodomain-containing protein 4 [Sus scrofa] >gi|321172828|gb|ADW77216.1| bromodomain-containing protein 4 [Sus scrofa]	1.000	0.575	1.145	0.883	0.932
gi|218664491|ref|NP_001136314.1| galectin-3 [Sus scrofa] >gi|215254098|gb|ACJ64061.1| lectin galactoside-binding soluble 2 protein [Sus scrofa]	1.000	1.047	1.249	0.849	0.939
gi|2833354|sp|Q29223.2|RL34_PIG RecName: Full=60S ribosomal protein L34	1.000	0.879	0.523	0.566	0.941
gi|350591034|ref|XP_003483187.1| PREDICTED: glycerol-3-phosphate dehydrogenase 1-like protein-like [Sus scrofa]	1.000	1.304	0.697	0.704	0.941
gi|350587641|ref|XP_003129114.3| PREDICTED: UDP-glucuronosyltransferase 2C1-like [Sus scrofa]	1.000	0.934	0.430	0.670	0.942
gi|335287882|ref|XP_003126232.2| PREDICTED: LOW QUALITY PROTEIN: sterol O-acyltransferase 2-like [Sus scrofa]	1.000	1.336	0.918	1.402	0.942
gi|346227222|ref|NP_001230997.1| ribosomal protein L13a isoform 1 [Sus scrofa]	1.000	0.802	0.636	0.500	0.943
gi|346421386|ref|NP_001231066.1| ATP synthase subunit g, mitochondrial [Sus scrofa]	1.000	0.905	0.362	0.382	0.946
gi|113205668|ref|NP_001038021.1| microsomal	1.000	1.689	0.870	0.986	0.950

glutathione S-transferase 3 [Sus scrofa] >gi|120564453|gb|ABM30152.1| microsomal glutathione S-transferase 3 [Sus scrofa] >gi|87047644|gb|ABD18455.1| microsomal glutathione S-transferase 3 [Sus scrofa]					
gi|311260243|ref|XP_001927987.2| PREDICTED: protein CutA isoform 1 [Sus scrofa]	1.000	0.621	2.449	1.975	0.951
gi|350597193|ref|XP_003484383.1| PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase B [Sus scrofa]	1.000	0.394	1.723	0.922	0.958
gi|311255888|ref|XP_003126410.1| PREDICTED: cullin-associated NEDD8-dissociated protein 1-like [Sus scrofa]	1.000	1.430	0.839	0.627	0.959
gi|311250237|ref|XP_003124024.1| PREDICTED: stress-70 protein, mitochondrial [Sus scrofa]	1.000	0.877	0.886	0.721	0.961
gi|45269029|gb|AAS55927.1| cytoskeletal beta actin, partial [Sus scrofa]	1.000	1.089	0.585	0.609	0.964
gi|350587231|ref|XP_003482373.1| PREDICTED: LOW QUALITY PROTEIN: cytoplasmic dynein 1 heavy chain 1 [Sus scrofa]	1.000	1.192	0.769	0.690	0.967
gi|335281560|ref|XP_003353830.1| PREDICTED: splicing factor 1 isoform 2 [Sus scrofa]	1.000	1.140	1.611	1.992	0.968
gi|343098455|ref|NP_001230202.1| ras-related protein Rab-6A [Sus scrofa]	1.000	1.156	0.719	0.616	0.970
gi|350582040|ref|XP_003481180.1| PREDICTED: U5 small nuclear ribonucleoprotein 200 kDa helicase-like [Sus scrofa]	1.000	1.299	0.968	0.982	0.974
gi|312283580|ref|NP_999292.2| superoxide dismutase [Mn], mitochondrial [Sus scrofa]	1.000	0.970	1.800	0.677	0.974
gi|335293826|ref|XP_003357065.1| PREDICTED: LOW QUALITY PROTEIN: short coiled-coil protein-like [Sus scrofa]	1.000	0.372	3.119	1.888	0.975
gi|385648282|ref|NP_001245314.1| glucosidase, beta (bile acid) 2 [Sus scrofa]	1.000	0.636	0.760	0.737	0.977
gi|124857|sp|P00998.1|ISK1_PIG RecName: Full=Pancreatic secretory trypsin inhibitor; AltName: Full=Serine protease inhibitor	1.000	0.546	1.059	0.297	0.980

Kazal-type 1 >gi|230351|pdb|1TGS|I Chain I, Three-Dimensional Structure Of The Complex Between Pancreatic Secretory Inhibitor (Kazal Type) And Trypsinogen					
gi|350592528|ref|XP_003483480.1| PREDICTED: endoplasmic reticulum resident protein 29 [Sus scrofa]	1.000	0.787	1.304	1.172	0.982
gi|350579445|ref|XP_003480606.1| PREDICTED: protein NipSnap homolog 3A-like [Sus scrofa]	1.000	0.842	1.427	1.801	0.984
gi|347543818|ref|NP_001231565.1| cytochrome P450, family 4, subfamily F, polypeptide 55 precursor [Sus scrofa]	1.000	0.959	0.472	0.472	0.986
gi|113205892|ref|NP_001038077.1| tubulin beta chain [Sus scrofa] >gi|75045190|sp|Q767L7.1|TBB5_PIG RecName: Full=Tubulin beta chain; AltName: Full=Tubulin beta-5 chain >gi|81174748|gb|ABB58916.1| beta 5-tubulin [Sus scrofa] >gi|41529175|dbj|BAD08435.1| beta 5-tubulin [Sus scrofa]	1.000	0.788	0.442	0.456	0.987
gi|45268981|gb|AAS55903.1| 60S ribosomal protein L12, partial [Sus scrofa]	1.000	0.878	0.609	0.594	0.987
gi|164543|gb|AAA31072.1| malate dehydrogenase (EC 1.1.1.37), partial [Sus scrofa]	1.000	0.973	0.715	0.601	0.988
gi|239504558|ref|NP_001155112.1| caspase-10 [Sus scrofa] >gi|229365449|dbj|BAH57972.1| caspase 10 [Sus scrofa]	1.000	1.116	0.668	0.738	0.988
gi|462384|sp|P33198.1|IDHP_PIG RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=ICD-M; AltName: Full=IDP; AltName: Full=NADP(+)-specific ICDH; AltName: Full=Oxalosuccinate decarboxylase; Flags: Precursor >gi|294223|gb|AAA31089.1| NADPH-specif	1.000	1.284	0.588	0.640	0.990
gi|157427728|ref|NP_001098772.1| ATP-citrate synthase isoform 2 [Sus scrofa] >gi|380509279|gb|AFD64642.1| ATP citrate lyase short isoform [Sus scrofa] >gi|156140098|gb|ABU51323.1| ATP citrate lyase [Sus scrofa]	1.000	0.960	0.574	0.853	0.991

gi|346716326|ref|NP_001231181.1| SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 [Sus scrofa]	1.000	0.627	0.547	0.905	0.991
gi|47522800|ref|NP_999152.1| 60S ribosomal protein L22 [Sus scrofa] >gi|54039123|sp|P67985.2|RL22_PIG RecName: Full=60S ribosomal protein L22; AltName: Full=Heparin-binding protein HBp15 >gi|409074|dbj|BAA04547.1| heparin binding protein [Sus scrofa]	1.000	0.815	0.549	0.479	0.997
gi|343478210|ref|NP_001230371.1| syntaxin 12 [Sus scrofa]	1.000	0.949	1.837	2.884	1.001
gi|311249251|ref|XP_003123542.1| PREDICTED: 6-phosphogluconolactonase-like [Sus scrofa]	1.000	1.405	0.796	0.756	1.009
gi|350587377|ref|XP_003356918.2| PREDICTED: cytosol aminopeptidase-like [Sus scrofa]	1.000	1.687	2.747	3.579	1.011
gi|350586674|ref|XP_001929500.4| PREDICTED: exportin-5 [Sus scrofa]	1.000	0.936	0.699	0.653	1.018
gi|351738777|gb|AEQ61487.1| ribokinase [Sus scrofa]	1.000	1.083	1.493	1.603	1.019
gi|350580256|ref|XP_003480773.1| PREDICTED: nucleobindin-2 [Sus scrofa]	1.000	0.608	1.207	1.564	1.020
gi|350593062|ref|XP_003133228.3| PREDICTED: xaa-Pro aminopeptidase 1 isoform 2 [Sus scrofa]	1.000	1.117	0.832	0.607	1.023
gi|335298834|ref|XP_003358406.1| PREDICTED: leucine-rich repeat flightless-interacting protein 2 [Sus scrofa]	1.000	0.894	1.546	1.044	1.027
gi|47522844|ref|NP_999174.1| complement C3 precursor [Sus scrofa] >gi|11869931|gb|AAG40565.1|AF154933_1 complement component C3 [Sus scrofa] >gi|27801787|emb|CAD38823.2| complement C3 precursor [Sus scrofa]	1.000	0.640	0.917	0.806	1.028
gi|342672022|ref|NP_001230144.1| exportin-2 [Sus scrofa]	1.000	1.359	0.529	0.497	1.030
gi|335284313|ref|XP_003124517.2| PREDICTED: RNA-binding protein FUS-like isoform 1 [Sus scrofa]	1.000	0.713	0.899	0.633	1.032

gi|350583346|ref|XP_003125776.3| PREDICTED: ubiquitin associated protein 2-like isoform 3 [Sus scrofa]	1.000	0.946	1.471	1.696	1.033
gi|335307509|ref|XP_003360867.1| PREDICTED: lipoma-preferred partner-like, partial [Sus scrofa]	1.000	0.795	1.317	1.276	1.036
gi|335297068|ref|XP_001927259.3| PREDICTED: CLYBL protein [Sus scrofa]	1.000	0.888	1.271	1.636	1.036
gi|311276332|ref|XP_003135175.1| PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2-like isoform 2 [Sus scrofa]	1.000	1.185	0.750	0.745	1.037
gi|311246780|ref|XP_003122339.1| PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2-like [Sus scrofa]	1.000	0.868	1.466	1.718	1.043
gi|350591495|ref|XP_003132454.3| PREDICTED: coatomer subunit gamma [Sus scrofa]	1.000	1.377	0.929	0.721	1.045
gi|311258000|ref|XP_003127386.1| PREDICTED: AP-2 complex subunit alpha-1 isoform 1 [Sus scrofa]	1.000	1.207	0.648	0.815	1.052
gi|311259466|ref|XP_003128111.1| PREDICTED: putative hydroxypyruvate isomerase-like isoform 1 [Sus scrofa]	1.000	1.019	2.107	1.793	1.053
gi|350582315|ref|XP_003481243.1| PREDICTED: NFU1 iron-sulfur cluster scaffold homolog, mitochondrial-like [Sus scrofa]	1.000	0.809	1.818	1.689	1.055
gi|212549623|ref|NP_001131101.1| endoplasmic reticulum resident protein 44 precursor [Sus scrofa] >gi|187480160|gb|ACD13000.1| thioredoxin domain-containing 4 [Sus scrofa]	1.000	1.194	0.716	0.968	1.059
gi|350586216|ref|XP_003128039.3| PREDICTED: thioredoxin domain-containing protein 12-like [Sus scrofa]	1.000	0.456	1.098	1.272	1.059
gi|350584903|ref|XP_003126945.3| PREDICTED: AP-1 complex subunit gamma-1 isoform 1 [Sus scrofa]	1.000	1.115	0.685	0.787	1.059
gi|346421347|ref|NP_001231022.1| glucosamine-6-phosphate isomerase 1 [Sus scrofa]	1.000	0.958	1.649	1.438	1.064
gi|113205878|ref|NP_001038072.1| delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase,	1.000	1.299	1.408	0.971	1.065

mitochondrial [Sus scrofa] >gi|90024980|gb|AAZ82038.2| peroxisomal enoyl coenzyme A hydratase 1 [Sus scrofa]					
gi|311275226|ref|XP_003134622.1| PREDICTED: glutathione S-transferase kappa 1-like isoform 2 [Sus scrofa]	1.000	0.864	0.619	0.577	1.072
gi|57528035|ref|NP_001009582.1| stathmin [Sus scrofa] >gi|75043336|sp|Q6DUB7.3|STMN1_PIG RecName: Full=Stathmin >gi|49615355|gb|AAT66936.1| stathmin-1 [Sus scrofa]	1.000	0.699	1.231	1.255	1.081
gi|343488538|ref|NP_001230424.1| cytoplasmic dynein 1 intermediate chain 2 [Sus scrofa]	1.000	0.686	1.581	1.663	1.087
gi|346716298|ref|NP_001231025.1| heterogeneous nuclear ribonucleoprotein G [Sus scrofa]	1.000	0.958	1.657	1.159	1.090
gi|298104082|ref|NP_001177109.1| dynein light chain roadblock-type 1 [Sus scrofa]	1.000	0.847	2.213	3.050	1.090
gi|335310032|ref|XP_003126353.2| PREDICTED: dynactin subunit 2-like isoform 3 [Sus scrofa]	1.000	1.748	1.035	0.915	1.093
gi|311246990|ref|XP_003122442.1| PREDICTED: mucin-2, partial [Sus scrofa]	1.000	1.835	0.865	0.677	1.098
gi|335280113|ref|XP_003121789.2| PREDICTED: LOW QUALITY PROTEIN: 60S ribosomal protein L4 [Sus scrofa]	1.000	0.772	0.477	0.419	1.100
gi|350595475|ref|XP_003360255.2| PREDICTED: proteasome subunit alpha type-2-like [Sus scrofa]	1.000	0.713	2.004	2.133	1.102
gi|350586921|ref|XP_003482304.1| PREDICTED: LOW QUALITY PROTEIN: apoptotic chromatin condensation inducer in the nucleus-like [Sus scrofa]	1.000	0.842	1.424	0.894	1.102
gi|311261483|ref|XP_003128742.1| PREDICTED: LOW QUALITY PROTEIN: golgin subfamily A member 5-like [Sus scrofa]	1.000	1.092	1.630	1.604	1.104
gi|350594033|ref|XP_003483821.1| PREDICTED: UDP-glucuronosyltransferase 1-10 isoform 2 [Sus scrofa]	1.000	0.806	0.583	0.609	1.105
gi|347300356|ref|NP_001231473.1| uncharacterized protein LOC100689297 [Sus	1.000	1.224	1.686	1.919	1.106

scrofa]					
gi|350581286|ref|XP_003124146.3| PREDICTED: hypothetical protein LOC100516425 [Sus scrofa]	1.000	1.102	1.883	1.285	1.111
gi|297591969|ref|NP_001172062.1| ubiquitin-conjugating enzyme E2 L3 [Sus scrofa] >gi|219563058|gb|ACL27888.1| ubiquitin-conjugating enzyme E2L 3 [Sus scrofa]	1.000	0.729	1.377	1.106	1.111
gi|75051712|sp|Q9TUB5.1|CLCA1_PIG RecName: Full=Calcium-activated chloride channel regulator 1; AltName: Full=Calcium-activated chloride channel family member 1; AltName: Full=pCLCA1; Flags: Precursor >gi|47523388|ref|NP_999313.1| calcium-activated chloride channel regulator 1 precu	1.000	1.042	1.503	1.076	1.117
gi|194038540|ref|XP_001929175.1| PREDICTED: ectonucleoside triphosphate diphosphohydrolase 5 [Sus scrofa]	1.000	0.769	0.948	0.509	1.118
gi|346986324|ref|NP_001231316.1| tumor protein D52 [Sus scrofa]	1.000	0.720	0.882	1.075	1.124
gi|329663924|ref|NP_001192332.1| tubulin-folding cofactor B-like [Sus scrofa] >gi|24528346|emb|CAD56044.1| cytoskeleton-associated protein 1 [Sus scrofa]	1.000	1.001	1.310	1.194	1.124
gi|335310868|ref|XP_003362230.1| PREDICTED: T-complex protein 1 subunit epsilon, partial [Sus scrofa]	1.000	1.491	0.598	0.472	1.125
gi|122064583|sp|P04178.2|SODC_PIG RecName: Full=Superoxide dismutase [Cu-Zn] >gi|298677090|ref|NP_001177351.1| superoxide dismutase [Cu-Zn] [Sus scrofa] >gi|297593564|gb|ADI47520.1| superoxide dismutase 1 [Sus scrofa]	1.000	0.935	1.540	1.450	1.125
gi|325652138|ref|NP_001191702.1| A-kinase anchor protein 1, mitochondrial [Sus scrofa] >gi|321267428|dbj|BAJ72691.1| A kinase anchor protein 1 [Sus scrofa]	1.000	0.686	1.180	1.032	1.126
gi|350585075|ref|XP_003481870.1| PREDICTED: xaa-Pro dipeptidase-like [Sus scrofa]	1.000	1.176	1.013	1.704	1.131
gi|335300836|ref|XP_003359054.1| PREDICTED: ES1 protein homolog,	1.000	0.485	1.208	0.769	1.133

mitochondrial-like [Sus scrofa]					
gi|350592730|ref|XP_003483523.1| PREDICTED: heterogeneous nuclear ribonucleoprotein F [Sus scrofa] >gi|335301642|ref|XP_003359253.1| PREDICTED: heterogeneous nuclear ribonucleoprotein F [Sus scrofa] >gi|194042674|ref|XP_001929089.1| PREDICTED: heterogeneous nuclear ribonucleoprotei	1.000	1.215	1.290	1.078	1.133
gi|350587966|ref|XP_003482525.1| PREDICTED: PDZ and LIM domain protein 5 isoform 3 [Sus scrofa]	1.000	0.779	1.597	1.479	1.140
gi|194037005|ref|XP_001928988.1| PREDICTED: ribonuclease UK114-like isoform 1 [Sus scrofa]	1.000	1.117	2.581	2.299	1.141
gi|350581741|ref|XP_003124660.3| PREDICTED: phosphomannomutase 2-like, partial [Sus scrofa]	1.000	1.863	1.052	1.590	1.141
gi|350586779|ref|XP_003482273.1| PREDICTED: LOW QUALITY PROTEIN: IQ motif containing GTPase activating protein 1 [Sus scrofa]	1.000	1.126	0.971	0.793	1.146
gi|1900|emb|CAA27575.1| unnamed protein product [Sus scrofa]	1.000	1.005	0.503	0.769	1.152
gi|350582471|ref|XP_003125244.3| PREDICTED: echinoderm microtubule associated protein like 4 [Sus scrofa]	1.000	0.952	1.303	1.407	1.152
gi|83921635|ref|NP_001033089.1| FKBP1A-like [Sus scrofa] >gi|61098747|gb|AAX37547.1| FKBP1A-like [Sus scrofa]	1.000	1.011	1.849	1.720	1.154
gi|350584176|ref|XP_003481686.1| PREDICTED: myosin-Ia-like [Sus scrofa]	1.000	0.968	0.862	0.644	1.164
gi|311259195|ref|XP_003127983.1| PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like isoform 2 [Sus scrofa]	1.000	1.114	1.411	1.334	1.164
gi|350583407|ref|XP_003481511.1| PREDICTED: cathepsin S [Sus scrofa]	1.000	0.807	3.109	2.841	1.171
gi|322510017|sp|Q007T2.2|CDC42_PIG RecName: Full=Cell division control protein 42 homolog; Flags: Precursor >gi|269994011|dbj|BAI50642.1| Cell division control protein 42 homolog [Sus scrofa]	1.000	1.125	0.764	0.921	1.172

gi|335291962|ref|XP_001928015.3| PREDICTED: E3 ubiquitin-protein ligase TRIM31 [Sus scrofa] >gi|211926941|dbj|BAG82682.1| tripartite motif-containing protein 31 [Sus scrofa]	1.000	0.990	0.644	1.319	1.179
gi|350590070|ref|XP_003131163.3| PREDICTED: paraspeckle component 1 [Sus scrofa]	1.000	1.256	0.892	0.844	1.179
gi|225450|prf||1303334A valosin precursor	1.000	1.408	0.778	0.889	1.181
gi|350590733|ref|XP_003131874.3| PREDICTED: pre-mRNA-processing-splicing factor 8, partial [Sus scrofa]	1.000	1.245	0.745	0.327	1.182
gi|343790906|ref|NP_001230510.1| calcineurin-like phosphoesterase domain containing 1 [Sus scrofa]	1.000	0.755	2.436	1.559	1.194
gi|178056532|ref|NP_001116688.1| Z-DNA-binding protein 1 [Sus scrofa] >gi|147223427|emb|CAN13344.1| Z-DNA binding protein 1 [Sus scrofa]	1.000	0.703	0.731	1.318	1.195
gi|350587405|ref|XP_003482406.1| PREDICTED: cytosolic beta-glucosidase-like, partial [Sus scrofa]	1.000	1.402	0.973	0.831	1.198
gi|335297344|ref|XP_003131243.2| PREDICTED: integrin beta-4-like [Sus scrofa]	1.000	0.730	1.151	1.519	1.199
gi|194038734|ref|XP_001929226.1| PREDICTED: protein transport protein Sec23A isoform 2 [Sus scrofa]	1.000	1.655	0.875	0.634	1.202
gi|311272700|ref|XP_003133549.1| PREDICTED: heterogeneous nuclear ribonucleoprotein A3-like isoform 1 [Sus scrofa]	1.000	1.347	0.704	0.642	1.203
gi|75053043|sp|Q6UAQ8.3|ETFB_PIG RecName: Full=Electron transfer flavoprotein subunit beta; Short=Beta-ETF >gi|328550534|ref|NP_001192208.1| electron transfer flavoprotein subunit beta [Sus scrofa] >gi|35384838|gb|AAQ84565.1| electron transfer flavoprotein beta subunit precursor [S	1.000	1.237	0.867	1.028	1.205
gi|350582454|ref|XP_003125231.3| PREDICTED: LOW QUALITY PROTEIN: leucine-rich PPR motif-containing protein, mitochondrial [Sus scrofa]	1.000	1.183	0.968	0.808	1.206
gi|356582293|ref|NP_001239141.1| DEAH	1.000	0.875	0.801	0.869	1.207

(Asp-Glu-Ala-His) box polypeptide 15 [Sus scrofa]					
gi|47523822|ref|NP_999549.1| glutamate carboxypeptidase 2 [Sus scrofa] >gi|20138100|sp|O77564.1|FOLH1_PIG RecName: Full=Glutamate carboxypeptidase 2; AltName: Full=Folate hydrolase 1; AltName: Full=Folylpoly-gamma-glutamate carboxypeptidase; Short=FGCP; AltName: Full=Glutamate	1.000	1.112	2.071	2.577	1.210
gi|194044822|ref|XP_001927404.1| PREDICTED: peroxiredoxin-4 [Sus scrofa]	1.000	0.450	1.472	1.707	1.213
gi|311250752|ref|XP_003124284.1| PREDICTED: NACHT, LRR and PYD domains-containing protein 6 [Sus scrofa]	1.000	1.000	2.178	1.782	1.213
gi|148231223|ref|NP_001090898.1| mitochondrial antiviral-signaling protein [Sus scrofa] >gi|156144883|gb|ABU53000.1| virus-induced signaling adapter [Sus scrofa] >gi|119507309|dbj|BAF42542.1| mitochondrial antiviral signaling protein [Sus scrofa]	1.000	0.771	1.333	1.416	1.219
gi|311247536|ref|XP_003122689.1| PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)-like [Sus scrofa]	1.000	1.863	0.874	0.935	1.222
gi|194036835|ref|XP_001924895.1| PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase [Sus scrofa]	1.000	1.684	0.809	0.783	1.223
gi|311250151|ref|XP_003123979.1| PREDICTED: heat shock 70 kDa protein 4 [Sus scrofa]	1.000	1.453	2.216	1.688	1.224
gi|148234672|ref|NP_001090881.1| porphobilinogen deaminase [Sus scrofa] >gi|112980813|gb|ABI29188.1| hydroxymethylbilane synthase [Sus scrofa]	1.000	0.860	2.163	1.615	1.225
gi|213021241|ref|NP_001132944.1| proteasome subunit alpha type-6 [Sus scrofa] >gi|210062872|gb|ACJ06406.1| proteasome subunit alpha type 6 [Sus scrofa]	1.000	1.055	1.229	1.076	1.231
gi|335303414|ref|XP_001928370.3| PREDICTED: tubulin alpha-4A chain [Sus scrofa]	1.000	1.239	0.760	0.683	1.233

gi|335296459|ref|XP_003130769.2| PREDICTED: vimentin-like [Sus scrofa]	1.000	0.816	1.537	1.283	1.234
gi|194033860|ref|XP_001927901.1| PREDICTED: UV excision repair protein RAD23 homolog B [Sus scrofa]	1.000	1.642	2.407	2.937	1.236
gi|164669|gb|AAA31120.1| succinyl-CoA synthetase beta-subunit, partial [Sus scrofa]	1.000	1.758	0.974	0.824	1.244
gi|148232214|ref|NP_001090964.1| ribose-5-phosphate isomerase [Sus scrofa] >gi|158512830|sp|A2TLM1.1|RPIA_PIG RecName: Full=Ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase >gi|124265188|gb|ABM98101.1| ribose 5-phosphate isomerase-like protein [Sus scrofa]	1.000	0.938	3.291	3.682	1.253
gi|194036975|ref|XP_001927782.1| PREDICTED: polyadenylate-binding protein 1 [Sus scrofa]	1.000	0.878	1.445	1.228	1.255
gi|190360593|ref|NP_001121945.1| interferon-induced guanylate-binding protein 1 [Sus scrofa] >gi|166202346|gb|ABY84597.1| guanylate binding protein 1 [Sus scrofa]	1.000	0.933	0.844	0.731	1.258
gi|47523692|ref|NP_999478.1| thioredoxin [Sus scrofa] >gi|20141821|sp|P82460.3|THIO_PIG RecName: Full=Thioredoxin; Short=Trx >gi|332368598|gb|AEE61373.1| thioredoxin [Sus scrofa] >gi|14326453|gb|AAK60272.1|AF382821_1 thioredoxin [Sus scrofa]	1.000	1.007	2.615	2.229	1.258
gi|343488474|ref|NP_001230453.1| elongation factor 1-beta [Sus scrofa]	1.000	0.927	1.277	2.426	1.258
gi|225735709|ref|NP_001139599.1| clathrin heavy chain 1 [Sus scrofa] >gi|224492556|emb|CAR65329.1| clathrin heavy chain [Sus scrofa]	1.000	1.218	0.807	0.717	1.260
gi|350582501|ref|XP_003481284.1| PREDICTED: atlastin-2-like isoform 2 [Sus scrofa]	1.000	1.596	1.146	0.929	1.273
gi|350584145|ref|XP_001929467.3| PREDICTED: nascent polypeptide-associated complex subunit alpha isoform 1 [Sus scrofa]	1.000	0.879	1.852	1.608	1.283
gi|335305558|ref|XP_003134901.2| PREDICTED: heterogeneous nuclear	1.000	1.127	0.765	0.745	1.284

ribonucleoproteins A2/B1 isoform 1 [Sus scrofa]					
gi|48675927|ref|NP_001001632.1| tropomyosin alpha-3 chain [Sus scrofa] >gi|45272586|gb|AAS57724.1| tropomyosin 3 [Sus scrofa]	1.000	0.426	1.649	1.820	1.290
gi|148225750|ref|NP_001090973.1| heat shock protein 105 kDa [Sus scrofa] >gi|141521428|gb|ABO88027.1| heat shock 105kDa/110kDa protein 1 [Sus scrofa]	1.000	0.908	1.023	0.959	1.296
gi|343790920|ref|NP_001230517.1| fumarate hydratase [Sus scrofa]	1.000	1.509	0.966	0.890	1.303
gi|60394813|sp|Q29201.4|RS16_PIG RecName: Full=40S ribosomal protein S16 >gi|212549659|ref|NP_001131092.1| 40S ribosomal protein S16 [Sus scrofa] >gi|335289675|ref|XP_003355953.1| PREDICTED: 40S ribosomal protein S16-like isoform 2 [Sus scrofa] >gi|335289677|ref|XP_003355954.1| PRE	1.000	1.010	0.711	0.563	1.304
gi|68532157|gb|AAY98813.1| proteasome subunit 10 [Sus scrofa] >gi|68532159|gb|AAY98814.1| proteasome subunit 10 [Sus scrofa]	1.000	1.961	1.767	3.009	1.305
gi|311244872|ref|XP_003121596.1| PREDICTED: creatine kinase U-type, mitochondrial-like isoform 2 [Sus scrofa] >gi|311244870|ref|XP_003121595.1| PREDICTED: creatine kinase U-type, mitochondrial-like isoform 1 [Sus scrofa]	1.000	1.676	1.552	1.153	1.306
gi|311276184|ref|XP_003135086.1| PREDICTED: FUN14 domain-containing protein 1-like [Sus scrofa]	1.000	0.718	1.337	1.354	1.308
gi|346421435|ref|NP_001231091.1| sorbitol dehydrogenase [Sus scrofa]	1.000	1.724	1.163	0.884	1.309
gi|122131841|sp|Q06A98.1|SRSF2_PIG RecName: Full=Serine/arginine-rich splicing factor 2; AltName: Full=Splicing component, 35 kDa; AltName: Full=Splicing factor SC35; Short=SC-35; AltName: Full=Splicing factor, arginine/serine-rich 2 >gi|116175283|ref|NP_001070697.1| serine/arginine-	1.000	1.196	1.380	1.786	1.313
gi|389618965|gb|AFK92990.1| U2 small nuclear	1.000	1.303	1.058	1.085	1.315

RNA auxiliary factor 2 [Sus scrofa]					
gi|335282599|ref|XP_003123290.2| PREDICTED: interleukin enhancer-binding factor 3 [Sus scrofa]	1.000	1.011	1.226	1.104	1.319
gi|335281715|ref|XP_003122673.2| PREDICTED: L-asparaginase-like [Sus scrofa]	1.000	1.844	2.260	2.082	1.320
gi|312062797|ref|NP_001185848.1| proactivator polypeptide precursor [Sus scrofa] >gi|310789269|gb|ADP24688.1| prosaposin variant 2 [Sus scrofa]	1.000	0.731	2.233	2.259	1.324
gi|335302965|ref|XP_001925033.2| PREDICTED: lupus La protein homolog [Sus scrofa]	1.000	1.032	0.677	0.571	1.326
gi|346644874|ref|NP_001231109.1| T-complex protein 1 subunit gamma [Sus scrofa]	1.000	1.406	0.959	0.898	1.328
gi|343790856|ref|NP_001230567.1| glutathione transferase zeta 1 [Sus scrofa]	1.000	1.644	0.741	0.595	1.333
gi|268607671|ref|NP_001161267.1| actin, alpha skeletal muscle [Sus scrofa] >gi|62287931|sp|P68137.1|ACTS_PIG RecName: Full=Actin, alpha skeletal muscle; AltName: Full=Alpha-actin-1; Flags: Precursor >gi|790202|gb|AAC48692.1| skeletal alpha actin [Sus scrofa]	1.000	1.216	0.517	0.418	1.334
gi|350585579|ref|XP_003481996.1| PREDICTED: alpha-enolase-like, partial [Sus scrofa]	1.000	1.597	1.466	1.565	1.341
gi|350577999|ref|XP_001928755.4| PREDICTED: ezrin-like [Sus scrofa]	1.000	1.848	0.828	1.314	1.341
gi|47523870|ref|NP_999573.1| peroxiredoxin-6 [Sus scrofa] >gi|75074817|sp|Q9TSX9.3|PRDX6_PIG RecName: Full=Peroxiredoxin-6; AltName: Full=Non-selenium glutathione peroxidase; Short=NSGPx >gi|6689393|emb|CAB65456.1| non-selenium glutathione phospholipid hydroperoxide peroxidase	1.000	1.132	2.008	1.577	1.343
gi|350593430|ref|XP_003483683.1| PREDICTED: glutathione reductase, mitochondrial isoform 1 [Sus scrofa]	1.000	0.713	1.184	1.473	1.349
gi|335280672|ref|XP_003353634.1| PREDICTED: aldehyde dehydrogenase X, mitochondrial [Sus scrofa]	1.000	1.944	0.802	0.591	1.353

gi|55583761|sp|Q64L94.1|PSME1_PIG RecName: Full=Proteasome activator complex subunit 1; AltName: Full=Proteasome activator 28 subunit alpha; Short=PA28a; Short=PA28alpha >gi|34978646|gb|AAQ83574.1| proteasome activator 28 alpha subunit [Sus scrofa]	1.000	1.531	1.257	1.253	1.363
gi|335281676|ref|XP_003353867.1| PREDICTED: heterogeneous nuclear ribonucleoprotein U-like 2 [Sus scrofa]	1.000	1.432	0.889	1.030	1.367
gi|335299026|ref|XP_003132223.2| PREDICTED: microtubule-associated protein 4-like [Sus scrofa]	1.000	0.901	1.857	1.532	1.377
gi|555827|gb|AAA65943.1| immunoglobulin alpha heavy chain constant region, partial [Sus scrofa] >gi|2136551|pir||I47175 Ig alpha chain C region - pig (fragment)	1.000	0.720	0.817	1.044	1.378
gi|350587586|ref|XP_003129077.3| PREDICTED: hypothetical protein LOC100522154 [Sus scrofa]	1.000	1.027	1.932	2.369	1.379
gi|120968|sp|P80147.2|GABT_PIG RecName: Full=4-aminobutyrate aminotransferase, mitochondrial; AltName: Full=(S)-3-amino-2-methylpropionate transaminase; AltName: Full=GABA aminotransferase; Short=GABA-AT; AltName: Full=Gamma-amino-N-butyrate transaminase; Short=GABA transaminase;	1.000	1.695	0.783	0.717	1.390
gi|62511144|sp|Q764M5.1|STAT1_PIG RecName: Full=Signal transducer and activator of transcription 1 >gi|47523306|ref|NP_998934.1| signal transducer and activator of transcription 1 [Sus scrofa] >gi|40363629|dbj|BAD06318.1| signal transducer and activator of transcription 1 [Sus scrof	1.000	1.669	1.216	1.570	1.391
gi|335309657|ref|XP_003361720.1| PREDICTED: 14-3-3 protein epsilon-like [Sus scrofa]	1.000	1.488	0.899	0.780	1.393
gi|335289143|ref|XP_003126912.2| PREDICTED: probable D-lactate dehydrogenase, mitochondrial [Sus scrofa]	1.000	1.998	1.083	2.112	1.394
gi|346644844|ref|NP_001231177.1| phosphotriesterase-related protein [Sus scrofa]	1.000	1.138	2.160	2.467	1.396

gi|345441750|ref|NP_001230836.1| heat shock 70kDa protein 8 [Sus scrofa]	1.000	1.383	0.961	0.980	1.398
gi|311271975|ref|XP_001926332.2| PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial [Sus scrofa]	1.000	1.307	0.714	0.940	1.408
gi|350580243|ref|XP_003123005.3| PREDICTED: harmonin-like [Sus scrofa]	1.000	0.886	2.100	1.767	1.414
gi|197251934|ref|NP_001127826.1| actin-related protein 2 [Sus scrofa] >gi|195562213|gb|ACG50178.1| actin-related protein 2-like protein [Sus scrofa]	1.000	1.397	0.500	0.574	1.417
gi|350591605|ref|XP_003483304.1| PREDICTED: plastin-1-like [Sus scrofa]	1.000	1.460	1.001	0.985	1.418
gi|346716348|ref|NP_001231189.1| arginine--tRNA ligase, cytoplasmic [Sus scrofa]	1.000	1.610	0.986	0.841	1.429
gi|47523086|ref|NP_999309.1| peroxiredoxin-5, mitochondrial [Sus scrofa] >gi|10305336|gb|AAG13452.2|AF110735_1 peroxiredoxin 5 [Sus scrofa]	1.000	1.866	0.912	0.881	1.432
gi|297591979|ref|NP_001172070.1| ornithine aminotransferase, mitochondrial [Sus scrofa] >gi|166244455|gb|ABY86572.1| mitochondrial ornithine aminotransferase [Sus scrofa]	1.000	1.701	1.067	0.856	1.434
gi|56788496|gb|AAW29969.1| unknown [Sus scrofa] >gi|56792880|gb|AAW30632.1| unknown [Sus scrofa]	1.000	0.647	1.212	0.768	1.437
gi|47117721|sp|P83884.2|RL36A_PIG RecName: Full=60S ribosomal protein L36a; AltName: Full=60S ribosomal protein L44 >gi|47522650|ref|NP_999082.1| 60S ribosomal protein L36a [Sus scrofa] >gi|335303998|ref|XP_003134062.2| PREDICTED: 60S ribosomal protein L36a-like [Sus scrofa] >gi|335	1.000	1.132	0.672	0.743	1.439
gi|1170740|sp|P00339.3|LDHA_PIG RecName: Full=L-lactate dehydrogenase A chain; Short=LDH-A; AltName: Full=LDH muscle subunit; Short=LDH-M >gi|473571|gb|AAA50436.1| lactate dehydrogenase-A [Sus scrofa domesticus]	1.000	1.799	0.825	0.705	1.440
gi|118403852|ref|NP_001072139.1| UBC1 [Sus	1.000	1.670	1.155	1.259	1.448

scrofa] >gi|115371727|gb|ABI96188.1| UBC1 [Sus scrofa]					
gi|311254260|ref|XP_001929592.2| PREDICTED: interleukin enhancer-binding factor 2 [Sus scrofa]	1.000	1.471	1.176	0.872	1.452
gi|155369760|ref|NP_001094498.1| peroxisomal acyl-coenzyme A oxidase 1 [Sus scrofa] >gi|112292673|gb|ABI14815.1| palmitoyl acyl-CoA oxidase 1 [Sus scrofa]	1.000	1.021	0.945	1.126	1.452
gi|194038542|ref|XP_001929208.1| PREDICTED: methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial [Sus scrofa]	1.000	1.593	0.928	0.929	1.458
gi|335296662|ref|XP_003130891.2| PREDICTED: 6-phosphofructokinase type C [Sus scrofa]	1.000	1.462	0.995	1.326	1.464
gi|194036227|ref|XP_001929678.1| PREDICTED: selenium-binding protein 1 [Sus scrofa]	1.000	1.132	1.756	2.005	1.465
gi|311248177|ref|XP_003123013.1| PREDICTED: proteasome subunit alpha type-1-like [Sus scrofa]	1.000	0.627	1.485	1.428	1.467
gi|350591320|ref|XP_003132344.3| PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 [Sus scrofa]	1.000	1.844	1.187	0.979	1.468
gi|51592135|ref|NP_001004043.1| cofilin-1 [Sus scrofa] >gi|116850|sp|P10668.3|COF1_PIG RecName: Full=Cofilin-1; AltName: Full=Cofilin, non-muscle isoform >gi|164425|gb|AAA31020.1| cofilin [Sus scrofa]	1.000	1.814	1.452	0.952	1.469
gi|113205888|ref|NP_001038076.1| aldehyde dehydrogenase, mitochondrial precursor [Sus scrofa] >gi|122138098|sp|Q2XQV4.1|ALDH2_PIG RecName: Full=Aldehyde dehydrogenase, mitochondrial; AltName: Full=ALDH class 2; AltName: Full=ALDH-E2; Flags: Precursor >gi|81295909|gb|ABB70228.1| mit	1.000	1.732	0.778	0.734	1.475
gi|194034199|ref|XP_001928042.1| PREDICTED: proteasome subunit alpha type-3 isoform 2 [Sus scrofa]	1.000	1.080	2.055	1.906	1.477
gi|45268975|gb|AAS55900.1| 60S ribosomal protein L11, partial [Sus scrofa]	1.000	2.079	1.202	2.070	1.478

gi|350595271|ref|XP_003134762.3| PREDICTED: hypothetical protein LOC100521760 [Sus scrofa]	1.000	1.787	1.246	1.200	1.484
gi|12055551|emb|CAC21172.1| diazepam binding inhibitor [Sus scrofa]	1.000	1.667	2.489	2.516	1.486
gi|350587882|ref|XP_003129304.3| PREDICTED: caspase-6-like [Sus scrofa]	1.000	0.925	2.035	1.475	1.488
gi|311255145|ref|XP_001926338.2| PREDICTED: thiosulfate sulfurtransferase [Sus scrofa]	1.000	1.947	0.819	1.357	1.494
gi|89573899|gb|ABD77175.1| ribosomal protein L18 [Sus scrofa]	1.000	0.920	0.907	0.779	1.498
gi|47523670|ref|NP_999471.1| peroxisomal multifunctional enzyme type 2 [Sus scrofa] >gi|499340|emb|CAA55037.1| 17beta-estradiol dehydrogenase [Sus scrofa]	1.000	1.407	1.131	1.217	1.501
gi|194018698|ref|NP_001123442.1| cytochrome c [Sus scrofa] >gi|119388070|sp|P62895.2|CYC_PIG RecName: Full=Cytochrome c >gi|62208258|gb|AAX77008.1| cytochrome c-like protein [Sus scrofa]	1.000	1.081	2.968	2.164	1.501
gi|335300802|ref|XP_003359038.1| PREDICTED: 6-phosphofructokinase, liver type-like [Sus scrofa]	1.000	1.026	0.859	0.933	1.510
gi|283993079|gb|ADB57036.1| L-gulonate 3-dehydrogenase [Sus scrofa]	1.000	2.065	0.888	1.278	1.510
gi|47169449|pdb|1VJD|A Chain A, Structure Of Pig Muscle Pgk Complexed With Atp >gi|47169448|pdb|1VJC|A Chain A, Structure Of Pig Muscle Pgk Complexed With Mgatp	1.000	1.879	0.606	0.764	1.515
gi|350579323|ref|XP_003122006.3| PREDICTED: retinal dehydrogenase 1-like, partial [Sus scrofa]	1.000	1.350	1.241	1.953	1.515
gi|335293690|ref|XP_003129163.2| PREDICTED: general vesicular transport factor p115-like [Sus scrofa]	1.000	0.836	2.522	2.176	1.516
gi|346986445|ref|NP_001231372.1| NSFL1 (p97) cofactor (p47) [Sus scrofa]	1.000	1.188	1.880	1.872	1.520
gi|47523818|ref|NP_999546.1| calcium/calmodulin-dependent protein kinase	1.000	1.253	1.013	0.852	1.523

type II subunit delta [Sus scrofa] >gi|75073672|sp|Q95266.1|KCC2D_PIG RecName: Full=Calcium/calmodulin-dependent protein kinase type II subunit delta; Short=CaM kinase II subunit delta; Short=CaMK-II subun					
gi|350592964|ref|XP_003483582.1| PREDICTED: PDZ and LIM domain protein 1 [Sus scrofa]	1.000	1.389	2.467	2.281	1.529
gi|350590394|ref|XP_003131590.3| PREDICTED: pyridoxine-5~-phosphate oxidase-like [Sus scrofa]	1.000	1.599	2.451	2.121	1.531
gi|330417958|ref|NP_001155225.1| phosphoenolpyruvate carboxykinase [GTP], mitochondrial [Sus scrofa] >gi|238863892|gb|ACR66222.1| phosphoenolpyruvate carboxykinase 2 [Sus scrofa]	1.000	2.689	1.250	0.996	1.532
gi|350593418|ref|XP_003359535.2| PREDICTED: hypothetical protein LOC100627320 [Sus scrofa]	1.000	1.522	1.994	2.167	1.535
gi|116175259|ref|NP_001070686.1| heterogeneous nuclear ribonucleoprotein A1 [Sus scrofa] >gi|115371763|gb|ABI96206.1| ROA1 [Sus scrofa]	1.000	1.325	0.865	0.712	1.539
gi|356460899|ref|NP_999466.2| catalase [Sus scrofa]	1.000	0.830	1.677	1.644	1.541
gi|118403904|ref|NP_001072131.1| protein DJ-1 [Sus scrofa] >gi|67038668|gb|AAY63803.1| DJ-1 protein [Sus scrofa]	1.000	1.060	2.156	1.948	1.543
gi|255683394|ref|NP_001157474.1| ornithine carbamoyltransferase, mitochondrial [Sus scrofa]	1.000	0.910	1.058	1.682	1.552
gi|219522018|ref|NP_001137196.1| Na(+)/H(+) exchange regulatory cofactor NHE-RF1 [Sus scrofa] >gi|217031226|gb|ACJ74160.1| solute carrier family 9 (sodium/hydrogen exchanger) member 3 regulator 1 [Sus scrofa]	1.000	1.571	2.608	2.407	1.557
gi|346716265|ref|NP_001231271.1| omega-amidase NIT2 [Sus scrofa]	1.000	1.536	1.113	0.832	1.558
gi|194035831|ref|XP_001928742.1| PREDICTED: coatomer subunit alpha isoform 2 [Sus scrofa]	1.000	1.561	1.003	0.878	1.562
gi|343780946|ref|NP_001230486.1| D-dopachrome decarboxylase [Sus scrofa]	1.000	1.248	1.873	1.422	1.566

gi|312062805|ref|NP_001185852.1| chloride intracellular channel protein 5 [Sus scrofa] >gi|197361201|gb|ACH70136.1| chloride intracellular channel 5 [Sus scrofa]	1.000	2.034	0.871	1.000	1.572
gi|194037373|ref|XP_001927584.1| PREDICTED: coatomer subunit zeta-1 isoform 1 [Sus scrofa]	1.000	1.781	1.371	1.598	1.578
gi|194040624|ref|XP_001929173.1| PREDICTED: plastin-2 isoform 1 [Sus scrofa]	1.000	1.786	1.252	1.164	1.583
gi|350591042|ref|XP_003132145.3| PREDICTED: programmed cell death 6-interacting protein [Sus scrofa]	1.000	1.284	0.954	1.220	1.590
gi|335310692|ref|XP_003362151.1| PREDICTED: protein LZIC-like [Sus scrofa]	1.000	1.219	2.177	2.930	1.599
gi|335309939|ref|XP_003133770.2| PREDICTED: nucleolin-like [Sus scrofa]	1.000	1.089	1.648	1.607	1.599
gi|47523784|ref|NP_999528.1| 40S ribosomal protein S12 [Sus scrofa] >gi|1173191|sp|P46405.2|RS12_PIG RecName: Full=40S ribosomal protein S12 >gi|872315|emb|CAA55946.1| 40S ribosomal protein S12 [Sus scrofa]	1.000	0.974	1.068	0.878	1.607
gi|335282345|ref|XP_003354038.1| PREDICTED: mitochondrial import inner membrane translocase subunit Tim13-like [Sus scrofa]	1.000	1.780	2.187	2.239	1.616
gi|21954744|gb|AAM83105.1|AF525487_1 Ran [Sus scrofa]	1.000	1.757	0.822	0.618	1.618
gi|348605274|ref|NP_001231762.1| alcohol dehydrogenase 5 (class III), chi polypeptide [Sus scrofa]	1.000	1.887	0.872	0.792	1.618
gi|112985|sp|P00506.2|AATM_PIG RecName: Full=Aspartate aminotransferase, mitochondrial; Short=mAspAT; AltName: Full=Fatty acid-binding protein; Short=FABP-1; AltName: Full=Glutamate oxaloacetate transaminase 2; AltName: Full=Plasma membrane-associated fatty acid-binding protein;	1.000	1.009	1.728	2.191	1.620
gi|350592969|ref|XP_003483583.1| PREDICTED: phosphoglycerate mutase 1-like [Sus scrofa]	1.000	1.569	0.987	1.190	1.621
gi|335292272|ref|XP_003356696.1| PREDICTED: fumarylacetoacetase-like [Sus	1.000	1.473	3.380	2.688	1.629

scrofa]					
gi|122064241|sp|Q06AT0.3|HPCL1_PIG RecName: Full=Hippocalcin-like protein 1 >gi|178056468|ref|NP_001116598.1| hippocalcin-like protein 1 [Sus scrofa] >gi|115394792|gb|ABI97190.1| HPCL1 [Sus scrofa]	1.000	1.122	1.907	2.156	1.642
gi|350582722|ref|XP_003481338.1| PREDICTED: 14-3-3 protein theta isoform 1 [Sus scrofa]	1.000	1.696	1.369	1.297	1.659
gi|335294002|ref|XP_003357106.1| PREDICTED: 3-hydroxybutyrate dehydrogenase type 2-like isoform 2 [Sus scrofa] >gi|335294000|ref|XP_003129333.2| PREDICTED: 3-hydroxybutyrate dehydrogenase type 2-like isoform 1 [Sus scrofa]	1.000	2.360	0.622	0.791	1.663
gi|335297787|ref|XP_003131575.2| PREDICTED: puromycin-sensitive aminopeptidase isoform 1 [Sus scrofa]	1.000	1.467	0.977	0.697	1.664
gi|211578376|ref|NP_001129984.1| beta,beta-carotene 15,15~-monooxygenase [Sus scrofa] >gi|209571749|gb|ACI62530.1| beta-carotene 15,15~-monooxygenase 1 [Sus scrofa]	1.000	1.281	1.155	1.164	1.667
gi|239977642|sp|Q29183.1|TFF3_PIG RecName: Full=Trefoil factor 3; AltName: Full=Intestinal trefoil factor; Flags: Precursor	1.000	0.853	4.328	3.069	1.667
gi|47523516|ref|NP_999381.1| inositol monophosphatase 1 [Sus scrofa] >gi|68568737|sp|O77591.1|IMPA1_PIG RecName: Full=Inositol monophosphatase 1; Short=IMP 1; Short=IMPase 1; AltName: Full=Inositol-1(or 4)-monophosphatase 1; AltName: Full=Lithium-sensitive myo-inositol monophos	1.000	1.006	2.592	2.528	1.676
gi|297591965|ref|NP_001172061.1| leukotriene A-4 hydrolase [Sus scrofa] >gi|262204898|dbj|BAI48029.1| leukotriene A4 hydrolase [Sus scrofa]	1.000	1.816	0.956	0.872	1.682
gi|47522738|ref|NP_999119.1| aconitate hydratase, mitochondrial precursor [Sus scrofa] >gi|113159|sp|P16276.1|ACON_PIG RecName: Full=Aconitate hydratase,	1.000	1.770	1.054	1.058	1.686

mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor >gi|164315|gb|AAA30987.1| heart aconitas					
gi|345441801|ref|NP_001230874.1| TNF receptor-associated protein 1 [Sus scrofa]	1.000	1.932	0.894	0.943	1.689
gi|84028320|sp|Q9GKX6.1|GALM_PIG RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase >gi|47523866|ref|NP_999571.1| aldose 1-epimerase [Sus scrofa] >gi|11611545|dbj|BAB18973.1| aldose 1-epimerase [Sus scrofa]	1.000	1.501	0.864	0.931	1.695
gi|335305925|ref|XP_003135119.2| PREDICTED: LOW QUALITY PROTEIN: ubiquitin-like modifier activating enzyme 1 [Sus scrofa]	1.000	1.971	0.991	0.967	1.697
gi|1352666|sp|P11493.2|PP2AB_PIG RecName: Full=Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform; Short=PP2A-beta >gi|164298|gb|AAA30982.1| protein phosphatase 2A beta subunit, partial [Sus scrofa]	1.000	2.065	1.224	0.936	1.719
gi|194044626|ref|XP_001927289.1| PREDICTED: 14-3-3 protein beta/alpha isoform 1 [Sus scrofa]	1.000	2.234	1.272	0.948	1.724
gi|311250943|ref|XP_003124353.1| PREDICTED: 28 kDa heat- and acid-stable phosphoprotein-like [Sus scrofa]	1.000	0.855	1.997	1.660	1.733
gi|347543782|ref|NP_001231554.1| glutathione synthetase [Sus scrofa]	1.000	1.749	1.676	2.554	1.735
gi|162951821|ref|NP_001106165.1| heterogeneous nuclear ribonucleoprotein A/B [Sus scrofa] >gi|160858224|dbj|BAF93845.1| CArG-binding factor A [Sus scrofa]	1.000	0.998	2.227	1.941	1.736
gi|311268173|ref|XP_003131919.1| PREDICTED: myb-binding protein 1A [Sus scrofa]	1.000	0.608	2.053	1.081	1.739
gi|71361861|gb|AAZ30034.1| Mx1 [Sus scrofa]	1.000	0.967	1.069	0.893	1.743
gi|47522916|ref|NP_999215.1| glutathione S-transferase omega-1 [Sus scrofa] >gi|20141290|sp|Q9N1F5.2|GSTO1_PIG RecName: Full=Glutathione S-transferase	1.000	1.410	0.791	0.625	1.755

omega-1; Short=GSTO-1; AltName: Full=Glutathione S-transferase omega 1-1; Short=GSTO 1-1; AltName: Full=Glutathione-dependent d					
gi|335310331|ref|XP_003361983.1| PREDICTED: poly(U)-binding-splicing factor PUF60-like [Sus scrofa]	1.000	1.293	1.065	0.792	1.760
gi|52000924|sp|Q29238.2|CLIC1_PIG RecName: Full=Chloride intracellular channel protein 1; AltName: Full=Nuclear chloride ion channel 27	1.000	1.730	0.733	0.748	1.761
gi|197251946|ref|NP_001127815.1| actin-related protein 3 [Sus scrofa] >gi|195562215|gb|ACG50179.1| actin-related protein 3-like protein [Sus scrofa]	1.000	1.498	1.237	1.031	1.763
gi|48675953|ref|NP_001001643.1| rab GDP dissociation inhibitor beta [Sus scrofa] >gi|75043802|sp|Q6Q7J2.1|GDIB_PIG RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2 >gi|45758488|gb|AAS76	1.000	2.866	1.102	0.916	1.781
gi|335281104|ref|XP_003353734.1| PREDICTED: argininosuccinate synthase [Sus scrofa]	1.000	1.671	2.308	2.587	1.797
gi|194041937|ref|XP_001928912.1| PREDICTED: alpha-centractin [Sus scrofa]	1.000	1.787	1.406	1.284	1.802
gi|319401915|ref|NP_001188313.1| rho GDP-dissociation inhibitor 1 [Sus scrofa] >gi|315321426|gb|ADU04840.1| Rho GDP dissociation inhibitor alpha [Sus scrofa]	1.000	2.584	0.973	1.127	1.810
gi|311277231|ref|XP_003135559.1| PREDICTED: trimethyllysine dioxygenase, mitochondrial-like [Sus scrofa]	1.000	1.143	5.553	3.922	1.817
gi|311252247|ref|XP_003124998.1| PREDICTED: macrophage-capping protein-like isoform 4 [Sus scrofa] >gi|311252243|ref|XP_003124996.1| PREDICTED: macrophage-capping protein-like isoform 2 [Sus scrofa] >gi|311252249|ref|XP_003124997.1| PREDICTED: macrophage-capping protein-like isofor	1.000	1.498	2.400	4.476	1.818

gi|311252615|ref|XP_003125184.1| PREDICTED: ubiquitin-40S ribosomal protein S27a-like [Sus scrofa] >gi|311252617|ref|XP_003125185.1| PREDICTED: ubiquitin-40S ribosomal protein S27a-like [Sus scrofa]	1.000	1.316	3.017	2.609	1.820
gi|350582355|ref|XP_003354851.2| PREDICTED: exportin-1 [Sus scrofa]	1.000	2.597	2.292	1.444	1.821
gi|223046|prf||0410468A aminotransferase,Asp	1.000	1.169	1.787	1.918	1.829
gi|999620|pdb|1MLD|D Chain D, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases >gi|999618|pdb|1MLD|B Chain B, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine	1.000	2.014	1.057	0.879	1.832
gi|311252403|ref|XP_003125080.1| PREDICTED: sepiapterin reductase-like [Sus scrofa]	1.000	1.394	1.350	1.971	1.837
gi|148237564|ref|NP_001090977.1| adenylosuccinate synthetase isozyme 2 [Sus scrofa] >gi|189031715|sp|A4Z6H1.1|PURA2_PIG RecName: Full=Adenylosuccinate synthetase isozyme 2; Short=AMPSase 2; Short=AdSS 2; AltName: Full=Adenylosuccinate synthetase, acidic isozyme; AltName: Full=Adeny	1.000	2.151	1.756	2.876	1.842
gi|311253255|ref|XP_003125488.1| PREDICTED: alanine aminotransferase 1-like [Sus scrofa]	1.000	1.108	1.782	2.460	1.848
gi|212549619|ref|NP_001131099.1| ERO1-like protein alpha precursor [Sus scrofa] >gi|226741411|sp|B6CVD7.1|ERO1A_PIG RecName: Full=ERO1-like protein alpha; Short=ERO1-L; Short=ERO1-L-alpha; AltName: Full=Endoplasmic oxidoreductin-1-like protein; AltName: Full=Oxidoreductin-1-L-alpha	1.000	1.314	1.946	1.577	1.857
gi|335300581|ref|XP_003358947.1| PREDICTED: T-complex protein 1 subunit theta-like isoform 1 [Sus scrofa]	1.000	1.545	0.974	0.794	1.863
gi|164414678|emb|CAO81735.1| Alternative Pig Liver Esterase [Sus scrofa]	1.000	0.927	1.243	1.579	1.871
gi|311270662|ref|XP_003132938.1| PREDICTED:	1.000	1.826	3.013	2.036	1.876

phosphatidylethanolamine-binding protein 1-like [Sus scrofa]					
gi|281427370|ref|NP_001163993.1| T-complex protein 1 subunit eta [Sus scrofa] >gi|262036937|dbj|BAI47603.1| chaperonin containing TCP1, subunit 7 (eta) [Sus scrofa]	1.000	1.904	0.901	0.911	1.878
gi|222136590|ref|NP_001138373.1| proteasome subunit alpha type-5 [Sus scrofa]	1.000	1.041	2.413	2.229	1.879
gi|311245810|ref|XP_001924714.2| PREDICTED: GTP:AMP phosphotransferase, mitochondrial isoform 1 [Sus scrofa]	1.000	1.660	0.785	1.152	1.897
gi|350583020|ref|XP_003481419.1| PREDICTED: zinc finger protein 706-like [Sus scrofa]	1.000	1.271	1.945	2.395	1.900
gi|335288894|ref|XP_003126772.2| PREDICTED: ubiquitin-conjugating enzyme E2 N-like [Sus scrofa]	1.000	1.780	2.226	1.835	1.902
gi|347300325|ref|NP_001231461.1| dehydrogenase/reductase SDR family member 11 [Sus scrofa]	1.000	2.520	1.354	1.392	1.907
gi|350578507|ref|XP_003121503.3| PREDICTED: asparaginyl-tRNA synthetase, cytoplasmic-like [Sus scrofa]	1.000	1.923	1.266	1.484	1.920
gi|47523456|ref|NP_999349.1| serine/threonine-protein phosphatase PP1-beta catalytic subunit [Sus scrofa] >gi|47116968|sp|P61292.3|PP1B_PIG RecName: Full=Serine/threonine-protein phosphatase PP1-beta catalytic subunit; Short=PP-1B >gi|89257972|gb|ABD65256.1| protein phosphatase	1.000	1.843	1.251	1.257	1.937
gi|195539476|ref|NP_001124208.1| bifunctional purine biosynthesis protein PURH [Sus scrofa] >gi|192383834|gb|ACF04802.1| 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Sus scrofa]	1.000	1.674	0.855	1.284	1.949
gi|350582612|ref|XP_003481312.1| PREDICTED: protein phosphatase 1G-like [Sus scrofa]	1.000	1.641	2.347	2.165	1.949
gi|335282386|ref|XP_003354050.1| PREDICTED: elongation factor 2 [Sus scrofa]	1.000	1.833	1.100	0.974	1.955

gi|335293373|ref|XP_003356947.1| PREDICTED: UDP-glucose 6-dehydrogenase-like isoform 1 [Sus scrofa]	1.000	1.734	1.612	1.136	1.981
gi|311273061|ref|XP_001925202.2| PREDICTED: villin 1 [Sus scrofa]	1.000	1.437	1.059	0.998	1.990
gi|122114359|gb|AAY42145.2| cathepsin D [Sus scrofa]	1.000	1.729	1.191	1.125	1.992
gi|345199288|ref|NP_001230831.1| protein phosphatase 1, regulatory (inhibitor) subunit 7 [Sus scrofa]	1.000	1.888	1.653	0.854	2.001
gi|346986388|ref|NP_001231345.1| profilin-1 [Sus scrofa]	1.000	2.107	1.375	1.305	2.004
gi|350596362|ref|XP_003361090.2| PREDICTED: CD2-associated protein-like [Sus scrofa]	1.000	1.357	5.830	3.915	2.031
gi|350586543|ref|XP_003482212.1| PREDICTED: glutamate--cysteine ligase catalytic subunit isoform 2 [Sus scrofa]	1.000	2.588	1.351	1.762	2.034
gi|350585077|ref|XP_003481871.1| PREDICTED: hypothetical protein LOC100739300 [Sus scrofa]	1.000	0.914	1.823	1.807	2.044
gi|335309827|ref|XP_003361787.1| PREDICTED: nuclear autoantigenic sperm protein, partial [Sus scrofa]	1.000	1.435	2.468	1.368	2.088
gi|47523618|ref|NP_999441.1| citrate synthase, mitochondrial precursor [Sus scrofa] >gi|116470|sp|P00889.2|CISY_PIG RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor >gi|164419|gb|AAA31017.1| citrate synthase precursor (EC 4.1.3.7) [Sus scrofa]	1.000	2.016	0.966	1.408	2.124
gi|112976|sp|P00503.3|AATC_PIG RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Glutamate oxaloacetate transaminase 1; AltName: Full=Transaminase A >gi|47522636|ref|NP_999092.1| aspartate aminotransferase, cytoplasmic [Sus scrofa] >gi|300557343|emb|CBV09643.1|	1.000	1.113	2.697	3.518	2.144
gi|262072939|dbj|BAI47777.1| CCHC-type zinc finger, nucleic acid binding protein [Sus scrofa]	1.000	1.380	2.221	1.925	2.168
gi|35384836|gb|AAQ84564.1| electron transfer flavoprotein alpha subunit precursor [Sus scrofa]	1.000	2.734	1.242	1.160	2.173

gi|24987656|pdb|1LXE|A Chain A, Crystal Structure Of The Cathelicidin Motif Of Protegrins >gi|24987482|pdb|1KWI|A Chain A, Crystal Structure Analysis Of The Cathelicidin Motif Of Protegrins	1.000	0.329	1.160	0.826	2.176
gi|311267406|ref|XP_003131549.1| PREDICTED: gasdermin-B-like [Sus scrofa]	1.000	1.558	1.337	1.747	2.213
gi|346644743|ref|NP_001231138.1| calmodulin 3 [Sus scrofa] >gi|346644746|ref|NP_001231139.1| calmodulin 1 [Sus scrofa] >gi|311252670|ref|XP_003125211.1| PREDICTED: calmodulin-like [Sus scrofa]	1.000	1.687	2.281	4.172	2.230
gi|194040450|ref|XP_001927992.1| PREDICTED: lactoylglutathione lyase isoform 1 [Sus scrofa]	1.000	1.245	1.591	3.199	2.250
gi|281500757|pdb|3FX4|A Chain A, Porcine Aldehyde Reductase In Ternary Complex With Inhibitor >gi|229597975|pdb|3H4G|A Chain A, Structure Of Aldehyde Reductase Holoenzyme In Complex With Potent Aldose Reductase Inhibitor Fidarestat: Implications For Inhibitor Binding And S	1.000	3.159	1.610	1.180	2.261
gi|311261988|ref|XP_003128958.1| PREDICTED: phosphoglucomutase-2 [Sus scrofa]	1.000	1.677	1.345	1.583	2.313
gi|194043292|ref|XP_001928111.1| PREDICTED: 14-3-3 protein eta [Sus scrofa]	1.000	3.227	1.275	1.172	2.330
gi|112980811|gb|ABI29187.1| glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]	1.000	2.033	1.297	0.982	2.414
gi|346986428|ref|NP_001231362.1| heat shock 90kD protein 1, beta [Sus scrofa]	1.000	1.860	1.323	0.967	2.418
gi|47523764|ref|NP_999518.1| peptidyl-prolyl cis-trans isomerase A [Sus scrofa] >gi|51702768|sp|P62936.2|PPIA_PIG RecName: Full=Peptidyl-prolyl cis-trans isomerase A; Short=PPIase A; AltName: Full=Cyclophilin A; AltName: Full=Cyclosporin A-binding protein; AltName: Full=Rotamas	1.000	2.721	1.273	0.985	2.422
gi|349732201|ref|NP_001231854.1| dpy-30 homolog [Sus scrofa]	1.000	0.546	1.038	2.141	2.438
gi|1845|emb|CAA48565.1| aminoacylase I [Sus scrofa]	1.000	1.855	2.955	3.909	2.438

gi|346644699|ref|NP_001231019.1| protein SET [Sus scrofa]	1.000	1.404	4.301	2.967	2.469
gi|237681312|ref|NP_001153744.1| protein S100-A12 [Sus scrofa] >gi|126302600|sp|P80310.2|S10AC_PIG RecName: Full=Protein S100-A12; AltName: Full=Calgranulin-C; Short=CAGC; AltName: Full=Extracellular newly identified RAGE-binding protein; Short=EN-RAGE; AltName: Full=S100 calcium-b	1.000	0.787	1.875	1.494	2.476
gi|122220|sp|P17630.1|TCO1_PIG RecName: Full=Transcobalamin-1; Short=TC-1; AltName: Full=Cobalophilin; AltName: Full=Haptocorrin; AltName: Full=Protein R; AltName: Full=Transcobalamin I; Short=TC I; Short=TCI; Flags: Precursor >gi|1964|emb|CAA36800.1| unnamed protein product [Sus	1.000	1.622	1.801	1.275	2.573
gi|335284301|ref|XP_003354567.1| PREDICTED: T-complex protein 1 subunit zeta-like isoform 2 [Sus scrofa]	1.000	2.957	1.740	1.338	2.699
gi|190360639|ref|NP_001121941.1| interferon-induced 17 kDa protein [Sus scrofa] >gi|182406743|gb|ACB87600.1| interferon stimulated gene 15 [Sus scrofa]	1.000	0.780	2.300	4.581	2.706
gi|1364248|emb|CAA82246.1| glucosephosphate isomerase [Sus scrofa]	1.000	2.652	1.874	1.372	2.710
gi|350583022|ref|XP_001927263.3| PREDICTED: 14-3-3 protein zeta/delta [Sus scrofa]	1.000	3.308	1.517	1.086	2.726
gi|343962597|ref|NP_001230636.1| cytosolic non-specific dipeptidase [Sus scrofa]	1.000	1.600	3.758	3.289	2.765
gi|335281222|ref|XP_003353764.1| PREDICTED: probable 2-ketogluconate reductase-like isoform 2 [Sus scrofa]	1.000	2.964	2.138	1.420	2.895
gi|194043017|ref|XP_001928354.1| PREDICTED: MGC159817 protein isoform 1 [Sus scrofa]	1.000	2.079	1.832	2.726	2.978
gi|311259408|ref|XP_003128090.1| PREDICTED: peroxiredoxin-1 isoform 5 [Sus scrofa]	1.000	2.943	1.704	1.309	3.046
gi|90200404|gb|ABD92704.1| triosephosphate isomerase 1 [Sus scrofa]	1.000	2.706	1.493	1.114	3.048
gi|219521990|ref|NP_001137182.1| granzyme B	1.000	1.167	3.528	4.173	3.057

precursor [Sus scrofa] >gi|216408333|gb|ACJ72857.1| granzyme B [Sus scrofa]					
gi|7288152|dbj|BAA92850.1| esterase D [Sus scrofa]	1.000	3.122	1.562	2.008	3.194
gi|229620|prf||770227A dehydrogenase H4,lactate	1.000	2.789	2.491	1.866	3.254
gi|264681436|ref|NP_001161113.1| copper transport protein ATOX1 [Sus scrofa] >gi|262036932|dbj|BAI47601.1| antioxidant protein 1 homolog (yeast) [Sus scrofa]	1.000	1.280	2.727	3.209	3.307
gi|335300686|ref|XP_003358992.1| PREDICTED: carbonyl reductase [NADPH] 1-like [Sus scrofa]	1.000	3.339	1.314	1.332	3.405
gi|47523158|ref|NP_999015.1| glutathione S-transferase A2 [Sus scrofa] >gi|1185280|emb|CAA93434.1| glutathione S-transferase [Sus scrofa]	1.000	2.229	1.726	1.798	3.489
gi|162952052|ref|NP_001106151.1| transketolase [Sus scrofa] >gi|159502444|gb|ABW97521.1| transketolase [Sus scrofa]	1.000	1.819	2.627	3.235	3.514
gi|116047849|gb|ABJ53147.1| glutathione S-transferase mu 2 [Sus scrofa]	1.000	2.290	1.598	1.589	3.519
gi|350597032|ref|XP_001925921.4| PREDICTED: aldehyde dehydrogenase family 1 member A3, partial [Sus scrofa]	1.000	2.310	4.200	3.338	3.713
gi|311251248|ref|XP_003124516.1| PREDICTED: apoptosis-associated speck-like protein containing a CARD-like isoform 1 [Sus scrofa]	1.000	3.139	6.012	6.925	3.814
gi|266018|gb|AAB25484.1| calmodulin=low affinity vasoactive intestinal polypeptide binding protein [swine, liver, Peptide Partial, 34 aa]	1.000	1.397	2.473	2.726	4.203