

Table S1. Proteins Quantified. The protein list is organized based upon the Sum PEP Score. All proteins listed had a q-value of zero.

Accession	Description	Sum PEP Score	Abundances (Scaled): F1: Breast	Abundances (Scaled): F2: Breast	Abundances (Scaled): F3: Breast	Abundances (Scaled): F4: Leg	Abundances (Scaled): F5: Leg	Abundances (Scaled): F6: Leg	Abundances (Scaled): F7: Thigh	Abundances (Scaled): F8: Thigh	Abundances (Scaled): F9: Thigh	Breast AVE	Leg AVE	Thigh AVE	TTEST B-L	TTEST B-T	TTEST L-T
XP_019472906.1	PREDICTED: LOW QUALITY PROTEIN: titin [Meleagris gallopavo]	15405.3	81.3	76.3	80.7	103.1	102.4	102.6	117.7	117.7	118.2	79.4	102.7	117.9	1.27E-04	1.72E-05	5.72E-07
XP_019474851.1	PREDICTED: pyruvate kinase PKM isoform X3 [Meleagris gallopavo]	1657.1	142.7	140.7	150.3	69.6	69.6	71.9	81.3	87.5	86.3	144.6	70.4	85.0	1.64E-05	6.90E-05	2.01E-03
NP_001290108.1	glyceraldehyde 3-phosphate dehydrogenase [Meleagris gallopavo]	1428.5	126.4	126.3	135.6	71.8	64.5	65.2	101.3	104.4	104.4	129.4	67.2	103.4	8.66E-05	1.31E-03	1.42E-04
XP_010707950.1	PREDICTED: serum albumin [Meleagris gallopavo]	938.7	49.5	45.5	47.7	138.7	148.9	146.4	112	107.6	103.7	47.6	144.7	107.8	7.75E-06	2.26E-05	6.92E-04
XP_010714343.2	PREDICTED: LOW QUALITY PROTEIN: phosphoglucotransferase 1 [Meleagris gallopavo]	900.3	166.3	146.4	151.5	64.9	65.2	68.3	80.6	78.4	78.4	154.7	66.1	79.1	1.28E-04	2.30E-04	5.81E-04
XP_003204057.2	PREDICTED: alpha-actinin-2 [Meleagris gallopavo]	832.2	55.2	50.3	53.1	148.7	149.2	144.6	97.1	101.8	100	52.9	147.5	99.6	1.28E-06	1.87E-05	1.81E-05
XP_010713665.1	PREDICTED: phosphoglycerate kinase 1 [Meleagris gallopavo]	798.1	158.7	143.6	162.6	64.2	63.8	70	77.8	79.1	80.1	155.0	66.0	79.0	1.31E-04	2.00E-04	3.53E-03
XP_010716042.1	PREDICTED: glucose-6-phosphate isomerase, partial [Meleagris gallopavo]	626.2	145	130.2	138.8	76.2	74.8	76.8	84.5	86	87.7	138.0	75.9	86.1	1.38E-04	2.92E-04	7.66E-04
XP_019469471.1	PREDICTED: myomesin-1 [Meleagris gallopavo]	602.1	103	96.7	109.1	105.4	105.2	105.3	90.7	93	91.7	102.9	105.3	91.8	5.45E-01	3.77E-02	3.55E-05
XP_010713041.1	PREDICTED: phosphoglycerate mutase 1 [Meleagris gallopavo]	545.7	136.6	122.5	133.8	70.5	103.7	72.6	98.8	81.7	79.8	131.0	82.3	86.8	1.36E-02	3.99E-03	7.33E-01
XP_019472960.1	PREDICTED: LOW QUALITY PROTEIN: nebulin, partial [Meleagris gallopavo]	540.4	59.2	52.7	56.3	125	121.7	124.6	122.1	120.2	118.3	56.1	123.8	120.2	6.04E-06	7.90E-06	7.77E-02
XP_010706094.1	PREDICTED: M-protein, striated muscle [Meleagris gallopavo]	526.0	99.9	94.1	103.8	104.8	104.6	105.5	92	97.6	97.7	99.3	105.0	95.8	1.14E-01	3.60E-01	8.44E-03
XP_010713921.1	PREDICTED: glycogen debranching enzyme isoform X1 [Meleagris gallopavo]	517.1	138.7	129.1	139.1	84.3	83.5	79.3	87	76.5	82.6	135.6	82.4	82.0	1.24E-04	2.76E-04	9.27E-01
XP_010716134.2	PREDICTED: triosephosphate isomerase [Meleagris gallopavo]	494.0	145.7	128.8	129.9	84	81.2	83.5	80.8	81.6	84.5	134.8	82.9	82.3	7.17E-04	7.08E-04	6.94E-01
XP_010710566.1	PREDICTED: LOW QUALITY PROTEIN: obscurin [Meleagris gallopavo]	451.0	111.5	103.1	106.5	88.1	86.2	88.7	105.4	105.4	105	107.0	87.7	105.3	1.62E-03	5.10E-01	2.12E-05
XP_010713505.1	PREDICTED: four and a half LIM domains protein 1 isoform X1 [Meleagris gallopavo]	435.1	2.4	2.6	2.9	137.3	136.5	135.4	162.4	158	162.6	2.6	136.4	161.0	1.97E-09	4.93E-08	1.04E-04
NP_001290122.1	myosin light chain 1/3, skeletal muscle isoform [Meleagris gallopavo]	419.5	19.4	17.2	19.5	178.8	178.8	177.4	102.7	96.9	109.3	18.7	178.3	103.0	5.64E-09	2.11E-05	3.12E-05
XP_010721062.1	PREDICTED: alpha-enolase isoform X2 [Meleagris gallopavo]	410.8	101.4	101	112.6	93.2	98.1	100	96.1	96	101.4	105.0	97.1	97.8	1.41E-01	1.63E-01	7.99E-01
XP_003202767.1	PREDICTED: calsequestrin-2 [Meleagris gallopavo]	410.0	28.8	28.3	29.8	158.2	157.1	158.5	119.8	111.1	108.4	29.0	157.9	113.1	3.06E-09	1.71E-05	2.06E-04
XP_010705319.1	PREDICTED: actin, alpha skeletal muscle [Meleagris gallopavo]	401.9	39	36.8	39.3	149.4	152.3	150.6	111.1	110	111.5	38.4	150.8	110.9	6.63E-08	1.47E-07	1.95E-06
XP_010724398.1	PREDICTED: creatine kinase S-type, mitochondrial [Meleagris gallopavo]	367.3	69.1	60.2	65.1	132.2	149.1	112.6	103.5	111.8	96.4	64.8	131.3	103.9	3.60E-03	1.60E-03	7.49E-02
XP_003205196.1	PREDICTED: carbonic anhydrase 3-like [Meleagris gallopavo]	354.4	101.6	91.6	98.2	158.1	147	142.7	53.9	55.6	51.3	97.1	149.3	53.6	6.66E-04	1.67E-04	3.60E-05
XP_019473010.1	PREDICTED: LIM domain-binding protein 3 isoform X6 [Meleagris gallopavo]	354.1	51.6	46.8	52.8	143.6	141.8	137.3	106.2	105.9	114.1	50.4	140.9	108.7	4.20E-06	5.67E-05	6.02E-04
XP_003206814.3	PREDICTED: LOW QUALITY PROTEIN: heat shock-related 70 kDa protein 2 [Meleagris gallopavo]	343.9	85.7	77.6	86.7	124.5	129.8	124.1	92.4	90	89.1	83.3	126.1	90.5	2.34E-04	7.82E-02	6.87E-05
XP_003212746.1	PREDICTED: heat shock cognate 71 kDa protein [Meleagris gallopavo]	330.4	93.2	87.5	105.1	113.2	109.3	110	87.6	99.4	94.7	95.3	110.8	93.9	4.30E-02	8.37E-01	9.59E-03
XP_003211747.1	PREDICTED: malate dehydrogenase, mitochondrial [Meleagris gallopavo]	328.3	56.2	53.2	56.2	144.2	151.8	145.4	98.1	98.2	96.7	55.2	147.1	97.7	3.60E-06	2.80E-06	3.32E-05
XP_019476563.1	PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Meleagris gallopavo]	318.7	65.7	63	67.4	126.2	116.5	119.8	112.7	114.3	114.7	65.4	120.8	113.9	5.90E-05	4.36E-06	7.59E-02
XP_010719135.1	PREDICTED: adenylate kinase isoenzyme 1 isoform X1 [Meleagris gallopavo]	317.5	128.6	121.7	121.3	80.2	76.4	86.8	102.7	90.5	91.9	123.9	81.1	95.0	3.76E-04	3.11E-03	4.72E-02
XP_010706093.1	PREDICTED: M-protein, striated muscle-like [Meleagris gallopavo]	313.8	98.1	94.1	104.1	101.5	104.9	108.6	92.4	100	96.3	98.8	105.0	96.2	1.55E-01	5.25E-01	4.33E-02
XP_010707718.1	PREDICTED: ATP synthase subunit beta, mitochondrial [Meleagris gallopavo]	290.9	25	20.2	24.5	158.1	158.5	159.5	115.6	121.3	117.4	23.2	158.7	118.1	1.11E-07	1.96E-06	1.97E-05
XP_003209725.3	PREDICTED: aspartate aminotransferase, mitochondrial [Meleagris gallopavo]	286.4	104.8	98.6	105.3	106.4	105.8	102.8	95.6	92.5	88.3	102.9	105.0	92.1	4.35E-01	2.35E-02	5.76E-03
XP_010724123.1	PREDICTED: fructose-1,6-bisphosphatase isozyme 2 isoform X1 [Meleagris gallopavo]	281.6	143.1	138.7	146.4	83.2	90.3	89.7	68.3	74.1	66.2	142.7	87.7	69.5	6.60E-05	2.30E-05	5.15E-03
XP_003210442.2	PREDICTED: annexin A6 isoform X1 [Meleagris gallopavo]	281.4	79.3	75	79.9	145.5	135.2	145.9	80.5	78.4	80.4	78.1	142.2	79.8	7.43E-05	3.71E-01	6.26E-05
XP_019467155.1	PREDICTED: LOW QUALITY PROTEIN: ATP-dependent 6-phosphofructokinase, muscle type [Meleagris gallopavo]	264.0	147.7	64.8	71.1	100.1	107.2	103.8	126.3	125.6	126.4	70.2	103.7	126.1	7.00E-04	4.29E-05	4.10E-04
XP_019477138.1	PREDICTED: myosin-1B-like [Meleagris gallopavo]	261.5	31	27.3	31.6	176.6	181.7	178.1	94.2	88.8	90.8	30.0	178.8	91.3	2.05E-07	7.77E-06	2.32E-06
XP_010723192.2	PREDICTED: elongation factor 2 [Meleagris gallopavo]	256.0	82.5	80.3	82.5	122.1	127.8	121.2	93.6	90	100	81.8	123.7	94.5	4.40E-05	1.33E-02	1.24E-03
XP_010709371.2	PREDICTED: L-lactate dehydrogenase A chain-like, partial [Meleagris gallopavo]	254.1	105.3	100.1	98.4	93.9	97.6	99.7	102.7	103.4	99.1	101.3	97.1	101.7	1.92E-01	8.59E-01	9.64E-02
XP_003206336.1	PREDICTED: troponin I, fast skeletal muscle [Meleagris gallopavo]	247.1	44	41.9	41.8	163.9	167.3	170.2	89.1	96.2	85.6	42.6	167.1	90.3	3.65E-07	1.18E-04	2.88E-05
NP_001290136.1	serotransferrin precursor [Meleagris gallopavo]	246.2	45.2	40	42.5	156.4	156	157.2	105.3	98.1	99.2	42.6	156.5	100.9	2.01E-07	2.71E-05	1.63E-05
XP_010718838.1	PREDICTED: glycerol 3-phosphate dehydrogenase [NAD(+)], cytoplasmic [Meleagris gallopavo]	245.6	187	170.2	179	41.1	44.1	43.7	77.5	79.2	78.2	178.7	43.0	78.3	1.04E-05	3.28E-05	4.87E-06
XP_019465869.1	PREDICTED: transitional endoplasmic reticulum ATPase isoform X1 [Meleagris gallopavo]	240.2	78.6	71.7	82.5	130.2	131.4	132.8	89.3	91.5	92	77.6	131.5	90.9	7.72E-05	1.50E-02	3.47E-06
XP_010708730.1	PREDICTED: aconitase hydratase, mitochondrial [Meleagris gallopavo]	235.9	35.2	39.1	30.5	133.2	143.6	153.2	120.8	122.9	121.4	34.9	143.3	121.7	6.64E-05	4.54E-06	2.04E-02
XP_010719484.2	PREDICTED: myosin heavy chain, skeletal muscle, adult [Meleagris gallopavo]	209.8	155.7	109.6	144.1	90.6	98.8	88.9	81.1	58.9	72.5	136.5	92.7	70.8	3.67E-02	1.27E-02	3.73E-02
XP_003211746.1	PREDICTED: heat shock protein beta-1 [Meleagris gallopavo]	198.8	21.9	21.8	24.4	120.4	137.1	175.7	122.8	137.8	138.1	22.7	144.4	132.9	1.76E-03	2.76E-05	5.39E-01
XP_010708318.1	PREDICTED: PDZ and LIM domain protein 5 isoform X6 [Meleagris gallopavo]	194.9	63.8	58.7	63.6	136.1	136.3	147.7	94	99.5	100.3	62.0	140.0	97.9	4.86E-05	1.17E-04	6.18E-04
XP_010710229.1	PREDICTED: heat shock protein HSP 90-alpha [Meleagris gallopavo]	194.6	75.3	70.6	74.8	120.9	125.8	127.4	102.7	99.2	103.2	73.6	124.7	101.7	3.16E-05	1.34E-04	5.86E-04
XP_003209375.1	PREDICTED: actin, cytoplasmic type 5 [Meleagris gallopavo]	193.4	39.4	35.2	15.8	163.1	150.2	127.4	121.6	127.9	119.4	30.1	146.9	123.0	7.82E-04	2.72E-04	8.98E-02
XP_003212096.2	PREDICTED: elongation factor 1-alpha 2 [Meleagris gallopavo]	181.2	80.6	76.3	75.6	109	106	114.4	114.9	115	108	77.5	109.8	112.6	3.76E-04	2.30E-04	4.49E-01
XP_010704712.1	PREDICTED: glycogen phosphorylase, brain form [Meleagris gallopavo]	179.6	131.3	128.9	135.4	82.1	78.7	78.7	86.6	90	88.2	131.9	79.8	88.3	1.93E-05	3.41E-05	4.92E-03
XP_010726365.1	PREDICTED: beta-enolase-like [Meleagris gallopavo]	179.3	122.2	113.1	121.4	85.5	83.6	89.1	86.8	85.4	112.8	118.9	86.1	95.0	5.91E-04	6.33E-02	3.80E-01
XP_010708319.1	PREDICTED: PDZ and LIM domain protein 5 isoform X7 [Meleagris gallopavo]	170.0	12.7	12.7	13.1	153.2	153.2	169.5	135.2	128.4	121.9	12.8	158.6	128.5	1.15E-05	7.25E-06	1.06E-02
XP_010711942.1	PREDICTED: desmin [Meleagris gallopavo]	161.7	42	34.8	36.5	145.8	142.2	133	125.7	120.5	119.6	37.8	140.3	121.9	1.98E-05	8.24E-06	1.24E-02
XP_010712691.1	PREDICTED: myozenin-1 isoform X1 [Meleagris gallopavo]	159.5	42.9	47	42.9	122.9	127.4	117.4	134.7	133.8	130.9	44.3	122.6	133.1	1.65E-05	9.72E-07	2.74E-02
XP_010722346.1	PREDICTED: immunoglobulin-like and fibronectin type III domain-containing protein 1 [Meleagris gallopavo]	159.4	290.2	281.2	301.7	3.3	9.9	4.7	2.6	3.2	3.1	291.0	6.0	3.0	1.39E-06	1.08E-06	2.11E-01
XP_010709311.1	PREDICTED: troponin T, fast skeletal muscle isoform X2 [Meleagris gallopavo]	159.2	48.9	48.2	66.2	159.3	153.9	175.1	83.1	86.9	78.6	54.4	162.8	82.9	2.36E-04	1.10E-02	3.00E-04
XP_010718246.1	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial [Meleagris gallopavo]	158.6	53.5	50.3	53.3	143	140.5	135.3	109.3	107.2	107.7	52.4	139.6	108.1	3.98E-06	1.35E-06	1.80E-04
XP_010713032.2	PREDICTED: aspartate aminotransferase, cytoplasmic, partial [Meleagris gallopavo]	157.7	54.6	55.3	52.3	118.3	119.4	119.7	136.2	122.8	121.3	54.1	119.1	126.8	3.36E-07	1.13E-04	1.84E-01
XP_010716826.1	PREDICTED: cytochrome b-c1 complex subunit 1, mitochondrial [Meleagris gallopavo]	157.7	53.4	52.1	53	136.											

XP_010723540.1	PREDICTED: transitional endoplasmic reticulum ATPase-like [Meleagris gallopavo]	138.7	47.7		56.6	235.8	89.2	229.9	125.5	64.1	51.1	52.2	185.0	80.2	1.21E-01	4.16E-01	1.20E-01
XP_010707027.1	PREDICTED: myomesin-1-like [Meleagris gallopavo]	137.8	81.4	75.9	79.3	103.8	100.4	110.5	121.6	107.9	119.2	78.9	104.9	116.2	1.52E-03	1.17E-03	9.31E-02
XP_010723474.1	PREDICTED: ATP synthase subunit alpha, mitochondrial [Meleagris gallopavo]	137.6	20.4	18.8	17.6	149.9	160	149.7	128	124.9	130.7	18.9	153.2	127.9	2.74E-06	5.11E-07	2.61E-03
XP_010711008.2	PREDICTED: vimentin [Meleagris gallopavo]	133.6	35.7	40.7	44.1	140	141.7	144.2	118.8	122.9	111.9	40.2	142.0	117.9	3.08E-06	4.27E-05	2.17E-03
XP_010717663.1	PREDICTED: sarcoplasmic reticulum protein X1 [Meleagris gallopavo]	132.2	53.6	56.2	53.9	124.1	108.9	109.7	139.7	129.7	124.3	54.6	114.2	131.2	2.84E-04	7.50E-05	6.39E-02
XP_003204233.1	PREDICTED: tropomyosin alpha-3 chain isoform X5 [Meleagris gallopavo]	129.5	51.6	52	33.4	142.1	251	153.9	74.8	71.2	70.1	45.7	182.3	72.0	1.75E-02	1.38E-02	3.31E-02
XP_010708361.1	PREDICTED: PDZ and LIM domain protein 3 isoform X1 [Meleagris gallopavo]	127.2	58.3	70.5	58.1	141.5	134.5	141	97.3	100.8	97.8	62.3	139.0	98.6	8.11E-05	1.02E-03	8.68E-05
XP_010715974.1	PREDICTED: isocitrate dehydrogenase (NADP), mitochondrial [Meleagris gallopavo]	127.2	12.8	12.5	16.5	174	170.3	171.5	112.9	118.1	114.1	13.9	171.9	114.1	7.77E-08	1.98E-06	1.50E-05
XP_010717664.1	PREDICTED: sarcoplasmic reticulum protein X2 [Meleagris gallopavo]	125.6				192	146.9	181.8	159.7	219.6		#DIV/0!	173.6	189.7	#DIV/0!	#DIV/0!	6.11E-01
XP_003212226.1	PREDICTED: protein deglycase DJ-1 [Meleagris gallopavo]	125.6	90.7	78.4	84	115.9	122.1	125.2	92.6	97.5	93.7	84.4	121.1	94.6	1.21E-03	5.66E-02	1.05E-03
XP_003207490.1	PREDICTED: 80 kDa heat shock protein, mitochondrial [Meleagris gallopavo]	124.3	88.2	75.1	84.1	118.5	121	125.1	98.5	94.8	94.8	82.5	121.5	96.0	8.29E-04	2.88E-02	3.67E-04
XP_010704813.2	PREDICTED: malate dehydrogenase, cytoplasmic, partial [Meleagris gallopavo]	124.2	39	35.8	39.8	148.2	138.1	150	117.7	116.6	114.9	38.2	145.4	116.4	1.04E-05	7.45E-07	1.56E-03
XP_003202395.1	PREDICTED: myoglobin [Meleagris gallopavo]	118.3	0.6	0.7		230.7	258.7	238.3	62.8	55.3	52.9	0.7	242.6	57.0	1.94E-04	6.91E-04	3.09E-05
XP_010706908.2	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial, partial [Meleagris gallopavo]	117.4	49.5	54	54	152.1	147.3	156.5	99.7	100.3	86.5	52.5	152.0	95.5	5.28E-06	8.23E-04	4.17E-04
XP_003204611.1	PREDICTED: trifunctional enzyme subunit alpha, mitochondrial [Meleagris gallopavo]	112.5	50.6	38.6	41.5	141.7	137.3	146.6	119.2	112.9	111.5	43.6	141.9	114.5	2.61E-05	8.05E-05	1.58E-03
NP_001290128.1	ryanodine receptor 1 (skeletal) [Meleagris gallopavo]	111.6	93.9	80.5	88.6	96.9	93.1	96.3	118.1	116.1	116.4	87.7	95.4	116.9	1.29E-01	1.78E-03	8.77E-05
XP_010708108.1	PREDICTED: hydroxyacyl-coenzyme A dehydrogenase, mitochondrial [Meleagris gallopavo]	108.6	51.1	45.1	48.6	151.6	155.7	145.4	92.7	107.4	102.5	48.3	150.9	100.9	7.72E-06	3.51E-04	6.80E-04
XP_010715203.1	PREDICTED: 3-ketoacyl-CoA thiolase, mitochondrial [Meleagris gallopavo]	106.7	49.4	45.4	49.3	136	131.8	130.8	111.2	125	121.1	48.0	132.9	119.1	2.11E-06	7.95E-05	3.54E-02
XP_010712078.1	PREDICTED: myc box-dependent-interacting protein 1 [Meleagris gallopavo]	106.7	66.9	71.2	60.3	118.9	136.3	128.3	110.7	105.5	101.9	66.1	127.8	106.0	4.86E-04	6.07E-04	1.81E-02
XP_003210796.1	PREDICTED: hemoglobin subunit alpha-A [Meleagris gallopavo]	105.8	29.3	36.8	38.6	144.3	136.4	138.3	124.6	126.7	125	34.9	139.7	125.4	9.38E-06	6.45E-06	4.47E-03
XP_010707648.1	PREDICTED: rab GNP dissociation inhibitor beta [Meleagris gallopavo]	104.2	67.5	74.9	70.9	124.7	124.7	138.3	94.7	101	103.2	71.1	129.2	99.6	3.16E-04	1.01E-03	4.70E-03
XP_010712670.1	PREDICTED: voltage-dependent anion-selective channel protein 2 isoform X1 [Meleagris gallopavo]	103.0	47.3	50.5	48.3	124.8	136	142.3	107.3	122.8	120.6	48.7	134.4	116.9	7.97E-05	1.59E-04	6.83E-02
XP_010716123.1	PREDICTED: gamma-enolase isoform X1 [Meleagris gallopavo]	100.2	119.3	108.9	114.4	90.9	90.4	93	97.1	92.8	93.3	114.2	91.4	94.4	1.85E-03	3.87E-03	1.33E-01
XP_010710458.1	PREDICTED: glycogen phosphorylase, liver form [Meleagris gallopavo]	97.3	152.7	145.5	154.2	70	69.2	64.7	85.1	76.9	81.6	150.8	68.0	81.2	1.24E-05	4.15E-05	1.02E-02
XP_003211726.3	PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Meleagris gallopavo]	95.5	3.1	72.6	89.4	150.7	102.7	114.2	109.5	161.1	96.7	55.0	122.5	122.4	8.85E-02	1.10E-01	9.97E-01
XP_010706095.1	PREDICTED: M-protein, striated muscle-like [Meleagris gallopavo]	95.2	115.8	115.1	112.5	90.1	92.8	95	95.5	98.6	84.6	114.5	92.6	92.9	2.30E-04	7.80E-03	9.55E-01
XP_010719463.1	PREDICTED: 78 kDa glucose-regulated protein [Meleagris gallopavo]	94.4	77.8	72.1	73.4	115	138	146	93.1	94.4	90.4	74.4	133.0	92.6	3.45E-03	9.55E-04	1.25E-02
XP_003202518.2	PREDICTED: LOW QUALITY PROTEIN: aldose reductase-like [Meleagris gallopavo]	94.2	60.3	53.7	64.2	138.4	133.5	126.6	112	107	106.3	59.4	132.2	108.4	1.37E-04	1.59E-04	5.81E-03
XP_019471366.1	PREDICTED: myosin-binding protein C, slow-type isoform X1 [Meleagris gallopavo]	92.9	34.1	31.5	34.4	160.4	151.7	156.3	114.6	109	107.9	33.3	156.1	110.5	1.35E-06	4.46E-06	1.51E-04
XP_010721169.1	PREDICTED: superoxide dismutase [Cu-Zn], partial [Meleagris gallopavo]	92.8	82	75.6	85.9	135.5	117	125.7	88.8	93.4	96.2	81.2	126.1	92.8	1.85E-03	3.46E-02	4.47E-03
XP_010713923.1	PREDICTED: glycogen debranching enzyme-like [Meleagris gallopavo]	91.1	119.8	118.4	115.6	85.5	84.4	86.2	95.3	97.9	96.8	117.9	85.4	96.7	1.71E-05	1.25E-04	2.50E-04
XP_010720198.1	PREDICTED: 14-3-3 protein gamma [Meleagris gallopavo]	90.4	53	45.5	42.4	124.2	137.1	133.9	124.4	111.4	128.2	47.0	131.7	121.3	7.07E-05	2.41E-04	1.79E-01
XP_010714482.1	PREDICTED: peroxiredoxin-1 [Meleagris gallopavo]	89.7	51.4	37.4	45.4	158.5	152.7	150.3	108	100.3	96	44.7	153.8	101.4	2.09E-05	4.53E-04	2.54E-04
XP_010705458.1	PREDICTED: soluble scavenger receptor cysteine-rich domain-containing protein SSC5D-like [Meleagris gallopavo]	87.7	74.1	77.3	78.7	124.7	124.3	120.9	103.3	97.2	99.5	76.7	123.3	100.0	1.38E-05	4.82E-04	4.10E-04
XP_019471455.1	PREDICTED: adenylosuccinate synthetase isozyme 1 isoform X1 [Meleagris gallopavo]	84.8	79.7	73.5	82.9	108.5	106.3	104.9	112.2	113.9	118.1	78.7	106.6	114.7	7.02E-04	3.85E-04	1.62E-02
XP_019476000.1	PREDICTED: myotilin isoform X2 [Meleagris gallopavo]	82.9		1.1	2.4	193.1	187.2	179.3	112.8	115.4	108.7	1.8	186.5	112.3	4.85E-05	2.75E-05	7.55E-05
NP_001290140.1	ryanodine receptor 3 [Meleagris gallopavo]	82.3	156.7	139.8	143.7	58.1	68.8	54.8	96.3	96.6	85.2	146.7	60.6	92.7	2.02E-04	1.04E-03	4.72E-03
XP_010714011.1	PREDICTED: peroxiredoxin-6, partial [Meleagris gallopavo]	81.0	65.1	93.2	92	115.5	119.2	110.1	98.5	108.5	97.9	83.4	114.9	101.6	2.99E-02	1.37E-01	3.74E-02
XP_019472959.1	PREDICTED: glyceral-3-phosphate dehydrogenase, mitochondrial [Meleagris gallopavo]	78.6	271.1	225.4	326.7	19.5	4.7	6.2	9.5	17.8	19.2	274.4	10.1	15.5	8.78E-04	9.23E-04	3.92E-01
XP_010712016.1	PREDICTED: kelch-like protein 41 [Meleagris gallopavo]	76.7	88.9	85.5	91.8	136.8	136.7	133.8	76	77.4	73.1	88.7	135.8	75.5	2.22E-05	3.96E-03	2.99E-06
XP_010720031.1	PREDICTED: 14-3-3 protein epsilon isoform X1 [Meleagris gallopavo]	73.1	39.4	28.6	38.2	176.6	155.4	185.5	97.6	85.3	93.4	35.4	172.5	92.1	1.37E-04	3.37E-04	1.13E-03
XP_010715145.1	PREDICTED: eukaryotic initiation factor 4A-II isoform X1 [Meleagris gallopavo]	70.3	104.5	104.6	118	92.3	92	97.8	88.1	108.3	94.3	109.0	94.0	96.9	3.68E-02	1.80E-01	6.71E-01
XP_019471732.1	PREDICTED: bisphosphoglycerate mutase isoform X1 [Meleagris gallopavo]	69.4	168.7	151.1	158.1	71	69.7	74	67.5	80	69.8	156.0	71.6	72.4	6.73E-06	5.18E-05	8.41E-01
XP_010708989.1	PREDICTED: adenylosuccinate lyase [Meleagris gallopavo]	68.0	139.1	130	145.2	65.1	57.8	63.4	96	107.6	95.7	138.1	62.1	99.8	1.04E-04	2.90E-03	1.11E-03
XP_010709971.1	PREDICTED: cofilin-2 [Meleagris gallopavo]	66.2	71.8	69.3	71.8	121.5	133.8	128.8	101.3	100	101.8	71.0	128.0	101.0	9.96E-05	7.03E-06	1.71E-03
XP_010725496.2	PREDICTED: citrate synthase, mitochondrial, partial [Meleagris gallopavo]	65.8	45	35.5	44.8	134.3	151.3	139	107.2	124.4	118.4	41.8	141.5	116.7	7.46E-05	2.27E-04	2.54E-02
XP_010726207.1	PREDICTED: glycogen phosphorylase, muscle form-like, partial [Meleagris gallopavo]	65.4	128.2	115.8	131.9	85.6	82.9	81.9	90.2	90.9	92.6	125.3	83.5	91.2	1.11E-03	2.28E-03	4.11E-03
XP_019477161.1	PREDICTED: nucleoside diphosphate kinase [Meleagris gallopavo]	64.4	94.8	88	88.7	113	120.6	116.9	94.3	94.8	88.9	90.5	116.8	92.7	1.03E-03	4.92E-01	1.13E-03
XP_019468449.1	PREDICTED: protein-L-isaspartate(D-aspartate) O-methyltransferase isoform X1 [Meleagris gallopavo]	56.8	32.7	35.5	51.2	121.3	168.4	160.8	103	116.8	110.3	39.8	150.2	110.0	2.15E-03	5.55E-04	5.69E-02
XP_010712906.1	PREDICTED: ankyrin repeat domain-containing protein 2 [Meleagris gallopavo]	56.8	11.2	4.3	10.3	244	229.7	221.5	63	52.2	63.7	8.6	231.7	59.6	5.52E-06	2.90E-04	2.20E-05
XP_010719949.1	PREDICTED: ATP synthase subunit d, mitochondrial [Meleagris gallopavo]	54.6	26	30	31	179.2	172.7	174.4	96.5	96.3	93.8	29.0	175.4	95.5	4.88E-07	2.91E-06	3.02E-06
XP_010711802.1	PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform X1 [Meleagris gallopavo]	54.3	28.2	29.5	32.7	153.7	153.5	155	119.5	110.8	117.3	30.1	154.1	115.9	1.03E-07	8.17E-06	1.35E-04
XP_003208605.2	PREDICTED: 4-trimethylaminobutylaldehyde dehydrogenase [Meleagris gallopavo]	53.8	57.6	56.1	57	136.1	132.2	128.5	122	109.5	101.1	56.9	132.3	110.9	4.63E-06	8.94E-04	2.95E-02
XP_010705220.1	PREDICTED: lactoylglutathione lyase [Meleagris gallopavo]	52.7	133.9	123.8	130.3	82.5	89.1	80.2	85.6	82.7	92.1	129.3	83.9	86.8	3.37E-04	4.68E-04	4.98E-01
XP_003204919.3	PREDICTED: fumarate hydratase, mitochondrial [Meleagris gallopavo]	52.1	16.2	23.3	23	162.6	158.4	149.4	116.9	132.8	117.5	20.8	156.8	122.4	7.35E-06	5.81E-05	6.11E-03
XP_003211138.2	PREDICTED: phosphatidylethanolamine-binding protein 1 [Meleagris gallopavo]	51.7	91.2	67.1	77.5	117.1	117.9	119	100.6	104.6	105	78.6	118.0	103.4	4.90E-03	2.53E-02	6.38E-04
XP_003203374.1	PREDICTED: translationally-controlled tumor protein [Meleagris gallopavo]	50.5	126.1	126.6	119.2	86.7	89.9	92.5	86	94	78.9	124.0	89.7	86.3	3.01E-04	1.63E-03	5.07E-01
XP_019474821.1	PREDICTED: annexin A2 [Meleagris gallopavo]	48.4	76.7	88.2	98	122.7	125.5	144	92.5	76.2	76.1	87.6	130.7	81.6	9.01E-03	5.04E-01	4.69E-03
XP_010715382.1	PREDICTED: glycogenin-1 isoform X1 [Meleagris gallopavo]	48.0	125	108.6	112.6	95.8	91.6	83	101.6	92.9	88.9	115.4	90.1	94.5	1.52E-02	2.79E-02	4.61E-01
XP_0107236																	

XP_010722913.1	PREDICTED: puromycin-sensitive aminopeptidase, partial [Meleagris gallopavo]	41.9	111.2	88.3	111.2	91.1	102.3	93.9	97.8	102	102.1	103.6	95.8	100.6	4.03E-01	7.25E-01	2.53E-01
XP_010704584.2	PREDICTED: hemopexin [Meleagris gallopavo]	40.8	163.8	43.1	31.9	136.8	119.7	118.7	103	94.7	88.5	79.6	125.1	95.4	3.46E-01	7.29E-01	1.48E-02
XP_010716572.1	PREDICTED: tropoin C, slow skeletal and cardiac muscles [Meleagris gallopavo]	40.7	45.6	35.7	38.1	198.8	191.4	201.6	57.4	67.6	63.6	39.8	197.3	62.9	3.20E-06	5.93E-03	5.96E-06
XP_010723825.2	PREDICTED: betaine-homocysteine S-methyltransferase 1 [Meleagris gallopavo]	39.9	159	154	171.2	61.8	68	73.8	69.4	68.7	74	161.4	67.9	70.7	1.11E-04	7.21E-05	5.02E-01
XP_019473127.1	PREDICTED: vinculin isoform X1 [Meleagris gallopavo]	39.2	53.7	61	53.1	155.3	156.7	162.2	83.1	85.1	89.8	55.9	158.1	86.0	6.48E-06	7.35E-04	1.54E-05
XP_010725238.1	PREDICTED: tubulin alpha-1B chain [Meleagris gallopavo]	38.7	165.2	155.6	170.2	68	66.6	64.6	69	70.4	70.4	163.7	66.4	69.9	2.47E-05	2.64E-05	3.17E-02
XP_010723063.1	PREDICTED: dihydroxyoloyl dehydrogenase, mitochondrial [Meleagris gallopavo]	37.8	36.9	33.6	42.5	145	145	141.4	126	107.7	121.8	37.7	143.8	118.5	3.15E-06	1.89E-04	1.11E-02
XP_010711617.1	PREDICTED: long-chain specific acyl-CoA dehydrogenase, mitochondrial, partial [Meleagris gallopavo]	37.7	33.2	17.7	17.8	192.8	186.9	178	122.8	78.4	72.3	22.9	185.9	91.2	1.70E-05	1.51E-02	4.55E-03
XP_003206068.2	PREDICTED: histone-lysine N-methyltransferase SMYD1 isoform X1 [Meleagris gallopavo]	37.1	100.4	94.2	88.8	130.1	112.1	111.3	82.5	85.4	95.2	94.5	117.8	87.7	2.88E-02	2.55E-01	1.41E-02
XP_019476911.1	PREDICTED: tubulin beta-4B chain [Meleagris gallopavo]	36.5	32.1	22.9	28.6	106.1	103.7	116	164.4	169.2	157.1	27.9	108.6	163.6	6.30E-05	6.72E-06	4.37E-04
XP_010721655.1	PREDICTED: ATP synthase subunit O, mitochondrial [Meleagris gallopavo]	35.8	34	29.3	30.5	161.8	157.5	159.5	110	110.5	106.9	31.3	159.6	109.1	2.75E-07	1.72E-06	7.26E-06
XP_010722287.1	PREDICTED: tropomodulin-4 isoform X1 [Meleagris gallopavo]	35.5	59.5	95.6	139.1	123	82.2	100	56.6	109.2	134.8	98.1	101.7	100.2	8.94E-01	9.51E-01	9.56E-01
XP_010724176.1	PREDICTED: histidine triad nucleotide-binding protein 1 [Meleagris gallopavo]	34.8	101.8	86.2	79.6	111.6	117.9	116.7	103.1	87.3	95.8	89.2	115.4	95.4	1.88E-02	4.82E-01	1.57E-02
XP_010704759.1	PREDICTED: UTP-glucose-1-phosphate uridylyltransferase [Meleagris gallopavo]	34.7	120.8	103.8	115.8	86.9	85.4	88.7	113.5	95.5	89.7	113.5	87.0	99.6	6.72E-03	1.88E-01	1.57E-01
XP_010725154.1	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 [Meleagris gallopavo]	34.2	38.6	44.7	57.7	136.8	139.1	136.1	112.9	98.2	136	47.0	137.3	115.7	9.30E-05	5.13E-03	1.22E-01
XP_010722464.1	PREDICTED: ES1 protein homolog, mitochondrial [Meleagris gallopavo]	32.7	12.2	21.9	31.3	94.2	103.1	136.8	182.1	165.2	153.3	21.8	111.4	166.9	3.14E-03	1.32E-04	2.28E-02
XP_003207855.3	PREDICTED: enoyl-CoA hydratase, mitochondrial [Meleagris gallopavo]	32.4	49.3	44.7	48.9	143.7	150.5	155.3	92.4	109.9	105.3	47.6	149.8	102.5	9.92E-06	5.43E-04	1.61E-03
XP_010724255.1	PREDICTED: ATP synthase subunit e, mitochondrial [Meleagris gallopavo]	31.8	41	32.2	39.3	164.4	155.7	152.5	102.4	107.5	105	37.5	157.5	105.0	1.13E-05	2.54E-05	1.66E-04
XP_003212221.2	PREDICTED: LOW QUALITY PROTEIN: succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	31.6	29.2	42	39.7	159.7	148.6	160.2	99.8	109	111.8	37.0	156.2	106.9	2.61E-05	1.99E-04	7.12E-04
XP_010716520.1	PREDICTED: cytochrome c oxidase subunit 4 isoform 1, mitochondrial isoform X1 [Meleagris gallopavo]	31.5	43.9	40.7	45	146.6	127.2	132.4	136.7	115.1	112.5	43.2	135.4	121.4	1.01E-04	5.49E-04	2.20E-01
NP_001290109.1	cytochrome c oxidase subunit 4 isoform 1, mitochondrial [Meleagris gallopavo]	31.5	36.5	35.4	38.2	146.5	152.7	156.6	104.6	120.1	109.3	36.7	151.9	111.3	2.94E-06	8.89E-05	1.73E-03
XP_010721496.1	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial isoform X1 [Meleagris gallopavo]	30.7	12.9	9.7	18.9	181.5	149.4	149.7	129.7	120.1	128	13.8	160.2	125.9	1.84E-04	9.67E-06	3.62E-02
XP_010726371.1	PREDICTED: cytochrome c oxidase subunit 6B1 [Meleagris gallopavo]	30.4	28.1	25.7	26.7	155	154.7	149.2	112.3	133.4	115	26.8	153.0	120.2	3.66E-07	1.51E-04	8.98E-03
XP_010720929.1	PREDICTED: neurofilament heavy polypeptide-like [Meleagris gallopavo]	30.2	109.6	35.5	103.7	100.3	104.2	117.1	121.7	101.2	106.7	82.9	107.2	109.9	3.75E-01	3.34E-01	7.54E-01
XP_003205760.1	PREDICTED: myozenin-2 isoform X1 [Meleagris gallopavo]	30.1	0.7	1.4	2.5	208.4	217	212.2	83.3	84	90.6	1.5	212.5	86.0	1.26E-07	3.79E-06	3.13E-06
XP_010708937.2	PREDICTED: dyferlin-like [Meleagris gallopavo]	29.8	90.6	89.9	76	121.5	144.3	132.6	75.2	92.1	77.8	85.5	132.8	81.7	4.33E-03	6.20E-01	3.73E-03
XP_010726718.1	PREDICTED: ATP synthase subunit delta, mitochondrial [Meleagris gallopavo]	29.6	38.9	31.6	36	113.8	145.3	206.8	128.4	118	81.3	35.5	155.3	109.2	1.19E-02	6.96E-03	2.09E-01
XP_019476651.1	PREDICTED: Ig lambda-1 chain V regions MOPC 1045/RPC20/U558/S104 isoform X1 [Meleagris gallopavo]	29.6	51	41.9	50.6	110.8	138.6	155.4	114.9	91.1	145.6	47.8	134.9	117.2	2.84E-03	1.24E-02	4.35E-01
XP_010716964.2	PREDICTED: pyruvate dehydrogenase E1 component subunit beta, mitochondrial [Meleagris gallopavo]	29.4	30.7	37.6	23.9	153.4	162	159.9	112.4	113	107.1	30.7	158.4	110.8	1.12E-05	5.24E-05	1.18E-04
XP_010726400.2	PREDICTED: tropoin T, slow skeletal muscle-like [Meleagris gallopavo]	29.0	31	27.3	30.5	190.9	194	178.2	92.2	94.6	61.4	29.6	187.7	82.7	5.82E-06	7.81E-03	8.63E-04
XP_010726217.2	PREDICTED: neuroblast differentiation-associated protein AHNAK-like, partial [Meleagris gallopavo]	28.7	67.6	69	75	121.5	110.7	110.1	121.2	116.8	108	70.5	114.1	115.3	5.56E-04	5.70E-04	8.29E-01
XP_019478418.1	PREDICTED: dihydroxylysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitoc	28.7	31.7	34.4	33.3	126	146.7	123.7	121.6	129.4	153.2	33.1	132.1	134.7	1.76E-04	4.40E-04	8.39E-01
XP_010706330.1	PREDICTED: infunational enzyme subunit beta, mitochondrial isoform X1 [Meleagris gallopavo]	28.1	58	46.8	47.9	136.8	145.5	141.7	100.1	110.6	112.7	50.9	141.3	107.8	3.20E-05	4.21E-04	1.94E-03
XP_003202173.1	PREDICTED: lumican [Meleagris gallopavo]	27.7	48	43.7	48.5	171	171.9	178.8	72.1	83.8	82.2	46.7	173.9	79.4	1.61E-06	1.19E-03	2.81E-05
XP_019471375.1	PREDICTED: calmodulin [Meleagris gallopavo]	27.3	80.9	73.5	86.6	140.2	132.7	131.5	89.9	86.5	78.3	80.3	134.8	84.9	3.08E-04	4.23E-01	3.41E-04
XP_003207548.1	PREDICTED: elongation factor 1-beta [Meleagris gallopavo]	27.2	89.6	80.8	92.2	109	118	117.5	96.4	99.6	96.8	87.5	114.8	97.6	3.79E-03	4.87E-02	5.06E-03
XP_010726564.2	PREDICTED: medium-chain specific acyl-CoA dehydrogenase, mitochondrial, partial [Meleagris gallopavo]	26.9	63.5	62.1	58.8	99.2	90.7	78.4	152	146.9	148.5	61.5	89.4	149.1	1.07E-02	1.79E-06	6.60E-04
XP_010711546.1	PREDICTED: collagen alpha-3(VI) chain isoform X1 [Meleagris gallopavo]	26.8	23.3	13.4	22.6	157.6	147.4	148.3	132	123.3	132.1	19.8	151.1	129.1	8.66E-06	1.45E-05	7.38E-03
XP_010726340.1	PREDICTED: calcitriol [Meleagris gallopavo]	26.8	79.4	77.4	64.3	128.4	105.5	127.8	119.7	96.3	101.1	73.7	120.6	105.7	6.23E-03	2.02E-02	2.25E-01
XP_010724594.1	PREDICTED: histone H1.11R, partial [Meleagris gallopavo]	26.4	1.1	1.8	2.5	198.7	212.6	207.4	90.5	94.7	90.6	1.8	206.2	91.9	9.45E-07	3.92E-07	1.17E-05
XP_010713339.1	PREDICTED: ribose-phosphate pyrophosphokinase 1 [Meleagris gallopavo]	26.3	121.2	117.1	132.4	97.2	93.9	100.9	95.1	70.4	71.8	123.6	97.3	79.1	6.31E-03	8.52E-03	9.19E-02
XP_010716010.1	PREDICTED: protein disulfide-isomerase A3 [Meleagris gallopavo]	26.3	73	61.8	67.3	130.5	123.9	136.8	100.1	105	101.7	67.4	130.4	102.3	2.16E-04	5.94E-04	2.14E-03
XP_003211808.1	PREDICTED: bleomycin hydrolase [Meleagris gallopavo]	26.3	82.6	79.7	104.9	102.9	104.5	106.3	119.5	95.2	104.3	89.1	104.6	106.3	1.25E-01	1.81E-01	8.17E-01
XP_010722978.1	PREDICTED: heat shock protein 30C-like [Meleagris gallopavo]	26.2	43.2	37.4	25.3	114.5	155.7	155.8	123.4	95.2	149.5	35.3	142.0	122.7	1.93E-03	6.16E-03	4.07E-01
XP_010716011.1	PREDICTED: creatine kinase U-type, mitochondrial, partial [Meleagris gallopavo]	25.7	51.1	55.2	36.3	148.5	132.6	140.7	110.6	115.3	109.6	47.5	140.6	111.8	2.24E-04	4.30E-04	4.25E-03
XP_019467633.1	PREDICTED: acetyl-CoA acetyltransferase, mitochondrial, partial [Meleagris gallopavo]	25.7	8.2	11.4	9.3	136.9	150	149.5	137.1	155.2	142.3	9.6	145.5	144.9	6.49E-06	1.58E-05	9.35E-01
XP_019477922.1	PREDICTED: aflatoxin B1 aldehyde reductase member 2-like [Meleagris gallopavo]	25.4	75.9	67.1	95.6	115.3	118.3	110.8	97	109.1	110.9	79.5	114.8	105.7	1.54E-02	5.12E-02	1.34E-01
XP_003202996.1	PREDICTED: SH3 domain-binding glutamic acid-rich-like protein [Meleagris gallopavo]	25.2	54.9	51.6	56.6	155.8	150.9	177.9	88.8	82.9	80.6	54.4	161.5	84.1	2.21E-04	4.76E-04	8.64E-04
XP_019473564.1	PREDICTED: CGSH iron-sulfur domain-containing protein 1 isoform X1 [Meleagris gallopavo]	25.0	55.1	59.2	81.9	122.2	116.8	118.9	101.9	123.3	120.6	65.4	119.3	115.3	3.14E-03	9.62E-03	5.91E-01
XP_010708189.1	PREDICTED: histone H2A.J [Meleagris gallopavo]	24.9	3.3	3.4	2.2	242.8	241.8	246.7	54.4	54.7	50.7	3.0	243.8	53.3	1.01E-08	3.03E-06	6.89E-08
XP_010720908.1	PREDICTED: microtubule-associated protein RPIEB family member 1 isoform X1 [Meleagris gallopavo]	24.6	65.1	68.7	69.7	127	124.6	128	100.9	108.4	107.5	67.8	126.5	105.6	4.43E-06	1.62E-04	1.24E-03
XP_019473001.1	PREDICTED: glutamate dehydrogenase 1, mitochondrial [Meleagris gallopavo]	24.6	46.1	55.8	30.9	174.2	172.9	143.7	83.5	104.6	88.2	44.3	163.6	92.1	6.35E-04	7.77E-03	3.78E-03
XP_010718264.2	PREDICTED: ubiquitin-conjugating enzyme E2 L3 [Meleagris gallopavo]	24.5	77.1	75.9	81.7	121.2	124.8	72.1	92.7	139.6	114.6	78.2	106.0	115.6	1.79E-01	5.21E-02	6.82E-01
XP_010722862.1	PREDICTED: prohibitin [Meleagris gallopavo]	24.4	82.3	80.9	80	130.9	126.2	104.8	80.4	106.6	107.9	81.1	120.6	98.3	7.99E-03	1.27E-01	1.37E-01
XP_010708917.1	PREDICTED: MICOS complex subunit MIC60-like [Meleagris gallopavo]	24.4	31.7	39	29.2	191.5	131.9	121	80.5	197.6	77.6	33.3	148.1	118.6	6.54E-03	9.78E-02	5.49E-01
XP_010709463.1	PREDICTED: rbonuclease inhibitor [Meleagris gallopavo]	23.7	112.3	107.6	100.2	90	88.2	92.8	111.4	86.7	110.8	106.7	90.3	103.0	1.22E-02	6.95E-01	2.00E-01
XP_010707400.1	PREDICTED: carbonic anhydrase 3-like [Meleagris gallopavo]	23.7	63.7	70.7	66.2	140.6	130	88.3	114.9	115.2	110.4	66.9	119.6	113.5	3.05E-02	5.42E-05	7.22E-01
XP_010716605.1	PREDICTED: prohibitin-2, partial [Meleagris gallopavo]	22.6	85.9	84	88.4	112.8	112	107.4	100	111.3	98.2	86.1	110.7	103.2	3.08E-04	1.65E-02	1.63E-01
XP_010721372.1	PREDICTED: dihydropyrimidinease-related protein 2 [Meleagris gallopavo]	22.2	33.7	33.3	29.1	127.4	142.6	177.6	101.1	117.9	135.2	32.7					

XP_019473935.1	PREDICTED: laminin subunit gamma-1, partial [Meleagris gallopavo]	19.4		11.4	84.2	194.8	101.3	118.1	139.3	133.4	117.5	47.8	138.1	130.1	1.45E-01	6.27E-02	8.00E-01
XP_003213488.3	PREDICTED: NAD(P) transhydrogenase, mitochondrial-like [Meleagris gallopavo]	19.3				160.8	159.3	172.8	140.6	138	128.5	#DIV/0!	164.3	135.7	#DIV/0!	#DIV/0!	7.11E-03
XP_003210067.1	PREDICTED: mimecan [Meleagris gallopavo]	19.1	32.2	65.4	61.4	217.2	180.4	192.1	40.3	64.6	46.4	53.0	196.6	50.4	6.79E-04	3.65E-04	
XP_019466703.1	PREDICTED: protein ADP-ribosylarginine hydrolase-like, partial [Meleagris gallopavo]	18.9	68.9	75	82.2	133.1	116	128.6	96	100.6	99.5	75.4	125.9	98.7	1.39E-03	4.65E-03	6.84E-03
XP_019468352.1	PREDICTED: LOW QUALITY PROTEIN: nidogen-1 [Meleagris gallopavo]	18.9	47.8	28.9	53.3	134.3	89.1	181.6	61.7	140.1	163.3	43.3	135.0	121.7	2.97E-02	6.83E-02	7.60E-01
XP_010709934.1	PREDICTED: cyanodine receptor 3-like isoform X1 [Meleagris gallopavo]	18.8	197.1	165.3	188	21.8	19.9	17.7	47.5	116.1	126.5	183.5	19.8	96.7	6.74E-05	3.08E-02	3.62E-02
XP_010720462.1	PREDICTED: laminin subunit beta-1 [Meleagris gallopavo]	18.8	94.1	99.3	60.7	96.8	104.6	99.1	152	95.6	97.8	84.7	100.2	115.1	2.77E-01	2.40E-01	4.66E-01
XP_003208621.1	PREDICTED: 14 kDa phosphotidine phosphatase-like [Meleagris gallopavo]	18.7	51.5	47.1	50.9	150.7	144.2	146.4	105.1	103.7	100.4	49.8	147.1	103.1	2.05E-06	1.09E-05	4.88E-05
XP_003212008.1	PREDICTED: 14-3-3 protein beta/alpha [Meleagris gallopavo]	18.6	25.3	29.8	31	159.1	167.1	166.1	112.5	107.1	102	28.7	164.1	107.2	1.55E-06	2.32E-05	1.34E-04
XP_010713240.1	PREDICTED: thioredoxin-dependent peroxide reductase, mitochondrial, partial [Meleagris gallopavo]	18.4	17.6	23.8	19.6	173.6	137.4	134.1	167	113.4	113.4	20.3	148.4	131.3	5.59E-04	3.49E-03	4.78E-01
XP_019471775.1	PREDICTED: LOW QUALITY PROTEIN: xin actin-binding repeat-containing protein 1 [Meleagris gallopavo]	18.3	124.5	135.3	145.3	108.2	91.5	96.7	83.3	37.4	77.7	135.0	98.8	66.1	9.58E-03	1.17E-02	9.93E-02
XP_010719753.1	PREDICTED: beta-2-glycoprotein 1 isoform X1 [Meleagris gallopavo]	18.1	33.2	36.2	33.7	113.7	198.9	186	83.7	105.4	109.2	34.4	166.2	99.4	7.65E-03	1.24E-03	7.34E-02
XP_003205566.2	PREDICTED: ADP/ATP translocase 1, partial [Meleagris gallopavo]	17.9	89	72.2	94.4	113.7	124.2	114	103.8	87.6	101.1	85.2	117.3	97.5	1.30E-02	2.15E-01	3.13E-02
XP_010705975.1	PREDICTED: NADP-dependent malic enzyme isoform X1 [Meleagris gallopavo]	17.8	159.6	121.3	157.8	51.1	75.2	88.3	69.6	83	94.1	146.2	71.5	82.2	1.07E-02	1.12E-02	4.57E-01
XP_010710255.1	PREDICTED: LOW QUALITY PROTEIN: creatine kinase B-type [Meleagris gallopavo]	17.8	47.3	44.5	46.5	162.7	157.7	156.4	99.1	93.8	92	46.1	158.9	95.0	7.09E-07	2.84E-05	2.39E-05
XP_010716394.1	PREDICTED: cadherin-13 isoform X1 [Meleagris gallopavo]	17.6	76.5	82.1	76.3	122.6	119.6	127.6	88.9	109.3	97	78.3	123.3	98.4	1.17E-04	3.20E-02	1.75E-02
XP_010709805.1	PREDICTED: 5-mercaptopyrivate sulfurtransferase isoform X1 [Meleagris gallopavo]	17.5	60.2	43.8	39.2	151.1	153.2	151.4	107.8	85.2	108.1	47.7	151.9	100.4	8.37E-05	6.03E-03	2.48E-03
XP_010718107.1	PREDICTED: glycerol-3-phosphate phosphatase, partial [Meleagris gallopavo]	17.4	70.1	65.8	67.8	122.6	117.6	119.5	101	118.4	117.1	67.9	119.9	112.2	1.09E-05	1.51E-03	2.52E-01
XP_010712598.1	PREDICTED: hexokinase-1 [Meleagris gallopavo]	17.4	78.8	38.7	38.4	144.6	139	147.2	80.1	112.7	120.5	52.0	143.6	104.4	2.55E-03	4.53E-02	3.60E-02
XP_010725164.1	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial-like [Meleagris gallopavo]	17.3	20.9	18.3	21.2	149.6	154.3	172.1	118.8	121.9	123	20.1	158.7	121.2	3.66E-05	3.38E-07	5.80E-03
XP_010713442.1	PREDICTED: phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform [Meleagris gallopavo]	17.1	114.9	22.8	16.1	100.3	92.8	125.8	138.2	136	153.1	51.3	106.3	142.4	1.75E-01	4.78E-02	3.33E-02
XP_010718484.1	PREDICTED: aldehyde dehydrogenase, mitochondrial [Meleagris gallopavo]	16.7	98	91.2	91	124.8	115.5	121.7	88.1	90.2	79.4	93.4	120.7	85.9	1.58E-03	1.36E-01	1.26E-03
XP_010715482.1	PREDICTED: mannose-6-phosphate isomerase [Meleagris gallopavo]	16.4	116.4	98	100.7	78.2	90.4	95.1	108.6	105	107.5	105.0	87.9	107.0	8.82E-02	7.49E-01	2.05E-02
XP_003207311.1	PREDICTED: 45S ribosomal protein SA [Meleagris gallopavo]	16.4	52.6	40	38.8	145.2	145.6	156.7	105.8	109.5	105.8	43.8	149.2	107.0	5.41E-05	1.60E-04	4.44E-04
XP_010709036.1	PREDICTED: cysteine and glycine-rich protein 3 isoform X2 [Meleagris gallopavo]	16.3	9.8	13.4	10.9	181.7	210.7	198.7	93.8	86.4	94.7	11.4	197.0	91.6	2.58E-05	9.00E-06	2.79E-04
XP_010722333.1	PREDICTED: tropoin 1, slow skeletal muscle [Meleagris gallopavo]	16.3				154.2	194.4	369.4	59.1	62.2	60.8	#DIV/0!	239.3	60.7	#DIV/0!	#DIV/0!	5.39E-02
XP_003207602.1	PREDICTED: C- U-editing enzyme APOBEC-2 [Meleagris gallopavo]	16.2	61.6	80.8	62	184.5	128	150.4	66.1	94.9	71.6	68.1	154.3	77.5	8.08E-03	4.36E-01	1.47E-02
XP_010723080.1	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 [Meleagris gallopavo]	15.9	35.9	21.4	35.6	161.2	157.1	144.1	115.5	116.7	112.6	31.0	154.1	114.9	6.24E-05	7.01E-05	1.78E-03
XP_010705429.1	PREDICTED: superoxide dismutase [Mn], mitochondrial [Meleagris gallopavo]	15.9	54.5	57.4	65.2	128.3	107.7	120	120.4	121.7	124.8	59.0	118.7	122.3	9.24E-04	5.21E-05	5.85E-01
XP_003209409.2	PREDICTED: isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial [Meleagris gallopavo]	15.8	23.2	42.9	24.1	147.3	104.2	136.9	175.3	123.6	122.5	30.1	129.5	140.5	2.36E-03	4.01E-03	6.39E-01
XP_010723313.1	PREDICTED: guanidinoacetate N-methyltransferase [Meleagris gallopavo]	15.6	136.2	128.9	146.9	89.4	112.8	118	39.9	93	34.8	106.7	55.9	4.03E-02	1.36E-02	6.90E-02	
XP_010725340.1	PREDICTED: protein NDGR2-like [Meleagris gallopavo]	15.6	48.2	44.8	45.9	152	125.3	160.8	120.2	93.1	109.8	46.3	146.0	107.7	7.43E-04	1.52E-03	4.47E-02
XP_010717168.1	PREDICTED: stress-70 protein, mitochondrial [Meleagris gallopavo]	15.6	88.4	76.3	105.9	123.9	119.4	127.4	87.2	105.9	65.6	90.2	123.6	86.2	2.00E-02	7.98E-01	3.47E-02
XP_010709097.1	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial [Meleagris gallopavo]	15.5	44.6	24	44	230.9	217.8	254.1	34.2	27.2	23.2	37.5	234.3	28.2	9.79E-05	2.81E-01	4.94E-05
XP_003202247.2	PREDICTED: histone H2B 8-like [Meleagris gallopavo]	15.5	5.3	6	5.7	248.8	222.4	244.5	49.3	56.1	62.1	5.7	238.6	55.8	9.06E-06	1.72E-04	3.44E-05
XP_010720926.2	PREDICTED: myosin light chain kinase 2, skeletal/cardiac muscle, partial [Meleagris gallopavo]	15.5	121.5	107.8	93.5	123.5	67.4	86.2	120.9	119.3	59.9	107.6	92.4	100.0	4.53E-01	7.44E-01	7.83E-01
XP_010720044.1	PREDICTED: protein NipSnap homolog 2 isoform X1 [Meleagris gallopavo]	15.4	11	40.1	27	146.6	118.6	122	149.3	144.2	141.3	26.0	129.1	144.9	1.07E-03	1.69E-04	1.57E-01
XP_010706217.1	PREDICTED: protein disulfide-isomerase A6 [Meleagris gallopavo]	15.1	125.3	80.3	82.3	90.4	95.1	112.8	99.9	71.4	142.6	96.0	99.4	104.6	8.41E-01	7.50E-01	8.23E-01
NP_001290084.1	glutathione S-transferase alpha class A1.3 [Meleagris gallopavo]	15.0	56.4	54.3	51.1	138.7	143.3	149.4	106.4	101.9	98.4	53.9	143.8	102.2	1.31E-05	6.45E-05	4.25E-04
XP_010707626.1	PREDICTED: elongation factor 1-delta isoform X1 [Meleagris gallopavo]	14.9	125.3	109.7	117.2	107.2	106.4	88.1	98.1	84.8	63.1	117.4	100.6	82.0	9.39E-02	3.37E-02	1.95E-01
XP_010720721.1	PREDICTED: ATP synthase-coupling factor 6, mitochondrial [Meleagris gallopavo]	14.8	47.6	40.9	43.1	164.9	158.4	162.5	96.4	103.5	82.6	43.9	161.9	94.2	1.73E-06	1.45E-03	4.56E-04
XP_010717684.1	PREDICTED: enoyl-CoA delta isomerase 1, mitochondrial [Meleagris gallopavo]	14.8	43	28.8	37.1	160.9	161.5	136.7	113.8	110.1	108.1	36.3	153.0	110.7	2.17E-04	7.47E-05	7.07E-03
XP_010715230.2	PREDICTED: eukaryotic translation initiation factor 5A-2, partial [Meleagris gallopavo]	14.7	99.1	96.3	105	103.1	96.6	95.8	105.9	97	101.2	100.1	98.5	101.4	6.61E-01	7.51E-01	4.54E-01
XP_010725971.1	PREDICTED: histone H4 [Meleagris gallopavo]	14.6				262.3	276.1	268.9	33.4	37.8	21.5	#DIV/0!	269.1	30.9	#DIV/0!	#DIV/0!	2.91E-06
XP_019468033.1	PREDICTED: acylphosphatase-2 isoform X1 [Meleagris gallopavo]	14.6	65.4	76	60.7	132.9	141.1	128.8	102.2	91.1	101.8	67.4	134.3	98.4	3.21E-04	5.92E-03	2.19E-03
XP_010713768.2	PREDICTED: NADH-cytochrome b5 reductase 3, partial [Meleagris gallopavo]	14.5	104.7	90.1	91.5	126.4	114.1	117.5	83.6	86.3	85.8	95.4	119.3	85.2	1.57E-02	9.70E-02	8.19E-04
XP_010726533.2	PREDICTED: neuroblast differentiation-associated protein AHNAK-like, partial [Meleagris gallopavo]	14.3	52	48.8	50.4	146.4	123.8	130	119.5	112.4	116.7	50.4	133.4	116.2	2.59E-04	8.31E-06	7.13E-02
XP_019474799.1	PREDICTED: profilin-2 isoform X2 [Meleagris gallopavo]	14.1	51.8	47.1	49.7	144	150.2	149.1	111.7	97.5	98.8	49.5	147.8	102.7	1.94E-06	3.58E-04	7.85E-04
XP_010704648.1	PREDICTED: reticulon-4 [Meleagris gallopavo]	13.9	71.2	71.3	65.2	119.1	115.6	123	99.6	114	120.9	69.2	119.2	111.5	7.00E-05	3.04E-03	3.08E-01
XP_003213185.1	PREDICTED: polymerase I and transcript release factor [Meleagris gallopavo]	13.8	29.2	28.4	34.3	168.1	164.8	154.9	108.3	104.1	108	30.6	162.6	106.8	7.20E-06	4.87E-06	1.84E-04
XP_010711822.1	PREDICTED: isocitrate dehydrogenase [NADP] cytoplasmic [Meleagris gallopavo]	13.8	72.7	67.5	75.9	131.8	145.1	113.9	100.6	89.3	103.2	72.0	130.3	97.7	3.40E-03	6.44E-03	3.11E-02
XP_019477394.1	PREDICTED: smoothenin-like protein 2, partial [Meleagris gallopavo]	13.7	6.5	7.4	8.2	175.2	173.1	188	116.6	111.2	113.9	7.4	178.8	113.9	3.32E-06	3.32E-07	1.90E-04
XP_010709306.1	PREDICTED: proline-rich protein 33 isoform X1 [Meleagris gallopavo]	13.7	66.3	82	56.9	134	139.2	131.7	57.6	113.4	118.9	68.4	135.0	96.6	9.60E-04	2.48E-01	1.24E-01
XP_010727123.1	PREDICTED: succinate-CoA ligase [ADP-forming] subunit beta, mitochondrial [Meleagris gallopavo]	13.7	14.6	9	20.1	144.6	146.7	142.8	146.2	135.3	140.7	14.6	144.7	140.7	2.77E-06	9.55E-06	3.01E-01
XP_019465497.1	PREDICTED: vicilin-like seed storage protein A2g18540 [Meleagris gallopavo]	13.7	22.3	17.9	55.2	124.9	141	150.1	134.4	133.1	121	31.8	138.7	129.5	1.53E-03	1.45E-03	3.42E-01
XP_003210226.1	PREDICTED: PRAT1 family protein 3 [Meleagris gallopavo]	13.6	62	114.3	76.6	116.6	104.7	66.5	100.1	105.8	153.5	84.3	95.9	119.8	6.20E-01	1.98E-01	3.52E-01
XP_003206523.1	PREDICTED: calpain-3 isoform X1 [Meleagris gallopavo]	13.3	62.6	119.2	65.8	112.9	111.4	112.4	112.2	102.7	100.7	82.5	112.2	105.2	1.81E-01	2.92E-01	1.21E-01
XP_010710203.1	PREDICTED: ubiquitin-conjugating enzyme E2 N [Meleagris gallopavo]	13.3	66.7	66.8	70	139	120	120.6	97.7	111.2	107.9	67.8	126.5	105.6	7.52E-04	8.51E-04	4.82E-02
XP_010726380.1	PREDICTED: LOW QUALITY PROTEIN: plectin-like, partial [Meleagris gallopavo]	13.3	39.3	42.5	38	139.6	169.2	138.9	123.6	98.5	110.5	39.9	149.2	110.9	4.10E-04	6.52E-	

XP_019473945.1	PREDICTED: cystathionine gamma-lyase, partial [Meleagris gallopavo]	11.7	83.6	88.5	44.7	126.2	114.9	92.6	108.2	105.9	135.3	72.3	111.2	116.5	8.38E-02	5.78E-02	7.21E-01
XP_003205251.1	PREDICTED: 14-3-3 protein zeta/delta [Meleagris gallopavo]	11.4	38.8	24.3	27.5	140.7	185.3	190.9	65.7	93.1	133.5	30.2	172.3	97.4	9.95E-04	2.90E-02	4.16E-02
XP_003207600.1	PREDICTED: O-acetyl-ADP-ribose deacetylase 1 isoform X1 [Meleagris gallopavo]	11.4	22.9	80.1	88	151.2	156.9	98.8	120.1	108.7	75.3	63.7	135.0	101.4	6.39E-02	1.99E-01	2.24E-01
XP_010721814.1	PREDICTED: myomesin-3 [Meleagris gallopavo]	11.4				198.4	211.1	209	61.5	108.7	111.2	#DIV/0!	206.2	93.8	#DIV/0!	#DIV/0!	2.51E-03
XP_010725827.1	PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1-like [Meleagris gallopavo]	11.3	57.3	51.8	56.7	155.2	162.1	156.6	76.2	90.9	93	55.3	158.0	86.7	2.99E-06	4.84E-03	2.34E-04
XP_010725666.1	PREDICTED: adenosylhomocysteinase [Meleagris gallopavo]	11.2	77.3	75.3	78.7	120.6	126.4	113.3	99.7	109.1	99.6	77.1	120.1	102.8	3.91E-04	1.47E-03	2.47E-02
XP_003214067.2	PREDICTED: delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial, partial [Meleagris gallopavo]	11.1	29.1	36.9	46.8	145.8	138.2	154	110.5	122.8	115.9	37.6	146.0	116.4	9.37E-05	2.26E-04	6.91E-03
XP_003209234.1	PREDICTED: alpha-2-HS-glycoprotein [Meleagris gallopavo]	11.0	63.4	54.2	65.2	95.7	145.4	239.4	83.9	50.3	102.4	60.9	160.2	78.9	7.87E-02	3.15E-01	1.44E-01
XP_003208024.2	PREDICTED: synaptopodin 2-like protein [Meleagris gallopavo]	11.0				40	434	425.9				#DIV/0!	300.0	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!
XP_010722077.1	PREDICTED: heat shock protein beta-2 [Meleagris gallopavo]	11.0				164.5	157.5	155.5	145.7	141.2	135.5	#DIV/0!	159.2	140.8	#DIV/0!	#DIV/0!	1.03E-02
XP_010707744.1	PREDICTED: electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial [Meleagris gallopavo]	10.9	35.2	25.1	2.7	146.7	192.6	165.1	129.1	106.2	97.4	21.0	168.1	110.9	8.61E-04	2.62E-03	2.49E-02
XP_010722917.1	PREDICTED: telethonin [Meleagris gallopavo]	10.9	96.7	96	101.2	92.7	104.7	91	91.7	116.9	109.1	98.0	96.1	105.9	7.11E-01	3.57E-01	3.20E-01
XP_010712046.1	PREDICTED: calcium-binding mitochondrial carrier protein Aralar1-like [Meleagris gallopavo]	10.8	48.7	74.7	21.5	167.6	167.6	35.4	142.8	124.3	117.4	48.3	123.5	128.2	1.82E-01	9.57E-03	9.22E-01
XP_010711091.1	PREDICTED: cytochrome c [Meleagris gallopavo]	10.6	24.2	17.8	24.8	184.8	195.3	151.8	121.8	86.9	92.6	22.3	177.3	100.4	3.09E-04	2.10E-03	1.06E-02
XP_003203488.2	PREDICTED: LOW QUALITY PROTEIN: radixin [Meleagris gallopavo]	10.5	20.1	13.9	42.8	181.8	173.9	163.1	83.7	124.7	95.9	25.6	172.9	101.4	1.40E-04	7.20E-03	5.80E-03
XP_010704870.1	PREDICTED: desrin [Meleagris gallopavo]	10.5	65.5	53.3	65.8	125.3	144.9	113.3	123.1	110.2	98.6	61.5	127.8	110.6	2.77E-03	3.89E-03	2.13E-01
XP_003203792.1	PREDICTED: atypical kinase COGBA, mitochondrial [Meleagris gallopavo]	10.5				108	230.9	226.1	104.7	230.3	#DIV/0!	169.5	187.0	#DIV/0!	#DIV/0!	#DIV/0!	8.18E-01
XP_010726006.1	PREDICTED: peptidyl-prolyl cis-trans isomerase D-like, partial [Meleagris gallopavo]	10.4	90.8	73.6	84	59.8	125.9	151.4	108.8	93.6	112.1	82.8	112.4	104.8	3.47E-01	4.38E-02	8.00E-01
XP_010712062.1	PREDICTED: obg-like ATPase 1 [Meleagris gallopavo]	10.0	119.3	101.5	111.2	105.9	105.3	98.7	78.7	86	93.5	110.7	103.3	86.1	2.61E-01	2.12E-02	2.38E-02
XP_010712570.1	PREDICTED: myopalladin [Meleagris gallopavo]	10.0	65.1	76.4	63.6	162	111.4	133.3	87.5	135.8	64.8	68.4	135.6	96.0	1.15E-02	2.64E-01	1.97E-01
XP_010714500.1	PREDICTED: 40S ribosomal protein S8 [Meleagris gallopavo]	9.9	88.8	71.6	86.1	89.7	83.8	105.7	128.7	121.6	124.1	82.2	93.1	124.8	2.66E-01	1.74E-03	9.86E-03
XP_010708859.1	PREDICTED: dysferlin-like [Meleagris gallopavo]	9.9	99	88.1	93.2	119.3	119.5	73.7	101.8	100.2	105.3	93.4	104.2	102.4	5.28E-01	6.14E-02	9.15E-01
XP_010708324.1	PREDICTED: alcohol dehydrogenase class-3 [Meleagris gallopavo]	9.9	162.6	130.1	5.5	118.4		92.5	140.5	138.7	111.9	99.4	105.5	130.4	9.29E-01	5.60E-01	2.03E-01
XP_010708353.1	PREDICTED: ubiquitin-conjugating enzyme E2 D3 isoform X1 [Meleagris gallopavo]	9.8	92.3	86.6	91.4	98.9	117.4	128.5	97.1	95.2	92.5	90.1	114.9	94.9	4.79E-02	9.46E-02	8.39E-02
XP_003206653.2	PREDICTED: methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial [Meleagris gallopavo]	9.8	17.9	6.5	7.3	136.8	142.1	133.1	158.9	158.6	138.7	10.6	137.3	152.1	9.51E-06	4.97E-05	1.09E-01
XP_003214052.3	PREDICTED: pre-B-cell leukemia transcription factor-interacting protein 1, partial [Meleagris gallopavo]	9.8	18.9	22.4	7.8	249.9	252.3	235.7	35.4	40.5	37.2	16.4	246.0	37.7	4.58E-06	1.01E-02	2.68E-06
XP_003212338.1	PREDICTED: heat shock protein beta-7 [Meleagris gallopavo]	9.8	59.4	65.6	4	173.9	185.8	151.7	95	87.3	77.3	43.0	170.5	86.5	4.40E-03	9.79E-02	1.71E-03
XP_010715962.1	PREDICTED: 60S ribosomal protein L4 [Meleagris gallopavo]	9.7	58.2	54.4		110.3	167.6	161.8	93.5	141.1	113.1	56.3	146.6	115.9	3.13E-02	4.47E-02	2.51E-01
XP_010726089.1	PREDICTED: titin-like [Meleagris gallopavo]	9.7				125.8	128.6	125.4	176.3	170.6	173.4	#DIV/0!	126.6	173.4	#DIV/0!	#DIV/0!	1.71E-05
XP_010719444.1	PREDICTED: 60S ribosomal protein L7a [Meleagris gallopavo]	9.6				195.7	197.4	169.9	119.2	105.7	112.1	#DIV/0!	187.7	112.3	#DIV/0!	#DIV/0!	1.49E-03
XP_010714799.1	PREDICTED: adiponectin [Meleagris gallopavo]	9.6	47	36.7	44.4	156	156.2	168.8	98.9	99.1	92.9	42.7	160.3	97.0	2.34E-05	1.26E-04	1.75E-04
XP_003205257.1	PREDICTED: cytochrome c oxidase subunit 6C [Meleagris gallopavo]	9.5	74.3	68.9	69.4	127	130	130.9	97.8	101.7	99.9	70.9	129.3	99.8	9.69E-06	1.49E-04	5.49E-05
XP_003203602.2	PREDICTED: mth838 domain-containing protein isoform X1 [Meleagris gallopavo]	9.4	9.4	48.9	41.6	136.6	137.3	150.2	135.2	132.4	108.4	33.3	141.4	125.3	1.12E-03	3.42E-03	1.70E-01
XP_010720775.1	PREDICTED: junctophilin-2 [Meleagris gallopavo]	9.3				80.8	135.1	138.5	178.7	186.2	180.7	#DIV/0!	118.1	181.9	#DIV/0!	#DIV/0!	2.76E-02
XP_010726681.1	PREDICTED: T-complex protein 1 subunit gamma [Meleagris gallopavo]	9.3	78.4	50.6	84.6	149.6	149.9	133.1	95.8	79.8	78.1	71.2	144.2	84.6	3.51E-03	3.23E-01	1.66E-03
XP_010706616.1	PREDICTED: NAD-dependent protein deacetylase sirutin-5, mitochondrial [Meleagris gallopavo]	9.2				282.9	97.4	307.6	65.3	105.5	41.2	#DIV/0!	229.3	70.7	#DIV/0!	#DIV/0!	8.28E-02
XP_010708968.1	PREDICTED: MICOS complex subunit MIC60, partial [Meleagris gallopavo]	9.2	68.4	51.5	56.2	156.4	97.9	163.4	64.7	122.6	118.9	58.7	139.2	102.1	1.96E-02	8.88E-02	2.54E-01
XP_010713434.1	PREDICTED: FUN14 domain-containing protein 2 [Meleagris gallopavo]	9.2	72.8	62.3	27	145.9	189	130.4	91.1	86.8	94.6	54.0	155.1	90.8	1.06E-02	5.87E-02	2.20E-02
XP_003205187.1	PREDICTED: fatty acid-binding protein, adipocyte-like [Meleagris gallopavo]	9.1			13.6	161	157.9	201.5	122.6	127.8	115.5	13.6	173.5	122.0	#DIV/0!	#DIV/0!	2.37E-02
XP_010710853.1	PREDICTED: RNA-splicing ligase RtcB homolog [Meleagris gallopavo]	9.0	85.4	111.2	81.5	95	84.3	80.6	94	92.1	175.9	92.7	86.6	120.7	5.86E-01	3.92E-01	2.90E-01
XP_010708237.1	PREDICTED: annexin A5 [Meleagris gallopavo]	8.9	41.5	37.3	43.7	135.7	154.5	163.1	114.7	96.3	113.1	40.8	151.1	108.0	1.86E-04	4.05E-04	1.26E-02
XP_019472815.1	PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial-like isoform X1 [Meleagris gallopavo]	8.9	324.2	291.4	284.4							300.0	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!
XP_019472940.1	PREDICTED: secernin-3, partial [Meleagris gallopavo]	8.8	110.1	106.8	112.5	100.5	91.2	101.3	91.3	93.3	93	109.8	97.7	92.5	2.90E-02	6.13E-04	1.95E-01
XP_010717643.1	PREDICTED: probable aminopeptidase NPEPL1 [Meleagris gallopavo]	8.8	82.1	80.5	86.8	104.3	113.1	116.5	109.6	103.5	103.7	83.1	111.3	105.6	2.35E-03	1.23E-03	2.41E-01
XP_010709117.1	PREDICTED: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial [Meleagris gallopavo]	8.8	37.8	32.8	20.3	129.8	127.4	215.1	141.8	97.7	97.2	30.3	157.4	112.2	1.23E-02	6.39E-03	2.36E-01
XP_003209240.2	PREDICTED: guanine nucleotide-binding protein subunit beta-4 [Meleagris gallopavo]	8.8	88.2	80.9	67.3	135.7	134.1	131.7	79.2	91.6	91.3	78.8	133.8	87.4	9.08E-04	3.09E-01	3.96E-04
XP_010709646.2	PREDICTED: MICOS complex subunit MIC19 [Meleagris gallopavo]	8.7	76.8	32.4	64.9	87.3	115.4	179.5	146.7	60.6	136.4	58.0	127.4	114.6	8.42E-02	1.35E-01	7.56E-01
XP_003203313.1	PREDICTED: ES1 protein homolog, mitochondrial-like isoform X1 [Meleagris gallopavo]	8.7	45.5	36.5	41.8	147.2	142.5	145.9	109.4	117.2	114	41.3	145.2	113.5	3.95E-06	3.09E-05	2.86E-04
XP_003204095.1	PREDICTED: proteasome subunit beta type-1 [Meleagris gallopavo]	8.7	6.3	72.9	90.2	138.6	149.3	120	111.1	114.4	97.3	56.5	136.0	107.6	4.21E-02	1.22E-01	4.75E-02
XP_010720097.1	PREDICTED: myosin regulatory light chain 10 isoform X2 [Meleagris gallopavo]	8.5		2.5		255.7	242.1	226.3	62.6	56.2	54.6	2.5	241.4	57.8	#DIV/0!	#DIV/0!	3.18E-05
NP_001290139.1	transforming protein RhoA [Meleagris gallopavo]	8.5	52.3	70.3	78.2	145.2	137.4	145.8	83	82.7	105.1	66.9	142.8	90.3	7.33E-04	9.39E-02	2.65E-03
XP_010711294.1	PREDICTED: programmed cell death 6-interacting protein [Meleagris gallopavo]	8.5	51.9	45.6	83.1	100.2	142.1	158.9	133.4	93.9	91	60.2	133.7	106.1	2.47E-02	6.26E-02	2.81E-01
XP_019469110.1	PREDICTED: LYR motif-containing protein 2 [Meleagris gallopavo]	8.4	82.9	52.7	55.2	128.3	153.5	150.3	98.2	86.5	92.4	63.6	144.0	92.4	3.00E-03	4.85E-02	3.88E-03
XP_010726200.2	PREDICTED: plectin-like [Meleagris gallopavo]	8.3	35.5	15.9	22.3	134.3	147.8	151.3	136.1	128.3	128.6	24.6	144.5	131.0	1.02E-04	7.24E-05	8.01E-02
XP_010714676.1	PREDICTED: protein phosphatase inhibitor 2 isoform X1 [Meleagris gallopavo]	8.2	118.8	135.4	176.4	116.4			101.8	143.3	107.8	143.5	116.4	117.6	#DIV/0!	2.94E-01	#DIV/0!
XP_010707388.1	PREDICTED: carbonic anhydrase 2 [Meleagris gallopavo]	8.1	61.2	58.6	73.4	135	107.9	142.1	112.9	103.1	105.9	64.4	128.3	107.3	4.93E-03	1.37E-03	1.24E-01
XP_010706534.1	PREDICTED: protein disulfide-isomerase A4 [Meleagris gallopavo]	8.1	75.7	67.9	66.5	90.2	138.4	129.5	124.1	108	99.5	70.0	119.4	110.5	3.08E-02	6.43E-03	6.20E-01
XP_003211790.1	PREDICTED: pigment epithelium-derived factor [Meleagris gallopavo]	8.0				332.6	262.6	231.3	73.5			#DIV/0!	275.5	73.5	#DIV/0!	#DIV/0!	#DIV/0!
XP_010717837.1	PREDICTED: hydroxyacylglutathione hydrolase, mitochondrial [Meleagris gallopavo]	8.0	59.2	10.1	57.5	151.5	150	159.3	106.4	106.5	99.4	42.3	153.6	104.1	2.43E-03	1.91E-02	1.84E-04
XP_010714872.1	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial [Meleagris gallopavo]	8.0	12.7	66.2	75.4	133.1	146.9	121	116.7	113.2	114.7	51.4	133.7	114.9	1.71E-02	3.17E-02	6.75E-02
XP_019478138.1	PREDICTED: prenylcysteine oxidase 1 [Meleagris gallopavo]	8.0	87.3	72.4	97.3	19.2	182.7	19.7	150.7	137	133.7	85.7	73.9	140			

XP_019472431.1	PREDICTED: putative methyltransferase DDB_G0268948 [Meleagris gallopavo]	6.8	83.8	80.1	75.4	103.7	81.5	73.1	113.3	154.6	134.5	79.8	86.1	134.1	5.39E-01	1.11E-02	3.29E-02	
XP_010719149.1	PREDICTED: prostaglandin E synthase 2 [Meleagris gallopavo]	6.8	23.7	29.9	30.6	166.1	139.1	170.5	102.2	132.8	105.2	28.1	158.6	113.4	2.04E-04	1.03E-03	3.09E-02	
XP_019471620.1	PREDICTED: ferritin heavy chain [Meleagris gallopavo]	6.8	57.8	68.4	78.3	115.6	98.2	121	101.3	129.6	129.7	68.2	111.6	120.2	8.74E-03	9.54E-03	5.03E-01	
XP_003211494.1	PREDICTED: histone H3.3 [Meleagris gallopavo]	6.6	26	30.5	15.1	243.5	242.8	256.8	18.3	31.8	35.2	23.9	247.7	28.4	4.12E-06	5.44E-01	5.79E-06	
XP_010706192.1	PREDICTED: low molecular weight phosphotyrosine protein phosphatase [Meleagris gallopavo]	6.6	104.1	103.1		166.9	55.7	47.5	139	142.2	141.5	103.6	90.0	140.9	8.03E-01	9.47E-05	2.57E-01	
XP_010721757.1	PREDICTED: adenylate kinase 2, mitochondrial isoform X1 [Meleagris gallopavo]	6.5	57		16	136.1	143.6	142.9	144.6	154	105.9	36.5	140.9	134.8	6.80E-03	2.74E-02	7.06E-01	
XP_019472938.1	PREDICTED: obg-like ATPase 1 [Meleagris gallopavo]	6.5	113.2	97.4	105.6	102.6	108.8	120.1	90.9	84	77.5	105.4	110.5	84.1	4.98E-01	2.37E-02	1.48E-02	
XP_010715142.1	PREDICTED: histidine-rich glycoprotein [Meleagris gallopavo]	6.4				175.8	194.1	186.6	113.1	127.7	102.8	#DIV/0!	185.5	114.5	#DIV/0!	#DIV/0!	1.38E-03	
XP_003207974.2	PREDICTED: inorganic pyrophosphatase [Meleagris gallopavo]	6.4	101.6	74.5	102.5	111.7	74.4	87	121.6	80.1	146.5	92.9	91.0	116.1	9.04E-01	3.40E-01	3.23E-01	
XP_010704829.1	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 [Meleagris gallopavo]	6.3	72.8		92.5		171.7	178.1		193.7	191.1	82.7	174.9	192.4	1.24E-02	8.10E-03	3.68E-02	
XP_010725100.2	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial [Meleagris gallopavo]	6.1	42.6	51.3	50.5	153.9	117.4	149.3	116.5	108.2	110.4	48.1	140.2	111.7	1.46E-03	6.91E-05	7.22E-02	
XP_003202723.1	PREDICTED: parathyrimosin [Meleagris gallopavo]	6.1	13.7	38.2		181.7	217.5	188.1	89.7	76.9	94.2	26.0	195.8	86.9	2.10E-03	1.25E-02	8.68E-04	
XP_019469887.1	PREDICTED: ubiquitin-conjugating enzyme E2 variant 2 [Meleagris gallopavo]	6.0	83.5	83.1	81.8	140.5	133	127.1	105	109.4	36.6	82.8	133.5	83.7	2.04E-04	9.72E-01	1.05E-01	
XP_019471930.1	PREDICTED: acyl-CoA-binding domain-containing protein 7 isoform X1 [Meleagris gallopavo]	5.9	28	25.4		162.1	180.2	182.7	110.7	105.5	105.5	26.7	175.0	107.2	4.01E-04	6.10E-05	5.43E-04	
XP_010717078.1	PREDICTED: cullin-associated NEDD8-dissociated protein 1-like [Meleagris gallopavo]	5.9	28.7	32.1	23.1	156.2	136.2	124.9	146.6	181.4	70.8	28.0	139.1	132.9	3.08E-04	3.28E-02	8.65E-01	
XP_010719340.1	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 [Meleagris gallopavo]	5.9				194.9	176.8	175.8	123.7	112.9	115.9	#DIV/0!	182.5	117.5	#DIV/0!	#DIV/0!	7.45E-04	
XP_003206625.1	PREDICTED: proteasome subunit alpha type-6 [Meleagris gallopavo]	5.9	50	52.5	69.5	156	148	151.4	92.5	88.4	91.6	57.3	151.8	90.8	1.34E-04	5.85E-03	2.05E-05	
XP_010717624.2	PREDICTED: nucleoside diphosphate kinase 3 [Meleagris gallopavo]	5.8	73.1	76.3	83.5	128.1	118.1	125.3	98	103.5	94.1	77.6	123.8	98.5	4.18E-04	7.06E-03	3.31E-03	
XP_010712047.1	PREDICTED: calcium-binding mitochondrial carrier protein Aralar1-like [Meleagris gallopavo]	5.8	56.7	57.7	60	127.4	125.5	151.8	83.9	119.9	117.1	58.1	134.9	107.0	8.42E-04	1.36E-02	1.23E-01	
XP_019469083.1	PREDICTED: laminin subunit alpha-2-like [Meleagris gallopavo]	5.8	58.8	70.5	36.2	127.6	183.4	105.2	87.9	144.4	86.1	55.2	138.7	106.1	3.00E-02	7.79E-02	3.40E-01	
XP_003212170.1	PREDICTED: ATP synthase subunit epsilon, mitochondrial [Meleagris gallopavo]	5.8	29.3	30.1	29.8	158.1	154.7	166.2	110.5	109	112.3	29.7	159.7	110.6	2.86E-06	1.30E-07	1.57E-04	
XP_003203975.1	PREDICTED: calpain-11 [Meleagris gallopavo]	5.7	99.1	97.1	115.2	117.5	120.2	113.9	78.3	80.4	78.3	103.8	117.2	79.0	8.98E-02	1.27E-02	4.04E-05	
XP_003208849.1	PREDICTED: alcohol dehydrogenase [NADP(+)] [Meleagris gallopavo]	5.6	90.8	83.3	82.6	123.5	127.1	135.7	82.9	97.4	76.7	85.6	128.8	85.7	6.42E-04	9.89E-01	3.76E-03	
XP_010705749.1	PREDICTED: cardiac phospholamban [Meleagris gallopavo]	5.6				216.2	226.5	245.8	73.4	78.2	59.8	#DIV/0!	229.5	70.5	#DIV/0!	#DIV/0!	1.02E-04	
XP_010723457.1	PREDICTED: halocacid dehalogenase-like hydrolase domain-containing protein 2 [Meleagris gallopavo]	5.6	65.8	64.8	55.4	107.8	133.3	114.2	104.6	121.2	132.8	62.0	118.4	119.5	2.49E-03	2.86E-03	9.27E-01	
XP_010706080.1	PREDICTED: ATP-binding cassette sub-family F member 2 [Meleagris gallopavo]	5.5	254.1	232.3	240.4			44.5			128.6	242.3	44.5	128.6	#DIV/0!	#DIV/0!	#DIV/0!	
XP_010720328.1	PREDICTED: 1,4-alpha-glucan-branching enzyme-like [Meleagris gallopavo]	5.3	29	30.8		59.8	56.1	70.8	207.1	219.2	227.3	29.9	62.2	217.9	1.11E-02	1.45E-04	2.93E-05	
XP_010707375.1	PREDICTED: inositol monophosphatase 1 [Meleagris gallopavo]	5.2	94.3	138.1	158.8	93.9	79.3	100.2	77.7	80.4	77.3	130.4	91.1	78.5	1.21E-01	5.26E-02	1.13E-01	
XP_003210533.1	PREDICTED: cytochrome b-c1 complex subunit 8 [Meleagris gallopavo]	5.2	62.7	69.2	75	144.1	116.7	124.6	105.9	100.2	101.7	69.0	128.5	102.6	2.59E-03	1.03E-03	3.59E-02	
XP_003211803.2	PREDICTED: vitronectin [Meleagris gallopavo]	5.2		18.5	21	157.6	170.7	176	131.6	120.4	104.3	19.8	168.1	118.8	2.42E-04	2.37E-03	6.86E-03	
XP_019474838.1	PREDICTED: eukaryotic translation initiation factor 3 subunit J [Meleagris gallopavo]	5.1	43.8	90	87.9	114.9	118.3	112.9	96.9	141.6	93.9	73.9	115.4	110.8	5.20E-02	1.62E-01	7.83E-01	
XP_003205354.1	PREDICTED: 60S acidic ribosomal protein P1 [Meleagris gallopavo]	5.1				169.1	166.4	170.5	124.6	142.2	127.3	#DIV/0!	168.7	131.4	#DIV/0!	#DIV/0!	2.64E-03	
XP_003206548.1	PREDICTED: eukaryotic translation initiation factor 2 subunit 1 [Meleagris gallopavo]	5.1	79.1	41.3	92.9	119.3	105.7	143.4	122.1	111.2	85	71.1	122.8	106.1	5.26E-02	1.38E-01	3.44E-01	
XP_010710388.2	PREDICTED: proteasome subunit alpha type-3, partial [Meleagris gallopavo]	4.9	66.8	67.7	77.7	124.4	125.2	131.8	85.6	106.2	114.6	70.7	127.1	102.1	1.79E-04	2.78E-02	4.88E-02	
XP_010706329.1	PREDICTED: ras-related protein Rab-10 [Meleagris gallopavo]	4.9	53.3	43.8	57.6	143.5	152.9	146.1	103.9	106	92.9	51.6	147.5	100.9	4.17E-05	1.01E-03	7.03E-04	
XP_019466080.1	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X1 [Meleagris gallopavo]	4.9	68.3	43.2	68.1	138.3	122.6	139.5	112.4	103.1	104.4	59.9	133.5	106.6	1.78E-03	6.09E-03	1.22E-02	
XP_010725594.1	PREDICTED: protein S100-A1 [Meleagris gallopavo]	4.9	516.1				267.2					116.7	516.1	267.2	116.7	#DIV/0!	#DIV/0!	#DIV/0!
XP_019478963.1	PREDICTED: phosphoethanolamine/phosphocholine phosphatase [Meleagris gallopavo]	4.8	175.1	191.4	153.2				125.1	141.4		113.7	173.2	#DIV/0!	126.7	#DIV/0!	2.73E-02	#DIV/0!
XP_010722856.1	PREDICTED: dual specificity protein phosphatase 3 [Meleagris gallopavo]	4.8	42.2	40	37.8	148.1	156.7	149.4	123.9	106.2	95.5	40.0	151.4	108.5	2.99E-06	1.22E-03	7.90E-03	

Table S2. Proteins Higher in Leg and Thigh Tissues.

Accession	Description	Sum PEP Score	Breast AVE	Leg AVE	Thigh AVE	p-value B-L	p-value B-T	p-value L-T
XP_019472906.1	titin	15405.3	79.4	102.7	117.9	1.27E-04	1.72E-05	5.72E-07
XP_010707950.1	serum albumin	938.7	47.6	144.7	107.8	7.75E-06	2.26E-05	6.92E-04
XP_003204057.2	alpha-actinin-2	832.2	52.9	147.5	99.6	1.28E-06	1.87E-05	1.81E-05
XP_019472960.1	nebulin, partial	540.4	56.1	123.8	120.2	6.04E-06	7.90E-06	7.77E-02
XP_010713505.1	four and a half LIM domains protein 1 isoform X1	435.1	2.6	136.4	161.0	1.97E-09	4.93E-08	1.04E-04
NP_001290122.1	myosin light chain 1/3, skeletal muscle isoform	419.5	18.7	178.3	103.0	5.64E-09	2.11E-05	3.12E-05
XP_003202767.1	calsequestrin-2	410.0	29.0	157.9	113.1	3.06E-09	1.71E-05	2.06E-04
XP_010705319.1	actin, alpha skeletal muscle	401.9	38.4	150.8	110.9	6.63E-08	1.47E-07	1.95E-06
XP_010724398.1	creatine kinase S-type, mitochondrial	367.3	64.8	131.3	103.9	3.60E-03	1.60E-03	7.49E-02
XP_019473010.1	LIM domain-binding protein 3 isoform X6	354.1	50.4	140.9	108.7	4.20E-06	5.67E-05	6.02E-04
XP_003211747.1	malate dehydrogenase, mitochondrial	328.3	55.2	147.1	97.7	3.60E-06	2.80E-06	3.32E-05
XP_019476563.1	sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1	318.7	65.4	120.8	113.9	5.90E-05	4.36E-06	7.59E-02
XP_010707718.1	ATP synthase subunit beta, mitochondrial	290.9	23.2	158.7	118.1	1.11E-07	1.96E-06	1.97E-05
XP_019467155.1	ATP-dependent 6-phosphofructokinase, muscle type	264.0	70.2	103.7	126.1	7.00E-04	4.29E-05	4.10E-04
XP_019477138.1	myosin-1B-like	261.5	30.0	178.8	91.3	2.05E-07	7.77E-06	2.32E-06
XP_010723192.2	elongation factor 2	256.0	81.8	123.7	94.5	4.40E-05	1.33E-02	1.24E-03
XP_003206336.1	troponin I, fast skeletal muscle	247.1	42.6	167.1	90.3	3.65E-07	1.18E-04	2.88E-05
NP_001290136.1	serotransferrin precursor	246.2	42.6	156.5	100.9	2.01E-07	2.71E-05	1.63E-05
XP_019465869.1	transitional endoplasmic reticulum ATPase isoform X1	240.2	77.6	131.5	90.9	7.72E-05	1.50E-02	3.47E-06
XP_010708730.1	aconitate hydratase, mitochondrial	235.9	34.9	143.3	121.7	6.64E-05	4.54E-06	2.04E-02
XP_003211746.1	heat shock protein beta-1	198.8	22.7	144.4	132.9	1.76E-03	2.76E-05	5.39E-01
XP_010708318.1	PDZ and LIM domain protein 5 isoform X6	194.9	62.0	140.0	97.9	4.86E-05	1.57E-04	6.18E-04
XP_010710229.1	heat shock protein HSP 90-alpha	194.6	73.6	124.7	101.7	3.16E-05	1.34E-04	5.86E-04
XP_003209375.1	actin, cytoplasmic type 5	193.4	30.1	146.9	123.0	7.82E-04	2.72E-04	8.98E-02
XP_003212096.2	elongation factor 1-alpha 2	181.2	77.5	109.8	112.6	3.76E-04	2.30E-04	4.49E-01
XP_010708319.1	PDZ and LIM domain protein 5 isoform X7	170.0	12.8	158.6	128.5	1.15E-05	7.25E-06	1.06E-02
XP_010711942.1	desmin	161.7	37.8	140.3	121.9	1.98E-05	8.24E-06	1.24E-02
XP_010712691.1	myozenin-1 isoform X1	159.5	44.3	122.6	133.1	1.65E-05	9.72E-07	2.74E-02
XP_010709311.1	troponin T, fast skeletal muscle isoform X2	159.2	54.4	162.8	82.9	2.36E-04	1.10E-02	3.00E-04
XP_010718246.1	cytochrome b-c1 complex subunit 2, mitochondrial	158.6	52.4	139.6	108.1	3.98E-06	1.35E-06	1.80E-04
XP_010713032.2	aspartate aminotransferase, cytoplasmic, partial	157.7	54.1	119.1	126.8	3.36E-07	1.13E-04	1.84E-01
XP_010716826.1	cytochrome b-c1 complex subunit 1, mitochondrial	157.7	52.8	131.3	115.9	7.09E-06	3.57E-07	4.82E-03
XP_003206959.1	myosin light chain 3	154.8	1.7	209.1	89.8	9.94E-05	4.97E-05	3.88E-05
XP_010722021.1	apolipoprotein A-I	154.0	27.2	152.4	120.4	1.15E-06	2.20E-07	1.80E-04
XP_003203314.1	hemoglobin subunit beta	153.8	34.8	139.2	126.1	4.67E-07	6.68E-06	1.01E-02
XP_003210790.1	hemoglobin subunit alpha-D	152.5	25.2	148.2	126.5	9.82E-06	3.28E-06	1.39E-02

XP_010720888.1	troponin C, skeletal muscle	147.9	38.1	173.2	88.7	1.34E-07	5.14E-05	5.50E-06
XP_010723380.1	tropomyosin alpha-4 chain isoform X1	145.8	63.5	158.9	77.6	4.81E-04	4.62E-03	9.91E-04
XP_003211805.1	fructose-bisphosphate aldolase C	145.4	n.d.	186.9	113.1	n.a.	n.a.	8.17E-02
XP_019465707.1	talín-1	145.4	42.1	171.1	86.8	4.96E-04	8.40E-03	2.32E-03
XP_010714086.1	L-lactate dehydrogenase B chain isoform X2	141.5	9.0	162.7	128.3	2.44E-09	1.94E-07	3.38E-05
XP_010723540.1	transitional endoplasmic reticulum ATPase-like	138.7	52.2	185.0	80.2	1.21E-01	4.16E-01	1.20E-01
XP_010707027.1	myomesin-1-like	137.8	78.9	104.9	116.2	1.52E-03	1.17E-03	9.31E-02
XP_010723474.1	ATP synthase subunit alpha, mitochondrial	137.6	18.9	153.2	127.9	2.74E-06	5.11E-07	2.61E-03
XP_010711008.2	vimentin	133.6	40.2	142.0	117.9	3.08E-06	4.27E-05	2.17E-03
XP_010717663.1	sarcalumenin isoform X1	132.2	54.6	114.2	131.2	2.84E-04	7.50E-05	6.39E-02
XP_003204233.1	tropomyosin alpha-3 chain isoform X5	129.5	45.7	182.3	72.0	1.75E-02	1.38E-02	3.31E-02
XP_010708361.1	PDZ and LIM domain protein 3 isoform X1	127.2	62.3	139.0	98.6	8.11E-05	1.02E-03	8.68E-05
XP_010715974.1	isocitrate dehydrogenase [NADP], mitochondrial	127.2	13.9	171.9	114.1	7.77E-08	1.98E-06	1.50E-05
XP_010717664.1	sarcalumenin isoform X2	125.6	n.d.	173.6	189.7	n.a.	n.a.	6.11E-01
XP_003212226.1	protein deglycase DJ-1	125.6	84.4	121.1	94.6	1.21E-03	5.66E-02	1.05E-03
XP_003207490.1	60 kDa heat shock protein, mitochondrial	124.3	82.5	121.5	96.0	8.29E-04	2.88E-02	3.67E-04
XP_010704813.2	malate dehydrogenase, cytoplasmic, partial	124.2	38.2	145.4	116.4	1.04E-05	7.45E-07	1.56E-03
XP_003202395.1	myoglobin	118.3	0.7	242.6	57.0	1.94E-04	6.91E-04	3.09E-05
XP_010706908.2	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondr	117.4	52.5	152.0	95.5	5.28E-06	8.23E-04	4.17E-04
XP_003204611.1	trifunctional enzyme subunit alpha, mitochondrial	112.5	43.6	141.9	114.5	2.61E-05	8.05E-05	1.58E-03
XP_010708108.1	hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	108.6	48.3	150.9	100.9	7.72E-06	3.51E-04	6.80E-04
XP_010715203.1	3-ketoacyl-CoA thiolase, mitochondrial	106.7	48.0	132.9	119.1	2.11E-06	7.95E-05	3.54E-02
XP_010712078.1	myc box-dependent-interacting protein 1	106.7	66.1	127.8	106.0	4.86E-04	6.07E-04	1.81E-02
XP_003210796.1	hemoglobin subunit alpha-A	105.8	34.9	139.7	125.4	9.38E-06	6.45E-06	4.47E-03
XP_010707648.1	rab GDP dissociation inhibitor beta	104.2	71.1	129.2	99.6	3.16E-04	1.01E-03	4.70E-03
XP_010712670.1	voltage-dependent anion-selective channel protein 2 isoform X1	103.0	48.7	134.4	116.9	7.97E-05	1.59E-04	6.83E-02
XP_003211726.3	sarcoplasmic/endoplasmic reticulum calcium ATPase 3	95.5	55.0	122.5	122.4	8.85E-02	1.10E-01	9.97E-01
XP_010719463.1	78 kDa glucose-regulated protein	94.4	74.4	133.0	92.6	3.45E-03	9.55E-04	1.25E-02
XP_003202518.2	aldose reductase-like	94.2	59.4	132.2	108.4	1.37E-04	1.59E-04	5.81E-03
XP_019471366.1	myosin-binding protein C, slow-type isoform X1	92.9	33.3	156.1	110.5	1.35E-06	4.46E-06	1.51E-04
XP_010721169.1	superoxide dismutase [Cu-Zn], partial	92.8	81.2	126.1	92.8	1.85E-03	3.46E-02	4.47E-03
XP_010720198.1	14-3-3 protein gamma	90.4	47.0	131.7	121.3	7.07E-05	2.41E-04	1.79E-01
XP_010714482.1	peroxiredoxin-1	89.7	44.7	153.8	101.4	2.09E-05	4.53E-04	2.54E-04
XP_010705458.1	soluble scavenger receptor cysteine-rich domain-containing protein SS	87.7	76.7	123.3	100.0	1.38E-05	4.82E-04	4.10E-04
XP_019471455.1	adenylosuccinate synthetase isozyme 1 isoform X1	84.8	78.7	106.6	114.7	7.02E-04	3.85E-04	1.62E-02
XP_019476000.1	myotilin isoform X2	82.9	1.8	186.5	112.3	4.85E-05	2.75E-05	7.55E-05
XP_010714011.1	peroxiredoxin-6, partial	81.0	83.4	114.9	101.6	2.99E-02	1.37E-01	3.74E-02
XP_010720031.1	14-3-3 protein epsilon isoform X1	73.1	35.4	172.5	92.1	1.37E-04	3.37E-04	1.13E-03

XP_010709971.1	cofilin-2	66.2	71.0	128.0	101.0	9.96E-05	7.03E-06	1.71E-03
XP_010725496.2	citrate synthase, mitochondrial, partial	65.8	41.8	141.5	116.7	7.46E-05	2.27E-04	2.54E-02
XP_019468449.1	protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform X1	56.8	39.8	150.2	110.0	2.15E-03	5.55E-04	5.69E-02
XP_010712906.1	ankyrin repeat domain-containing protein 2	56.8	8.6	231.7	59.6	5.52E-06	2.90E-04	2.20E-05
XP_010719949.1	ATP synthase subunit d, mitochondrial	54.6	29.0	175.4	95.5	4.88E-07	2.91E-06	3.02E-06
XP_010711802.1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform X1	54.3	30.1	154.1	115.9	1.03E-07	8.17E-06	1.35E-04
XP_003208605.2	4-trimethylaminobutyraldehyde dehydrogenase	53.8	56.9	132.3	110.9	4.63E-06	8.94E-04	2.95E-02
XP_003204919.3	fumarate hydratase, mitochondrial	52.1	20.8	156.8	122.4	7.35E-06	5.81E-05	6.11E-03
XP_003211138.2	phosphatidylethanolamine-binding protein 1	51.7	78.6	118.0	103.4	4.90E-03	2.53E-02	6.38E-04
XP_010723580.1	tropomyosin beta chain isoform X2	47.0	4.5	212.0	83.5	1.68E-05	9.48E-07	1.10E-04
XP_010721582.1	fatty acid-binding protein, heart	45.6	28.0	163.7	108.4	2.96E-05	5.15E-05	2.05E-03
XP_010715653.1	electron transfer flavoprotein subunit alpha, mitochondrial	45.1	20.1	157.9	122.1	2.58E-04	5.46E-05	3.77E-02
XP_010725978.1	myosin heavy chain, skeletal muscle, adult-like, partial	44.9	7.5	170.6	121.9	6.99E-05	7.67E-06	9.10E-03
XP_010715481.1	cytochrome c oxidase subunit 5A, mitochondrial	44.3	28.6	161.8	109.6	8.51E-07	1.71E-06	2.13E-05
XP_003203382.1	S-formylglutathione hydrolase	44.0	67.2	133.5	99.4	5.31E-05	1.17E-02	1.28E-02
XP_019472831.1	nebulin-like isoform X1	43.9	25.1	105.7	169.3	1.30E-05	1.99E-06	1.24E-04
XP_010726361.2	filamin-C-like, partial	43.6	55.9	125.7	118.4	1.51E-04	1.01E-02	6.12E-01
XP_003212977.1	ATP synthase F(0) complex subunit B1, mitochondrial, partial	43.2	47.3	143.1	109.5	1.18E-05	1.11E-03	9.91E-03
XP_003204773.1	adenylyl cyclase-associated protein 2	43.1	51.2	154.3	94.4	7.66E-04	1.99E-03	6.25E-03
XP_010711895.1	myc box-dependent-interacting protein 1-like	42.4	52.6	139.5	107.9	2.66E-06	5.16E-05	4.32E-04
XP_010716572.1	troponin C, slow skeletal and cardiac muscles	40.7	39.8	197.3	62.9	3.20E-06	5.39E-03	5.96E-06
XP_019473127.1	vinculin isoform X1	39.2	55.9	158.1	86.0	6.48E-06	7.35E-04	1.54E-05
XP_010720363.1	dihydrolipoyl dehydrogenase, mitochondrial	37.8	37.7	143.8	118.5	3.15E-06	1.89E-04	1.11E-02
XP_010711617.1	long-chain specific acyl-CoA dehydrogenase, mitochondrial, partial	37.7	22.9	185.9	91.2	1.70E-05	1.51E-02	4.55E-03
XP_019476911.1	tubulin beta-4B chain	36.5	27.9	108.6	163.6	6.30E-05	6.72E-06	4.37E-04
XP_010721655.1	ATP synthase subunit O, mitochondrial	35.8	31.3	159.6	109.1	2.75E-07	1.72E-06	7.26E-06
XP_010725154.1	sodium/potassium-transporting ATPase subunit alpha-2	34.2	47.0	137.3	115.7	9.30E-05	5.13E-03	1.22E-01
XP_010722464.1	ES1 protein homolog, mitochondrial	32.7	21.8	111.4	166.9	3.14E-03	1.32E-04	2.28E-02
XP_003207855.3	enoyl-CoA hydratase, mitochondrial	32.4	47.6	149.8	102.5	9.92E-06	5.43E-04	1.61E-03
XP_010724255.1	ATP synthase subunit e, mitochondrial	31.8	37.5	157.5	105.0	1.13E-05	2.54E-05	1.66E-04
XP_003212221.2	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	31.6	37.0	156.2	106.9	2.61E-05	1.99E-04	7.12E-04
NP_001290109.1	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	31.5	36.7	151.9	111.3	2.94E-06	8.89E-05	1.73E-03
XP_010716520.1	cytochrome c oxidase subunit 4 isoform 1, mitochondrial isoform X1	31.5	43.2	135.4	121.4	1.01E-04	5.49E-04	2.20E-01
XP_010721496.1	2-oxoglutarate dehydrogenase, mitochondrial isoform X1	30.7	13.8	160.2	125.9	1.84E-04	9.67E-06	3.62E-02
XP_010726371.1	cytochrome c oxidase subunit 6B1	30.4	26.8	153.0	120.2	3.86E-07	1.51E-04	8.98E-03
XP_010720929.1	neurofilament heavy polypeptide-like	30.2	82.9	107.2	109.9	3.75E-01	3.34E-01	7.54E-01
XP_003205760.1	myozenin-2 isoform X1	30.1	1.5	212.5	86.0	1.26E-07	3.79E-06	3.13E-06
XP_019476651.1	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 isoform X1	29.6	47.8	134.9	117.2	2.84E-03	1.24E-02	4.35E-01

XP_010716964.2	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	29.4	30.7	158.4	110.8	1.12E-05	5.24E-05	1.18E-04
XP_010726400.2	troponin T, slow skeletal muscle-like	29.0	29.6	187.7	82.7	5.82E-06	7.81E-03	8.63E-04
XP_010726217.2	neuroblast differentiation-associated protein AHNAK-like, partial	28.7	70.5	114.1	115.3	5.56E-04	5.70E-04	8.29E-01
XP_019478418.1	dihydrolipoyllysine-residue acetyltransferase component of pyruvate de	28.7	33.1	132.1	134.7	1.76E-04	4.40E-04	8.39E-01
XP_010706330.1	trifunctional enzyme subunit beta, mitochondrial isoform X1	28.1	50.9	141.3	107.8	3.20E-05	4.21E-04	1.94E-03
XP_003202173.1	lumican	27.7	46.7	173.9	79.4	1.61E-06	1.19E-03	2.81E-05
XP_003207548.1	elongation factor 1-beta	27.2	87.5	114.8	97.6	3.79E-03	4.87E-02	5.06E-03
XP_010711546.1	collagen alpha-3(VI) chain isoform X1	26.8	19.8	151.1	129.1	8.66E-06	1.45E-05	7.38E-03
XP_010726340.1	calreticulin	26.8	73.7	120.6	105.7	6.23E-03	2.02E-02	2.25E-01
XP_010724594.1	histone H1.11R, partial	26.4	1.8	206.2	91.9	9.45E-07	3.92E-07	1.17E-05
XP_010716010.1	protein disulfide-isomerase A3	26.3	67.4	130.4	102.3	2.16E-04	5.94E-04	2.14E-03
XP_003211808.1	bleomycin hydrolase	26.3	89.1	104.6	106.3	1.25E-01	1.81E-01	8.17E-01
XP_010722978.1	heat shock protein 30C-like	26.2	35.3	142.0	122.7	1.93E-03	6.16E-03	4.07E-01
XP_010716011.1	creatine kinase U-type, mitochondrial, partial	25.7	47.5	140.6	111.8	2.24E-04	4.30E-04	4.25E-03
XP_019467633.1	acetyl-CoA acetyltransferase, mitochondrial, partial	25.7	9.6	145.5	144.9	6.49E-06	1.58E-05	9.35E-01
XP_019477922.1	aflatoxin B1 aldehyde reductase member 2-like	25.4	79.5	114.8	105.7	1.54E-02	5.12E-02	1.34E-01
XP_003202996.1	SH3 domain-binding glutamic acid-rich-like protein	25.2	54.4	161.5	84.1	2.21E-04	4.76E-04	8.64E-04
XP_019473564.1	CDGS8 iron-sulfur domain-containing protein 1 isoform X1	25.0	65.4	119.3	115.3	3.14E-03	9.62E-03	5.91E-01
XP_010708189.1	histone H2A.J	24.9	3.0	243.8	53.3	1.01E-08	3.03E-06	6.89E-08
XP_010720908.1	microtubule-associated protein RP/EB family member 1 isoform X1	24.6	67.8	126.5	105.6	4.43E-06	1.62E-04	1.24E-03
XP_019473001.1	glutamate dehydrogenase 1, mitochondrial	24.6	44.3	163.6	92.1	6.35E-04	7.77E-03	3.78E-03
XP_010718264.2	ubiquitin-conjugating enzyme E2 L3	24.5	78.2	106.0	115.6	1.79E-01	5.21E-02	6.82E-01
XP_010722862.1	prohibitin	24.4	81.1	120.6	98.3	7.99E-03	1.27E-01	1.37E-01
XP_010708917.1	MICOS complex subunit MIC60-like	24.4	33.3	148.1	118.6	6.54E-03	9.78E-02	5.49E-01
XP_010707400.1	carbonic anhydrase 2-like	23.7	66.9	119.6	113.5	3.05E-02	5.42E-05	7.22E-01
XP_010716605.1	prohibitin-2, partial	22.6	86.1	110.7	103.2	3.08E-04	1.65E-02	1.63E-01
XP_010721372.1	dihydropyrimidinase-related protein 2	22.2	32.7	149.2	118.1	1.48E-03	1.05E-03	1.56E-01
NP_001278332.1	transferrin precursor	22.2	15.8	174.1	110.1	4.92E-05	2.02E-04	2.48E-03
XP_010711141.1	3-hydroxyisobutyrate dehydrogenase, mitochondrial isoform X1	21.8	91.9	105.1	103.0	3.18E-02	6.07E-02	3.21E-01
XP_010726059.1	hemopexin-like, partial	21.8	40.7	153.7	105.6	8.38E-05	1.55E-04	8.11E-04
XP_003206087.3	succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	21.7	7.3	147.4	147.8	1.13E-04	7.50E-04	9.68E-01
XP_003209829.2	cytochrome b-c1 complex subunit Rieske, mitochondrial	21.1	63.9	140.5	95.6	5.63E-04	3.68E-02	8.92E-03
XP_010711708.1	10 kDa heat shock protein, mitochondrial isoform X1	21.1	77.0	127.6	95.4	6.60E-04	2.30E-02	1.45E-03
XP_010718676.2	14-3-3 protein eta	21.0	65.8	120.0	114.2	6.63E-02	1.33E-01	8.58E-01
XP_010707416.1	2,4-dienoyl-CoA reductase, mitochondrial	21.0	54.1	114.5	131.4	6.18E-06	5.91E-06	5.59E-03
YP_004243711.1	cytochrome c oxidase subunit II (mitochondrion)	20.8	35.2	159.8	105.0	3.36E-07	3.71E-05	1.07E-04
XP_010717306.1	ovoinhibitor isoform X1	20.6	25.3	166.0	108.7	1.62E-04	2.03E-02	5.08E-02
XP_019466271.1	alpha-aminoadipic semialdehyde dehydrogenase	19.7	29.2	144.3	126.4	1.01E-04	2.26E-04	7.47E-02

XP_010718554.1	short-chain specific acyl-CoA dehydrogenase, mitochondrial	19.7	29.3	152.4	118.3	1.96E-06	1.78E-05	1.52E-04
XP_019473935.1	laminin subunit gamma-1, partial	19.4	47.8	138.1	130.1	1.45E-01	6.27E-02	8.00E-01
XP_003213488.3	NAD(P) transhydrogenase, mitochondrial-like	19.3	n.d.	164.3	135.7	n.a.	n.a.	7.11E-03
XP_019466703.1	protein ADP-ribosylarginine hydrolase-like, partial	18.9	75.4	125.9	98.7	1.39E-03	4.65E-03	6.84E-03
XP_019468352.1	nidogen-1	18.9	43.3	135.0	121.7	2.97E-02	6.83E-02	7.60E-01
XP_010720462.1	laminin subunit beta-1	18.8	84.7	100.2	115.1	2.77E-01	2.40E-01	4.66E-01
XP_003208621.1	14 kDa phosphohistidine phosphatase-like	18.7	49.8	147.1	103.1	2.05E-06	1.09E-05	4.88E-05
XP_003212008.1	14-3-3 protein beta/alpha	18.6	28.7	164.1	107.2	1.55E-06	2.32E-05	1.34E-04
XP_010713240.1	thioredoxin-dependent peroxide reductase, mitochondrial, partial	18.4	20.3	148.4	131.3	5.59E-04	3.49E-03	4.78E-01
XP_010719753.1	beta-2-glycoprotein 1 isoform X1	18.1	34.4	166.2	99.4	7.65E-03	1.24E-03	7.34E-02
XP_003205566.2	ADP/ATP translocase 1, partial	17.9	85.2	117.3	97.5	1.30E-02	2.15E-01	3.13E-02
XP_010710255.1	creatine kinase B-type	17.8	46.1	158.9	95.0	7.09E-07	2.84E-05	2.39E-05
XP_010716394.1	cadherin-13 isoform X1	17.6	78.3	123.3	98.4	1.17E-04	3.20E-02	1.75E-02
XP_010709805.1	3-mercaptopyruvate sulfurtransferase isoform X1	17.5	47.7	151.9	100.4	8.37E-05	6.03E-03	2.48E-03
XP_010718107.1	glycerol-3-phosphate phosphatase, partial	17.4	67.9	119.9	112.2	1.09E-05	1.51E-03	2.52E-01
XP_010712598.1	hexokinase-1	17.4	52.0	143.6	104.4	2.55E-03	4.53E-02	3.60E-02
XP_010725164.1	2-oxoglutarate dehydrogenase, mitochondrial-like	17.3	20.1	158.7	121.2	3.66E-05	3.38E-07	5.80E-03
XP_003207311.1	40S ribosomal protein SA	16.4	43.8	149.2	107.0	5.41E-05	1.60E-04	4.44E-04
XP_010709036.1	cysteine and glycine-rich protein 3 isoform X2	16.3	11.4	197.0	91.6	2.58E-05	9.00E-06	2.79E-04
XP_010722333.1	troponin I, slow skeletal muscle	16.3	n.d.	239.3	60.7	n.a.	n.a.	5.39E-02
XP_010723080.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	15.9	31.0	154.1	114.9	6.24E-05	7.01E-05	1.78E-03
XP_010705429.1	superoxide dismutase [Mn], mitochondrial	15.9	59.0	118.7	122.3	9.24E-04	5.21E-05	5.85E-01
XP_003209409.2	isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	15.8	30.1	129.5	140.5	2.36E-03	4.01E-03	6.39E-01
XP_010725340.1	protein NDRG2-like	15.6	46.3	146.0	107.7	7.43E-04	1.52E-03	4.47E-02
XP_003202247.2	histone H2B 8-like	15.5	5.7	238.6	55.8	9.06E-06	1.72E-04	3.44E-05
XP_010720044.1	protein NipSnap homolog 2 isoform X1	15.4	26.0	129.1	144.9	1.07E-03	1.69E-04	1.57E-01
NP_001290084.1	glutathione S-transferase alpha class A1.3	15.0	53.9	143.8	102.2	1.31E-05	6.45E-05	4.25E-04
XP_010720721.1	ATP synthase-coupling factor 6, mitochondrial	14.8	43.9	161.9	94.2	1.73E-06	1.45E-03	4.56E-04
XP_010717684.1	enoyl-CoA delta isomerase 1, mitochondrial	14.8	36.3	153.0	110.7	2.17E-04	7.47E-05	7.07E-03
XP_010725971.1	histone H4	14.6	n.d.	269.1	30.9	n.a.	n.a.	2.91E-06
XP_019468033.1	acylphosphatase-2 isoform X1	14.6	67.4	134.3	98.4	3.21E-04	5.92E-03	2.19E-03
XP_010726533.2	neuroblast differentiation-associated protein AHNAK-like, partial	14.3	50.4	133.4	116.2	2.59E-04	8.31E-06	7.13E-02
XP_019474799.1	profilin-2 isoform X2	14.1	49.5	147.8	102.7	1.94E-06	3.58E-04	7.85E-04
XP_010704648.1	reticulon-4	13.9	69.2	119.2	111.5	7.00E-05	3.04E-03	3.08E-01
XP_003213185.1	polymerase I and transcript release factor	13.8	30.6	162.6	106.8	7.20E-06	4.87E-06	1.84E-04
XP_010711822.1	isocitrate dehydrogenase [NADP] cytoplasmic	13.8	72.0	130.3	97.7	3.40E-03	6.44E-03	3.11E-02
XP_019477394.1	smoothelin-like protein 2, partial	13.7	7.4	178.8	113.9	3.32E-06	3.32E-07	1.90E-04
XP_010709306.1	proline-rich protein 33 isoform X1	13.7	68.4	135.0	96.6	9.60E-04	2.48E-01	1.24E-01

XP_010727123.1	succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	13.7	14.6	144.7	140.7	2.77E-06	9.55E-06	3.01E-01
XP_019465497.1	vicilin-like seed storage protein At2g18540	13.7	31.8	138.7	129.5	1.53E-03	1.45E-03	3.42E-01
XP_003206523.1	calpain-3 isoform X1	13.3	82.5	112.2	105.2	1.81E-01	2.92E-01	1.21E-01
XP_010710203.1	ubiquitin-conjugating enzyme E2 N	13.3	67.8	126.5	105.6	7.52E-04	8.51E-04	4.82E-02
XP_010726380.1	plectin-like, partial	13.3	39.9	149.2	110.9	4.10E-04	6.52E-04	3.59E-02
XP_010723898.2	pyruvate dehydrogenase E1 component subunit alpha, somatic form, m	13.1	12.8	157.3	134.1	2.66E-05	8.52E-04	3.28E-02
XP_010722250.1	transgelin-2	12.9	11.7	210.3	78.0	2.21E-05	4.81E-02	5.03E-03
XP_010710036.1	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglut	12.6	41.3	149.7	109.0	2.02E-04	1.23E-03	2.21E-02
XP_003202174.1	decorin	12.4	n.d.	195.1	104.9	n.a.	n.a.	2.40E-04
XP_010706914.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	12.4	36.3	154.0	121.8	8.96E-02	9.95E-02	5.22E-01
XP_010712175.1	aldo-keto reductase family 1 member B10-like isoform X2	12.2	59.4	123.8	116.8	4.29E-04	1.13E-03	4.00E-01
XP_010716902.2	laminin subunit beta-2	12.2	62.0	130.6	107.4	1.23E-04	4.82E-02	2.25E-01
XP_003202424.1	endoplasmin	11.9	85.2	110.9	103.9	2.67E-02	1.54E-01	5.57E-01
XP_010709395.1	cathepsin D, partial	11.9	70.2	144.2	85.5	6.18E-04	1.78E-02	2.17E-03
XP_003203240.1	protein ADP-ribosylarginine hydrolase-like protein 1	11.8	n.d.	147.9	152.1	n.a.	n.a.	2.93E-01
XP_003208853.1	cytochrome b-c1 complex subunit 6, mitochondrial	11.8	54.0	132.2	113.8	5.65E-05	3.20E-05	1.20E-02
XP_010710492.1	peptidyl-prolyl cis-trans isomerase FKBP3, partial	11.7	18.7	163.9	129.9	n.a.	n.a.	3.69E-01
XP_019473945.1	cystathionine gamma-lyase, partial	11.7	72.3	111.2	116.5	8.38E-02	5.78E-02	7.21E-01
XP_003205251.1	14-3-3 protein zeta/delta	11.4	30.2	172.3	97.4	9.95E-04	2.90E-02	4.16E-02
XP_003207600.1	O-acetyl-ADP-ribose deacetylase 1 isoform X1	11.4	63.7	135.0	101.4	6.39E-02	1.99E-01	2.24E-01
XP_010725827.1	voltage-dependent calcium channel subunit alpha-2/delta-1-like	11.3	55.3	158.0	86.7	2.99E-06	4.84E-03	2.34E-04
XP_010720566.1	adenosylhomocysteinase	11.2	77.1	120.1	102.8	3.91E-04	1.47E-03	2.47E-02
XP_003214067.2	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial, partial	11.1	37.6	146.0	116.4	9.37E-05	2.26E-04	6.91E-03
XP_003208024.2	synaptopodin 2-like protein	11.0	n.d.	300.0	n.d.	n.a.	n.a.	#DIV/0!
XP_010722077.1	heat shock protein beta-2	11.0	n.d.	159.2	140.8	n.a.	n.a.	1.03E-02
XP_010707744.1	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondria	10.9	21.0	168.1	110.9	8.61E-04	2.62E-03	2.49E-02
XP_010712046.1	calcium-binding mitochondrial carrier protein Aralar1-like	10.8	48.3	123.5	128.2	1.82E-01	9.57E-03	9.22E-01
XP_010711091.1	cytochrome c	10.6	22.3	177.3	100.4	3.09E-04	2.10E-03	1.06E-02
XP_003203488.2	radixin	10.5	25.6	172.9	101.4	1.40E-04	7.20E-03	5.80E-03
XP_010704870.1	destrin	10.5	61.5	127.8	110.6	2.77E-03	3.89E-03	2.13E-01
XP_003203792.1	atypical kinase COQ8A, mitochondrial	10.5	n.d.	169.5	187.0	n.a.	n.a.	8.18E-01
XP_010726006.1	peptidyl-prolyl cis-trans isomerase D-like, partial	10.4	82.8	112.4	104.8	3.47E-01	4.38E-02	8.00E-01
XP_003206653.2	methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	9.8	10.6	137.3	152.1	9.51E-06	4.97E-05	1.09E-01
XP_003214052.3	pre-B-cell leukemia transcription factor-interacting protein 1, partial	9.8	16.4	246.0	37.7	4.58E-06	1.01E-02	2.68E-06
XP_003212338.1	heat shock protein beta-7	9.8	43.0	170.5	86.5	4.40E-03	9.79E-02	1.71E-03
XP_010715962.1	60S ribosomal protein L4	9.7	56.3	146.6	115.9	3.13E-02	4.47E-02	2.51E-01
XP_010726089.1	titin-like	9.7	n.d.	126.6	173.4	n.a.	n.a.	1.71E-05
XP_010719444.1	60S ribosomal protein L7a	9.6	n.d.	187.7	112.3	n.a.	n.a.	1.49E-03

XP_010714799.1	adiponectin	9.6	42.7	160.3	97.0	2.34E-05	1.26E-04	1.75E-04
XP_003205257.1	cytochrome c oxidase subunit 6C	9.5	70.9	129.3	99.8	9.69E-06	1.49E-04	5.49E-05
XP_003203602.2	mtH938 domain-containing protein isoform X1	9.4	33.3	141.4	125.3	1.12E-03	3.42E-03	1.70E-01
XP_010720775.1	junctophilin-2	9.3	n.d.	118.1	181.9	n.a.	n.a.	2.76E-02
XP_010726681.1	T-complex protein 1 subunit gamma	9.3	71.2	144.2	84.6	3.51E-03	3.23E-01	1.66E-03
XP_010706616.1	NAD-dependent protein deacetylase sirtuin-5, mitochondrial	9.2	n.d.	229.3	70.7	n.a.	n.a.	8.28E-02
XP_010708968.1	MICOS complex subunit MIC60, partial	9.2	58.7	139.2	102.1	1.96E-02	8.88E-02	2.54E-01
XP_010713434.1	FUN14 domain-containing protein 2	9.2	54.0	155.1	90.8	1.06E-02	5.87E-02	2.20E-02
XP_003205187.1	fatty acid-binding protein, adipocyte-like	9.1	13.6	173.5	122.0	n.a.	n.a.	2.37E-02
XP_010708237.1	annexin A5	8.9	40.8	151.1	108.0	1.86E-04	4.05E-04	1.26E-02
XP_019477643.1	probable aminopeptidase NPEPL1	8.8	83.1	111.3	105.6	2.35E-03	1.23E-03	2.41E-01
XP_010709117.1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	8.8	30.3	157.4	112.2	1.23E-02	6.39E-03	2.36E-01
XP_003203313.1	ES1 protein homolog, mitochondrial-like isoform X1	8.7	41.3	145.2	113.5	3.95E-06	3.09E-05	2.86E-04
XP_003204095.1	proteasome subunit beta type-1	8.7	56.5	136.0	107.6	4.21E-02	1.22E-01	4.75E-02
XP_010720097.1	myosin regulatory light chain 10 isoform X2	8.5	2.5	241.4	57.8	n.a.	n.a.	3.18E-05
NP_001290139.1	transforming protein RhoA	8.5	66.9	142.8	90.3	7.33E-04	9.39E-02	2.65E-03
XP_010711294.1	programmed cell death 6-interacting protein	8.5	60.2	133.7	106.1	2.47E-02	6.26E-02	2.81E-01
XP_019469110.1	LYR motif-containing protein 2	8.4	63.6	144.0	92.4	3.00E-03	4.85E-02	3.88E-03
XP_010726200.2	plectin-like	8.3	24.6	144.5	131.0	1.02E-04	7.24E-05	8.01E-02
XP_010707388.1	carbonic anhydrase 2	8.1	64.4	128.3	107.3	4.93E-03	1.37E-03	1.24E-01
XP_010706534.1	protein disulfide-isomerase A4	8.1	70.0	119.4	110.5	3.08E-02	6.43E-03	6.20E-01
XP_003211790.1	pigment epithelium-derived factor	8.0	n.d.	275.5	73.5	n.a.	n.a.	#DIV/0!
XP_010717837.1	hydroxyacylglutathione hydrolase, mitochondrial	8.0	42.3	153.6	104.1	2.43E-03	1.91E-02	1.84E-04
XP_010714872.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	8.0	51.4	133.7	114.9	1.71E-02	3.17E-02	6.75E-02
XP_019475865.1	synaptopodin	7.9	n.d.	154.3	145.8	n.a.	n.a.	3.69E-01
XP_019474689.1	omega-amidase NIT2	7.9	53.1	130.3	116.6	3.34E-03	2.87E-02	5.70E-01
XP_003212771.2	apolipoprotein A-IV	7.8	40.7	167.5	105.4	3.20E-03	3.53E-02	2.51E-02
XP_010725400.1	stress-induced-phosphoprotein 1-like	7.7	98.7	128.2	106.0	1.79E-02	5.37E-01	7.90E-02
NP_001295581.1	glutathione peroxidase 1	7.6	35.3	151.6	113.2	1.08E-03	1.86E-03	7.31E-02
XP_003213740.2	thioredoxin	7.6	70.7	138.2	91.0	9.78E-04	9.46E-03	5.11E-03
XP_003205398.1	fibrinogen alpha chain	7.3	23.5	126.3	150.2	4.76E-04	2.73E-04	2.82E-02
XP_010713455.1	apoptosis-inducing factor 1, mitochondrial	7.2	48.1	150.8	101.0	4.10E-04	4.74E-03	8.99E-03
XP_010720043.1	coiled-coil-helix-coiled-coil-helix domain-containing protein 2	7.2	n.d.	159.7	140.3	n.a.	n.a.	3.95E-01
XP_010722641.1	40S ribosomal protein S10	7.1	43.4	159.4	97.1	2.54E-04	4.19E-03	6.24E-03
XP_003205762.2	synaptopodin-2 isoform X1	6.8	53.1	139.2	107.7	1.13E-04	7.06E-04	1.46E-02
XP_019471644.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	6.8	64.5	130.9	104.6	4.67E-03	2.75E-02	7.94E-03
XP_010719149.1	prostaglandin E synthase 2	6.8	28.1	158.6	113.4	2.04E-04	1.03E-03	3.09E-02
XP_019471620.1	ferritin heavy chain	6.8	68.2	111.6	120.2	8.74E-03	9.54E-03	5.03E-01

XP_010721757.1	adenylate kinase 2, mitochondrial isoform X1	6.5	36.5	140.9	134.8	6.80E-03	2.74E-02	7.06E-01
XP_010715142.1	histidine-rich glycoprotein	6.4	n.d.	185.5	114.5	#DIV/0!	#DIV/0!	1.38E-03
XP_010704829.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	6.3	82.7	174.9	192.4	1.24E-02	8.10E-03	3.68E-02
XP_010725100.2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	6.1	48.1	140.2	111.7	1.46E-03	6.91E-05	7.22E-02
XP_003202723.1	parathymosin	6.1	26.0	195.8	86.9	2.10E-03	1.25E-02	8.68E-04
XP_019471930.1	acyl-CoA-binding domain-containing protein 7 isoform X1	5.9	26.7	175.0	107.2	4.01E-04	6.10E-05	5.43E-04
XP_010717078.1	cullin-associated NEDD8-dissociated protein 1-like	5.9	28.0	139.1	132.9	3.08E-04	3.28E-02	8.65E-01
XP_010719340.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	5.9	n.d.	182.5	117.5	#DIV/0!	#DIV/0!	7.45E-04
XP_003206625.1	proteasome subunit alpha type-6	5.9	57.3	151.8	90.8	1.34E-04	5.85E-03	2.05E-05
XP_010717624.2	nucleoside diphosphate kinase 3	5.8	77.6	123.8	98.5	4.18E-04	7.06E-03	3.31E-03
XP_010712047.1	calcium-binding mitochondrial carrier protein Aralar1-like	5.8	58.1	134.9	107.0	8.42E-04	1.36E-02	1.23E-01
XP_019469083.1	laminin subunit alpha-2-like	5.8	55.2	138.7	106.1	3.00E-02	7.79E-02	3.40E-01
XP_003212170.1	ATP synthase subunit epsilon, mitochondrial	5.8	29.7	159.7	110.6	2.86E-06	1.30E-07	1.57E-04
XP_010705749.1	cardiac phospholamban	5.6	n.d.	229.5	70.5	#DIV/0!	#DIV/0!	1.02E-04
XP_010723457.1	haloacid dehalogenase-like hydrolase domain-containing protein 2	5.6	62.0	118.4	119.5	2.49E-03	2.86E-03	9.27E-01
XP_003210533.1	cytochrome b-c1 complex subunit 8	5.2	69.0	128.5	102.6	2.59E-03	1.03E-03	3.59E-02
XP_003211803.2	vitronectin	5.2	19.8	168.1	118.8	2.42E-04	2.37E-03	6.86E-03
XP_019474838.1	eukaryotic translation initiation factor 3 subunit J	5.1	73.9	115.4	110.8	5.20E-02	1.62E-01	7.83E-01
XP_003205354.1	60S acidic ribosomal protein P1	5.1	n.d.	168.7	131.4	n.a.	#DIV/0!	2.64E-03
XP_003206548.1	eukaryotic translation initiation factor 2 subunit 1	5.1	71.1	122.8	106.1	5.26E-02	1.38E-01	3.44E-01
XP_010710388.2	proteasome subunit alpha type-3, partial	4.9	70.7	127.1	102.1	1.79E-04	2.78E-02	4.88E-02
XP_010706329.1	ras-related protein Rab-10	4.9	51.6	147.5	100.9	4.17E-05	1.01E-03	7.03E-04
XP_019466080.1	heterogeneous nuclear ribonucleoprotein K isoform X1	4.9	59.9	133.5	106.6	1.78E-03	6.09E-03	1.22E-02
XP_010722856.1	dual specificity protein phosphatase 3	4.8	40.0	151.4	108.5	2.99E-06	1.22E-03	7.90E-03