Supplemental Table 1 Protein identifications from TCDD treated and control zebrafish hearts

TCDD replicate 1

Protein #	Accession ID	Protein name	Protein coverage	length	peptide *m/z*	peptide Mr*expt*	peptide Mr*calc*	peptide score	pep_expect	peptide sequence
1	gi|41053652	myoglobin [Danio rerio]	94.6	147	550.49	1098.97	1098.58	69.68	0.00012	AGLDAAGQGALR
					780.21	1558.40	1557.74	111.12	7.70E-09	VMDAVIGDIDGYYK
					1010.02	2018.03	2020.10	89.88	8.80E-07	GDHAALLKPLANTHANIHK
					1110.00	2217.98	2219.23	105.42	2.30E-08	AKGDHAALLKPLANTHANIHK
					1128.60	2255.18	2253.18	112.98	4.10E-09	FSGISQGDLAGSPAVAAHGATV
					946.49	2836.43	2834.54	64.80	0.00021	GDHAALLKPLANTHANIHKVAL
					1012.84	3035.50	3033.67	45.05	0.019	AKGDHAALLKPLANTHANIHKV
2	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	52.6	1936	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1180.66	1179.65	1179.58	47.68	0.017	DFEISQLNSK
					609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					621.00	1239.98	1237.63	51.96	0.0065	EADVLQQNPPK
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					645.12	1288.22	1288.63	47.26	0.02	DSQLQLDDSLR
					654.30	1306.58	1305.58	40.69	0.089	ELECEVEAEQK
					655.46	1308.91	1307.64	77.55	1.70E-05	NSFSQQLEDLK
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					699.56	1397.10	1397.75	86.37	2.20E-06	NALLQAELEELR
					708.41	1414.80	1414.73	99.51	1.20E-07	LAEQELLDVTER
					733.14	1464.26	1463.74	77.88	1.60E-05	NSFSQQLEDLKR
					738.45	1474.89	1473.68	79.64	1.10E-05	VEELEEELEAER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					751.13	1500.24	1499.75	107.00	2.00E-08	LQEAEEAVEAVNAK
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					1540.74	1539.73	1539.77	67.06	0.00019	DYHIFYQILSNK
					771.81	1541.61	1541.83	41.93	0.063	IDDEQSIIIQLQK
					772.48	1542.94	1542.83	83.14	4.90E-06	KLAEQELLDVTER
					772.58	1543.15	1541.83	79.18	1.20E-05	IDDEQSIIIQLQK
					773.18	1544.35	1542.83	89.45	1.20E-06	KLAEQELLDVTER
					778.74	1555.46	1553.85	77.67	1.70E-05	RNALLQAELEELR
					779.46	1556.90	1556.79	66.68	0.00021	LLGSLDIDHQQYR
					802.72	1603.42	1602.78	73.08	5.00E-05	SNDDLKENTAIVER
					806.41	1610.80	1610.75	87.04	1.90E-06	AAEESEEQANVHLGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					825.24	1648.47	1645.82	53.20	0.0049	NLTEEMAALDDIIAK
					843.71	1685.41	1684.83	67.36	0.00018	LELDDVASSMEHIVK
					845.72	1689.42	1688.88	91.16	7.80E-07	GQNVQQVNYAIGALSK
					1713.93	1712.92	1711.91	50.75	0.0079	ILNPAAIPEGQFIDSK
					860.59	1719.16	1717.85	95.23	3.00E-07	NEDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLINQK
					895.49	1788.97	1786.87	93.20	4.70E-07	TIDTLQSALESETHSR
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					934.83	1867.65	1867.93	118.48	1.30E-09	DLEEATLQHEATAATLR
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR

					979.93	1957.84	1957.98	122.26	5.20E-10	ILQEEISDLTEQLGEGGK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1021.70	2041.38	2040.98	102.96	4.40E-08	LLSNLFANYAGADSATGDGGK
					1044.21	2086.41	2086.04	81.55	5.80E-06	VKLEQQVDDLEGSLEQEK
					1069.85	2137.69	2139.00	132.48	4.70E-11	AEIQAALEEAEGSLEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.24	2200.46	2199.12	98.84	1.10E-07	GTLEDQIIQANPALEAFGNAK
					1145.88	2289.75	2290.10	89.15	9.60E-07	LTQESIMDLENDKQQLEEK
					1241.45	2480.89	2481.17	111.86	4.70E-09	KLETDLSQFQTEVEEAVQECR
					1278.53	2555.04	2554.18	49.27	0.0082	TEAPPHIYSISDNAYQYMLADR
3	gi|74315904	alpha globin-like [Danio rerio]	67.8	143	1117.39	1116.38	1114.56	42.40	0.07	ADEIGAEALAR
					588.76	1175.51	1175.62	78.14	1.80E-05	TIMGAVGEAISK
					684.64	1367.27	1365.73	80.52	8.50E-06	FFNNLALALSEK
					932.23	1862.44	1863.88	119.89	9.30E-10	TYFSHWSDLSPGSGPVK
					934.14	1866.26	1868.00	104.77	3.00E-08	IDDLVGGLAALSELHAFK
					934.17	1866.32	1863.88	96.10	2.20E-07	TYFSHWSDLSPGSGPVK
					934.23	1866.44	1868.00	116.08	2.20E-09	IDDLVGGLAALSELHAFK
					934.30	1866.58	1863.88	93.17	4.30E-07	TYFSHWSDLSPGSGPVK
					934.46	1866.90	1868.00	133.85	3.70E-11	IDDLVGGLAALSELHAFK
					998.22	1994.42	1991.97	69.02	0.00011	TYFSHWSDLSPGSGPVKK
4	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	67.8	143	1117.39	1116.38	1114.56	42.40	0.07	ADEIGAEALAR
					582.09	1162.17	1161.61	80.71	9.20E-06	TIMGAVGEAVSK
					684.64	1367.27	1365.73	80.52	8.50E-06	FFNNLALALSEK
					925.24	1848.46	1847.88	108.85	1.20E-08	TYFSHWADLSPGSGPVK
					934.46	1866.90	1868.00	133.85	3.70E-11	IDDLVGGLAALSELHAFK
5	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	63.1	333	748.67	1495.33	1494.84	73.96	3.70E-05	VPTPNVSVVDLTVR
					787.22	1572.42	1571.83	87.49	1.80E-06	LVIDGHAITVYSER
					931.70	1861.39	1860.94	91.36	6.60E-07	SSIFDAGAGIALNDHFVK
					1105.92	2209.83	2210.17	74.16	3.10E-05	LVIDGHAITVYSERDPANIK
					1117.27	2232.53	2230.08	109.24	9.40E-09	WGDAGATYVVESTGVFTTIEK
					1300.97	2599.93	2599.37	115.89	1.80E-09	VINDNFVIVEGLMSTVHAITATQ
6	gi|38488753	myosin, heavy polypeptide 6, cardiac muscle, alpha [Dan	47	1936	602.49	1202.96	1202.57	64.97	0.00035	DGDVHPQNPPK
					659.27	1316.53	1316.61	44.94	0.034	ELENELDAEQK
					671.85	1341.68	1341.65	84.88	3.20E-06	AFDVLGFTSEEK
					1375.67	1374.66	1374.66	66.79	0.00022	LAEQELTDATER
					702.67	1403.32	1403.72	76.66	2.20E-05	KDFEINQLNQR
					737.76	1473.50	1473.68	50.23	0.0097	IEELEEELDAER
					742.19	1482.37	1480.77	58.83	0.0012	LSSADIETYLLEK
					755.38	1508.74	1509.74	59.37	0.0011	KLQHELEEAEER
					774.42	1546.82	1546.71	67.01	0.0002	SAEEAEELANANTAK
					794.15	1586.29	1585.79	48.54	0.014	IRELENELDAEQK
					795.70	1589.38	1588.75	98.08	1.50E-07	IEDEEEINADLTAK
					809.11	1616.20	1615.81	111.35	7.20E-09	LEEAGGATSAQVELNK
					846.60	1691.19	1690.81	85.65	2.70E-06	NSYEETLDHLETIK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					1744.97	1743.96	1742.92	44.84	0.031	ILNASAIPEGQFIENK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					950.87	1899.73	1899.92	88.36	1.30E-06	DLEESTLQHEATTASLR
					967.26	1932.50	1931.91	114.53	3.10E-09	NLQEEISDLTDQVSEGR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1029.23	2056.45	2056.02	50.36	0.0076	RDLEESTLQHEATTASLR
					1044.21	2086.41	2086.04	81.55	5.80E-06	VKLEQQVDDLEGSLEQEK

					1086.81	2171.61	2170.99	90.81	6.70E-07	TELQSALEEADASVEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.24	2200.46	2199.12	98.84	1.10E-07	GTLEDQIIQANPALEAFGNAK
					1145.86	2289.71	2289.08	53.91	0.0032	LTQENVMDLENDKQQLEDK
					1158.89	2315.76	2316.11	145.85	2.10E-12	NDLLLQVQSEQDTLTDAEER
					1278.78	2555.54	2554.29	56.67	0.0015	KQESDLLQLQNELEELVQENR
					1341.94	2681.86	2682.38	81.75	4.50E-06	KKQESDLLQLQNELEELVQENR
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
7	gi|70778800	actin, alpha, cardiac muscle [Danio rerio]	58.4	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.20E-08	SYELPDGQVITIGNER
					977.68	1953.34	1955.04	80.29	7.90E-06	VAPEEHPTLLTEAPLNPK
					1114.80	2227.58	2227.06	62.75	0.00044	DLYANNVLSGGTTMYPGIADR
8	gi|163644331	ventricular myosin heavy chain [Danio rerio]	50.2	1938	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	IQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KIQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					825.24	1648.47	1645.82	53.20	0.0049	NLTEEMAALDDIIAK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					934.83	1867.65	1867.93	118.48	1.30E-09	DLEEATLQHEATAATLR
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					980.32	1958.63	1958.94	90.94	7.10E-07	NLQEEISDLTEQLGEGGK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1094.51	2187.00	2185.00	73.03	4.20E-05	SEIQSALEEAEASLEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.24	2200.46	2199.12	98.84	1.10E-07	GTLEDQIIQANPALEAFGNAK
					1165.44	2328.86	2327.21	37.90	0.13	KGTLEDQIIQANPALEAFGNAK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
9	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	58.4	551	1199.65	1198.64	1196.64	38.38	0.16	VVDALGNPIDGK
					644.36	1286.71	1286.69	72.45	6.20E-05	HALIIYDDLSK
					650.86	1299.70	1299.74	95.06	3.20E-07	TAIAIDTIINQK
					682.29	1362.56	1362.69	80.70	8.60E-06	TGTAEVSSILEEK
					766.34	1530.67	1530.75	131.50	7.20E-11	ILGADTGAELEETGR
					1031.84	2061.66	2059.13	79.24	9.90E-06	AFLQHVISQHQDLLAAIR
					1182.76	2363.50	2364.17	82.77	4.00E-06	EVAAFAQFGSDLDAATQQLLNR
10	gi|66472252	slow myosin heavy chain 1 [Danio rerio]	43.3	1938	1180.66	1179.65	1179.58	47.68	0.017	DFEISQLNSK
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					751.13	1500.24	1499.75	107.00	2.00E-08	LQEAEEAVEAVNAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					934.83	1867.65	1867.93	118.48	1.30E-09	DLEEATLQHEATAATLR

					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2002.97	56.10	0.002	NLQEEISDLTEQLGETGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.24	2200.46	2199.12	98.84	1.10E-07	GTLEDQIIQANPALEAFGNAK
					1165.44	2328.86	2327.21	37.90	0.13	KGTLEDQIIQANPALEAFGNAK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
11	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	52	196	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
					780.26	1558.50	1559.82	92.64	5.50E-07	KEEAPAPAPVPETPK
					889.30	1776.58	1777.85	48.44	0.015	SVPLDFSPDQIEEFR
					973.35	1944.68	1944.08	96.37	1.90E-07	ALGHNPTNADVLTVLGKPK
					790.88	2369.61	2370.23	93.88	3.20E-07	KEEAPAPAPVPETPKEPEVDLK
12	gi|18858329	ba1 globin [Danio rerio]	83.8	148	713.59	1425.16	1424.76	91.43	6.90E-07	LNIDEIGPQALSR
					726.37	1450.72	1449.69	68.09	0.00015	NTYAALSVMHSEK
					898.52	1795.02	1794.83	130.34	8.40E-11	FGQAGFNADVQEAWQK
					994.50	1986.99	1984.97	94.14	3.30E-07	YFATFGNLSSPAAIMGNPK
13	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio re	75	517	975.59	974.58	974.55	36.11	0.31	IGLFGGAGVGK
					704.65	1407.28	1405.67	96.20	2.30E-07	AHGGYSVFAGVGER
					1436.69	1435.68	1434.75	46.62	0.022	FTQAGSEVSALLGR
					720.34	1438.67	1438.78	103.02	4.80E-08	VALTGLTVAEYFR
					729.69	1457.36	1456.83	72.54	5.60E-05	TVLIMELINNVAK
					839.46	1676.91	1676.92	102.54	5.60E-08	LVLEVAQHLGENTVR
					961.83	1921.65	1920.96	84.87	2.80E-06	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	1.10E-07	AIAELGIYPAVDPLDSTSR
					1004.29	2006.57	2004.05	85.99	2.10E-06	FLSQPFQVAEVFTGHLGK
					687.83	2060.47	2059.99	39.81	0.087	EGNDLYHEMIESGVINLK
					1330.59	2659.17	2658.38	122.66	3.80E-10	SLQDIIAILGMDELSEEDKLTVA
					1282.31	3843.90	3841.97	53.23	0.002	KGSITSVQAIYVPADDLTDPAPA
14	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	70	433	687.71	1373.40	1372.70	80.72	8.70E-06	HITGEQLGDLYK
					719.54	1437.06	1435.72	59.66	0.001	GNPTVEVDLYTTK
					1054.07	2106.12	2104.07	111.53	6.00E-09	FTGSVDIQVVGDDLTVTNPK
					1060.84	2119.67	2118.12	102.85	4.30E-08	DVILPVPAFNVINGGSHAGNK
					1013.17	3036.49	3037.61	62.59	0.00033	HIADLAGNKDVILPVPAFNVING
15	gi|18858539	desmin [Danio rerio]	56.7	473	773.44	772.43	772.43	35.04	0.45	LEAEIAK
					527.61	1053.20	1052.56	39.51	0.11	KIHEEEIR
					545.18	1088.34	1086.57	41.12	0.095	VSDLNQAVNK
					1254.56	1253.55	1253.56	38.11	0.15	NISEAEDWYK
					888.41	1774.80	1775.91	99.92	1.00E-07	FLEQQNSALTVEIER
					989.77	1977.53	1978.97	108.45	1.20E-08	LDFNLADAINQDFLNTR
					1094.31	2186.61	2186.00	145.27	2.50E-12	TFGSGLGSSIFAGHGSSGSSGS
16	gi|23097290	troponin T2, cardiac [Danio rerio]	18.4	282	609.45	1216.89	1216.66	49.43	0.013	KEEEEIISLK
					672.95	1343.88	1344.75	79.90	1.10E-05	KKEEEEIISLK
					855.86	1709.71	1710.90	55.88	0.0024	RKPLDIDNANESALR
					957.92	1913.82	1913.95	94.24	3.30E-07	DLNELQTLIEAHFESR
17	gi|189536981	PREDICTED: similar to slow myosin heavy chain 3 isofor	48.2	1940	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1182.71	1181.70	1180.57	49.07	0.012	DFEISQLSSR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK

					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					949.82	1897.63	1895.90	59.47	0.00096	HADSVSDLGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
18	gi|189536979	PREDICTED: similar to slow myosin heavy chain 3 isofor	46.4	1934	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1182.71	1181.70	1180.57	49.07	0.012	DFEISQLSSR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					949.82	1897.63	1895.90	59.47	0.00096	HADSVSDLGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
19	gi|83025080	actinin, alpha 2 [Danio rerio]	42.3	895	671.13	1340.24	1338.79	55.24	0.0029	QAILGIQQEVLK
					826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
					842.75	1683.49	1680.90	72.26	5.60E-05	LLETVDQLFLEYAK
					860.29	1718.57	1715.95	46.08	0.024	ILAADKPYILSDELR
					873.76	1745.51	1743.87	73.20	4.60E-05	DDPLGNLNLAFDIAEK
					885.39	1768.76	1768.81	108.07	1.40E-08	KHEAFESDLSAHQDR
					916.62	1831.23	1828.89	71.45	6.70E-05	MLDAEDILSTPKPDER
					969.28	1936.54	1934.98	74.47	3.10E-05	GDLTNPYSTITAEEIAIK
					1000.26	1998.50	1998.01	57.54	0.0015	LEGDHQLIQESLIFDNK
					1050.91	2099.81	2099.09	86.17	2.00E-06	LNKDDPLGNLNLAFDIAEK
					1412.81	2823.60	2824.40	93.56	2.80E-07	VEQIAAIAQELNELDYHDVASVN
20	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple:	69.8	517	975.59	974.58	974.55	36.11	0.31	IGLFGGAGVGK
					704.65	1407.28	1405.67	96.20	2.30E-07	AHGGYSVFAGVGER
					1436.69	1435.68	1434.75	46.62	0.022	FTQAGSEVSALLGR
					720.34	1438.67	1438.78	103.02	4.80E-08	VALTGLTVAEYFR
					729.69	1457.36	1456.83	72.54	5.60E-05	TVLIMELINNVAK
					839.46	1676.91	1676.92	102.54	5.60E-08	LVLEVAQHLGENTVR
					961.83	1921.65	1920.96	84.87	2.80E-06	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	1.10E-07	AIAELGIYPAVDPLDSTSR
					1004.29	2006.57	2004.05	85.99	2.10E-06	FLSQPFQVAEVFTGHLGK
					687.83	2060.47	2059.99	39.81	0.087	EGNDLYHEMIESGVINLK
					1282.31	3843.90	3841.97	53.23	0.002	KGSITSVQAIYVPADDLTDPAPA
21	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	87.2	172	1274.59	1273.58	1273.67	40.26	0.1	LFDPNATGVVNK
					842.26	1682.51	1681.91	98.27	1.40E-07	GPINFTVFLTLFGEK
					897.81	1793.60	1792.84	50.73	0.0079	LNVSDEELESMLTEGK

					1047.20	2092.38	2091.96	104.81	2.80E-08	GSSNVFSMFEQSQIQEFK
					1292.50	2582.99	2582.25	108.90	8.90E-09	FTAEEVDQAFAVAPIDVAGNIDY
22	gi|189520343	PREDICTED: similar to myosin heavy chain fast skeletal	40.8	1933	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					846.60	1691.19	1690.81	85.65	2.70E-06	NSYEETLDHLETLK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1010.39	2018.76	2016.00	68.23	0.00013	NLQQEITDLTEQLGETGK
					1108.55	2215.08	2213.03	110.50	7.20E-09	SEIQAALEEAEATLEHEESK
23	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	67.9	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.20E-08	SYELPDGQVITIGNER
					1954.17	1953.16	1953.06	81.42	6.10E-06	VAPEEHPVLLTEAPLNPK
24	gi|50344802	hypothetical protein LOC415164 [Danio rerio]	68.7	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.20E-08	SYELPDGQVITIGNER
					1954.17	1953.16	1953.06	81.42	6.10E-06	VAPEEHPVLLTEAPLNPK
25	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio re	35.1	1937	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.002	NLQQEISDLTEQLGETGK
26	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	78.7	334	710.69	1419.36	1417.79	76.48	2.30E-05	LITPLASGPAEPPR
					770.19	1538.36	1537.77	74.86	3.10E-05	IVADKDYSVTANSR
					843.74	1685.46	1684.85	114.34	3.60E-09	ELADELALVDVVEDR
27	gi|18858335	bactin1 [Danio rerio]	62.1	375	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.20E-08	SYELPDGQVITIGNER
28	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	54.3	782	786.18	1570.35	1568.82	59.32	0.0012	FKLEPPTGDELPAR
					1695.68	1694.67	1694.78	51.72	0.0066	FNPETDYLTAPNGEK
					857.83	1713.65	1711.84	77.20	1.80E-05	EVNQEVYSFLASAGAK
					878.27	1754.52	1752.88	68.60	0.00013	IVYGHLDDPAGQEIAR
					954.55	1907.08	1905.98	68.05	0.00014	KQGLLPLTFSNPADYDK
					1041.84	2081.67	2080.94	61.45	0.00059	NNISWVVVGDENYGEGSSR
					1106.24	2210.46	2209.04	53.72	0.0034	KNNISWVVVGDENYGEGSSR
					1267.35	2532.69	2532.29	120.88	5.90E-10	GHLDNISNNLLIGAVNIENDGVN
					1361.62	2721.22	2721.43	65.92	0.00017	NDANPATHAFVTSPEIVTALAIA
					1178.33	3531.95	3531.63	40.47	0.044	HTDGSSETIELNHTFNETQIEWF
29	gi|189523699	PREDICTED: titin a [Danio rerio]	49.5	32757	622.64	1243.26	1243.73	45.32	0.033	KPKPPVQEPPK
					804.70	1607.39	1605.88	52.60	0.0054	AEDPLFLPSPPAKPK
					831.24	1660.46	1658.82	50.71	0.0084	VNVEVEYTEPVPER
					863.58	1725.14	1722.92	52.16	0.0057	AGSDLVLDAAVGGKPEPK
					947.83	1893.64	1892.90	52.96	0.0043	HTVTLSWEKPDHDGGSK
					968.75	1935.49	1936.07	49.40	0.0099	AVNEAGASRPSVTAGPIVIK
					1015.88	2029.75	2029.15	63.89	0.00033	KVPAKPVEAITVPTEEPPK
					1029.07	2056.13	2056.09	70.98	6.60E-05	ELPISFVTPLADVHVYEK
					1035.13	2068.25	2067.07	47.02	0.017	NKFDVPDAPQNVIVGNVNK
					1049.90	2097.79	2095.07	51.75	0.0057	LQGEVLSPSPDVEIIEDGAK

					1052.35	2102.69	2102.05	79.10	1.10E-05	EQVTHQAALLQSHEVQER
					1058.69	2115.37	2113.11	54.55	0.003	VLAENEHGIGLPAETPEPLK
					708.80	2123.37	2122.13	68.98	0.0001	VLDRPGPSSGPLDITGLTAEK
					1070.08	2138.14	2137.14	45.22	0.025	EQHKPVVLSVNETTQTLSK
					1079.92	2157.82	2157.24	49.64	0.0092	KVPAKPVEAITVPTEEPPKK
					1098.94	2195.87	2196.14	55.19	0.0025	VLDRPGPPDGPISIYGVTSEK
					1101.80	2201.58	2199.25	68.20	0.00013	KLPAKPDETIAVPIEEPPKK
					1140.29	2278.57	2276.23	39.60	0.088	VKEPPSIIEKPESQDVIPGSK
					1177.07	2352.13	2351.12	38.63	0.1	VSWRPPSDDGGSDIFGYIVER
					1224.99	2447.97	2447.27	40.79	0.062	VNDAENLHPSTVFTIPNLPELK
					1299.87	2597.72	2597.14	69.48	7.90E-05	EKEVEEPEEPEEEYHPSLNER
					1072.88	3215.61	3213.65	67.41	0.0001	SHAIDSAPIVAQYPFTPPGPPTS
					1108.51	3322.51	3321.81	37.42	0.099	YTITATNNIGTVTEEVAIIILDKPG
30	gi|66472732	myosin heavy chain 4 [Danio rerio]	43.9	1935	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.002	NLQQEISDLTEQIGETGK
					1044.21	2086.41	2088.02	74.04	3.30E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	1.20E-06	NDLQLAVASEAENLSDAEER
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
31	gi|189519129	PREDICTED: similar to myosin heavy chain 4 [Danio reri	41	1933	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.002	NLQQEISDLTEQIGETGK
					1044.21	2086.41	2088.02	74.04	3.30E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	1.20E-06	NDLQLAVASEAENLSDAEER
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
32	gi|148596963	spectrin alpha 2 [Danio rerio]	43.8	2480	787.22	1572.42	1571.78	80.51	9.20E-06	HQALQAEISGHEPR
					567.84	1700.48	1699.88	49.54	0.01	KHQALQAEISGHEPR
					869.56	1737.10	1736.82	56.93	0.0019	TATDEAYKDPSNLQGK
					873.61	1745.21	1744.82	38.53	0.14	LSDDNTIGQEEIQQR
					926.15	1850.29	1848.86	74.98	2.80E-05	KFEEFQTDLAAHEER
					964.07	1926.13	1924.90	93.25	4.10E-07	SSLSSAEADFSQLAELDR
					698.23	2091.67	2091.08	70.44	7.60E-05	LEAELGAHEPAIQSVLETGK
					1077.98	2153.95	2153.10	123.55	3.70E-10	ALINADELANDVAGAEALLDR
					1109.34	2216.67	2215.12	36.12	0.2	RDELITNWEQIQTLATER
					1110.83	2219.64	2219.03	45.13	0.025	STDEAGQALLNTGHYASEEVK
					750.39	2248.15	2247.19	67.14	0.00016	RLEAELGAHEPAIQSVLETGK
					831.34	2490.98	2489.22	39.47	0.081	EKEPIVGSPDYGKDEDSAEALL
33	gi|169259784	myosin, heavy polypeptide 1, skeletal muscle [Danio reri	37.4	1937	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.002	NLQQEISDLTEQLGETGK
					1044.21	2086.41	2088.02	74.04	3.30E-05	TKLEQQVDDLEGSLEQEK
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
34	gi|18858427	creatine kinase, muscle a [Danio rerio]	26.2	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR

					999.17	1996.33	1993.93	107.13	1.60E-08	GTGGVDTASVGGVFDISNADR
35	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	38	1936	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.002	NLQQEISDLTEQLGETGK
36	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	51.2	28836	671.64	1341.26	1340.73	47.09	0.019	VTEHTVTGLLSGK
					700.80	1399.58	1399.71	67.53	0.00017	HVSVEALDFIDR
					710.47	1418.92	1418.74	37.16	0.2	FGLGEALESEIVR
					808.51	1615.01	1612.87	52.28	0.0058	ALDPVFKPGPPHNPK
					830.81	1659.61	1660.95	47.43	0.018	VIILSKPDEPQGPIR
					856.20	1710.38	1709.82	61.51	0.00064	ADSGNYTITIQNAAGSK
					863.58	1725.14	1722.92	52.16	0.0057	AGSDLVLDAAVGGKPEPK
					885.45	1768.89	1768.91	37.29	0.17	SSVTLTWVKPAHDGGSK
					920.85	1839.68	1838.93	50.02	0.0089	STVSLAWEKPLHDGGSR
					924.84	1847.66	1845.01	54.27	0.0034	VQILDKPGPPAGHIEFK
					929.14	1856.27	1854.92	68.20	0.00013	TSVSLSWEKPIHDGGSR
					951.67	1901.33	1898.91	43.42	0.039	TTVTLSWEKPEHDGGSR
					648.76	1943.24	1941.02	43.23	0.04	IGESFEIDVPISGRPTPK
					989.31	1976.60	1976.14	42.13	0.052	SQLERPGAPLKPVVSGITK
					1013.79	2025.56	2025.09	38.16	0.13	ITIDTKPGHSTLSIANTTR
					1040.51	2079.00	2077.08	49.15	0.01	HGTGEAFINLDVIDVPGPVK
					1045.73	2089.44	2089.14	70.70	7.20E-05	DATIEIITLDKPGPPTGPVR
					1047.74	2093.46	2092.96	51.97	0.0054	WTEPDSDGGSPITNYVVEK
					1112.56	2223.10	2222.18	41.11	0.064	VTAENEIGTGDPSVPSKPILAK
					1146.20	2290.39	2289.16	55.90	0.002	KGEWVAVTTDEIHQTVYSVK
					1152.84	2303.67	2302.28	45.00	0.025	SEPKPLAAPVIANDLTIEPSLK
					884.78	2651.30	2651.51	60.57	0.0006	KKPTLPATILTKPQSLTVSEGES
37	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	93.2	337	661.18	1320.35	1319.67	78.24	1.50E-05	GYIGADQLGDALK
					753.50	1504.98	1502.77	81.33	7.40E-06	VEFPADQLSALTGR
					1545.20	3088.39	3088.58	91.67	4.00E-07	NSPLVSELSLFDIAHTPGVAADL
38	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	63.6	283	588.48	1174.94	1173.56	62.94	0.00059	SEYGLTFTEK
					1429.74	1428.73	1427.69	59.35	0.0012	LTFDTTFSPNTGK
					1052.33	2102.65	2102.15	73.62	3.70E-05	VNNTSLVGVGYTQSLRPGIK
					1088.83	2175.64	2174.05	81.62	5.60E-06	WNTDNTLGTEINIEDQIAK
					1258.10	2514.18	2513.15	75.22	2.10E-05	TGDFQLHTNVNDGSEFGGSIY
39	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	52.1	449	578.00	1153.98	1153.57	40.85	0.086	DIFQDIFEK
					678.57	1355.13	1354.68	66.05	0.00024	TIEAEAAHGTVTR
					716.02	1430.02	1428.73	77.71	1.70E-05	FKDIFQDIFEK
					861.13	1720.25	1719.82	116.07	2.40E-09	DQTDDQVTIDSAIATK
					1894.09	1893.08	1891.93	57.87	0.0014	LNEHYVNTTDFLDAIK
40	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	54.9	284	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					1298.84	1297.83	1297.76	53.23	0.0047	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.64	1417.26	1416.75	48.43	0.015	DAQEKLELSEKK
					770.52	1539.02	1537.71	105.07	3.00E-08	SIDDLEDELYAQK
					845.36	1688.70	1688.78	68.99	0.00013	YSEKEDKYEEEIK
					770.52	2308.54	2307.18	67.97	0.00013	TVAKLEKSIDDLEDELYAQK
41	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	35.7	1945	609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR

					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
42	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	35.1	1938	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
43	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	44.8	143	934.97	1867.93	1867.99	120.19	8.40E-10	IDDLLGALSSLSDLHATK
44	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	52.9	119	599.32	1196.62	1195.75	37.92	0.16	AKLEPVVLSLK
					1050.98	2099.94	2100.09	88.07	1.30E-06	ELTELGEQVKPHFEGIFK
					1115.07	2228.12	2228.18	64.05	0.00032	KELTELGEQVKPHFEGIFK
45	gi|41387136	hypothetical protein LOC393781 [Danio rerio]	74.2	128	902.23	1802.45	1801.94	110.64	8.20E-09	YHVSETPFAISAQKPK
					915.41	2743.19	2742.29	43.40	0.03	LFPGDVILETGEVVPDFPEDSH
46	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Dani	56.1	659	837.57	1673.13	1671.94	104.71	3.30E-08	AIEQFGAVIEELLLK
					872.48	2614.41	2614.37	42.99	0.035	AGLGSGLTLQGTVHPELNHSGE
47	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	63.4	153	550.56	1099.10	1098.53	38.00	0.18	NLIHGSDSEK
					795.46	1588.90	1588.88	60.32	0.00091	LVAAKFVQASEDLAK
					651.01	1950.01	1949.07	55.39	0.0024	GFRLVAAKFVQASEDLAK
					1040.53	2079.05	2077.09	74.03	3.40E-05	YTSSGPLLAMVWEGLNVIK
					1106.98	2211.95	2211.12	83.98	3.20E-06	SAATEVSLWFKPEELVSYR
48	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	68.8	397	594.84	1187.66	1187.68	73.04	6.00E-05	ITAHLVHELR
					649.07	1296.12	1294.70	56.75	0.0021	RTPFGTYGGVLK
					683.58	1365.14	1364.63	58.96	0.0012	DHSATDLAEHAAK
					931.96	1861.91	1861.98	116.41	2.10E-09	TNVNGGAIAIGHPLGASGTR
49	gi|48762657	enolase 1, (alpha) [Danio rerio]	56.5	432	1002.93	3005.75	3006.57	90.40	5.60E-07	HIADLAGNPDVILPVPAFNVING
50	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	91.5	248	542.18	1082.34	1081.57	37.83	0.17	KFFVGGNWK
					696.12	1390.22	1388.71	83.57	4.70E-06	SIEELANTLNSAK
					1458.87	1457.86	1457.72	49.98	0.01	HVFGESDELIGQK
					801.94	1601.87	1601.88	47.81	0.017	VVLAYEPVWAIGTGK
					808.77	1615.53	1613.82	72.55	5.40E-05	RHVFGESDELIGQK
					1216.87	2431.73	2431.30	60.01	0.00072	DLDGFLVGGASLKPEFIDIINAK
51	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	73.3	202	999.09	2994.24	2996.41	41.19	0.046	TLAAGSHAEHDGQPYCHKPCY
					1008.14	3021.39	3023.42	48.04	0.0094	TLNPGGHAEHDGKPYCHKPCY
					1008.49	3022.44	3022.46	54.27	0.0022	GVNIGGAGSYVYDTPVGDDSV
					1008.85	3023.53	3023.42	54.78	0.002	TLNPGGHAEHDGKPYCHKPCY
52	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	34.1	331	969.23	1936.45	1936.93	114.30	3.20E-09	HLTTLVDDIWYYAGDR
53	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio reri	52	410	844.84	1687.67	1687.84	100.98	8.00E-08	NIDYVAESIHEAVTK
					1115.18	2228.34	2226.03	63.50	0.00036	NLFAFFDSAYQGFASGDLEK
54	gi|38488731	natriuretic peptide precursor A [Danio rerio]	77.4	106	1025.48	2048.94	2049.99	105.81	2.20E-08	SLLQQFEEALATEEASER
					1182.83	2363.65	2362.99	79.64	8.30E-06	DREEAAAPGEDSNPSDGFDTQI
55	gi|156713467	vitellogenin 7 [Danio rerio]	52.7	1358	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
					1069.54	2137.07	2135.16	100.74	7.00E-08	ISDATAQIVEVLTHLVANNK
56	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	48.5	357	1112.08	2222.15	2220.13	106.28	1.90E-08	NAITVEMYNELIEALELAGK
					1315.03	2628.05	2626.36	76.50	1.50E-05	QQYVDLISSLVGAEAPAVAAQP
57	gi|47086523	ictacalcin [Danio rerio]	76.8	95	697.11	1392.20	1390.73	104.53	3.60E-08	ELLSAELGDIFGK
58	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	41.7	532	882.38	1762.75	1763.98	115.54	2.70E-09	KGVNLPGAAVDLPAVSEK
					937.95	1873.89	1872.82	46.17	0.021	MNFSHGSHEYHGETIK
59	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	16.1	230	1068.17	2134.32	2133.18	94.22	3.10E-07	ILVSAEDVLHSWAVPSLGIK
60	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	94.6	260	851.87	1701.73	1702.86	109.48	1.10E-08	HGASAVILDLPSSDGHK
61	gi|40254659	bactin2 [Danio rerio]	53.1	375	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK

					1954.17	1953.16	1953.06	81.42	6.10E-06	VAPEEHPVLLTEAPLNPK
62	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	57.7	603	1379.96	2757.90	2756.52	38.69	0.09	TLEEVVETIKPTAIIGVAAIGGAF
					1006.36	3016.04	3013.43	94.02	2.40E-07	HISDDIFLTTAEAISEMVTEEHLA
63	gi|18858587	elongation factor 1-alpha [Danio rerio]	60.4	462	530.41	1588.19	1587.87	51.62	0.0068	THINIVVIGHVDSGK
					1244.91	2487.80	2486.35	68.46	0.0001	VETGVLKPGMVVTFAPANVTTE
					973.65	2917.91	2917.55	69.48	7.00E-05	EGNASGTTLLDALDAILPPSRPT
					1015.61	3043.79	3045.65	67.12	0.00011	KEGNASGTTLLDALDAILPPSRP
64	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	59.1	763	653.09	1304.16	1303.71	82.76	5.60E-06	MQLLEIITTDK
					804.74	1607.47	1606.81	72.46	5.50E-05	DVNTEALEILEAYK
					1049.90	2097.78	2095.02	66.49	0.00019	AGVEQGPTTGYLVESQQFGK
					1195.44	3583.28	3583.84	76.05	1.20E-05	KLDSLTTGFGFPVGAATLADEV
65	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	31.9	364	530.65	1059.29	1058.57	51.67	0.0086	KELSDIAQR
					568.04	1134.06	1132.66	42.00	0.07	LFSQLIKER
					660.09	1318.16	1317.68	91.48	7.50E-07	GILAADESTGSVAK
					876.65	1751.28	1749.80	94.12	3.70E-07	GDTGAAAGESLFVANHAY
					1174.96	2347.90	2347.17	50.36	0.007	GVVPLAGTNGETTTQGLDGLYE
66	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Co	68.5	761	653.09	1304.16	1303.71	82.76	5.60E-06	MQLLEIITTDK
					698.19	1394.36	1392.67	54.97	0.0032	LSGQLDYHGFEK
					837.73	1673.45	1672.93	67.82	0.00016	MGLVHQLVDPLGPGLK
					1167.77	3500.29	3497.79	58.92	0.00062	LDSLTTGFGFPVGLATLADEVGI
					1210.60	3628.77	3625.89	38.77	0.061	KLDSLTTGFGFPVGLATLADEV
67	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	48.8	248	542.18	1082.34	1081.57	37.83	0.17	KFFVGGNWK
					1458.87	1457.86	1457.72	49.98	0.01	HVFGESDELIGQK
					801.94	1601.87	1601.88	47.81	0.017	VVLAYEPVWAIGTGK
					808.77	1615.53	1613.82	72.55	5.40E-05	RHVFGESDELIGQK
68	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (as	47.4	428	644.14	1286.26	1284.69	49.82	0.011	GALDDISKIPEK
					706.10	1410.19	1408.72	67.95	0.00015	EYLPIGGLADFSK
					723.85	1445.68	1445.81	66.36	0.00024	IAATILNTPELYK
					947.98	1893.94	1893.02	70.95	6.90E-05	KLDKEYLPIGGLADFSK
					998.97	1995.92	1994.03	41.92	0.054	YFIEQGHNILLSQSFAK
					784.61	2350.79	2350.26	62.99	0.00038	ISVAGVTSANVEYLAHAIHAVTK
69	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	65.7	283	930.44	1858.86	1858.82	97.79	1.50E-07	SQSGVEFTTGGSSNTDTGK
					1030.87	2059.73	2058.12	72.35	4.80E-05	VNNASLVGVGYTQSLRPGVK
70	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio r	52.6	454	1246.66	1245.65	1244.68	77.74	2.00E-05	KVDFAAAGEPLK
					696.14	1390.27	1390.71	74.71	3.60E-05	GVEAVGGSLSVSSSR
					1265.98	3794.90	3793.99	58.55	0.00057	HQTGAGLVHALVAIEGASATSA
71	gi|68448530	vitellogenin 5 [Danio rerio]	44	1360	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
					1074.23	3219.66	3217.64	49.60	0.0064	DIHLPITVPINPDGTFSINEDFLS
72	gi|166795887	vitellogenin 1 [Danio rerio]	48.2	1362	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					682.95	1363.89	1363.69	44.02	0.039	HILTAAYDTGFR
					691.81	1381.61	1381.78	51.39	0.007	ISDAPAQIVEVLK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
73	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	46.1	1358	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					691.81	1381.61	1381.78	51.39	0.007	ISDAPAQIVEVLK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
74	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	45.6	1631	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					925.36	1848.71	1847.86	65.37	0.00026	LSSENADSEIETETPVK
75	gi|41054193	hypothetical protein LOC327506 [Danio rerio]	47.2	178	1042.49	2082.96	2079.97	96.83	1.70E-07	GTGGVDTAAVGDTFDISNLDR
76	gi|117606264	sarcalumenin [Danio rerio]	58.5	482	731.19	1460.36	1459.77	63.21	0.00048	VTFVDTPGIIENR

					1738.02	1737.01	1735.95	88.70	1.30E-06	AITHELPSLLGSINSGK
					1036.41	2070.80	2069.08	65.94	0.00022	REEISLLEDLNQVIENR
77	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio reric	54.2	413	1503.86	1502.85	1501.78	37.62	0.18	GQDITVPSPVSQFK
					1042.49	2082.96	2079.97	96.83	1.70E-07	GTGGVDTAAVGDTFDISNLDR
78	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	54.8	104	745.36	1488.71	1487.65	60.28	0.00096	TGQAEGFSYTDANK
					997.04	1992.06	1992.95	90.95	6.70E-07	GIVWGEDTLMEYLENPK
79	gi|189529437	PREDICTED: similar to plectin 1 isoform 1 [Danio rerio]	36.8	4530	669.70	2006.06	2004.06	42.99	0.041	LLDAQLATGGIIDPVESHR
					1032.88	2063.74	2062.11	98.98	1.00E-07	DGHNLISLLEVLSGETLPR
					1163.62	2325.22	2323.14	48.85	0.01	IDTAEWGIDLPTVESQLGSHR
80	gi|189529439	PREDICTED: similar to plectin 1 isoform 2 [Danio rerio]	36.6	4506	669.70	2006.06	2004.06	42.99	0.041	LLDAQLATGGIIDPVESHR
					1032.88	2063.74	2062.11	98.98	1.00E-07	DGHNLISLLEVLSGETLPR
					1163.62	2325.22	2323.14	48.85	0.01	IDTAEWGIDLPTVESQLGSHR
81	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	85.2	305	855.23	1708.45	1706.82	92.94	4.90E-07	EIAAFDAVNDESWLK
					877.76	2630.26	2631.29	87.23	1.30E-06	NVTIWGNHSSTQYPDVHHAIVTI
82	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	36.5	364	530.65	1059.29	1058.57	51.67	0.0086	KELSDIAQR
					660.09	1318.16	1317.68	91.48	7.50E-07	GILAADESTGSVAK
					1174.96	2347.90	2347.17	50.36	0.007	GVVPLAGTNGETTTQGLDGLYE
83	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	46.5	284	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					1298.84	1297.83	1297.76	53.23	0.0047	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.10	1416.18	1415.73	49.47	0.012	DAQEKLEQAEKK
84	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	34.5	1079	1271.84	1270.83	1269.68	44.80	0.036	SLGAEPLEVDIK
					707.70	1413.39	1412.74	49.47	0.011	GVIHVGYTDIPSR
					790.14	1578.26	1577.77	42.94	0.049	QGFNVVVESGAGESAK
					922.59	2764.74	2763.39	66.57	0.00015	DGSVVVDLAAEAGGNIETTVPG
85	gi|162287365	hemopexin [Danio rerio]	48.8	447	1339.69	1338.68	1338.61	51.90	0.0061	FHSDTIESEFK
					901.36	1800.71	1800.00	63.19	0.00045	VGKPHTHLEGYPKPLK
86	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	43.8	1974	808.09	1614.16	1612.69	40.36	0.089	DLEEHLEEEEDAR
					1000.25	1998.48	1997.92	83.36	3.90E-06	ELEGHISDLQEDLESER
					1066.46	2130.91	2131.00	57.42	0.0015	QVEAERDELADELASNASGK
87	gi|47086819	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	43.9	255	1044.76	2087.51	2086.96	98.21	1.30E-07	AAFDDAIAELDTLSEESYK
88	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	57.9	164	820.79	1639.56	1637.91	94.27	3.50E-07	HVVFGQVVEGLDVIK
89	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	41.9	284	623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.64	1417.26	1416.75	48.43	0.015	DAQEKLEISEKK
					770.52	2308.54	2307.18	67.97	0.00013	SVAKLEKTIDDLEDELYAQK
90	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	35.1	359	880.53	1759.04	1758.94	75.76	2.60E-05	SIRPLDADTIETSITK
91	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	63.1	141	565.40	1128.79	1128.63	54.53	0.0041	RLDDLASAIR
					1105.94	3314.79	3313.73	63.69	0.00023	EIYPYVIQELRPTLDELGIATPEE
					1693.85	3385.68	3384.77	50.22	0.0049	EIYPYVIQELRPTLDELGIATPEE
92	gi|47087077	phosphoglycerate kinase 1 [Danio rerio]	63.5	417	666.83	1331.65	1331.73	46.32	0.025	ITLPVDFITADK
					818.96	1635.91	1633.78	39.91	0.097	LGDVYVNDAFGTAHR
					1740.87	1739.86	1739.91	58.16	0.0014	VSHVSTGGGASLELLEGK
					925.89	1849.76	1850.97	62.41	0.00052	ITLPVDFITADKFDEK
					801.08	2400.20	2400.17	46.35	0.017	QIVWNGPVGVFEWDNFAHGTK
93	gi|41054435	hypothetical protein LOC324244 [Danio rerio]	33.5	248	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					1298.84	1297.83	1297.76	53.23	0.0047	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
94	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	47.5	242	1074.12	2146.22	2143.98	91.19	6.40E-07	TAFDEAIAELDTLNEDSYK
95	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	58.2	244	1074.12	2146.22	2143.98	91.19	6.40E-07	TAFDEAIAELDTLNEDSYK

96	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	49.6	996	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					765.37	1528.72	1526.87	36.19	0.24	AIGVVVATGVNTEIGK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
97	gi|189526600	PREDICTED: similar to dystonin [Danio rerio]	39.3	8365	1032.88	2063.74	2062.11	98.98	1.00E-07	DGHNLISLLEVLSGETLPR
98	gi|153792369	si:dkey-151c10.1 [Danio rerio]	38.1	4577	1032.88	2063.74	2062.11	98.98	1.00E-07	DGHNLISLLEVLSGETLPR
99	gi|189516972	PREDICTED: similar to Myosin light polypeptide 4 (Myos	72.2	187	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
100	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio r	48.3	151	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
101	gi|62955689	hypothetical protein LOC550556 [Danio rerio]	33.7	270	842.61	1683.21	1682.84	86.73	2.00E-06	AFAEFLTEEIKEEK
102	gi|18859505	alpha-tropomyosin [Danio rerio]	31.7	284	623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					770.52	2308.54	2307.18	67.97	0.00013	SVAKLEKTIDDLEDELYAQK
103	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	49.9	1056	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVLK
104	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	41.1	1035	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
105	gi|41055855	aldehyde dehydrogenase 4 family, member A1 [Danio re	33.8	556	1044.85	2087.69	2086.97	84.57	2.90E-06	VGDPVEDFSTFFSAVIDDK
106	gi|46358344	isocitrate dehydrogenase 3 (NAD+) alpha [Danio rerio]	52.9	365	1251.50	2500.99	2501.23	87.86	1.20E-06	ENTEGEYSGIEHVIVDGVVQSIK
107	gi|41054770	WD repeat domain 1 [Danio rerio]	51.3	606	1296.44	2590.87	2589.21	86.27	1.60E-06	AHDGGIYAVSWSPDSTQLISAS
108	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	38.1	134	1339.12	2676.23	2675.32	66.46	0.00016	ITFTNEEFLVTLPDGSEIHFPNR
109	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	73.8	164	686.49	1370.97	1370.73	87.95	1.60E-06	VVDGLDVVDAIEK
110	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	38.3	3730	637.94	1273.86	1273.71	79.51	1.20E-05	SKVEEILSELK
					1036.49	3106.45	3105.49	56.25	0.0014	YDAEEIEAEVSSDVTTEIHNIITT
111	gi|51571925	hypothetical protein LOC445486 [Danio rerio]	44.8	194	902.31	1802.60	1800.95	59.54	0.0011	INSELPVDEVFAIVEK
					965.71	1929.41	1929.05	73.55	3.90E-05	KINSELPVDEVFAIVEK
112	gi|27545193	creatine kinase, brain [Danio rerio]	40.7	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR
					894.58	1787.15	1785.94	47.27	0.018	GIESLSVEALGALDGDLK
					990.39	1978.76	1977.94	66.42	0.0002	GTGGVDTAAVGGVFDISNADR
113	gi|56118753	troponin C, slow [Danio rerio]	44.1	161	602.40	1202.78	1202.58	47.42	0.02	AAAEQLTDEQK
					603.43	1204.85	1202.58	56.44	0.0025	AAAEQLTDEQK
					684.11	1366.20	1364.65	62.15	0.00058	NADGYIDLDELK
114	gi|58801524	LIM domain containing preferred translocation partner in	47.1	556	732.30	2193.86	2193.06	41.09	0.064	AEPSHHPAPTPSQGYQPAPPK
					1398.18	2794.34	2793.39	116.45	1.50E-09	SSLDAEIDSLTSILADLESSSPYK
115	gi|47087349	coagulation factor II [Danio rerio]	46.8	524	674.22	1346.42	1345.80	77.10	2.10E-05	IVAIDEIIVHPK
					674.76	1347.50	1345.80	80.64	8.90E-06	IVAIDEIIVHPK
116	gi|41055546	hypothetical protein LOC393186 [Danio rerio]	45.9	281	973.05	1944.09	1942.85	73.38	3.90E-05	SQNGVEFNTSGSTNTDTGK
					1044.26	2086.51	2086.15	55.93	0.0021	VNNASLIGIGYTQSLRPGVK
117	gi|62955483	NADH dehydrogenase (ubiquinone) Fe-S protein 3, (NAD	42	255	1179.48	2356.94	2358.17	88.22	1.20E-06	DPVTHSQLSEFGEYVAEILPK
					1410.75	2819.48	2817.31	58.87	0.00082	TYTDELTPLDSSVPVFQASNWY
118	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	59.8	433	1008.31	3021.90	3020.58	67.54	0.00011	HIADLAGNPEVILPVPAFNVING
119	gi|40538764	ceruloplasmin [Danio rerio]	31.1	1087	828.53	1655.05	1654.78	117.55	1.70E-09	LVDDIVSDTFFDNR
120	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	61.4	757	978.83	1955.65	1955.09	75.99	2.20E-05	KPETVKPLQISSLSEATK
					1066.23	2130.45	2130.11	36.16	0.21	AELDALAALTAGLEETLGSSAK
					732.09	2193.24	2192.18	53.19	0.0039	VTLQAIGAQEAALTAIAAHTDK
121	gi|41282194	glutamate dehydrogenase 1 [Danio rerio]	48.2	542	785.85	1569.68	1568.77	91.97	6.30E-07	IIAEGANGPTTPDADK
122	gi|51972166	radixin isoform 1 [Danio rerio]	41.3	579	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
					1683.89	1682.88	1682.85	73.28	4.40E-05	NQEHLATELAELTSK
123	gi|189535578	PREDICTED: fetuin B [Danio rerio]	32.7	498	1117.51	2233.01	2233.01	59.36	0.00092	KDETHEHDHEIVLDHDHK
					797.59	2389.73	2389.01	53.15	0.0035	AHEHGQDEWEHQHHQYGHK
124	gi|41055654	hypothetical protein LOC393165 isoform 2 [Danio rerio]	61.3	628	1025.69	2049.36	2049.07	51.32	0.0062	KPVLETEVNHVSPLSDASK
					1079.64	2157.27	2155.09	92.58	4.70E-07	ILAQITGTENDQAQESRPGK
125	gi|18859045	mitochondrial carrier homolog 2 [Danio rerio]	40.3	300	824.74	1647.47	1647.80	48.34	0.015	SDEGSLQQVINETTK
					843.43	1684.84	1684.96	56.86	0.002	VLVQVGHEPLAPTLGR

126	gi|116004537	hypothetical protein LOC564694 [Danio rerio]	50.4	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR
					990.39	1978.76	1977.94	66.42	0.0002	GTGGVDTAAVGGVFDISNADR
127	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio reri	48.7	199	667.37	1332.73	1332.69	69.63	0.00011	KYTLPPGVDSEK
					921.78	1841.54	1839.94	54.79	0.003	ISLDVNHFSPEELNVK
128	gi|41152448	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	51	355	1228.12	2454.22	2454.31	90.23	7.00E-07	LLQYSDAVEHLLTTGQGVILER
129	gi|41055718	fumarate hydratase precursor [Danio rerio]	51.5	509	1077.99	2153.96	2153.18	63.34	0.00039	EVHEVLLPGLQTLHDALAAK
					1251.93	2501.85	2501.26	77.23	1.30E-05	THTQDAVPLSLGQEFGGYVQQ
130	gi|41151982	major vault protein [Danio rerio]	53.1	863	1019.64	2037.26	2036.88	108.34	1.20E-08	AVEAFIDTQGDEAEEEER
131	gi|80751141	solute carrier family 8 (sodium/calcium exchanger), mem	30.3	974	985.15	1968.29	1968.04	63.87	0.00035	EGVILPIWTPVNPSFGDK
					1212.35	2422.69	2422.06	42.42	0.043	GGGEDFEDTHGVLEFQNDEISK
132	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprotei	55.7	661	738.79	1475.57	1473.75	60.59	0.00088	KHTLSYVDPETGK
133	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	54.4	226	724.13	1446.24	1445.78	60.12	0.001	VIFEAETEKPGVK
					881.73	2642.17	2641.29	65.66	0.00019	SPDPAAVEHKPEESKPEESKPE
134	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	46.9	682	406.52	811.02	810.48	45.06	0.026	FGLHLPK
					622.59	1243.16	1240.68	51.93	0.0073	LQVAGEITTGPR
					1325.61	1324.60	1324.74	85.06	3.00E-06	TVHLLAGVADTTK
135	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	46.1	523	789.78	1577.54	1577.76	37.55	0.17	YDVQVQIENVEDK
					790.64	1579.27	1577.76	97.12	1.80E-07	YDVQVQIENVEDK
136	gi|189526930	PREDICTED: similar to c-Cbl associated protein [Danio r	40.5	1015	918.74	1835.46	1834.94	67.53	0.00016	HAGLVVTHQQFITNDR
137	gi|41053732	aldehyde dehydrogenase 2 precursor [Danio rerio]	56.6	516	881.60	1761.19	1760.83	67.29	0.00018	TFVQESIYDEFVER
					778.04	2331.08	2330.19	63.12	0.00038	VAFTGSTDVGHLIQQASSASNL
138	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	32.6	380	691.30	1380.58	1379.71	71.30	7.10E-05	FFEAAVGEAKPSK
					1079.82	2157.62	2155.10	42.96	0.043	YPDLPGLEDLGITPASIEQK
139	gi|56118264	actinin alpha 3 [Danio rerio]	32.7	896	826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
140	gi|153791915	hypothetical protein LOC100006671 [Danio rerio]	31.1	151	826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
141	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dani	57.3	731	1570.82	3139.63	3139.56	75.20	1.70E-05	DSFIVYQGHHGDVGAPIADVILP
142	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	73	575	814.72	2441.14	2439.35	53.75	0.0031	TALLDAAGVASLLSTAEAVVTEI
					942.68	2825.01	2825.53	73.70	2.70E-05	TALLDAAGVASLLSTAEAVVTEI
143	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	33.3	306	700.18	1398.35	1398.75	68.66	0.00013	REEEANLLGQIK
144	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	39.3	679	553.22	1104.42	1102.64	47.20	0.022	YKDVVVGVPK
					1153.05	2304.08	2303.11	75.64	2.10E-05	SFGAEPLEVHIAESGEGVGGYA
145	gi|41056085	keratin 8 [Danio rerio]	30.6	520	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
					744.37	1486.73	1485.71	41.88	0.065	ANLENQIAEAEER
					1009.39	2016.76	2017.16	59.54	0.00094	SLLAPLNLEIDPNIQIVR
146	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio reri	51.9	133	749.63	1497.24	1496.63	69.94	9.50E-05	LGEEFDETTADDR
147	gi|18858657	fatty acid binding protein 7, brain, a [Danio rerio]	33.3	132	749.63	1497.24	1496.63	69.94	9.50E-05	LGEEFDETTADDR
148	gi|66472610	hypothetical protein LOC553595 [Danio rerio]	48.7	275	1284.63	2567.24	2566.31	88.00	1.10E-06	STPTDLVTEADHQVEELIISTLR
149	gi|18859423	spectrin, beta, erythrocytic [Danio rerio]	39.9	2357	714.77	1427.52	1425.74	43.23	0.047	HRPDLVDYGNLK
					945.01	1888.00	1887.93	72.39	5.20E-05	KKHDAIETDIAAYEER
					733.65	2197.91	2197.09	36.78	0.18	IIDELIEGGHSESATLAEWK
150	gi|47085999	hypothetical protein LOC406484 [Danio rerio]	30.7	361	722.75	1443.49	1443.76	85.59	2.80E-06	GQAFLDDLILDPK
151	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	29.8	245	782.16	1562.31	1560.73	50.70	0.0084	AVTEGDIELSNEER
					1073.02	2144.03	2143.98	56.16	0.002	TAFDEAIAELDSLNEESYK
152	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	57.8	116	839.77	1677.52	1677.88	62.40	0.00058	TTGLVGLAVSQNPHER
153	gi|52219158	aquaporin 8 [Danio rerio]	20.4	260	1057.84	2113.66	2113.97	41.95	0.054	SELFTVATGDGGDNHQNQPK
					1058.64	2115.26	2113.97	55.18	0.0026	SELFTVATGDGGDNHQNQPK
154	gi|58801528	SET translocation (myeloid leukemia-associated) A [Dani	22.7	269	1098.65	2195.28	2194.01	56.17	0.002	EQQEAIEHIDEVQNEIDR
155	gi|58801526	SET translocation (myeloid leukemia-associated) B [Dani	16.7	275	1098.65	2195.28	2194.01	56.17	0.002	EQQEAIEHIDEVQNEIDR
156	gi|117606266	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	46.6	991	789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
157	gi|55741944	wu:cegs655 [Danio rerio]	45.8	994	789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
158	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [	57.8	709	825.71	1649.40	1649.84	62.28	0.0006	TVAVHSDVDSSAVHVK
					945.77	1889.53	1887.95	48.08	0.014	LTGAQAVHPGYGFLSENK

159	gi|50344731	fibrinogen alpha chain [Danio rerio]	56.1	684	677.11	1352.21	1350.70	80.92	7.60E-06	LGISDSEFLTAAK
160	gi|54400460	fibulin 5 [Danio rerio]	31.2	477	1111.43	2220.84	2220.00	80.84	6.70E-06	NSPLPYPEASYPEEPYPDR
161	gi|55925387	carnitine palmitoyltransferase II [Danio rerio]	49.9	668	1127.33	2252.65	2252.11	56.20	0.002	YLAAQRPLLNDEQYSNTEK
					1193.60	2385.19	2384.18	44.83	0.025	DTTEKPLVGPGSQPASVDSSSA
162	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	61.5	283	1045.96	2089.91	2088.16	80.68	7.20E-06	VNNSSLVGLGYTQTLKPGIK
163	gi|113679439	hypothetical protein LOC751638 [Danio rerio]	47.6	126	637.26	1272.51	1272.68	49.46	0.012	GQDPYSILRPK
					468.43	1402.27	1400.78	36.47	0.24	KGQDPYSILRPK
					1471.59	1470.58	1470.70	64.81	0.00032	GIPTDDEQAAGLER
164	gi|41387118	ubiquinol-cytochrome c reductase core I protein [Danio re	48.7	474	943.51	1885.00	1882.98	79.05	1.10E-05	MVLATAGGVSHDEVVSLAK
165	gi|68362804	PREDICTED: similar to Histone H4 replacement CG3379	61.2	103	495.60	989.18	988.57	47.01	0.025	VFLENVIR
					591.57	1181.13	1179.61	59.87	0.001	ISGLIYEETR
166	gi|189538855	PREDICTED: similar to sarcalumenin [Danio rerio]	31	882	731.19	1460.36	1459.77	63.21	0.00048	VTFVDTPGIIENR
					783.21	1564.40	1564.67	41.58	0.067	SEELSQEEAASEEK
167	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reric	41.1	858	703.72	1405.42	1404.80	77.74	1.70E-05	TFAQLILDPIFK
168	gi|18858399	cadherin 2, neuronal [Danio rerio]	22.7	783	1148.25	3441.71	3440.82	76.41	1.10E-05	YSVTGPGADQNPTGLFIIDPISGI
169	gi|189530625	PREDICTED: similar to spectrin repeat containing, nuclea	36.9	8621	550.38	1098.74	1097.66	63.31	0.00054	QLADAIAKLR
170	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	70.2	238	778.40	1554.79	1553.87	76.16	2.30E-05	KGGIVAIDNVLWGGR
171	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	40	255	827.80	1653.58	1653.91	71.00	7.40E-05	ALPFWNEVIVPEIK
172	gi|50540420	branched chain aminotransferase 2, mitochondrial [Danic	20	415	900.83	1799.64	1799.02	46.62	0.02	SSVLKPKPDPSTLVFGK
173	gi|52219190	hypothetical protein LOC447942 [Danio rerio]	30.1	103	1168.02	3501.04	3500.62	45.24	0.014	TKPWPWGDGNHSLFHNPHTNA
174	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	64.6	455	824.81	1647.61	1645.83	39.41	0.12	KCPDCPGLLPLHEPK
					654.65	1960.93	1959.96	43.44	0.039	FHDHRPGSVHPLGPDHR
175	gi|189525434	PREDICTED: im:7157373 [Danio rerio]	59.3	545	1430.98	2859.95	2859.32	74.75	2.10E-05	SAAAPPKEEAPPANAPDGDAPA
176	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio r	77.9	172	565.40	1128.79	1127.64	45.39	0.034	RLNDLASAIR
					1106.47	3316.39	3314.75	67.87	8.70E-05	EIYPYVIQELKPTLQELGISTPEE
177	gi|62122813	3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]	52.4	382	897.46	1792.91	1790.92	71.86	6.10E-05	WKPSTLAGVSEQFVDK
178	gi|189517274	PREDICTED: hypothetical protein [Danio rerio]	39.1	797	602.97	1203.92	1201.66	58.26	0.0016	MRNLTEGILR
179	gi|18858281	apolipoprotein A-I [Danio rerio]	48.5	262	822.99	1643.96	1643.73	71.47	7.00E-05	ALDNLDGTDYEQYK
180	gi|50540186	hypothetical protein LOC436833 [Danio rerio]	32.3	229	1079.82	2157.63	2156.16	60.52	0.00075	AGLTASEVDELLTLATSQPIK
181	gi|150378483	heat shock protein, alpha-crystallin-related, b11 [Danio re	23.4	205	1113.16	2224.31	2223.99	70.86	6.80E-05	NPALQNSEPENQAVEAEAAEN
182	gi|49274617	tropomyosin 1 alpha [Danio rerio]	44.4	284	623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
183	gi|41393141	tropomyosin 3 [Danio rerio]	37.5	248	623.18	1244.35	1242.65	53.21	0.0056	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
184	gi|136429	Trypsin precursor	66.8	232	737.73	2210.15	2210.10	70.33	7.40E-05	LGEHNIDVLEGNEQFINAAK
185	gi|57528846	hypothetical protein LOC445255 [Danio rerio]	37.7	207	770.14	1538.26	1537.87	69.95	9.50E-05	AEEDKIPLLLVGNK
186	gi|123706335	hypothetical protein LOC791136 [Danio rerio]	52.7	313	1223.67	2445.33	2443.21	48.42	0.01	QILANPFQDYVNTHPVSHAHR
					1296.63	2591.25	2589.22	42.49	0.038	GTKDDPIEPQQAIPDAQSFEFEK
187	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	37.2	484	904.58	1807.15	1806.90	69.69	0.0001	HEVISQGGVTHPIDYR
188	gi|189517050	PREDICTED: glycine C-acetyltransferase [Danio rerio]	58.5	458	785.77	1569.52	1568.74	69.25	0.00012	VQISAAHTDEDIDR
189	gi|114326248	elastin b [Danio rerio]	16.6	2054	888.60	1775.19	1772.86	68.41	0.00015	SYGGAGALGGAGQGGIGGGPG
190	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	41.7	1368	1212.77	2423.53	2422.19	68.39	0.00011	GQNHLEEVELAFPQNVIEGSGR
191	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	34.7	1754	575.38	1723.12	1721.89	38.26	0.14	KQELEEILHDLEAR
					958.30	1914.58	1913.91	68.34	0.00013	HSQAFDELNEQLEQVK
192	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filamir	53.2	2523	1207.46	2412.90	2411.15	54.31	0.0028	EGPYSINVLYADEEIPQSPYK
					1178.80	3533.36	3531.58	47.45	0.0089	DLGDGTYQVEYTPYEEGTHSVE
193	gi|51571951	aldehyde dehydrogenase 2b [Danio rerio]	41.5	516	881.60	1761.19	1760.83	67.29	0.00018	TFVQESIYDEFVER
194	gi|41054571	citrate synthase [Danio rerio]	39.5	468	564.10	1126.18	1126.65	40.48	0.095	ALGFPLERPK
					881.85	1761.69	1761.88	63.55	0.00044	GLVYETSVLDPDEGIR
195	gi|27545305	laminin, gamma 1 [Danio rerio]	55.8	1593	1175.40	2348.79	2346.18	66.83	0.00016	LLDLQNLIDSLDNTETTVSDK
196	gi|41055614	hypothetical protein LOC393478 [Danio rerio]	59.3	86	1465.66	1464.65	1464.65	41.10	0.075	WDSQIEDGSFPGK
					733.65	1465.28	1464.65	61.22	0.00072	WDSQIEDGSFPGK

197	gi|55742559	Rho GDP dissociation inhibitor (GDI) alpha [Danio rerio]	47.3	203	960.67	1919.32	1916.90	52.99	0.0045	SLQEIQELDQDDESLR
					1023.83	2045.64	2044.99	51.22	0.0065	SLQEIQELDQDDESLRK
198	gi|121583986	hypothetical protein LOC557972 [Danio rerio]	36.5	562	1071.25	2140.48	2138.14	66.20	0.0002	TFLVIPELAQELHVWTDK
199	gi|41152334	ATP synthase, H+ transporting, mitochondrial F0 comple	44.7	161	573.43	1144.85	1144.54	66.01	0.00029	IDAQEQEANK
200	gi|41053347	mitochondrial trifunctional protein, beta subunit [Danio re	41	471	710.16	1418.30	1415.77	65.85	0.00027	DQLLLGPTYATPK
201	gi|189522849	PREDICTED: similar to oxoglutarate (alpha-ketoglutarate	31.8	961	834.04	1666.06	1665.82	38.69	0.13	VITDDGPPAQNPSEVK
					1201.44	2400.87	2399.32	54.83	0.0025	NITLSLVANPSHLEAVNPVVQG
202	gi|189518755	PREDICTED: similar to malic enzyme 2, NAD(+)-depend	66.3	581	1093.78	2185.54	2184.23	53.23	0.004	SFLDAVNVIKPTAIIGVSGAGR
203	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	50.8	6009	579.12	1156.23	1155.65	54.20	0.0041	LKGDVDVSVPK
					1033.94	2065.86	2062.98	46.95	0.017	SDASLSGGIENQEGNLTFPK
204	gi|148596955	ATP synthase, H+ transporting, mitochondrial F0 comple	19.7	71	817.37	1632.73	1631.83	63.17	0.00049	RYDNLKPIAEEER
205	gi|41055939	sorting and assembly machinery component 50 homolog	38.4	469	997.86	1993.70	1992.02	64.82	0.00028	TKEDILTYEIADVFHAK
206	gi|41056175	programmed cell death 8 (apoptosis-inducing factor) [Da	37.7	751	736.65	1471.28	1471.66	64.47	0.00036	SAGLEVDSDFGGYR
207	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	53.1	697	1302.96	1301.95	1301.66	64.35	0.00039	SHIDELYANIK
208	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	37.8	606	1090.76	2179.50	2179.07	64.20	0.00031	GGENIYPAEIEQFLHTHPK
209	gi|51011067	pyruvate kinase, muscle, b [Danio rerio]	40.8	530	904.59	1807.16	1806.98	63.88	0.00038	KGVNLPGANVDLPAVSEK
210	gi|189538766	PREDICTED: similar to mitogen-activated protein kinase-	54	535	778.04	2331.08	2330.19	63.12	0.00038	VAFTGSTDVGHLIQQASSASNL
211	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	70.2	329	865.98	1729.95	1729.95	62.94	0.00049	KGSLLIDSSTIDPAVSK
212	gi|125828659	PREDICTED: hypothetical protein LOC449551 [Danio re	63.5	126	1270.39	2538.76	2538.31	62.53	0.00039	LVVNDGPDGGQSVYHIHIHVLG
213	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Da	37	2115	1419.48	2836.94	2835.44	62.39	0.00037	GAFTPSPLDPASTSDSHIASLSI
214	gi|113678245	hypothetical protein LOC558738 [Danio rerio]	62.2	111	846.23	1690.45	1689.84	61.33	0.00074	IEFSPLDAWNSGVQK
215	gi|189526598	PREDICTED: similar to COASTER [Danio rerio]	40.7	916	657.73	1313.44	1312.78	53.00	0.0051	QAVALSLKEARK
216	gi|68444865	PREDICTED: dodecenoyl-Coenzyme A delta isomerase	56.1	301	663.69	1325.37	1325.71	52.34	0.0058	IGLVDELVPEDK
217	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	30.4	204	853.72	1705.42	1704.91	61.21	0.00075	GATYGKPVHHGVNQIK
218	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	40.5	2633	1230.41	2458.81	2458.19	61.14	0.00054	HAINQEINAYNTPAQFGLEGSG
219	gi|54400426	ATP synthase, H+ transporting, mitochondrial F0 comple	67.1	252	764.44	1526.87	1526.78	52.48	0.0055	LDYQVELQNLHR
220	gi|41152175	ribosomal protein S7 [Danio rerio]	60.3	194	733.47	1464.93	1464.94	60.08	0.00094	KAIIIFVPVPQLK
221	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	25.7	2113	653.09	1304.16	1303.77	57.14	0.002	RCLIEIFGILK
222	gi|189532434	PREDICTED: im:7160733 [Danio rerio]	25.1	1248	653.09	1304.16	1303.77	57.14	0.002	RCLIEIFGILK
223	gi|189516256	PREDICTED: similar to phosphofructokinase, platelet [D	56.8	782	707.25	1412.48	1411.69	59.91	0.001	DLQSNVEHLTEK
224	gi|52219010	EH-domain containing 3, like [Danio rerio]	21.6	532	853.20	1704.38	1703.91	58.84	0.0013	KKDPELFQTVSDGLK
225	gi|125854185	PREDICTED: hypothetical protein [Danio rerio]	16.6	645	672.86	1343.71	1346.62	48.88	0.014	EEEEEQLKADK
226	gi|74315945	hypothetical protein LOC613246 [Danio rerio]	51.2	422	1048.40	2094.79	2092.98	58.42	0.0012	ALVGNEASEELQSADGNPHR
227	gi|47086875	glutamate dehydrogenase 1a [Danio rerio]	48.5	544	862.40	1722.79	1722.87	57.43	0.0017	HGGAIPIVPTSDFQER
228	gi|123858772	protein phosphatase 1, catalytic subunit, beta [Danio reri	79.5	327	978.50	1954.99	1952.12	57.82	0.0014	EIFLSQPILLELEAPLK
229	gi|189518709	PREDICTED: wu:fi22e08 [Danio rerio]	49.2	323	978.50	1954.99	1952.12	57.82	0.0014	EIFLSQPILLELEAPLK
230	gi|47550715	heterogeneous nuclear ribonucleoprotein A0 [Danio rerio	44.9	314	843.62	1685.23	1683.72	57.64	0.0017	GFGFVHFEDNDSADK
231	gi|41056209	hypothetical protein LOC393532 [Danio rerio]	35.3	490	1012.59	2023.16	2022.00	56.97	0.0017	HILDTHGLDPHQATASGPR
232	gi|33667057	calmodulin 2, gamma [Danio rerio]	20.1	149	923.68	1845.34	1843.88	56.77	0.0019	EAFSLFDKDGDGTITTK
233	gi|189532998	PREDICTED: similar to calmodulin 2 [Danio rerio]	21.7	152	923.68	1845.34	1843.88	56.77	0.0019	EAFSLFDKDGDGTITTK
234	gi|56693257	hypothetical protein LOC494050 [Danio rerio]	53.3	368	1035.13	3102.35	3100.58	51.88	0.0038	ILLDQGQEHTVETPHGVLHVTV
235	gi|41053611	hypothetical protein LOC393828 [Danio rerio]	27.2	213	1200.94	2399.87	2399.16	56.18	0.0018	SYHSPWEEAIINDPTLADTLK
236	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio r	41.4	333	713.59	1425.17	1424.81	56.10	0.0024	LDVAPISDIIEIK
237	gi|41053746	RNA binding protein with multiple splicing 2 [Danio rerio]	45.5	200	772.69	1543.36	1542.88	56.08	0.0025	TLFVSGLPTDIKPR
238	gi|56790313	homeo box B9a [Danio rerio]	14.1	255	710.16	1418.30	1416.74	55.87	0.0027	MEPLLGHLGEPPK
239	gi|44917595	alcohol dehydrogenase 8b [Danio rerio]	61.2	376	966.09	2895.25	2894.48	55.82	0.0017	GFPTILGHEAAGVVESVGPGVT
240	gi|154707842	methylmalonyl Coenzyme A mutase [Danio rerio]	39.5	757	786.15	1570.29	1568.84	47.95	0.016	NTQIIIQEESGIPK
					976.35	1950.69	1948.02	44.18	0.032	TPEGISIKPVYTQTDTAK
241	gi|62955301	hypothetical protein LOC550355 [Danio rerio]	39.6	255	925.67	1849.32	1848.92	55.56	0.0025	VLPGVDVTVGHEEEQGGK
242	gi|68438153	PREDICTED: similar to predicted protein [Danio rerio]	60.5	124	872.20	1742.39	1742.81	55.55	0.0027	AMGIMNSFVNDIFER
243	gi|41152402	histone 2, H2, like [Danio rerio]	35.7	126	872.20	1742.39	1742.81	55.55	0.0027	AMGIMNSFVNDIFER
244	gi|56693297	hypothetical protein LOC494070 [Danio rerio]	45.1	182	952.62	1903.22	1902.91	55.04	0.0028	AKEELEQELADKEDEK

245	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple	58.4	209	920.66	1839.30	1838.03	54.42	0.0032	VSPITINLINVLSENGR
246	gi|83523754	chimera galectin Gal3 [Danio rerio]	18.4	228	705.77	1409.53	1408.73	54.11	0.0037	RGNDIAFHINPR
247	gi|50539806	hypothetical protein LOC436642 [Danio rerio]	23.5	323	976.35	1950.69	1950.01	53.72	0.0036	ALESAYGSEKPSLTSAAIR
248	gi|66472400	NADH dehydrogenase (ubiquinone) Fe-S protein 4, (NA	48.2	168	827.09	1652.17	1650.88	53.50	0.0041	LDISTLTGVPEEHIK
249	gi|125995404	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 [Danio rerio]	55	709	695.11	2082.30	2082.02	53.31	0.0038	HVINFDLPSDIEEYVHR
250	gi|41282082	pl10 [Danio rerio]	50.3	688	695.11	2082.30	2082.02	53.31	0.0038	HVINFDLPSDIEEYVHR
251	gi|55742591	telomerase binding protein, p23 [Danio rerio]	20.8	159	974.86	1947.70	1944.92	53.01	0.0043	HHNEVDLLEAIDPNDSK
252	gi|55926092	heat shock 10kD protein 1 (chaperonin 10) [Danio rerio]	65	100	770.78	1539.54	1539.86	52.40	0.0055	VLQATVVAVGPGSTNK
253	gi|125842393	PREDICTED: zgc:103738 [Danio rerio]	36.4	77	987.76	2960.25	2961.35	52.44	0.0034	TLSAGSHAEHEGKPYCNNPCY
254	gi|52218912	enoyl Coenzyme A hydratase, short chain, 1, mitochondr	43	291	1056.69	2111.36	2110.12	52.29	0.005	AQFGQPEILLGTIPGAGGTQR
255	gi|189532637	PREDICTED: similar to Calcium-binding mitochondrial ca	26.9	774	622.59	1243.16	1240.68	51.93	0.0073	LQVAGEITTGPR
256	gi|30410758	keratin 18 [Danio rerio]	73.8	431	1000.00	1997.99	1998.02	51.86	0.0055	GNIQHQTQEYEALLNIK
257	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	49.7	298	617.63	1233.24	1232.68	51.16	0.0084	DFLAGGIAAAISK
258	gi|167621510	hypothetical protein LOC100136853 [Danio rerio]	31.6	424	654.89	1307.76	1306.71	46.23	0.023	KNSSSLKSTIDK
					655.46	1308.91	1306.71	47.37	0.018	KNSSSLKSTIDK
259	gi|68357456	PREDICTED: similar to mCG1046517 [Danio rerio]	46.1	1561	766.34	1530.67	1530.94	47.44	0.018	LLEKSKELAFILK
260	gi|59933260	cardiomyopathy associated 1 [Danio rerio]	49.8	2297	915.95	1829.89	1827.92	51.47	0.0066	SHTWLFETQPLDNIK
261	gi|53292609	clathrin, heavy polypeptide a (Hc) [Danio rerio]	34.9	1680	1170.75	2339.48	2338.23	51.37	0.0057	ISGETIFVTAPHDATAGIIGVNR
262	gi|57770449	hypothetical protein LOC393165 isoform 1 [Danio rerio]	42.1	197	1025.69	2049.36	2049.07	51.32	0.0062	KPVLETEVNHVSPLSDASK
263	gi|80751159	hypothetical protein LOC641325 [Danio rerio]	46	313	1296.63	2591.25	2589.22	42.49	0.038	GTKDDPIEPQQAIPDAQSFEFE
264	gi|50344970	hypothetical protein LOC415247 [Danio rerio]	52.1	382	604.82	1207.63	1205.69	50.73	0.0088	HNNLDLVIIR
265	gi|189523865	PREDICTED: myosin 1b-like 2 [Danio rerio]	46.9	1078	752.61	2254.79	2255.13	46.51	0.019	SLRHQDKDQCILITGESGAGK
266	gi|18858981	lamin b2 [Danio rerio]	66.2	583	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
267	gi|125849603	PREDICTED: similar to keratin 8 [Danio rerio]	41.8	438	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
268	gi|157743314	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	33.3	186	866.17	1730.33	1729.87	50.53	0.0086	EKGDGPWFQIPTIDK
269	gi|50540060	ubiquinol-cytochrome c reductase, complex III subunit VI	76.8	82	915.14	2742.38	2740.48	50.26	0.0063	GLHFGNLAKVRHVITYSISPFEQ
270	gi|68448495	hypothetical protein LOC100003906 isoform 1 [Danio reri	29.6	915	1373.97	4118.89	4117.98	50.23	0.0034	SGTPGFSHHHYTTNSGQPGLH
271	gi|37497110	ribophorin I [Danio rerio]	40	598	813.09	2436.23	2435.30	50.20	0.0069	VETVFSHVLKPFPTHITQAER
272	gi|189516116	PREDICTED: similar to ribophorin I [Danio rerio]	27.1	505	813.09	2436.23	2435.30	50.20	0.0069	VETVFSHVLKPFPTHITQAER
273	gi|62955727	NADH dehydrogenase (ubiquinone) 1 beta subcomplex,	19.4	175	814.41	1626.81	1625.79	50.13	0.0095	EVQQLQSETPADGPK
274	gi|54261767	succinate-CoA ligase, ADP-forming, beta subunit [Danio	63.1	466	1294.16	2586.30	2585.29	50.09	0.0067	LHGGTPANFLDVGGGATAQQV
275	gi|68379126	PREDICTED: hypothetical protein LOC767664 [Danio re	74.1	81	1494.87	1493.86	1493.82	50.07	0.0092	IFLEDNGLPVHIK
276	gi|112363126	dynein, cytoplasmic 1, heavy chain 1 [Danio rerio]	33.7	4643	843.40	2527.16	2526.32	49.04	0.0088	VLRPQVSAVPQHAQGESAEPA
277	gi|189533132	PREDICTED: A kinase anchor protein 12 [Danio rerio]	27.5	1533	1075.96	3224.86	3224.59	48.92	0.0074	QSSVIVQEIIQNVVENFAEAHGE
278	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	57.1	448	780.37	1558.73	1557.89	48.92	0.013	LLEVIDGHIPLPSR
279	gi|47087201	RIO kinase 2 [Danio rerio]	16.8	512	896.26	1790.51	1790.03	47.93	0.016	NHEIVPVSLIASIASLK
280	gi|189545630	PREDICTED: hypothetical protein [Danio rerio]	28	403	1429.65	1428.64	1427.78	47.74	0.017	LYEVFIKNFQK
281	gi|160333682	heat shock protein 8 [Danio rerio]	35.7	649	1131.27	2260.52	2259.14	47.51	0.014	SINPDEAVAYGAAVQAAILSGD
282	gi|130494136	ubiquitin-conjugating enzyme E2L 3, like [Danio rerio]	70	190	828.62	2482.83	2482.32	47.47	0.013	TDQVIQSLIALVNDPQPEHPLR
283	gi|57222259	talin 1 [Danio rerio]	46.9	2538	1059.58	3175.71	3174.57	47.34	0.011	EAVDDLGSTLAEVASAAGAVG
284	gi|55925219	sorting and assembly machinery component 50 homolog	38.8	469	768.63	1535.24	1533.83	47.24	0.018	DVVVQHVNIEGLGR
285	gi|189537996	PREDICTED: similar to sorting and assembly machinery	42.8	201	768.63	1535.24	1533.83	47.24	0.018	DVVVQHVNIEGLGR
286	gi|47086623	monocarboxylate transporter 4 [Danio rerio]	65	508	946.72	1891.42	1889.91	47.08	0.017	ELESIEVDSIEVENASK
287	gi|50539996	peroxiredoxin 2 [Danio rerio]	84.8	197	922.51	2764.51	2762.45	47.00	0.013	KIGVELIAASTDSHFSHLAWINT
288	gi|125814831	PREDICTED: similar to zinc finger protein 585B [Danio re	51.7	298	838.32	1674.63	1672.88	46.69	0.021	EESEDVKIEEIIIK
289	gi|189527553	PREDICTED: hypothetical protein LOC553434 [Danio re	47.2	568	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
290	gi|71892458	villin 2 [Danio rerio]	40	583	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
291	gi|125833577	PREDICTED: similar to Galectin-3 (Galactose-specific le	15.5	368	670.74	1339.46	1337.66	46.62	0.021	GHEVVFHFNPR
292	gi|189519969	PREDICTED: myosin, heavy polypeptide 10, non-muscle	43.3	1973	580.54	1738.58	1737.89	46.55	0.021	KQELEEILHDLESR
293	gi|189519965	PREDICTED: similar to nonmuscle myosin heavy chain [	43.5	1857	580.54	1738.58	1737.89	46.55	0.021	KQELEEILHDLESR
294	gi|61651682	fibronectin 1b [Danio rerio]	40.9	2408	806.73	2417.17	2416.31	46.22	0.018	SAPLVGTATTQLISGLPSLPSHG
295	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	64.3	308	550.57	1099.13	1098.61	44.93	0.037	QLADALKANR

296	gi|189523776	PREDICTED: hypothetical protein LOC798920 isoform 1	74	265	685.11	1368.20	1367.61	45.43	0.027	TRMYNTQDDPK
297	gi|50233897	FLJ12716-like protein [Danio rerio]	29.8	1132	596.22	1190.42	1187.63	45.26	0.034	TAYSLVHELR
298	gi|73611922	histone 2, H2a [Danio rerio]	60.2	128	972.56	2914.65	2914.58	45.22	0.019	VGAGAPVYLAAVLEYLTAEILEL
299	gi|41055102	H2A histone family, member X [Danio rerio]	60.6	142	972.56	2914.65	2914.58	45.22	0.019	VGAGAPVYLAAVLEYLTAEILEL
300	gi|21426835	glucose phosphate isomerase a [Danio rerio]	15	553	593.18	1184.34	1183.63	45.16	0.033	HFVALSTNAPK
301	gi|189525785	PREDICTED: similar to AT rich interactive domain 5B (M	31.1	935	673.32	1344.62	1344.72	45.14	0.032	KQEGSVQESIIK
302	gi|61806508	signal peptidase complex subunit 2 homolog [Danio rerio	48.3	201	650.50	1298.98	1299.73	45.04	0.032	AARNGKNSILEK
303	gi|189523571	PREDICTED: similar to mcf.2 transforming sequence-like	30.5	929	889.20	1776.39	1774.95	44.83	0.033	ESSPLFAADVITELKR
304	gi|125850307	PREDICTED: CFH protein [Danio rerio]	63.1	751	1101.66	2201.30	2200.96	44.39	0.031	DDITYENVEPVSEASYADGK
305	gi|189528635	PREDICTED: similar to odorant receptor [Danio rerio]	4.6	305	797.72	1593.43	1591.89	44.35	0.035	LLTDLLSDTHLVPR
306	gi|125843259	PREDICTED: polymerase (RNA) III (DNA directed) polyp	44.7	1130	585.65	1169.29	1169.70	44.34	0.039	VILIQEQLSK
307	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	21.9	448	710.11	1418.20	1415.74	44.34	0.038	EALGAENIQSTKR
308	gi|47085781	ubiquitin-like modifier activating enzyme 1 [Danio rerio]	37.1	1058	733.03	2196.05	2196.12	44.01	0.033	FDRPGQLHVGFQALHAFEK
309	gi|189526852	PREDICTED: similar to G2/M-phase specific E3 ubiquitin	43	762	898.52	1795.02	1794.80	44.16	0.035	SNMEFAINNTHGFGKE
310	gi|50344798	ubiquitin-conjugating enzyme E2L 3 [Danio rerio]	53.2	154	828.62	2482.83	2482.32	47.47	0.013	TDQVIQSLIALVNDPQPEHPLR
311	gi|189532554	PREDICTED: similar to karyopherin alpha 6 (importin alp	33.9	537	609.19	1216.37	1216.62	44.01	0.046	NKALNLEEMR
312	gi|52219050	hypothetical protein LOC447859 [Danio rerio]	41.7	617	928.92	2783.72	2782.39	43.84	0.028	ITDENLQSQTTGLYIPEYEEALK
313	gi|47086477	ribosomal protein L13a [Danio rerio]	39	205	634.75	1267.49	1265.65	43.73	0.042	YQAITATLEEK
314	gi|189517523	PREDICTED: hypothetical protein [Danio rerio]	66	147	713.74	1425.46	1424.76	43.62	0.042	INVDEIGPQTLAR
315	gi|121583897	hypothetical protein LOC562692 [Danio rerio]	46.6	384	816.81	1631.60	1631.81	43.59	0.045	ELEEKVAMLEAENK
316	gi|50539832	lysyl-tRNA synthetase [Danio rerio]	28.1	602	750.82	2249.44	2247.14	43.46	0.037	YNHLQPGDHLTDVVLNLSGR
317	gi|52218992	hypothetical protein LOC447834 [Danio rerio]	48.8	248	662.36	1322.70	1321.71	43.45	0.044	TLLGGGGVDGAIHR
318	gi|189536881	PREDICTED: hypothetical protein LOC402880 [Danio re	28.3	173	684.43	1366.84	1367.74	43.41	0.044	LDTPLPDVPFVR
319	gi|189541652	PREDICTED: similar to Myosin-3 (Myosin heavy chain 3)	40.6	882	659.27	1316.53	1315.65	43.35	0.049	ELELELDAEQK
320	gi|189531190	PREDICTED: im:7145859 isoform 1 [Danio rerio]	38.3	677	1052.47	2102.92	2102.03	42.90	0.044	EVDEVDAALSDLEITLEGGK
321	gi|57525959	BCL2-associated athanogene 3 [Danio rerio]	20	459	1015.59	3043.75	3041.54	42.71	0.031	VSEVPQQIHHQPVQQQQQPTQ
322	gi|62955581	hypothetical protein LOC550502 [Danio rerio]	50.8	455	1113.39	2224.76	2224.07	42.61	0.045	AHIVFDFHQAVDGVQEQER
323	gi|136256027	phosphorylase, glycogen; brain [Danio rerio]	33.9	843	953.65	1905.28	1905.00	42.55	0.049	LITSVGEVVNHDPVVGDR
324	gi|41055708	proteasome (prosome, macropain) 26S subunit, non-ATF	31.4	503	1294.90	2587.79	2586.35	42.35	0.04	EFLLGFLEQPVEIEGDVPFRPR
325	gi|41053395	glutamate oxaloacetate transaminase 2 [Danio rerio]	47	428	998.97	1995.92	1994.03	41.92	0.054	YFIEQGHNILLSQSFAK
326	gi|52219194	fatty acid binding protein 11 [Danio rerio]	64.2	134	769.63	1537.24	1535.67	41.74	0.063	LNEPFEETTADDR
327	gi|131889079	hypothetical protein LOC100034487 [Danio rerio]	60.5	850	544.27	543.26	543.31	41.53	0.034	INAAR
328	gi|39752649	kelch repeat and BTB (POZ) domain containing 10 [Dani	28.1	605	544.27	543.26	543.31	41.53	0.034	LNAAR
329	gi|28201964	erythrocyte membrane protein band 4.1 (elliptocytosis 1,	28.6	1534	583.60	1165.19	1164.71	41.44	0.071	IELVLPEKPK
330	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [Da	50.4	789	1115.74	2229.46	2229.10	41.20	0.062	TSYDVSDSGQLEHVVVNRPK

TCDD replicate 2

Protein #	Accession ID	Protein name	Protein coverage	length	peptide *m/z*	peptide Mr*expt*	peptide Mr*calc*	peptide score	pep_expect	peptide sequence
1	gi|41053652	myoglobin [Danio rerio]	100	147	550.49	1098.97	1098.58	69.68	0.00012	AGLDAAGQGALR
					780.21	1558.40	1557.74	111.12	7.70E-09	VMDAVIGDIDGYYK
					1010.42	2018.82	2020.10	106.78	1.80E-08	GDHAALLKPLANTHANIHK
					1110.91	2219.80	2219.23	91.96	5.10E-07	AKGDHAALLKPLANTHANIHK
					1128.60	2255.18	2253.18	112.98	4.10E-09	FSGISQGDLAGSPAVAAHGATV
					946.49	2836.43	2834.54	64.80	0.00021	GDHAALLKPLANTHANIHKVAL
					1012.59	3034.75	3033.67	57.28	0.0011	AKGDHAALLKPLANTHANIHKV
2	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	53.6	1936	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1180.66	1179.65	1179.58	47.68	0.017	DFEISQLNSK
					609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					621.00	1239.98	1237.63	51.96	0.0063	EADVLQQNPPK

					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					645.12	1288.22	1288.63	47.26	0.02	DSQLQLDDSLR
					654.30	1306.58	1305.58	40.69	0.088	ELECEVEAEQK
					655.46	1308.91	1307.64	77.55	1.70E-05	NSFSQQLEDLK
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					699.56	1397.10	1397.75	86.37	2.20E-06	NALLQAELEELR
					708.41	1414.80	1414.73	99.51	1.20E-07	LAEQELLDVTER
					733.14	1464.26	1463.74	77.88	1.60E-05	NSFSQQLEDLKR
					738.45	1474.89	1473.68	79.64	1.10E-05	VEELEEELEAER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					751.13	1500.24	1499.75	107.00	2.00E-08	LQEAEEAVEAVNAK
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					1540.74	1539.73	1539.77	67.06	0.00019	DYHIFYQILSNK
					771.81	1541.61	1541.83	41.93	0.063	IDDEQSIIIQLQK
					772.07	1542.12	1539.77	43.86	0.041	DYHIFYQILSNK
					772.48	1542.94	1542.83	83.14	4.90E-06	KLAEQELLDVTER
					772.58	1543.15	1541.83	79.18	1.20E-05	IDDEQSIIIQLQK
					773.18	1544.35	1542.83	89.45	1.20E-06	KLAEQELLDVTER
					778.74	1555.46	1553.85	77.67	1.70E-05	RNALLQAELEELR
					779.46	1556.90	1556.79	66.68	0.00021	LLGSLDIDHQQYR
					802.72	1603.42	1602.78	73.08	4.90E-05	SNDDLKENTAIVER
					806.41	1610.80	1610.75	87.04	1.90E-06	AAEESEEQANVHLGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					825.24	1648.47	1645.82	53.20	0.0049	NLTEEMAALDDIIAK
					843.71	1685.41	1684.83	67.36	0.00018	LELDDVASSMEHIVK
					845.72	1689.42	1688.88	91.16	7.80E-07	GQNVQQVNYAIGALSK
					1713.93	1712.92	1711.91	50.75	0.0078	ILNPAAIPEGQFIDSK
					860.59	1719.16	1717.85	95.23	3.00E-07	NEDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLINQK
					895.49	1788.97	1786.87	93.20	4.50E-07	TIDTLQSALESETHSR
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					934.83	1867.65	1867.93	118.48	1.30E-09	DLEEATLQHEATAATLR
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					979.93	1957.84	1957.98	122.26	5.20E-10	ILQEEISDLTEQLGEGGK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1021.70	2041.38	2040.98	102.96	4.30E-08	LLSNLFANYAGADSATGDGGK
					1044.21	2086.41	2086.04	81.55	5.80E-06	VKLEQQVDDLEGSLEQEK
					1069.85	2137.69	2139.00	132.48	4.70E-11	AEIQAALEEAEGSLEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.39	2200.76	2199.12	103.60	3.70E-08	GTLEDQIIQANPALEAFGNAK
					1145.88	2289.75	2290.10	89.15	9.70E-07	LTQESIMDLENDKQQLEEK
					1241.45	2480.89	2481.17	111.86	4.70E-09	KLETDLSQFQTEVEEAVQECR
3	gi|74315904	alpha globin-like [Danio rerio]	67.8	143	1117.39	1116.38	1114.56	42.40	0.07	ADEIGAEALAR
					588.76	1175.51	1175.62	78.14	1.80E-05	TIMGAVGEAISK
					684.64	1367.27	1365.73	80.52	8.50E-06	FFNNLALALSEK
					932.23	1862.44	1863.88	119.89	9.30E-10	TYFSHWSDLSPGSGPVK
					934.14	1866.26	1868.00	104.77	3.00E-08	IDDLVGGLAALSELHAFK
					934.17	1866.32	1863.88	96.10	2.20E-07	TYFSHWSDLSPGSGPVK
					934.23	1866.44	1868.00	116.08	2.20E-09	IDDLVGGLAALSELHAFK

					934.30	1866.58	1863.88	93.17	4.40E-07	TYFSHWSDLSPGSGPVK
					934.46	1866.90	1868.00	133.85	3.70E-11	IDDLVGGLAALSELHAFK
					998.22	1994.42	1991.97	69.02	0.00011	TYFSHWSDLSPGSGPVKK
4	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	67.8	143	1117.39	1116.38	1114.56	42.40	0.07	ADEIGAEALAR
					582.09	1162.17	1161.61	80.71	9.20E-06	TIMGAVGEAVSK
					684.64	1367.27	1365.73	80.52	8.50E-06	FFNNLALALSEK
					924.26	1846.50	1847.88	123.11	4.40E-10	TYFSHWADLSPGSGPVK
					934.46	1866.90	1868.00	133.85	3.70E-11	IDDLVGGLAALSELHAFK
5	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	79.3	333	748.67	1495.33	1494.84	73.96	3.80E-05	VPTPNVSVVDLTVR
					787.22	1572.42	1571.83	87.49	1.80E-06	LVIDGHAITVYSER
					882.65	1763.28	1762.80	54.62	0.0034	LVTWYDNEFGYSNR
					931.70	1861.39	1860.94	91.36	6.60E-07	SSIFDAGAGIALNDHFVK
					1105.92	2209.83	2210.17	74.16	3.10E-05	LVIDGHAITVYSERDPANIK
					1117.33	2232.65	2230.08	125.99	2.00E-10	WGDAGATYVVESTGVFTTIEK
					1301.14	2600.27	2599.37	90.28	6.60E-07	VINDNFVIVEGLMSTVHAITATQ
6	gi|38488753	myosin, heavy polypeptide 6, cardiac muscle, alpha [Dan	46.9	1936	602.49	1202.96	1202.57	64.97	0.00035	DGDVHPQNPPK
					659.27	1316.53	1316.61	44.94	0.034	ELENELDAEQK
					671.85	1341.68	1341.65	84.88	3.20E-06	AFDVLGFTSEEK
					1375.67	1374.66	1374.66	66.79	0.00022	LAEQELTDATER
					702.67	1403.32	1403.72	76.66	2.30E-05	KDFEINQLNQR
					737.76	1473.50	1473.68	50.23	0.0097	IEELEEELDAER
					742.19	1482.37	1480.77	58.83	0.0012	LSSADIETYLLEK
					755.38	1508.74	1509.74	59.37	0.0011	KLQHELEEAEER
					774.42	1546.82	1546.71	67.01	0.0002	SAEEAEELANANTAK
					794.15	1586.29	1585.79	48.54	0.014	IRELENELDAEQK
					795.70	1589.38	1588.75	98.08	1.50E-07	IEDEEEINADLTAK
					809.11	1616.20	1615.81	111.35	7.20E-09	LEEAGGATSAQVELNK
					846.60	1691.19	1690.81	85.65	2.80E-06	NSYEETLDHLETIK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					862.98	1723.94	1723.90	72.40	5.40E-05	MQLLHSQNTGLINQK
					1744.97	1743.96	1742.92	44.84	0.031	ILNASAIPEGQFIENK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					950.87	1899.73	1899.92	88.36	1.30E-06	DLEESTLQHEATTASLR
					967.26	1932.50	1931.91	114.53	3.00E-09	NLQEEISDLTDQVSEGR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1029.23	2056.45	2056.02	50.36	0.0077	RDLEESTLQHEATTASLR
					1044.21	2086.41	2086.04	81.55	5.80E-06	VKLEQQVDDLEGSLEQEK
					1086.81	2171.61	2170.99	90.81	6.80E-07	TELQSALEEADASVEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.39	2200.76	2199.12	103.60	3.70E-08	GTLEDQIIQANPALEAFGNAK
					1145.86	2289.71	2289.08	53.91	0.0032	LTQENVMDLENDKQQLEDK
					1158.89	2315.76	2316.11	145.85	2.10E-12	NDLLLQVQSEQDTLTDAEER
					1278.37	2554.72	2554.29	64.17	0.00027	KQESDLLQLQNELEELVQENR
					1341.94	2681.86	2682.38	81.75	4.50E-06	KKQESDLLQLQNELEELVQENR
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVN
7	gi|51592073	actin, alpha, cardiac muscle 1 like [Danio rerio]	57	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.10E-08	SYELPDGQVITIGNER
					977.68	1953.34	1955.04	80.29	8.00E-06	VAPEEHPTLLTEAPLNPK
					1114.80	2227.58	2227.06	62.75	0.00044	DLYANNVLSGGTTMYPGIADR
8	gi|62955473	hypothetical protein LOC550445 [Danio rerio]	50.7	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK

					895.36	1788.71	1789.88	109.27	1.10E-08	SYELPDGQVITIGNER
					977.68	1953.34	1955.04	80.29	8.00E-06	VAPEEHPTLLTEAPLNPK
					1114.80	2227.58	2227.06	62.75	0.00044	DLYANNVLSGGTTMYPGIADR
9	gi|163644331	ventricular myosin heavy chain [Danio rerio]	53.4	1938	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	IQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KIQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					825.24	1648.47	1645.82	53.20	0.0049	NLTEEMAALDDIIAK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					934.83	1867.65	1867.93	118.48	1.30E-09	DLEEATLQHEATAATLR
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					981.20	1960.38	1958.94	97.52	1.50E-07	NLQEEISDLTEQLGEGGK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1094.51	2187.00	2185.00	73.03	4.20E-05	SEIQSALEEAEASLEHEEGK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1101.39	2200.76	2199.12	103.60	3.70E-08	GTLEDQIIQANPALEAFGNAK
					1165.44	2328.86	2327.21	37.90	0.13	KGTLEDQIIQANPALEAFGNAK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
10	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	65.3	551	1199.65	1198.64	1196.64	38.38	0.16	VVDALGNPIDGK
					644.36	1286.71	1286.69	72.45	6.20E-05	HALIIYDDLSK
					650.86	1299.70	1299.74	95.06	3.20E-07	TAIAIDTIINQK
					682.29	1362.56	1362.69	80.70	8.60E-06	TGTAEVSSILEEK
					766.34	1530.67	1530.75	131.50	7.20E-11	ILGADTGAELEETGR
					1031.84	2061.66	2059.13	79.24	9.90E-06	AFLQHVISQHQDLLAAIR
					1182.76	2363.50	2364.17	82.77	4.00E-06	EVAAFAQFGSDLDAATQQLLNR
11	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	61.7	196	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
					780.26	1558.50	1559.82	92.64	5.40E-07	KEEAPAPAPVPETPK
					889.30	1776.58	1777.85	48.44	0.014	SVPLDFSPDQIEEFR
					973.35	1944.68	1944.08	96.37	1.90E-07	ALGHNPTNADVLTVLGKPK
					790.88	2369.61	2370.23	93.88	3.20E-07	KEEAPAPAPVPETPKEPEVDLK
12	gi|18858329	ba1 globin [Danio rerio]	93.2	148	713.59	1425.16	1424.76	91.43	7.00E-07	LNIDEIGPQALSR
					726.37	1450.72	1449.69	68.09	0.00015	NTYAALSVMHSEK
					898.52	1795.02	1794.83	130.34	8.60E-11	FGQAGFNADVQEAWQK
					994.50	1986.99	1984.97	94.14	3.30E-07	YFATFGNLSSPAAIMGNPK
13	gi|23097290	troponin T2, cardiac [Danio rerio]	22.7	282	609.45	1216.89	1216.66	49.43	0.013	KEEEEIISLK
					672.95	1343.88	1344.75	79.90	1.10E-05	KKEEEEIISLK
					855.86	1709.71	1710.90	55.88	0.0024	RKPLDIDNANESALR
					957.92	1913.82	1913.95	94.24	3.30E-07	DLNELQTLIEAHFESR
14	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	78.3	433	687.71	1373.40	1372.70	80.72	8.70E-06	HITGEQLGDLYK
					719.54	1437.06	1435.72	59.66	0.001	GNPTVEVDLYTTK
					1054.07	2106.12	2104.07	111.53	6.00E-09	FTGSVDIQVVGDDLTVTNPK
					1060.84	2119.67	2118.12	102.85	4.30E-08	DVILPVPAFNVINGGSHAGNK
					1147.92	2293.83	2295.13	40.61	0.067	SGETEDTFIADLVVGLCTGQIK
					1013.17	3036.49	3037.61	62.59	0.00033	HIADLAGNKDVILPVPAFNVING
15	gi|18858539	desmin [Danio rerio]	62.8	473	527.61	1053.20	1052.56	39.51	0.11	KIHEEEIR

					545.18	1088.34	1086.57	41.12	0.096	VSDLNQAVNK
					1254.56	1253.55	1253.56	38.11	0.15	NISEAEDWYK
					888.41	1774.80	1775.91	99.92	1.00E-07	FLEQQNSALTVEIER
					989.77	1977.53	1978.97	108.45	1.20E-08	LDFNLADAINQDFLNTR
					1094.31	2186.61	2186.00	145.27	2.50E-12	TFGSGLGSSIFAGHGSSGSSGS
16	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio rei	80.7	517	975.59	974.58	974.55	36.11	0.31	IGLFGGAGVGK
					704.65	1407.28	1405.67	96.20	2.30E-07	AHGGYSVFAGVGER
					1436.69	1435.68	1434.75	46.62	0.022	FTQAGSEVSALLGR
					720.70	1439.39	1438.78	77.81	1.60E-05	VALTGLTVAEYFR
					730.22	1458.43	1456.83	60.63	0.00086	TVLIMELINNVAK
					839.46	1676.91	1676.92	102.54	5.60E-08	LVLEVAQHLGENTVR
					961.83	1921.65	1920.96	84.87	2.80E-06	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	1.10E-07	AIAELGIYPAVDPLDSTSR
					1003.42	2004.82	2004.05	79.87	8.60E-06	FLSQPFQVAEVFTGHLGK
					687.83	2060.47	2059.99	39.81	0.087	EGNDLYHEMIESGVINLK
					1330.59	2659.17	2658.38	122.66	3.80E-10	SLQDIIAILGMDELSEEDKLTVAF
					1282.47	3844.39	3841.97	52.51	0.0024	KGSITSVQAIYVPADDLTDPAPA
17	gi|189536981	PREDICTED: similar to slow myosin heavy chain 3 isofor	48.7	1940	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1182.71	1181.70	1180.57	49.07	0.012	DFEISQLSSR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					949.82	1897.63	1895.90	59.47	0.00096	HADSVSDLGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
18	gi|189536979	PREDICTED: similar to slow myosin heavy chain 3 isofor	48.2	1934	496.09	990.16	989.50	39.61	0.13	SNNFQKPR
					1182.71	1181.70	1180.57	49.07	0.012	DFEISQLSSR
					1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					685.16	1368.31	1367.63	47.57	0.017	LQHELDEAEER
					748.98	1495.95	1495.73	61.03	0.00074	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					810.75	1619.49	1620.72	57.80	0.0016	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					860.59	1719.16	1716.90	95.15	3.00E-07	NKDPLNETVVGLYQK
					862.60	1723.18	1721.94	75.88	2.50E-05	VQLLHSQNTSLLNQK
					897.20	1792.39	1790.76	52.36	0.0056	QREEQAEADGTEDADK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					949.82	1897.63	1895.90	59.47	0.00096	HADSVSDLGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	1.60E-07	ALQEAHQQTLDDLQSEEDK

					1427.49	2852.97	2853.40	96.93	1.30E-07	ALQEAHQQTLDDLQSEEDKVNT
19	gi|83025080	actinin, alpha 2 [Danio rerio]	40.1	895	671.13	1340.24	1338.79	55.24	0.0029	QAILGIQQEVLK
					826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
					860.29	1718.57	1715.95	46.08	0.024	ILAADKPYILSDELR
					873.76	1745.51	1743.87	73.20	4.60E-05	DDPLGNLNLAFDIAEK
					885.47	1768.93	1768.81	104.59	3.20E-08	KHEAFESDLSAHQDR
					916.62	1831.23	1828.89	71.45	6.60E-05	MLDAEDILSTPKPDER
					969.28	1936.54	1934.98	74.47	3.10E-05	GDLTNPYSTITAEEIAIK
					1001.17	2000.32	1998.01	68.34	0.00013	LEGDHQLIQESLIFDNK
					1050.91	2099.81	2099.09	86.17	2.00E-06	LNKDDPLGNLNLAFDIAEK
					1412.81	2823.60	2824.40	93.56	2.70E-07	VEQIAAIAQELNELDYHDVASVN
20	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple	76	517	975.59	974.58	974.55	36.11	0.31	IGLFGGAGVGK
					704.65	1407.28	1405.67	96.20	2.30E-07	AHGGYSVFAGVGER
					1436.69	1435.68	1434.75	46.62	0.022	FTQAGSEVSALLGR
					720.70	1439.39	1438.78	77.81	1.60E-05	VALTGLTVAEYFR
					730.22	1458.43	1456.83	60.63	0.00086	TVLIMELINNVAK
					839.46	1676.91	1676.92	102.54	5.60E-08	LVLEVAQHLGENTVR
					961.83	1921.65	1920.96	84.87	2.80E-06	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	1.10E-07	AIAELGIYPAVDPLDSTSR
					1003.42	2004.82	2004.05	79.87	8.60E-06	FLSQPFQVAEVFTGHLGK
					687.83	2060.47	2059.99	39.81	0.087	EGNDLYHEMIESGVINLK
					1282.47	3844.39	3841.97	52.51	0.0024	KGSITSVQAIYVPADDLTDPAPA
21	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	77.9	172	1274.59	1273.58	1273.67	40.26	0.1	LFDPNATGVVNK
					897.81	1793.60	1792.84	50.73	0.0081	LNVSDEELESMLTEGK
					1048.00	2093.99	2091.96	79.59	9.30E-06	GSSNVFSMFEQSQIQEFK
					1292.50	2582.99	2582.25	108.90	9.00E-09	FTAEEVDQAFAVAPIDVAGNIDY
22	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	48.3	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.10E-08	SYELPDGQVITIGNER
					1954.17	1953.16	1953.06	81.42	6.20E-06	VAPEEHPVLLTEAPLNPK
23	gi|50344802	hypothetical protein LOC415164 [Danio rerio]	48.3	377	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.10E-08	SYELPDGQVITIGNER
					1954.17	1953.16	1953.06	81.42	6.20E-06	VAPEEHPVLLTEAPLNPK
24	gi|189520343	PREDICTED: similar to myosin heavy chain fast skeletal	47.5	1933	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.067	EQYEEEQEAK
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					846.60	1691.19	1690.81	85.65	2.80E-06	NSYEETLDHLETLK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1010.39	2018.76	2016.00	68.23	0.00013	NLQQEITDLTEQLGETGK
					1108.55	2215.08	2213.03	110.50	7.20E-09	SEIQAALEEAEATLEHEESK
25	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	55.2	782	786.18	1570.35	1568.82	59.32	0.0012	FKLEPPTGDELPAR
					1695.68	1694.67	1694.78	51.72	0.0067	FNPETDYLTAPNGEK
					857.83	1713.65	1711.84	77.20	1.80E-05	EVNQEVYSFLASAGAK
					878.27	1754.52	1752.88	68.60	0.00013	IVYGHLDDPAGQEIAR
					954.55	1907.08	1905.98	68.05	0.00014	KQGLLPLTFSNPADYDK
					1041.84	2081.67	2080.94	61.45	0.0006	NNISWVVVGDENYGEGSSR
					1106.24	2210.46	2209.04	53.72	0.0034	KNNISWVVVGDENYGEGSSR
					1267.35	2532.69	2532.29	120.88	5.80E-10	GHLDNISNNLLIGAVNIENDGVN
					1361.62	2721.22	2721.43	65.92	0.00017	NDANPATHAFVTSPEIVTALAIA

26	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio rer	44.2	1937	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					752.60	1503.19	1502.76	72.06	6.30E-05	ENQSILITGESGAGK
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.0019	NLQQEISDLTEQLGETGK
27	gi|18858335	bactin1 [Danio rerio]	46.1	375	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					895.36	1788.71	1789.88	109.27	1.10E-08	SYELPDGQVITIGNER
28	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	65.3	334	710.69	1419.36	1417.79	76.48	2.30E-05	LITPLASGPAEPPR
					770.19	1538.36	1537.77	74.86	3.10E-05	IVADKDYSVTANSR
					843.74	1685.46	1684.85	114.34	3.50E-09	ELADELALVDVVEDR
29	gi|148596963	spectrin alpha 2 [Danio rerio]	43.5	2480	787.22	1572.42	1571.78	80.51	9.20E-06	HQALQAEISGHEPR
					851.84	1701.66	1699.88	93.88	3.80E-07	KHQALQAEISGHEPR
					869.56	1737.10	1736.82	56.93	0.0019	TATDEAYKDPSNLQGK
					873.61	1745.21	1744.82	38.53	0.14	LSDDNTIGQEEIQQR
					882.85	1763.69	1760.88	36.14	0.24	KHQLLEADISAHEDR
					926.15	1850.29	1848.86	74.98	2.80E-05	KFEEFQTDLAAHEER
					964.07	1926.13	1924.90	93.25	4.10E-07	SSLSSAEADFSQLAELDR
					698.23	2091.67	2091.08	70.44	7.60E-05	LEAELGAHEPAIQSVLETGK
					1077.98	2153.95	2153.10	123.55	3.70E-10	ALINADELANDVAGAEALLDR
					1110.83	2219.64	2219.03	45.13	0.025	STDEAGQALLNTGHYASEEVK
					750.39	2248.15	2247.19	67.14	0.00016	RLEAELGAHEPAIQSVLETGK
					831.34	2490.98	2489.22	39.47	0.08	EKEPIVGSPDYGKDEDSAEALL
30	gi|189523699	PREDICTED: titin a [Danio rerio]	52	32757	804.70	1607.39	1605.88	52.60	0.0054	AEDPLFLPSPPAKPK
					831.24	1660.46	1658.82	50.71	0.0084	VNVEVEYTEPVPER
					863.58	1725.14	1722.92	52.16	0.0057	AGSDLVLDAAVGGKPEPK
					947.83	1893.64	1892.90	52.96	0.0043	HTVTLSWEKPDHDGGSK
					968.75	1935.49	1936.07	49.40	0.0099	AVNEAGASRPSVTAGPIVIK
					1015.88	2029.75	2029.15	63.89	0.00033	KVPAKPVEAITVPTEEPPK
					1029.07	2056.13	2056.09	70.98	6.60E-05	ELPISFVTPLADVHVYEK
					1035.13	2068.25	2067.07	47.02	0.017	NKFDVPDAPQNVIVGNVNK
					1049.90	2097.79	2095.07	51.75	0.0057	LQGEVLSPSPDVEIIEDGAK
					1052.35	2102.69	2102.05	79.10	1.10E-05	EQVTHQAALLQSHEVQER
					1058.69	2115.37	2113.11	54.55	0.003	VLAENEHGIGLPAETPEPLK
					708.80	2123.37	2122.13	68.98	0.0001	VLDRPGPSSGPLDITGLTAEK
					1070.08	2138.14	2137.14	45.22	0.025	EQHKPVVLSVNETTQTLSK
					1079.92	2157.82	2157.24	49.64	0.0092	KVPAKPVEAITVPTEEPPKK
					1098.94	2195.87	2196.14	55.19	0.0025	VLDRPGPPDGPISIYGVTSEK
					1101.80	2201.58	2199.25	68.20	0.00013	KLPAKPDETIAVPIEEPPKK
					1140.29	2278.57	2276.23	39.60	0.087	VKEPPSIIEKPESQDVIPGSK
					1177.07	2352.13	2351.12	38.63	0.1	VSWRPPSDDGGSDIFGYIVER
					1224.99	2447.97	2447.27	40.79	0.062	VNDAENLHPSTVFTIPNLPELK
					1299.87	2597.72	2597.14	69.48	7.90E-05	EKEVEEPEEPEEEYHPSLNER
					1072.88	3215.61	3213.65	67.41	0.0001	SHAIDSAPIVAQYPFTPPGPPTS
31	gi|66472732	myosin heavy chain 4 [Danio rerio]	41.7	1935	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.0019	NLQQEISDLTEQIGETGK

					1044.21	2086.41	2088.02	74.04	3.20E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	1.20E-06	NDLQLAVASEAENLSDAEER
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
32	gi|189519129	PREDICTED: similar to myosin heavy chain 4 [Danio reri	41.2	1933	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.0019	NLQQEISDLTEQIGETGK
					1044.21	2086.41	2088.02	74.04	3.20E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	1.20E-06	NDLQLAVASEAENLSDAEER
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
33	gi|169259784	myosin, heavy polypeptide 1, skeletal muscle [Danio reri	36.4	1937	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.0019	NLQQEISDLTEQLGETGK
					1044.21	2086.41	2088.02	74.04	3.20E-05	TKLEQQVDDLEGSLEQEK
					738.94	2213.78	2213.03	41.26	0.061	AEIQTALEEAEGTLEHEESK
34	gi|18858427	creatine kinase, muscle a [Danio rerio]	40.2	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR
					999.17	1996.33	1993.93	107.13	1.60E-08	GTGGVDTASVGGVFDISNADR
35	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	46	1936	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					816.81	1631.60	1631.78	96.03	2.60E-07	LEEAGGATAAQIEMNK
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	3.90E-05	QADSVAELGEQIDNLQR
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2001.99	56.30	0.0019	NLQQEISDLTEQLGETGK
36	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	55.1	28836	671.64	1341.26	1340.73	47.09	0.019	VTEHTVTGLLSGK
					700.80	1399.58	1399.71	67.53	0.00017	HVSVEALDFIDR
					710.47	1418.92	1418.74	37.16	0.2	FGLGEALESEIVR
					808.51	1615.01	1612.87	52.28	0.0058	ALDPVFKPGPPHNPK
					830.81	1659.61	1660.95	47.43	0.018	VIILSKPDEPQGPIR
					856.20	1710.38	1709.82	61.51	0.00065	ADSGNYTITIQNAAGSK
					863.58	1725.14	1722.92	52.16	0.0057	AGSDLVLDAAVGGKPEPK
					885.45	1768.89	1768.91	37.29	0.17	SSVTLTWVKPAHDGGSK
					920.85	1839.68	1838.93	50.02	0.009	STVSLAWEKPLHDGGSR
					924.84	1847.66	1845.01	54.27	0.0034	VQILDKPGPPAGHIEFK
					929.14	1856.27	1854.92	68.20	0.00013	TSVSLSWEKPIHDGGSR
					951.67	1901.33	1898.91	43.42	0.04	TTVTLSWEKPEHDGGSR
					648.76	1943.24	1941.02	43.23	0.04	IGESFEIDVPISGRPTPK
					989.31	1976.60	1976.14	42.13	0.052	SQLERPGAPLKPVVSGITK
					1013.79	2025.56	2025.09	38.16	0.13	ITIDTKPGHSTLSIANTTR
					1033.20	2064.39	2064.06	43.67	0.035	VISGVQDLEYTVTDVIEGK
					1039.66	2077.30	2077.08	43.93	0.035	HGTGEAFINLDVIDVPGPVK
					1045.73	2089.44	2089.14	70.70	7.20E-05	DATIEIITLDKPGPPTGPVR
					1047.74	2093.46	2092.96	51.97	0.0054	WTEPDSDGGSPITNYVVEK
					1112.56	2223.10	2222.18	41.11	0.064	VTAENEIGTGDPSVPSKPILAK
					1146.20	2290.39	2289.16	55.90	0.002	KGEWVAVTTDEIHQTVYSVK
					1152.84	2303.67	2302.28	45.00	0.024	SEPKPLAAPVIANDLTIEPSLK
37	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	76.9	337	661.18	1320.35	1319.67	78.24	1.50E-05	GYIGADQLGDALK
					753.50	1504.98	1502.77	81.33	7.40E-06	VEFPADQLSALTGR

					1545.20	3088.39	3088.58	91.67	4.10E-07	NSPLVSELSLFDIAHTPGVAADL
38	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	89.4	283	588.48	1174.94	1173.56	62.94	0.00059	SEYGLTFTEK
					1429.74	1428.73	1427.69	59.35	0.0012	LTFDTTFSPNTGK
					1052.33	2102.65	2102.15	73.62	3.70E-05	VNNTSLVGVGYTQSLRPGIK
					1088.83	2175.64	2174.05	81.62	5.60E-06	WNTDNTLGTEINIEDQIAK
					1258.10	2514.18	2513.15	75.22	2.20E-05	TGDFQLHTNVNDGSEFGGSIY
39	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	50.6	449	578.00	1153.98	1153.57	40.85	0.086	DIFQDIFEK
					678.57	1355.13	1354.68	66.05	0.00024	TIEAEAAHGTVTR
					716.02	1430.02	1428.73	77.71	1.70E-05	FKDIFQDIFEK
					861.13	1720.25	1719.82	116.07	2.40E-09	DQTDDQVTIDSAIATK
					1894.09	1893.08	1891.93	57.87	0.0014	LNEHYVNTTDFLDAIK
40	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	62	284	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	0.00013	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.64	1417.26	1416.75	48.43	0.015	DAQEKLELSEKK
					770.52	1539.02	1537.71	105.07	2.90E-08	SIDDLEDELYAQK
					845.36	1688.70	1688.78	68.99	0.00013	YSEKEDKYEEEIK
					770.52	2308.54	2307.18	67.97	0.00013	TVAKLEKSIDDLEDELYAQK
41	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	63.4	153	550.56	1099.10	1098.53	38.00	0.18	NLIHGSDSEK
					795.45	1588.88	1588.88	78.54	1.40E-05	LVAAKFVQASEDLAK
					975.95	1949.88	1949.07	83.51	3.80E-06	GFRLVAAKFVQASEDLAK
					1040.04	2078.06	2077.09	38.09	0.13	YTSSGPLLAMVWEGLNVIK
					1106.98	2211.95	2211.12	83.98	3.20E-06	SAATEVSLWFKPEELVSYR
42	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	41.3	143	934.97	1867.93	1867.99	120.19	8.40E-10	IDDLLGALSSLSDLHATK
43	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	36.8	1945	609.19	1216.37	1215.63	54.25	0.0044	AGLLGQLEEMR
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
44	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	39.7	1938	1224.67	1223.66	1223.61	43.14	0.046	TKYETDAIQR
					643.04	1284.06	1282.57	37.91	0.16	ELTYQTEEDR
					931.62	1861.22	1858.88	99.10	1.10E-07	LEQQVDDLEGSLEQEK
					995.29	1988.57	1986.97	72.80	4.40E-05	LEQQVDDLEGSLEQEKK
45	gi|41387136	hypothetical protein LOC393781 [Danio rerio]	77.3	128	902.23	1802.45	1801.94	110.64	8.00E-09	YHVSETPFAISAQKPK
					915.41	2743.19	2742.29	43.40	0.03	LFPGDVILETGEVVPDFPEDSH
46	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	34.4	331	969.23	1936.45	1936.93	114.30	3.20E-09	HLTTLVDDIWYYAGDR
47	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio reri	52.7	410	844.84	1687.67	1687.84	100.98	7.90E-08	NIDYVAESIHEAVTK
					1115.35	2228.68	2226.03	103.90	3.40E-08	NLFAFFDSAYQGFASGDLEK
48	gi|48762657	enolase 1, (alpha) [Danio rerio]	57.9	432	1147.92	2293.83	2295.13	40.61	0.067	SGETEDTFIADLVVGLCTGQIK
					1002.93	3005.75	3006.57	90.40	5.70E-07	HIADLAGNPDVILPVPAFNVING
49	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	79.3	397	594.84	1187.66	1187.68	73.04	6.00E-05	ITAHLVHELR
					649.07	1296.12	1294.70	56.75	0.0021	RTPFGTYGGVLK
					683.58	1365.14	1364.63	58.96	0.0012	DHSATDLAEHAAK
					931.96	1861.91	1861.98	116.41	2.10E-09	TNVNGGAIAIGHPLGASGTR
50	gi|38488731	natriuretic peptide precursor A [Danio rerio]	77.4	106	1025.48	2048.94	2049.99	105.81	2.20E-08	SLLQQFEEALATEEASER
					1182.83	2363.65	2362.99	79.64	8.30E-06	DREEAAAPGEDSNPSDGFDTQ
51	gi|162287365	hemopexin [Danio rerio]	54.1	447	1339.69	1338.68	1338.61	51.90	0.0061	FHSDTIESEFK
					900.94	1799.87	1800.00	65.16	0.00028	VGKPHTHLEGYPKPLK
52	gi|18858587	elongation factor 1-alpha [Danio rerio]	50.2	462	530.52	1588.54	1587.87	53.53	0.0044	THINIVVIGHVDSGK
					1244.91	2487.80	2486.35	68.46	0.0001	VETGVLKPGMVVTFAPANVTTE
					973.65	2917.91	2917.55	69.48	7.00E-05	EGNASGTTLLDALDAILPPSRPT
					1015.61	3043.79	3045.65	67.12	0.00011	KEGNASGTTLLDALDAILPPSRP

53	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio	51.1	454	1245.78	1244.77	1244.68	74.35	4.30E-05	KVDFAAAGEPLK
					1246.66	1245.65	1244.68	77.74	2.00E-05	KVDFAAAGEPLK
					696.14	1390.27	1390.71	74.71	3.70E-05	GVEAVGGSLSVSSSR
					1265.56	3793.64	3793.99	160.27	4.00E-14	HQTGAGLVHALVAIEGASATSA
54	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	45.4	119	599.32	1196.62	1195.75	37.92	0.16	AKLEPVVLSLK
					1050.98	2099.94	2100.09	88.07	1.30E-06	ELTELGEQVKPHFEGIFK
					1115.07	2228.12	2228.18	64.05	0.00032	KELTELGEQVKPHFEGIFK
55	gi|47086523	ictacalcin [Danio rerio]	86.3	95	697.11	1392.20	1390.73	104.53	3.60E-08	ELLSAELGDIFGK
56	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	66.4	532	882.38	1762.75	1763.98	115.54	2.70E-09	KGVNLPGAAVDLPAVSEK
					938.02	1874.03	1872.82	42.98	0.045	MNFSHGSHEYHGETIK
57	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Dani	66.2	659	837.57	1673.13	1671.94	104.71	3.20E-08	AIEQFGAVIEELLLK
					872.48	2614.41	2614.37	42.99	0.034	AGLGSGLTLQGTVHPELNHSG
58	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	70.4	260	851.87	1701.73	1702.86	109.48	1.00E-08	HGASAVILDLPSSDGHK
59	gi|156713467	vitellogenin 7 [Danio rerio]	55.7	1358	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
					1069.54	2137.07	2135.16	100.74	6.90E-08	ISDATAQIVEVLTHLVANNK
60	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	62.4	763	653.09	1304.16	1303.71	82.76	5.60E-06	MQLLEIITTDK
					804.74	1607.47	1606.81	72.46	5.60E-05	DVNTEALEILEAYK
					1049.90	2097.78	2095.02	66.49	0.00019	AGVEQGPTTGYLVESQQFGK
					1195.44	3583.28	3583.84	76.05	1.20E-05	KLDSLTTGFGFPVGAATLADEV
61	gi|40254659	bactin2 [Danio rerio]	44	375	489.47	976.93	975.44	36.02	0.29	AGFAGDDAPR
					600.05	1198.08	1197.51	75.20	3.20E-05	DSYVGDEAQSK
					1954.17	1953.16	1953.06	81.42	6.20E-06	VAPEEHPVLLTEAPLNPK
62	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Co	74.6	761	653.09	1304.16	1303.71	82.76	5.60E-06	MQLLEIITTDK
					698.19	1394.36	1392.67	54.97	0.0032	LSGQLDYHGFEK
					837.73	1673.45	1672.93	67.82	0.00016	MGLVHQLVDPLGPGLK
					1167.77	3500.29	3497.79	58.92	0.00062	LDSLTTGFGFPVGLATLADEVG
63	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	64.8	364	530.65	1059.29	1058.57	51.67	0.0085	KELSDIAQR
					568.04	1134.06	1132.66	42.00	0.069	LFSQLIKER
					660.09	1318.16	1317.68	91.48	7.50E-07	GILAADESTGSVAK
					876.65	1751.28	1749.80	94.12	3.70E-07	GDTGAAAGESLFVANHAY
					1174.96	2347.90	2347.17	50.36	0.007	GVVPLAGTNGETTTQGLDGLY
64	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	88.3	248	696.12	1390.22	1388.71	83.57	4.70E-06	SIEELANTLNSAK
					1458.87	1457.86	1457.72	49.98	0.01	HVFGESDELIGQK
					801.94	1601.87	1601.88	47.81	0.017	VVLAYEPVWAIGTGK
					808.26	1614.50	1613.82	63.83	0.0004	RHVFGESDELIGQK
					1216.87	2431.73	2431.30	60.01	0.00071	DLDGFLVGGASLKPEFIDIINAK
65	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	31.7	230	1068.17	2134.32	2133.18	94.22	3.20E-07	ILVSAEDVLHSWAVPSLGIK
66	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	47	164	820.79	1639.56	1637.91	94.27	3.60E-07	HVVFGQVVEGLDVIK
67	gi|117606264	sarcalumenin [Danio rerio]	52.1	482	731.19	1460.36	1459.77	63.21	0.00049	VTFVDTPGIIENR
					1738.02	1737.01	1735.95	88.70	1.30E-06	AITHELPSLLGSINSGK
					1036.41	2070.80	2069.08	65.94	0.00022	REEISLLEDLNQVIENR
68	gi|62955689	hypothetical protein LOC550556 [Danio rerio]	38.1	270	842.00	1681.99	1682.84	89.42	1.10E-06	AFAEFLTEEIKEEK
69	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	60.4	603	1379.96	2757.90	2756.52	38.69	0.09	TLEEVVETIKPTAIIGVAAIGGAF
					1006.36	3016.04	3013.43	94.02	2.40E-07	HISDDIFLTTAEAISEMVTEEHLA
70	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (as	49.8	428	644.14	1286.26	1284.69	49.82	0.011	GALDDISKIPEK
					706.10	1410.19	1408.72	67.95	0.00015	EYLPIGGLADFSK
					723.85	1445.68	1445.81	66.36	0.00024	IAATILNTPELYK
					947.98	1893.94	1893.02	70.95	6.90E-05	KLDKEYLPIGGLADFSK
					998.97	1995.92	1994.03	41.92	0.054	YFIEQGHNILLSQSFAK
					784.61	2350.79	2350.26	62.99	0.00038	ISVAGVTSANVEYLAHAIHAVTK

71	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	79.2	202	999.96	2996.84	2996.41	42.81	0.031	TLAAGSHAEHDGQPYCHKPCY
					1008.19	3021.55	3023.42	63.54	0.00026	TLNPGGHAEHDGKPYCHKPCY
					1008.49	3022.44	3022.46	54.27	0.0022	GVNIGGAGSYVYDTPVGDDSV
					1009.02	3024.02	3023.42	61.13	0.00046	TLNPGGHAEHDGKPYCHKPCY
72	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	72.1	283	930.44	1858.86	1858.82	97.79	1.50E-07	SQSGVEFTTGGSSNTDTGK
					1030.87	2059.73	2058.12	72.35	4.90E-05	VNNASLVGVGYTQSLRPGVK
73	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	52.5	284	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	0.00013	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.10	1416.18	1415.73	49.47	0.012	DAQEKLEQAEKK
74	gi|166795887	vitellogenin 1 [Danio rerio]	51.8	1362	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					682.95	1363.89	1363.69	44.02	0.039	HILTAAYDTGFR
					691.81	1381.61	1381.78	51.39	0.0071	ISDAPAQIVEVLK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
75	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio reric	47.7	413	1503.86	1502.85	1501.78	37.62	0.18	GQDITVPSPVSQFK
					1042.49	2082.96	2079.97	96.83	1.70E-07	GTGGVDTAAVGDTFDISNLDR
76	gi|41054193	hypothetical protein LOC327506 [Danio rerio]	38.2	178	1042.49	2082.96	2079.97	96.83	1.70E-07	GTGGVDTAAVGDTFDISNLDR
77	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	51.3	1358	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					691.81	1381.61	1381.78	51.39	0.0071	ISDAPAQIVEVLK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
78	gi|41054435	hypothetical protein LOC324244 [Danio rerio]	38.3	248	586.14	1170.26	1169.67	66.30	0.00025	LVILEGELER
					623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	0.00013	KLVILEGELER
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
79	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	54.8	1631	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					925.36	1848.71	1847.86	65.37	0.00026	LSSENADSEIETETPVK
80	gi|189529437	PREDICTED: similar to plectin 1 isoform 1 [Danio rerio]	41.9	4530	669.70	2006.06	2004.06	42.99	0.042	LLDAQLATGGIIDPVESHR
					1032.88	2063.74	2062.11	98.98	1.10E-07	DGHNLISLLEVLSGETLPR
					1163.62	2325.22	2323.14	48.85	0.01	IDTAEWGIDLPTVESQLGSHR
81	gi|189529439	PREDICTED: similar to plectin 1 isoform 2 [Danio rerio]	42.2	4506	669.70	2006.06	2004.06	42.99	0.042	LLDAQLATGGIIDPVESHR
					1032.88	2063.74	2062.11	98.98	1.10E-07	DGHNLISLLEVLSGETLPR
					1163.62	2325.22	2323.14	48.85	0.01	IDTAEWGIDLPTVESQLGSHR
82	gi|47087077	phosphoglycerate kinase 1 [Danio rerio]	63.1	417	666.83	1331.65	1331.73	46.32	0.025	ITLPVDFITADK
					818.96	1635.91	1633.78	39.91	0.097	LGDVYVNDAFGTAHR
					1740.87	1739.86	1739.91	58.16	0.0014	VSHVSTGGGASLELLEGK
					925.89	1849.76	1850.97	62.41	0.00052	ITLPVDFITADKFDEK
					801.08	2400.20	2400.17	46.35	0.017	QIVWNGPVGVFEWDNFAHGTK
83	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	54.4	305	855.23	1708.45	1706.82	92.94	5.00E-07	EIAAFDAVNDESWLK
					877.76	2630.26	2631.29	87.23	1.30E-06	NVTIWGNHSSTQYPDVHHAIVTI
84	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	60.2	364	530.65	1059.29	1058.57	51.67	0.0085	KELSDIAQR
					660.09	1318.16	1317.68	91.48	7.50E-07	GILAADESTGSVAK
					1174.96	2347.90	2347.17	50.36	0.007	GVVPLAGTNGETTTQGLDGLYE
85	gi|68448530	vitellogenin 5 [Danio rerio]	43.6	1360	587.59	1173.17	1172.62	60.66	0.001	LEFEVQVGPR
					1299.73	1298.72	1298.71	49.73	0.011	EIELTAALPSQK
					1706.13	1705.12	1705.02	40.57	0.087	WLLDALPAVGTPVIIK
86	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	38.6	1079	1271.84	1270.83	1269.68	44.80	0.036	SLGAEPLEVDIK
					707.70	1413.39	1412.74	49.47	0.011	GVIHVGYTDIPSR
					790.14	1578.26	1577.77	42.94	0.049	QGFNVVVESGAGESAK
					922.59	2764.74	2763.39	66.57	0.00015	DGSVVVDLAAEAGGNIETTVPG
87	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	38.4	3730	637.94	1273.86	1273.71	79.51	1.20E-05	SKVEEILSELK

					1036.97	3107.89	3105.49	62.90	0.0003	YDAEEIEAEVSSDVTTEIHNIITT
88	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	42.9	1974	808.09	1614.16	1612.69	40.36	0.089	DLEEHLEEEEDAR
					1000.25	1998.48	1997.92	83.36	3.90E-06	ELEGHISDLQEDLESER
					1066.46	2130.91	2131.00	57.42	0.0015	QVEAERDELADELASNASGK
89	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	69.5	455	824.81	1647.61	1645.83	39.41	0.12	KCPDCPGLLPLHEPK
					654.45	1960.33	1959.96	51.31	0.0063	FHDHRPGSVHPLGPDHR
90	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	36.5	359	880.53	1759.04	1758.94	75.76	2.50E-05	SIRPLDADTIETSITK
91	gi|47086819	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	59.2	255	1044.76	2087.51	2086.96	98.21	1.30E-07	AAFDDAIAELDTLSEESYK
92	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	69	284	623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					709.64	1417.26	1416.75	48.43	0.015	DAQEKLEISEKK
					770.52	2308.54	2307.18	67.97	0.00013	SVAKLEKTIDDLEDELYAQK
93	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	49.7	996	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					765.37	1528.72	1526.87	36.19	0.24	AIGVVVATGVNTEIGK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
94	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	44.8	1056	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVLK
95	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	39.7	1035	1526.85	1525.84	1524.80	69.48	0.00011	DIVPGDIVEVAVGDK
					789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
96	gi|189526600	PREDICTED: similar to dystonin [Danio rerio]	42	8365	1032.88	2063.74	2062.11	98.98	1.10E-07	DGHNLISLLEVLSGETLPR
97	gi|153792369	si:dkey-151c10.1 [Danio rerio]	37.6	4577	1032.88	2063.74	2062.11	98.98	1.10E-07	DGHNLISLLEVLSGETLPR
98	gi|68448513	hypothetical protein LOC574004 [Danio rerio]	42.2	187	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
99	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio r	39.7	151	757.17	1512.33	1511.69	84.44	3.40E-06	DQGTFEDFVEGLR
100	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	59	244	1074.12	2146.22	2143.98	91.19	6.40E-07	TAFDEAIAELDTLNEDSYK
101	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	50.8	242	1074.12	2146.22	2143.98	91.19	6.40E-07	TAFDEAIAELDTLNEDSYK
102	gi|41151982	major vault protein [Danio rerio]	55	863	1019.64	2037.26	2036.88	108.34	1.20E-08	AVEAFIDTQGDEAEEEER
					713.28	2136.80	2137.12	52.17	0.005	IPPHHYIHVLDQNTNIAR
103	gi|18859505	alpha-tropomyosin [Danio rerio]	47.2	284	623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
					770.52	2308.54	2307.18	67.97	0.00013	SVAKLEKTIDDLEDELYAQK
104	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	75.9	141	565.40	1128.79	1128.63	54.53	0.0041	RLDDLASAIR
					1105.94	3314.79	3313.73	63.69	0.00023	EIYPYVIQELRPTLDELGIATPEE
					1693.85	3385.68	3384.77	50.22	0.0049	EIYPYVIQELRPTLDELGIATPEE
105	gi|46358344	isocitrate dehydrogenase 3 (NAD+) alpha [Danio rerio]	34.5	365	1251.50	2500.99	2501.23	87.86	1.20E-06	ENTEGEYSGIEHVIVDGVVQSIK
106	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	66.9	248	1458.87	1457.86	1457.72	49.98	0.01	HVFGESDELIGQK
					801.94	1601.87	1601.88	47.81	0.017	VVLAYEPVWAIGTGK
					808.26	1614.50	1613.82	63.83	0.0004	RHVFGESDELIGQK
107	gi|41054770	WD repeat domain 1 [Danio rerio]	63	606	1296.44	2590.87	2589.21	86.27	1.60E-06	AHDGGIYAVSWSPDSTQLISAS
108	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	55.7	433	1147.92	2293.83	2295.13	40.61	0.067	SGETEDTFIADLVVGLCTGQIK
					1008.31	3021.90	3020.58	67.54	0.00011	HIADLAGNPEVILPVPAFNVING
109	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	43.9	164	686.49	1370.97	1370.73	87.95	1.60E-06	VVDGLDVVDAIEK
110	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprote	65.5	661	738.51	1475.00	1473.75	73.92	4.10E-05	KHTLSYVDPETGK
					889.00	2663.98	2662.42	46.42	0.015	GVGPDKDHVHLQLHHLPPQQL
111	gi|27545193	creatine kinase, brain [Danio rerio]	38.3	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR
					894.58	1787.15	1785.94	47.27	0.018	GIESLSVEALGALDGDLK
					990.39	1978.76	1977.94	66.42	0.00019	GTGGVDTAAVGGVFDISNADR
112	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	38.1	134	1339.12	2676.23	2675.32	66.46	0.00016	ITFTNEEFLVTLPDGSEIHFPNR
113	gi|56118753	troponin C, slow [Danio rerio]	32.3	161	602.40	1202.78	1202.58	47.42	0.02	AAAEQLTDEQK
					603.43	1204.85	1202.58	56.44	0.0025	AAAEQLTDEQK
					684.11	1366.20	1364.65	62.15	0.00058	NADGYIDLDELK
114	gi|58801524	LIM domain containing preferred translocation partner in	55.2	556	732.30	2193.86	2193.06	41.09	0.064	AEPSHHPAPTPSQGYQPAPPK
					1398.18	2794.34	2793.39	116.45	1.50E-09	SSLDAEIDSLTSILADLESSSPY

115	gi|47087349	coagulation factor II [Danio rerio]	44.3	524	674.22	1346.42	1345.80	77.10	2.10E-05	IVAIDEIIVHPK
					674.76	1347.50	1345.80	80.64	8.90E-06	IVAIDEIIVHPK
116	gi|41055546	hypothetical protein LOC393186 [Danio rerio]	59.8	281	973.05	1944.09	1942.85	73.38	3.90E-05	SQNGVEFNTSGSTNTDTGK
					1044.26	2086.51	2086.15	55.93	0.0021	VNNASLIGIGYTQSLRPGVK
117	gi|62955483	NADH dehydrogenase (ubiquinone) Fe-S protein 3, (NAD	37.3	255	1179.48	2356.94	2358.17	88.22	1.20E-06	DPVTHSQLSEFGEYVAEILPK
					1410.75	2819.48	2817.31	58.87	0.00083	TYTDELTPLDSSVPVFQASNWY
118	gi|41055855	aldehyde dehydrogenase 4 family, member A1 [Danio rer	39.2	556	1044.85	2087.69	2086.97	84.57	2.90E-06	VGDPVEDFSTFFSAVIDDK
119	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	56.6	357	1315.03	2628.05	2626.36	76.50	1.50E-05	QQYVDLISSLVGAEAPAVAAQPT
120	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	45.6	757	978.83	1955.65	1955.09	75.99	2.20E-05	KPETVKPLQISSLSEATK
					1066.23	2130.45	2130.11	36.16	0.21	AELDALAALTAGLEETLGSSAK
					732.09	2193.24	2192.18	53.19	0.0039	VTLQAIGAQEAALTAIAAHTDK
121	gi|40538764	ceruloplasmin [Danio rerio]	36.8	1087	828.53	1655.05	1654.78	117.55	1.70E-09	LVDDIVSDTFFDNR
122	gi|41282194	glutamate dehydrogenase 1 [Danio rerio]	44.1	542	785.85	1569.68	1568.77	91.97	6.30E-07	IIAEGANGPTTPDADK
123	gi|189535578	PREDICTED: fetuin B [Danio rerio]	42	498	1117.51	2233.01	2233.01	59.36	0.00092	KDETHEHDHEIVLDHDHK
					808.91	2423.70	2423.12	39.35	0.086	HLLGGEVDHSHTTGSSTAHDHT
124	gi|51972166	radixin isoform 1 [Danio rerio]	41.3	579	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
					1683.89	1682.88	1682.85	73.28	4.40E-05	NQEHLATELAELTSK
125	gi|189522028	PREDICTED: similar to myomesin [Danio rerio]	70.7	923	1302.32	3903.94	3901.05	74.82	1.30E-05	KGASAPWTGQIIVTEEEPVEGV
126	gi|41055654	hypothetical protein LOC393165 isoform 2 [Danio rerio]	65.6	628	1025.69	2049.36	2049.07	51.32	0.0062	KPVLETEVNHVSPLSDASK
					1079.64	2157.27	2155.09	92.58	4.70E-07	ILAQITGTENDQAQESRPGK
127	gi|18859045	mitochondrial carrier homolog 2 [Danio rerio]	40.7	300	824.74	1647.47	1647.80	48.34	0.015	SDEGSLQQVINETTK
					843.43	1684.84	1684.96	56.86	0.002	VLVQVGHEPLAPTLGR
128	gi|18859423	spectrin, beta, erythrocytic [Danio rerio]	38.1	2357	945.35	1888.69	1887.93	76.88	1.80E-05	KKHDAIETDIAAYEER
					733.65	2197.91	2197.09	36.78	0.18	IIDELIEGGHSESATLAEWK
129	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio rerio	46.7	199	667.37	1332.73	1332.69	69.63	0.00011	KYTLPPGVDSEK
					921.78	1841.54	1839.94	54.79	0.003	ISLDVNHFSPEELNVK
130	gi|41152448	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	56.9	355	1228.12	2454.22	2454.31	90.23	6.90E-07	LLQYSDAVEHLLTTGQGVILER
131	gi|116004537	hypothetical protein LOC564694 [Danio rerio]	36	381	754.73	1507.44	1506.70	57.40	0.0017	GGDDLDPNYVLSSR
					990.39	1978.76	1977.94	66.42	0.00019	GTGGVDTAAVGGVFDISNADR
132	gi|41055718	fumarate hydratase precursor [Danio rerio]	49.1	509	1077.99	2153.96	2153.18	63.34	0.00039	EVHEVLLPGLQTLHDALAAK
					1251.93	2501.85	2501.26	77.23	1.40E-05	THTQDAVPLSLGQEFGGYVQQ
133	gi|51571925	hypothetical protein LOC445486 [Danio rerio]	43.8	194	902.31	1802.60	1800.95	59.54	0.001	INSELPVDEVFAIVEK
					965.71	1929.41	1929.05	73.55	3.90E-05	KINSELPVDEVFAIVEK
134	gi|80751141	solute carrier family 8 (sodium/calcium exchanger), memb	33.3	974	985.15	1968.29	1968.04	63.87	0.00035	EGVILPIWTPVNPSFGDK
					1212.35	2422.69	2422.06	42.42	0.043	GGGEDFEDTHGVLEFQNDEISK
135	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	61.5	226	724.13	1446.24	1445.78	60.12	0.001	VIFEAETEKPGVK
					881.73	2642.17	2641.29	65.66	0.00019	SPDPAAVEHKPEESKPEESKPE
136	gi|41387118	ubiquinol-cytochrome c reductase core I protein [Danio re	61	474	943.51	1885.00	1882.98	79.05	1.10E-05	MVLATAGGVSHDEVVSLAK
					1307.43	2612.84	2610.26	57.63	0.0012	KHPQSALEQAVESMGGHLNAYT
137	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	49.3	682	622.59	1243.16	1240.68	51.93	0.0072	LQVAGEITTGPR
					1325.61	1324.60	1324.74	85.06	3.00E-06	TVHLLAGVADTTK
138	gi|189526930	PREDICTED: similar to c-Cbl associated protein [Danio r	35.6	1015	918.74	1835.46	1834.94	67.53	0.00016	HAGLVVTHQQFITNDR
139	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	49.7	523	790.64	1579.27	1577.76	97.12	1.80E-07	YDVQVQIENVEDK
140	gi|136429	Trypsin precursor	63.4	232	737.73	2210.15	2210.10	70.33	7.50E-05	LGEHNIDVLEGNEQFINAAK
141	gi|21426835	glucose phosphate isomerase a [Danio rerio]	25	553	593.18	1184.34	1183.63	45.16	0.033	HFVALSTNAPK
					1127.48	3379.42	3376.65	58.76	0.00069	VNYHTGPIVWGEPGTNGQHAF
142	gi|51011067	pyruvate kinase, muscle, b [Danio rerio]	54	530	904.59	1807.16	1806.98	63.88	0.00038	KGVNLPGANVDLPAVSEK
					942.87	1883.72	1882.90	67.23	0.00016	LNFSHGTHEYHAETIK
143	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	41.1	679	553.22	1104.42	1102.64	47.20	0.022	YKDVVVGVPK
					1153.05	2304.08	2303.11	75.64	2.10E-05	SFGAEPLEVHIAESGEGVGGYA
144	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	36.8	380	691.30	1380.58	1379.71	71.30	7.20E-05	FFEAAVGEAKPSK
					1079.82	2157.62	2155.10	42.96	0.043	YPDLPGLEDLGITPASIEQK

145	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	76.5	575	814.72	2441.14	2439.35	53.75	0.0031	TALLDAAGVASLLSTAEAVVTEI
					942.68	2825.01	2825.53	73.70	2.70E-05	TALLDAAGVASLLSTAEAVVTEI
146	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio reri	63.9	133	749.63	1497.24	1496.63	69.94	9.50E-05	LGEEFDETTADDR
147	gi|41054603	actinin alpha 4 [Danio rerio]	36.6	901	826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
148	gi|56118264	actinin alpha 3 [Danio rerio]	31.4	896	826.12	1650.22	1648.81	71.27	7.40E-05	KAGTQIENIEEDFR
149	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	45.4	306	700.18	1398.35	1398.75	68.66	0.00013	REEEANLLGQIK
150	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dan	63.5	731	1570.82	3139.63	3139.56	75.20	1.70E-05	DSFIVYQGHHGDVGAPIADVILP
151	gi|41056085	keratin 8 [Danio rerio]	26	520	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
					744.37	1486.73	1485.71	41.88	0.065	ANLENQIAEAEER
					1009.39	2016.76	2017.16	59.54	0.00094	SLLAPLNLEIDPNIQIVR
152	gi|66472610	hypothetical protein LOC553595 [Danio rerio]	44.4	275	1284.63	2567.24	2566.31	88.00	1.10E-06	STPTDLVTEADHQVEELIISTLR
153	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filami	55.7	2523	824.65	1647.29	1645.89	49.61	0.011	VHGPGLQSGITNKPNK
					1207.46	2412.90	2411.15	54.31	0.0028	EGPYSINVLYADEEIPQSPYK
					1178.80	3533.36	3531.58	47.45	0.0089	DLGDGTYQVEYTPYEEGTHSV
154	gi|47085999	hypothetical protein LOC406484 [Danio rerio]	26.9	361	722.75	1443.49	1443.76	85.59	2.80E-06	GQAFLDDLILDPK
155	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	41.2	245	782.16	1562.31	1560.73	50.70	0.0084	AVTEGDIELSNEER
					1073.02	2144.03	2143.98	56.16	0.002	TAFDEAIAELDSLNEESYK
156	gi|21426837	glucose phosphate isomerase b [Danio rerio]	40.9	553	1127.48	3379.42	3376.65	58.76	0.00069	VNYHTGPIVWGEPGTNGQHAF
157	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	78.4	116	839.77	1677.52	1677.88	62.40	0.00057	TTGLVGLAVSQNPHER
158	gi|117606266	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	50.3	991	789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
159	gi|189519111	PREDICTED: similar to ATPase, Ca++ transporting, fast	50	1005	789.18	1576.34	1573.86	86.39	2.30E-06	VDQSILTGESVSVIK
160	gi|58801528	SET translocation (myeloid leukemia-associated) A [Dani	22.7	269	1098.65	2195.28	2194.01	56.17	0.002	EQQEAIEHIDEVQNEIDR
161	gi|58801526	SET translocation (myeloid leukemia-associated) B [Dani	18.5	275	1098.65	2195.28	2194.01	56.17	0.002	EQQEAIEHIDEVQNEIDR
162	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [	53.7	709	825.71	1649.40	1649.84	62.28	0.00059	TVAVHSDVDSSAVHVK
					945.77	1889.53	1887.95	48.08	0.014	LTGAQAVHPGYGFLSENK
163	gi|50344731	fibrinogen alpha chain [Danio rerio]	64.5	684	677.11	1352.21	1350.70	80.92	7.60E-06	LGISDSEFLTAAK
164	gi|54400460	fibulin 5 [Danio rerio]	40.3	477	1111.43	2220.84	2220.00	80.84	6.70E-06	NSPLPYPEASYPEEPYPDR
165	gi|55925387	carnitine palmitoyltransferase II [Danio rerio]	46.1	668	1127.33	2252.65	2252.11	56.20	0.0019	YLAAQRPLLNDEQYSNTEK
					1193.60	2385.19	2384.18	44.83	0.025	DTTEKPLVGPGSQPASVDSSS
166	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	56.2	283	1045.96	2089.91	2088.16	80.68	7.30E-06	VNNSSLVGLGYTQTLKPGIK
167	gi|52219158	aquaporin 8 [Danio rerio]	20.4	260	1057.84	2113.66	2113.97	41.95	0.054	SELFTVATGDGGDNHQNQPK
					1058.64	2115.26	2113.97	55.18	0.0026	SELFTVATGDGGDNHQNQPK
168	gi|113679439	hypothetical protein LOC751638 [Danio rerio]	55.6	126	637.26	1272.51	1272.68	49.46	0.012	GQDPYSILRPK
					468.43	1402.27	1400.78	36.47	0.23	KGQDPYSILRPK
					1471.59	1470.58	1470.70	64.81	0.00032	GIPTDDEQAAGLER
169	gi|68362804	PREDICTED: similar to Histone H4 replacement CG337	55.3	103	495.60	989.18	988.57	47.01	0.025	VFLENVIR
					591.57	1181.13	1179.61	59.87	0.001	ISGLIYEETR
170	gi|41055939	sorting and assembly machinery component 50 homolog	52	469	997.86	1993.70	1992.02	64.82	0.00028	TKEDILTYEIADVFHAK
171	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reri	57.5	858	703.72	1405.42	1404.80	77.74	1.70E-05	TFAQLILDPIFK
172	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	55.7	255	827.80	1653.58	1653.91	71.00	7.40E-05	ALPFWNEVIVPEIK
173	gi|18858399	cadherin 2, neuronal [Danio rerio]	26.2	783	1148.25	3441.71	3440.82	76.41	1.10E-05	YSVTGPGADQNPTGLFIIDPISG
174	gi|189530625	PREDICTED: similar to spectrin repeat containing, nucle	41.4	8621	550.38	1098.74	1097.66	63.31	0.00054	QLADAIAKLR
175	gi|50540420	branched chain aminotransferase 2, mitochondrial [Dani	31.3	415	900.83	1799.64	1799.02	46.62	0.02	SSVLKPKPDPSTLVFGK
176	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	81.9	238	778.40	1554.79	1553.87	76.16	2.40E-05	KGGIVAIDNVLWGGR
177	gi|189538855	PREDICTED: similar to sarcalumenin [Danio rerio]	23.4	882	731.19	1460.36	1459.77	63.21	0.00049	VTFVDTPGIIENR
					783.21	1564.40	1564.67	41.58	0.068	SEELSQEEAASEEK
178	gi|189525434	PREDICTED: im:7157373 [Danio rerio]	55	545	1430.98	2859.95	2859.32	74.75	2.10E-05	SAAAPPKEEAPPANAPDGDAP
179	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio	67.4	172	565.40	1128.79	1127.64	45.39	0.034	RLNDLASAIR
					1106.47	3316.39	3314.75	67.87	8.70E-05	EIYPYVIQELKPTLQELGISTPEE
180	gi|123706335	hypothetical protein LOC791136 [Danio rerio]	50.5	313	1223.67	2445.33	2443.21	48.42	0.011	QILANPFQDYVNTHPVSHAHR
					1296.63	2591.25	2589.22	42.49	0.038	GTKDDPIEPQQAIPDAQSFEFE
181	gi|168229163	cysteine-rich protein 2 [Danio rerio]	76.2	206	990.03	2967.06	2968.41	48.11	0.0093	TLTAGGHAEHDGKPYCHKPCY

					999.96	2996.84	2996.41	42.81	0.031	TLAAGSHAEHDGQPYCHKPCY
182	gi|62122813	3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]	49	382	897.46	1792.91	1790.92	71.86	6.20E-05	WKPSTLAGVSEQFVDK
183	gi|52219190	hypothetical protein LOC447942 [Danio rerio]	57.3	103	1167.53	3499.56	3500.62	52.81	0.0025	TKPWPWGDGNHSLFHNPHTNA
184	gi|189517274	PREDICTED: hypothetical protein [Danio rerio]	33	797	602.97	1203.92	1201.66	58.26	0.0016	MRNLTEGILR
185	gi|18858281	apolipoprotein A-I [Danio rerio]	42	262	822.99	1643.96	1643.73	71.47	6.90E-05	ALDNLDGTDYEQYK
186	gi|50540186	hypothetical protein LOC436833 [Danio rerio]	32.3	229	1079.82	2157.63	2156.16	60.52	0.00075	AGLTASEVDELLTLATSQPIK
187	gi|150378483	heat shock protein, alpha-crystallin-related, b11 [Danio re	47.8	205	1113.16	2224.31	2223.99	70.86	6.80E-05	NPALQNSEPENQAVEAEAAEN
188	gi|41393141	tropomyosin 3 [Danio rerio]	59.3	248	623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
189	gi|49274617	tropomyosin 1 alpha [Danio rerio]	40.8	284	623.18	1244.35	1242.65	53.21	0.0055	IQLVEEELDR
					700.61	1399.21	1398.75	51.35	0.0072	RIQLVEEELDR
190	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	38.5	104	745.36	1488.71	1487.65	60.28	0.00096	TGQAEGFSYTDANK
191	gi|57528846	hypothetical protein LOC445255 [Danio rerio]	50.2	207	770.14	1538.26	1537.87	69.95	9.50E-05	AEEDKIPLLLVGNK
192	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	47.5	484	904.58	1807.15	1806.90	69.69	0.0001	HEVISQGGVTHPIDYR
193	gi|189517050	PREDICTED: glycine C-acetyltransferase [Danio rerio]	69.4	458	785.77	1569.52	1568.74	69.25	0.00012	VQISAAHTDEDIDR
194	gi|114326248	elastin b [Danio rerio]	16.6	2054	888.60	1775.19	1772.86	68.41	0.00015	SYGGAGALGGAGQGGIGGGPG
195	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	43.1	1368	1212.77	2423.53	2422.19	68.39	0.00011	GQNHLEEVELAFPQNVIEGSGR
196	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	39.7	1754	575.38	1723.12	1721.89	38.26	0.14	KQELEEILHDLEAR
					958.30	1914.58	1913.91	68.34	0.00013	HSQAFDELNEQLEQVK
197	gi|41055614	hypothetical protein LOC393478 [Danio rerio]	15.1	86	1465.66	1464.65	1464.65	41.10	0.076	WDSQIEDGSFPGK
					733.65	1465.28	1464.65	61.22	0.00072	WDSQIEDGSFPGK
198	gi|41054571	citrate synthase [Danio rerio]	24.6	468	564.10	1126.18	1126.65	40.48	0.094	ALGFPLERPK
					881.85	1761.69	1761.88	63.55	0.00043	GLVYETSVLDPDEGIR
199	gi|27545305	laminin, gamma 1 [Danio rerio]	55.8	1593	1175.40	2348.79	2346.18	66.83	0.00016	LLDLQNLIDSLDNTETTVSDK
200	gi|55742559	Rho GDP dissociation inhibitor (GDI) alpha [Danio rerio]	45.8	203	960.67	1919.32	1916.90	52.99	0.0044	SLQEIQELDQDDESLR
					1023.83	2045.64	2044.99	51.22	0.0065	SLQEIQELDQDDESLRK
201	gi|121583986	hypothetical protein LOC557972 [Danio rerio]	35.6	562	1071.25	2140.48	2138.14	66.20	0.0002	TFLVIPELAQELHVWTDK
202	gi|41152334	ATP synthase, H+ transporting, mitochondrial F0 comple	59.6	161	573.43	1144.85	1144.54	66.01	0.00029	IDAQEQEANK
203	gi|41053347	mitochondrial trifunctional protein, beta subunit [Danio re	48.8	471	710.16	1418.30	1415.77	65.85	0.00027	DQLLLGPTYATPK
204	gi|189522849	PREDICTED: similar to oxoglutarate (alpha-ketoglutarate	49	961	834.04	1666.06	1665.82	38.69	0.13	VITDDGPPAQNPSEVK
					1201.44	2400.87	2399.32	54.83	0.0025	NITLSLVANPSHLEAVNPVVQG
205	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	52.1	6009	579.12	1156.23	1155.65	54.20	0.0042	LKGDVDVSVPK
					1033.94	2065.86	2062.98	46.95	0.017	SDASLSGGIENQEGNLTFPK
206	gi|148596955	ATP synthase, H+ transporting, mitochondrial F0 comple	69	71	816.74	1631.46	1631.83	43.32	0.048	RYDNLKPIAEEER
					817.37	1632.73	1631.83	63.17	0.00049	RYDNLKPIAEEER
207	gi|189518755	PREDICTED: similar to malic enzyme 2, NAD(+)-depend	59.9	581	1093.78	2185.54	2184.23	53.23	0.004	SFLDAVNVIKPTAIIGVSGAGR
208	gi|41056175	programmed cell death 8 (apoptosis-inducing factor) [Da	43.4	751	736.65	1471.28	1471.66	64.47	0.00036	SAGLEVDSDFGGYR
209	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	62.3	697	1302.96	1301.95	1301.66	64.35	0.00039	SHIDELYANIK
210	gi|189526598	PREDICTED: similar to COASTER [Danio rerio]	54.5	916	657.73	1313.44	1312.78	53.00	0.0052	QAVALSLKEARK
211	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	45.7	606	1090.76	2179.50	2179.07	64.20	0.00031	GGENIYPAEIEQFLHTHPK
212	gi|189515773	PREDICTED: amylo-1, 6-glucosidase, 4-alpha-glucanotra	45.3	1532	894.83	1787.64	1787.00	63.95	0.00039	GLPALIQDHPHLHAIR
213	gi|41053732	aldehyde dehydrogenase 2 precursor [Danio rerio]	38.6	516	778.04	2331.08	2330.19	63.12	0.00038	VAFTGSTDVGHLIQQASSASNL
214	gi|189538766	PREDICTED: similar to mitogen-activated protein kinase-	32	535	778.04	2331.08	2330.19	63.12	0.00038	VAFTGSTDVGHLIQQASSASNL
215	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	52.3	329	865.98	1729.95	1729.95	62.94	0.00049	KGSLLIDSSTIDPAVSK
216	gi|47271384	cofilin 2, like [Danio rerio]	40.6	165	996.00	1989.98	1989.06	62.79	0.00044	KEDLVFIFWAPESAPLK
217	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	44.1	2633	1230.41	2458.81	2458.19	61.14	0.00055	HAINQEINAYNTPAQFGLEGSG
218	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	31.2	2113	653.09	1304.16	1303.77	57.14	0.002	RCLIEIFGILK
219	gi|189532434	PREDICTED: im:7160733 [Danio rerio]	34.8	1248	653.09	1304.16	1303.77	57.14	0.002	RCLIEIFGILK
220	gi|125828659	PREDICTED: hypothetical protein LOC449551 [Danio re	38.1	126	1270.39	2538.76	2538.31	62.53	0.0004	LVVNDGPDGGQSVYHIHIHVLG
221	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Da	35.1	2115	1419.48	2836.94	2835.44	62.39	0.00037	GAFTPSPLDPASTSDSHIASLSI
222	gi|54400426	ATP synthase, H+ transporting, mitochondrial F0 comple	68.7	252	764.44	1526.87	1526.78	52.48	0.0055	LDYQVELQNLHR
223	gi|113678245	hypothetical protein LOC558738 [Danio rerio]	62.2	111	846.23	1690.45	1689.84	61.33	0.00075	IEFSPLDAWNSGVQK

224	gi|68444865	PREDICTED: dodecenoyl-Coenzyme A delta isomerase	39.5	301	663.69	1325.37	1325.71	52.34	0.0058	IGLVDELVPEDK
225	gi|41152175	ribosomal protein S7 [Danio rerio]	35.1	194	733.47	1464.93	1464.94	60.08	0.00094	KAIIIFVPVPQLK
226	gi|189516256	PREDICTED: similar to phosphofructokinase, platelet [Da	49.4	782	707.25	1412.48	1411.69	59.91	0.00099	DLQSNVEHLTEK
227	gi|57525624	malic enzyme 2, NAD(+)-dependent, mitochondrial [Dani	56.5	581	1093.78	2185.54	2184.23	53.23	0.004	SFLDAVNVIKPTAIIGVSGAGR
228	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	48.7	448	780.37	1558.73	1557.89	48.92	0.013	LLEVIDGHIPLPSR
					920.26	1838.50	1836.96	44.61	0.031	DKPHLNIGTIGHVDHGK
229	gi|52219010	EH-domain containing 3, like [Danio rerio]	35.2	532	853.20	1704.38	1703.91	58.84	0.0013	KKDPELFQTVSDGLK
230	gi|125854185	PREDICTED: hypothetical protein [Danio rerio]	15.7	645	672.86	1343.71	1346.62	48.88	0.014	EEEEEQLKADK
231	gi|61806608	hypothetical protein LOC541390 [Danio rerio]	60	110	1161.83	2321.64	2319.22	58.56	0.0011	NSVWLGLLGWANAVLHNSVNR
232	gi|74315945	hypothetical protein LOC613246 [Danio rerio]	51.9	422	1048.40	2094.79	2092.98	58.42	0.0012	ALVGNEASEELQSADGNPHR
233	gi|125842393	PREDICTED: zgc:103738 [Danio rerio]	57.1	77	987.76	2960.25	2961.35	52.44	0.0035	TLSAGSHAEHEGKPYCNNPCY
234	gi|47086875	glutamate dehydrogenase 1a [Danio rerio]	33.5	544	862.40	1722.79	1722.87	57.43	0.0018	HGGAIPIVPTSDFQER
235	gi|47551331	hypothetical protein LOC407980 [Danio rerio]	52.3	331	978.50	1954.99	1952.12	57.82	0.0014	EIFLSQPILLELEAPLK
236	gi|123858772	protein phosphatase 1, catalytic subunit, beta [Danio reri	21.4	327	978.50	1954.99	1952.12	57.82	0.0014	EIFLSQPILLELEAPLK
237	gi|189518709	PREDICTED: wu:fi22e08 [Danio rerio]	49.8	323	978.50	1954.99	1952.12	57.82	0.0014	EIFLSQPILLELEAPLK
238	gi|56693257	hypothetical protein LOC494050 [Danio rerio]	48.9	368	1035.13	3102.35	3100.58	51.88	0.0038	ILLDQGQEHTVETPHGVLHVTV
239	gi|47550715	heterogeneous nuclear ribonucleoprotein A0 [Danio rerio	28.3	314	843.62	1685.23	1683.72	57.64	0.0016	GFGFVHFEDNDSADK
240	gi|41056209	hypothetical protein LOC393532 [Danio rerio]	35.1	490	1012.59	2023.16	2022.00	56.97	0.0017	HILDTHGLDPHQATASGPR
241	gi|189532998	PREDICTED: similar to calmodulin 2 [Danio rerio]	21.7	152	923.68	1845.34	1843.88	56.77	0.0019	EAFSLFDKDGDGTITTK
242	gi|41053611	hypothetical protein LOC393828 [Danio rerio]	33.8	213	1200.94	2399.87	2399.16	56.18	0.0018	SYHSPWEEAIINDPTLADTLK
243	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio r	70.3	333	713.59	1425.17	1424.81	56.10	0.0024	LDVAPISDIIEIK
244	gi|41053746	RNA binding protein with multiple splicing 2 [Danio rerio]	39.5	200	772.69	1543.36	1542.88	56.08	0.0025	TLFVSGLPTDIKPR
245	gi|41393119	valosin containing protein [Danio rerio]	56.1	806	905.89	1809.76	1809.99	55.96	0.0023	NAPAIIFIDELDAIAPK
246	gi|56790313	homeo box B9a [Danio rerio]	20.8	255	710.16	1418.30	1416.74	55.87	0.0027	MEPLLGHLGEPPK
247	gi|44917595	alcohol dehydrogenase 8b [Danio rerio]	70.7	376	966.09	2895.25	2894.48	55.82	0.0016	GFPTILGHEAAGVVESVGPGVT
248	gi|154707842	methylmalonyl Coenzyme A mutase [Danio rerio]	42.1	757	786.15	1570.29	1568.84	47.95	0.016	NTQIIIQEESGIPK
					976.35	1950.69	1948.02	44.18	0.032	TPEGISIKPVYTQTDTAK
249	gi|62955301	hypothetical protein LOC550355 [Danio rerio]	41.6	255	925.67	1849.32	1848.92	55.56	0.0025	VLPGVDVTVGHEEEQGGK
250	gi|56693297	hypothetical protein LOC494070 [Danio rerio]	58.2	182	952.62	1903.22	1902.91	55.04	0.0027	AKEELEQELADKEDEK
251	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple	66	209	920.66	1839.30	1838.03	54.42	0.0033	VSPITINLINVLSENGR
252	gi|80751159	hypothetical protein LOC641325 [Danio rerio]	43.8	313	1296.63	2591.25	2589.22	42.49	0.038	GTKDDPIEPQQAIPDAQSFEFE
253	gi|50539806	hypothetical protein LOC436642 [Danio rerio]	27.6	323	976.35	1950.69	1950.01	53.72	0.0036	ALESAYGSEKPSLTSAAIR
254	gi|66472400	NADH dehydrogenase (ubiquinone) Fe-S protein 4, (NA	48.2	168	827.09	1652.17	1650.88	53.50	0.0042	LDISTLTGVPEEHIK
255	gi|125995404	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 [Danio rerio]	52	709	695.11	2082.30	2082.02	53.31	0.0038	HVINFDLPSDIEEYVHR
256	gi|41282082	pl10 [Danio rerio]	50.6	688	695.11	2082.30	2082.02	53.31	0.0038	HVINFDLPSDIEEYVHR
257	gi|55742591	telomerase binding protein, p23 [Danio rerio]	45.3	159	974.86	1947.70	1944.92	53.01	0.0043	HHNEVDLLEAIDPNDSK
258	gi|55926092	heat shock 10kD protein 1 (chaperonin 10) [Danio rerio]	34	100	770.78	1539.54	1539.86	52.40	0.0054	VLQATVVAVGPGSTNK
259	gi|52218912	enoyl Coenzyme A hydratase, short chain, 1, mitochondr	36.1	291	1056.69	2111.36	2110.12	52.29	0.005	AQFGQPEILLGTIPGAGGTQR
260	gi|189532637	PREDICTED: similar to Calcium-binding mitochondrial ca	45.1	774	622.59	1243.16	1240.68	51.93	0.0072	LQVAGEITTGPR
261	gi|30410758	keratin 18 [Danio rerio]	54.5	431	1000.00	1997.99	1998.02	51.86	0.0055	GNIQHQTQEYEALLNIK
262	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	48	298	617.63	1233.24	1232.68	51.16	0.0084	DFLAGGIAAAISK
263	gi|167621510	hypothetical protein LOC100136853 [Danio rerio]	28.5	424	654.89	1307.76	1306.71	46.23	0.023	KNSSSLKSTIDK
					655.46	1308.91	1306.71	47.37	0.018	KNSSSLKSTIDK
264	gi|68357456	PREDICTED: similar to mCG1046517 [Danio rerio]	51.4	1561	766.34	1530.67	1530.94	47.44	0.018	LLEKSKELAFILK
265	gi|59933260	cardiomyopathy associated 1 [Danio rerio]	55	2297	915.95	1829.89	1827.92	51.47	0.0066	SHTWLFETQPLDNIK
266	gi|53292609	clathrin, heavy polypeptide a (Hc) [Danio rerio]	35	1680	1170.75	2339.48	2338.23	51.37	0.0057	ISGETIFVTAPHDATAGIIGVNR
267	gi|57770449	hypothetical protein LOC393165 isoform 1 [Danio rerio]	52.3	197	1025.69	2049.36	2049.07	51.32	0.0062	KPVLETEVNHVSPLSDASK
268	gi|50344970	hypothetical protein LOC415247 [Danio rerio]	41.4	382	604.82	1207.63	1205.69	50.73	0.0088	HNNLDLVIIR
269	gi|189523865	PREDICTED: myosin 1b-like 2 [Danio rerio]	44.3	1078	752.61	2254.79	2255.13	46.51	0.018	SLRHQDKDQCILITGESGAGK
270	gi|18858981	lamin b2 [Danio rerio]	64.5	583	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
271	gi|125849603	PREDICTED: similar to keratin 8 [Danio rerio]	41.1	438	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR
272	gi|189523135	PREDICTED: similar to type II keratin E1 [Danio rerio]	27.3	311	545.21	1088.41	1087.55	50.59	0.011	KLLEGEEDR

273	gi|157743314	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5	33.3	186	866.17	1730.33	1729.87	50.53	0.0085	EKGDGPWFQIPTIDK
274	gi|37497110	ribophorin I [Danio rerio]	47	598	813.09	2436.23	2435.30	50.20	0.0069	VETVFSHVLKPFPTHITQAER
275	gi|189516116	PREDICTED: similar to ribophorin I [Danio rerio]	29.3	505	813.09	2436.23	2435.30	50.20	0.0069	VETVFSHVLKPFPTHITQAER
276	gi|62955727	NADH dehydrogenase (ubiquinone) 1 beta subcomplex,	22.3	175	814.41	1626.81	1625.79	50.13	0.0093	EVQQLQSETPADGPK
277	gi|54261767	succinate-CoA ligase, ADP-forming, beta subunit [Danio	58.2	466	1294.16	2586.30	2585.29	50.09	0.0067	LHGGTPANFLDVGGGATAQQV
278	gi|68379126	PREDICTED: hypothetical protein LOC767664 [Danio rer	80.2	81	1494.87	1493.86	1493.82	50.07	0.0093	IFLEDNGLPVHIK
279	gi|162138946	hypothetical protein LOC562705 [Danio rerio]	52.8	307	549.17	1096.33	1094.59	49.23	0.012	KYGSVTVWR
280	gi|112363126	dynein, cytoplasmic 1, heavy chain 1 [Danio rerio]	36	4643	843.40	2527.16	2526.32	49.04	0.0088	VLRPQVSAVPQHAQGESAEPA
281	gi|189533132	PREDICTED: A kinase anchor protein 12 [Danio rerio]	46.4	1533	1075.96	3224.86	3224.59	48.92	0.0074	QSSVIVQEIIQNVVENFAEAHGE
282	gi|18859107	non-metastatic cells 2, protein (NM23B) expressed in [Da	62.7	153	1088.81	3263.40	3261.62	48.41	0.0082	NIIHGSDSVDSANTEISLWFKPE
283	gi|47087201	RIO kinase 2 [Danio rerio]	24	512	896.26	1790.51	1790.03	47.93	0.016	NHEIVPVSLIASIASLK
284	gi|189545630	PREDICTED: hypothetical protein [Danio rerio]	31.3	403	1429.65	1428.64	1427.78	47.74	0.017	LYEVFIKNFQK
285	gi|47086529	hypothetical protein LOC336641 [Danio rerio]	40.2	184	891.22	1780.42	1777.96	47.58	0.017	GLDVDSLVIEHIQVNK
286	gi|160333682	heat shock protein 8 [Danio rerio]	43	649	1131.27	2260.52	2259.14	47.51	0.014	SINPDEAVAYGAAVQAAILSGDK
287	gi|130494136	ubiquitin-conjugating enzyme E2L 3, like [Danio rerio]	58.4	190	828.62	2482.83	2482.32	47.47	0.013	TDQVIQSLIALVNDPQPEHPLR
288	gi|57222259	talin 1 [Danio rerio]	52.9	2538	1059.58	3175.71	3174.57	47.34	0.011	EAVDDLGSTLAEVASAAGAVGG
289	gi|55925219	sorting and assembly machinery component 50 homolog	48.8	469	768.63	1535.24	1533.83	47.24	0.018	DVVVQHVNIEGLGR
290	gi|51467931	enolase 2 [Danio rerio]	61.5	434	1147.92	2293.83	2295.13	40.61	0.067	SGETEDTFIADLVVGLCTGQIK
					1008.90	3023.68	3024.58	36.03	0.15	HIADLAGNTELVLPVPAFNVING
291	gi|47086623	monocarboxylate transporter 4 [Danio rerio]	65	508	946.72	1891.42	1889.91	47.08	0.017	ELESIEVDSIEVENASK
292	gi|71892458	villin 2 [Danio rerio]	45.6	583	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
293	gi|189527553	PREDICTED: hypothetical protein LOC553434 [Danio rer	37.5	568	481.06	960.10	958.59	46.63	0.028	FVIKPIDK
294	gi|189519969	PREDICTED: myosin, heavy polypeptide 10, non-muscle	41.9	1973	580.54	1738.58	1737.89	46.55	0.021	KQELEEILHDLESR
295	gi|189519965	PREDICTED: similar to nonmuscle myosin heavy chain [	40.6	1857	580.54	1738.58	1737.89	46.55	0.021	KQELEEILHDLESR
296	gi|189522138	PREDICTED: similar to paxillin [Danio rerio]	43.6	527	1147.86	2293.70	2294.99	42.47	0.044	TWHPEHFVCTHCQEEIGSR
297	gi|61651682	fibronectin 1b [Danio rerio]	47.3	2408	806.73	2417.17	2416.31	46.22	0.018	SAPLVGTATTQLISGLPSLPSHG
298	gi|50539996	peroxiredoxin 2 [Danio rerio]	69.5	197	1318.69	2635.36	2634.36	36.61	0.15	IGVELIAASTDSHFSHLAWINTP
299	gi|113678121	ATPase inhibitory factor 1-like [Danio rerio]	43	107	655.66	1309.30	1308.60	46.03	0.024	HHQEEIDHHK
300	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	33.1	308	550.57	1099.13	1098.61	44.93	0.037	QLADALKANR
301	gi|189523776	PREDICTED: hypothetical protein LOC798920 isoform 1	80	265	685.11	1368.20	1367.61	45.43	0.027	TRMYNTQDDPK
302	gi|50233897	FLJ12716-like protein [Danio rerio]	39.9	1132	596.22	1190.42	1187.63	45.26	0.034	TAYSLVHELR
303	gi|189525785	PREDICTED: similar to AT rich interactive domain 5B (M	44.6	935	1080.49	1079.48	1077.58	36.93	0.21	LGGYEVITAR
					673.32	1344.62	1344.72	45.14	0.032	KQEGSVQESIIK
304	gi|61806508	signal peptidase complex subunit 2 homolog [Danio rerio	54.2	201	650.50	1298.98	1299.73	45.04	0.032	AARNGKNSILEK
305	gi|189532951	PREDICTED: hypothetical protein [Danio rerio]	41.1	570	1001.67	2001.32	2000.01	44.93	0.027	YVIDTSDVVTNYKELNK
306	gi|189523571	PREDICTED: similar to mcf.2 transforming sequence-like	44.3	929	889.20	1776.39	1774.95	44.83	0.033	ESSPLFAADVITELKR
307	gi|189523947	PREDICTED: similar to Poly [ADP-ribose] polymerase 14	72	683	788.66	1575.31	1572.84	44.72	0.034	LLDCKDGLGLVLEK
308	gi|125850307	PREDICTED: CFH protein [Danio rerio]	64.8	751	1101.66	2201.30	2200.96	44.39	0.031	DDITYENVEPVSEASYADGK
309	gi|189528635	PREDICTED: similar to odorant receptor [Danio rerio]	27.9	305	797.72	1593.43	1591.89	44.35	0.035	LLTDLLSDTHLVPR
310	gi|125843259	PREDICTED: polymerase (RNA) III (DNA directed) polyp	41.8	1130	585.65	1169.29	1169.70	44.34	0.039	VILIQEQLSK
311	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	43.5	448	710.11	1418.20	1415.74	44.34	0.038	EALGAENIQSTKR
312	gi|189526852	PREDICTED: similar to G2/M-phase specific E3 ubiquitin	44.9	762	898.52	1795.02	1794.80	44.16	0.036	SNMEFAINNTHGFGKE
313	gi|189519924	PREDICTED: similar to Uncharacterized protein KIAA046	33.5	2775	664.74	1991.18	1992.00	44.09	0.033	VGEDSMSGDPLSKLPVPHK
314	gi|50344798	ubiquitin-conjugating enzyme E2L 3 [Danio rerio]	69.5	154	828.62	2482.83	2482.32	47.47	0.013	TDQVIQSLIALVNDPQPEHPLR
315	gi|189532554	PREDICTED: similar to karyopherin alpha 6 (importin alp	37.4	537	609.19	1216.37	1216.62	44.01	0.046	NKALNLEEMR
316	gi|47086477	ribosomal protein L13a [Danio rerio]	46.8	205	634.75	1267.49	1265.65	43.73	0.043	YQAITATLEEK
317	gi|189517523	PREDICTED: hypothetical protein [Danio rerio]	58.5	147	713.74	1425.46	1424.76	43.62	0.042	INVDEIGPQTLAR
318	gi|121583897	hypothetical protein LOC562692 [Danio rerio]	39.8	384	816.81	1631.60	1631.81	43.59	0.045	ELEEKVAMLEAENK
319	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	39.2	204	853.67	1705.32	1704.91	43.53	0.044	GATYGKPVHHGVNQIK
320	gi|41053395	glutamate oxaloacetate transaminase 2 [Danio rerio]	66.1	428	998.97	1995.92	1994.03	41.92	0.054	YFIEQGHNILLSQSFAK
321	gi|50539832	lysyl-tRNA synthetase [Danio rerio]	37.2	602	750.82	2249.44	2247.14	43.46	0.036	YNHLQPGDHLTDVVLNLSGR
322	gi|52218992	hypothetical protein LOC447834 [Danio rerio]	52.8	248	662.36	1322.70	1321.71	43.45	0.044	TLLGGGGVDGAIHR

323	gi|189536881	PREDICTED: hypothetical protein LOC402880 [Danio re	26.6	173	684.43	1366.84	1367.74	43.41	0.044	LDTPLPDVPFVR
324	gi|189541652	PREDICTED: similar to Myosin-3 (Myosin heavy chain 3)	52.7	882	659.27	1316.53	1315.65	43.35	0.049	ELELELDAEQK
325	gi|52219050	hypothetical protein LOC447859 [Danio rerio]	61.6	617	928.92	2783.72	2782.39	43.84	0.028	ITDENLQSQTTGLYIPEYEEALK
326	gi|113682189	glutaminase, like [Danio rerio]	44.5	591	652.45	1954.32	1951.90	42.93	0.044	ASSSRRALCTQTDAANDK
327	gi|189531190	PREDICTED: im:7145859 isoform 1 [Danio rerio]	28.8	677	1052.47	2102.92	2102.03	42.90	0.044	EVDEVDAALSDLEITLEGGK
328	gi|57525959	BCL2-associated athanogene 3 [Danio rerio]	24.6	459	1015.59	3043.75	3041.54	42.71	0.031	VSEVPQQIHHQPVQQQQQPTQ
329	gi|189529567	PREDICTED: glutamate receptor, ionotropic, kainate 5 [	48.9	1052	808.26	1614.50	1612.91	42.69	0.052	AECLLRLEELIRR
330	gi|18858379	carbonic anhydrase [Danio rerio]	55.8	260	745.25	1488.49	1489.64	39.21	0.12	QFHFHWGSSDDK
331	gi|62955581	hypothetical protein LOC550502 [Danio rerio]	53.8	455	1113.39	2224.76	2224.07	42.61	0.045	AHIVFDFHQAVDGVQEQER
332	gi|136256027	phosphorylase, glycogen; brain [Danio rerio]	43.2	843	953.65	1905.28	1905.00	42.55	0.049	LITSVGEVVNHDPVVGDR
333	gi|41055708	proteasome (prosome, macropain) 26S subunit, non-AT	32.4	503	1294.90	2587.79	2586.35	42.35	0.04	EFLLGFLEQPVEIEGDVPFRPR
334	gi|52219194	fatty acid binding protein 11 [Danio rerio]	48.5	134	769.63	1537.24	1535.67	41.74	0.063	LNEPFEETTADDR
335	gi|131889079	hypothetical protein LOC100034487 [Danio rerio]	60.5	850	544.27	543.26	543.31	41.53	0.034	INAAR
336	gi|39752649	kelch repeat and BTB (POZ) domain containing 10 [Dani	35	605	544.27	543.26	543.31	41.53	0.034	LNAAR
337	gi|28201964	erythrocyte membrane protein band 4.1 (elliptocytosis 1,	25.8	1534	583.60	1165.19	1164.71	41.44	0.071	IELVLPEKPK
338	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [D	49.6	789	1115.74	2229.46	2229.10	41.20	0.062	TSYDVSDSGQLEHVVVNRPK

TCDD replicate 3

Protein #	Accession ID	Protein name	Protein coverage	length	peptide *m/z*	peptide Mr*expt*	peptide Mr*calc*	peptide score	pep_expect	peptide sequence
1	gi|41053652	myoglobin [Danio rerio]	88.4	147	550.28	1098.55	1098.58	95.61	1.60E-07	AGLDAAGQGALR
					780.21	1558.40	1557.74	111.12	3.40E-09	VMDAVIGDIDGYYK
					1010.42	2018.82	2020.10	106.78	7.00E-09	GDHAALLKPLANTHANIHK
					1110.00	2217.98	2219.23	105.42	8.80E-09	AKGDHAALLKPLANTHANIHK
					1127.60	2253.19	2253.18	118.45	4.30E-10	FSGISQGDLAGSPAVAAHGATV
					1191.71	2381.41	2381.27	87.39	4.80E-07	FSGISQGDLAGSPAVAAHGATV
					946.49	2836.43	2834.54	64.80	7.10E-05	GDHAALLKPLANTHANIHKVAL
2	gi|74315904	alpha globin-like [Danio rerio]	60.1	143	559.18	1116.34	1114.56	48.72	0.0082	ADEIGAEALAR
					589.10	1176.18	1175.62	80.21	5.50E-06	TIMGAVGEAISK
					684.61	1367.21	1365.73	77.39	8.40E-06	FFNNLALALSEK
					933.31	1864.61	1863.88	111.04	2.90E-09	TYFSHWSDLSPGSGPVK
					934.31	1866.60	1868.00	124.17	1.40E-10	IDDLVGGLAALSELHAFK
					997.30	1992.58	1991.97	54.63	0.0012	TYFSHWSDLSPGSGPVKK
					1008.94	3023.79	3025.62	41.79	0.013	TIMGAVGEAISKIDDLVGGLAAL
3	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	68.5	143	559.18	1116.34	1114.56	48.72	0.0082	ADEIGAEALAR
					582.09	1162.17	1161.61	80.71	4.70E-06	TIMGAVGEAVSK
					684.61	1367.21	1365.73	77.39	8.40E-06	FFNNLALALSEK
					924.26	1846.50	1847.88	123.11	1.70E-10	TYFSHWADLSPGSGPVK
					934.31	1866.60	1868.00	124.17	1.40E-10	IDDLVGGLAALSELHAFK
4	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	57.6	1936	496.07	990.13	989.50	55.65	0.0018	SNNFQKPR
					609.16	1216.30	1215.63	44.72	0.019	AGLLGQLEEMR
					1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					620.08	1238.15	1237.63	47.53	0.0085	EADVLQQNPPK
					641.99	1281.96	1281.54	41.73	0.032	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					645.12	1288.22	1288.63	47.26	0.0099	DSQLQLDDSLR
					654.30	1306.58	1305.58	40.69	0.044	ELECEVEAEQK
					655.60	1309.19	1307.64	67.02	9.30E-05	NSFSQQLEDLK
					1368.62	1367.61	1367.63	55.83	0.0012	LQHELDEAEER
					699.73	1397.44	1397.75	84.68	1.50E-06	NALLQAELEELR
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK

					708.66	1415.30	1414.73	99.30	5.60E-08	LAEQELLDVTER
					732.18	1462.35	1463.74	67.18	8.90E-05	NSFSQQLEDLKR
					733.09	1464.16	1463.68	57.89	0.00074	LSEKDEEMEQVK
					733.14	1464.26	1463.74	77.88	7.40E-06	NSFSQQLEDLKR
					733.64	1465.26	1463.68	65.89	0.00012	LSEKDEEMEQVK
					738.45	1474.89	1473.68	79.64	5.10E-06	VEELEEELEAER
					748.98	1495.95	1495.73	61.03	0.00034	KLQHELDEAEER
					751.13	1500.24	1499.75	107.00	8.80E-09	LQEAEEAVEAVNAK
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					771.09	1540.17	1539.77	71.72	2.90E-05	DYHIFYQILSNK
					771.81	1541.61	1541.83	41.93	0.028	IDDEQSIIIQLQK
					771.90	1541.78	1542.83	96.87	8.70E-08	KLAEQELLDVTER
					772.41	1542.81	1541.83	31.84	0.29	IDDEQSIIIQLQK
					772.48	1542.94	1542.83	83.14	2.10E-06	KLAEQELLDVTER
					772.58	1543.15	1541.83	79.18	5.30E-06	IDDEQSIIIQLQK
					773.18	1544.35	1542.83	89.45	5.10E-07	KLAEQELLDVTER
					779.46	1556.90	1556.79	66.68	9.80E-05	LLGSLDIDHQQYR
					802.68	1603.34	1602.78	88.85	5.80E-07	SNDDLKENTAIVER
					806.78	1611.54	1610.75	87.12	8.00E-07	AAEESEEQANVHLGK
					810.75	1619.49	1620.72	57.80	0.00071	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					824.65	1647.28	1645.82	84.14	1.80E-06	NLTEEMAALDDIIAK
					843.71	1685.41	1684.83	61.27	0.00031	LELDDVASSMEHIVK
					845.69	1689.37	1688.88	93.45	1.90E-07	GQNVQQVNYAIGALSK
					1712.88	1711.87	1711.91	36.88	0.079	ILNPAAIPEGQFIDSK
					859.79	1717.56	1717.85	96.85	8.30E-08	NEDPLNETVVGLYQK
					862.23	1722.44	1721.94	96.71	9.10E-08	VQLLHSQNTSLINQK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					894.72	1787.43	1786.87	93.16	1.90E-07	TIDTLQSALESETHSR
					896.63	1791.24	1790.76	101.34	3.10E-08	QREEQAEADGTEDADK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					935.63	1869.25	1867.93	118.69	5.00E-10	DLEEATLQHEATAATLR
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
5	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	79	333	748.28	1494.55	1494.84	92.12	2.60E-07	VPTPNVSVVDLTVR
					787.22	1572.42	1571.83	87.49	7.80E-07	LVIDGHAITVYSER
					882.65	1763.28	1762.80	54.62	0.0014	LVTWYDNEFGYSNR
					931.70	1861.39	1860.94	91.36	2.70E-07	SSIFDAGAGIALNDHFVK
					1105.92	2209.83	2210.17	74.16	1.20E-05	LVIDGHAITVYSERDPANIK
					1108.00	2213.98	2212.10	70.66	2.60E-05	VIISAPSADAPMFVMGVNHEK
					1116.28	2230.55	2230.08	112.38	1.70E-09	WGDAGATYVVESTGVFTTIEK
					1300.97	2599.93	2599.37	115.89	6.60E-10	VINDNFVIVEGLMSTVHAITATQ
6	gi|189536977	PREDICTED: similar to slow myosin heavy chain 3 [Dani	46.2	1938	496.07	990.13	989.50	55.65	0.0018	SNNFQKPR
					1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.032	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					1368.62	1367.61	1367.63	55.83	0.0012	LQHELDEAEER
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					748.98	1495.95	1495.73	61.03	0.00034	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					810.75	1619.49	1620.72	57.80	0.00071	LEDEEEMNAELTAK

					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					858.95	1715.88	1716.90	88.94	5.30E-07	NKDPLNETVVGLYQK
					862.23	1722.44	1721.94	96.71	9.10E-08	VQLLHSQNTSLLNQK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					896.63	1791.24	1790.76	101.34	3.10E-08	QREEQAEADGTEDADK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					948.33	1894.65	1895.90	70.16	3.40E-05	HADSVSDLGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1070.77	2139.52	2139.00	135.28	9.50E-12	AEIQAALEEAEGSLEHEEGK
					1099.79	2197.57	2197.01	97.21	6.10E-08	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	4.10E-08	ALQEAHQQTLDDLQSEEDKVNT
7	gi|70778800	actin, alpha, cardiac muscle [Danio rerio]	71.6	377	600.05	1198.08	1197.51	75.20	1.60E-05	DSYVGDEAQSK
					896.17	1790.32	1789.88	102.64	2.10E-08	SYELPDGQVITIGNER
					978.36	1954.70	1955.04	95.38	1.00E-07	VAPEEHPTLLTEAPLNPK
					1114.80	2227.58	2227.06	62.75	0.00016	DLYANNVLSGGTTMYPGIADR
					1178.43	2354.85	2355.15	135.42	8.00E-12	KDLYANNVLSGGTTMYPGIADR
					1178.43	2354.85	2355.15	135.42	8.00E-12	KDLYANNVLSGGTTMYPGIADR
8	gi|62955473	hypothetical protein LOC550445 [Danio rerio]	69.2	377	600.05	1198.08	1197.51	75.20	1.60E-05	DSYVGDEAQSK
					896.17	1790.32	1789.88	102.64	2.10E-08	SYELPDGQVITIGNER
					978.36	1954.70	1955.04	95.38	1.00E-07	VAPEEHPTLLTEAPLNPK
					1114.80	2227.58	2227.06	62.75	0.00016	DLYANNVLSGGTTMYPGIADR
					1178.43	2354.85	2355.15	135.42	8.00E-12	KDLYANNVLSGGTTMYPGIADR
9	gi|66472252	slow myosin heavy chain 1 [Danio rerio]	43.1	1938	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					1368.62	1367.61	1367.63	55.83	0.0012	LQHELDEAEER
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					748.98	1495.95	1495.73	61.03	0.00034	KLQHELDEAEER
					751.13	1500.24	1499.75	107.00	8.80E-09	LQEAEEAVEAVNAK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					783.19	1564.37	1562.78	31.72	0.29	VVDTLQSSLESETR
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					896.63	1791.24	1790.76	101.34	3.10E-08	QREEQAEADGTEDADK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					935.63	1869.25	1867.93	118.69	5.00E-10	DLEEATLQHEATAATLR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1003.16	2004.30	2002.97	56.10	0.00081	NLQEEISDLTEQLGETGK
					1099.79	2197.57	2197.01	97.21	6.10E-08	ALQEAHQQTLDDLQSEEDK
					1101.39	2200.76	2199.12	103.60	1.40E-08	GTLEDQIIQANPALEAFGNAK
					1165.44	2328.86	2327.21	37.90	0.047	KGTLEDQIIQANPALEAFGNAK
					1427.49	2852.97	2853.40	96.93	4.10E-08	ALQEAHQQTLDDLQSEEDKVNT
10	gi|18858329	ba1 globin [Danio rerio]	71.6	148	480.00	957.99	957.56	46.94	0.013	TAILGLWGK
					713.66	1425.30	1424.76	77.10	8.90E-06	LNIDEIGPQALSR
					725.37	1448.72	1449.69	86.81	9.90E-07	NTYAALSVMHSEK
					898.52	1795.02	1794.83	130.34	3.50E-11	FGQAGFNADVQEAWQK
					993.79	1985.57	1984.97	94.94	1.10E-07	YFATFGNLSSPAAIMGNPK
11	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	52.3	551	645.10	1288.19	1286.69	73.63	2.30E-05	HALIIYDDLSK
					651.12	1300.22	1299.74	86.95	1.00E-06	TAIAIDTIINQK
					682.71	1363.40	1362.69	82.87	2.50E-06	TGTAEVSSILEEK
					720.11	1438.21	1437.84	47.15	0.0085	GIRPAINVGLSVSR
					766.34	1530.67	1530.75	131.50	3.30E-11	ILGADTGAELEETGR

					1031.14	2060.27	2059.13	83.36	1.50E-06	AFLQHVISQHQDLLAAIR
					1182.76	2363.50	2364.17	82.77	1.50E-06	EVAAFAQFGSDLDAATQQLLNR
12	gi|189536981	PREDICTED: similar to slow myosin heavy chain 3 isofor	45.4	1940	496.07	990.13	989.50	55.65	0.0018	SNNFQKPR
					1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.032	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					1368.62	1367.61	1367.63	55.83	0.0012	LQHELDEAEER
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					748.98	1495.95	1495.73	61.03	0.00034	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					810.75	1619.49	1620.72	57.80	0.00071	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					858.95	1715.88	1716.90	88.94	5.30E-07	NKDPLNETVVGLYQK
					862.23	1722.44	1721.94	96.71	9.10E-08	VQLLHSQNTSLLNQK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					896.63	1791.24	1790.76	101.34	3.10E-08	QREEQAEADGTEDADK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					948.33	1894.65	1895.90	70.16	3.40E-05	HADSVSDLGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	6.10E-08	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	4.10E-08	ALQEAHQQTLDDLQSEEDKVNT
13	gi|189536979	PREDICTED: similar to slow myosin heavy chain 3 isofor	45.3	1934	496.07	990.13	989.50	55.65	0.0018	SNNFQKPR
					1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.032	EQYEEEQEAK
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					1368.62	1367.61	1367.63	55.83	0.0012	LQHELDEAEER
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					748.98	1495.95	1495.73	61.03	0.00034	KLQHELDEAEER
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					810.75	1619.49	1620.72	57.80	0.00071	LEDEEEMNAELTAK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					858.95	1715.88	1716.90	88.94	5.30E-07	NKDPLNETVVGLYQK
					862.23	1722.44	1721.94	96.71	9.10E-08	VQLLHSQNTSLLNQK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					896.63	1791.24	1790.76	101.34	3.10E-08	QREEQAEADGTEDADK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					948.33	1894.65	1895.90	70.16	3.40E-05	HADSVSDLGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1099.79	2197.57	2197.01	97.21	6.10E-08	ALQEAHQQTLDDLQSEEDK
					1427.49	2852.97	2853.40	96.93	4.10E-08	ALQEAHQQTLDDLQSEEDKVNT
14	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio rer	85.9	517	488.47	974.92	974.55	46.55	0.015	IGLFGGAGVGK
					1435.70	1434.69	1434.75	48.04	0.0074	FTQAGSEVSALLGR
					720.70	1439.39	1438.78	77.81	7.50E-06	VALTGLTVAEYFR
					729.72	1457.43	1456.83	62.88	0.00023	TVLIMELINNVAK
					838.90	1675.79	1676.92	111.15	3.30E-09	LVLEVAQHLGENTVR
					916.22	1830.42	1828.88	72.59	2.10E-05	IMDPNIVGTEHYDVAR
					961.34	1920.66	1920.96	43.02	0.018	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	4.30E-08	AIAELGIYPAVDPLDSTSR
					1003.03	2004.05	2004.05	112.09	2.00E-09	FLSQPFQVAEVFTGHLGK
					687.59	2059.73	2059.99	41.30	0.024	EGNDLYHEMIESGVINLK

					1060.02	2118.03	2118.04	38.73	0.042	SLQDIIAILGMDELSEEDK
					1331.03	2660.05	2658.38	97.51	4.40E-08	SLQDIIAILGMDELSEEDKLTVAF
					1282.28	3843.82	3841.97	47.77	0.002	KGSITSVQAIYVPADDLTDPAPA
15	gi|23097290	troponin T2, cardiac [Danio rerio]	34.8	282	718.46	717.45	717.35	31.99	0.54	ELEAEK
					509.03	1016.05	1015.47	58.74	0.00085	VDFDDIHR
					609.45	1216.89	1216.66	49.43	0.0062	KEEEEIISLK
					855.86	1709.71	1710.90	55.88	0.001	RKPLDIDNANESALR
					957.35	1912.69	1913.95	95.06	1.10E-07	DLNELQTLIEAHFESR
16	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple	81.2	517	488.47	974.92	974.55	46.55	0.015	IGLFGGAGVGK
					1435.70	1434.69	1434.75	48.04	0.0074	FTQAGSEVSALLGR
					720.70	1439.39	1438.78	77.81	7.50E-06	VALTGLTVAEYFR
					729.72	1457.43	1456.83	62.88	0.00023	TVLIMELINNVAK
					838.90	1675.79	1676.92	111.15	3.30E-09	LVLEVAQHLGENTVR
					916.22	1830.42	1828.88	72.59	2.10E-05	IMDPNIVGTEHYDVAR
					961.34	1920.66	1920.96	43.02	0.018	DQEGQDVLLFIDNIFR
					994.82	1987.63	1987.03	98.94	4.30E-08	AIAELGIYPAVDPLDSTSR
					1003.03	2004.05	2004.05	112.09	2.00E-09	FLSQPFQVAEVFTGHLGK
					687.59	2059.73	2059.99	41.30	0.024	EGNDLYHEMIESGVINLK
					1282.28	3843.82	3841.97	47.77	0.002	KGSITSVQAIYVPADDLTDPAPA
17	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	62.8	196	968.51	967.50	966.55	60.55	0.00047	HVLATLGEK
					757.17	1512.33	1511.69	84.44	1.60E-06	DQGTFEDFVEGLR
					780.26	1558.50	1559.82	92.64	2.40E-07	KEEAPAPAPVPETPK
					856.49	1710.96	1710.82	92.16	2.40E-07	AKDQGTFEDFVEGLR
					889.30	1776.58	1777.85	48.44	0.0061	SVPLDFSPDQIEEFR
					973.03	1944.05	1944.08	97.32	6.10E-08	ALGHNPTNADVLTVLGKPK
18	gi|18858539	desmin [Danio rerio]	52.2	473	527.61	1053.20	1052.56	39.51	0.06	KIHEEEIR
					545.18	1088.34	1086.57	41.12	0.048	VSDLNQAVNK
					888.41	1774.80	1775.91	99.92	4.00E-08	FLEQQNSALTVEIER
					989.77	1977.53	1978.97	108.45	4.80E-09	LDFNLADAINQDFLNTR
					1094.31	2186.61	2186.00	145.27	9.40E-13	TFGSGLGSSIFAGHGSSGSSGS
19	gi|83025080	actinin, alpha 2 [Danio rerio]	44.7	895	670.69	1339.36	1338.79	39.36	0.054	QAILGIQQEVLK
					547.73	1640.17	1640.72	43.32	0.019	HEAFESDLSAHQDR
					826.12	1650.22	1648.81	71.27	3.30E-05	KAGTQIENIEEDFR
					873.76	1745.51	1743.87	73.20	1.90E-05	DDPLGNLNLAFDIAEK
					885.47	1768.93	1768.81	104.59	1.30E-08	KHEAFESDLSAHQDR
					916.17	1830.33	1828.89	73.78	1.60E-05	MLDAEDILSTPKPDER
					969.28	1936.54	1934.98	74.47	1.30E-05	GDLTNPYSTITAEEIAIK
					1000.26	1998.50	1998.01	57.54	0.00059	LEGDHQLIQESLIFDNK
					1050.91	2099.81	2099.09	86.17	7.90E-07	LNKDDPLGNLNLAFDIAEK
					942.63	2824.85	2824.40	71.67	1.40E-05	VEQIAAIAQELNELDYHDVASVN
20	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	64.4	433	469.64	937.27	937.50	41.97	0.034	HIADLAGNK
					687.75	1373.49	1372.70	48.62	0.0067	HITGEQLGDLYK
					719.54	1437.06	1435.72	59.66	0.00049	GNPTVEVDLYTTK
					1053.98	2105.94	2104.07	85.69	8.90E-07	FTGSVDIQVVGDDLTVTNPK
					1060.86	2119.71	2118.12	60.54	0.00029	DVILPVPAFNVINGGSHAGNK
					1147.92	2293.83	2295.13	40.61	0.024	SGETEDTFIADLVVGLCTGQIK
					1013.17	3036.49	3037.61	62.59	0.0001	HIADLAGNKDVILPVPAFNVING
21	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio re	38.7	1937	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK

					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
22	gi|189520343	PREDICTED: similar to myosin heavy chain fast skeletal	48.6	1933	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					641.99	1281.96	1281.54	41.73	0.032	EQYEEEQEAK
					684.76	1367.50	1366.65	31.95	0.29	VQHELEEAQER
					752.60	1503.19	1502.76	72.06	3.00E-05	ENQSILITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					824.74	1647.46	1647.78	35.76	0.12	LEEAGGATSAQIEMNK
					847.15	1692.29	1690.81	82.30	2.70E-06	NSYEETLDHLETLK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
23	gi|66472732	myosin heavy chain 4 [Danio rerio]	37.1	1935	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					684.76	1367.50	1367.63	44.43	0.017	VQHELEEAEER
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1044.21	2086.41	2088.02	74.04	1.30E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	4.40E-07	NDLQLAVASEAENLSDAEER
24	gi|189519129	PREDICTED: similar to myosin heavy chain 4 [Danio reri	37.4	1933	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					684.76	1367.50	1367.63	44.43	0.017	VQHELEEAEER
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1044.21	2086.41	2088.02	74.04	1.30E-05	TKLEQQVDDLEGSLEQEK
					1087.82	2173.62	2173.01	88.30	4.40E-07	NDLQLAVASEAENLSDAEER
25	gi|50512294	myosin, heavy polypeptide 2, fast muscle specific [Danio	37.8	1935	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					684.76	1367.50	1367.63	44.43	0.017	VQHELEEAEER
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1044.21	2086.41	2088.02	74.04	1.30E-05	TKLEQQVDDLEGSLEQEK
26	gi|169259784	myosin, heavy polypeptide 1, skeletal muscle [Danio reri	36.2	1937	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					684.76	1367.50	1367.63	44.43	0.017	VQHELEEAEER
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK

					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
					1044.21	2086.41	2088.02	74.04	1.30E-05	TKLEQQVDDLEGSLEQEK
27	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	79.1	172	690.02	1378.03	1377.66	55.55	0.0013	SLCYIITHGDEK
					809.72	1617.43	1617.83	31.87	0.28	LNGTDPEETILAAFK
					842.26	1682.51	1681.91	98.27	6.00E-08	GPINFTVFLTLFGEK
					1047.36	2092.71	2091.96	75.34	9.40E-06	GSSNVFSMFEQSQIQEFK
					1292.50	2582.99	2582.25	108.90	3.10E-09	FTAEEVDQAFAVAPIDVAGNIDY
28	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	43	1936	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					816.81	1631.60	1631.78	96.03	1.10E-07	LEEAGGATAAQIEMNK
					880.79	1759.56	1759.88	84.54	1.40E-06	LEEAGGATAAQIEMNKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					943.56	1885.10	1884.92	73.56	1.60E-05	QADSVAELGEQIDNLQR
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
29	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	72.7	377	600.05	1198.08	1197.51	75.20	1.60E-05	DSYVGDEAQSK
					896.17	1790.32	1789.88	102.64	2.10E-08	SYELPDGQVITIGNER
					1954.17	1953.16	1953.06	81.42	2.40E-06	VAPEEHPVLLTEAPLNPK
30	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	83.5	334	710.40	1418.78	1417.79	55.13	0.0015	LITPLASGPAEPPR
					769.90	1537.78	1537.77	102.60	2.30E-08	IVADKDYSVTANSR
					843.74	1685.46	1684.85	114.34	1.50E-09	ELADELALVDVVEDR
					858.16	1714.30	1714.82	48.64	0.0057	LNPDIGTDKDAENWK
31	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	52.7	782	786.18	1570.35	1568.82	59.32	0.00051	FKLEPPTGDELPAR
					857.83	1713.65	1711.84	77.20	7.70E-06	EVNQEVYSFLASAGAK
					878.27	1754.52	1752.88	68.60	5.40E-05	IVYGHLDDPAGQEIAR
					954.55	1907.08	1905.98	68.05	5.40E-05	KQGLLPLTFSNPADYDK
					1041.84	2081.67	2080.94	61.45	0.00023	NNISWVVVGDENYGEGSSR
					1267.44	2532.86	2532.29	120.13	2.40E-10	GHLDNISNNLLIGAVNIENDGVN
					1362.08	2722.14	2721.43	48.21	0.0033	NDANPATHAFVTSPEIVTALAIA
32	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	81.3	337	661.47	1320.92	1319.67	72.08	3.00E-05	GYIGADQLGDALK
					751.89	1501.77	1502.77	93.73	2.00E-07	VEFPADQLSALTGR
					1545.56	3089.10	3088.58	102.99	1.00E-08	NSPLVSELSLFDIAHTPGVAADL
33	gi|189523699	PREDICTED: titin a [Danio rerio]	50.7	32757	824.59	823.58	822.50	52.54	0.0028	VHIVIDK
					567.69	1133.36	1133.57	50.68	0.005	KGDVTLSDSGR
					616.63	1231.24	1230.66	42.57	0.031	DTATLAWTKPK
					681.12	1360.22	1359.75	38.80	0.064	VLDRPGPPDGPLK
					781.54	1561.07	1560.75	40.14	0.042	EHSEVIPHTQQEK
					804.70	1607.39	1605.88	52.60	0.0023	AEDPLFLPSPPAKPK
					831.24	1660.46	1658.82	50.71	0.0037	VNVEVEYTEPVPER
					862.77	1723.52	1722.92	49.25	0.005	AGSDLVLDAAVGGKPEPK
					877.52	1753.03	1752.99	43.02	0.02	EAEILKPLASVEVVEK
					940.78	1879.54	1878.92	96.56	7.60E-08	TPLHDGGAEVSHYIVER
					947.83	1893.64	1892.90	52.96	0.0018	HTVTLSWEKPDHDGGSK
					968.75	1935.49	1936.07	49.40	0.004	AVNEAGASRPSVTAGPIVIK
					1005.77	2009.52	2009.11	51.51	0.0023	AAPAPLHLQAVHSENLLTK
					1014.48	2026.94	2024.95	48.72	0.0044	GNTELQSDDKYEIISEGK
					1035.13	2068.25	2067.07	47.02	0.0063	NKFDVPDAPQNVIVGNVNK
					1052.34	2102.66	2102.05	88.77	4.40E-07	EQVTHQAALLQSHEVQER
					708.80	2123.37	2122.13	68.98	3.90E-05	VLDRPGPSSGPLDITGLTAEK
					1082.45	2162.89	2161.14	39.72	0.032	VLDRPGPPEGPLTVSGVTNEK
					1098.94	2195.87	2196.14	55.19	0.00093	VLDRPGPPDGPISIYGVTSEK

					1100.60	2199.18	2199.29	64.34	0.00012	KEPKPESILQVISTPVPLPK
					1114.26	2226.51	2226.10	51.16	0.0024	EHVIIEWFKPENDGGSEIK
					1151.50	2300.99	2300.07	51.59	0.0019	EVTSNSVTLSWEKPDHDGGSR
					1177.07	2352.13	2351.12	38.63	0.037	VSWRPPSDDGGSDIFGYIVER
					1299.87	2597.72	2597.14	69.48	2.80E-05	EKEVEEPEEPEEEYHPSLNER
					895.44	2683.29	2684.42	50.51	0.002	TPILAIDPLQKPGEPENFHVGDI
					1108.51	3322.51	3321.81	37.42	0.031	YTITATNNIGTVTEEVAIIILDKPG
34	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	36	1945	609.16	1216.30	1215.63	44.72	0.019	AGLLGQLEEMR
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					824.74	1647.46	1647.78	35.76	0.12	LEEAGGATSAQIEMNK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
35	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	36	1938	1224.67	1223.66	1223.61	43.14	0.023	TKYETDAIQR
					643.04	1284.06	1282.57	37.91	0.078	ELTYQTEEDR
					706.52	1411.03	1410.66	59.01	0.00056	ELTYQTEEDRK
					761.34	1520.66	1520.76	65.72	0.00012	AITDAAMMAEELKK
					930.48	1858.95	1858.88	100.27	3.50E-08	LEQQVDDLEGSLEQEK
					993.73	1985.45	1986.97	82.42	2.00E-06	LEQQVDDLEGSLEQEKK
36	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	57.7	449	578.00	1153.98	1153.57	40.85	0.042	DIFQDIFEK
					678.77	1355.52	1354.68	97.84	7.70E-08	TIEAEAAHGTVTR
					716.14	1430.27	1428.73	81.19	3.50E-06	FKDIFQDIFEK
					861.13	1720.25	1719.82	116.07	1.10E-09	DQTDDQVTIDSAIATK
					1893.05	1892.04	1891.93	83.81	1.50E-06	LNEHYVNTTDFLDAIK
37	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	52.6	28836	671.64	1341.26	1340.73	47.09	0.0091	VTEHTVTGLLSGK
					701.73	1401.45	1399.71	64.74	0.00016	HVSVEALDFIDR
					738.17	1474.33	1473.71	56.64	0.001	RLDETDEAQLER
					807.69	1613.36	1612.87	47.29	0.0078	ALDPVFKPGPPHNPK
					830.81	1659.61	1660.95	47.43	0.0078	VIILSKPDEPQGPIR
					856.20	1710.38	1709.82	61.51	0.00027	ADSGNYTITIQNAAGSK
					862.77	1723.52	1722.92	49.25	0.005	AGSDLVLDAAVGGKPEPK
					872.18	1742.35	1742.87	33.61	0.17	AISVNIQEDENSPTVK
					877.52	1753.03	1752.99	43.02	0.02	EAEILKPLASVEVVEK
					885.70	1769.38	1768.91	59.08	0.00048	SSVTLTWVKPAHDGGSK
					894.79	1787.56	1787.83	38.15	0.061	GENKVDVEYDEHINK
					905.42	1808.83	1807.91	39.53	0.042	VTLTWTAPHEDGGSPIK
					920.77	1839.53	1838.93	62.48	0.00021	STVSLAWEKPLHDGGSR
					923.72	1845.43	1845.01	63.56	0.00016	VQILDKPGPPAGHIEFK
					928.68	1855.35	1854.92	75.30	1.00E-05	TSVSLSWEKPIHDGGSR
					935.40	1868.78	1867.88	35.85	0.097	TSADLQWTRPEHDGGAK
					939.89	1877.77	1877.90	33.61	0.15	VLNYDEEVDDTRPVSK
					950.74	1899.47	1898.91	53.37	0.0016	TTVTLSWEKPEHDGGSR
					1002.79	2003.56	2002.96	75.42	9.50E-06	KDNTSDDIGWVTVTSTHK
					1009.78	2017.54	2017.97	31.43	0.23	TVQPEPEEEFHPPLVDR
					1028.52	2055.03	2055.07	32.17	0.2	LKGDVLSASPDVEIIEDGAK
					1033.20	2064.39	2064.06	43.67	0.014	VISGVQDLEYTVTDVIEGK
					1039.66	2077.30	2077.08	43.93	0.014	HGTGEAFINLDVIDVPGPVK
					1045.72	2089.43	2089.14	87.49	5.70E-07	DATIEIITLDKPGPPTGPVR
					1258.45	2514.89	2514.23	109.45	2.80E-09	HTLPVDSDISSSDTTSVVTIPES
					903.21	2706.60	2706.41	44.80	0.0077	TPVLAVDPVEKPGEPENFQITEI
38	gi|148596963	spectrin alpha 2 [Danio rerio]	49.1	2480	624.57	1247.12	1246.55	41.19	0.042	GEIDAHEDSFK

					773.69	1545.36	1544.77	82.66	2.50E-06	HALLEADVAAHQDR
					787.22	1572.42	1571.78	80.51	3.90E-06	HQALQAEISGHEPR
					567.84	1700.48	1699.88	49.54	0.0044	KHQALQAEISGHEPR
					861.63	1721.25	1720.86	47.63	0.0076	LIQSHPEAVDDIQEK
					873.61	1745.21	1744.82	38.53	0.056	LSDDNTIGQEEIQQR
					925.80	1849.59	1848.86	86.05	9.10E-07	KFEEFQTDLAAHEER
					964.07	1926.13	1924.90	93.25	1.70E-07	SSLSSAEADFSQLAELDR
					1010.83	2019.65	2018.99	84.45	1.20E-06	LQIASDENYKDPSNLQGK
					1077.98	2153.95	2153.10	123.55	1.40E-10	ALINADELANDVAGAEALLDR
					1108.81	2215.60	2215.12	41.10	0.024	RDELITNWEQIQTLATER
					1110.29	2218.56	2219.03	35.74	0.08	STDEAGQALLNTGHYASEEVK
					750.41	2248.19	2247.19	55.90	0.00076	RLEAELGAHEPAIQSVLETGK
39	gi|18858335	bactin1 [Danio rerio]	60.8	375	1198.50	1197.49	1197.51	54.95	0.0016	DSYVGDEAQSK
					600.05	1198.08	1197.51	75.20	1.60E-05	DSYVGDEAQSK
					896.17	1790.32	1789.88	102.64	2.10E-08	SYELPDGQVITIGNER
40	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	54.6	119	599.36	1196.71	1195.75	42.35	0.03	AKLEPVVLSLK
					1050.98	2099.94	2100.09	88.07	5.10E-07	ELTELGEQVKPHFEGIFK
					1115.07	2228.12	2228.18	64.05	0.00012	KELTELGEQVKPHFEGIFK
41	gi|162287365	hemopexin [Danio rerio]	61.7	447	1339.71	1338.70	1338.61	63.12	0.00022	FHSDTIESEFK
					900.94	1799.87	1800.00	65.16	0.00011	VGKPHTHLEGYPKPLK
					720.76	2159.26	2159.07	35.56	0.086	GKPGGEGHKHELHHGAQLDR
42	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	29	331	969.23	1936.45	1936.93	114.30	1.30E-09	HLTTLVDDIWYYAGDR
43	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	52	202	999.96	2996.84	2996.41	42.81	0.01	TLAAGSHAEHDGQPYCHKPCY
					1008.19	3021.55	3023.42	63.54	8.50E-05	TLNPGGHAEHDGKPYCHKPCY
44	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	74.6	283	588.48	1174.94	1173.56	62.94	0.0003	SEYGLTFTEK
					665.84	1329.67	1329.66	41.35	0.037	RSEYGLTFTEK
					1052.41	2102.81	2102.15	74.40	1.20E-05	VNNTSLVGVGYTQSLRPGIK
					1088.83	2175.64	2174.05	69.95	3.00E-05	WNTDNTLGTEINIEDQIAK
					1258.26	2514.51	2513.15	43.86	0.01	TGDFQLHTNVNDGSEFGGSIY
45	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	42.3	284	777.37	776.36	776.33	34.17	0.29	AADESER
					537.38	1072.75	1072.55	46.75	0.013	LDKENAIDR
					586.14	1170.26	1169.67	66.30	0.00013	LVILEGELER
					622.72	1243.43	1242.65	73.33	2.50E-05	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	6.10E-05	KLVILEGELER
					701.18	1400.34	1399.71	101.39	3.40E-08	KAADAEGDVAALNR
					770.10	1538.18	1537.71	79.43	4.80E-06	SIDDLEDELYAQK
46	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	94.2	397	594.84	1187.66	1187.68	73.04	2.90E-05	ITAHLVHELR
					649.07	1296.12	1294.70	56.75	0.00099	RTPFGTYGGVLK
					683.58	1365.14	1364.63	58.96	0.00059	DHSATDLAEHAAK
					931.96	1861.91	1861.98	116.41	8.40E-10	TNVNGGAIAIGHPLGASGTR
47	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	60.4	364	530.65	1059.29	1058.57	51.67	0.0044	KELSDIAQR
					660.09	1318.16	1317.68	91.48	3.60E-07	GILAADESTGSVAK
					777.08	1552.14	1550.70	74.99	1.40E-05	FQSINAENTEENR
					876.65	1751.28	1749.80	94.12	1.60E-07	GDTGAAAGESLFVANHAY
					1174.96	2347.90	2347.17	50.36	0.0025	GVVPLAGTNGETTTQGLDGLYE
48	gi|18858587	elongation factor 1-alpha [Danio rerio]	48.7	462	530.52	1588.54	1587.87	53.53	0.0019	THINIVVIGHVDSGK
					973.27	2916.77	2917.55	75.00	6.50E-06	EGNASGTTLLDALDAILPPSRPT
49	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	85.6	153	1099.44	1098.43	1098.53	56.37	0.0013	NLIHGSDSEK
					665.79	1329.57	1329.74	31.80	0.32	TFIAVKPDGVQR
					795.45	1588.88	1588.88	78.54	6.10E-06	LVAAKFVQASEDLAK
					1040.08	2078.14	2077.09	80.53	3.00E-06	YTSSGPLLAMVWEGLNVIK
					1106.98	2211.95	2211.12	83.98	1.20E-06	SAATEVSLWFKPEELVSYR

50	gi|40254659	bactin2 [Danio rerio]	42.7	375	1198.50	1197.49	1197.51	54.95	0.0016	DSYVGDEAQSK
					600.05	1198.08	1197.51	75.20	1.60E-05	DSYVGDEAQSK
					1954.17	1953.16	1953.06	81.42	2.40E-06	VAPEEHPVLLTEAPLNPK
51	gi|41387136	hypothetical protein LOC393781 [Danio rerio]	52.3	128	902.23	1802.45	1801.94	110.64	3.40E-09	YHVSETPFAISAQKPK
					915.41	2743.19	2742.29	43.40	0.01	LFPGDVILETGEVVPDFPEDSHC
52	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	37.4	230	442.41	882.81	882.46	55.83	0.0013	LLETDHR
					1068.14	2134.27	2133.18	99.87	3.30E-08	ILVSAEDVLHSWAVPSLGIK
					905.75	2714.23	2715.50	31.08	0.18	ESPIRILVSAEDVLHSWAVPSLG
53	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	58.5	532	819.21	1636.41	1635.88	37.13	0.081	GVNLPGAAVDLPAVSEK
					882.38	1762.75	1763.98	115.54	1.20E-09	KGVNLPGAAVDLPAVSEK
					938.02	1874.03	1872.82	42.98	0.018	MNFSHGSHEYHGETIK
54	gi|62955689	hypothetical protein LOC550556 [Danio rerio]	66.3	270	843.26	1684.50	1682.84	89.86	4.20E-07	AFAEFLTEEIKEEK
55	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	61.3	364	530.65	1059.29	1058.57	51.67	0.0044	KELSDIAQR
					660.09	1318.16	1317.68	91.48	3.60E-07	GILAADESTGSVAK
					1427.77	1426.76	1426.72	45.39	0.013	PHAYPFLTPEQK
					777.08	1552.14	1550.70	74.99	1.40E-05	FQSINAENTEENR
					1174.96	2347.90	2347.17	50.36	0.0025	GVVPLAGTNGETTTQGLDGLYE
56	gi|38488731	natriuretic peptide precursor A [Danio rerio]	60.4	106	1026.70	2051.39	2049.99	106.07	8.20E-09	SLLQQFEEALATEEASER
					1182.79	2363.56	2362.99	76.92	5.70E-06	DREEAAAPGEDSNPSDGFDTQI
57	gi|48762657	enolase 1, (alpha) [Danio rerio]	51.4	432	1147.92	2293.83	2295.13	40.61	0.024	SGETEDTFIADLVVGLCTGQIK
					1504.37	3006.73	3006.57	90.04	1.90E-07	HIADLAGNPDVILPVPAFNVING
58	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Danic	57.1	659	577.56	1153.10	1152.61	48.98	0.0064	VEEHTLQGLK
					638.66	1275.30	1275.65	46.36	0.012	SFGGVSSGPPEKK
					837.28	1672.54	1671.94	94.37	1.50E-07	AIEQFGAVIEELLLK
					872.48	2614.41	2614.37	42.99	0.012	AGLGSGLTLQGTVHPELNHSGE
59	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	70.1	603	1059.42	2116.82	2115.97	81.90	2.00E-06	GKEYDDLIDEFMQAVTDK
					736.20	2205.58	2204.05	33.56	0.13	SHLNHEKEEFAHDHPHIK
					1380.08	2758.14	2756.52	35.10	0.071	TLEEVVETIKPTAIIGVAAIGGAFT
					1005.22	3012.64	3013.43	105.12	6.00E-09	HISDDIFLTTAEAISEMVTEEHLA
60	gi|18858427	creatine kinase, muscle a [Danio rerio]	50.4	381	754.52	1507.03	1506.70	35.38	0.12	GGDDLDPNYVLSSR
					998.78	1995.54	1993.93	91.51	2.40E-07	GTGGVDTASVGGVFDISNADR
					1076.62	2151.22	2150.04	34.27	0.12	RGTGGVDTASVGGVFDISNADF
61	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	36.4	143	935.31	1868.61	1867.99	94.68	1.30E-07	IDDLLGALSSLSDLHATK
62	gi|157787181	creatine kinase CKM3 [Danio rerio]	51.3	380	754.52	1507.03	1506.70	35.38	0.12	GGDDLDPNYVLSSR
					998.78	1995.54	1993.93	91.51	2.40E-07	GTGGVDTASVGGVFDISNADR
					1076.62	2151.22	2150.04	34.27	0.12	RGTGGVDTASVGGVFDISNADF
63	gi|117606264	sarcalumenin [Danio rerio]	62.7	482	1738.02	1737.01	1735.95	88.70	5.50E-07	AITHELPSLLGSINSGK
					957.65	1913.29	1912.97	35.94	0.091	EEISLLEDLNQVIENR
					1036.33	2070.65	2069.08	98.98	4.10E-08	REEISLLEDLNQVIENR
64	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio reric	44.4	410	844.91	1687.81	1687.84	103.16	2.10E-08	NIDYVAESIHEAVTK
					1114.35	2226.68	2226.03	41.35	0.023	NLFAFFDSAYQGFASGDLEK
					1291.46	2580.90	2579.28	55.51	0.00067	MIADDHSLNHEYLPILGLPEFR
					1103.95	3308.81	3308.59	32.16	0.1	TPVYVSAPTWENHNAVFSNAGF
65	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	82.3	248	1458.82	1457.81	1457.72	75.26	1.40E-05	HVFGESDELIGQK
					802.24	1602.47	1601.88	64.30	0.00016	VVLAYEPVWAIGTGK
					808.26	1614.50	1613.82	63.83	0.00018	RHVFGESDELIGQK
					1216.41	2430.81	2431.30	86.70	5.30E-07	DLDGFLVGGASLKPEFIDIINAK
66	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	33.5	284	777.37	776.36	776.33	34.17	0.29	AADESER
					537.38	1072.75	1072.55	46.75	0.013	LDKENAIDR
					586.14	1170.26	1169.67	66.30	0.00013	LVILEGELER
					622.72	1243.43	1242.65	73.33	2.50E-05	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	6.10E-05	KLVILEGELER

67	gi|189538466	PREDICTED: similar to alpha 2 actin [Danio rerio]	46.2	132	1114.80	2227.58	2227.06	62.75	0.00016	DLYANNVLSGGTTMYPGIADR
					1178.43	2354.85	2355.15	135.42	8.00E-12	KDLYANNVLSGGTTMYPGIADR
68	gi|41054435	tropomyosin alpha-4 chain [Danio rerio]	20.6	248	777.37	776.36	776.33	34.17	0.29	AADESER
					586.14	1170.26	1169.67	66.30	0.00013	LVILEGELER
					622.72	1243.43	1242.65	73.33	2.50E-05	IQLVEEELDR
					649.69	1297.36	1297.76	68.97	6.10E-05	KLVILEGELER
69	gi|50539808	hypothetical protein LOC436647 [Danio rerio]	49.7	525	968.42	1934.82	1932.99	40.30	0.032	VNAGDQPGADVGPLISPQAK
					1006.23	2010.44	2009.00	95.36	9.20E-08	SSQWLDIHNPATSEVIGR
70	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	55.1	305	730.84	1459.66	1459.79	56.96	0.00094	EVIPTDKVEVGFK
					855.08	1708.14	1706.82	100.12	4.20E-08	EIAAFDAVNDESWLK
					877.76	2630.26	2631.29	87.23	4.40E-07	NVTIWGNHSSTQYPDVHHAIVTI
71	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	66.7	357	1252.70	1251.69	1251.62	69.12	6.10E-05	LHAVNDAEVER
					1111.95	2221.88	2220.13	94.16	1.10E-07	NAITVEMYNELIEALELAGK
					1315.03	2628.05	2626.36	76.50	5.20E-06	QQYVDLISSLVGAEAPAVAAQP
72	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	37.7	1974	1000.33	1998.64	1997.92	68.53	4.70E-05	ELEGHISDLQEDLESER
					1007.71	2013.41	2012.04	58.97	0.00041	TLEAELLQLQEDLAAAER
					1066.71	2131.40	2131.00	69.02	4.10E-05	QVEAERDELADELASNASGK
73	gi|47087077	phosphoglycerate kinase 1 [Danio rerio]	60.4	417	916.46	915.45	915.45	52.89	0.0034	FHVAEEGK
					818.24	1634.46	1633.78	84.76	1.40E-06	LGDVYVNDAFGTAHR
					1740.87	1739.86	1739.91	58.16	0.00059	VSHVSTGGGASLELLEGK
					926.88	1851.75	1850.97	49.52	0.004	ITLPVDFITADKFDEK
					801.08	2400.20	2400.17	46.35	0.0065	QIVWNGPVGVFEWDNFAHGTK
74	gi|40538764	ceruloplasmin [Danio rerio]	36.1	1087	805.83	1609.65	1609.72	87.83	6.90E-07	SVNKEDADFQESNK
					828.53	1655.05	1654.78	117.55	7.00E-10	LVDDIVSDTFFDNR
					1287.86	2573.71	2573.23	102.88	1.20E-08	VSWHLSGLGSETDIHGLYFEGN
75	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	47.1	104	608.49	1214.96	1214.66	57.95	0.0009	VGPNLWGLFGR
					745.36	1488.71	1487.65	60.28	0.00043	TGQAEGFSYTDANK
					808.82	1615.63	1615.75	107.78	7.00E-09	KTGQAEGFSYTDANK
					998.19	1994.37	1992.95	53.43	0.0015	GIVWGEDTLMEYLENPK
76	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Co	66.4	761	653.09	1304.16	1303.71	82.76	2.70E-06	MQLLEIITTDK
					698.19	1394.36	1392.67	54.97	0.0015	LSGQLDYHGFEK
					837.73	1673.45	1672.93	67.82	6.80E-05	MGLVHQLVDPLGPGLK
77	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	74.6	283	1348.76	1347.75	1347.70	53.27	0.0022	LGLDTSFVPNTGK
					930.44	1858.86	1858.82	97.79	6.00E-08	SQSGVEFTTGGSSNTDTGK
					1030.87	2059.73	2058.12	72.35	1.90E-05	VNNASLVGVGYTQSLRPGVK
78	gi|136429	Trypsin precursor	75.4	232	1105.98	2209.95	2210.10	98.95	3.90E-08	LGEHNIDVLEGNEQFINAAK
79	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	67.7	226	723.80	1445.58	1445.78	65.41	0.00014	VIFEAETEKPGVK
					881.46	2641.36	2641.29	69.67	2.50E-05	SPDPAAVEHKPEESKPEESKPE
80	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio r	46.9	454	1245.76	1244.75	1244.68	78.80	7.70E-06	KVDFAAAGEPLK
					696.14	1390.27	1390.71	74.71	1.70E-05	GVEAVGGSLSVSSSR
81	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	66.4	116	840.79	1679.57	1677.88	85.12	1.30E-06	TTGLVGLAVSQNPHER
82	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	52.9	433	1147.92	2293.83	2295.13	40.61	0.024	SGETEDTFIADLVVGLCTGQIK
					1008.42	3022.23	3020.58	72.22	1.20E-05	HIADLAGNPEVILPVPAFNVING
83	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	78.6	248	1458.82	1457.81	1457.72	75.26	1.40E-05	HVFGESDELIGQK
					802.24	1602.47	1601.88	64.30	0.00016	VVLAYEPVWAIGTGK
					808.26	1614.50	1613.82	63.83	0.00018	RHVFGESDELIGQK
84	gi|41055718	fumarate hydratase precursor [Danio rerio]	42.2	509	719.05	2154.12	2153.18	71.07	2.50E-05	EVHEVLLPGLQTLHDALAAK
					1251.93	2501.85	2501.26	77.23	4.70E-06	THTQDAVPLSLGQEFGGYVQQ
85	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	68.9	763	653.09	1304.16	1303.71	82.76	2.70E-06	MQLLEIITTDK
					804.74	1607.47	1606.81	72.46	2.40E-05	DVNTEALEILEAYK
					1195.44	3583.28	3583.84	76.05	3.50E-06	KLDSLTTGFGFPVGAATLADEV
86	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	54.6	359	880.40	1758.79	1758.94	83.05	1.90E-06	SIRPLDADTIETSITK

87	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	55.3	682	1325.66	1324.65	1324.74	91.10	3.60E-07	TVHLLAGVADTTK
					677.63	1353.24	1352.69	51.33	0.0033	SSGISTIHPETPK
					1057.39	2112.76	2113.04	73.43	1.50E-05	WLYVDFGGHRPAGSEPTPK
88	gi|58801524	LIM domain containing preferred translocation partner in	62.2	556	1097.90	2193.79	2193.06	52.39	0.0018	AEPSHHPAPTPSQGYQPAPPK
					1398.18	2794.34	2793.39	116.45	5.10E-10	SSLDAEIDSLTSILADLESSSPYK
89	gi|189530625	PREDICTED: similar to spectrin repeat containing, nucle	37.7	8621	550.32	1098.62	1097.66	69.95	6.10E-05	QLADAIAKLR
90	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	69.5	455	759.60	1517.19	1517.74	36.85	0.096	CPDCPGLLPLHEPK
					824.81	1647.61	1645.83	39.41	0.053	KCPDCPGLLPLHEPK
					654.45	1960.33	1959.96	51.31	0.0025	FHDHRPGSVHPLGPDHR
91	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	45.8	996	732.69	1463.37	1463.67	47.19	0.0088	IRDEMASTEQER
					733.60	1465.19	1464.92	72.90	2.30E-05	ISLPVILLDELLK
					733.61	1465.21	1463.67	49.86	0.0046	IRDEMASTEQER
					1526.85	1525.84	1524.80	69.48	4.90E-05	DIVPGDIVEVAVGDK
92	gi|156713467	vitellogenin 7 [Danio rerio]	50.7	1358	587.14	1172.27	1172.62	59.04	0.00071	LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.028	THYVINEDPK
					1069.54	2137.07	2135.16	100.74	2.60E-08	ISDATAQIVEVLTHLVANNK
93	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	42.5	2633	1230.46	2458.90	2458.19	90.98	2.00E-07	HAINQEINAYNTPAQFGLEGSG
94	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprotei	65.4	661	738.51	1475.00	1473.75	73.92	1.90E-05	KHTLSYVDPETGK
					1291.54	2581.07	2582.14	56.25	0.00057	DGQDHVVPGLYACGEAGCASV
95	gi|47086523	ictacalcin [Danio rerio]	57.9	95	696.55	1391.08	1390.73	96.62	1.10E-07	ELLSAELGDIFGK
96	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	35.9	1368	1212.60	2423.18	2422.19	102.56	1.50E-08	GQNHLEEVELAFPQNVIEGSGR
					988.87	2963.58	2964.31	50.87	0.0017	VFSSDGSSTVTVQSAGDSHHF
97	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	53.4	283	660.08	1318.14	1317.64	60.19	0.00048	WAEHGLTFTEK
					1045.46	2088.90	2088.16	88.25	4.80E-07	VNNSSLVGLGYTQTLKPGIK
98	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dani	54.9	731	1570.97	3139.92	3139.56	100.34	1.60E-08	DSFIVYQGHHGDVGAPIADVILP
99	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	70.7	164	820.21	1638.40	1637.91	103.88	1.70E-08	HVVFGQVVEGLDVIK
100	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	31.4	1754	575.27	1722.79	1721.89	60.94	0.00033	KQELEEILHDLEAR
					958.30	1914.58	1913.91	68.34	5.30E-05	HSQAFDELNEQLEQVK
					893.88	2678.62	2678.38	79.43	2.70E-06	KLEGDSTELHDQIAELQAQIAEL
101	gi|189522028	PREDICTED: similar to myomesin [Danio rerio]	52.9	923	1508.67	1507.66	1507.73	82.72	2.30E-06	FKGEFDESLPSPR
					1301.70	3902.07	3901.05	52.45	0.00066	KGASAPWTGQIIVTEEEPVEGV
102	gi|82658182	cytochrome c-1 [Danio rerio]	59.9	307	714.58	1427.15	1425.71	80.63	4.00E-06	NLVGVSHTEDEVK
					1310.72	2619.42	2618.22	38.78	0.031	TLAEEIEVVDGPDDNGEMFTRP
103	gi|68448513	hypothetical protein LOC574004 [Danio rerio]	56.1	187	968.51	967.50	966.55	60.55	0.00047	HVLATLGEK
					757.17	1512.33	1511.69	84.44	1.60E-06	DQGTFEDFVEGLR
104	gi|70778734	ATPase, Na+/K+ transporting, alpha 3b polypeptide [Dan	46.3	1023	924.66	1847.31	1846.81	86.28	8.50E-07	YQLSIHETEDNNDNR
105	gi|51972166	radixin isoform 1 [Danio rerio]	43.5	579	704.77	1407.53	1407.78	68.51	6.30E-05	HLLALTSELANAR
					1683.89	1682.88	1682.85	73.28	1.90E-05	NQEHLATELAELTSK
					1027.33	2052.65	2052.96	44.28	0.012	FYPEDVSEELIQEATQR
106	gi|189529437	PREDICTED: similar to plectin 1 isoform 1 [Danio rerio]	42.4	4530	1032.88	2063.74	2062.11	98.98	4.10E-08	DGHNLISLLEVLSGETLPR
107	gi|189529439	PREDICTED: similar to plectin 1 isoform 2 [Danio rerio]	42.4	4506	1032.88	2063.74	2062.11	98.98	4.10E-08	DGHNLISLLEVLSGETLPR
108	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [	56.6	709	1164.68	1163.67	1164.65	55.10	0.0016	HIEIQVLADK
					826.01	1650.00	1649.84	65.94	0.00011	TVAVHSDVDSSAVHVK
					945.77	1889.53	1887.95	48.08	0.0055	LTGAQAVHPGYGFLSENK
109	gi|189526600	PREDICTED: similar to dystonin [Danio rerio]	43.8	8365	1032.88	2063.74	2062.11	98.98	4.10E-08	DGHNLISLLEVLSGETLPR
110	gi|153792369	si:dkey-151c10.1 [Danio rerio]	32.9	4577	1032.88	2063.74	2062.11	98.98	4.10E-08	DGHNLISLLEVLSGETLPR
111	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	82.1	134	1339.12	2676.23	2675.32	66.46	5.40E-05	ITFTNEEFLVTLPDGSEIHFPNR
112	gi|41055546	hypothetical protein LOC393186 [Danio rerio]	38.1	281	1348.76	1347.75	1347.70	51.96	0.003	VALDTSFVPNTGK
					973.05	1944.09	1942.85	73.38	1.50E-05	SQNGVEFNTSGSTNTDTGK
					1044.26	2086.51	2086.15	55.93	0.00082	VNNASLIGIGYTQSLRPGVK
113	gi|18858959	lactate dehydrogenase A4 [Danio rerio]	48.3	333	755.98	1509.94	1509.77	80.77	3.60E-06	IVADKDYSVTANSK
114	gi|74315945	hypothetical protein LOC613246 [Danio rerio]	54	422	1047.77	2093.53	2092.98	84.98	1.00E-06	ALVGNEASEELQSADGNPHR

115	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (as	62.1	428	644.14	1286.26	1284.69	49.82	0.0053	GALDDISKIPEK
					665.76	1994.24	1994.03	43.33	0.016	YFIEQGHNILLSQSFAK
					784.38	2350.11	2350.26	58.13	0.00043	ISVAGVTSANVEYLAHAIHAVTK
116	gi|47085679	electron-transfer-flavoprotein, beta polypeptide [Danio re	63.8	254	924.89	923.88	924.50	63.43	0.00023	GIHVEVSGK
					601.23	1200.44	1199.71	71.48	3.90E-05	KEEASLIILGK
117	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	52.4	3730	637.94	1273.86	1273.71	79.51	5.90E-06	SKVEEILSELK
					967.39	1932.77	1931.96	72.74	1.80E-05	TLHLDDSIDSVHPIQDK
					1036.26	3105.74	3105.49	38.48	0.027	YDAEEIEAEVSSDVTTEIHNIITT
118	gi|47086819	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	48.6	255	1044.76	2087.51	2086.96	98.21	4.80E-08	AAFDDAIAELDTLSEESYK
119	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	40.3	1035	733.61	1465.21	1463.67	49.86	0.0046	IRDEMASTEQER
					1526.85	1525.84	1524.80	69.48	4.90E-05	DIVPGDIVEVAVGDK
120	gi|41054770	WD repeat domain 1 [Danio rerio]	56.6	606	1296.44	2590.87	2589.21	86.27	5.70E-07	AHDGGIYAVSWSPDSTQLISAS
121	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	64	164	686.49	1370.97	1370.73	87.95	7.60E-07	VVDGLDVVDAIEK
122	gi|47271384	cofilin 2, like [Danio rerio]	80.6	165	996.00	1989.98	1989.06	62.79	0.00017	KEDLVFIFWAPESAPLK
					1207.39	2412.76	2412.16	63.61	0.00012	HIIMEQGQEILQGDEGDPYLK
123	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	52.8	606	810.47	1618.93	1617.74	31.69	0.29	QLCPEMETASPGGIK
					1091.31	2180.60	2179.07	79.39	3.60E-06	GGENIYPAEIEQFLHTHPK
124	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio	69.5	151	757.17	1512.33	1511.69	84.44	1.60E-06	DQGTFEDFVEGLR
125	gi|41055855	aldehyde dehydrogenase 4 family, member A1 [Danio re	40.6	556	1044.55	2087.08	2086.97	68.40	4.60E-05	VGDPVEDFSTFFSAVIDDK
126	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	58.9	141	565.40	1128.79	1128.63	54.53	0.0021	RLDDLASAIR
					1658.57	3315.12	3313.73	47.65	0.0028	EIYPYVIQELRPTLDELGIATPEE
					1694.17	3386.32	3384.77	46.69	0.0032	EIYPYVIQELRPTLDELGIATPEE
127	gi|47087349	coagulation factor II [Danio rerio]	63.5	524	674.76	1347.50	1345.80	80.64	4.30E-06	IVAIDEIIVHPK
128	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio reri	56.4	133	749.63	1497.24	1496.63	69.94	4.40E-05	LGEEFDETTADDR
					813.62	1625.23	1624.72	62.83	0.00022	LGEEFDETTADDRK
129	gi|189519969	PREDICTED: myosin, heavy polypeptide 10, non-muscle	39.7	1973	580.67	1738.97	1737.89	69.98	4.00E-05	KQELEEILHDLESR
					1093.83	2185.64	2184.99	76.48	7.20E-06	HAEQERDELADEISNSASGK
130	gi|41282194	glutamate dehydrogenase 1 [Danio rerio]	51.7	542	785.85	1569.68	1568.77	91.97	2.80E-07	IIAEGANGPTTPDADK
131	gi|51571925	hypothetical protein LOC445486 [Danio rerio]	51	194	902.00	1801.98	1800.95	49.53	0.0043	INSELPVDEVFAIVEK
					965.71	1929.41	1929.05	73.55	1.50E-05	KINSELPVDEVFAIVEK
132	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	56.8	1631	587.14	1172.27	1172.62	59.04	0.00071	LEFEVQVGPR
					925.36	1848.71	1847.86	65.37	0.00011	LSSENADSEIETETPVK
133	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio reri	48.2	413	1041.29	2080.57	2079.97	95.84	8.60E-08	GTGGVDTAAVGDTFDISNLDR
					1119.27	2236.53	2236.07	41.96	0.018	RGTGGVDTAAVGDTFDISNLDR
134	gi|80751141	solute carrier family 8 (sodium/calcium exchanger), mem	31.8	974	985.15	1968.29	1968.04	63.87	0.00014	EGVILPIWTPVNPSFGDK
					1002.61	3004.79	3003.40	32.64	0.11	TEDGTANAGSDYQFTEGVIIFK
135	gi|49274617	tropomyosin 1 alpha [Danio rerio]	39.1	284	777.37	776.36	776.33	34.17	0.29	AADESER
					537.38	1072.75	1072.55	46.75	0.013	LDKENALDR
					622.72	1243.43	1242.65	73.33	2.50E-05	IQLVEEELDR
136	gi|18859505	alpha-tropomyosin [Danio rerio]	29.2	284	777.37	776.36	776.33	34.17	0.29	AADESER
					537.38	1072.75	1072.55	46.75	0.013	LDKENALDR
					622.72	1243.43	1242.65	73.33	2.50E-05	IQLVEEELDR
137	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	48.2	380	691.30	1380.58	1379.71	71.30	3.40E-05	FFEAAVGEAKPSK
138	gi|189535578	PREDICTED: fetuin B [Danio rerio]	48.2	498	1117.51	2233.01	2233.01	59.36	0.00035	KDETHEHDHEIVLDHDHK
					797.59	2389.73	2389.01	53.15	0.0012	AHEHGQDEWEHQHHQYGHK
139	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	71.5	575	602.23	1202.45	1200.63	35.42	0.16	NAGVEGSLVVEK
					814.72	2441.14	2439.35	53.75	0.0011	TALLDAAGVASLLSTAEAVVTEI
					942.90	2825.66	2825.53	79.28	2.50E-06	TALLDAAGVASLLSTAEAVVTEI
140	gi|41151982	major vault protein [Danio rerio]	58.6	863	804.76	1607.51	1607.71	34.39	0.15	DDEGQVQFDGSGQVK
					1019.64	2037.26	2036.88	108.34	4.70E-09	AVEAFIDTQGDEAEEEER
141	gi|27545193	creatine kinase, brain [Danio rerio]	35.4	381	754.52	1507.03	1506.70	35.38	0.12	GGDDLDPNYVLSSR
					894.58	1787.15	1785.94	47.27	0.0074	GIESLSVEALGALDGDLK

					990.39	1978.76	1977.94	66.42	7.80E-05 GTGGVDTAAVGGVFDISNADR
142	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	65.4	697	1302.96	1301.95	1301.66	64.35	0.00018 SHIDELYANIK
143	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filami	62.8	2523	650.58	1299.14	1298.73	38.57	0.068 VTVLFAGQHISK
					720.86	1439.70	1437.71	32.98	0.22 TFEPAEFIIDTR
					824.65	1647.29	1645.89	49.61	0.0051 VHGPGLQSGITNKPNK
					901.26	1800.50	1799.96	62.58	0.00021 VAKPDITDNKDGTVTVK
					1207.46	2412.90	2411.15	54.31	0.001 EGPYSINVLYADEEIPQSPYK
144	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	44.6	1056	1526.85	1525.84	1524.80	69.48	4.90E-05 DIVPGDIVEVAVGDK
145	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	33.1	284	777.37	776.36	776.33	34.17	0.29 AADESER
					622.72	1243.43	1242.65	73.33	2.50E-05 IQLVEEELDR
146	gi|41393141	tropomyosin 3 [Danio rerio]	35.9	248	777.37	776.36	776.33	34.17	0.29 AADESER
					622.72	1243.43	1242.65	73.33	2.50E-05 IQLVEEELDR
147	gi|50345022	small muscle protein, X-linked [Danio rerio]	83.1	83	1037.69	2073.37	2072.97	79.66	3.70E-06 REDTVETEEVSPVTPEEK
148	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	38	757	1066.23	2130.45	2130.11	36.16	0.08 AELDALAALTAGLEETLGSSAK
					732.40	2194.16	2192.18	37.50	0.053 VTLQAIGAQEAALTAIAAHTDK
					893.21	2676.59	2677.37	79.30	2.70E-06 IDSARPQILAAEENLHSMIVDLD
149	gi|21426837	glucose phosphate isomerase b [Danio rerio]	40.3	553	780.76	1559.51	1558.78	80.43	4.10E-06 KELEAGGLSGDNLEK
					1127.20	3378.58	3376.65	55.39	0.00044 VNYHTGPIVWGEPGTNGQHAF
150	gi|59858543	gelsolin a [Danio rerio]	33.3	730	1071.90	2141.79	2141.06	98.83	4.30E-08 MLEVLGEKPDLPEGASDDVK
151	gi|189526930	PREDICTED: similar to c-Cbl associated protein [Danio r	34.1	1015	918.74	1835.46	1834.94	67.53	6.80E-05 HAGLVVTHQQFITNDR
152	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	36.3	523	789.78	1577.54	1577.76	37.55	0.077 YDVQVQIENVEDK
					790.64	1579.27	1577.76	97.12	8.10E-08 YDVQVQIENVEDK
153	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio r	75.1	333	552.89	1103.76	1102.56	37.70	0.099 SDRPELTSAK
					713.59	1425.17	1424.81	56.10	0.0011 LDVAPISDIIEIK
					1105.34	2208.66	2207.12	63.10	0.00015 DPEAPIFQVADYGLVADLFK
154	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	34.2	1079	1268.85	1267.84	1266.75	32.36	0.28 VAISPAGVEALIK
					707.70	1413.39	1412.74	49.47	0.0051 GVIHVGYTDIPSR
					790.14	1578.26	1577.77	42.94	0.021 QGFNVVVESGAGESAK
					922.25	2763.71	2763.39	60.04	0.00022 DGSVVVDLAAEAGGNIETTVPG
155	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reri	55.5	858	1073.30	2144.58	2144.05	65.62	8.60E-05 ARPFPDGLAEDIDKGDVSSR
156	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	52	298	525.09	1048.16	1047.57	57.91	0.00098 VFLDGVDKR
					617.63	1233.24	1232.68	51.16	0.0042 DFLAGGIAAAISK
157	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	64	308	550.28	1098.55	1098.61	51.62	0.004 QLADALKANR
158	gi|51011067	pyruvate kinase, muscle, b [Danio rerio]	59.2	530	904.59	1807.16	1806.98	63.88	0.00016 KGVNLPGANVDLPAVSEK
					942.87	1883.72	1882.90	67.23	6.40E-05 LNFSHGTHEYHAETIK
159	gi|41152448	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	46.2	355	1228.47	2454.93	2454.31	67.96	4.20E-05 LLQYSDAVEHLLTTGQGVILER
160	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	35.9	306	700.18	1398.35	1398.75	68.66	6.10E-05 REEEANLLGQIK
161	gi|52219190	hypothetical protein LOC447942 [Danio rerio]	46.6	103	1167.53	3499.56	3500.62	52.81	0.00075 TKPWPWGDGNHSLFHNPHTN
162	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	43.4	484	818.92	1635.82	1635.85	57.52	0.00075 GLDIVLDPLGGSDTHK
					904.73	1807.45	1806.90	69.62	4.20E-05 HEVISQGGVTHPIDYR
163	gi|166795887	vitellogenin 1 [Danio rerio]	52.3	1362	587.14	1172.27	1172.62	59.04	0.00071 LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.028 THYVINEDPK
164	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	55	1358	587.14	1172.27	1172.62	59.04	0.00071 LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.028 THYVINEDPK
165	gi|68448530	vitellogenin 5 [Danio rerio]	48	1360	587.14	1172.27	1172.62	59.04	0.00071 LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.028 THYVINEDPK
166	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	52.5	244	1073.02	2144.03	2143.98	72.71	1.70E-05 TAFDEAIAELDTLNEDSYK
167	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	43.8	242	1073.02	2144.03	2143.98	72.71	1.70E-05 TAFDEAIAELDTLNEDSYK
168	gi|154707842	methylmalonyl Coenzyme A mutase [Danio rerio]	48.7	757	786.15	1570.29	1568.84	47.95	0.007 NTQIIIQEESGIPK
					870.13	1738.25	1737.81	79.76	4.30E-06 SEFGEHEEIALAHNR
169	gi|116004537	hypothetical protein LOC564694 [Danio rerio]	47	381	754.52	1507.03	1506.70	35.38	0.12 GGDDLDPNYVLSSR
					990.39	1978.76	1977.94	66.42	7.80E-05 GTGGVDTAAVGGVFDISNADR

170	gi|68444865	PREDICTED: dodecenoyl-Coenzyme A delta isomerase	49.5	301	663.70	1325.39	1325.71	64.04	0.00019	IGLVDELVPEDK
171	gi|41393119	valosin containing protein [Danio rerio]	63	806	905.89	1809.76	1809.99	55.96	0.00096	NAPAIIFIDELDAIAPK
					912.63	1823.24	1822.91	66.85	7.70E-05	ELQELVQYPVEHPDK
172	gi|68362804	PREDICTED: similar to Histone H4 replacement CG337	76.7	103	447.35	446.34	445.26	32.55	0.015	GKGGK
					495.62	989.22	988.57	40.93	0.054	VFLENVIR
					591.57	1181.13	1179.61	59.87	0.00053	ISGLIYEETR
					664.19	1326.36	1324.75	49.37	0.0057	DNIQGITKPAIR
173	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	63.1	260	852.76	1703.51	1702.86	86.75	8.30E-07	HGASAVILDLPSSDGHK
174	gi|113679439	hypothetical protein LOC751638 [Danio rerio]	46	126	636.68	1271.35	1272.68	66.20	0.00012	GQDPYSILRPK
					468.43	1402.27	1400.78	36.47	0.11	KGQDPYSILRPK
175	gi|18858399	cadherin 2, neuronal [Danio rerio]	38.8	783	938.76	1875.50	1873.93	45.48	0.01	SAAPHPGDIGEFIHEGLK
					1148.53	3442.55	3440.82	72.69	8.00E-06	YSVTGPGADQNPTGLFIIDPISG
176	gi|47086189	propionyl Coenzyme A carboxylase, beta polypeptide [Da	70.7	557	874.24	1746.46	1744.85	85.36	1.20E-06	AYDMLDIVHGIVDER
177	gi|45387563	ADP-ribosylation factor-like 8Ba [Danio rerio]	45.2	186	1276.92	2551.83	2551.45	68.47	3.50E-05	NELHNLLDKPQLQGIPVLVLGN
178	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio reri	48.2	199	581.73	1161.44	1159.64	63.81	0.00023	TKDGVLEITGK
					920.97	1839.93	1839.94	50.96	0.0029	ISLDVNHFSPEELNVK
179	gi|136256027	phosphorylase, glycogen; brain [Danio rerio]	42.2	843	954.50	1906.99	1905.00	61.61	0.00024	LITSVGEVVNHDPVVGDR
180	gi|50344731	fibrinogen alpha chain [Danio rerio]	41.5	684	677.11	1352.21	1350.70	80.92	3.60E-06	LGISDSEFLTAAK
181	gi|54400460	fibulin 5 [Danio rerio]	40.7	477	1111.43	2220.84	2220.00	80.84	2.50E-06	NSPLPYPEASYPEEPYPDR
182	gi|50540420	branched chain aminotransferase 2, mitochondrial [Dani	55.4	415	900.90	1799.79	1799.02	52.09	0.0023	SSVLKPKPDPSTLVFGK
183	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	54.5	255	633.57	1265.13	1263.70	50.58	0.0042	NVIIAAHGNSLR
					672.48	1342.95	1342.57	41.92	0.031	HGESSWNQENR
					1058.87	2115.72	2115.10	36.73	0.068	DLKPIKPMQFLGDEETVR
184	gi|189517050	PREDICTED: glycine C-acetyltransferase [Danio rerio]	57.9	458	785.68	1569.34	1568.74	68.82	5.70E-05	VQISAAHTDEDIDR
185	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio	61	172	565.40	1128.79	1127.64	45.39	0.017	RLNDLASAIR
					1106.47	3316.39	3314.75	67.87	2.60E-05	EIYPYVIQELKPTLQELGISTPEE
186	gi|41056085	keratin 8 [Danio rerio]	35.6	520	545.21	1088.41	1087.55	50.59	0.0054	KLLEGEEDR
					1009.39	2016.76	2017.16	59.54	0.00036	SLLAPLNLEIDPNIQIVR
187	gi|168229163	cysteine-rich protein 2 [Danio rerio]	65.5	206	990.03	2967.06	2968.41	48.11	0.0031	TLTAGGHAEHDGKPYCHKPCY
					999.96	2996.84	2996.41	42.81	0.01	TLAAGSHAEHDGQPYCHKPCY
188	gi|41053395	glutamate oxaloacetate transaminase 2 [Danio rerio]	62.4	428	926.44	1850.87	1850.98	45.42	0.011	ALDKEYLGIVGLGDFNK
					665.76	1994.24	1994.03	43.33	0.016	YFIEQGHNILLSQSFAK
189	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple	72.7	209	638.04	1274.07	1272.67	50.07	0.0052	SLDKVEQELGR
					920.66	1839.30	1838.03	54.42	0.0013	VSPITINLINVLSENGR
190	gi|18859045	mitochondrial carrier homolog 2 [Danio rerio]	43.7	300	843.43	1684.84	1684.96	56.86	0.00085	VLVQVGHEPLAPTLGR
191	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	65.3	329	865.98	1729.95	1729.95	62.94	0.0002	KGSLLIDSSTIDPAVSK
192	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	40.4	245	782.16	1562.31	1560.73	50.70	0.0038	AVTEGDIELSNEER
					1073.02	2144.03	2143.98	56.16	0.00077	TAFDEAIAELDSLNEESYK
193	gi|50540382	hypothetical protein LOC436930 [Danio rerio]	51.3	460	1078.38	2154.75	2154.01	73.62	1.40E-05	ISVDHLQQFFDNNYTSAR
194	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	33.9	2113	653.09	1304.16	1303.77	57.14	0.00099	RCLIEIFGILK
195	gi|189532434	PREDICTED: im:7160733 [Danio rerio]	36.5	1248	653.09	1304.16	1303.77	57.14	0.00099	RCLIEIFGILK
196	gi|56118264	actinin alpha 3 [Danio rerio]	35.6	896	826.12	1650.22	1648.81	71.27	3.30E-05	KAGTQIENIEEDFR
197	gi|41054603	actinin alpha 4 [Danio rerio]	39.7	901	826.12	1650.22	1648.81	71.27	3.30E-05	KAGTQIENIEEDFR
198	gi|153791915	hypothetical protein LOC100006671 [Danio rerio]	37.7	151	826.12	1650.22	1648.81	71.27	3.30E-05	KAGTQIENIEEDFR
199	gi|51467931	enolase 2 [Danio rerio]	56.7	434	1147.92	2293.83	2295.13	40.61	0.024	SGETEDTFIADLVVGLCTGQIK
					1009.55	3025.62	3024.58	41.01	0.015	HIADLAGNTELVLPVPAFNVING
200	gi|150378483	heat shock protein, alpha-crystallin-related, b11 [Danio r	57.6	205	1113.16	2224.31	2223.99	70.86	2.50E-05	NPALQNSEPENQAVEAEAAEN
201	gi|61651682	fibronectin 1b [Danio rerio]	47.9	2408	806.73	2417.17	2416.31	46.22	0.0064	SAPLVGTATTQLISGLPSLPSHG
					1070.65	3208.93	3208.44	59.70	0.00019	INTVGPTGHDSTDAHGQHVEYT
202	gi|47085833	glyceraldehyde-3-phosphate dehydrogenase, spermatog	21.2	335	718.69	1435.37	1434.76	70.02	4.60E-05	GAHQNIIPASTGAAK
203	gi|57528846	hypothetical protein LOC445255 [Danio rerio]	49.3	207	770.14	1538.26	1537.87	69.95	4.30E-05	AEEDKIPLLLVGNK
204	gi|18858657	fatty acid binding protein 7, brain, a [Danio rerio]	28.8	132	749.63	1497.24	1496.63	69.94	4.40E-05	LGEEFDETTADDR

205	gi|54606886	hexokinase 1 [Danio rerio]	60.1	918	638.68	1275.35	1274.50	64.37	0.00019	HMDMVEGDEGR
					862.32	1722.62	1723.83	36.50	0.096	TKYDDAVDDLSLNAGK
206	gi|55925387	carnitine palmitoyltransferase II [Danio rerio]	53	668	816.40	1630.78	1631.90	43.55	0.02	DGNLIKPAEVQAHLK
					1127.33	2252.65	2252.11	56.20	0.00073	YLAAQRPLLNDEQYSNTEK
207	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	80.7	238	1028.82	2055.62	2055.00	68.70	4.40E-05	SHEGDDPLLQYVVNNSLR
208	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [Da	55.5	789	1115.74	2229.46	2229.10	60.89	0.00024	TSYDVSDSGQLEHVVVNRPK
209	gi|52219158	aquaporin 8 [Danio rerio]	20.4	260	1058.75	2115.49	2113.97	68.39	4.60E-05	SELFTVATGDGGDNHQNQPK
210	gi|189546569	PREDICTED: complement component 3 [Danio rerio]	40.6	1648	763.11	1524.21	1523.75	66.87	8.80E-05	AAVVHGEMVGDVQGR
211	gi|51010955	hypothetical protein LOC445042 [Danio rerio]	39.4	104	608.74	1215.47	1215.65	66.19	0.00014	ALTAGSEASGKPK
212	gi|41152334	ATP synthase, H+ transporting, mitochondrial F0 comple	46	161	573.43	1144.85	1144.54	66.01	0.00015	IDAQEQEANK
213	gi|57526735	glutaredoxin 5 [Danio rerio]	29	155	1106.67	2211.33	2209.97	64.91	9.70E-05	MHGVDNYASYNVLDDQDVR
214	gi|41056175	programmed cell death 8 (apoptosis-inducing factor) [Dar	43.7	751	736.65	1471.28	1471.66	64.47	0.00016	SAGLEVDSDFGGYR
215	gi|27545305	laminin, gamma 1 [Danio rerio]	63.3	1593	665.17	1328.32	1327.68	63.97	0.0002	RAEAALGNAAADAK
216	gi|189515773	PREDICTED: amylo-1, 6-glucosidase, 4-alpha-glucanotra	49.9	1532	894.83	1787.64	1787.00	63.95	0.00016	GLPALIQDHPHLHAIR
217	gi|189536606	PREDICTED: id:ibd5057 [Danio rerio]	50.6	1830	418.88	835.75	837.47	57.52	0.0011	VVAAPPER
					1051.37	3151.07	3149.88	40.31	0.017	TASEKPPKPLEKPVKPALEKPLK
218	gi|41054571	citrate synthase [Danio rerio]	29.1	468	550.50	1098.99	1097.53	33.89	0.25	HLPNDPMFK
					881.85	1761.69	1761.88	63.55	0.00018	GLVYETSVLDPDEGIR
219	gi|54400426	ATP synthase, H+ transporting, mitochondrial F0 comple	68.3	252	764.44	1526.87	1526.78	52.48	0.0025	LDYQVELQNLHR
220	gi|125828659	PREDICTED: hypothetical protein LOC449551 [Danio re	84.1	126	1270.39	2538.76	2538.31	62.53	0.00014	LVVNDGPDGGQSVYHIHIHVLG
221	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	39.5	6009	579.12	1156.23	1155.65	54.20	0.0021	LKGDVDVSVPK
					651.60	1301.18	1299.69	35.67	0.13	LMGSNVDLNLPK
222	gi|32401408	annexin A11b [Danio rerio]	29.5	485	822.76	1643.51	1642.75	58.18	0.00061	SLYTHISGDTSGDYK
					886.82	1771.62	1770.84	42.54	0.022	SLYTHISGDTSGDYKK
223	gi|50344950	hypothetical protein LOC415237 [Danio rerio]	74.6	118	859.19	1716.36	1715.99	61.34	0.0003	ILVLFYPLEPSQIGK
224	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	26.5	204	853.72	1705.42	1704.91	61.21	0.00033	GATYGKPVHHGVNQIK
225	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	65.2	448	780.37	1558.73	1557.89	48.92	0.0056	LLEVIDGHIPLPSR
					920.26	1838.50	1836.96	44.61	0.013	DKPHLNIGTIGHVDHGK
226	gi|41055823	hypothetical protein LOC393488 [Danio rerio]	75.3	186	968.51	967.50	966.55	60.55	0.00047	HVLATLGEK
227	gi|50540186	hypothetical protein LOC436833 [Danio rerio]	35.4	229	1079.82	2157.63	2156.16	60.52	0.00028	AGLTASEVDELLTLATSQPIK
228	gi|54261767	succinate-CoA ligase, ADP-forming, beta subunit [Danio	53.9	466	1294.16	2586.30	2585.29	50.09	0.0023	LHGGTPANFLDVGGGATAQQV
229	gi|125842393	PREDICTED: zgc:103738 [Danio rerio]	40.3	77	987.76	2960.25	2961.35	52.44	0.0011	TLSAGSHAEHEGKPYCNNPCY
230	gi|56693257	hypothetical protein LOC494050 [Danio rerio]	55.4	368	1035.13	3102.35	3100.58	51.88	0.0013	ILLDQGQEHTVETPHGVLHVTV
231	gi|41152175	ribosomal protein S7 [Danio rerio]	53.6	194	733.47	1464.93	1464.94	60.08	0.00044	KAIIIFVPVPQLK
232	gi|116487349	carboxylesterase 2-like [Danio rerio]	53.3	555	806.67	2416.99	2415.27	57.57	0.00048	GSPAVVEQYLGIPFAQPPVGPH
233	gi|125843378	PREDICTED: si:dkey-38l12.3 [Danio rerio]	53.4	549	806.67	2416.99	2415.27	57.57	0.00048	GSPAVVEQYLGIPFAQPPVGPH
234	gi|40363541	S-adenosylhomocysteine hydrolase [Danio rerio]	44.1	433	480.61	1438.81	1437.75	58.91	0.00057	KLDEEVAAAHLDK
235	gi|189520524	PREDICTED: similar to Troponin T2, cardiac [Danio rerio	31.7	243	509.03	1016.05	1015.47	58.74	0.00085	VDFDDIHR
236	gi|31377814	troponin T1, skeletal, slow [Danio rerio]	25.2	290	509.03	1016.05	1015.47	58.74	0.00085	VDFDDLHR
237	gi|189517959	PREDICTED: hypothetical protein LOC556703 [Danio re	23.7	249	509.03	1016.05	1015.47	58.74	0.00085	VDFDDIHR
238	gi|68357880	PREDICTED: similar to slow troponin T 1 [Danio rerio]	7.8	268	509.03	1016.05	1015.47	58.74	0.00085	VDFDDIHR
239	gi|50539832	lysyl-tRNA synthetase [Danio rerio]	29.9	602	1124.52	2247.02	2247.14	58.56	0.00042	YNHLQPGDHLTDVVLNLSGR
240	gi|41056209	hypothetical protein LOC393532 [Danio rerio]	51.6	490	1012.59	2023.16	2022.00	56.97	0.00068	HILDTHGLDPHQATASGPR
241	gi|189517274	PREDICTED: hypothetical protein [Danio rerio]	42.3	797	602.46	1202.91	1201.66	47.02	0.011	MRNLTEGILR
242	gi|47550715	heterogeneous nuclear ribonucleoprotein A0 [Danio rerio	43.9	314	843.62	1685.23	1683.72	57.64	0.00071	GFGFVHFEDNDSADK
243	gi|189540123	PREDICTED: similar to Filamin-C (Gamma-filamin) (Filar	61.2	2702	1277.89	2553.77	2553.25	56.45	0.00055	FNNEHIPDSPFIVPVATLSDDAR
244	gi|68379126	PREDICTED: hypothetical protein LOC767664 [Danio re	38.3	81	1494.55	1493.54	1493.82	45.21	0.014	IFLEDNGLPVHIK
					1494.87	1493.86	1493.82	50.07	0.0042	IFLEDNGLPVHIK
245	gi|41053611	hypothetical protein LOC393828 [Danio rerio]	73.2	213	1200.94	2399.87	2399.16	56.18	0.00068	SYHSPWEEAIINDPTLADTLK
246	gi|47085891	cytochrome b5 [Danio rerio]	38	137	1090.16	2178.31	2177.91	56.12	0.00073	EQAGGDATESFEDVGHSTDAR
247	gi|189540214	PREDICTED: similar to myosin heavy chain, partial [Dani	45.5	809	1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
248	gi|189540222	PREDICTED: similar to myosin, heavy polypeptide 2, fas	42.1	950	1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK

249	gi|156616344	hypothetical protein LOC100124599 [Danio rerio]	71.2	278	1489.81	1488.80	1488.74	50.47	0.0042	ENQSVLITGESGAGK
250	gi|41053746	RNA binding protein with multiple splicing 2 [Danio rerio]	33.5	200	772.69	1543.36	1542.88	56.08	0.0011	TLFVSGLPTDIKPR
251	gi|90093334	hypothetical protein LOC563679 [Danio rerio]	63	805	905.89	1809.76	1809.99	55.96	0.00096	NAPAIIFIDELDAIAPK
252	gi|56790313	homeo box B9a [Danio rerio]	50.6	255	710.16	1418.30	1416.74	55.87	0.0013	MEPLLGHLGEPPK
253	gi|44917595	alcohol dehydrogenase 8b [Danio rerio]	88.6	376	966.09	2895.25	2894.48	55.82	0.00051	GFPTILGHEAAGVVESVGPGVT
254	gi|168229182	zgc:171912 [Danio rerio]	56	459	562.97	1123.92	1123.61	48.49	0.0073	IIEKNAGHSR
255	gi|47085971	eukaryotic translation initiation factor 5A [Danio rerio]	61.9	155	678.36	1354.70	1354.76	55.66	0.0012	VHLVGIDIFTNK
256	gi|21426835	glucose phosphate isomerase a [Danio rerio]	44.7	553	1127.20	3378.58	3376.65	55.39	0.00044	VNYHTGPIVWGEPGTNGQHAF
257	gi|90652819	hypothetical protein LOC664756 [Danio rerio]	53.7	462	972.67	2914.99	2915.57	39.60	0.023	EGGANGVTLLEALDSILPPSRPT
258	gi|41152375	mitochondrial ATP synthase gamma-subunit [Danio rerio	54.5	292	1097.58	1096.57	1095.60	55.25	0.0015	HLIIGVSSDR
259	gi|160333682	heat shock protein 8 [Danio rerio]	45.9	649	562.34	1122.67	1122.53	35.62	0.14	YKAEDDVQR
					887.36	1772.70	1772.81	39.80	0.043	NQTAEREEFEHQQK
					1131.27	2260.52	2259.14	47.51	0.0053	SINPDEAVAYGAAVQAAILSGD
260	gi|41055654	hypothetical protein LOC393165 isoform 2 [Danio rerio]	81.5	628	537.56	1073.11	1074.49	34.53	0.22	DQDESVVQR
					1079.28	2156.54	2155.09	56.88	0.00064	ILAQITGTENDQAQESRPGK
261	gi|47086649	F-actin capping protein alpha-1 subunit [Danio rerio]	47.6	286	717.26	2148.76	2147.02	54.51	0.0011	LDGSEDQVLITEHGDLGHGR
262	gi|50539806	hypothetical protein LOC436642 [Danio rerio]	54.2	323	976.35	1950.69	1950.01	53.72	0.0014	ALESAYGSEKPSLTSAAIR
263	gi|189518755	PREDICTED: similar to malic enzyme 2, NAD(+)-depend	65.4	581	1093.78	2185.54	2184.23	53.23	0.0015	SFLDAVNVIKPTAIIGVSGAGR
264	gi|57525624	malic enzyme 2, NAD(+)-dependent, mitochondrial [Dani	62	581	1093.78	2185.54	2184.23	53.23	0.0015	SFLDAVNVIKPTAIIGVSGAGR
265	gi|38488700	phosphoglycerate mutase 1 [Danio rerio]	42.5	254	835.62	1669.22	1668.89	52.44	0.0023	ALPFWNDEIVPQIK
266	gi|55926092	heat shock 10kD protein 1 (chaperonin 10) [Danio rerio]	65	100	770.78	1539.54	1539.86	52.40	0.0024	VLQATVVAVGPGSTNK
267	gi|52218912	enoyl Coenzyme A hydratase, short chain, 1, mitochondr	54.3	291	1056.69	2111.36	2110.12	52.29	0.0019	AQFGQPEILLGTIPGAGGTQR
268	gi|30410758	keratin 18 [Danio rerio]	54.3	431	1000.00	1997.99	1998.02	51.86	0.0022	GNIQHQTQEYEALLNIK
269	gi|18858281	apolipoprotein A-I [Danio rerio]	40.1	262	912.77	1823.53	1821.93	50.61	0.0032	EKLEPVFQEYSALNR
270	gi|51011113	hydroxyacyl-Coenzyme A dehydrogenase [Danio rerio]	70.6	309	923.36	2767.06	2767.42	51.37	0.0017	NVSTSTDAASVVHGTDLVVEAI
271	gi|47271398	ribosomal protein L7 [Danio rerio]	41.5	246	680.91	1359.81	1359.62	51.36	0.0036	TTHFVEGGDAGNR
272	gi|41055997	hypothetical protein LOC393098 [Danio rerio]	54.5	343	863.60	1725.19	1724.92	50.74	0.0034	DSTVLAHVMKLLNER
273	gi|18858981	lamin b2 [Danio rerio]	49.7	583	545.21	1088.41	1087.55	50.59	0.0054	KLLEGEEDR
274	gi|125849603	PREDICTED: similar to keratin 8 [Danio rerio]	31.3	438	545.21	1088.41	1087.55	50.59	0.0054	KLLEGEEDR
275	gi|189523135	PREDICTED: similar to type II keratin E1 [Danio rerio]	48.2	311	545.21	1088.41	1087.55	50.59	0.0054	KLLEGEEDR
276	gi|157743314	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	28.5	186	866.17	1730.33	1729.87	50.53	0.0035	EKGDGPWFQIPTIDK
277	gi|148229906	hypothetical protein LOC100037332 [Danio rerio]	30.1	302	550.67	1099.32	1098.64	50.39	0.0056	LKQELAELR
278	gi|68448495	hypothetical protein LOC100003906 isoform 1 [Danio reri	47.3	915	1373.97	4118.89	4117.98	50.23	0.00095	SGTPGFSHHHYTTNSGQPGLH
279	gi|37497110	ribophorin I [Danio rerio]	34.4	598	813.09	2436.23	2435.30	50.20	0.0024	VETVFSHVLKPFPTHITQAER
280	gi|189516116	PREDICTED: similar to ribophorin I [Danio rerio]	21.6	505	813.09	2436.23	2435.30	50.20	0.0024	VETVFSHVLKPFPTHITQAER
281	gi|62955727	NADH dehydrogenase (ubiquinone) 1 beta subcomplex,	22.9	175	814.41	1626.81	1625.79	50.13	0.0041	EVQQLQSETPADGPK
282	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Dar	40.8	2115	1419.69	2837.37	2835.44	49.72	0.0023	GAFTPSPLDPASTSDSHIASLS
283	gi|50539996	peroxiredoxin 2 [Danio rerio]	67	197	1318.69	2635.36	2634.36	36.61	0.051	IGVELIAASTDSHFSHLAWINTP
284	gi|189522138	PREDICTED: similar to paxillin [Danio rerio]	38.3	527	1147.86	2293.70	2294.99	42.47	0.016	TWHPEHFVCTHCQEEIGSR
285	gi|41055688	diaphorase (NADH) (cytochrome b-5 reductase) [Danio re	77	304	842.95	1683.88	1683.90	49.44	0.0046	DILLKDELEEIQAR
286	gi|189517210	PREDICTED: similar to ATP-binding cassette, sub-family	47.5	1518	551.55	1101.08	1099.59	49.30	0.0077	IIEAAEGEIR
287	gi|162138946	hypothetical protein LOC562705 [Danio rerio]	48.5	307	549.17	1096.33	1094.59	49.23	0.0062	KYGSVTVWR
288	gi|125854185	PREDICTED: hypothetical protein [Danio rerio]	24.3	645	673.68	1345.35	1346.62	48.11	0.0079	EEEEEQLKADK
289	gi|189528839	PREDICTED: similar to LOC567732 protein [Danio rerio]	46.6	1442	988.87	2963.58	2964.31	50.87	0.0017	VFSSDGSSTVTVQSAGDSHHF
290	gi|189528837	PREDICTED: similar to LOC567732 protein [Danio rerio]	47.4	1157	988.87	2963.58	2964.31	50.87	0.0017	VFSSDGSSTVTVQSAGDSHHF
291	gi|68354684	PREDICTED: coiled-coil domain containing 47 [Danio rer	55.7	492	851.10	1700.18	1698.86	45.80	0.01	IQRPPEDSIQPYEK
292	gi|30231250	cholinergic receptor, muscarinic 2 [Danio rerio]	34.5	495	418.31	417.30	418.22	37.37	0.0012	AGGSK
293	gi|50345068	dehydrogenase/reductase (SDR family) member 1 [Dani	69.4	310	909.43	1816.84	1815.86	47.68	0.0063	YKDVFTNGETTELSGR
294	gi|56118753	troponin C, slow [Danio rerio]	36	161	602.40	1202.78	1202.58	47.42	0.0099	AAAEQLTDEQK
295	gi|57222259	talin 1 [Danio rerio]	53	2538	1059.58	3175.71	3174.57	47.34	0.0035	EAVDDLGSTLAEVASAAGAVG
296	gi|47086623	monocarboxylate transporter 4 [Danio rerio]	56.7	508	946.72	1891.42	1889.91	47.08	0.0069	ELESIEVDSIEVENASK
297	gi|125814831	PREDICTED: similar to zinc finger protein 585B [Danio re	64.1	298	838.32	1674.63	1672.88	46.69	0.009	EESEDVKIEEIIIK

298	gi|189530311	PREDICTED: hypothetical LOC555629 [Danio rerio]	61.6	401	796.88	1591.74	1591.82	46.57	0.0093	QKMSLLSSNTEINK
299	gi|189524989	PREDICTED: neurobeachin-like 2 [Danio rerio]	48	1495	596.25	1190.48	1188.58	45.64	0.015	GSYAIEIHDGK
300	gi|189533816	PREDICTED: hypothetical protein [Danio rerio]	41.2	1020	493.60	985.18	983.60	45.55	0.018	QLIEQLLK
301	gi|189523776	PREDICTED: hypothetical protein LOC798920 isoform 1	83.4	265	685.11	1368.20	1367.61	45.43	0.013	TRMYNTQDDPK
302	gi|48597012	ribosomal protein L23a [Danio rerio]	25.2	155	621.67	1241.33	1240.68	45.28	0.014	VNTLIRPDGEK
303	gi|189522914	PREDICTED: similar to RAS and EF-hand domain contai	49.2	551	506.72	1011.42	1012.59	45.19	0.016	IVLAGDAAVGK
304	gi|189525785	PREDICTED: similar to AT rich interactive domain 5B (M	51.6	935	673.32	1344.62	1344.72	45.14	0.015	KQEGSVQESIIK
305	gi|189532951	PREDICTED: hypothetical protein [Danio rerio]	29.3	570	1001.67	2001.32	2000.01	44.93	0.011	YVIDTSDVVTNYKELNK
306	gi|41152024	glycoprotein, synaptic 2 [Danio rerio]	31.2	308	608.63	1215.25	1215.61	44.90	0.018	HYEVEILDAK
307	gi|189523571	PREDICTED: similar to mcf.2 transforming sequence-like	53.3	929	889.20	1776.39	1774.95	44.83	0.014	ESSPLFAADVITELKR
308	gi|125806044	PREDICTED: similar to 19.9kD myosin light chain [Danio	28.3	173	669.26	2004.76	2002.97	42.20	0.02	DGFIDKEDLHDMLASLGK
309	gi|47550703	myosin, light polypeptide 9, like [Danio rerio]	45.9	172	669.26	2004.76	2002.97	42.20	0.02	DGFIDKEDLHDMLASLGK
310	gi|125850307	PREDICTED: CFH protein [Danio rerio]	72	751	1101.66	2201.30	2200.96	44.39	0.011	DDITYENVEPVSEASYADGK
311	gi|189528635	PREDICTED: similar to odorant receptor [Danio rerio]	50.5	305	797.72	1593.43	1591.89	44.35	0.016	LLTDLLSDTHLVPR
312	gi|47086899	par-6 partitioning defective 6-like protein gamma [Danio r	6	434	442.43	882.85	882.51	42.80	0.026	LIMTIHR
313	gi|125843259	PREDICTED: polymerase (RNA) III (DNA directed) polyp	55.9	1130	585.65	1169.29	1169.70	44.34	0.02	VILIQEQLSK
314	gi|45387877	par-3 partitioning defective 3 homolog [Danio rerio]	40.3	1127	470.48	1408.42	1408.67	44.24	0.017	TLSPSPDDHERR
315	gi|189526852	PREDICTED: similar to G2/M-phase specific E3 ubiquitin	41.9	762	898.52	1795.02	1794.80	44.16	0.014	SNMEFAINNTHGFGKE
316	gi|189519924	PREDICTED: similar to Uncharacterized protein KIAA046	40.1	2775	664.74	1991.18	1992.00	44.09	0.013	VGEDSMSGDPLSKLPVPHK
317	gi|189519630	PREDICTED: similar to centrosomal protein 110kDa [Dar	38	1959	551.48	1100.95	1099.62	43.75	0.027	LEIAEKELR
318	gi|125815320	PREDICTED: similar to Cystine/glutamate transporter (Ar	52.4	492	476.65	951.28	952.38	43.97	0.022	VCTDGGSEK
319	gi|189529618	PREDICTED: similar to Glutamate [NMDA] receptor subu	36.7	1924	418.31	417.30	418.22	37.37	0.0012	AGGSK
					501.48	500.47	501.28	31.42	0.096	RGGGR
320	gi|122114635	hypothetical protein LOC613021 [Danio rerio]	36.4	1176	418.31	417.30	418.22	37.37	0.0012	AGGSK
321	gi|55926060	seven in absentia 2-like [Danio rerio]	39	331	418.31	417.30	418.22	37.37	0.0012	AGGSK
322	gi|47086263	phosphoglucomutase 2 [Danio rerio]	45.8	611	522.11	1042.20	1043.57	43.80	0.025	ELNRNTAVK
323	gi|123708080	hypothetical protein LOC791153 [Danio rerio]	38.8	304	916.46	915.45	914.55	43.74	0.028	IVATAKAGGK
					566.56	1131.11	1129.61	35.10	0.18	GEELSAAAVKR
324	gi|47086477	ribosomal protein L13a [Danio rerio]	20	205	634.75	1267.49	1265.65	43.73	0.02	YQAITATLEEK
325	gi|121583897	hypothetical protein LOC562692 [Danio rerio]	24.5	384	816.81	1631.60	1631.81	43.59	0.019	ELEEKVAMLEAENK
326	gi|52218992	hypothetical protein LOC447834 [Danio rerio]	60.1	248	662.36	1322.70	1321.71	43.45	0.021	TLLGGGGVDGAIHR
327	gi|68435369	PREDICTED: similar to Histone H1.5 (H1 VAR.5) (H1b) [	53.9	206	512.62	1023.22	1022.62	43.39	0.025	HGVSLAALKK
328	gi|113679269	hypothetical protein LOC751661 [Danio rerio]	39.6	202	512.62	1023.22	1022.62	43.39	0.025	HGVSLAALKK
329	gi|189541652	PREDICTED: similar to Myosin-3 (Myosin heavy chain 3)	30.8	882	659.27	1316.53	1315.65	43.35	0.024	ELELELDAEQK
330	gi|189530862	PREDICTED: wu:fb54a03 [Danio rerio]	32.7	727	401.07	800.12	800.46	43.33	0.032	ELEGLLK
331	gi|125848202	PREDICTED: similar to arachidonate lipoxygenase 3 [Da	29.5	722	635.12	1268.23	1267.71	39.82	0.05	LADLPTQVINGK
332	gi|18859107	non-metastatic cells 2, protein (NM23B) expressed in [Da	57.5	153	1088.81	3263.40	3261.62	48.41	0.0024	NIIHGSDSVDSANTEISLWFKPE
333	gi|189529038	PREDICTED: similar to Insulin receptor substrate 1-B (IR	45.4	1136	418.17	834.32	833.40	42.96	0.036	ELSCPGTK
334	gi|189531190	PREDICTED: im:7145859 isoform 1 [Danio rerio]	33.2	677	1052.47	2102.92	2102.03	42.90	0.017	EVDEVDAALSDLEITLEGGK
335	gi|189528657	PREDICTED: hypothetical protein LOC503600 [Danio rer	44.7	1677	472.54	943.07	942.49	42.73	0.034	HELIEFR
336	gi|53292609	clathrin, heavy polypeptide a (Hc) [Danio rerio]	47.4	1680	472.54	943.07	942.49	42.73	0.034	HELIEFR
337	gi|121583924	hypothetical protein LOC335781 [Danio rerio]	48.3	147	552.33	1102.64	1102.65	42.54	0.034	FIAVAVSALGR
338	gi|55925317	hypothetical protein LOC492525 [Danio rerio]	33.7	398	530.65	1059.29	1059.57	42.47	0.037	EKNNSLSLR
339	gi|123702724	hypothetical protein LOC791201 [Danio rerio]	50	440	737.77	1473.52	1472.75	39.98	0.046	QDLELQMENLLK
340	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	49.2	679	552.60	1103.19	1102.64	42.41	0.035	YKDVVVGVPK
341	gi|41055969	hypothetical protein LOC393494 [Danio rerio]	35.2	244	472.13	942.24	943.42	42.38	0.034	QDVDGDAPK
342	gi|41055708	proteasome (prosome, macropain) 26S subunit, non-ATF	43.3	503	1294.90	2587.79	2586.35	42.35	0.014	EFLLGFLEQPVEIEGDVPFRPR
343	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	18.1	448	709.08	1416.14	1415.74	42.27	0.029	EALGAENIQSTKR
344	gi|60279665	protocadherin 15b [Danio rerio]	36.4	1907	401.07	800.12	799.52	41.99	0.043	ELKGILK
345	gi|189521167	PREDICTED: MAP/microtubule affinity-regulating kinase	49.8	739	551.27	1100.52	1100.67	41.68	0.043	FLILNPTKR
346	gi|55742450	coiled-coil domain containing 80 [Danio rerio]	24.7	867	551.27	1100.52	1099.59	41.66	0.043	EEEIVPTKR
347	gi|189518076	PREDICTED: filamin C, gamma b (actin binding protein 2	44.8	2732	1277.89	2553.77	2554.23	37.76	0.041	FNDEHIPDSPFIVPIASLSDDAR

348	gi|39752649	kelch repeat and BTB (POZ) domain containing 10 [Dani	37	605	544.27	543.26	543.31	41.53	0.022	LNAAR
349	gi|28201964	erythrocyte membrane protein band 4.1 (elliptocytosis 1,	33.5	1534	583.60	1165.19	1164.71	41.44	0.036	IELVLPEKPK
350	gi|157073897	ubiquinol-cytochrome c reductase, Rieske iron-sulfur poly	42.1	273	1132.71	2263.40	2263.11	41.41	0.021	EIETEAGVNLAELRDPQHDK
351	gi|189530012	PREDICTED: wu:fb94b04 [Danio rerio]	43.8	762	550.32	1098.62	1098.61	41.37	0.044	KLNEAQQLR
352	gi|56693225	F-box protein 44 [Danio rerio]	54.7	276	665.84	1329.67	1330.68	36.18	0.02	KEPIDTFQPEK

DMSO replicate 1

Protein #	Accession ID	Protein name	Protein coverage	length	peptide *m/z*	peptide Mr*expt*	peptide Mr*calc*	peptide score	pep_expe ct	peptide sequence
1	gi|74315904	alpha globin-like [Danio rerio]	72	143	559.16	1116.30	1114.56	62.82	0.00064	ADEIGAEALAR
					590.05	1178.09	1175.62	81.86	7.00E-06	TIMGAVGEAISK
					684.20	1366.38	1365.73	83.43	4.40E-06	FFNNLALALSEK
					932.40	1862.78	1863.88	123.63	3.90E-10	TYFSHWSDLSPGSGPVK
					934.07	1866.12	1868.00	127.17	1.70E-10	IDDLVGGLAALSELHAFK
					623.13	1866.35	1863.88	43.57	0.039	TYFSHWSDLSPGSGPVK
					934.35	1866.68	1868.00	120.89	7.30E-10	IDDLVGGLAALSELHAFK
					996.15	1990.29	1991.97	89.92	8.50E-07	TYFSHWSDLSPGSGPVKK
					1009.90	3026.67	3025.62	60.45	0.00053	TIMGAVGEAISKIDDLVGGLAAL
2	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	74.1	143	559.16	1116.30	1114.56	62.82	0.00064	ADEIGAEALAR
					582.04	1162.06	1161.61	77.01	2.20E-05	TIMGAVGEAVSK
					684.20	1366.38	1365.73	83.43	4.40E-06	FFNNLALALSEK
					924.15	1846.28	1847.88	110.05	9.00E-09	TYFSHWADLSPGSGPVK
					934.07	1866.12	1868.00	127.17	1.70E-10	IDDLVGGLAALSELHAFK
					660.43	1978.26	1975.98	65.55	0.00024	TYFSHWADLSPGSGPVKK
3	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	58.1	1936	918.52	917.51	917.48	44.02	0.054	VTVETQGGK
					496.07	990.13	989.50	55.65	0.0033	SNNFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					554.06	1106.11	1104.58	44.72	0.036	SNTAAASLDKK
					1182.68	1181.67	1179.58	42.70	0.053	DFEISQLNSK
					1208.62	1207.61	1207.55	55.68	0.0028	LQAENDEFSR
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					619.88	1237.74	1237.63	49.48	0.011	EADVLQQNPPK
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					646.59	1291.16	1288.63	51.30	0.008	DSQLQLDDSLR
					650.14	1298.26	1297.56	53.69	0.0042	TLEDQMNEYR
					654.56	1307.11	1307.64	84.62	3.50E-06	NSFSQQLEDLK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00022	LQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					699.61	1397.21	1397.75	78.26	1.40E-05	NALLQAELEELR
					708.42	1414.83	1414.73	99.72	1.10E-07	LAEQELLDVTER
					733.10	1464.19	1463.68	59.68	0.001	LSEKDEEMEQVK
					738.40	1474.78	1473.68	90.43	9.20E-07	VEELEEELEAER
					748.76	1495.50	1495.73	54.59	0.0032	KLQHELDEAEER
					751.66	1501.31	1499.75	102.78	5.30E-08	LQEAEEAVEAVNAK
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					754.50	1506.99	1506.60	38.10	0.15	EEQAEADGTEDADK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					770.71	1539.41	1539.77	76.29	2.20E-05	DYHIFYQILSNK
					771.84	1541.67	1541.83	91.51	6.90E-07	IDDEQSIIIQLQK

					771.90	1541.78	1542.83	96.87	2.00E-07	KLAEQELLDVTER
					772.38	1542.74	1541.83	64.33	0.00037	IDDEQSIIIQLQK
					1543.94	1542.93	1542.83	92.72	5.40E-07	KLAEQELLDVTER
					772.73	1543.45	1541.83	60.07	0.00099	IDDEQSIIIQLQK
					802.72	1603.43	1602.78	73.98	4.00E-05	SNDDLKENTAIVER
					806.68	1611.34	1610.75	79.68	1.00E-05	AAEESEEQANVHLGK
					810.76	1619.50	1619.78	68.97	0.00012	LSEKDEEMEQVKR
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					823.93	1645.84	1645.82	111.90	6.60E-09	NLTEEMAALDDIIAK
					844.34	1686.67	1684.83	55.53	0.0028	LELDDVASSMEHIVK
					845.48	1688.95	1688.88	92.61	5.60E-07	GQNVQQVNYAIGALSK
					852.23	1702.45	1701.82	98.48	1.30E-07	LQNEIEDLMVDVER
					859.76	1717.51	1717.85	103.10	4.80E-08	NEDPLNETVVGLYQK
					862.60	1723.19	1721.94	82.68	5.10E-06	VQLLHSQNTSLINQK
					893.74	1785.47	1786.87	131.68	6.40E-11	TIDTLQSALESETHSR
					896.44	1790.86	1790.76	78.77	1.30E-05	QREEQAEADGTEDADK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					934.34	1866.67	1867.93	130.58	7.80E-11	DLEEATLQHEATAATLR
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					981.26	1960.50	1957.98	104.58	3.00E-08	ILQEEISDLTEQLGEGGK
					989.22	1976.43	1976.89	60.09	0.00084	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2086.04	94.86	2.70E-07	VKLEQQVDDLEGSLEQEK
4	gi|41053652	myoglobin [Danio rerio]	74.1	147	550.57	1099.12	1098.58	99.70	1.20E-07	AGLDAAGQGALR
					779.82	1557.62	1557.74	87.48	1.80E-06	VMDAVIGDIDGYYK
					1011.43	2020.84	2020.10	84.28	3.20E-06	GDHAALLKPLANTHANIHK
					1110.88	2219.75	2219.23	113.23	3.80E-09	AKGDHAALLKPLANTHANIHK
					1127.78	2253.55	2253.18	110.97	6.60E-09	FSGISQGDLAGSPAVAAHGATV
					1192.16	2382.31	2381.27	90.70	6.40E-07	FSGISQGDLAGSPAVAAHGATV
					946.44	2836.30	2834.54	54.67	0.0022	GDHAALLKPLANTHANIHKVALN
5	gi|163644331	ventricular myosin heavy chain [Danio rerio]	45.9	1938	496.07	990.13	989.50	55.65	0.0033	SNNFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00022	IQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					748.76	1495.50	1495.73	54.59	0.0032	KIQHELDEAEER
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					823.93	1645.84	1645.82	111.90	6.60E-09	NLTEEMAALDDIIAK
					862.60	1723.19	1721.94	82.68	5.10E-06	VQLLHSQNTSLLNQK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					934.34	1866.67	1867.93	130.58	7.80E-11	DLEEATLQHEATAATLR
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					1959.10	1958.09	1958.94	81.61	6.10E-06	NLQEEISDLTEQLGEGGK
					989.22	1976.43	1976.89	60.09	0.00084	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1100.79	2199.56	2199.12	117.61	1.50E-09	GTLEDQIIQANPALEAFGNAK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK

6	gi|18858329	ba1 globin [Danio rerio]	72.3	148	480.10	958.19	957.56	43.70	0.054	TAILGLWGK
					713.75	1425.48	1424.76	77.05	1.90E-05	LNIDEIGPQALSR
					726.09	1450.16	1449.69	79.72	1.00E-05	NTYAALSVMHSEK
					898.71	1795.40	1794.83	122.27	5.40E-10	FGQAGFNADVQEAWQK
					993.19	1984.36	1984.97	87.75	1.50E-06	YFATFGNLSSPAAIMGNPK
7	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	53.9	551	820.50	819.49	819.40	36.13	0.29	ISEASDAK
					1197.66	1196.65	1196.64	46.09	0.024	VVDALGNPIDGK
					644.18	1286.34	1286.69	72.39	6.10E-05	HALIIYDDLSK
					651.57	1301.13	1299.74	86.66	2.30E-06	TAIAIDTIINQK
					682.65	1363.29	1362.69	91.50	7.00E-07	TGTAEVSSILEEK
					766.40	1530.79	1530.75	121.91	6.70E-10	ILGADTGAELEETGR
					1625.03	1624.02	1623.88	75.60	2.60E-05	TGAIVDVPVGEELLGR
					1030.06	2058.11	2059.13	80.08	8.20E-06	AFLQHVISQHQDLLAAIR
					1054.00	2105.98	2103.03	59.97	0.00087	GMSLNLEPDNVGVVVFGNDK
					1183.48	2364.95	2364.17	140.40	7.10E-12	EVAAFAQFGSDLDAATQQLLNR
8	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	53.5	172	639.21	1276.41	1273.67	43.69	0.046	LFDPNATGVVNK
					810.67	1619.33	1617.83	96.66	2.10E-07	LNGTDPEETILAAFK
					1046.91	2091.80	2091.96	87.94	1.30E-06	GSSNVFSMFEQSQIQEFK
					1292.44	2582.87	2582.25	104.64	2.40E-08	FTAEEVDQAFAVAPIDVAGNIDY
9	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	67	333	1385.73	1384.72	1384.73	62.36	0.0006	GASQNIIPASTGAAK
					787.81	1573.60	1571.83	72.23	6.20E-05	LVIDGHAITVYSER
					882.67	1763.32	1762.80	80.71	8.20E-06	LVTWYDNEFGYSNR
					931.72	1861.42	1860.94	86.98	1.80E-06	SSIFDAGAGIALNDHFVK
					1106.31	2210.60	2210.17	52.13	0.0049	LVIDGHAITVYSERDPANIK
					1116.84	2231.66	2230.08	106.14	1.90E-08	WGDAGATYVVESTGVFTTIEK
					867.26	2598.76	2599.37	72.63	3.90E-05	VINDNFVIVEGLMSTVHAITATQ
10	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio re	39.1	1937	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
11	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	69.9	196	968.51	967.50	966.55	60.55	0.00082	HVLATLGEK
					757.12	1512.23	1511.69	84.28	3.50E-06	DQGTFEDFVEGLR
					855.80	1709.59	1710.82	89.24	1.10E-06	AKDQGTFEDFVEGLR
					889.86	1777.70	1777.85	80.93	8.20E-06	SVPLDFSPDQIEEFR
					972.94	1943.87	1944.08	94.30	3.10E-07	ALGHNPTNADVLTVLGKPK
					791.08	2370.22	2370.23	69.50	8.90E-05	KEEAPAPAPVPETPKEPEVDLK
12	gi|50512294	myosin, heavy polypeptide 2, fast muscle specific [Danio	49.2	1935	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.77	1495.52	1495.73	65.05	0.00029	KVQHELEEAEER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK

					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2088.02	75.58	2.30E-05	TKLEQQVDDLEGSLEQEK
					1107.99	2213.97	2213.03	75.84	2.10E-05	AEIQTALEEAEGTLEHEESK
					739.60	2215.76	2216.12	50.27	0.0076	TKLEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
13	gi|189519131	PREDICTED: ns:zf-e68 [Danio rerio]	46.1	1935	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.77	1495.52	1495.73	65.05	0.00029	KVQHELEEAEER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2088.02	75.58	2.30E-05	TKLEQQVDDLEGSLEQEK
					1107.99	2213.97	2213.03	75.84	2.10E-05	AEIQTALEEAEGTLEHEESK
					739.60	2215.76	2216.12	50.27	0.0076	TKLEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
14	gi|66472732	myosin heavy chain 4 [Danio rerio]	50.9	1935	612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.77	1495.52	1495.73	65.05	0.00029	KVQHELEEAEER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2088.02	75.58	2.30E-05	TKLEQQVDDLEGSLEQEK
					1107.99	2213.97	2213.03	75.84	2.10E-05	AEIQTALEEAEGTLEHEESK
					739.60	2215.76	2216.12	50.27	0.0076	TKLEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
15	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio re	90.1	517	471.62	941.22	940.53	45.28	0.03	VLDTGAPIR
					545.57	1089.13	1087.63	44.02	0.048	VVDLLAPYAK
					693.70	1385.39	1384.70	73.21	5.00E-05	IMNVIGEPIDER
					1407.02	1406.01	1405.67	38.39	0.14	AHGGYSVFAGVGER
					718.44	1434.87	1434.75	96.54	2.20E-07	FTQAGSEVSALLGR
					730.24	1458.47	1456.83	71.39	7.30E-05	TVLIMELINNVAK
					839.54	1677.07	1676.92	99.39	1.20E-07	LVLEVAQHLGENTVR
					916.20	1830.39	1828.88	61.80	0.00061	IMDPNIVGTEHYDVAR
					962.57	1923.13	1920.96	72.13	5.30E-05	DQEGQDVLLFIDNIFR
					994.51	1987.01	1987.03	85.08	2.70E-06	AIAELGIYPAVDPLDSTSR
					1004.49	2006.96	2004.05	45.00	0.026	FLSQPFQVAEVFTGHLGK
					688.51	2062.50	2059.99	44.65	0.029	EGNDLYHEMIESGVINLK
					1060.47	2118.93	2118.04	99.97	8.30E-08	SLQDIIAILGMDELSEEDK

					1330.37	2658.73	2658.38	88.28	1.00E-06	SLQDIIAILGMDELSEEDKLTVAR
					1492.02	2982.02	2981.47	59.23	0.00072	SILGGEYDALPEQAFYMVGPIEE
					1239.89	3716.65	3713.88	38.82	0.059	GSITSVQAIYVPADDLTDPAPAT
					1281.83	3842.46	3841.97	37.36	0.078	KGSITSVQAIYVPADDLTDPAPA
16	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	41.7	1936	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.40E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
17	gi|23097290	troponin T2, cardiac [Danio rerio]	28	282	718.41	717.40	717.35	38.58	0.21	ELEAEK
					431.68	861.35	861.41	41.02	0.1	KEEEEAK
					580.62	1159.23	1158.57	37.45	0.21	FELQYQFGK
					1217.66	1216.65	1216.66	71.14	9.10E-05	KEEEEIISLK
					674.08	1346.15	1344.75	80.98	8.50E-06	KKEEEEIISLK
					571.64	1711.88	1710.90	63.71	0.00039	RKPLDIDNANESALR
					957.91	1913.80	1913.95	85.11	2.70E-06	DLNELQTLIEAHFESR
18	gi|83025080	actinin, alpha 2 [Danio rerio]	48.2	895	410.26	1227.75	1226.64	56.49	0.0025	HRPDLIDYAK
					762.20	1522.39	1520.71	50.51	0.0085	AGTQIENIEEDFR
					547.73	1640.17	1640.72	43.32	0.044	HEAFESDLSAHQDR
					842.32	1682.63	1680.90	63.92	0.00038	LLETVDQLFLEYAK
					859.65	1717.29	1715.95	47.07	0.019	ILAADKPYILSDELR
					885.64	1769.26	1768.81	74.13	3.60E-05	KHEAFESDLSAHQDR
					916.28	1830.54	1828.89	57.77	0.0015	MLDAEDILSTPKPDER
					933.28	1864.55	1861.89	100.43	8.10E-08	MVSDIASAWQGLEQAEK
					969.81	1937.61	1934.98	110.25	8.20E-09	GDLTNPYSTITAEEIAIK
					667.40	1999.16	1998.01	38.70	0.11	LEGDHQLIQESLIFDNK
					701.57	2101.67	2099.09	78.17	1.30E-05	LNKDDPLGNLNLAFDIAEK
					968.50	2902.48	2899.50	71.13	4.90E-05	IFQSYGIRGDLTNPYSTITAEEIA
19	gi|51592073	actin, alpha, cardiac muscle 1 like [Danio rerio]	70.3	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.94	1953.87	1955.04	84.21	3.20E-06	VAPEEHPTLLTEAPLNPK
					1115.18	2228.34	2227.06	49.56	0.009	DLYANNVLSGGTTMYPGIADR
					1066.60	3196.78	3195.60	56.69	0.0012	TTGIVLDSGDGVTHNVPIYEGYA
20	gi|50344786	cardiac muscle alpha actin 1 [Danio rerio]	69.2	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.94	1953.87	1955.04	84.21	3.20E-06	VAPEEHPTLLTEAPLNPK
					1115.18	2228.34	2227.06	49.56	0.009	DLYANNVLSGGTTMYPGIADR

					1066.60	3196.78	3195.60	56.69	0.0012	TTGIVLDSGDGVTHNVPIYEGYA
21	gi|62955473	hypothetical protein LOC550445 [Danio rerio]	63.7	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.94	1953.87	1955.04	84.21	3.20E-06	VAPEEHPTLLTEAPLNPK
					1115.18	2228.34	2227.06	49.56	0.009	DLYANNVLSGGTTMYPGIADR
					1066.60	3196.78	3195.60	56.69	0.0012	TTGIVLDSGDGVTHNVPIYEGYA
22	gi|18858249	actin, alpha 1, skeletal muscle [Danio rerio]	64.2	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.94	1953.87	1955.04	84.21	3.20E-06	VAPEEHPTLLTEAPLNPK
					1115.18	2228.34	2227.06	49.56	0.009	DLYANNVLSGGTTMYPGIADR
23	gi|18858539	desmin [Danio rerio]	49.3	473	544.45	1086.88	1086.57	53.90	0.005	VSDLNQAVNK
					549.51	1097.01	1094.55	50.25	0.01	AELQHLNDR
					591.47	1180.92	1179.55	48.04	0.016	EAGGYQDTIAR
					1254.56	1253.55	1253.56	47.66	0.017	NISEAEDWYK
					642.15	1282.28	1281.59	37.33	0.18	IAELYEEEMR
					889.27	1776.52	1775.91	103.59	4.40E-08	FLEQQNSALTVEIER
					991.08	1980.14	1978.97	91.31	6.40E-07	LDFNLADAINQDFLNTR
					1094.09	2186.17	2186.00	151.75	5.70E-13	TFGSGLGSSIFAGHGSSGSSGS
24	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple	85.5	517	471.62	941.22	940.53	45.28	0.03	VLDTGAPIR
					545.57	1089.13	1087.63	44.02	0.048	VVDLLAPYAK
					693.70	1385.39	1384.70	73.21	5.00E-05	IMNVIGEPIDER
					1407.02	1406.01	1405.67	38.39	0.14	AHGGYSVFAGVGER
					718.44	1434.87	1434.75	96.54	2.20E-07	FTQAGSEVSALLGR
					730.24	1458.47	1456.83	71.39	7.30E-05	TVLIMELINNVAK
					839.54	1677.07	1676.92	99.39	1.20E-07	LVLEVAQHLGENTVR
					916.20	1830.39	1828.88	61.80	0.00061	IMDPNIVGTEHYDVAR
					962.57	1923.13	1920.96	72.13	5.30E-05	DQEGQDVLLFIDNIFR
					994.51	1987.01	1987.03	85.08	2.70E-06	AIAELGIYPAVDPLDSTSR
					1004.49	2006.96	2004.05	45.00	0.026	FLSQPFQVAEVFTGHLGK
					688.51	2062.50	2059.99	44.65	0.029	EGNDLYHEMIESGVINLK
					1492.02	2982.02	2981.47	59.23	0.00072	SILGGEYDALPEQAFYMVGPIEE
					1239.89	3716.65	3713.88	38.82	0.059	GSITSVQAIYVPADDLTDPAPAT
					1281.83	3842.46	3841.97	37.36	0.078	KGSITSVQAIYVPADDLTDPAPA
25	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	58.7	433	469.64	937.27	937.50	41.97	0.059	HIADLAGNK
					573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					687.18	1372.35	1372.70	64.40	0.00037	HITGEQLGDLYK
					719.58	1437.14	1435.72	86.91	2.00E-06	GNPTVEVDLYTTK
					1053.67	2105.32	2104.07	89.76	9.10E-07	FTGSVDIQVVGDDLTVTNPK
					1060.03	2118.04	2118.12	91.79	5.50E-07	DVILPVPAFNVINGGSHAGNK
					1372.83	2743.65	2742.33	73.97	2.70E-05	DATNVGDEGGFAPNILENNEAL
26	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	75.7	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENAIDR
					586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					628.87	1255.73	1256.66	64.85	0.00034	QLDDELVGLQK
					637.15	1272.29	1271.61	72.43	6.20E-05	AADAEGDVAALNR

					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
					700.72	1399.42	1399.71	107.10	1.90E-08	KAADAEGDVAALNR
					770.15	1538.28	1537.71	100.31	8.80E-08	SIDDLEDELYAQK
					700.72	2099.13	2099.09	80.39	7.70E-06	LELSEKKAADAEGDVAALNR
					747.65	2239.92	2239.05	56.88	0.0017	QTEDELDKYSEALKDAQEK
					770.15	2307.42	2307.18	54.59	0.0027	TVAKLEKSIDDLEDELYAQK
27	gi|189523699	PREDICTED: titin a [Danio rerio]	43.9	32757	824.59	823.58	822.50	52.54	0.0048	VHIVIDK
					511.18	1020.34	1019.54	37.43	0.21	ITDQYRPK
					567.76	1133.51	1133.57	64.96	0.00036	KGDVTLSDSGR
					705.08	1408.14	1407.69	57.46	0.0017	TDDKFEVLQEGK
					749.20	1496.39	1495.81	47.75	0.016	KFDNLFFIEVPK
					781.54	1561.07	1560.75	40.14	0.095	EHSEVIPHTQQEK
					819.76	1637.51	1636.89	41.42	0.067	VEIPDIELPDELKK
					878.68	1755.35	1752.99	47.59	0.016	EAEILKPLASVEVVEK
					907.31	1812.60	1811.95	45.44	0.026	IGVGETADIPGSVIIEDK
					908.46	1814.91	1812.91	55.97	0.0023	ASQAPSAPDDLIVTDVSK
					926.82	1851.63	1850.96	67.65	0.00015	STVILGWEKPLHDGGSR
					623.27	1866.79	1866.98	62.77	0.00047	RRDEEAPTQIVPDITK
					940.78	1879.54	1878.92	96.56	1.90E-07	TPLHDGGAEVSHYIVER
					947.81	1893.61	1892.90	71.72	5.80E-05	HTVTLSWEKPDHDGGSK
					962.72	1923.43	1922.99	53.01	0.0043	AVNAAGVGEPGEVADVIEVK
					976.57	1951.13	1950.02	85.98	2.10E-06	SSDIVQISSTPTSSTLSIK
					1029.44	2056.87	2056.09	59.01	0.001	ELPISFVTPLADVHVYEK
					1052.34	2102.66	2102.05	88.77	1.10E-06	EQVTHQAALLQSHEVQER
					1060.46	2118.90	2118.12	44.96	0.026	ASIEITPSFTTLLIENVDR
					1062.63	2123.25	2122.13	56.57	0.0018	VLDRPGPSSGPLDITGLTAEK
					1080.01	2158.01	2157.24	74.26	3.20E-05	KVPAKPVEAITVPTEEPPKK
					734.17	2199.49	2199.29	49.32	0.0099	KEPKPESILQVISTPVPLPK
					1114.26	2226.51	2226.10	51.16	0.0064	EHVIIEWFKPENDGGSEIK
					1133.96	2265.91	2265.23	36.44	0.18	KEQHKPVVLSVNETTQTLSK
					1137.55	2273.09	2271.31	36.90	0.16	VEIQDKPLLPEGPVVVDALLK
					1151.39	2300.76	2300.07	97.12	1.50E-07	EVTSNSVTLSWEKPDHDGGSR
					1682.58	5044.72	5042.61	49.40	0.0026	HQLQADQSSLIPGLDSAISVQPL
28	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	55.2	782	854.52	853.51	853.47	42.30	0.051	IHETNLK
					1160.53	1159.52	1159.57	47.24	0.022	GEIATLADENK
					1362.65	1361.64	1361.61	50.84	0.0084	FEPSSYINYDK
					786.32	1570.62	1568.82	42.98	0.051	FKLEPPTGDELPAR
					1695.86	1694.85	1694.78	63.98	0.00039	FNPETDYLTAPNGEK
					878.21	1754.41	1752.88	63.36	0.00043	IVYGHLDDPAGQEIAR
					890.24	1778.47	1777.89	41.25	0.074	QGLLPLTFSNPADYDK
					1041.78	2081.55	2080.94	106.96	1.70E-08	NNISWVVVGDENYGEGSSR
					1080.47	2158.92	2157.96	40.01	0.084	DFDPGQDTYQHPPADGSALK
					1267.12	2532.23	2532.29	157.81	1.20E-13	GHLDNISNNLLIGAVNIENDGVN
					1363.00	2723.98	2721.43	42.38	0.038	NDANPATHAFVTSPEIVTALAIA
29	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	67.7	449	588.63	1175.24	1174.60	50.29	0.011	ATDFVVNQPGK
					677.67	1353.33	1354.68	79.89	9.70E-06	TIEAEAAHGTVTR
					716.14	1430.27	1428.73	81.19	7.70E-06	FKDIFQDIFEK
					861.03	1720.05	1719.82	124.78	3.30E-10	DQTDDQVTIDSAIATK
					947.29	1892.57	1891.93	67.72	0.00015	LNEHYVNTTDFLDAIK
30	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	42.3	28836	431.68	861.35	860.46	39.18	0.16	KKEEEAK
					701.73	1401.45	1399.71	64.74	0.00035	HVSVEALDFIDR
					763.17	1524.32	1523.73	49.92	0.0097	SDSGVYYLHLENK

					787.63	1573.25	1572.78	78.62	1.40E-05	FGQSGPSEPSGPVVTK
					802.58	1603.15	1602.86	37.57	0.18	YGVSEPLVSQNVIAK
					823.16	1644.31	1642.77	62.59	0.00054	VHGLIEDHEYEFR
					878.68	1755.35	1752.99	47.59	0.016	EAEILKPLASVEVVEK
					885.70	1769.38	1768.91	59.08	0.0011	SSVTLTWVKPAHDGGSK
					894.79	1787.56	1787.83	38.15	0.15	GENKVDVEYDEHINK
					920.77	1839.53	1838.93	62.48	0.00051	STVSLAWEKPLHDGGSR
					923.72	1845.43	1845.01	63.56	0.0004	VQILDKPGPPAGHIEFK
					928.68	1855.35	1854.92	75.30	2.60E-05	TSVSLSWEKPIHDGGSR
					940.54	1879.06	1877.90	56.82	0.0018	VLNYDEEVDDTRPVSK
					950.74	1899.47	1898.91	53.37	0.004	TTVTLSWEKPEHDGGSR
					988.99	1975.96	1976.14	61.35	0.00062	SQLERPGAPLKPVVSGITK
					1002.79	2003.56	2002.96	75.42	2.40E-05	KDNTSDDIGWVTVTSTHK
					1028.44	2054.86	2055.07	95.10	2.60E-07	LKGDVLSASPDVEIIEDGAK
					1047.32	2092.62	2092.08	64.74	0.00028	INVSALNSEGVGEAAPVPGSPK
					1073.03	2144.05	2142.23	51.74	0.0055	SFHVQVITLGPPSKPIGPIR
					1258.48	2514.94	2514.23	83.61	3.10E-06	HTLPVDSDISSSDTTSVVTIPES
					902.92	2705.72	2706.41	50.47	0.0062	TPVLAVDPVEKPGEPENFQITEI
31	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	82.5	337	465.05	928.09	927.46	41.82	0.074	HGVYNPNK
					537.92	1073.83	1072.58	43.90	0.05	IQEAGTEVVK
					661.60	1321.18	1319.67	86.06	2.40E-06	GYIGADQLGDALK
					728.21	1454.40	1453.70	37.29	0.18	AGAGSATLSMAYAGAR
					751.99	1501.97	1502.77	100.04	1.00E-07	VEFPADQLSALTGR
					1544.85	3087.69	3088.58	95.05	1.80E-07	NSPLVSELSLFDIAHTPGVAADL
32	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	39.8	1945	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLEITLAK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLEITLAK
					504.06	1509.15	1507.70	37.65	0.16	SDSSKELEELSER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					825.52	1649.02	1647.78	50.84	0.0083	LEEAGGATSAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1107.99	2213.97	2213.03	64.44	0.00029	TEIQAALEEAEGTLEHEESK
33	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	70.7	283	588.19	1174.36	1173.56	42.41	0.068	SEYGLTFTEK
					665.84	1329.67	1329.66	41.35	0.078	RSEYGLTFTEK
					779.53	1557.05	1555.79	43.02	0.05	LTFDTTFSPNTGKK
					1051.96	2101.91	2102.15	84.24	3.30E-06	VNNTSLVGVGYTQSLRPGIK
					1088.43	2174.84	2174.05	117.04	1.60E-09	WNTDNTLGTEINIEDQIAK
34	gi|148596963	spectrin alpha 2 [Danio rerio]	39.3	2480	625.55	1249.08	1246.55	45.75	0.028	GEIDAHEDSFK
					773.69	1545.36	1544.77	82.66	5.60E-06	HALLEADVAAHQDR
					787.68	1573.34	1571.78	67.18	0.0002	HQALQAEISGHEPR
					537.25	1608.71	1607.74	39.91	0.098	HQAFEAELHANADR
					850.21	1698.40	1699.88	81.65	6.40E-06	KHQALQAEISGHEPR
					862.42	1722.82	1720.86	58.01	0.0015	LIQSHPEAVDDIQEK
					925.80	1849.59	1848.86	86.05	2.20E-06	KFEEFQTDLAAHEER
					1010.84	2019.66	2018.99	60.19	0.00081	LQIASDENYKDPSNLQGK
					1077.78	2153.55	2153.10	88.67	1.10E-06	ALINADELANDVAGAEALLDR
					1109.09	2216.17	2215.12	57.78	0.0014	RDELITNWEQIQTLATER
					740.44	2218.30	2219.18	48.35	0.012	LEAELGAHEPAIQSVLETGKK
					1110.70	2219.39	2219.03	79.75	8.60E-06	STDEAGQALLNTGHYASEEVK
					792.49	2374.44	2375.28	66.34	0.00018	RLEAELGAHEPAIQSVLETGKK

					1246.00	2489.99	2489.22	66.52	0.00016	EKEPIVGSPDYGKDEDSAEALL
35	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	66.8	334	474.43	946.84	946.60	41.19	0.093	HIIPQIVK
					1205.61	1204.60	1204.61	48.45	0.016	SSADTLWGIQK
					628.45	1254.88	1252.64	54.64	0.0035	MVVDSAYEVIK
					769.60	1537.18	1537.77	108.51	1.30E-08	IVADKDYSVTANSR
					844.16	1686.31	1684.85	113.65	4.30E-09	ELADELALVDVVEDR
					857.97	1713.92	1714.82	40.76	0.08	LNPDIGTDKDAENWK
36	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	30.4	1938	612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DLDDLEITLAK
					687.67	1373.32	1372.74	51.55	0.0072	KDLDDLEITLAK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
37	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	70.6	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					978.73	1955.44	1953.06	67.08	0.00017	VAPEEHPVLLTEAPLNPK
38	gi|18858335	bactin1 [Danio rerio]	58.9	375	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1131.52	37.35	0.22	GYSFTTTAER
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
39	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	43.1	153	1100.63	1099.62	1098.53	52.09	0.0074	NLIHGSDSEK
					795.69	1589.36	1588.88	74.37	3.60E-05	LVAAKFVQASEDLAK
					651.06	1950.14	1949.07	70.76	7.00E-05	GFRLVAAKFVQASEDLAK
					1106.96	2211.90	2211.12	85.26	2.40E-06	SAATEVSLWFKPEELVSYR
40	gi|18858587	elongation factor 1-alpha [Danio rerio]	52.6	462	766.50	765.49	765.39	39.76	0.09	FEEITK
					794.93	1587.84	1587.87	74.02	4.00E-05	THINIVVIGHVDSGK
					974.39	2920.14	2917.55	69.01	7.60E-05	EGNASGTTLLDALDAILPPSRPT
					1016.88	3047.61	3045.65	53.55	0.0026	KEGNASGTTLLDALDAILPPSRP
41	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	47.2	532	587.69	1173.36	1170.61	37.35	0.22	GDLGIEIPTEK
					820.11	1638.21	1635.88	86.12	2.30E-06	GVNLPGAAVDLPAVSEK
					882.32	1762.62	1763.98	104.58	3.40E-08	KGVNLPGAAVDLPAVSEK
					1286.58	2571.15	2569.21	90.02	7.00E-07	GIFPIYYNSPSNDVWAEDVDLR
42	gi|162287365	hemopexin [Danio rerio]	34.7	447	1211.64	1210.63	1210.61	43.92	0.04	GHHFLSITGDK
					1339.66	1338.65	1338.61	63.11	0.00046	FHSDTIESEFK
					600.27	1797.79	1800.00	61.55	0.00064	VGKPHTHLEGYPKPLK
					720.67	2158.98	2159.07	62.14	0.00052	GKPGGEGHKHELHHGAQLDR
43	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	64.7	119	529.66	1057.30	1056.56	77.57	2.10E-05	VAENVQELR
					599.58	1197.14	1195.75	45.88	0.027	AKLEPVVLSLK
					1050.75	2099.49	2100.09	79.52	9.40E-06	ELTELGEQVKPHFEGIFK
					743.41	2227.20	2228.18	62.96	0.00042	KELTELGEQVKPHFEGIFK
44	gi|48762657	enolase 1, (alpha) [Danio rerio]	61.1	432	573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					1504.37	3006.73	3006.57	90.04	5.90E-07	HIADLAGNPDVILPVPAFNVING
45	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	39.6	1974	864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
					586.03	1755.05	1753.87	55.57	0.0026	KQELEEILHEMEAR
					1000.03	1998.04	1997.92	75.62	2.30E-05	ELEGHISDLQEDLESER
					1007.31	2012.60	2012.04	100.39	7.70E-08	TLEAELLQLQEDLAAAER
					1066.77	2131.52	2131.00	43.65	0.037	QVEAERDELADELASNASGK

					1131.02	2260.02	2259.10	76.40	1.90E-05	KQVEAERDELADELASNASGK
					895.73	2684.15	2682.37	52.91	0.0034	KLEAESNDLQEQIADLQAQIADL
46	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Dani	44.3	659	836.68	1671.35	1671.94	114.36	3.50E-09	AIEQFGAVIEELLLK
47	gi|18858427	creatine kinase, muscle a [Danio rerio]	45.1	381	589.71	1177.41	1175.58	37.81	0.19	DLFDPVISDR
					755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
					836.18	1670.35	1670.77	59.49	0.0011	LNYSVDEEYPDLSK
					999.00	1995.98	1993.93	93.47	3.80E-07	GTGGVDTASVGGVFDISNADR
					1077.13	2152.25	2150.04	41.65	0.057	RGTGGVDTASVGGVFDISNAD
48	gi|41054435	hypothetical protein LOC324244 [Danio rerio]	29.4	248	586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					638.09	1274.16	1271.65	65.71	0.00029	EKAEGDVAALNR
					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
49	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	72	143	589.05	1176.08	1173.64	42.73	0.061	IVMGAITDAVGK
					767.47	1532.93	1532.73	89.40	1.20E-06	IASQADSIGQEAMGR
					1869.06	1868.05	1867.99	101.03	6.90E-08	IDDLLGALSSLSDLHATK
					978.64	1955.26	1954.97	58.28	0.0013	IYFAHWPDHSLGSAQVK
50	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	47.8	575	602.58	1203.14	1200.63	46.52	0.025	NAGVEGSLVVEK
					984.90	1967.78	1967.90	75.41	2.50E-05	VNEIAEQLESTNSDYEK
					943.10	2826.27	2825.53	118.08	1.00E-09	TALLDAAGVASLLSTAEAVVTEI
51	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	52.6	603	1359.62	1358.61	1358.64	59.74	0.0011	EEFAHDHPHIK
					1103.45	2204.88	2204.05	68.40	0.00012	SHLNHEKEEFAHDHPHIK
					1005.22	3012.64	3013.43	105.12	1.90E-08	HISDDIFLTTAEAISEMVTEEHLA
52	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	79.8	104	608.49	1214.96	1214.66	57.95	0.0019	VGPNLWGLFGR
					744.56	1487.11	1487.65	83.55	4.50E-06	TGQAEGFSYTDANK
					808.82	1615.63	1615.75	107.78	1.60E-08	KTGQAEGFSYTDANK
					998.19	1994.36	1992.95	50.68	0.0073	GIVWGEDTLMEYLENPK
53	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	48.9	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENAIDR
					586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
					708.64	1415.26	1415.73	37.18	0.2	DAQEKLEQAEKK
54	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	48.6	364	660.17	1318.33	1317.68	104.23	4.00E-08	GILAADESTGSVAK
					776.51	1551.00	1550.70	71.66	6.60E-05	FQSINAENTEENR
					932.72	1863.42	1862.90	38.48	0.13	RFQSINAENTEENRR
					1055.50	2108.98	2107.16	65.57	0.00023	ITPTTPSNLAIIENANVLAR
					1175.04	2348.06	2347.17	73.65	3.30E-05	GVVPLAGTNGETTTQGLDGLYE
55	gi|47086523	ictacalcin [Danio rerio]	46.3	95	696.65	1391.29	1390.73	90.39	9.70E-07	ELLSAELGDIFGK
56	gi|38488731	natriuretic peptide precursor A [Danio rerio]	84	106	1026.57	2051.12	2049.99	90.71	7.10E-07	SLLQQFEEALATEEASER
					1182.38	2362.75	2362.99	76.85	1.60E-05	DREEAAAPGEDSNPSDGFDTQ
					1248.96	2495.90	2495.11	43.62	0.03	AVDYEDSNTVLEQSPPSTSWD
57	gi|157787181	creatine kinase CKM3 [Danio rerio]	47.6	380	755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
					999.00	1995.98	1993.93	93.47	3.80E-07	GTGGVDTASVGGVFDISNADR
					1077.13	2152.25	2150.04	41.65	0.057	RGTGGVDTASVGGVFDISNAD
58	gi|40538764	ceruloplasmin [Danio rerio]	29.7	1087	806.08	1610.15	1609.72	91.54	6.70E-07	SVNKEDADFQESNK
					828.99	1655.97	1654.78	85.47	2.70E-06	LVDDIVSDTFFDNR
					859.48	2575.40	2573.23	60.57	0.00061	VSWHLSGLGSETDIHGLYFEGN
59	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	58.8	364	660.17	1318.33	1317.68	104.23	4.00E-08	GILAADESTGSVAK
					1427.77	1426.76	1426.72	45.39	0.028	PHAYPFLTPEQK
					776.51	1551.00	1550.70	71.66	6.60E-05	FQSINAENTEENR
					932.72	1863.42	1862.90	38.48	0.13	RFQSINAENTEENRR
					1175.04	2348.06	2347.17	73.65	3.30E-05	GVVPLAGTNGETTTQGLDGLYE
60	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filami	50.2	2523	823.47	1644.92	1645.89	81.60	6.80E-06	VHGPGLQSGITNKPNK

					886.49	1770.96	1770.93	63.28	0.00045	SGVELNKPTHFTVNTK
					901.26	1800.50	1799.96	62.58	0.00052	VAKPDITDNKDGTVTVK
					1115.87	2229.73	2228.05	63.53	0.00036	DGSSGVSYIVQEPGDYEVSIK
					1206.85	2411.68	2411.15	89.21	9.10E-07	EGPYSINVLYADEEIPQSPYK
61	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	64.3	305	662.59	1323.17	1320.67	70.62	8.40E-05	VVDGLSINDFSR
					730.42	1458.82	1459.79	53.60	0.0044	EVIPTDKVEVGFK
					878.99	2633.93	2631.29	81.11	5.40E-06	NVTIWGNHSSTQYPDVHHAIVTI
62	gi|41393131	dihydrolipoamide S-succinyltransferase [Danio rerio]	34.5	458	1075.38	2148.75	2147.07	114.26	3.20E-09	AAAYALTDQPAVNAVIDDTTK
63	gi|18858959	lactate dehydrogenase A4 [Danio rerio]	45	333	596.12	1190.22	1188.61	84.43	4.20E-06	VIGSGTNLDSAR
					628.45	1254.88	1252.64	54.64	0.0035	MVVDSAYEVIK
					756.18	1510.35	1509.77	73.74	4.00E-05	IVADKDYSVTANSK
64	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	47.3	283	930.98	1859.95	1858.82	94.89	3.00E-07	SQSGVEFTTGGSSNTDTGK
					1030.85	2059.68	2058.12	82.00	5.30E-06	VNNASLVGVGYTQSLRPGVK
65	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio rerio	36.3	413	1040.87	2079.72	2079.97	91.39	6.20E-07	GTGGVDTAAVGDTFDISNLDR
					1119.31	2236.61	2236.07	52.22	0.0048	RGTGGVDTAAVGDTFDISNLDR
66	gi|41054193	hypothetical protein LOC327506 [Danio rerio]	40.4	178	1040.87	2079.72	2079.97	91.39	6.20E-07	GTGGVDTAAVGDTFDISNLDR
					1119.31	2236.61	2236.07	52.22	0.0048	RGTGGVDTAAVGDTFDISNLDR
67	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (asp	44.2	428	555.50	1108.99	1107.59	39.28	0.12	KMNLGVGAYR
					705.68	1409.35	1408.72	46.27	0.023	EYLPIGGLADFSK
					724.76	1447.51	1445.81	72.14	6.30E-05	IAATILNTPELYK
					946.71	1891.41	1893.02	95.60	2.40E-07	KLDKEYLPIGGLADFSK
					666.36	1996.04	1994.03	36.92	0.17	YFIEQGHNILLSQSFAK
					784.38	2350.11	2350.26	58.13	0.0012	ISVAGVTSANVEYLAHAIHAVTK
68	gi|50539808	hypothetical protein LOC436647 [Danio rerio]	41.3	525	908.92	1815.83	1815.92	76.41	2.10E-05	ENTLNQLVGAAFGAAGQR
					967.82	1933.62	1932.99	63.67	0.00037	VNAGDQPGADVGPLISPQAK
					1005.87	2009.73	2009.00	85.54	2.30E-06	SSQWLDIHNPATSEVIGR
69	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio rerio	51.2	410	538.75	1075.48	1075.61	66.82	0.00025	KVNLGVGAYR
					1113.61	1112.60	1112.61	43.19	0.053	IALGEDSPAIK
					845.28	1688.54	1687.84	84.95	3.20E-06	NIDYVAESIHEAVTK
					861.05	2580.13	2579.28	45.87	0.018	MIADDHSLNHEYLPILGLPEFR
70	gi|68362804	PREDICTED: similar to Histone H4 replacement CG3379	73.8	103	1134.59	1133.58	1133.54	39.08	0.14	DAVTYTEHAK
					591.69	1181.36	1179.61	63.27	0.00047	ISGLIYEETR
					657.23	1312.44	1309.70	58.02	0.0016	TVTAMDVVYALK
					664.19	1326.36	1324.75	43.50	0.044	DNIQGITKPAIR
71	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprotei	49.2	661	666.56	1331.11	1329.65	45.28	0.031	GEGGILINSEGER
					1474.80	1473.79	1473.75	85.53	2.90E-06	KHTLSYVDPETGK
					704.36	2110.06	2109.13	36.94	0.17	DHVHLQLHHLPPQQLAAR
					861.14	2580.40	2582.14	47.38	0.013	DGQDHVVPGLYACGEAGCASV
					888.37	2662.07	2662.42	51.70	0.0047	GVGPDKDHVHLQLHHLPPQQLA
72	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio rerio	39.1	133	749.12	1496.23	1496.63	92.69	5.00E-07	LGEEFDETTADDR
					813.60	1625.18	1624.72	56.89	0.0019	LGEEFDETTADDRK
					1081.42	2160.82	2160.13	62.50	0.00047	EVSDNNLTLTLTLGDIVSTR
73	gi|58801524	LIM domain containing preferred translocation partner in	63.1	556	1097.90	2193.79	2193.06	52.39	0.0047	AEPSHHPAPTPSQGYQPAPPK
					1397.62	2793.23	2793.39	108.68	9.00E-09	SSLDAEIDSLTSILADLESSSPYK
74	gi|189535578	PREDICTED: fetuin B [Danio rerio]	35.9	498	1053.80	2105.59	2104.92	74.74	2.90E-05	DETHEHDHEIVLDHDHK
					1117.31	2232.61	2233.01	77.52	1.40E-05	KDETHEHDHEIVLDHDHK
					797.16	2388.45	2389.01	42.74	0.039	AHEHGQDEWEHQHHQYGHK
75	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	83.7	141	487.46	972.90	972.52	66.23	0.0003	LDDLASAIR
					487.46	1459.36	1458.77	41.65	0.069	ACRRLDDLASAIR
					1659.34	3316.67	3313.73	65.34	0.00015	EIYPYVIQELRPTLDELGIATPEE
					1694.78	3387.54	3384.77	59.62	0.00055	EIYPYVIQELRPTLDELGIATPEE
76	gi|41055718	fumarate hydratase precursor [Danio rerio]	50.7	509	829.24	1656.46	1655.84	48.58	0.013	LGSKDPVHPNDHVNK

					719.09	2154.25	2153.18	65.75	0.00022	EVHEVLLPGLQTLHDALAAK
					1251.94	2501.87	2501.26	85.96	1.80E-06	THTQDAVPLSLGQEFGGYVQQ
77	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	30.3	1754	569.07	1136.13	1135.60	36.18	0.25	VLQEQGTHPK
					613.09	1224.17	1222.63	64.72	0.00033	AGVLAHLEEER
					575.27	1722.79	1721.89	60.94	0.00077	KQELEEILHDLEAR
					864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
					893.88	2678.62	2678.38	79.43	7.80E-06	KLEGDSTELHDQIAELQAQIAEL
78	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	39.2	757	740.20	1478.39	1478.76	78.83	1.30E-05	IVSQYSELVNEAK
					978.64	1955.26	1955.09	67.25	0.00016	KPETVKPLQISSLSEATK
					1065.82	2129.63	2130.11	49.26	0.01	AELDALAALTAGLEETLGSSAK
79	gi|18858281	apolipoprotein A-I [Danio rerio]	55	262	585.45	1168.88	1166.55	57.61	0.0018	AFESNIEETK
					822.74	1643.47	1643.73	81.96	6.20E-06	ALDNLDGTDYEQYK
					912.03	1822.04	1821.93	58.57	0.0012	EKLEPVFQEYSALNR
					1580.96	3159.90	3159.53	45.88	0.015	LQEYAQTTSQALTPYAETISTQL
80	gi|57222259	talin 1 [Danio rerio]	52.6	2538	1526.50	3050.98	3050.51	110.47	5.30E-09	GTEWVDPEDPTVIAENELLGAA
					1588.48	3174.95	3174.57	84.08	2.30E-06	EAVDDLGSTLAEVASAAGAVGG
81	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	11.7	230	442.31	882.61	882.46	41.11	0.072	LLETDHR
					712.46	2134.35	2133.18	59.60	0.00091	ILVSAEDVLHSWAVPSLGIK
82	gi|56693297	hypothetical protein LOC494070 [Danio rerio]	44	182	952.64	1903.26	1902.91	92.17	5.30E-07	AKEELEQELADKEDEK
83	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dani	46.9	731	805.71	1609.40	1607.78	75.77	2.50E-05	FASEVAGVEDLGTTGR
					1571.20	3140.38	3139.56	89.52	6.40E-07	DSFIVYQGHHGDVGAPIADVILP
84	gi|117606264	sarcalumenin [Danio rerio]	39.4	482	869.43	1736.85	1735.95	50.99	0.0074	AITHELPSLLGSINSGK
					1036.37	2070.72	2069.08	87.62	1.50E-06	REEISLLEDLNQVIENR
85	gi|189517523	PREDICTED: hypothetical protein [Danio rerio]	59.9	147	1060.96	1059.95	1060.52	40.46	0.11	LNVDPDNFK
					714.17	1426.32	1424.76	90.93	7.90E-07	INVDEIGPQTLAR
86	gi|189530625	PREDICTED: similar to spectrin repeat containing, nucle	35	8621	550.57	1099.13	1097.66	68.83	0.00015	QLADAIAKLR
87	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	54.9	226	724.23	1446.44	1445.78	47.73	0.018	VIFEAETEKPGVK
					881.46	2641.36	2641.29	69.67	7.30E-05	SPDPAAVEHKPEESKPEESKPE
					1421.57	2841.12	2840.42	49.82	0.0068	AKSPDPAAVEHKPEESKPEESK
88	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	65.3	248	695.75	1389.49	1388.71	69.76	0.00011	SIEELANTLNSAK
					1458.82	1457.81	1457.72	75.26	3.00E-05	HVFGESDELIGQK
					808.43	1614.84	1613.82	57.16	0.0019	RHVFGESDELIGQK
					812.06	2433.15	2431.30	52.48	0.0041	DLDGFLVGGASLKPEFIDIINAK
89	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	36.4	1079	1270.68	1269.67	1269.68	49.62	0.011	SLGAEPLEVDIK
					707.79	1413.56	1412.74	41.33	0.073	GVIHVGYTDIPSR
					789.81	1577.60	1577.77	66.87	0.0002	QGFNVVVESGAGESAK
					922.38	2764.11	2763.39	47.00	0.013	DGSVVVDLAAEAGGNIETTVPG
90	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	68.9	164	686.63	1371.24	1370.73	82.70	5.50E-06	VVDGLDVVDAIEK
91	gi|52219194	fatty acid binding protein 11 [Danio rerio]	23.9	134	769.06	1536.10	1535.67	89.09	1.20E-06	LNEPFEETTADDR
					833.41	1664.80	1663.77	68.69	0.00013	LNEPFEETTADDRK
92	gi|114326248	elastin b [Danio rerio]	21.6	2054	880.55	1759.08	1759.92	38.98	0.12	SYGGAGSLGAGGILPGTGIR
					887.73	1773.45	1772.86	55.25	0.0029	SYGGAGALGGAGQGGIGGGPG
					1647.81	4940.40	4937.47	122.27	1.40E-10	LGVGPGGAGGIGGGLGVGPGG
93	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	37.6	3730	638.85	1275.69	1273.71	40.14	0.11	SKVEEILSELK
					967.82	1933.62	1931.96	84.94	2.80E-06	TLHLDDSIDSVHPIQDK
					1036.40	3106.17	3105.49	46.59	0.013	YDAEEIEAEVSSDVTTEIHNIITT
94	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	38.8	996	1072.60	1071.59	1071.56	41.86	0.079	NAENAIEALK
					732.73	1463.44	1463.67	45.15	0.03	IRDEMASTEQER
					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
95	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	28.7	1035	1072.60	1071.59	1071.56	41.86	0.079	NAENAIEALK
					732.73	1463.44	1463.67	45.15	0.03	IRDEMASTEQER

					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
96	gi|50540008	zgc:92882 [Danio rerio]	60.8	334	474.43	946.84	946.60	41.19	0.093	HIIPQIVK
					596.12	1190.22	1188.61	84.43	4.20E-06	VIGSGTNLDSAR
97	gi|189537196	PREDICTED: similar to L-lactate dehydrogenase B chain	52.3	285	474.43	946.84	946.60	41.19	0.093	HIIPQIVK
					596.12	1190.22	1188.61	84.43	4.20E-06	VIGSGTNLDSAR
98	gi|189520789	PREDICTED: si:ch211-239j9.2 [Danio rerio]	68.4	76	675.31	1348.61	1348.63	71.30	7.50E-05	EAGIFESARPSGE
					787.29	1572.56	1571.68	64.31	0.00038	AYADFYTQYDSTK
99	gi|51571925	hypothetical protein LOC445486 [Danio rerio]	36.1	194	902.32	1802.62	1800.95	39.68	0.1	INSELPVDEVFAIVEK
					966.43	1930.84	1929.05	82.64	4.70E-06	KINSELPVDEVFAIVEK
100	gi|166795887	vitellogenin 1 [Danio rerio]	43.8	1362	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					644.61	1287.21	1286.66	65.73	0.00029	AEAGVLGEFPAAR
					692.52	1383.03	1381.78	54.77	0.0034	ISDAPAQIVEVLK
101	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	34.6	1056	1072.60	1071.59	1071.56	41.86	0.079	NAENAIEALK
					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVLK
102	gi|136429	Trypsin precursor	63.4	232	737.53	2209.57	2210.10	85.13	2.50E-06	LGEHNIDVLEGNEQFINAAK
103	gi|50345022	small muscle protein, X-linked [Danio rerio]	61.4	83	1037.75	2073.48	2072.97	83.71	3.70E-06	REDTVETEEVSPVTPEEK
					1115.86	2229.71	2229.08	60.21	0.00077	RREDTVETEEVSPVTPEEK
104	gi|18859505	alpha-tropomyosin [Danio rerio]	35.6	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENALDR
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					770.15	2307.42	2307.18	51.55	0.0055	SVAKLEKTIDDLEDELYAQK
105	gi|160333682	heat shock protein 8 [Danio rerio]	56.2	649	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
					847.03	1692.05	1690.72	44.48	0.035	STAGDTHLGGEDFDNR
					887.36	1772.70	1772.81	39.80	0.1	NQTAEREEFEHQQK
					1131.58	2261.14	2259.14	47.52	0.014	SINPDEAVAYGAAVQAAILSGDK
106	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	26.3	331	969.31	1936.60	1936.93	83.84	3.60E-06	HLTTLVDDIWYYAGDR
107	gi|32308153	annexin A2a [Danio rerio]	27	337	633.21	1264.40	1263.66	53.64	0.0045	SLHQTIAEHTK
					723.17	1444.33	1443.78	90.36	9.60E-07	GVDEQTIIDILTK
108	gi|18858299	ATPase, Na+/K+ transporting, alpha 1a.3 polypeptide [Da	35.5	1024	877.83	1753.65	1751.85	85.52	2.60E-06	DAFQNAYLELGGLGER
					906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
109	gi|18858295	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Danic	35	1028	877.83	1753.65	1751.85	85.52	2.60E-06	DAFQNAYLELGGLGER
					906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
110	gi|189540222	PREDICTED: similar to myosin, heavy polypeptide 2, fas	43.1	950	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
111	gi|189540214	PREDICTED: similar to myosin heavy chain, partial [Dani	41	809	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
112	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	55.4	202	998.94	2993.79	2996.41	52.99	0.003	TLAAGSHAEHDGQPYCHKPCY
					1008.39	3022.14	3023.42	68.79	7.90E-05	TLNPGGHAEHDGKPYCHKPCY
113	gi|156713467	vitellogenin 7 [Danio rerio]	49.4	1358	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					644.61	1287.21	1286.66	65.73	0.00029	AEAGVLGEFPAAR
114	gi|189516972	PREDICTED: similar to Myosin light polypeptide 4 (Myos	37.4	187	968.51	967.50	966.55	60.55	0.00082	HVLATLGEK
					757.12	1512.23	1511.69	84.28	3.50E-06	DQGTFEDFVEGLR
115	gi|46358344	isocitrate dehydrogenase 3 (NAD+) alpha [Danio rerio]	40.5	365	1251.43	2500.84	2501.23	114.90	2.30E-09	ENTEGEYSGIEHVIVDGVVQSIK
116	gi|119943123	apolipoprotein A-IV [Danio rerio]	62.7	255	903.92	1805.82	1802.94	78.36	1.40E-05	AQIVQQSLTPYAEDLK
117	gi|189526598	PREDICTED: similar to COASTER [Danio rerio]	35.3	916	657.65	1313.29	1312.78	53.16	0.005	QAVALSLKEARK
118	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	43.3	284	623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					770.15	2307.42	2307.18	51.55	0.0055	SVAKLEKTIDDLEDELYAQK

119	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	40.3	134	892.64	2674.90	2675.32	93.26	3.30E-07	ITFTNEEFLVTLPDGSEIHFPNR
120	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	39.6	1368	1212.43	2422.84	2422.19	114.22	2.80E-09	GQNHLEEVELAFPQNVIEGSGR
121	gi|41055614	hypothetical protein LOC393478 [Danio rerio]	37.2	86	733.58	1465.15	1464.65	91.10	7.40E-07	WDSQIEDGSFPGK
122	gi|56118753	troponin C, slow [Danio rerio]	37.9	161	602.42	1202.83	1202.58	56.98	0.0022	AAAEQLTDEQK
					684.15	1366.28	1364.65	68.52	0.00013	NADGYIDLDELK
					726.33	1450.65	1448.65	60.34	0.0009	IDYDEFLEFMK
123	gi|189529657	PREDICTED: similar to nonmuscle myosin heavy chain [	34.9	1962	613.09	1224.17	1222.63	64.72	0.00033	AGVLAHLEEER
					864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
124	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	33.3	484	904.66	1807.30	1806.90	75.89	2.40E-05	HEVISQGGVTHPIDYR
125	gi|18859423	spectrin, beta, erythrocytic [Danio rerio]	29.6	2357	669.07	1336.13	1335.74	59.62	0.0011	HLLEVEDLLQK
					713.72	1425.42	1425.74	42.84	0.05	HRPDLVDYGNLK
					945.11	1888.20	1887.93	88.71	1.20E-06	KKHDAIETDIAAYEER
126	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	40.4	679	567.07	1132.13	1130.59	54.85	0.0038	SVAELEAEKR
					649.69	1297.36	1296.77	64.75	0.00033	VSVSPAGVELLVK
					1771.82	3541.62	3538.84	66.53	0.00011	VHEAELLSPGSTLVSFIYPAQNP
127	gi|41055387	hypothetical protein LOC393586 [Danio rerio]	48.4	647	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
					847.03	1692.05	1690.72	44.48	0.035	STAGDTHLGGEDFDNR
128	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reri	56.4	858	703.70	1405.38	1404.80	59.08	0.0013	TFAQLILDPIFK
					1073.30	2144.58	2144.05	65.62	0.00023	ARPFPDGLAEDIDKGDVSSR
129	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	33.9	682	1325.55	1324.54	1324.74	84.55	3.40E-06	TVHLLAGVADTTK
					677.29	1352.56	1352.69	36.67	0.2	SSGISTIHPETPK
					979.83	1957.64	1956.00	38.79	0.12	IAPLEEGSLPYNVAEAQR
130	gi|49274617	tropomyosin 1 alpha [Danio rerio]	33.5	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENALDR
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
131	gi|189522028	PREDICTED: similar to myomesin [Danio rerio]	61.5	923	1508.67	1507.66	1507.73	82.72	5.00E-06	FKGEFDESLPSPR
					1259.63	3775.87	3772.95	53.75	0.0018	GASAPWTGQIIVTEEEPVEGVV
					1301.58	3901.72	3901.05	47.40	0.0073	KGASAPWTGQIIVTEEEPVEGV
132	gi|55925387	carnitine palmitoyltransferase II [Danio rerio]	37.9	668	816.40	1630.78	1631.90	43.55	0.045	DGNLIKPAEVQAHLK
					1128.50	2254.98	2252.11	37.68	0.14	YLAAQRPLLNDEQYSNTEK
					1194.52	2387.02	2384.18	59.47	0.00084	DTTEKPLVGPGSQPASVDSSS
133	gi|30410758	keratin 18 [Danio rerio]	34.8	431	843.64	1685.27	1683.84	107.62	1.70E-08	NQISQSGVQVDVDAPK
134	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	43	433	573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					1008.42	3022.23	3020.58	72.22	3.60E-05	HIADLAGNPEVILPVPAFNVING
135	gi|189517055	PREDICTED: similar to heat shock protein 8 [Danio rerio]	42.6	698	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
136	gi|41053611	hypothetical protein LOC393828 [Danio rerio]	55.4	213	1602.92	3203.82	3202.41	103.90	2.40E-08	YTFESIQNEANALFNNENQANA
137	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	57.3	164	820.21	1638.40	1637.91	103.88	3.90E-08	HVVFGQVVEGLDVIK
138	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	46.2	1358	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					692.52	1383.03	1381.78	54.77	0.0034	ISDAPAQIVEVLK
139	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio r	56.6	454	1245.76	1244.75	1244.68	78.80	1.50E-05	KVDFAAAGEPLK
					693.59	1385.16	1385.75	63.33	0.00049	INAVSSADVVNVAK
140	gi|52219050	hypothetical protein LOC447859 [Danio rerio]	58.3	617	701.31	1400.60	1400.70	64.79	0.00034	HSGSDYAQLKPAK
					928.87	2783.58	2782.39	77.52	1.20E-05	ITDENLQSQTTGLYIPEYEEALK
141	gi|70778734	ATPase, Na+/K+ transporting, alpha 3b polypeptide [Dan	35.7	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
					924.65	1847.29	1846.81	64.13	0.00035	YQLSIHETEDNNDNR
142	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio r	48.3	151	757.12	1512.23	1511.69	84.28	3.50E-06	DQGTFEDFVEGLR
143	gi|113678245	hypothetical protein LOC558738 [Danio rerio]	57.7	111	845.40	1688.79	1689.84	97.41	1.80E-07	IEFSPLDAWNSGVQK
144	gi|38198639	TAR DNA binding protein, like [Danio rerio]	14.5	303	846.16	1690.31	1688.83	72.42	5.80E-05	HNNIHHLFSNFPGR
145	gi|150378483	heat shock protein, alpha-crystallin-related, b11 [Danio re	31.2	205	1113.54	2225.06	2223.99	95.53	2.30E-07	NPALQNSEPENQAVEAEAAEN
146	gi|41393141	tropomyosin 3 [Danio rerio]	28.2	248	623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
147	gi|47085999	hypothetical protein LOC406484 [Danio rerio]	41	361	850.81	1699.60	1700.90	94.54	3.30E-07	EKGQAFLDDLILDPK

148	gi|189517144	PREDICTED: similar to adaptor-related protein complex	43.7	930	835.88	1669.75	1668.88	78.67	1.30E-05	KGPGAVSVNELEEGKR
149	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	58.7	298	525.02	1048.03	1047.57	38.02	0.18	VFLDGVDKR
					589.21	1176.41	1175.67	69.50	0.00013	KVFLDGVDKR
					618.00	1233.99	1232.68	66.02	0.00027	DFLAGGIAAAISK
150	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	75.9	357	1252.70	1251.69	1251.62	69.12	0.00012	LHAVNDAEVER
151	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	38.7	248	1458.82	1457.81	1457.72	75.26	3.00E-05	HVFGESDELIGQK
					808.43	1614.84	1613.82	57.16	0.0019	RHVFGESDELIGQK
152	gi|154707842	methylmalonyl Coenzyme A mutase [Danio rerio]	37.1	757	595.61	1189.21	1188.61	47.59	0.02	AGLTIDEFAPR
					870.13	1738.25	1737.81	79.76	9.90E-06	SEFGEHEEIALAHNR
153	gi|40254659	bactin2 [Danio rerio]	51.5	375	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1131.52	37.35	0.22	GYSFTTTAER
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					758.70	1515.39	1514.74	39.42	0.12	IWHHTFYNELR
					978.73	1955.44	1953.06	67.08	0.00017	VAPEEHPVLLTEAPLNPK
154	gi|153791419	si:ch73-252g14.4 [Danio rerio]	22.3	386	1244.37	2486.73	2486.30	90.43	6.50E-07	VQQLLHAHTFGPQHNPTVHGL
155	gi|68379126	PREDICTED: hypothetical protein LOC767664 [Danio re	35.8	81	1494.75	1493.74	1493.82	56.01	0.0024	IFLEDNGLPVHIK
					748.64	1495.27	1493.82	76.25	2.20E-05	IFLEDNGLPVHIK
156	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	36.6	306	659.22	1316.43	1315.59	65.54	0.0003	VYGENIDYSEK
					701.50	1400.99	1398.75	66.80	0.00022	REEEANLLGQIK
157	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	66.1	283	660.08	1318.14	1317.64	60.19	0.001	WAEHGLTFTEK
					1045.44	2088.86	2088.16	70.82	7.00E-05	VNNSSLVGLGYTQTLKPGIK
158	gi|68448530	vitellogenin 5 [Danio rerio]	55.4	1360	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
159	gi|54262125	heat shock protein 9 [Danio rerio]	38.1	682	823.69	1645.37	1644.87	88.91	1.30E-06	VINEPTAAALAYGLDK
160	gi|41055939	sorting and assembly machinery component 50 homolog	50.3	469	665.33	1992.95	1992.02	77.36	1.50E-05	TKEDILTYEIADVFHAK
161	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	55.4	397	1188.77	1187.76	1187.68	48.56	0.017	ITAHLVHELR
					932.43	1862.85	1861.98	75.84	2.40E-05	TNVNGGAIAIGHPLGASGTR
162	gi|189533701	PREDICTED: calpastatin [Danio rerio]	62.6	824	1343.80	1342.79	1342.74	71.34	7.70E-05	HGAGVPAGVPEKPK
					736.38	1470.75	1470.83	48.01	0.016	KHGAGVPAGVPEKPK
163	gi|189519111	PREDICTED: similar to ATPase, Ca++ transporting, fast	43.2	1005	1072.60	1071.59	1071.56	41.86	0.079	NAENAIEALK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
164	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	62	255	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					633.57	1265.13	1263.70	50.58	0.0088	NVIIAAHGNSLR
					672.48	1342.95	1342.57	41.92	0.067	HGESSWNQENR
					828.27	1654.52	1653.91	60.12	0.00091	ALPFWNEVIVPEIK
					1058.87	2115.72	2115.10	36.73	0.18	DLKPIKPMQFLGDEETVR
165	gi|50344731	fibrinogen alpha chain [Danio rerio]	53.7	684	676.59	1351.17	1350.70	72.52	5.30E-05	LGISDSEFLTAAK
					750.64	1499.26	1498.69	57.20	0.0018	FPTSGTGSTSQTSNK
166	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	46.2	260	852.76	1703.51	1702.86	86.75	2.10E-06	HGASAVILDLPSSDGHK
167	gi|120952565	reticulon 4a isoform 4-l [Danio rerio]	16.5	322	843.32	1684.62	1684.83	86.64	2.10E-06	HQAQIDHYYGLVNK
168	gi|40254661	annexin A5 [Danio rerio]	47.9	317	530.21	1058.40	1058.56	40.72	0.1	SEVDLLDIR
					1144.59	2287.17	2284.98	86.60	1.70E-06	EHDKDLEEDVTGDTGGHFER
169	gi|41387146	peroxiredoxin 6 [Danio rerio]	64.9	222	1052.48	2102.95	2103.09	75.38	2.50E-05	PGILLGDVFPNFEADTTIGK
170	gi|62955301	hypothetical protein LOC550355 [Danio rerio]	62	255	925.29	1848.57	1848.92	77.21	1.70E-05	VLPGVDVTVGHEEEQGGK
171	gi|54400460	fibulin 5 [Danio rerio]	23.1	477	1111.23	2220.45	2220.00	85.10	2.50E-06	NSPLPYPEASYPEEPYPDR
172	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	30.4	359	879.64	1757.27	1758.94	53.19	0.0045	SIRPLDADTIETSITK
					901.77	1801.52	1800.89	51.77	0.0063	VFLLGEEVAQYDGAYK
					967.33	1932.65	1932.85	44.87	0.028	DALNQAMDEELERDER
173	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [	63.2	709	1164.68	1163.67	1164.65	55.10	0.0031	HIEIQVLADK
					827.11	1652.21	1649.84	62.11	0.00057	TVAVHSDVDSSAVHVK
174	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	46.7	763	653.21	1304.41	1303.71	61.87	0.00069	MQLLEIITTDK

					752.68	1503.34	1503.72	64.87	0.00033	TAEEVTGLSQEGQR
175	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	42.9	238	1029.00	2055.99	2055.00	84.28	3.10E-06	SHEGDDPLLQYVVNNSLR
176	gi|41055748	integrin linked kinase [Danio rerio]	24.6	452	792.72	1583.43	1582.76	83.90	4.00E-06	GDDTPLHLAASHGHR
177	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	35.3	116	1121.07	2240.13	2240.16	83.69	3.50E-06	INAGQIEEVIAQAEAELSLSR
178	gi|117606266	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	31.2	991	788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
179	gi|189519965	PREDICTED: similar to nonmuscle myosin heavy chain [	37.8	1857	1093.83	2185.64	2184.99	76.48	1.90E-05	HAEQERDELADEISNSASGK
180	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	50.3	523	790.68	1579.35	1577.76	83.48	4.20E-06	YDVQVQIENVEDK
					945.67	1889.33	1888.04	37.61	0.16	ASVNIQIVDVPGPPQNLK
181	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	60.2	244	903.52	902.51	902.51	42.18	0.083	VISSIEQK
					1155.50	1154.49	1154.55	60.78	0.00087	YLSEVASGDSK
					587.18	1172.34	1170.56	41.88	0.074	AYQDAFEISK
					745.40	1488.78	1488.71	51.91	0.0066	AVTEGGVELSNEER
182	gi|113678344	BCL2-like 13 (apoptosis facilitator) [Danio rerio]	18.8	485	1030.15	3087.41	3085.41	61.28	0.00044	SLDSAEGVALAEEQSENNSSNS
183	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	67.2	448	919.82	1837.62	1836.96	64.83	0.00029	DKPHLNIGTIGHVDHGK
184	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	34.7	242	903.52	902.51	902.51	42.18	0.083	VISSIEQK
					1155.50	1154.49	1154.55	60.78	0.00087	YLSEVASGDSK
					745.40	1488.78	1488.71	51.91	0.0066	AVTEGGVELSNEER
185	gi|58801526	SET translocation (myeloid leukemia-associated) B [Dani	16	275	605.37	1208.73	1207.60	35.37	0.3	VEVTEFEDIK
					1098.47	2194.92	2194.01	81.47	5.90E-06	EQQEAIEHIDEVQNEIDR
186	gi|58801528	SET translocation (myeloid leukemia-associated) A [Dani	15.2	269	605.37	1208.73	1207.60	35.37	0.3	VEVTEFEDIK
					1098.47	2194.92	2194.01	81.47	5.90E-06	EQQEAIEHIDEVQNEIDR
187	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple	52.6	209	637.34	1272.66	1272.67	64.58	0.00038	SLDKVEQELGR
					782.72	1563.43	1561.80	42.52	0.055	SDASILGGMIVSIGDK
188	gi|47086189	propionyl Coenzyme A carboxylase, beta polypeptide [Da	38.8	557	838.80	1675.58	1675.79	55.44	0.0029	SVTNEDVTQEELGGAK
					872.59	1743.16	1744.85	63.94	0.00039	AYDMLDIVHGIVDER
189	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	33.6	2633	1230.28	2458.55	2458.19	81.11	5.50E-06	HAINQEINAYNTPAQFGLEGSG
190	gi|67514531	ubiquitin specific protease 5 [Danio rerio]	27.9	834	602.99	1805.95	1804.92	67.29	0.00018	RREEAESSGAPPPVAPR
191	gi|50540382	hypothetical protein LOC436930 [Danio rerio]	32.2	460	735.25	1468.49	1467.79	63.52	0.00043	ALADQSPQIGVLEK
					832.57	1663.12	1662.89	52.80	0.0051	SAAPPVLQPQDVQVSK
192	gi|54606886	hexokinase 1 [Danio rerio]	46.3	918	864.33	1726.64	1723.83	79.77	9.80E-06	TKYDDAVDDLSLNAGK
193	gi|189518076	PREDICTED: filamin C, gamma b (actin binding protein 2	43.7	2732	805.13	1608.25	1607.78	36.13	0.23	VDVGKDEEFTVNTR
					1115.87	2229.73	2228.03	42.68	0.044	DGSCGVAYIVQEPGDYEVSIK
					1152.87	2303.73	2303.14	72.02	4.90E-05	GQHVPGSPFQFTVGPLGEGGA
194	gi|45356143	tumor protein D52-like 2 isoform 1 [Danio rerio]	50.2	201	737.80	1473.58	1473.69	79.41	1.20E-05	GLGSDSISDLPEER
195	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	56.5	1631	587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
196	gi|27545305	laminin, gamma 1 [Danio rerio]	48.2	1593	559.44	1116.86	1115.56	37.28	0.23	DAENLINTAR
					665.17	1328.32	1327.68	63.97	0.00042	RAEAALGNAAADAK
					963.13	1924.24	1924.06	50.87	0.007	EVLNTINALLGQLGNIDK
197	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Dar	26.4	2115	643.71	1285.40	1284.76	57.60	0.0018	KSPTPVPLPPPR
198	gi|47085823	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight c	54.5	424	924.30	1846.58	1846.92	75.34	2.70E-05	AFTGFIVDADTPGVQPGR
199	gi|47085679	electron-transfer-flavoprotein, beta polypeptide [Danio re	56.3	254	924.89	923.88	924.50	63.43	0.00041	GIHVEVSGK
200	gi|30017425	ATPase, Na+/K+ transporting, alpha 1a.5 polypeptide [Da	32.1	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
201	gi|18858303	ATPase, Na+/K+ transporting, alpha 1b polypeptide [Dan	34.1	1025	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
202	gi|66472494	phosphorylase, glycogen (muscle) A [Danio rerio]	37.2	842	594.42	1186.83	1184.64	74.74	4.00E-05	GLAGVENVADLK
203	gi|41054784	phosphorylase, glycogen (muscle) b [Danio rerio]	38.1	315	594.42	1186.83	1184.64	74.74	4.00E-05	GLAGVENVADLK
204	gi|41387136	hypothetical protein LOC393781 [Danio rerio]	57	128	902.80	1803.58	1801.94	74.18	3.60E-05	YHVSETPFAISAQKPK
205	gi|53933242	cytochrome c oxidase subunit VIa polypeptide 1 [Danio re	69.4	108	781.74	2342.19	2341.05	50.66	0.0067	TLFHNPHVNALPDGYEHHDE
206	gi|41282137	ATPase, Na+/K+ transporting, alpha 3a polypeptide [Dan	34.8	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
207	gi|35902900	aldolase c, fructose-bisphosphate [Danio rerio]	47.9	363	1136.95	2271.88	2271.13	72.97	4.10E-05	GVVPLAGTNGETTTQGLDGLSE
208	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	35	697	652.16	1302.30	1301.66	63.04	0.00053	SHIDELYANIK
209	gi|66472480	NADH dehydrogenase (ubiquinone) Fe-S protein 5 [Dani	52.8	106	643.28	1284.55	1283.66	72.00	6.40E-05	WLLAQSGEQPR
210	gi|41151982	major vault protein [Danio rerio]	34.2	863	1069.61	2137.21	2137.12	65.00	0.00026	IPPHHYIHVLDQNTNIAR

					1353.45	2704.89	2704.43	36.37	0.16	STLITDGSSPINLFTTANGLLGSL
211	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [Da	49.2	789	699.53	1397.05	1395.70	71.84	6.30E-05	DLQANVEHLTEK
212	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coe	57.4	761	653.21	1304.41	1303.71	61.87	0.00069	MQLLEIITTDK
					697.27	1392.52	1392.67	46.97	0.021	LSGQLDYHGFEK
					882.60	1763.19	1760.86	42.36	0.056	LTAPPAVSSDEDIQYR
213	gi|51010955	hypothetical protein LOC445042 [Danio rerio]	52.9	104	609.53	1217.04	1215.65	71.12	8.90E-05	ALTAGSEASGKPK
214	gi|38488700	phosphoglycerate mutase 1 [Danio rerio]	46.9	254	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					835.57	1669.12	1668.89	60.67	0.0008	ALPFWNDEIVPQIK
215	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio re	52.9	333	713.78	1425.54	1424.81	70.23	9.10E-05	LDVAPISDIIEIK
216	gi|47086009	ribosomal protein L19 [Danio rerio]	33.2	196	972.51	1943.00	1941.92	70.00	8.40E-05	VWLDPNETNEIANANSR
217	gi|189523865	PREDICTED: myosin 1b-like 2 [Danio rerio]	42.5	1078	752.67	2254.98	2255.13	50.39	0.0076	SLRHQDKDQCILITGESGAGK
218	gi|18858873	heat shock protein 90-alpha 1 [Danio rerio]	24.2	726	868.56	1735.10	1734.74	69.58	0.00011	IEDLGADEDEDSKDGK
219	gi|18858379	carbonic anhydrase [Danio rerio]	50.4	260	502.52	1003.03	1000.54	37.51	0.22	VLDALDDIK
					824.38	2470.10	2471.13	63.52	0.00032	QFHFHWGSSDDKGSEHTIAGTK
220	gi|189517212	PREDICTED: similar to myosin, heavy polypeptide 11, sr	32.1	1994	864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
221	gi|116235424	hypothetical protein LOC572011 [Danio rerio]	35.1	823	715.67	1429.33	1429.70	69.18	0.00012	ELQEAQELANTGK
222	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	38.2	204	853.75	1705.49	1704.91	69.08	0.00012	GATYGKPVHHGVNQIK
223	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	38.7	380	690.97	1379.93	1379.71	69.07	0.00012	FFEAAVGEAKPSK
224	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	46.3	6009	578.82	1155.63	1155.65	55.90	0.0027	LKGDVDVSVPK
					651.29	1300.57	1299.69	36.73	0.22	LMGSNVDLNLPK
225	gi|47550733	SERPINE1 mRNA binding protein 1 [Danio rerio]	32.5	391	1118.80	2235.59	2235.08	68.31	0.00012	RFDKPADEKPAEGGEFSVEK
226	gi|189515773	PREDICTED: amylo-1, 6-glucosidase, 4-alpha-glucanotra	41.6	1532	895.72	1789.43	1787.00	68.18	0.00015	GLPALIQDHPHLHAIR
227	gi|189521867	PREDICTED: similar to histone cluster 2, H2ab [Danio re	66.7	144	1136.50	2270.98	2270.37	45.74	0.021	LLGGVTIAQGGVLPNIQAVLLPK
					973.15	2916.42	2914.58	54.31	0.0023	VGAGAPVYLAAVLEYLTAEILEL
228	gi|41055102	H2A histone family, member X [Danio rerio]	62	142	1136.50	2270.98	2270.37	45.74	0.021	LLGGVTIAQGGVLPNIQAVLLPK
					973.15	2916.42	2914.58	54.31	0.0023	VGAGAPVYLAAVLEYLTAEILEL
229	gi|68441421	PREDICTED: similar to Mid1ip1 protein [Danio rerio]	62.5	128	1136.50	2270.98	2270.37	45.74	0.021	LLGGVTIAQGGVLPNIQAVLLPK
					973.15	2916.42	2914.58	54.31	0.0023	VGAGAPVYLAAVLEYLTAEILEL
230	gi|41152365	ATP synthase, H+ transporting, mitochondrial F1 comple	68.6	159	732.54	1463.06	1462.69	70.61	8.60E-05	AQSELVSASDEATR
231	gi|70887615	hypothetical protein LOC558711 [Danio rerio]	52.6	367	656.84	1311.67	1311.74	67.35	0.00018	VKVESQVAVPEK
232	gi|51467931	enolase 2 [Danio rerio]	59.7	434	1008.42	3022.23	3024.58	66.73	0.00013	HIADLAGNTELVLPVPAFNVING
233	gi|82658182	cytochrome c-1 [Danio rerio]	36.8	307	715.11	1428.21	1425.71	66.24	0.00024	NLVGVSHTEDEVK
234	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	25	308	550.57	1099.13	1098.61	50.09	0.011	QLADALKANR
235	gi|41053309	hydroxyacylglutathione hydrolase [Danio rerio]	28.5	260	970.86	1939.71	1938.91	65.72	0.00023	TVLTTHHHWDHAGGNEK
236	gi|41056085	keratin 8 [Danio rerio]	37.3	520	1308.67	1307.66	1307.65	40.71	0.085	NKYEDEINKR
					744.60	1487.19	1485.71	65.58	0.00028	ANLENQIAEAEER
237	gi|113681458	Ndrg4 [Danio rerio]	32.4	352	939.29	1876.56	1876.00	63.58	0.00039	GNKPAILTYHDVGLNHK
238	gi|21426835	glucose phosphate isomerase a [Danio rerio]	36.2	553	717.59	1433.16	1432.70	63.47	0.00045	ELQASGLSGDSLEK
239	gi|41152026	phosphoglycerate mutase 1 like b [Danio rerio]	39.8	254	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					1051.63	2101.25	2100.10	47.40	0.016	NLKPVKPMQFLGDEETVR
240	gi|41054573	hydroxysteroid dehydrogenase like 2 [Danio rerio]	50.1	415	1588.03	3174.05	3171.54	58.77	0.00079	DFDVYAVEPGHPLLPDFFLDGQ
241	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	61.5	455	759.60	1517.19	1517.74	36.85	0.21	CPDCPGLLPLHEPK
					654.05	1959.11	1959.96	47.27	0.016	FHDHRPGSVHPLGPDHR
242	gi|116235416	hypothetical protein LOC553452 [Danio rerio]	36.7	316	1009.26	2016.51	2014.96	62.10	0.00052	HIDGAAVYNNETEVGEGIK
243	gi|45387723	hypothetical protein LOC402952 [Danio rerio]	38.4	331	1181.37	3541.08	3539.71	48.56	0.0067	GEDYYPPPPPHYPPHPHDHPH
244	gi|61651682	fibronectin 1b [Danio rerio]	36	2408	1070.65	3208.93	3208.44	59.70	0.00061	INTVGPTGHDSTDAHGQHVEYT
245	gi|47087077	phosphoglycerate kinase 1 [Danio rerio]	59.5	417	916.46	915.45	915.45	52.89	0.0065	FHVAEEGK
					817.60	1633.19	1633.78	36.82	0.21	LGDVYVNDAFGTAHR
246	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	26.1	2113	651.79	1301.56	1299.71	37.15	0.2	EIGGLTQVNKNK
					653.21	1304.41	1303.77	60.26	0.001	RCLIEIFGILK
247	gi|189532434	PREDICTED: im:7160733 [Danio rerio]	29.2	1248	653.21	1304.41	1303.77	60.26	0.001	RCLIEIFGILK
248	gi|66472386	hypothetical protein LOC553711 [Danio rerio]	49.7	163	763.67	2287.99	2287.11	59.91	0.00081	GDRPLTYEQAHHPHHISHR

249	gi|32308156	annexin A1a [Danio rerio]	48.2	340	783.03	1564.04	1563.83	59.90	0.00099	GVDEPTIIDTLVHR
250	gi|189536881	PREDICTED: hypothetical protein LOC402880 [Danio re	35.8	173	685.99	1369.96	1367.74	50.88	0.0081	LDTPLPDVPFVR
251	gi|51011113	hydroxyacyl-Coenzyme A dehydrogenase [Danio rerio]	71.8	309	819.15	1636.29	1636.85	49.33	0.011	DPDNPLFAPSPLLNK
					923.59	2767.73	2767.42	36.64	0.14	NVSTSTDAASVVHGTDLVVEAI
252	gi|40363541	S-adenosylhomocysteine hydrolase [Danio rerio]	47.8	433	480.61	1438.81	1437.75	58.91	0.0012	KLDEEVAAAHLDK
253	gi|50344812	ribosomal protein S13 [Danio rerio]	45	151	848.35	1694.68	1692.91	58.79	0.0013	GLAPDLPEDLYHLIK
254	gi|41054351	ribosomal protein L27 [Danio rerio]	30.1	136	752.58	2254.71	2255.09	58.76	0.0011	NIDDGTADRPYSHALVAGIDR
255	gi|50539832	lysyl-tRNA synthetase [Danio rerio]	29.4	602	1124.52	2247.02	2247.14	58.56	0.0011	YNHLQPGDHLTDVVLNLSGR
256	gi|189518755	malic enzyme 2, NAD(+)-dependent, mitochondrial isofor	40.3	581	1093.30	2184.59	2184.23	58.56	0.0012	SFLDAVNVIKPTAIIGVSGAGR
257	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio	76.7	172	487.46	972.90	971.54	40.97	0.1	LNDLASAIR
					1659.13	3316.24	3314.75	50.52	0.0047	EIYPYVIQELKPTLQELGISTPEE
258	gi|47551341	adenylosuccinate synthase like 1 [Danio rerio]	52	456	643.44	1284.87	1284.72	56.83	0.0021	LDILDVLDEIK
259	gi|189526054	PREDICTED: hypothetical protein LOC335621, partial [D	47.5	530	721.66	1441.30	1439.87	56.81	0.002	AKLAAQEVELKLK
260	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	37.6	606	1090.85	2179.69	2179.07	56.63	0.0018	GGENIYPAEIEQFLHTHPK
261	gi|41152189	hypothetical protein LOC393720 [Danio rerio]	71.7	244	820.65	1639.28	1638.85	49.87	0.0098	RVEAIINNYPEGHK
262	gi|41152375	mitochondrial ATP synthase gamma-subunit [Danio rerio	54.5	292	1097.58	1096.57	1095.60	55.25	0.003	HLIIGVSSDR
263	gi|47086943	ATP synthase, H+ transporting, mitochondrial F0 comple	61.6	112	905.44	904.43	904.45	39.81	0.14	NLAEETTK
					674.56	1347.10	1346.68	55.37	0.003	ASGGVVDAGPVYQK
264	gi|52219158	aquaporin 8 [Danio rerio]	22.7	260	1058.86	2115.71	2113.97	55.02	0.0027	SELFTVATGDGGDNHQNQPK
265	gi|41054699	hypothetical protein LOC393530 [Danio rerio]	42.6	516	1059.44	1058.43	1058.47	54.82	0.004	EHDFSEAPK
266	gi|189516256	PREDICTED: similar to phosphofructokinase, platelet [Da	45.8	782	706.78	1411.55	1411.69	54.77	0.0032	DLQSNVEHLTEK
267	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	12.5	448	710.05	1418.09	1415.74	54.44	0.0037	EALGAENIQSTKR
268	gi|47085781	ubiquitin-like modifier activating enzyme 1 [Danio rerio]	41.1	1058	733.66	2197.94	2196.12	54.35	0.0031	FDRPGQLHVGFQALHAFEK
269	gi|47086817	bscv (C20orf3) homolog [Danio rerio]	23.9	415	1046.78	2091.54	2090.05	54.31	0.0031	LNRPHIITDETHEPQYK
270	gi|189524989	PREDICTED: neurobeachin-like 2 [Danio rerio]	45.2	1495	655.96	1309.91	1308.70	53.90	0.004	NNVAIEPLSAPGK
271	gi|189521058	PREDICTED: similar to cysteine and glycine-rich protein	81.3	193	1251.74	2501.47	2503.17	53.78	0.003	KGLDSTTVAAHESEIYCKTCYG
272	gi|189527668	PREDICTED: similar to janus kinase and microtubule int	37.2	807	773.19	1544.36	1543.91	52.30	0.006	FQLKIAELQSVIR
273	gi|168229163	cysteine-rich protein 2 [Danio rerio]	56.3	206	998.94	2993.79	2996.41	52.99	0.003	TLAAGSHAEHDGQPYCHKPCY
274	gi|46518516	interferon 1 [Danio rerio]	25.1	179	495.32	988.63	989.50	52.78	0.0066	MDIIASNAR
275	gi|55925377	peptidase (mitochondrial processing) alpha [Danio rerio]	44.9	517	1388.81	2775.60	2773.44	52.53	0.0038	SKPAVAALGDLTELPSYEDIQA
276	gi|189541652	PREDICTED: similar to Myosin-3 (Myosin heavy chain 3)	31.4	882	660.22	1318.42	1315.65	52.39	0.0061	ELELELDAEQK
277	gi|189546569	PREDICTED: complement component 3 [Danio rerio]	30.9	1648	652.15	1302.28	1301.65	52.01	0.0067	EGTDQVIEGQVK
278	gi|66773104	branched chain keto acid dehydrogenase E1, alpha poly	29.1	446	827.55	1653.08	1652.84	51.96	0.0059	QGQIINPSEDPQLSK
279	gi|189534068	PREDICTED: nuclear RNA export factor 1 [Danio rerio]	50	642	731.60	1461.18	1460.65	51.91	0.0065	FGGRGGGGGGGGPSDGR
280	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio reri	29.1	199	668.10	1334.18	1332.69	51.50	0.007	KYTLPPGVDSEK
281	gi|148229906	hypothetical protein LOC100037332 [Danio rerio]	28.8	302	550.58	1099.15	1098.64	46.82	0.024	LKQELAELR
282	gi|47271398	ribosomal protein L7 [Danio rerio]	46.3	246	680.91	1359.81	1359.62	51.36	0.0076	TTHFVEGGDAGNR
283	gi|125854185	PREDICTED: hypothetical protein [Danio rerio]	12.2	645	674.08	1346.15	1346.62	50.90	0.0086	EEEEEQLKADK
284	gi|189532605	PREDICTED: thrombospondin, type I, domain containing	52	1684	1194.55	3580.61	3581.73	50.77	0.0039	EVTCVHRSGSTASISQCTQQTL
285	gi|41055997	hypothetical protein LOC393098 [Danio rerio]	30.3	343	863.60	1725.19	1724.92	50.74	0.0079	DSTVLAHVMKLLNER
286	gi|125832538	PREDICTED: nucleolar and coiled-body phosphoprotein	72.4	1001	1088.39	2174.77	2173.28	50.71	0.0069	KKPATTPVSKPTPAKPTPTVK
287	gi|125833577	PREDICTED: similar to Galectin-3 (Galactose-specific le	29.6	368	670.63	1339.24	1337.66	50.69	0.0082	GHEVVFHFNPR
288	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	45.3	329	867.36	1732.71	1729.95	50.68	0.0085	KGSLLIDSSTIDPAVSK
289	gi|41054603	actinin alpha 4 [Danio rerio]	32.4	901	762.20	1522.39	1520.71	50.51	0.0085	AGTQIENIEEDFR
290	gi|66773056	proteasome (prosome, macropain) subunit, alpha type, 2	56	234	734.65	2200.92	2200.13	50.39	0.0077	YNEDLELEDAIHTAILTLK
291	gi|189522138	PREDICTED: similar to paxillin [Danio rerio]	39.7	527	1147.34	2292.67	2294.99	39.91	0.08	TWHPEHFVCTHCQEEIGSR
292	gi|189518402	PREDICTED: similar to NLR family, CARD domain conta	34.9	995	951.97	950.96	951.47	46.42	0.022	CFDDIVLK
293	gi|116875779	hypothetical protein LOC768287 [Danio rerio]	49.2	474	549.51	1097.01	1094.55	50.25	0.01	AELQHLNDR
294	gi|156616344	hypothetical protein LOC100124599 [Danio rerio]	55	278	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
295	gi|189524320	PREDICTED: similar to family with sequence similarity 8	37.4	174	533.18	1064.34	1063.51	49.33	0.013	SRVSDCLER
296	gi|148224341	hypothetical protein LOC100038781 [Danio rerio]	21.2	226	538.13	1074.25	1073.56	49.09	0.015	GGIHHISPEK
297	gi|55742519	vesicle-associated membrane protein 2 [Danio rerio]	64.5	110	833.77	1665.53	1664.80	48.94	0.012	ADALQAGASQFETSAAK

298	gi|50344800	vesicle-associated membrane protein 3 (cellubrevin) [Dar	58.8	102	833.77	1665.53	1664.80	48.94	0.012	ADALQAGASQFETSAAK
299	gi|47085833	glyceraldehyde-3-phosphate dehydrogenase, spermatog	40	335	718.66	1435.30	1434.76	48.73	0.013	GAHQNIIPASTGAAK
300	gi|189522849	PREDICTED: similar to oxoglutarate (alpha-ketoglutarate	21.9	961	1201.03	2400.04	2399.32	48.47	0.011	NITLSLVANPSHLEAVNPVVQG
301	gi|125814522	PREDICTED: si:dkey-261e22.2 [Danio rerio]	37.5	1868	653.21	1304.41	1303.69	48.31	0.016	DTSSDALELLIK
302	gi|47086525	ribosomal protein S15a [Danio rerio]	65.4	130	567.82	1700.43	1699.80	48.27	0.014	HGYIGEFEIIDDHR
303	gi|41055407	potassium channel, subfamily K, member 5 [Danio rerio]	29.5	448	609.35	1216.68	1216.64	47.76	0.02	KQEEELARSK
304	gi|68448495	hypothetical protein LOC100003906 isoform 1 [Danio reri	29	915	911.39	1820.76	1820.84	47.56	0.016	SDASYDEIQGSQPPSLK
305	gi|125817349	PREDICTED: similar to CAP-GLY domain containing link	44.6	1041	686.11	1370.20	1368.68	47.37	0.018	HEIDAAVMAKER
306	gi|116004537	creatine kinase, brain [Danio rerio]	58.3	381	755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
307	gi|35902802	chromobox homolog 2 [Danio rerio]	51.6	510	609.35	1216.68	1215.67	47.20	0.022	EQEKELLISK
308	gi|41282163	protein disulfide isomerase-related protein (provisional) [	38.2	440	559.48	1116.95	1114.60	49.77	0.013	GSTATVGGGALPK
309	gi|41054003	Cap1 CAP, adenylate cyclase-associated protein 1 [Dani	50.3	463	994.76	1987.51	1985.99	46.71	0.018	VENQEGAQNLVISDTELK
310	gi|189530311	PREDICTED: hypothetical LOC555629 [Danio rerio]	72.3	401	796.88	1591.74	1591.82	46.57	0.021	QKMSLLSSNTEINK
311	gi|46309527	hypothetical protein LOC404610 [Danio rerio]	36.6	325	724.76	1447.51	1447.76	46.36	0.024	DALGILDELQAYK
312	gi|113674674	DEK oncogene-like [Danio rerio]	48	442	867.38	1732.74	1729.98	46.20	0.024	KLLKTICQTLDLER
313	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	29	245	605.07	1208.12	1206.61	46.19	0.025	YLAEVAVGEEK
314	gi|125806044	PREDICTED: similar to 19.9kD myosin light chain [Danio	29.5	173	699.83	1397.64	1398.63	46.09	0.024	FTDEEVDELFR
315	gi|157073897	ubiquinol-cytochrome c reductase, Rieske iron-sulfur pol	29.7	273	773.42	1544.82	1542.79	45.70	0.028	EIETEAGVNLAELR
316	gi|189525434	PREDICTED: im:7157373 [Danio rerio]	46.6	545	954.39	2860.13	2859.32	45.68	0.017	SAAAPPKEEAPPANAPDGDAP
317	gi|189523403	PREDICTED: NADH dehydrogenase (ubiquinone) flavop	49.2	516	994.20	1986.38	1983.93	45.62	0.023	TTDSPPADTAAADVAVEEPK
318	gi|189516010	PREDICTED: similar to leucine rich repeat containing 16	40.1	1347	730.20	1458.38	1458.79	45.60	0.028	GTVLVNALGSNACLK
319	gi|189533816	PREDICTED: hypothetical protein [Danio rerio]	36	1020	493.60	985.18	983.60	45.55	0.032	QLIEQLLK
320	gi|189530783	PREDICTED: hypothetical protein isoform 2 [Danio rerio]	31.1	222	493.60	985.18	983.65	45.55	0.032	QILKKNLK
321	gi|50540198	hypothetical protein LOC436839 [Danio rerio]	48.3	201	721.18	1440.35	1439.63	45.52	0.027	NIDEHANEDVER
322	gi|116487349	carboxylesterase 2-like [Danio rerio]	42	555	1027.86	2053.71	2052.99	45.38	0.024	TGSPNPAPVPWPVYDQSNK
323	gi|125843378	PREDICTED: si:dkey-38l12.3 [Danio rerio]	25.3	549	1027.86	2053.71	2052.99	45.38	0.024	TGSPNPAPVPWPVYDQSNK
324	gi|189522914	PREDICTED: similar to RAS and EF-hand domain contai	40.1	551	506.72	1011.42	1012.59	45.19	0.03	IVLAGDAAVGK
325	gi|189523254	PREDICTED: similar to CD22 antigen [Danio rerio]	46.2	392	770.71	1539.41	1540.76	45.09	0.029	IFSISKISSDDSDK
326	gi|61806508	signal peptidase complex subunit 2 homolog [Danio rerio	63.7	201	650.84	1299.66	1299.73	44.33	0.037	AARNGKNSILEK
327	gi|68438157	PREDICTED: similar to Histone H1.5 (H1 VAR.5) (H1b) [	62.7	204	627.68	1253.35	1251.76	46.77	0.021	ALVLNGTLVQPK
328	gi|189536629	PREDICTED: similar to DEP domain containing 2 [Danio	47.3	1600	611.27	1220.52	1218.70	44.63	0.037	FNTIAIIDGKK
329	gi|90652819	hypothetical protein LOC664756 [Danio rerio]	53.9	462	766.50	765.49	765.39	39.76	0.09	FEEITK
					973.85	2918.52	2915.57	44.47	0.022	EGGANGVTLLEALDSILPPSRP
330	gi|50233897	FLJ12716-like protein [Danio rerio]	35.3	1132	1188.77	1187.76	1187.63	44.42	0.043	TAYSLVHELR
331	gi|189529141	PREDICTED: similar to NLR family, pyrin domain contain	44.4	789	487.46	972.90	973.52	44.41	0.046	DSAALASALR
332	gi|153945891	hypothetical protein LOC100101652 [Danio rerio]	39.2	293	713.31	1424.60	1424.85	44.33	0.035	RALTIQEIAALAR
333	gi|189530012	PREDICTED: wu:fb94b04 [Danio rerio]	33.9	762	551.34	1100.67	1098.61	44.29	0.045	KLNEAQQLR
334	gi|41056221	hypothetical protein LOC393533 [Danio rerio]	30.1	617	566.38	1130.75	1129.72	44.21	0.045	SSLRLKVLSK
335	gi|18858525	death associated protein 1b [Danio rerio]	77.1	109	469.10	1404.27	1403.80	44.20	0.039	VRPSVEKPHISR
336	gi|125814831	PREDICTED: similar to zinc finger protein 585B [Danio r	44.3	298	836.68	1671.35	1672.88	44.11	0.037	EESEDVKIEEIIIK
337	gi|47086263	phosphoglucomutase 2 [Danio rerio]	41.4	611	522.11	1042.20	1043.57	43.80	0.048	ELNRNTAVK
338	gi|125821665	PREDICTED: similar to Putative S-adenosyl-L-methionin	26.4	394	448.88	1343.62	1340.72	43.80	0.044	FLRGEDLAAPPR
339	gi|189530864	PREDICTED: similar to RIKEN cDNA 2810405J04 gene	52.3	516	581.62	1161.23	1160.63	43.73	0.047	LCAWLVSELK
340	gi|189525167	PREDICTED: hypothetical protein [Danio rerio]	39.7	1100	762.20	1522.39	1520.80	43.56	0.042	VQLLQDLQDFFR
341	gi|189533677	PREDICTED: hypothetical protein [Danio rerio]	39.1	128	531.01	1060.01	1058.51	43.41	0.057	MQNHFGAVR
342	gi|189530862	PREDICTED: wu:fb54a03 [Danio rerio]	27.9	727	401.07	800.12	800.46	43.33	0.056	ELEGLLK
343	gi|189520791	PREDICTED: family with sequence similarity 62 (C2 dom	27.7	1700	738.59	1475.17	1473.84	40.52	0.089	IDFGGKPMKVVGVK
					1094.98	3281.90	3280.56	43.09	0.028	QKPVVEDHSTGEEHEEKGPAT
344	gi|189528097	PREDICTED: similar to sushi-repeat-containing protein,	46.6	436	537.92	1073.83	1072.61	43.02	0.062	LKCPLSREK
345	gi|45433520	hypothetical protein LOC327237 [Danio rerio]	40.1	157	707.70	1413.38	1413.81	42.98	0.05	ISREVIQMVLAR
346	gi|113678297	nudix (nucleoside diphosphate linked moiety X)-type moti	45.5	242	1056.28	2110.55	2110.04	42.84	0.044	SKPKPLQPAEEESESTEPK
347	gi|45120100	calcium channel, voltage-dependent, L type, alpha 1D su	32.2	2082	701.36	2101.06	2100.08	38.30	0.13	TAGKIKTEGNLEQANEELR

348	gi|53292609	clathrin, heavy polypeptide a (Hc) [Danio rerio]	34.6	1680	472.54	943.07	942.49	42.73	0.064	HELIEFR
349	gi|41053833	hypothetical protein LOC393213 [Danio rerio]	25.2	333	542.49	1624.45	1623.84	42.64	0.052	GHPDEAAAALKELFR
350	gi|189532250	PREDICTED: si:ch211-81a5.3 [Danio rerio]	46	2962	771.84	1541.67	1540.86	42.63	0.053	TDDPRSQLLQLKK
351	gi|32401408	annexin A11b [Danio rerio]	36.9	485	886.82	1771.62	1770.84	42.54	0.053	SLYTHISGDTSGDYKK
352	gi|125842393	PREDICTED: zgc:103738 [Danio rerio]	54.5	77	987.88	2960.60	2961.35	42.46	0.035	TLSAGSHAEHEGKPYCNNPCY
353	gi|47086993	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, ne	54.1	303	752.86	2255.55	2254.08	42.45	0.047	HLVQAQYWHDPLNDDLYK
354	gi|189522065	PREDICTED: similar to Histone H1.2 (H1 VAR.1) (H1c) [	82	200	456.60	1366.76	1365.83	44.67	0.032	AKKAGPGVGELIVK
355	gi|47086505	fibrinogen, B beta polypeptide [Danio rerio]	48	485	1376.63	1375.62	1375.70	48.45	0.015	DTVDVTFPQNIK
356	gi|82658210	protein phosphatase 1, regulatory (inhibitor) subunit 7 [D	33.6	345	1090.76	2179.50	2178.14	41.86	0.053	VIENLDSLSSLESLFLGTNK
357	gi|160333235	lyric-like [Danio rerio]	60.5	542	760.76	1519.50	1518.87	41.82	0.067	SVTVKPHPPPHVPK
358	gi|41053347	mitochondrial trifunctional protein, beta subunit [Danio re	32.3	471	1197.60	1196.59	1196.57	41.61	0.068	DFVYVSQDPK
359	gi|189531881	PREDICTED: solute carrier family 8 (sodium-calcium exc	24.2	967	770.74	1539.47	1536.85	41.54	0.067	RPSIGGELGGPRVSR
360	gi|52219178	high-mobility group box 2 [Danio rerio]	55.1	214	705.76	1409.50	1407.74	41.51	0.067	SEHPNLTIGEIAK
361	gi|189526982	PREDICTED: similar to G protein-coupled receptor 103 [	20.6	422	500.54	999.06	998.59	41.05	0.091	IGIELWIR

DMSO replicate 2

Protein #	**Accession ID**	**Protein name**	**Protein coverage**	**length**	**peptide *m/z***	**peptide Mr*expt***	**peptide Mr*calc***	**peptide score**	**pep_expect**	**peptide sequence**
1	gi|74315904	alpha globin-like [Danio rerio]	72.7	143	559.21	1116.41	1114.56	61.51	0.00086	ADEIGAEALAR
					589.48	1176.94	1175.62	79.59	1.20E-05	TIMGAVGEAISK
					684.19	1366.37	1365.73	77.20	1.80E-05	FFNNLALALSEK
					933.26	1864.50	1863.88	127.77	1.50E-10	TYFSHWSDLSPGSGPVK
					934.01	1866.01	1868.00	50.86	0.0073	IDDLVGGLAALSELHAFK
					623.03	1866.07	1863.88	50.21	0.0085	TYFSHWSDLSPGSGPVK
					934.08	1866.14	1868.00	112.49	5.00E-09	IDDLVGGLAALSELHAFK
					934.14	1866.26	1868.00	110.20	8.50E-09	IDDLVGGLAALSELHAFK
					934.20	1866.38	1863.88	99.86	9.20E-08	TYFSHWSDLSPGSGPVK
					934.23	1866.45	1868.00	90.05	8.80E-07	IDDLVGGLAALSELHAFK
					934.24	1866.46	1863.88	89.80	9.40E-07	TYFSHWSDLSPGSGPVK
					934.28	1866.55	1868.00	95.93	2.30E-07	IDDLVGGLAALSELHAFK
					934.40	1866.79	1868.00	128.55	1.30E-10	IDDLVGGLAALSELHAFK
					996.85	1991.69	1991.97	65.99	0.00021	TYFSHWSDLSPGSGPVKK
					1008.94	3023.79	3025.62	41.79	0.039	TIMGAVGEAISKIDDLVGGLAAL
2	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	75.5	143	559.21	1116.41	1114.56	61.51	0.00086	ADEIGAEALAR
					582.03	1162.04	1161.61	84.54	3.80E-06	TIMGAVGEAVSK
					684.19	1366.37	1365.73	77.20	1.80E-05	FFNNLALALSEK
					924.16	1846.30	1847.88	127.55	1.60E-10	TYFSHWADLSPGSGPVK
					934.40	1866.79	1868.00	128.55	1.30E-10	IDDLVGGLAALSELHAFK
					989.42	1976.83	1975.98	76.11	2.10E-05	TYFSHWADLSPGSGPVKK
3	gi|41053652	myoglobin [Danio rerio]	82.3	147	456.00	909.98	909.49	40.70	0.076	ADHDLVLK
					551.01	1100.01	1098.58	83.28	5.60E-06	AGLDAAGQGALR
					780.67	1559.33	1557.74	81.26	7.40E-06	VMDAVIGDIDGYYK
					1010.16	2018.30	2020.10	87.97	1.40E-06	GDHAALLKPLANTHANIHK
					1110.11	2218.21	2219.23	109.00	1.00E-08	AKGDHAALLKPLANTHANIHK
					1126.98	2251.95	2253.18	117.85	1.30E-09	FSGISQGDLAGSPAVAAHGATV
					1191.84	2381.67	2381.27	91.45	5.30E-07	FSGISQGDLAGSPAVAAHGATV
4	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	62.4	1936	699.39	698.38	698.33	40.99	0.077	HATENK
					977.46	976.45	976.48	41.31	0.09	SNTAAASLDK
					1074.55	1073.54	1073.54	51.70	0.0085	ADIAESQVNK
					1180.76	1179.75	1179.58	64.75	0.00034	DFEISQLNSK
					609.12	1216.22	1215.63	46.69	0.025	AGLLGQLEEMR
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR

					619.21	1236.41	1237.63	57.60	0.0018	EADVLQQNPPK
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					646.42	1290.83	1288.63	52.39	0.0062	DSQLQLDDSLR
					654.83	1307.64	1307.64	84.75	3.40E-06	NSFSQQLEDLK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					1368.62	1367.61	1367.63	55.83	0.0025	LQHELDEAEER
					700.52	1399.02	1397.75	81.11	7.60E-06	NALLQAELEELR
					708.70	1415.39	1414.73	99.59	1.10E-07	LAEQELLDVTER
					719.30	1436.59	1435.77	68.95	0.00012	KKDFEISQLNSK
					733.09	1464.16	1463.68	57.89	0.0016	LSEKDEEMEQVK
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					733.64	1465.26	1463.68	65.89	0.00025	LSEKDEEMEQVK
					738.67	1475.32	1473.68	90.98	8.00E-07	VEELEEELEAER
					749.34	1496.67	1495.73	47.12	0.018	KLQHELDEAEER
					750.83	1499.65	1499.75	102.22	5.70E-08	LQEAEEAVEAVNAK
					752.68	1503.34	1502.76	91.89	6.50E-07	ENQSILITGESGAGK
					770.85	1539.68	1539.77	62.84	0.00049	DYHIFYQILSNK
					1543.82	1542.81	1542.83	88.50	1.40E-06	KLAEQELLDVTER
					772.48	1542.94	1541.83	49.13	0.012	IDDEQSIIIQLQK
					772.63	1543.25	1542.83	87.98	1.60E-06	KLAEQELLDVTER
					773.15	1544.28	1542.83	81.30	7.50E-06	KLAEQELLDVTER
					802.71	1603.40	1602.78	81.83	6.60E-06	SNDDLKENTAIVER
					806.37	1610.72	1610.75	74.36	3.50E-05	AAEESEEQANVHLGK
					810.77	1619.52	1619.78	62.50	0.00055	LSEKDEEMEQVKR
					812.45	1622.88	1620.72	56.59	0.0021	LEDEEEMNAELTAK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					824.64	1647.26	1645.82	101.28	7.60E-08	NLTEEMAALDDIIAK
					843.61	1685.21	1684.83	51.88	0.0063	LELDDVASSMEHIVK
					846.74	1691.46	1688.88	86.26	2.40E-06	GQNVQQVNYAIGALSK
					852.23	1702.45	1701.82	84.74	3.10E-06	LQNEIEDLMVDVER
					859.79	1717.56	1717.85	96.85	2.00E-07	NEDPLNETVVGLYQK
					861.94	1721.86	1721.94	81.68	6.60E-06	VQLLHSQNTSLINQK
					895.79	1789.56	1786.87	89.81	1.00E-06	TIDTLQSALESETHSR
					896.63	1791.24	1790.76	101.34	7.20E-08	QREEQAEADGTEDADK
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					935.63	1869.25	1867.93	118.69	1.20E-09	DLEEATLQHEATAATLR
					980.80	1959.58	1957.98	95.64	2.40E-07	ILQEEISDLTEQLGEGGK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					676.68	2027.00	2024.03	61.34	0.0006	RDLEEATLQHEATAATLR
					696.78	2087.32	2086.04	53.87	0.0034	VKLEQQVDDLEGSLEQEK
5	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	63.4	333	693.68	1385.34	1384.73	88.31	1.50E-06	GASQNIIPASTGAAK
					748.77	1495.53	1494.84	79.92	9.50E-06	VPTPNVSVVDLTVR
					787.60	1573.18	1571.83	60.74	0.00088	LVIDGHAITVYSER
					882.39	1762.77	1762.80	51.00	0.0078	LVTWYDNEFGYSNR
					930.86	1859.70	1860.94	111.65	6.20E-09	SSIFDAGAGIALNDHFVK
					1105.96	2209.91	2210.17	49.58	0.0089	LVIDGHAITVYSERDPANIK
					1116.33	2230.64	2230.08	140.10	7.80E-12	WGDAGATYVVESTGVFTTIEK
					1301.52	2601.03	2599.37	84.74	2.40E-06	VINDNFVIVEGLMSTVHAITATQ
6	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	60.3	551	555.35	1108.68	1108.51	51.81	0.0067	RFNEGTEEK
					600.61	1199.21	1196.64	55.34	0.0032	VVDALGNPIDGK
					645.62	1289.23	1286.69	66.41	0.00025	HALIIYDDLSK
					651.16	1300.30	1299.74	84.49	3.70E-06	TAIAIDTIINQK

					682.43	1362.84	1362.69	79.10	1.20E-05	TGTAEVSSILEEK
					720.33	1438.65	1437.84	41.57	0.067	GIRPAINVGLSVSR
					766.41	1530.80	1530.75	116.75	2.20E-09	ILGADTGAELEETGR
					813.24	1624.46	1623.88	87.21	1.80E-06	TGAIVDVPVGEELLGR
					1030.47	2058.93	2059.13	90.44	7.60E-07	AFLQHVISQHQDLLAAIR
					1052.89	2103.76	2103.03	81.26	6.40E-06	GMSLNLEPDNVGVVVFGNDK
					1156.38	2310.75	2308.15	46.53	0.018	QGQYSPMAIEEQVAVIYAGVR
					1183.60	2365.19	2364.17	65.54	0.00022	EVAAFAQFGSDLDAATQQLLNR
7	gi|18858329	ba1 globin [Danio rerio]	79.1	148	480.00	957.99	957.56	46.94	0.025	TAILGLWGK
					713.68	1425.34	1424.76	95.35	2.80E-07	LNIDEIGPQALSR
					725.33	1448.65	1449.69	87.32	1.90E-06	NTYAALSVMHSEK
					897.94	1793.87	1794.83	116.77	1.90E-09	FGQAGFNADVQEAWQK
					994.87	1987.72	1984.97	87.00	1.70E-06	YFATFGNLSSPAAIMGNPK
8	gi|163644331	ventricular myosin heavy chain [Danio rerio]	44.6	1938	699.39	698.38	698.33	40.99	0.077	HATENK
					1074.55	1073.54	1073.54	51.70	0.0085	ADIAESQVNK
					609.12	1216.22	1215.63	46.69	0.025	AGLLGQLEEMR
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					1368.62	1367.61	1367.63	55.83	0.0025	IQHELDEAEER
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					749.34	1496.67	1495.73	47.12	0.018	KIQHELDEAEER
					752.68	1503.34	1502.76	91.89	6.50E-07	ENQSILITGESGAGK
					812.45	1622.88	1620.72	56.59	0.0021	LEDEEEMNAELTAK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					824.64	1647.26	1645.82	101.28	7.60E-08	NLTEEMAALDDIIAK
					861.94	1721.86	1721.94	81.68	6.60E-06	VQLLHSQNTSLLNQK
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					935.63	1869.25	1867.93	118.69	1.20E-09	DLEEATLQHEATAATLR
					980.80	1959.58	1958.94	88.78	1.10E-06	NLQEEISDLTEQLGEGGK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					676.68	2027.00	2024.03	61.34	0.0006	RDLEEATLQHEATAATLR
					1100.81	2199.61	2199.12	88.83	1.10E-06	GTLEDQIIQANPALEAFGNAK
					1163.71	2325.40	2325.11	68.24	0.00012	KALQEAHQQTLDDLQSEEDK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
					1427.67	2853.33	2853.40	73.52	2.80E-05	ALQEAHQQTLDDLQSEEDKVNT
9	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	79.6	196	966.89	965.88	966.55	56.68	0.0021	HVLATLGEK
					781.14	1560.27	1559.82	71.73	6.70E-05	KEEAPAPAPVPETPK
					851.66	1701.30	1700.76	74.67	3.20E-05	DAFTLFDETPTGEMK
					856.49	1710.96	1710.82	92.16	5.60E-07	AKDQGTFEDFVEGLR
					891.17	1780.32	1777.85	71.23	7.20E-05	SVPLDFSPDQIEEFR
					972.50	1942.98	1944.08	90.30	7.90E-07	ALGHNPTNADVLTVLGKPK
					1186.43	2370.84	2370.23	75.39	2.30E-05	KEEAPAPAPVPETPKEPEVDLK
10	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	74.4	172	638.69	1275.36	1273.67	65.53	0.0003	LFDPNATGVVNK
					690.02	1378.03	1377.66	55.55	0.0027	SLCYIITHGDEK
					809.36	1616.70	1617.83	57.27	0.0018	LNGTDPEETILAAFK
					1795.81	1794.80	1792.84	40.43	0.083	LNVSDEELESMLTEGK
					1046.59	2091.17	2091.96	85.68	2.30E-06	GSSNVFSMFEQSQIQEFK
					1292.61	2583.21	2582.25	108.90	9.00E-09	FTAEEVDQAFAVAPIDVAGNIDY
11	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio re	75.4	517	488.39	974.76	974.55	41.25	0.095	IGLFGGAGVGK
					1406.84	1405.83	1405.67	77.72	1.70E-05	AHGGYSVFAGVGER
					718.59	1435.16	1434.75	102.43	5.70E-08	FTQAGSEVSALLGR

					729.47	1456.93	1456.83	90.05	9.90E-07	TVLIMELINNVAK
					839.67	1677.33	1676.92	83.08	5.00E-06	LVLEVAQHLGENTVR
					994.51	1987.00	1987.03	85.12	2.60E-06	AIAELGIYPAVDPLDSTSR
					1003.03	2004.05	2004.05	112.09	5.20E-09	FLSQPFQVAEVFTGHLGK
					687.82	2060.42	2059.99	42.32	0.049	EGNDLYHEMIESGVINLK
					1329.90	2657.78	2658.38	94.91	2.30E-07	SLQDIIAILGMDELSEEDKLTVAF
					1282.42	3844.24	3841.97	68.79	5.70E-05	KGSITSVQAIYVPADDLTDPAPA
12	gi|18858539	desmin [Danio rerio]	55.2	473	445.53	889.04	887.48	40.63	0.11	SRVEIER
					541.10	1080.18	1079.54	46.55	0.023	ASGSFGGGSVVR
					558.63	1115.25	1114.57	66.66	0.00026	GQVEALTNQR
					591.00	1179.98	1179.55	52.94	0.0052	EAGGYQDTIAR
					1254.61	1253.60	1253.56	42.27	0.058	NISEAEDWYK
					888.78	1775.55	1775.91	99.94	1.00E-07	FLEQQNSALTVEIER
					990.94	1979.86	1978.97	94.70	2.90E-07	LDFNLADAINQDFLNTR
					1094.25	2186.48	2186.00	133.47	3.80E-11	TFGSGLGSSIFAGHGSSGSSGS
13	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple	70.8	517	488.39	974.76	974.55	41.25	0.095	IGLFGGAGVGK
					1406.84	1405.83	1405.67	77.72	1.70E-05	AHGGYSVFAGVGER
					718.59	1435.16	1434.75	102.43	5.70E-08	FTQAGSEVSALLGR
					729.47	1456.93	1456.83	90.05	9.90E-07	TVLIMELINNVAK
					839.67	1677.33	1676.92	83.08	5.00E-06	LVLEVAQHLGENTVR
					994.51	1987.00	1987.03	85.12	2.60E-06	AIAELGIYPAVDPLDSTSR
					1003.03	2004.05	2004.05	112.09	5.20E-09	FLSQPFQVAEVFTGHLGK
					687.82	2060.42	2059.99	42.32	0.049	EGNDLYHEMIESGVINLK
					1282.42	3844.24	3841.97	68.79	5.70E-05	KGSITSVQAIYVPADDLTDPAPA
14	gi|70778800	actin, alpha, cardiac muscle [Danio rerio]	58.9	377	488.23	974.45	975.44	46.37	0.03	AGFAGDDAPR
					896.27	1790.52	1789.88	98.03	1.50E-07	SYELPDGQVITIGNER
					978.36	1954.70	1955.04	95.38	2.50E-07	VAPEEHPTLLTEAPLNPK
					1115.49	2228.97	2227.06	77.92	1.30E-05	DLYANNVLSGGTTMYPGIADR
					1067.01	3197.99	3195.60	47.46	0.01	TTGIVLDSGDGVTHNVPIYEGY
15	gi|62955473	hypothetical protein LOC550445 [Danio rerio]	58.1	377	488.23	974.45	975.44	46.37	0.03	AGFAGDDAPR
					896.27	1790.52	1789.88	98.03	1.50E-07	SYELPDGQVITIGNER
					978.36	1954.70	1955.04	95.38	2.50E-07	VAPEEHPTLLTEAPLNPK
					1115.49	2228.97	2227.06	77.92	1.30E-05	DLYANNVLSGGTTMYPGIADR
					1067.01	3197.99	3195.60	47.46	0.01	TTGIVLDSGDGVTHNVPIYEGY
16	gi|23097290	troponin T2, cardiac [Danio rerio]	38.3	282	509.03	1016.05	1015.47	58.74	0.0017	VDFDDIHR
					1217.73	1216.72	1216.66	46.97	0.023	KEEEEIISLK
					673.42	1344.83	1344.75	59.81	0.0011	KKEEEEIISLK
					957.35	1912.69	1913.95	95.06	2.70E-07	DLNELQTLIEAHFESR
17	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio re	48.5	1937	699.39	698.38	698.33	40.99	0.077	HATENK
					1074.55	1073.54	1073.54	51.70	0.0085	ADIAESQVNK
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					752.68	1503.34	1502.76	91.89	6.50E-07	ENQSILITGESGAGK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					928.91	1855.81	1853.91	74.52	3.10E-05	DLEESTLQHEATAAALR
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
18	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	46.9	28836	701.17	1400.33	1399.71	64.53	0.00036	HVSVEALDFIDR
					738.17	1474.33	1473.71	56.64	0.0022	RLDETDEAQLER

					772.58	1543.15	1541.72	71.52	7.10E-05	NDGGAPVTHYNIER
					787.22	1572.42	1572.78	45.27	0.031	FGQSGPSEPSGPVVTK
					807.77	1613.53	1612.87	43.79	0.04	ALDPVFKPGPPHNPK
					856.64	1711.26	1709.82	63.47	0.00041	ADSGNYTITIQNAAGSK
					894.75	1787.49	1787.83	55.94	0.0025	GENKVDVEYDEHINK
					920.70	1839.38	1838.93	41.66	0.061	STVSLAWEKPLHDGGSR
					923.92	1845.82	1845.01	55.76	0.0024	VQILDKPGPPAGHIEFK
					928.62	1855.22	1854.92	96.97	1.80E-07	TSVSLSWEKPIHDGGSR
					932.27	1862.52	1860.85	50.26	0.0085	NAQPDDVAEYAVEVEGR
					935.34	1868.66	1867.88	48.75	0.012	TSADLQWTRPEHDGGAK
					950.65	1899.28	1898.91	73.18	4.20E-05	TTVTLSWEKPEHDGGSR
					971.98	1941.94	1941.02	49.42	0.0096	IGESFEIDVPISGRPTPK
					1002.92	2003.83	2002.96	91.81	5.50E-07	KDNTSDDIGWVTVTSTHK
					1033.83	2065.64	2064.06	76.98	1.70E-05	VISGVQDLEYTVTDVIEGK
					1047.30	2092.59	2092.08	59.72	0.0009	INVSALNSEGVGEAAPVPGSPK
					1073.16	2144.30	2142.23	64.16	0.00032	SFHVQVITLGPPSKPIGPIR
					742.60	2224.76	2222.18	45.25	0.025	VTAENEIGTGDPSVPSKPILAK
					757.52	2269.52	2270.33	62.36	0.00047	KSFHVQVITLGPPSKPIGPIR
					1258.45	2514.89	2514.23	109.45	8.10E-09	HTLPVDSDISSSDTTSVVTIPES
					1326.96	2651.91	2651.51	61.01	0.00054	KKPTLPATILTKPQSLTVSEGES
					966.81	2897.40	2895.47	44.42	0.022	RLDIIDTTDTSVTLAWLKPEHDG
19	gi|66472732	myosin heavy chain 4 [Danio rerio]	47.7	1935	699.39	698.38	698.33	40.99	0.077	HATENK
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					928.91	1855.81	1853.91	74.52	3.10E-05	DLEESTLQHEATAAALR
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					696.78	2087.32	2088.02	50.20	0.008	TKLEQQVDDLEGSLEQEK
					1107.82	2213.62	2213.03	72.78	4.30E-05	AEIQTALEEAEGTLEHEESK
					1107.97	2213.93	2216.12	46.28	0.019	TKLEQQVDDLEGSLEQEKK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
20	gi|189519129	PREDICTED: similar to myosin heavy chain 4 [Danio reri	46.8	1933	699.39	698.38	698.33	40.99	0.077	HATENK
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					928.91	1855.81	1853.91	74.52	3.10E-05	DLEESTLQHEATAAALR
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					696.78	2087.32	2088.02	50.20	0.008	TKLEQQVDDLEGSLEQEK
					1107.82	2213.62	2213.03	72.78	4.30E-05	AEIQTALEEAEGTLEHEESK
					1107.97	2213.93	2216.12	46.28	0.019	TKLEQQVDDLEGSLEQEKK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
21	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	63.9	377	488.23	974.45	975.44	46.37	0.03	AGFAGDDAPR
					896.27	1790.52	1789.88	98.03	1.50E-07	SYELPDGQVITIGNER
					977.46	1952.91	1953.06	79.89	8.60E-06	VAPEEHPVLLTEAPLNPK

22	gi|83025080	actinin, alpha 2 [Danio rerio]	48.9	895	717.70	1433.39	1432.71	40.30	0.094	ISNRPAFMPSEGK
					761.94	1521.86	1520.71	64.59	0.00033	AGTQIENIEEDFR
					821.59	1641.17	1640.72	81.70	6.40E-06	HEAFESDLSAHQDR
					826.70	1651.38	1648.81	54.98	0.0031	KAGTQIENIEEDFR
					842.04	1682.07	1680.90	75.94	2.40E-05	LLETVDQLFLEYAK
					885.69	1769.37	1768.81	68.26	0.00014	KHEAFESDLSAHQDR
					933.07	1864.13	1861.89	64.74	0.0003	MVSDIASAWQGLEQAEK
					968.96	1935.91	1934.98	100.27	8.10E-08	GDLTNPYSTITAEEIAIK
					1050.84	2099.67	2099.09	87.13	1.60E-06	LNKDDPLGNLNLAFDIAEK
23	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	86.3	153	1099.44	1098.43	1098.53	56.37	0.0026	NLIHGSDSEK
					554.51	1107.00	1106.56	66.61	0.00023	FVQASEDLAK
					974.87	1947.73	1949.07	126.73	1.80E-10	GFRLVAAKFVQASEDLAK
					1106.09	2210.17	2211.12	91.07	6.30E-07	SAATEVSLWFKPEELVSYR
24	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	73.9	284	518.13	1034.24	1032.50	53.91	0.0047	ASDLEEELK
					585.81	1169.61	1169.67	62.93	0.00053	LVILEGELER
					1182.60	1181.59	1181.55	44.09	0.039	EDKYEEEIK
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
					629.66	1257.30	1256.66	60.54	0.00095	QLDDELVGLQK
					638.22	1274.42	1271.61	70.63	9.40E-05	AADAEGDVAALNR
					1298.67	1297.66	1297.76	56.35	0.0022	KLVILEGELER
					701.18	1400.34	1399.71	101.39	7.40E-08	KAADAEGDVAALNR
					770.64	1539.26	1537.71	73.76	4.00E-05	SIDDLEDELYAQK
					701.18	2100.51	2099.09	73.57	3.70E-05	LELSEKKAADAEGDVAALNR
					746.96	2237.85	2239.05	53.72	0.0034	QTEDELDKYSEALKDAQEK
25	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	49.2	1936	699.39	698.38	698.33	40.99	0.077	HATENK
					1074.55	1073.54	1073.54	51.70	0.0085	ADIAESQVNK
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLELTLAK
					662.12	1322.23	1320.66	65.34	0.00029	KLEDECSELKK
					733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
					816.69	1631.36	1631.78	82.84	5.40E-06	LEEAGGATAAQIEMNK
					928.91	1855.81	1853.91	74.52	3.10E-05	DLEESTLQHEATAAALR
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
26	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	51.8	782	1362.60	1361.59	1361.61	48.23	0.015	FEPSSYINYDK
					848.96	1695.90	1694.78	47.33	0.018	FNPETDYLTAPNGEK
					857.36	1712.71	1711.84	91.07	7.30E-07	EVNQEVYSFLASAGAK
					878.73	1755.45	1752.88	51.30	0.0069	IVYGHLDDPAGQEIAR
					890.73	1779.44	1777.89	40.99	0.078	QGLLPLTFSNPADYDK
					1042.22	2082.42	2080.94	98.48	1.20E-07	NNISWVVVGDENYGEGSSR
					1267.59	2533.16	2532.29	83.06	3.50E-06	GHLDNISNNLLIGAVNIENDGVN
					1362.50	2722.98	2721.43	68.33	9.60E-05	NDANPATHAFVTSPEIVTALAIA
27	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	79.5	337	538.47	1074.93	1072.58	56.67	0.0026	IQEAGTEVVK
					661.99	1321.96	1319.67	84.23	3.70E-06	GYIGADQLGDALK
					752.74	1503.47	1502.77	94.91	3.30E-07	VEFPADQLSALTGR
					1030.54	3088.58	3088.58	95.29	1.80E-07	NSPLVSELSLFDIAHTPGVAADL
28	gi|189523699	PREDICTED: titin a [Danio rerio]	46.8	32757	567.69	1133.36	1133.57	50.68	0.0096	KGDVTLSDSGR
					636.39	1270.77	1268.52	54.53	0.0038	NYDEEVDETR
					652.84	1303.66	1303.63	57.03	0.0021	AVNEAGEIETSGK
					666.15	1330.28	1328.66	54.57	0.0037	SLVEDSQLPEGR

					718.53	1435.05	1434.70	50.80	0.0082	YGVGPPLYSEPEK
					907.47	1812.93	1811.95	39.91	0.092	IGVGETADIPGSVIIEDK
					915.70	1829.39	1828.83	47.26	0.017	TTASLSWDKPDHDGGSR
					940.81	1879.60	1878.92	73.48	3.90E-05	TPLHDGGAEVSHYIVER
					945.92	1889.83	1889.94	46.07	0.022	NAAGLFSEPSESTGPVTVK
					947.53	1893.04	1892.90	100.70	7.30E-08	HTVTLSWEKPDHDGGSK
					975.71	1949.41	1948.02	49.13	0.01	VLDVPGPPGPIEASSVSAEK
					1015.41	2028.81	2029.15	70.81	6.80E-05	KVPAKPVEAITVPTEEPPK
					1079.59	2157.17	2157.24	74.29	3.10E-05	KVPAKPVEAITVPTEEPPKK
					1099.34	2196.66	2196.14	46.05	0.021	VLDRPGPPDGPISIYGVTSEK
					734.33	2199.95	2199.29	72.00	5.30E-05	KEPKPESILQVISTPVPLPK
					1133.89	2265.77	2265.23	56.10	0.002	KEQHKPVVLSVNETTQTLSK
					1682.35	5044.02	5042.61	45.61	0.0064	HQLQADQSSLIPGLDSAISVQPL
29	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	70.4	433	572.55	1143.09	1142.61	54.32	0.0042	IGAEVYHNLK
					687.75	1373.49	1372.70	48.62	0.014	HITGEQLGDLYK
					718.78	1435.54	1435.72	83.08	4.90E-06	GNPTVEVDLYTTK
					1053.85	2105.69	2104.07	109.40	9.80E-09	FTGSVDIQVVGDDLTVTNPK
					1060.42	2118.82	2118.12	86.64	1.80E-06	DVILPVPAFNVINGGSHAGNK
30	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	63.9	119	530.06	1058.11	1056.56	89.53	1.40E-06	VAENVQELR
					701.10	1400.18	1399.67	54.77	0.0034	TMLEPYVQEYK
					1050.46	2098.90	2100.09	80.87	7.00E-06	ELTELGEQVKPHFEGIFK
					744.06	2229.14	2228.18	67.52	0.00014	KELTELGEQVKPHFEGIFK
31	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	70.1	334	603.57	1205.13	1204.61	51.19	0.0083	SSADTLWGIQK
					627.64	1253.27	1252.64	69.43	0.00011	MVVDSAYEVIK
					709.79	1417.56	1417.79	62.74	0.00055	LITPLASGPAEPPR
					769.81	1537.61	1537.77	83.72	4.00E-06	IVADKDYSVTANSR
					843.79	1685.56	1684.85	107.47	1.80E-08	ELADELALVDVVEDR
					858.16	1714.30	1714.82	48.64	0.013	LNPDIGTDKDAENWK
32	gi|18858335	bactin1 [Danio rerio]	51.7	375	488.23	974.45	975.44	46.37	0.03	AGFAGDDAPR
					896.27	1790.52	1789.88	98.03	1.50E-07	SYELPDGQVITIGNER
33	gi|117606264	sarcalumenin [Danio rerio]	41.7	482	957.14	1912.26	1912.97	52.75	0.0046	EEISLLEDLNQVIENR
					1036.33	2070.65	2069.08	98.98	1.10E-07	REEISLLEDLNQVIENR
34	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	67.1	143	768.07	1534.13	1532.73	97.00	1.90E-07	IASQADSIGQEAMGR
					934.49	1866.97	1867.99	114.49	3.20E-09	IDDLLGALSSLSDLHATK
35	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	43.1	1945	699.39	698.38	698.33	40.99	0.077	HATENK
					1074.55	1073.54	1073.54	51.70	0.0085	ADIAESQVNK
					609.12	1216.22	1215.63	46.69	0.025	AGLLGQLEEMR
					624.15	1246.28	1244.65	73.73	4.80E-05	DIDDLEITLAK
					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
					1107.82	2213.62	2213.03	72.49	4.60E-05	TEIQAALEEAEGTLEHEESK
36	gi|162287365	hemopexin [Danio rerio]	39.6	447	569.58	1137.14	1136.57	39.76	0.11	GQSIYDVDLK
					1211.60	1210.59	1210.61	42.67	0.054	GHHFLSITGDK
					1339.63	1338.62	1338.61	67.37	0.00018	FHSDTIESEFK
					900.94	1799.87	1800.00	65.94	0.00024	VGKPHTHLEGYPKPLK
					721.15	2160.41	2159.07	59.48	0.00093	GKPGGEGHKHELHHGAQLDR
37	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Danic	52.2	659	575.21	1148.40	1147.55	48.86	0.015	SFGGVSSGPPEK
					638.66	1275.30	1275.65	46.36	0.025	SFGGVSSGPPEKK
					837.23	1672.45	1671.94	109.89	9.80E-09	AIEQFGAVIEELLLK
38	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	40.4	1938	699.39	698.38	698.33	40.99	0.077	HATENK
					614.04	1226.07	1223.61	44.28	0.039	TKYETDAIQR
					624.15	1246.28	1244.65	73.73	4.80E-05	DLDDLEITLAK

					930.22	1858.43	1858.88	83.59	3.90E-06	LEQQVDDLEGSLEQEK
					994.76	1987.50	1986.97	80.63	7.40E-06	LEQQVDDLEGSLEQEKK
39	gi|18858587	elongation factor 1-alpha [Danio rerio]	55.4	462	513.65	1025.28	1024.60	76.05	2.60E-05	IGGIGTVPVGR
					530.56	1588.66	1587.87	53.86	0.0041	THINIVVIGHVDSGK
					1250.51	2499.01	2497.15	74.77	2.30E-05	SVEMHHESLTEATPGDNVGFN
					973.28	2916.80	2917.55	73.61	2.70E-05	EGNASGTTLLDALDAILPPSRPT
40	gi|148596963	spectrin alpha 2 [Danio rerio]	36.6	2480	624.43	1246.84	1246.55	52.54	0.0064	GEIDAHEDSFK
					787.63	1573.25	1571.78	60.14	0.001	HQALQAEISGHEPR
					851.20	1700.38	1699.88	108.80	1.20E-08	KHQALQAEISGHEPR
					861.63	1721.25	1720.86	47.63	0.017	LIQSHPEAVDDIQEK
					869.56	1737.10	1736.82	45.62	0.026	TATDEAYKDPSNLQGK
					935.51	1869.01	1867.94	45.64	0.024	HQAFEAEVQANAEAIIK
					1010.83	2019.65	2018.99	84.45	3.10E-06	LQIASDENYKDPSNLQGK
					1109.12	2216.23	2215.12	46.89	0.017	RDELITNWEQIQTLATER
					1245.85	2489.69	2489.22	70.75	6.00E-05	EKEPIVGSPDYGKDEDSAEALL
41	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	60.4	283	1052.41	2102.81	2102.15	74.40	3.10E-05	VNNTSLVGVGYTQSLRPGIK
					1087.84	2173.67	2174.05	116.05	2.00E-09	WNTDNTLGTEINIEDQIAK
42	gi|41054435	hypothetical protein LOC324244 [Danio rerio]	42.7	248	585.81	1169.61	1169.67	62.93	0.00053	LVILEGELER
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
					638.22	1274.42	1271.65	70.93	8.80E-05	EKAEGDVAALNR
					1298.67	1297.66	1297.76	56.35	0.0022	KLVILEGELER
43	gi|48762657	enolase 1, (alpha) [Danio rerio]	50.7	432	572.55	1143.09	1142.61	54.32	0.0042	IGAEVYHNLK
					1002.86	3005.54	3006.57	91.47	4.40E-07	HIADLAGNPDVILPVPAFNVING
44	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	45.4	757	673.45	1344.88	1344.66	47.10	0.021	STQALNEALNER
					978.50	1954.98	1955.09	105.92	2.20E-08	KPETVKPLQISSLSEATK
					1066.66	2131.30	2130.11	113.88	3.50E-09	AELDALAALTAGLEETLGSSAK
45	gi|18858281	apolipoprotein A-I [Danio rerio]	48.5	262	585.48	1168.94	1166.55	54.76	0.0035	AFESNIEETK
					823.18	1644.35	1643.73	85.28	2.90E-06	ALDNLDGTDYEQYK
					912.77	1823.53	1821.93	50.61	0.0077	EKLEPVFQEYSALNR
46	gi|18858427	creatine kinase, muscle a [Danio rerio]	41.2	381	753.75	1505.48	1506.70	58.71	0.0013	GGDDLDPNYVLSSR
					836.64	1671.27	1670.77	106.29	2.20E-08	LNYSVDEEYPDLSK
					997.90	1993.79	1993.93	89.39	9.70E-07	GTGGVDTASVGGVFDISNADR
47	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	50.7	284	585.81	1169.61	1169.67	62.93	0.00053	LVILEGELER
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
					1298.67	1297.66	1297.76	56.35	0.0022	KLVILEGELER
48	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	47.4	449	1175.64	1174.63	1174.60	43.69	0.051	ATDFVVNQPGK
					679.50	1356.98	1354.68	79.06	1.30E-05	TIEAEAAHGTVTR
					716.09	1430.17	1428.73	77.41	1.80E-05	FKDIFQDIFEK
49	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	62	305	576.11	1150.21	1149.58	50.48	0.0096	GDFISTVQQR
					662.69	1323.36	1320.67	44.96	0.031	VVDGLSINDFSR
					855.66	1709.31	1706.82	87.43	1.70E-06	EIAAFDAVNDESWLK
					1316.66	2631.30	2631.29	93.78	2.90E-07	NVTIWGNHSSTQYPDVHHAIVT
50	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	62.6	575	985.23	1968.44	1967.90	120.13	8.30E-10	VNEIAEQLESTNSDYEK
					813.97	2438.88	2439.35	87.01	1.50E-06	TALLDAAGVASLLSTAEAVVTEI
					942.93	2825.75	2825.53	52.54	0.0036	TALLDAAGVASLLSTAEAVVTEI
51	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	41.2	364	660.49	1318.96	1317.68	70.58	9.10E-05	GILAADESTGSVAK
					776.69	1551.36	1550.70	66.10	0.00024	FQSINAENTEENR
					1175.44	2348.86	2347.17	81.77	5.00E-06	GVVPLAGTNGETTTQGLDGLYE
52	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	61.3	364	660.49	1318.96	1317.68	70.58	9.10E-05	GILAADESTGSVAK
					776.69	1551.36	1550.70	66.10	0.00024	FQSINAENTEENR
					1175.44	2348.86	2347.17	81.77	5.00E-06	GVVPLAGTNGETTTQGLDGLYE
53	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	44.8	1974	807.63	1613.25	1612.69	67.76	0.00016	DLEEHLEEEEDAR

					865.31	1728.60	1725.94	53.58	0.0041	QLLQANPILEAFGNAK
					956.63	1911.25	1910.93	69.96	8.70E-05	HEVPPHIYSITDNAYR
					1000.06	1998.11	1997.92	89.03	1.10E-06	ELEGHISDLQEDLESER
					1066.71	2131.40	2131.00	69.02	0.00011	QVEAERDELADELASNASGK
54	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	35.1	1079	1270.65	1269.64	1269.68	49.70	0.011	SLGAEPLEVDIK
					922.45	2764.32	2763.39	83.48	3.00E-06	DGSVVVDLAAEAGGNIETTVPG
55	gi|50539808	hypothetical protein LOC436647 [Danio rerio]	57	525	709.08	1416.14	1415.73	72.48	5.90E-05	VNSLIQSGVDEGAK
					967.79	1933.56	1932.99	56.50	0.0019	VNAGDQPGADVGPLISPQAK
					1006.23	2010.44	2009.00	95.36	2.40E-07	SSQWLDIHNPATSEVIGR
56	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	85.2	283	675.75	1349.49	1347.70	62.29	0.00058	LGLDTSFVPNTGK
					930.64	1859.26	1858.82	76.85	1.90E-05	SQSGVEFTTGGSSNTDTGK
					1031.44	2060.86	2058.12	66.10	0.0002	VNNASLVGVGYTQSLRPGVK
					1096.63	2191.25	2189.09	81.74	5.50E-06	WNTDNVLTTEVTLEDQLAK
57	gi|56118753	troponin C, slow [Danio rerio]	50.9	161	602.33	1202.64	1202.58	59.08	0.0014	AAAEQLTDEQK
					684.05	1366.08	1364.65	70.76	8.10E-05	NADGYIDLDELK
					723.66	1445.31	1444.73	60.51	0.00093	GRPEEELAELFR
58	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio reri	61.5	410	1113.63	1112.62	1112.61	44.28	0.042	IALGEDSPAIK
					846.06	1690.11	1687.84	80.71	8.60E-06	NIDYVAESIHEAVTK
					1114.87	2227.73	2226.03	124.06	3.30E-10	NLFAFFDSAYQGFASGDLEK
59	gi|136429	Trypsin precursor	87.1	232	1105.98	2209.94	2210.10	125.54	2.30E-10	LGEHNIDVLEGNEQFINAAK
60	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	51.6	996	732.86	1463.71	1463.67	54.55	0.0034	IRDEMASTEQER
					1525.87	1524.86	1524.80	73.09	4.60E-05	DIVPGDIVEVAVGDK
					788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVIK
61	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	47.7	1035	732.86	1463.71	1463.67	54.55	0.0034	IRDEMASTEQER
					1525.87	1524.86	1524.80	73.09	4.60E-05	DIVPGDIVEVAVGDK
					788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVIK
62	gi|18858399	cadherin 2, neuronal [Danio rerio]	27.3	783	843.88	1685.75	1683.81	61.16	0.00075	VIDVNESPNFDPNPK
					1148.47	3442.39	3440.82	98.83	6.30E-08	YSVTGPGADQNPTGLFIIDPISG
63	gi|54606886	hexokinase 1 [Danio rerio]	50.3	918	749.15	1496.28	1494.68	69.18	0.00011	YDDAVDDLSLNAGK
					863.58	1725.15	1723.83	106.79	2.00E-08	TKYDDAVDDLSLNAGK
64	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dani	57.3	731	805.44	1608.86	1607.78	102.93	4.80E-08	FASEVAGVEDLGTTGR
					1570.97	3139.92	3139.56	100.34	5.30E-08	DSFIVYQGHHGDVGAPIADVILP
65	gi|40254659	bactin2 [Danio rerio]	52	375	488.23	974.45	975.44	46.37	0.03	AGFAGDDAPR
					977.46	1952.91	1953.06	79.89	8.60E-06	VAPEEHPVLLTEAPLNPK
66	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	60.2	603	1059.42	2116.82	2115.97	81.90	5.40E-06	GKEYDDLIDEFMQAVTDK
					1004.66	3010.94	3013.43	129.45	6.80E-11	HISDDIFLTTAEAISEMVTEEHLA
67	gi|38488731	natriuretic peptide precursor A [Danio rerio]	74.5	106	1046.85	2091.68	2091.86	77.93	1.40E-05	EEAAAPGEDSNPSDGFDTQR
					1182.86	2363.71	2362.99	77.03	1.50E-05	DREEAAAPGEDSNPSDGFDTQ
68	gi|27545193	creatine kinase, brain [Danio rerio]	40.4	381	753.75	1505.48	1506.70	58.71	0.0013	GGDDLDPNYVLSSR
					989.80	1977.58	1977.94	102.38	5.00E-08	GTGGVDTAAVGGVFDISNADR
69	gi|68383957	PREDICTED: apolipoprotein C-II isoform 1 [Danio rerio]	41	100	1013.75	2025.48	2024.92	111.62	5.70E-09	SYYDQSVDTASGYVETIK
70	gi|116004537	hypothetical protein LOC564694 [Danio rerio]	43.6	381	753.75	1505.48	1506.70	58.71	0.0013	GGDDLDPNYVLSSR
					989.80	1977.58	1977.94	102.38	5.00E-08	GTGGVDTAAVGGVFDISNADR
71	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprotei	61	661	1474.72	1473.71	1473.75	73.86	4.20E-05	KHTLSYVDPETGK
					1055.70	2109.39	2109.13	43.11	0.041	DHVHLQLHHLPPQQLAAR
					1291.54	2581.07	2582.14	56.25	0.0017	DGQDHVVPGLYACGEAGCASV
					888.17	2661.47	2662.42	60.65	0.00059	GVGPDKDHVHLQLHHLPPQQL
72	gi|40538764	ceruloplasmin [Danio rerio]	32.1	1087	805.83	1609.65	1609.72	87.83	1.60E-06	SVNKEDADFQESNK
					827.90	1653.79	1654.78	103.86	3.80E-08	LVDDIVSDTFFDNR
73	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	52.3	532	819.19	1636.36	1635.88	66.50	0.00021	GVNLPGAAVDLPAVSEK
					884.20	1766.38	1763.98	94.81	3.00E-07	KGVNLPGAAVDLPAVSEK
74	gi|32308153	annexin A2a [Danio rerio]	44.8	337	606.76	1211.50	1211.57	72.36	6.00E-05	STAQYDASEIK

					634.06	1266.11	1263.66	55.02	0.0032	SLHQTIAEHTK
					722.94	1443.86	1443.78	88.15	1.60E-06	GVDEQTIIDILTK
75	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	56.9	283	1319.68	1318.67	1317.64	51.79	0.007	WAEHGLTFTEK
					1045.46	2088.90	2088.16	88.25	1.30E-06	VNNSSLVGLGYTQTLKPGIK
					1097.43	2192.85	2191.06	103.87	3.30E-08	WNTDNTLGTEITLEDQLTK
76	gi|18858959	lactate dehydrogenase A4 [Danio rerio]	54.1	333	480.22	958.43	956.61	50.92	0.01	FIIPNIIK
					595.62	1189.23	1188.61	71.56	8.00E-05	VIGSGTNLDSAR
					627.64	1253.27	1252.64	69.43	0.00011	MVVDSAYEVIK
					756.27	1510.52	1509.77	63.97	0.00038	IVADKDYSVTANSK
77	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	49.4	164	686.47	1370.93	1370.73	98.39	1.50E-07	VVDGLDVVDAIEK
78	gi|125805081	PREDICTED: similar to LOC495046 protein [Danio rerio]	42.7	1050	1525.87	1524.86	1524.80	73.09	4.60E-05	DIVPGDIVEVAVGDK
					788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVLK
					920.62	1839.22	1837.88	39.20	0.11	SLPSVETLGCTSVICSDK
79	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	41.5	1056	1525.87	1524.86	1524.80	73.09	4.60E-05	DIVPGDIVEVAVGDK
					788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVLK
					920.62	1839.22	1837.88	39.20	0.11	SLPSVETLGCTSVICSDK
80	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (as	61.4	428	555.66	1109.31	1107.59	56.05	0.0025	KMNLGVGAYR
					644.57	1287.13	1284.69	49.72	0.012	GALDDISKIPEK
					947.18	1892.34	1893.02	103.02	4.30E-08	KLDKEYLPIGGLADFSK
					665.76	1994.24	1994.03	43.33	0.04	YFIEQGHNILLSQSFAK
					784.30	2349.87	2350.26	70.31	7.10E-05	ISVAGVTSANVEYLAHAIHAVTK
81	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	52.4	397	595.17	1188.32	1187.68	66.98	0.00024	ITAHLVHELR
					932.38	1862.75	1861.98	91.68	6.10E-07	TNVNGGAIAIGHPLGASGTR
82	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	44.6	242	1155.55	1154.54	1154.55	53.71	0.0044	YLSEVASGDSK
					648.46	1294.90	1293.66	56.75	0.0021	YLIANASQAESK
					1073.03	2144.04	2143.98	120.68	7.10E-10	TAFDEAIAELDTLNEDSYK
83	gi|189522028	PREDICTED: similar to myomesin [Danio rerio]	59.6	923	755.82	1509.62	1507.73	68.34	0.00014	FKGEFDESLPSPR
					1258.77	3773.27	3772.95	53.64	0.0019	GASAPWTGQIIVTEEEPVEGVV
					1301.49	3901.45	3901.05	67.56	7.10E-05	KGASAPWTGQIIVTEEEPVEGV
84	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	26.5	230	1068.52	2135.02	2133.18	60.00	0.00083	ILVSAEDVLHSWAVPSLGIK
85	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	45.9	244	1155.55	1154.54	1154.55	53.71	0.0044	YLSEVASGDSK
					1073.03	2144.04	2143.98	120.68	7.10E-10	TAFDEAIAELDTLNEDSYK
86	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	75.2	226	723.80	1445.58	1445.78	65.41	0.0003	VIFEAETEKPGVK
					881.39	2641.15	2641.29	64.07	0.00027	SPDPAAVEHKPEESKPEESKPE
					1221.79	3662.33	3660.68	76.94	9.30E-06	EPPPAPTENSAPESTGPPSDGV
87	gi|189517523	PREDICTED: hypothetical protein [Danio rerio]	83.7	147	714.14	1426.27	1424.76	97.25	1.80E-07	INVDEIGPQTLAR
88	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio reri	50.1	413	1040.92	2079.82	2079.97	104.18	3.20E-08	GTGGVDTAAVGDTFDISNLDR
					1119.27	2236.53	2236.07	41.96	0.051	RGTGGVDTAAVGDTFDISNLDR
89	gi|41054193	hypothetical protein LOC327506 [Danio rerio]	62.9	178	1040.92	2079.82	2079.97	104.18	3.20E-08	GTGGVDTAAVGDTFDISNLDR
					1119.27	2236.53	2236.07	41.96	0.051	RGTGGVDTAAVGDTFDISNLDR
90	gi|47085887	MARCKS-like 1 [Danio rerio]	55.9	213	939.32	1876.63	1874.84	89.22	1.10E-06	TEEGDGIEAAPATEAEASK
					980.98	1959.94	1959.89	70.18	8.20E-05	AEEPAQQTETAPTEETTK
91	gi|41393141	tropomyosin 3 [Danio rerio]	63.3	248	1182.60	1181.59	1181.55	44.09	0.039	EDKYEEEIK
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
					708.62	1415.23	1414.67	59.89	0.0011	VLQQQADEAEER
92	gi|189535578	PREDICTED: fetuin B [Danio rerio]	42.8	498	456.37	910.72	910.50	56.67	0.002	ASASLHLGR
					1117.00	2231.98	2233.01	86.29	1.90E-06	KDETHEHDHEIVLDHDHK
					797.00	2387.96	2389.01	42.38	0.043	AHEHGQDEWEHQHHQYGHK
93	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	79.8	104	745.23	1488.45	1487.65	58.76	0.0014	TGQAEGFSYTDANK
					809.10	1616.18	1615.75	91.49	7.00E-07	KTGQAEGFSYTDANK
					1061.98	2121.94	2121.05	45.63	0.022	GIVWGEDTLMEYLENPKK
94	gi|157787181	creatine kinase CKM3 [Danio rerio]	43.9	380	753.75	1505.48	1506.70	58.71	0.0013	GGDDLDPNYVLSSR

					997.90	1993.79	1993.93	89.39	9.70E-07	GTGGVDTASVGGVFDISNADR
95	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	79.4	141	488.03	974.05	972.52	54.91	0.0041	LDDLASAIR
					1659.06	3316.11	3313.73	60.17	0.00051	EIYPYVIQELRPTLDELGIATPEE
					1694.32	3386.62	3384.77	59.50	0.00056	EIYPYVIQELRPTLDELGIATPEE
96	gi|119943123	apolipoprotein A-IV [Danio rerio]	38	255	903.11	1804.21	1802.94	108.11	1.50E-08	AQIVQQSLTPYAEDLK
97	gi|68448530	vitellogenin 5 [Danio rerio]	45.1	1360	588.13	1174.25	1172.62	53.92	0.0048	LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.056	THYVINEDPK
					706.51	1411.00	1410.81	47.98	0.015	IKDAPAQTVEVLK
					759.43	1516.84	1514.74	75.85	2.70E-05	VFGQEVAYVNFDK
98	gi|189530625	PREDICTED: similar to spectrin repeat containing, nucle	38.9	8621	551.01	1100.01	1097.66	70.18	0.00012	QLADAIAKLR
99	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [	64.2	709	826.20	1650.38	1649.84	74.99	3.10E-05	TVAVHSDVDSSAVHVK
100	gi|115495857	hypothetical protein LOC767650 [Danio rerio]	75.7	103	567.82	1133.63	1133.54	49.53	0.012	DAVTYTEHAK
					591.66	1181.30	1179.61	66.87	0.00021	ISGLIYEETR
					657.35	1312.68	1309.70	53.96	0.004	TVTAMDVVYALK
					664.19	1326.36	1324.75	49.37	0.011	DNIQGITKPAIR
101	gi|68362804	PREDICTED: similar to Histone H4 replacement CG337	75.7	103	567.82	1133.63	1133.54	49.53	0.012	DAVTYTEHAK
					591.66	1181.30	1179.61	66.87	0.00021	ISGLIYEETR
					657.35	1312.68	1309.70	53.96	0.004	TVTAMDVVYALK
					664.19	1326.36	1324.75	49.37	0.011	DNIQGITKPAIR
102	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	49.2	1358	588.13	1174.25	1172.62	53.92	0.0048	LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.056	THYVINEDPK
					759.43	1516.84	1514.74	75.85	2.70E-05	VFGQEVAYVNFDK
103	gi|156713467	vitellogenin 7 [Danio rerio]	44.8	1358	588.13	1174.25	1172.62	53.92	0.0048	LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.056	THYVINEDPK
					759.43	1516.84	1514.74	75.85	2.70E-05	VFGQEVAYVNFDK
104	gi|166795887	vitellogenin 1 [Danio rerio]	42.6	1362	588.13	1174.25	1172.62	53.92	0.0048	LEFEVQVGPR
					1215.56	1214.55	1214.59	42.98	0.056	THYVINEDPK
					759.43	1516.84	1514.74	75.85	2.70E-05	VFGQEVAYVNFDK
105	gi|47086009	ribosomal protein L19 [Danio rerio]	49	196	972.16	1942.31	1941.92	89.34	9.90E-07	VWLDPNETNEIANANSR
106	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	73.9	284	1182.60	1181.59	1181.55	44.09	0.039	EDKYEEEIK
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
107	gi|18859505	alpha-tropomyosin [Danio rerio]	56.7	284	1182.60	1181.59	1181.55	44.09	0.039	EDKYEEEIK
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
108	gi|49274617	tropomyosin 1 alpha [Danio rerio]	36.3	284	1182.60	1181.59	1181.55	44.09	0.039	EDKYEEEIK
					622.64	1243.26	1242.65	73.35	5.20E-05	IQLVEEELDR
109	gi|70778734	ATPase, Na+/K+ transporting, alpha 3b polypeptide [Dan	50.9	1023	717.77	1433.53	1433.75	73.01	5.00E-05	FQTDIVQGLTNAK
					907.46	1812.91	1810.94	70.66	7.70E-05	QGAIVAVTGDGVNDSPALK
					924.90	1847.78	1846.81	66.68	0.00019	YQLSIHETEDNNDNR
110	gi|54400460	fibulin 5 [Danio rerio]	46.3	477	1111.45	2220.88	2220.00	92.28	4.80E-07	NSPLPYPEASYPEEPYPDR
111	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	35.6	3730	816.24	1630.47	1628.74	82.22	6.10E-06	FTSNNEANVGSFNTK
					967.39	1932.77	1931.96	72.74	4.60E-05	TLHLDDSIDSVHPIQDK
					1036.96	3107.84	3105.49	44.71	0.02	YDAEEIEAEVSSDVTTEIHNIITT
112	gi|47086523	ictacalcin [Danio rerio]	82.1	95	696.63	1391.25	1390.73	79.96	1.10E-05	ELLSAELGDIFGK
113	gi|41055614	hypothetical protein LOC393478 [Danio rerio]	15.1	86	733.60	1465.19	1464.65	43.84	0.039	WDSQIEDGSFPGK
					734.13	1466.25	1464.65	86.49	2.10E-06	WDSQIEDGSFPGK
114	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio reri	46.6	133	749.60	1497.18	1496.63	63.80	0.00039	LGEEFDETTADDR
					1081.31	2160.60	2160.13	61.63	0.00057	EVSDNNLTLTLTLGDIVSTR
115	gi|55741944	wu:cegs655 [Danio rerio]	47.9	994	788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVIK
					920.62	1839.22	1837.88	39.20	0.11	SLPSVETLGCTSVICSDK
116	gi|117606266	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	43.2	991	788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVIK
					920.62	1839.22	1837.88	39.20	0.11	SLPSVETLGCTSVICSDK
117	gi|189519111	PREDICTED: similar to ATPase, Ca++ transporting, fast	49.7	1005	788.66	1575.30	1573.86	86.17	2.50E-06	VDQSILTGESVSVIK

118	gi|21426837	glucose phosphate isomerase b [Danio rerio]	43.4	553	716.54	1431.06	1430.69	66.29	0.00024	ELEAGGLSGDNLEK
					780.76	1559.51	1558.78	80.43	9.00E-06	KELEAGGLSGDNLEK
					821.74	1641.46	1640.79	63.28	0.00044	TFTTQETITNAESAK
119	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	78.6	248	1458.72	1457.71	1457.72	88.87	1.30E-06	HVFGESDELIGQK
					808.17	1614.32	1613.82	47.68	0.016	RHVFGESDELIGQK
120	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	51.2	248	1458.72	1457.71	1457.72	88.87	1.30E-06	HVFGESDELIGQK
					808.17	1614.32	1613.82	47.68	0.016	RHVFGESDELIGQK
121	gi|189540214	PREDICTED: similar to myosin heavy chain, partial [Dani	58.6	809	733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
122	gi|189540222	PREDICTED: similar to myosin, heavy polypeptide 2, fas	51.6	950	733.28	1464.55	1464.77	90.20	9.20E-07	LASADIETYLLEK
					745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
					790.32	2367.93	2366.12	47.04	0.016	LQQFFNHHMFVLEQEEYK
123	gi|50345022	small muscle protein, X-linked [Danio rerio]	59	83	1038.53	2075.05	2072.97	88.25	1.30E-06	REDTVETEEVSPVTPEEK
124	gi|189522849	PREDICTED: similar to oxoglutarate (alpha-ketoglutarate	30	961	834.79	1667.56	1665.82	81.39	6.90E-06	VITDDGPPAQNPSEVK
					1201.09	2400.17	2399.32	50.61	0.0065	NITLSLVANPSHLEAVNPVVQGK
125	gi|41055855	aldehyde dehydrogenase 4 family, member A1 [Danio rei	34.5	556	1044.08	2086.14	2086.97	105.00	2.60E-08	VGDPVEDFSTFFSAVIDDK
126	gi|41282194	glutamate dehydrogenase 1 [Danio rerio]	47.8	542	786.25	1570.48	1568.77	84.15	3.90E-06	IIAEGANGPTTPDADK
127	gi|41151982	major vault protein [Danio rerio]	48.8	863	580.37	1158.73	1156.71	41.00	0.093	KEVTVLEVIK
					1069.52	2137.03	2137.12	86.26	2.00E-06	IPPHHYIHVLDQNTNIAR
128	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	65.3	202	999.01	2993.99	2996.41	51.77	0.004	TLAAGSHAEHDGQPYCHKPCY
					1008.93	3023.75	3023.42	65.34	0.00017	TLNPGGHAEHDGKPYCHKPCY
129	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	30.6	359	635.80	1269.58	1268.70	46.61	0.022	ILEDNSIPQIK
					879.64	1757.27	1758.94	85.04	3.00E-06	SIRPLDADTIETSITK
130	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	58.5	260	852.69	1703.36	1702.86	87.04	1.90E-06	HGASAVILDLPSSDGHK
131	gi|52219194	fatty acid binding protein 11 [Danio rerio]	53	134	769.55	1537.08	1535.67	70.79	7.80E-05	LNEPFEETTADDR
					832.91	1663.80	1663.77	81.11	7.50E-06	LNEPFEETTADDRK
132	gi|45387533	hypothetical protein LOC323320 [Danio rerio]	43.3	890	717.70	1433.39	1432.71	40.30	0.094	LSNRPAFMPSEGK
					761.94	1521.86	1520.71	64.59	0.00033	AGTQIENIEEDFR
					826.70	1651.38	1648.81	54.98	0.0031	KAGTQIENIEEDFR
					877.58	1753.15	1752.82	74.90	3.00E-05	KHEAFESDLAAHQDR
133	gi|56118264	actinin alpha 3 [Danio rerio]	30.4	896	717.70	1433.39	1432.71	40.30	0.094	LSNRPAFMPSEGK
					761.94	1521.86	1520.71	64.59	0.00033	AGTQIENIEEDFR
					826.70	1651.38	1648.81	54.98	0.0031	KAGTQIENIEEDFR
					877.58	1753.15	1752.82	74.90	3.00E-05	KHEAFESDLAAHQDR
134	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	51.2	523	790.73	1579.45	1577.76	96.77	2.00E-07	YDVQVQIENVEDK
					945.77	1889.52	1888.04	53.82	0.0037	ASVNIQIVDVPGPPQNLK
135	gi|41054603	actinin alpha 4 [Danio rerio]	27.3	901	761.94	1521.86	1520.71	64.59	0.00033	AGTQIENIEEDFR
					826.70	1651.38	1648.81	54.98	0.0031	KAGTQIENIEEDFR
					877.58	1753.15	1752.82	74.90	3.00E-05	KHEAFESDLAAHQDR
136	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	39.6	331	969.85	1937.69	1936.93	109.86	8.90E-09	HLTTLVDDIWYYAGDR
137	gi|51011113	hydroxyacyl-Coenzyme A dehydrogenase [Danio rerio]	62.8	309	797.76	1593.50	1593.77	45.57	0.027	FAEKPEDGEAFVQK
					819.87	1637.72	1636.85	62.69	0.0005	DPDNPLFAPSPLLNK
					942.81	1883.61	1882.93	68.33	0.00013	TPATSQQTFDALLEFSK
138	gi|18858295	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Danic	47.8	1028	877.21	1752.40	1751.85	64.06	0.00037	DAFQNAYLELGGLGER
					907.46	1812.91	1810.94	70.66	7.70E-05	QGAIVAVTGDGVNDSPALK
					987.65	1973.29	1972.92	40.48	0.075	YQLSIHQNPNSNNTESK
139	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	56.6	357	626.78	1251.55	1251.62	49.54	0.011	LHAVNDAEVER
					1111.50	2220.99	2220.13	92.38	4.70E-07	NAITVEMYNELIEALELAGK
140	gi|41056175	programmed cell death 8 (apoptosis-inducing factor) [Dar	36.4	751	614.32	1226.63	1226.57	73.89	4.20E-05	LSDGSEISYEK
					616.35	1230.68	1228.64	73.63	5.10E-05	VENGGVAVLTDR
141	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	58.2	763	653.19	1304.36	1303.71	57.40	0.0019	MQLLEIITTDK

					753.25	1504.48	1503.72	81.80	6.60E-06	TAEEVTGLSQEGQR
142	gi|189526598	PREDICTED: similar to COASTER [Danio rerio]	42.9	916	657.66	1313.30	1312.78	53.15	0.005	QAVALSLKEARK
143	gi|47085679	electron-transfer-flavoprotein, beta polypeptide [Danio re	70.1	254	925.57	924.56	924.50	51.93	0.0058	GIHVEVSGK
					601.23	1200.44	1199.71	71.48	8.00E-05	KEEASLIILGK
144	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	55.2	116	839.84	1677.67	1677.88	70.20	9.60E-05	TTGLVGLAVSQNPHER
145	gi|18859423	spectrin, beta, erythrocytic [Danio rerio]	34.8	2357	713.91	1425.80	1425.74	51.18	0.0074	HRPDLVDYGNLK
					945.14	1888.27	1887.93	93.31	4.20E-07	KKHDAIETDIAAYEER
146	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	31.1	1368	1212.60	2423.18	2422.19	102.56	4.20E-08	GQNHLEEVELAFPQNVIEGSGR
147	gi|54261777	NADH dehydrogenase (ubiquinone) Fe-S protein 8, (NAD	22.9	210	748.62	1495.22	1495.66	70.62	8.00E-05	YVNNQEEATDWK
					963.49	1924.97	1926.95	64.51	0.0003	LCEAICPAQAITIEAEPR
148	gi|62955689	hypothetical protein LOC550556 [Danio rerio]	40	270	585.09	1168.17	1167.62	45.88	0.026	FLEDLGTFVK
					843.24	1684.46	1682.84	80.84	8.00E-06	AFAEFLTEEIKEEK
					1125.33	2248.64	2246.10	46.64	0.017	SQEEEPDIVSTPNFVVEVTK
149	gi|90652819	hypothetical protein LOC664756 [Danio rerio]	72.1	462	513.65	1025.28	1024.60	76.05	2.60E-05	IGGIGTVPVGR
					972.45	2914.31	2915.57	43.03	0.031	EGGANGVTLLEALDSILPPSRPT
150	gi|59858543	gelsolin a [Danio rerio]	27.3	730	1071.90	2141.79	2141.06	98.83	1.10E-07	MLEVLGEKPDLPEGASDDVK
151	gi|41387146	peroxiredoxin 6 [Danio rerio]	49.1	222	1052.57	2103.13	2103.09	78.77	1.10E-05	PGILLGDVFPNFEADTTIGK
152	gi|18858299	ATPase, Na+/K+ transporting, alpha 1a.3 polypeptide [Da	36.8	1024	877.21	1752.40	1751.85	64.06	0.00037	DAFQNAYLELGGLGER
					907.46	1812.91	1810.94	70.66	7.70E-05	QGAIVAVTGDGVNDSPALK
153	gi|41055718	fumarate hydratase precursor [Danio rerio]	40.1	509	719.05	2154.12	2153.18	71.07	6.50E-05	EVHEVLLPGLQTLHDALAAK
					1251.82	2501.63	2501.26	47.13	0.014	THTQDAVPLSLGQEFGGYVQQ
154	gi|189533701	PREDICTED: calpastatin [Danio rerio]	68.8	824	1343.82	1342.81	1342.74	51.69	0.0071	HGAGVPAGVPEKPK
					735.92	1469.83	1470.83	57.29	0.0018	KHGAGVPAGVPEKPK
					903.69	2708.03	2705.32	45.36	0.02	QAVEDSSATDLLSSKPSSDVVP
155	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	65.8	298	525.09	1048.16	1047.57	57.91	0.0019	VFLDGVDKR
					589.15	1176.28	1175.67	51.37	0.0084	KVFLDGVDKR
					618.38	1234.75	1232.68	68.88	0.00014	DFLAGGIAAAISK
156	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio r	33	454	1245.66	1244.65	1244.68	89.06	1.50E-06	KVDFAAAGEPLK
					694.50	1386.98	1385.75	48.37	0.016	INAVSSADVVNVAK
157	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	42.2	2633	1230.46	2458.90	2458.19	90.98	5.60E-07	HAINQEINAYNTPAQFGLEGSG
158	gi|48762667	collagen, type I, alpha 2 [Danio rerio]	89.3	1352	819.00	1635.98	1635.80	93.63	4.10E-07	GELGPAGPTGPSGAQGQR
159	gi|116875789	hypothetical protein LOC768289 [Danio rerio]	52.2	431	674.15	1346.28	1345.65	93.62	4.60E-07	AALENSLGDTEAR
160	gi|59933260	cardiomyopathy associated 1 [Danio rerio]	41.7	2297	1039.06	2076.11	2075.93	93.51	3.90E-07	SSLFEHSTFDSQHAAGAER
161	gi|68444865	PREDICTED: dodecenoyl-Coenzyme A delta isomerase	62.8	301	663.31	1324.60	1325.71	84.33	3.50E-06	IGLVDELVPEDK
162	gi|41055939	sorting and assembly machinery component 50 homolog	49.9	469	665.69	1994.04	1992.02	64.06	0.00033	TKEDILTYEIADVFHAK
163	gi|40363541	S-adenosylhomocysteine hydrolase [Danio rerio]	45	433	719.94	1437.87	1437.75	80.32	8.90E-06	KLDEEVAAAHLDK
164	gi|189519969	PREDICTED: myosin, heavy polypeptide 10, non-muscle	37.6	1973	580.60	1738.78	1737.89	50.92	0.0075	KQELEEILHDLESR
					1093.81	2185.60	2184.99	80.53	7.50E-06	HAEQERDELADEISNSASGK
165	gi|189519965	PREDICTED: similar to nonmuscle myosin heavy chain [	37.3	1857	580.60	1738.78	1737.89	50.92	0.0075	
					1093.81	2185.60	2184.99	80.53	7.50E-06	
166	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	37.5	682	1325.66	1324.65	1324.74	91.10	7.40E-07	TVHLLAGVADTTK
					668.73	1335.44	1333.80	38.77	0.13	GLLPQLIGVAPEK
167	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	41.7	1754	613.78	1225.54	1222.63	38.19	0.15	AGVLAHLEEER
					575.06	1722.16	1721.89	51.85	0.0064	KQELEEILHDLEAR
					865.31	1728.60	1725.94	53.58	0.0041	QLLQANPILEAFGNAK
					894.30	2679.86	2678.38	56.37	0.0016	KLEGDSTELHDQIAELQAQIAEL
168	gi|41152365	ATP synthase, H+ transporting, mitochondrial F1 comple	18.2	159	733.15	1464.28	1462.69	89.95	9.80E-07	AQSELVSASDEATR
169	gi|189537549	PREDICTED: similar to carnitine O-palmitoyltransferase I	44.5	773	944.52	1887.03	1886.90	89.00	1.10E-06	SEPQPGEEFLAALTAGDR
170	gi|189537551	PREDICTED: similar to carnitine O-palmitoyltransferase I	40.9	753	944.52	1887.03	1886.90	89.00	1.10E-06	
171	gi|58801526	SET translocation (myeloid leukemia-associated) B [Dani	30.9	275	1098.28	2194.55	2194.01	88.55	1.10E-06	EQQEAIEHIDEVQNEIDR
172	gi|58801528	SET translocation (myeloid leukemia-associated) A [Dani	20.1	269	1098.28	2194.55	2194.01	88.55	1.10E-06	
173	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Co	61.2	761	653.19	1304.36	1303.71	57.40	0.0019	MQLLEIITTDK

					881.72	1761.43	1760.86	59.25	0.0012	LTAPPAVSSDEDIQYR
174	gi|189517055	PREDICTED: similar to heat shock protein 8 [Danio rerio	60.9	698	831.22	1660.43	1658.89	86.78	2.10E-06	IINEPTAAAIAYGLDK
175	gi|47085775	heat shock 70kDa protein 5 [Danio rerio]	40.6	650	831.22	1660.43	1658.89	86.78	2.10E-06	IINEPTAAAIAYGLDK
176	gi|116235424	hypothetical protein LOC572011 [Danio rerio]	38.2	823	1268.25	2534.48	2533.22	86.76	1.50E-06	YEVEISNLQASFQLQSQHQER
177	gi|41152028	prohibitin [Danio rerio]	62.7	271	575.24	1148.46	1148.58	43.36	0.052	FDAGELITQR
					576.00	1149.98	1148.58	84.24	4.00E-06	
178	gi|160333682	heat shock protein 8 [Danio rerio]	56.4	649	831.22	1660.43	1658.89	86.78	2.10E-06	IINEPTAAAIAYGLDK
179	gi|41055742	selenium binding protein 1 [Danio rerio]	52.3	457	846.88	2537.62	2537.25	89.21	8.50E-07	LNENFLVDFGAEPEGPALAHELI
180	gi|148922856	hypothetical protein LOC559194 [Danio rerio]	36.8	106	1069.99	2137.96	2136.73	83.54	3.70E-06	GADDDEDEDEDDEDDVDPK
181	gi|45356145	tumor protein D52-like 2 isoform 2 [Danio rerio]	45.9	185	737.79	1473.56	1473.69	75.37	3.00E-05	GLGSDSISDLPEER
182	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	73.8	164	820.04	1638.07	1637.91	82.77	5.00E-06	HVVFGQVVEGLDVIK
183	gi|47086875	glutamate dehydrogenase 1a [Danio rerio]	49.6	544	793.50	1584.99	1582.78	52.69	0.0054	IIAEGANGPTTPEADK
					863.73	1725.45	1722.87	56.83	0.0019	HGGAIPIVPTSDFQER
184	gi|18858379	carbonic anhydrase [Danio rerio]	57.7	260	501.56	1001.11	1000.54	65.27	0.00038	VLDALDDIK
					824.69	2471.05	2471.13	51.80	0.0048	QFHFHWGSSDDKGSEHTIAGT
185	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	39.7	204	853.63	1705.25	1704.91	79.51	1.10E-05	GATYGKPVHHGVNQIK
186	gi|45387723	hypothetical protein LOC402952 [Danio rerio]	54.1	331	1181.36	3541.04	3539.71	57.14	0.00093	GEDYYPPPPPHYPPHPHDHPH
187	gi|41152189	hypothetical protein LOC393720 [Danio rerio]	46.7	244	820.76	1639.51	1638.85	68.04	0.00015	RVEAIINNYPEGHK
188	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	56.7	238	777.69	1553.37	1553.87	47.03	0.019	KGGIVAIDNVLWGGR
					1028.82	2055.62	2055.00	68.70	0.00011	SHEGDDPLLQYVVNNSLR
189	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reri	53	858	703.58	1405.14	1404.80	48.13	0.016	TFAQLILDPIFK
					715.78	2144.30	2144.05	61.83	0.00055	ARPFPDGLAEDIDKGDVSSR
190	gi|189521142	PREDICTED: similar to phosphatidylinositol-binding clath	37.3	587	1258.24	3771.69	3770.92	78.08	6.70E-06	VAEQVGIDQGDIPDLTQAPSSLL
191	gi|41152448	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	34.6	355	680.96	1359.90	1358.56	78.04	1.60E-05	YAEGYNEDVGDK
192	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filami	51.1	2523	719.89	1437.77	1437.71	66.30	0.00022	TFEPAEFIIDTR
					825.27	1648.52	1645.89	44.74	0.034	VHGPGLQSGITNKPNK
193	gi|41054571	citrate synthase [Danio rerio]	37.8	468	882.18	1762.35	1761.88	77.97	1.60E-05	GLVYETSVLDPDEGIR
194	gi|189538466	PREDICTED: similar to alpha 2 actin [Danio rerio]	71.2	132	1115.49	2228.97	2227.06	77.92	1.30E-05	DLYANNVLSGGTTMYPGIADR
195	gi|47086703	dihydrolipoamide S-acetyltransferase (E2 component of	57.5	652	736.66	1471.31	1471.73	77.62	1.70E-05	GVDITQVTGTGPDGR
196	gi|153791915	hypothetical protein LOC100006671 [Danio rerio]	46.4	151	761.94	1521.86	1520.71	64.59	0.00033	AGTQIENIEEDFR
					826.70	1651.38	1648.81	54.98	0.0031	KAGTQIENIEEDFR
197	gi|125852449	PREDICTED: wu:fb57a10 [Danio rerio]	30.2	603	1108.23	2214.44	2213.98	77.43	1.50E-05	KDDGTFYEFGEDIPEAPER
198	gi|52219050	hypothetical protein LOC447859 [Danio rerio]	63.2	617	639.24	1276.47	1274.63	40.56	0.094	NLAIYDGPEQR
					928.72	2783.12	2782.39	76.93	1.40E-05	ITDENLQSQTTGLYIPEYEEALK
199	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	50.5	380	691.63	1381.25	1379.71	59.25	0.0012	FFEAAVGEAKPSK
200	gi|50539810	hypothetical protein LOC436644 [Danio rerio]	65	463	513.65	1025.28	1024.60	76.05	2.60E-05	IGGIGTVPVGR
201	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	49.7	6009	578.98	1155.95	1155.65	43.42	0.05	LKGDVDVSVPK
					586.18	1170.34	1169.67	37.19	0.21	LKGEVDVSVPK
					844.25	1686.48	1685.81	76.64	2.20E-05	VELEGPEIEGPEGGFK
202	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Da	35.2	2115	643.76	1285.50	1284.76	43.24	0.049	KSPTPVPLPPPR
					1418.91	2835.81	2835.44	67.01	0.00013	GAFTPSPLDPASTSDSHIASLSI
203	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	37.6	306	659.50	1316.99	1315.59	65.66	0.00029	VYGENIDYSEK
204	gi|50344731	fibrinogen alpha chain [Danio rerio]	46.6	684	750.41	1498.80	1498.69	74.11	3.70E-05	FPTSGTGSTSQTSNK
205	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	45.8	448	919.52	1837.03	1836.96	73.38	4.10E-05	DKPHLNIGTIGHVDHGK
206	gi|113679439	hypothetical protein LOC751638 [Danio rerio]	73	126	491.53	981.05	980.52	44.06	0.039	LVHHELPH
					636.68	1271.35	1272.68	66.20	0.00026	GQDPYSILRPK
207	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	49	308	549.82	1097.62	1098.61	47.95	0.017	QLADALKANR
					551.01	1100.01	1098.61	51.89	0.0078	
208	gi|21426835	glucose phosphate isomerase a [Danio rerio]	36.5	553	717.61	1433.21	1432.70	72.64	5.50E-05	ELQASGLSGDSLEK
209	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	27.3	484	904.88	1807.74	1806.90	72.42	5.30E-05	HEVISQGGVTHPIDYR
210	gi|66472610	hypothetical protein LOC553595 [Danio rerio]	53.8	275	1285.40	2568.79	2566.31	71.92	4.50E-05	STPTDLVTEADHQVEELIISTLR
211	gi|50540008	zgc:92882 [Danio rerio]	41	334	595.62	1189.23	1188.61	71.56	8.00E-05	VIGSGTNLDSAR

212	gi|189537196	PREDICTED: similar to L-lactate dehydrogenase B chain	32.3	285	595.62	1189.23	1188.61	71.56	8.00E-05	
213	gi|46358344	isocitrate dehydrogenase 3 (NAD+) alpha [Danio rerio]	35.1	365	1251.99	2501.97	2501.23	71.48	5.10E-05	ENTEGEYSGIEHVIVDGVVQSIK
214	gi|56693297	hypothetical protein LOC494070 [Danio rerio]	53.8	182	952.76	1903.50	1902.91	71.41	6.40E-05	AKEELEQELADKEDEK
215	gi|157073897	ubiquinol-cytochrome c reductase, Rieske iron-sulfur poly	72.9	273	773.18	1544.35	1542.79	77.14	2.00E-05	EIETEAGVNLAELR
216	gi|30017425	ATPase, Na+/K+ transporting, alpha 1a.5 polypeptide [Da	44.4	1023	907.46	1812.91	1810.94	70.66	7.70E-05	QGAIVAVTGDGVNDSPALK
217	gi|189517050	PREDICTED: glycine C-acetyltransferase [Danio rerio]	43.9	458	610.07	1218.13	1217.64	47.64	0.02	ALGGAAGGYTVGPK
					610.91	1219.80	1217.64	59.61	0.0012	
218	gi|41053309	hydroxyacylglutathione hydrolase [Danio rerio]	46.2	260	970.67	1939.33	1938.91	70.11	8.40E-05	TVLTTHHHWDHAGGNEK
219	gi|47085833	glyceraldehyde-3-phosphate dehydrogenase, spermatog	52.8	335	718.69	1435.37	1434.76	70.02	9.90E-05	GAHQNIIPASTGAAK
220	gi|50300477	coatomer protein complex, subunit beta 1 [Danio rerio]	52.4	953	830.92	2489.74	2489.26	69.90	7.30E-05	NFEHLIPDAPELIHDFLVNEK
221	gi|47086505	fibrinogen, B beta polypeptide [Danio rerio]	61.4	485	1376.68	1375.67	1375.70	48.29	0.015	DTVDVTFPQNIK
					916.63	1831.25	1828.90	54.48	0.0033	ETYSPGPVSQPPISGGTR
222	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	46.7	1631	588.13	1174.25	1172.62	53.92	0.0048	LEFEVQVGPR
223	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	43	697	651.91	1301.80	1301.66	68.64	0.00015	SHIDELYANIK
224	gi|189536555	PREDICTED: hypothetical protein [Danio rerio]	31.7	454	774.22	1546.42	1545.72	68.37	0.00015	YPEPVEGEAEGELK
225	gi|54400408	myosin, light chain 6, alkali, smooth muscle and non-mus	41.1	151	997.69	996.68	996.56	60.30	0.00094	HVLTTLGEK
					677.17	1352.33	1351.75	49.02	0.012	ALGQNPVNAEVLK
226	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio r	29.8	151	997.69	996.68	996.56	60.30	0.00094	
					677.17	1352.33	1351.75	49.02	0.012	
227	gi|189516972	PREDICTED: similar to Myosin light polypeptide 4 (Myos	44.4	187	966.89	965.88	966.55	56.68	0.0021	HVLATLGEK
228	gi|41055823	hypothetical protein LOC393488 [Danio rerio]	28	186	966.89	965.88	966.55	56.68	0.0021	
229	gi|156616344	hypothetical protein LOC100124599 [Danio rerio]	57.6	278	745.69	1489.36	1488.74	65.97	0.00026	ENQSVLITGESGAGK
230	gi|41393125	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	58	245	640.25	1278.49	1278.65	60.54	0.00091	YLAEVAAGDDKK
					691.66	1381.30	1379.66	48.36	0.014	YLIENSSNPESK
231	gi|58801524	LIM domain containing preferred translocation partner in	40.5	556	1098.63	2195.24	2193.06	60.16	0.00079	AEPSHHPAPTPSQGYQPAPPK
232	gi|113865949	zgc:161979 [Danio rerio]	48.5	130	628.15	1254.29	1253.63	67.07	0.0002	YFQDLVDNLK
233	gi|49227667	popeye domain containing 1 [Danio rerio]	42.4	316	660.79	1319.56	1319.63	66.75	0.00022	GGSTGSSLPVTSDR
234	gi|148596955	ATP synthase, H+ transporting, mitochondrial F0 comple	54.9	71	817.25	1632.48	1631.83	66.73	0.00022	RYDNLKPIAEEER
235	gi|62955727	NADH dehydrogenase (ubiquinone) 1 beta subcomplex,	31.4	175	814.44	1626.87	1625.79	66.52	0.00022	EVQQLQSETPADGPK
236	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	44.6	679	567.50	1132.99	1130.59	41.62	0.077	SVAELEAEKR
					649.20	1296.39	1296.77	66.51	0.00022	VSVSPAGVELLVK
237	gi|41056085	keratin 8 [Danio rerio]	43.8	520	1486.79	1485.78	1485.71	50.29	0.0093	ANLENQIAEAEER
					1009.90	2017.79	2017.16	48.42	0.012	SLLAPLNLEIDPNIQIVR
238	gi|51010955	hypothetical protein LOC445042 [Danio rerio]	71.2	104	608.74	1215.47	1215.65	66.19	0.00028	ALTAGSEASGKPK
239	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio reri	42.7	199	667.73	1333.44	1332.69	62.89	0.00053	KYTLPPGVDSEK
240	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	44	134	893.49	2677.44	2675.32	54.23	0.0026	ITFTNEEFLVTLPDGSEIHFPNR
241	gi|41053395	glutamate oxaloacetate transaminase 2 [Danio rerio]	43.2	428	555.66	1109.31	1107.59	56.05	0.0025	KMNLGVGAYR
					926.44	1850.87	1850.98	45.42	0.025	ALDKEYLGIVGLGDFNK
					665.76	1994.24	1994.03	43.33	0.04	YFIEQGHNILLSQSFAK
242	gi|189521842	PREDICTED: similar to Histone H1.5 (Histone H1a) isofo	80.4	194	556.09	1110.16	1108.54	64.97	0.00033	ALSAGGYDVEK
243	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio r	82	172	614.69	1227.37	1225.51	50.85	0.0088	VETDEEFDSR
					1144.30	3429.88	3427.84	47.59	0.0089	EIYPYVIQELKPTLQELGISTPEE
244	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	42.2	606	1090.87	2179.73	2179.07	64.88	0.00027	GGENIYPAEIEQFLHTHPK
245	gi|18858657	fatty acid binding protein 7, brain, a [Danio rerio]	54.5	132	749.60	1497.18	1496.63	63.80	0.00039	LGEEFDETTADDR
246	gi|27545301	laminin, beta 1 [Danio rerio]	53.4	1785	1065.04	2128.06	2128.10	63.70	0.00037	VGSLTDVEDILNQSAADILR
247	gi|47271384	cofilin 2, like [Danio rerio]	67.9	165	1207.39	2412.76	2412.16	63.61	0.00033	HIIMEQGQEILQGDEGDPYLK
248	gi|41055546	hypothetical protein LOC393186 [Danio rerio]	73	281	675.75	1349.49	1347.70	62.34	0.00057	VALDTSFVPNTGK
249	gi|40548314	H1 histone family, member X [Danio rerio]	56.8	192	866.08	1730.15	1729.89	62.32	0.00057	PAVVEESAPAPAPAPAEK
250	gi|52218912	enoyl Coenzyme A hydratase, short chain, 1, mitochondr	48.1	291	1056.37	2110.72	2110.12	62.20	0.00051	AQFGQPEILLGTIPGAGGTQR
251	gi|113678344	BCL2-like 13 (apoptosis facilitator) [Danio rerio]	45.8	485	1029.90	3086.66	3085.41	61.92	0.00038	SLDSAEGVALAEEQSENNSSNS
252	gi|38198629	solute carrier family 4, anion exchanger, member 1 [Dani	24.5	905	826.71	1651.40	1649.80	61.90	0.00062	RGDAESYVELNELR
253	gi|53933242	cytochrome c oxidase subunit VIa polypeptide 1 [Danio re	52.8	108	1171.65	2341.28	2341.05	61.51	0.00055	TLFHNPHVNALPDGYEHHDE

254	gi|40254661	annexin A5 [Danio rerio]	50.8	317	1143.81	2285.61	2284.98	61.28	0.0006	EHDKDLEEDVTGDTGGHFER
255	gi|52219022	hypothetical protein LOC447845 [Danio rerio]	33.5	462	990.77	1979.53	1977.05	49.87	0.0089	VLIFQEENEIPSSVFVK
256	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [Da	62.1	789	1115.74	2229.46	2229.10	60.89	0.00066	TSYDVSDSGQLEHVVVNRPK
257	gi|189522065	PREDICTED: similar to Histone H1.2 (H1 VAR.1) (H1c) [I	60.5	200	521.08	1040.14	1038.61	54.49	0.0037	AGPGVGELIVK
					456.55	1366.61	1365.83	44.62	0.033	AKKAGPGVGELIVK
258	gi|61651682	fibronectin 1b [Danio rerio]	43.9	2408	766.21	1530.41	1529.75	50.29	0.0095	GGQGPTFSELVGPER
					995.13	1988.24	1987.01	41.68	0.057	ILEEVVTAGNTVPGDATSSK
					1070.96	3209.84	3208.44	37.88	0.093	INTVGPTGHDSTDAHGQHVEYT
259	gi|189534068	PREDICTED: nuclear RNA export factor 1 [Danio rerio]	45.8	642	731.21	1460.40	1460.65	60.46	0.00091	FGGRGGGGGGGGGPSDGR
260	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	66.9	329	667.28	1332.54	1331.67	45.39	0.03	DLGLAQNSATNTK
					865.58	1729.14	1729.95	49.58	0.01	KGSLLIDSSTIDPAVSK
261	gi|55742376	sex hormone binding globulin [Danio rerio]	51.4	381	495.50	988.99	987.52	59.46	0.0014	LAEEQLTGK
262	gi|41053347	mitochondrial trifunctional protein, beta subunit [Danio rei	48	471	561.19	1120.36	1119.56	49.10	0.014	LEQDEFALR
					709.86	1417.70	1415.77	53.33	0.0049	DQLLLGPTYATPK
263	gi|189517202	PREDICTED: NADH dehydrogenase (ubiquinone) 1, alph	70.6	153	812.60	1623.19	1621.83	58.87	0.0013	LMTPEEIVTYIADK
264	gi|68357880	PREDICTED: similar to slow troponin T 1 [Danio rerio]	21.3	268	509.03	1016.05	1015.47	58.74	0.0017	VDFDDIHR
265	gi|31377814	troponin T1, skeletal, slow [Danio rerio]	15.9	290	509.03	1016.05	1015.47	58.74	0.0017	VDFDDLHR
266	gi|189520524	PREDICTED: similar to Troponin T2, cardiac [Danio rerio	25.1	243	509.03	1016.05	1015.47	58.74	0.0017	
267	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	48.6	245	1073.03	2144.04	2143.98	57.93	0.0013	TAFDEAIAELDSLNEESYK
268	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple:	73.2	209	637.58	1273.14	1272.67	52.09	0.0067	SLDKVEQELGR
					920.90	1839.79	1838.03	36.05	0.22	VSPITINLINVLSENGR
269	gi|189530481	PREDICTED: similar to LIM domain-containing protein 1	61	490	843.76	1685.51	1684.80	56.53	0.0022	HHSTIIQHNDGPSSR
270	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	72.7	455	758.93	1515.84	1517.74	37.74	0.17	CPDCPGLLPLHEPK
					654.52	1960.54	1959.96	44.47	0.031	FHDHRPGSVHPLGPDHR
271	gi|189530774	PREDICTED: ryanodine receptor 2b (cardiac) [Danio reri	38.7	4882	727.63	2179.85	2177.92	36.56	0.18	EEDFHAVQDEEEDTETKK
					779.29	2334.84	2333.25	50.22	0.0073	HLTTGSFLGLIHDQGLQLVER
272	gi|68362968	PREDICTED: similar to TAF6-like RNA polymerase II, p3	55.9	641	819.52	1637.03	1636.94	56.28	0.0022	EINLVELALATNIPK
273	gi|74315945	hypothetical protein LOC613246 [Danio rerio]	54	422	1048.00	2093.99	2092.98	56.22	0.002	ALVGNEASEELQSADGNPHR
274	gi|68365370	PREDICTED: hypothetical protein LOC325885 [Danio rei	33	276	445.53	889.04	887.48	56.13	0.0032	RSVELER
275	gi|32401408	annexin A11b [Danio rerio]	39.2	485	886.76	1771.51	1770.84	56.08	0.0023	SLYTHISGDTSGDYKK
276	gi|125822895	PREDICTED: similar to phospholipase A2, group IVC (cy	47.6	548	878.65	1755.29	1754.84	56.05	0.0023	IQEFFTQSTPAEETK
277	gi|47085823	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight cl	58.7	424	609.57	1217.13	1216.67	56.22	0.0028	GITFEDVVIPK
278	gi|50080164	5'-3' exoribonuclease 2 [Danio rerio]	28.7	540	530.06	1058.11	1060.53	55.24	0.0037	MREEVIER
279	gi|41054573	hydroxysteroid dehydrogenase like 2 [Danio rerio]	59	415	785.87	1569.72	1568.74	55.00	0.0031	HMEAHGATPAFTTAK
280	gi|47086649	F-actin capping protein alpha-1 subunit [Danio rerio]	15.4	286	717.26	2148.76	2147.02	54.51	0.003	LDGSEDQVLITEHGDLGHGR
281	gi|189525013	PREDICTED: im:7145727 [Danio rerio]	74.5	561	530.57	1059.12	1057.54	54.32	0.0046	AVEIVEAGDR
282	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	58.2	433	572.55	1143.09	1142.61	54.32	0.0042	IGAEVYHNLK
283	gi|47086189	propionyl Coenzyme A carboxylase, beta polypeptide [Da	65.2	557	847.73	1693.44	1692.80	54.30	0.0036	GKQNQAEAEAEYVEK
284	gi|57525801	hypothetical protein LOC445183 [Danio rerio]	34	200	518.13	1034.24	1032.60	54.10	0.0045	TGNIFLQLK
285	gi|113678245	hypothetical protein LOC558738 [Danio rerio]	64	111	873.28	1744.54	1744.90	52.89	0.0049	SIHALSVAPSTVGDYTK
286	gi|189532065	PREDICTED: similar to acyl-Coenzyme A dehydrogenase	34.6	442	771.24	1540.46	1539.72	53.98	0.0038	AQDTAELFFEDVR
287	gi|41056265	acyl-Coenzyme A dehydrogenase, long chain [Danio reri	33.5	442	771.24	1540.46	1539.72	53.98	0.0038	
288	gi|52219190	hypothetical protein LOC447942 [Danio rerio]	81.6	103	1167.88	3500.62	3500.62	53.66	0.0021	TKPWPWGDGNHSLFHNPHTNA
289	gi|189517212	PREDICTED: similar to myosin, heavy polypeptide 11, sr	40.6	1994	865.31	1728.60	1725.94	53.58	0.0041	QLLQANPILEAFGNAK
290	gi|168229163	cysteine-rich protein 2 [Danio rerio]	68.9	206	999.01	2993.99	2996.41	51.77	0.004	TLAAGSHAEHDGQPYCHKPCY/
291	gi|189529657	PREDICTED: similar to nonmuscle myosin heavy chain [I	40.8	1962	865.31	1728.60	1725.94	53.58	0.0041	QLLQANPILEAFGNAK
292	gi|189525028	PREDICTED: wu:fi27h03 [Danio rerio]	44.9	3392	483.04	964.07	963.54	53.06	0.0054	INLSAATFK
293	gi|123858772	protein phosphatase 1, catalytic subunit, beta [Danio reric	50.2	327	977.65	1953.29	1952.12	53.02	0.0042	EIFLSQPILLELEAPLK
294	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	49.8	255	632.78	1263.55	1263.70	49.54	0.012	NVIIAAHGNSLR
					828.74	1655.46	1653.91	42.52	0.053	ALPFWNEVIVPEIK
295	gi|41054025	adenylosuccinate lyase [Danio rerio]	36.1	482	762.75	2285.22	2284.20	52.32	0.0047	VQADPYFAPILGELDALLDPK
296	gi|189522138	PREDICTED: similar to paxillin [Danio rerio]	41.7	527	1149.87	2297.72	2294.99	45.75	0.021	TWHPEHFVCTHCQEEIGSR

297	gi|189521681	PREDICTED: im:7139872 [Danio rerio]	35.8	584	842.74	1683.47	1682.82	51.16	0.0072	HQVETSQEANTQALK
298	gi|55925233	suppressor of variegation 4-20 [Danio rerio]	45.5	808	601.52	1201.02	1199.66	51.06	0.009	RSQANISSLPK
299	gi|27545305	laminin, gamma 1 [Danio rerio]	58.4	1593	665.17	1328.32	1327.68	51.01	0.0083	RAEAALGNAAADAK
300	gi|89886285	endothelial PAS domain protein 1 [Danio rerio]	32.6	832	576.62	1151.22	1150.59	50.92	0.0084	LFSLDTQEAK
301	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	30.8	2113	653.19	1304.36	1303.77	48.47	0.015	RCLIEIFGILK
302	gi|41152161	Rho GTPase activating protein 12 [Danio rerio]	30.6	817	530.06	1058.11	1060.49	48.93	0.016	SSNENLNQR
					530.07	1587.17	1586.76	44.57	0.035	SSNENLNQRAPTEK
303	gi|56790313	homeo box B9a [Danio rerio]	27.1	255	709.86	1417.70	1416.74	49.99	0.01	MEPLLGHLGEPPK
304	gi|55926092	heat shock 10kD protein 1 (chaperonin 10) [Danio rerio]	50	100	771.64	1541.27	1539.86	49.56	0.011	VLQATVVAVGPGSTNK
305	gi|189527715	PREDICTED: similar to dentin sialophosphoprotein [Dani	31.2	998	729.47	1456.93	1457.71	47.26	0.019	SDNDPGSKINLGNK
306	gi|125814831	PREDICTED: similar to zinc finger protein 585B [Danio r	47.7	298	837.97	1673.92	1672.88	46.67	0.021	EESEDVKIEEIIIK
307	gi|66472430	hypothetical protein LOC553684 [Danio rerio]	42.6	324	477.16	952.30	952.52	49.28	0.011	FMSKSVVR
308	gi|18858981	lamin b2 [Danio rerio]	34.6	583	624.69	1247.37	1245.61	48.79	0.015	VELEESSTAGPK
309	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio r	57.1	333	714.44	1426.86	1424.81	52.98	0.005	LDVAPISDIIEIK
310	gi|153791419	si:ch73-252g14.4 [Danio rerio]	28.2	386	829.77	2486.28	2486.30	48.59	0.0099	VQQLLHAHTFGPQHNPTVHGL
311	gi|148229906	hypothetical protein LOC100037332 [Danio rerio]	45.4	302	551.01	1100.01	1098.64	48.48	0.017	LKQELAELR
312	gi|148922926	succinate dehydrogenase complex, subunit B, iron sulfur	68.2	280	634.14	1266.26	1264.60	48.26	0.015	QQYLQSVEDR
313	gi|189518965	PREDICTED: similar to Acetyl-CoA carboxylase 2 (ACC-	35.4	2240	836.89	1671.76	1672.86	48.19	0.014	ESRGGVLEAEGTVEIK
314	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	25.2	448	708.70	1415.39	1415.74	48.18	0.016	EALGAENIQSTKR
315	gi|41055754	sarcolemma associated protein [Danio rerio]	38.8	376	902.65	1803.28	1801.84	48.03	0.015	LNQELQEANEQANSSK
316	gi|50345068	dehydrogenase/reductase (SDR family) member 1 [Dani	78.1	310	909.43	1816.84	1815.86	47.68	0.016	YKDVFTNGETTELSGR
317	gi|55742454	signal transducer and activator of transcription 4 [Danio r	44.5	667	635.80	1269.58	1268.77	47.68	0.017	QLDKLGELILK
318	gi|189533166	PREDICTED: similar to G protein-coupled receptor 126 b	22	1236	581.81	1161.61	1161.64	47.63	0.019	LTSTVAWGLSK
319	gi|121583897	hypothetical protein LOC562692 [Danio rerio]	22.1	384	816.69	1631.36	1631.81	47.64	0.018	ELEEKVAMLEAENK
320	gi|68357456	PREDICTED: similar to mCG1046517 [Danio rerio]	38.3	1561	767.11	1532.20	1530.94	47.56	0.018	LLEKSKELAFILK
321	gi|51870938	cortactin [Danio rerio]	50.4	504	843.14	1684.27	1683.84	47.32	0.018	TVQGSGHQEHINIHK
322	gi|50233897	FLJ12716-like protein [Danio rerio]	30.7	1132	595.17	1188.32	1187.63	46.86	0.025	TAYSLVHELR
323	gi|47086425	cytochrome P450, family 17, subfamily A, polypeptide 1 [	43.5	519	531.43	1060.84	1061.51	46.84	0.025	MNGFVPAGNR
324	gi|168229182	zgc:171912 [Danio rerio]	52.7	459	562.80	1123.58	1123.61	46.57	0.022	IIEKNAGHSR
325	gi|189530003	PREDICTED: hypothetical protein [Danio rerio]	72.4	261	664.65	1327.28	1325.80	46.21	0.024	CALLALRGLALR
326	gi|115529393	hypothetical protein LOC767787 [Danio rerio]	46.4	168	1304.73	1303.72	1303.63	46.05	0.026	GIEFDAIAPDEK
327	gi|189532603	PREDICTED: im:7151086 [Danio rerio]	24.2	15951	690.69	1379.37	1379.61	46.02	0.024	ELEDQMMDLTR
328	gi|123708080	hypothetical protein LOC791153 [Danio rerio]	50	304	459.01	916.00	914.55	45.98	0.033	IVATAKAGGK
329	gi|189518402	PREDICTED: similar to NLR family, CARD domain conta	48.8	995	952.59	951.58	951.47	45.61	0.025	CFDDIVLK
330	gi|189523575	PREDICTED: similar to gag-pol polyprotein [Danio rerio]	58.8	1555	550.82	1099.63	1098.64	45.59	0.033	LELAAAVVSAR
331	gi|18858907	islet2 [Danio rerio]	51.8	359	656.53	1966.55	1963.95	45.44	0.024	VDILPHPSFLGDMGDHSK
332	gi|189520388	PREDICTED: similar to helentron 4 helitron-like transpos	30.3	2363	799.26	1596.50	1595.81	45.40	0.028	QNNYNLFKSNNLK
333	gi|57525891	hypothetical protein LOC445162 [Danio rerio]	36.3	306	799.26	1596.50	1593.85	45.32	0.028	NKMLSAAFKSAAVEK
334	gi|189529618	PREDICTED: similar to Glutamate [NMDA] receptor sub	27.5	1924	418.31	417.30	418.22	37.37	0.0013	AGGSK
335	gi|122114635	hypothetical protein LOC613021 [Danio rerio]	52.3	1176	418.31	417.30	418.22	37.37	0.0013	AGGSK
336	gi|189516062	PREDICTED: similar to cadherin-like 24 [Danio rerio]	32.3	725	577.37	1152.73	1152.52	45.16	0.031	EMSVDSRSSR
337	gi|189523771	PREDICTED: wu:fa11e05 [Danio rerio]	25.5	715	664.43	1990.27	1988.96	45.09	0.026	HHTILSDMASVPNFQHR
338	gi|189514468	PREDICTED: similar to tropomodulin [Danio rerio]	42.4	356	844.25	1686.48	1684.83	45.05	0.031	SNDPDLTEVNLNNIK
339	gi|189529885	PREDICTED: similar to Si:dkey-204a24.2 protein [Danio	39.4	1182	607.51	1213.01	1212.65	44.95	0.035	LLQAQLDEQR
340	gi|41152024	glycoprotein, synaptic 2 [Danio rerio]	27.3	308	608.63	1215.25	1215.61	44.90	0.038	HYEVEILDAK
341	gi|189537716	PREDICTED: similar to kinesin family member 21A, parti	39.2	1581	410.34	818.67	818.47	44.82	0.043	KLSVMNK
342	gi|164414411	hypothetical protein LOC561896 [Danio rerio]	37.8	423	719.94	1437.87	1439.78	44.47	0.034	ENLQVVRSRDPK
343	gi|189536525	PREDICTED: similar to carbohydrate (N-acetylglucosami	24.6	423	719.94	1437.87	1439.78	44.47	0.034	
344	gi|189529867	PREDICTED: similar to transforming growth factor beta r	33	2317	635.80	1269.58	1268.77	44.44	0.037	IIQLSETKPLK
345	gi|189517917	PREDICTED: similar to family with sequence similarity 4	42.1	789	589.15	1176.28	1177.49	44.15	0.044	VEMESDSPER
346	gi|189515647	PREDICTED: similar to Choline transporter-like protein 5	37	737	478.48	954.95	952.49	44.15	0.04	FLLCCLK
347	gi|189522362	PREDICTED: similar to Choline transporter-like protein 5	41.5	730	478.48	954.95	952.49	44.15	0.04	

348	gi|189533245	PREDICTED: ryanodine receptor 3 [Danio rerio]	38.1	4863	701.10	1400.18	1398.71	44.00	0.041	GRPQKTEEEPTK
349	gi|66773104	branched chain keto acid dehydrogenase E1, alpha poly	25.3	446	827.53	1653.04	1652.84	43.92	0.038	QGQIINPSEDPQLSK
350	gi|189519010	PREDICTED: similar to dynein, axonemal, heavy chain 1	39.1	4616	558.63	1115.25	1114.58	45.21	0.036	VWQADVLER
351	gi|45387519	short chain dehydrogenase/reductase [Danio rerio]	45.6	320	529.67	1585.97	1586.92	43.87	0.041	VITVSSGGMLVQKLR
352	gi|160333235	lyric-like [Danio rerio]	72.1	542	1176.76	2351.51	2350.20	43.69	0.032	KRPEEEGSAVEVIPEVSAPAEK
353	gi|68399071	PREDICTED: similar to rCG63619 [Danio rerio]	37.5	104	530.07	1587.17	1586.77	43.63	0.043	KESAQMPGDVQELR
354	gi|125848595	PREDICTED: similar to procollagen I N-proteinase [Dani	45	1270	1059.42	2116.82	2114.97	43.57	0.037	CGVCGGDNSTCKIVKGNFTR
355	gi|57770377	homeo box HB9 like a [Danio rerio]	57.6	309	599.59	1197.16	1196.70	43.36	0.048	RSINVGVSLPR
356	gi|189519045	PREDICTED: similar to Armadillo repeat protein deleted i	36.4	986	866.31	1730.60	1729.84	43.34	0.045	FQDPSALQAPGSAGTQR
357	gi|68399197	PREDICTED: cathepsin K, like [Danio rerio]	18.1	349	605.86	1209.71	1209.58	43.27	0.048	NLAMAGISDYR
358	gi|50344729	annexin A6 [Danio rerio]	46.7	492	565.88	1129.74	1129.63	43.17	0.057	EAILDLITSR
359	gi|18858253	adenosine deaminase, RNA-specific [Danio rerio]	41.8	1382	539.50	1076.99	1076.55	43.08	0.056	LFQEASAPSK
360	gi|47086899	par-6 partitioning defective 6-like protein gamma [Danio r	11.1	434	442.43	882.85	882.51	42.80	0.049	LIMTIHR
361	gi|55742346	receptor interacting protein kinase 5 [Danio rerio]	44.6	857	1217.37	3649.08	3647.74	42.72	0.025	VSDGGGGGALFTQLASLQLISA
362	gi|189525434	PREDICTED: im:7157373 [Danio rerio]	51.2	545	954.04	2859.08	2859.32	42.64	0.035	SAAAPPKEEAPPANAPDGDAP
363	gi|189524989	PREDICTED: neurobeachin-like 2 [Danio rerio]	38.9	1495	741.60	1481.19	1480.68	42.56	0.053	NEQEVVSDDRYK
364	gi|41393105	plasminogen [Danio rerio]	51.5	818	825.87	1649.73	1649.83	42.31	0.059	WEGTFPHVPNITPR
365	gi|125852544	PREDICTED: hypothetical protein [Danio rerio]	24.1	174	669.26	2004.76	2002.97	42.20	0.05	DGFIDKEDLHDMLASLGK
366	gi|47550703	myosin, light polypeptide 9, like [Danio rerio]	37.8	172	669.26	2004.76	2002.97	42.20	0.05	
367	gi|189523637	PREDICTED: hypothetical protein [Danio rerio]	16.6	650	548.40	1642.16	1644.80	41.90	0.062	GCPNGHLASVTSSFIR
368	gi|125852977	PREDICTED: similar to Zinc finger protein 776 [Danio rer	50.1	499	617.69	1850.04	1850.86	41.48	0.063	CPRSLSVCQTCNGKMPK
369	gi|54400554	cysteine and glycine-rich protein 3 (cardiac LIM protein) [	75.6	193	818.62	2452.82	2452.15	42.68	0.04	SLESTTVTDKDGELYCKVCYAK

DMSO replicate 3

Protein #	**Accession ID**	**Protein name**	**Protein coverage**	**length**	**peptide *m/z***	**peptide Mr*expt***	**peptide Mr*calc***	**peptide score**	**pep_expect**	**peptide sequence**
1	gi|74315904	alpha globin-like [Danio rerio]	76.2	143	559.16	1116.30	1114.56	62.82	0.00064	ADEIGAEALAR
					588.80	1175.58	1175.62	75.69	3.10E-05	TIMGAVGEAISK
					684.20	1366.38	1365.73	83.43	4.30E-06	FFNNLALALSEK
					932.40	1862.78	1863.88	123.63	3.90E-10	TYFSHWSDLSPGSGPVK
					934.07	1866.12	1868.00	127.17	1.70E-10	IDDLVGGLAALSELHAFK
					934.16	1866.31	1863.88	71.94	5.80E-05	TYFSHWSDLSPGSGPVK
					934.21	1866.40	1868.00	95.14	2.80E-07	IDDLVGGLAALSELHAFK
					934.24	1866.46	1863.88	89.80	9.50E-07	TYFSHWSDLSPGSGPVK
					934.40	1866.79	1868.00	128.55	1.30E-10	IDDLVGGLAALSELHAFK
					996.15	1990.29	1991.97	89.92	8.60E-07	TYFSHWSDLSPGSGPVKK
					1009.90	3026.67	3025.62	60.45	0.00053	TIMGAVGEAISKIDDLVGGLAAL
2	gi|47271417	hemoglobin alpha adult-1 [Danio rerio]	75.5	143	559.16	1116.30	1114.56	62.82	0.00064	ADEIGAEALAR
					582.03	1162.04	1161.61	84.54	3.80E-06	TIMGAVGEAVSK
					684.20	1366.38	1365.73	83.43	4.30E-06	FFNNLALALSEK
					924.44	1846.87	1847.88	123.87	3.70E-10	TYFSHWADLSPGSGPVK
					934.40	1866.79	1868.00	128.55	1.30E-10	IDDLVGGLAALSELHAFK
					660.43	1978.26	1975.98	65.55	0.00024	TYFSHWADLSPGSGPVKK
3	gi|163644263	ventricular myosin heavy chain-like [Danio rerio]	59.4	1936	918.52	917.51	917.48	44.02	0.053	VTVETQGGK
					496.07	990.13	989.50	55.65	0.0033	SNNFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					554.06	1106.11	1104.58	44.72	0.036	SNTAAASLDKK
					1182.68	1181.67	1179.58	42.70	0.053	DFEISQLNSK
					1208.62	1207.61	1207.55	55.68	0.0028	LQAENDEFSR
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					619.88	1237.74	1237.63	49.48	0.011	EADVLQQNPPK

					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					646.59	1291.16	1288.63	51.30	0.008	DSQLQLDDSLR
					650.14	1298.26	1297.56	53.69	0.0043	TLEDQMNEYR
					654.56	1307.11	1307.64	84.62	3.50E-06	NSFSQQLEDLK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00023	LQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					699.61	1397.21	1397.75	78.26	1.40E-05	NALLQAELEELR
					708.42	1414.83	1414.73	99.72	1.10E-07	LAEQELLDVTER
					733.10	1464.19	1463.68	59.68	0.0011	LSEKDEEMEQVK
					738.40	1474.78	1473.68	90.43	9.10E-07	VEELEEELEAER
					748.76	1495.50	1495.73	54.59	0.0032	KLQHELDEAEER
					751.66	1501.31	1499.75	102.78	5.30E-08	LQEAEEAVEAVNAK
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					754.50	1506.99	1506.60	38.10	0.15	EEQAEADGTEDADK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					770.71	1539.41	1539.77	76.29	2.20E-05	DYHIFYQILSNK
					771.84	1541.67	1541.83	91.51	6.90E-07	IDDEQSIIIQLQK
					771.84	1541.67	1539.77	45.03	0.031	DYHIFYQILSNK
					771.90	1541.78	1542.83	96.87	2.00E-07	KLAEQELLDVTER
					772.38	1542.74	1541.83	64.33	0.00036	IDDEQSIIIQLQK
					1543.94	1542.93	1542.83	92.72	5.40E-07	KLAEQELLDVTER
					772.73	1543.45	1541.83	60.07	0.00099	IDDEQSIIIQLQK
					773.15	1544.28	1542.83	81.30	7.50E-06	KLAEQELLDVTER
					802.72	1603.43	1602.78	73.98	4.00E-05	SNDDLKENTAIVER
					806.68	1611.34	1610.75	79.68	1.00E-05	AAEESEEQANVHLGK
					810.76	1619.50	1619.78	68.97	0.00012	LSEKDEEMEQVKR
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					823.93	1645.84	1645.82	111.90	6.50E-09	NLTEEMAALDDIIAK
					844.34	1686.67	1684.83	55.53	0.0028	LELDDVASSMEHIVK
					845.48	1688.95	1688.88	92.61	5.60E-07	GQNVQQVNYAIGALSK
					852.23	1702.45	1701.82	98.48	1.30E-07	LQNEIEDLMVDVER
					859.76	1717.51	1717.85	103.10	4.80E-08	NEDPLNETVVGLYQK
					862.60	1723.19	1721.94	82.68	5.20E-06	VQLLHSQNTSLINQK
					893.74	1785.47	1786.87	131.68	6.40E-11	TIDTLQSALESETHSR
					896.44	1790.86	1790.76	78.77	1.30E-05	QREEQAEADGTEDADK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					934.68	1867.34	1867.93	113.91	3.70E-09	DLEEATLQHEATAATLR
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					981.26	1960.50	1957.98	104.58	3.00E-08	ILQEEISDLTEQLGEGGK
					989.22	1976.43	1976.89	60.09	0.00083	MEGDLNEMEIQLSQANR
4	gi|41053652	myoglobin [Danio rerio]	100	147	550.57	1099.12	1098.58	99.70	1.20E-07	AGLDAAGQGALR
					779.82	1557.62	1557.74	87.48	1.80E-06	VMDAVIGDIDGYYK
					1010.16	2018.30	2020.10	87.97	1.40E-06	GDHAALLKPLANTHANIHK
					1110.11	2218.21	2219.23	109.00	1.00E-08	AKGDHAALLKPLANTHANIHK
					1127.78	2253.55	2253.18	110.97	6.50E-09	FSGISQGDLAGSPAVAAHGATV
					1192.16	2382.31	2381.27	90.70	6.30E-07	FSGISQGDLAGSPAVAAHGATV
					946.44	2836.30	2834.54	54.67	0.0022	GDHAALLKPLANTHANIHKVALN
5	gi|38488753	myosin, heavy polypeptide 6, cardiac muscle, alpha [Dan	52	1936	494.37	986.73	986.54	50.96	0.0099	ENITLLER
					502.45	1002.89	1002.56	48.51	0.018	TNIFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					1203.58	1202.57	1202.57	53.53	0.005	DGDVHPQNPPK

					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					660.22	1318.42	1316.61	57.05	0.0021	ELENELDAEQK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					672.56	1343.10	1341.65	93.60	4.50E-07	AFDVLGFTSEEK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					1375.67	1374.66	1374.66	54.13	0.004	LAEQELTDATER
					1382.63	1381.62	1381.65	62.31	0.00057	LQHELEEAEER
					737.89	1473.76	1473.68	57.30	0.0019	IEELEEELDAER
					741.38	1480.74	1480.77	83.35	4.40E-06	LSSADIETYLLEK
					743.81	1485.60	1485.73	96.91	2.00E-07	LQDAEEAVEAVNAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					752.72	1503.42	1502.76	81.10	7.90E-06	KLAEQELTDATER
					757.12	1512.23	1509.74	64.70	0.00032	KLQHELEEAEER
					760.38	1518.75	1517.74	68.41	0.00015	IEDEQMASVQLQK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					774.60	1547.19	1546.71	99.75	1.10E-07	SAEEAEELANANTAK
					775.73	1549.44	1547.71	74.44	3.60E-05	LTQENVMDLENDK
					796.14	1590.26	1588.75	92.29	5.80E-07	IEDEEEINADLTAK
					809.57	1617.12	1615.81	113.60	4.30E-09	LEEAGGATSAQVELNK
					823.31	1644.61	1644.83	36.65	0.21	RNNLMQTELEELR
					846.53	1691.04	1690.81	65.90	0.00026	NSYEETLDHLETIK
					849.50	1696.99	1697.86	118.55	1.30E-09	GQSVDQVYYSIGALAK
					859.76	1717.51	1716.90	83.45	4.40E-06	NKDPLNETVVGLYQK
					865.98	1729.95	1729.86	86.09	2.40E-06	LQNEIEDLMLDLER
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					948.63	1895.24	1893.92	99.40	9.90E-08	HADSVAELGEQIDNLQR
					950.98	1899.94	1899.92	113.63	3.80E-09	DLEESTLQHEATTASLR
					966.99	1931.97	1931.91	121.29	6.40E-10	NLQEEISDLTDQVSEGR
					989.22	1976.43	1976.89	60.09	0.00083	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					686.73	2057.16	2056.02	50.86	0.0068	RDLEESTLQHEATTASLR
					1044.14	2086.27	2086.04	94.86	2.70E-07	VKLEQQVDDLEGSLEQEK
					1087.63	2173.25	2170.99	47.59	0.014	TELQSALEEADASVEHEEGK
					1099.84	2197.66	2199.12	116.43	1.90E-09	GTLEDQIIQANPALEAFGNAK
					739.60	2215.76	2214.14	72.91	4.10E-05	VKLEQQVDDLEGSLEQEKK
					1158.56	2315.10	2316.11	61.10	0.00062	NDLLLQVQSEQDTLTDAEER
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
					1214.26	2426.50	2426.19	36.45	0.17	QESDLLQLQNELEELVQENR
					1278.27	2554.53	2554.29	59.63	0.00076	KQESDLLQLQNELEELVQENR
					1341.92	2681.83	2682.38	99.52	7.50E-08	KKQESDLLQLQNELEELVQENR
6	gi|169403947	glyceraldehyde-3-phosphate dehydrogenase [Danio rerio	67	333	1385.73	1384.72	1384.73	62.36	0.0006	GASQNIIPASTGAAK
					787.81	1573.60	1571.83	72.23	6.20E-05	LVIDGHAITVYSER
					882.67	1763.32	1762.80	80.71	8.30E-06	LVTWYDNEFGYSNR
					931.72	1861.42	1860.94	86.98	1.80E-06	SSIFDAGAGIALNDHFVK
					1106.31	2210.60	2210.17	52.13	0.0049	LVIDGHAITVYSERDPANIK
					1116.33	2230.64	2230.08	140.10	7.90E-12	WGDAGATYVVESTGVFTTIEK
					1301.52	2601.03	2599.37	84.74	2.40E-06	VINDNFVIVEGLMSTVHAITATQ
7	gi|163644331	ventricular myosin heavy chain [Danio rerio]	46.1	1938	496.07	990.13	989.50	55.65	0.0033	SNNFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK

					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00023	IQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					748.76	1495.50	1495.73	54.59	0.0032	KIQHELDEAEER
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					823.93	1645.84	1645.82	111.90	6.50E-09	NLTEEMAALDDIIAK
					862.60	1723.19	1721.94	82.68	5.20E-06	VQLLHSQNTSLLNQK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					934.68	1867.34	1867.93	113.91	3.70E-09	DLEEATLQHEATAATLR
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					1959.10	1958.09	1958.94	81.61	6.10E-06	NLQEEISDLTEQLGEGGK
					989.22	1976.43	1976.89	60.09	0.00083	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1099.84	2197.66	2199.12	116.43	1.90E-09	GTLEDQIIQANPALEAFGNAK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
8	gi|18858329	ba1 globin [Danio rerio]	71.6	148	480.10	958.19	957.56	43.70	0.054	TAILGLWGK
					713.32	1424.63	1424.76	73.16	4.70E-05	LNIDEIGPQALSR
					726.09	1450.16	1449.69	79.72	1.00E-05	NTYAALSVMHSEK
					898.71	1795.40	1794.83	122.27	5.50E-10	FGQAGFNADVQEAWQK
					993.19	1984.36	1984.97	87.75	1.50E-06	YFATFGNLSSPAAIMGNPK
9	gi|66472252	slow myosin heavy chain 1 [Danio rerio]	49.7	1938	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					1182.68	1181.67	1179.58	42.70	0.053	DFEISQLNSK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00023	LQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.76	1495.50	1495.73	54.59	0.0032	KLQHELDEAEER
					751.66	1501.31	1499.75	102.78	5.30E-08	LQEAEEAVEAVNAK
					754.50	1506.99	1506.60	38.10	0.15	EEQAEADGTEDADK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					796.88	1591.74	1591.75	40.27	0.091	LSEKDEEMEQAKR
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					852.23	1702.45	1701.82	98.48	1.30E-07	LQNEIEDLMVDVER
					896.44	1790.86	1790.76	78.77	1.30E-05	QREEQAEADGTEDADK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					934.68	1867.34	1867.93	113.91	3.70E-09	DLEEATLQHEATAATLR
					989.22	1976.43	1976.89	60.09	0.00083	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1099.84	2197.66	2199.12	116.43	1.90E-09	GTLEDQIIQANPALEAFGNAK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
10	gi|116325975	ATP synthase, H+ transporting, mitochondrial F1 comple	63	551	820.50	819.49	819.40	36.13	0.29	ISEASDAK
					1197.66	1196.65	1196.64	46.09	0.025	VVDALGNPIDGK
					644.18	1286.34	1286.69	72.39	6.10E-05	HALIIYDDLSK
					651.57	1301.13	1299.74	86.66	2.30E-06	TAIAIDTIINQK
					682.65	1363.29	1362.69	91.50	7.00E-07	TGTAEVSSILEEK
					766.40	1530.79	1530.75	121.91	6.70E-10	ILGADTGAELEETGR
					1625.03	1624.02	1623.88	75.60	2.70E-05	TGAIVDVPVGEELLGR
					1030.06	2058.11	2059.13	80.08	8.20E-06	AFLQHVISQHQDLLAAIR

					1054.00	2105.98	2103.03	59.97	0.00086	GMSLNLEPDNVGVVVFGNDK
					1156.38	2310.75	2308.15	46.53	0.018	QGQYSPMAIEEQVAVIYAGVR
					1183.48	2364.95	2364.17	140.40	7.00E-12	EVAAFAQFGSDLDAATQQLLNR
11	gi|189536979	PREDICTED: similar to slow myosin heavy chain 3 isofor	55	1934	496.07	990.13	989.50	55.65	0.0033	SNNFQKPR
					538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					1182.68	1181.67	1180.57	49.43	0.011	DFEISQLSSR
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					1368.64	1367.63	1367.63	66.26	0.00023	LQHELDEAEER
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					743.81	1485.60	1485.73	96.91	2.00E-07	LQDAEEAVEAVNAK
					748.76	1495.50	1495.73	54.59	0.0032	KLQHELDEAEER
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					754.50	1506.99	1506.60	38.10	0.15	EEQAEADGTEDADK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					796.88	1591.74	1591.75	40.27	0.091	LSEKDEEMEQAKR
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					852.23	1702.45	1701.82	98.48	1.30E-07	LQNEIEDLMVDVER
					859.76	1717.51	1716.90	83.45	4.40E-06	NKDPLNETVVGLYQK
					862.60	1723.19	1721.94	82.68	5.20E-06	VQLLHSQNTSLLNQK
					896.44	1790.86	1790.76	78.77	1.30E-05	QREEQAEADGTEDADK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					948.63	1895.24	1895.90	67.35	0.00016	HADSVSDLGEQIDNLQR
					989.22	1976.43	1976.89	60.09	0.00083	MEGDLNEMEIQLSQANR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
12	gi|29725603	myosin, light polypeptide 7, regulatory [Danio rerio]	59.9	172	639.21	1276.41	1273.67	43.69	0.046	LFDPNATGVVNK
					810.67	1619.33	1617.83	96.66	2.10E-07	LNGTDPEETILAAFK
					1046.59	2091.17	2091.96	85.68	2.30E-06	GSSNVFSMFEQSQIQEFK
					1292.44	2582.87	2582.25	104.64	2.40E-08	FTAEEVDQAFAVAPIDVAGNIDY
13	gi|189540220	PREDICTED: hypothetical protein LOC393472 [Danio re	42.1	1937	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
14	gi|189525553	PREDICTED: hypothetical protein LOC336197 [Danio re	85.1	517	471.62	941.22	940.53	45.28	0.03	VLDTGAPIR
					545.57	1089.13	1087.63	44.02	0.048	VVDLLAPYAK
					693.70	1385.39	1384.70	73.21	5.00E-05	IMNVIGEPIDER
					1407.02	1406.01	1405.67	38.39	0.15	AHGGYSVFAGVGER
					718.44	1434.87	1434.75	96.54	2.20E-07	FTQAGSEVSALLGR
					729.47	1456.93	1456.83	90.05	9.80E-07	TVLIMELINNVAK
					839.54	1677.07	1676.92	99.39	1.10E-07	LVLEVAQHLGENTVR
					916.20	1830.39	1828.88	61.80	0.00061	IMDPNIVGTEHYDVAR
					994.51	1987.01	1987.03	85.08	2.70E-06	AIAELGIYPAVDPLDSTSR

					1004.49	2006.96	2004.05	45.00	0.026	FLSQPFQVAEVFTGHLGK
					688.51	2062.50	2059.99	44.65	0.029	EGNDLYHEMIESGVINLK
					1060.47	2118.93	2118.04	99.97	8.40E-08	SLQDIIAILGMDELSEEDK
					1329.90	2657.78	2658.38	94.91	2.30E-07	SLQDIIAILGMDELSEEDKLTVAR
					1492.02	2982.02	2981.47	59.23	0.00072	SILGGEYDALPEQAFYMVGPIEE
					1239.89	3716.65	3713.88	38.82	0.059	GSITSVQAIYVPADDLTDPAPAT
					1282.42	3844.24	3841.97	68.79	5.60E-05	KGSITSVQAIYVPADDLTDPAPA
15	gi|189520343	PREDICTED: similar to myosin heavy chain fast skeletal	48.5	1933	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					748.77	1495.52	1494.74	53.40	0.0043	KVQHELEEAQER
					752.63	1503.25	1502.76	89.35	1.20E-06	ENQSILITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					825.52	1649.02	1647.78	50.84	0.0082	LEEAGGATSAQIEMNK
					846.53	1691.04	1690.81	65.90	0.00026	NSYEETLDHLETLK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
16	gi|66472732	myosin heavy chain 4 [Danio rerio]	45.7	1935	612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.77	1495.52	1495.73	65.05	0.00029	KVQHELEEAEER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2088.02	75.58	2.30E-05	TKLEQQVDDLEGSLEQEK
					1107.99	2213.97	2213.03	75.84	2.10E-05	AEIQTALEEAEGTLEHEESK
					739.60	2215.76	2216.12	50.27	0.0076	TKLEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
17	gi|189519131	PREDICTED: ns:zf-e68 [Danio rerio]	47.8	1935	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					748.77	1495.52	1495.73	65.05	0.00029	KVQHELEEAEER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1044.14	2086.27	2088.02	75.58	2.30E-05	TKLEQQVDDLEGSLEQEK
					1107.99	2213.97	2213.03	75.84	2.10E-05	AEIQTALEEAEGTLEHEESK
					739.60	2215.76	2216.12	50.27	0.0076	TKLEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK

18	gi|23097290	troponin T2, cardiac [Danio rerio]	29.8	282	718.41	717.40	717.35	38.58	0.21	ELEAEK
					431.68	861.35	861.41	41.02	0.1	KEEEEAK
					580.62	1159.23	1158.57	37.45	0.21	FELQYQFGK
					1217.66	1216.65	1216.66	71.14	9.10E-05	KEEEEIISLK
					674.08	1346.15	1344.75	80.98	8.40E-06	KKEEEEIISLK
					571.64	1711.88	1710.90	63.71	0.00039	RKPLDIDNANESALR
					958.25	1914.48	1913.95	89.43	1.00E-06	DLNELQTLIEAHFESR
19	gi|189540216	PREDICTED: wu:fd14a01 [Danio rerio]	47.3	1936	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLELTLAK
					661.87	1321.73	1320.66	42.87	0.05	KLEDECSELKK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLELTLAK
					745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					817.80	1633.58	1631.78	111.28	7.50E-09	LEEAGGATAAQIEMNK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					942.98	1883.95	1884.92	100.93	7.00E-08	QADSVAELGEQIDNLQR
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
20	gi|55926111	cardiac myosin light chain-1 [Danio rerio]	71.9	196	968.51	967.50	966.55	60.55	0.00083	HVLATLGEK
					757.12	1512.23	1511.69	84.28	3.60E-06	DQGTFEDFVEGLR
					855.80	1709.59	1710.82	89.24	1.10E-06	AKDQGTFEDFVEGLR
					889.86	1777.70	1777.85	80.93	8.10E-06	SVPLDFSPDQIEEFR
					972.94	1943.87	1944.08	94.30	3.10E-07	ALGHNPTNADVLTVLGKPK
					1186.45	2370.88	2370.23	71.44	5.60E-05	KEEAPAPAPVPETPKEPEVDLK
21	gi|66773080	ATP synthase, H+ transporting, mitochondrial F1 comple	80.5	517	471.62	941.22	940.53	45.28	0.03	VLDTGAPIR
					545.57	1089.13	1087.63	44.02	0.048	VVDLLAPYAK
					693.70	1385.39	1384.70	73.21	5.00E-05	IMNVIGEPIDER
					1407.02	1406.01	1405.67	38.39	0.15	AHGGYSVFAGVGER
					718.44	1434.87	1434.75	96.54	2.20E-07	FTQAGSEVSALLGR
					729.47	1456.93	1456.83	90.05	9.80E-07	TVLIMELINNVAK
					839.54	1677.07	1676.92	99.39	1.10E-07	LVLEVAQHLGENTVR
					916.20	1830.39	1828.88	61.80	0.00061	IMDPNIVGTEHYDVAR
					994.51	1987.01	1987.03	85.08	2.70E-06	AIAELGIYPAVDPLDSTSR
					1004.49	2006.96	2004.05	45.00	0.026	FLSQPFQVAEVFTGHLGK
					688.51	2062.50	2059.99	44.65	0.029	EGNDLYHEMIESGVINLK
					1492.02	2982.02	2981.47	59.23	0.00072	SILGGEYDALPEQAFYMVGPIEE
					1239.89	3716.65	3713.88	38.82	0.059	GSITSVQAIYVPADDLTDPAPAT
					1282.42	3844.24	3841.97	68.79	5.60E-05	KGSITSVQAIYVPADDLTDPAPA
22	gi|51592073	actin, alpha, cardiac muscle 1 like [Danio rerio]	59.9	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.94	1953.87	1955.04	84.21	3.20E-06	VAPEEHPTLLTEAPLNPK
					1115.18	2228.34	2227.06	49.56	0.0091	DLYANNVLSGGTTMYPGIADR
					1066.60	3196.78	3195.60	56.69	0.0012	TTGIVLDSGDGVTHNVPIYEGY
23	gi|18858539	desmin [Danio rerio]	49.5	473	544.45	1086.88	1086.57	53.90	0.005	VSDLNQAVNK
					549.51	1097.01	1094.55	50.25	0.01	AELQHLNDR
					591.47	1180.92	1179.55	48.04	0.016	EAGGYQDTIAR
					1254.56	1253.55	1253.56	47.66	0.017	NISEAEDWYK
					642.15	1282.28	1281.59	37.33	0.18	IAELYEEEMR

					889.27	1776.52	1775.91	103.59	4.40E-08	FLEQQNSALTVEIER
					991.08	1980.14	1978.97	91.31	6.40E-07	LDFNLADAINQDFLNTR
					1094.25	2186.48	2186.00	133.47	3.80E-11	TFGSGLGSSIFAGHGSSGSSGS
24	gi|47551317	enolase 3, (beta, muscle) [Danio rerio]	68.1	433	469.64	937.27	937.50	41.97	0.061	HIADLAGNK
					573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					719.58	1437.14	1435.72	86.91	2.00E-06	GNPTVEVDLYTTK
					1053.67	2105.32	2104.07	89.76	9.10E-07	FTGSVDIQVVGDDLTVTNPK
					1060.03	2118.04	2118.12	91.79	5.50E-07	DVILPVPAFNVINGGSHAGNK
					1372.83	2743.65	2742.33	73.97	2.70E-05	DATNVGDEGGFAPNILENNEAL
25	gi|189523697	PREDICTED: im:6911926 [Danio rerio]	47.4	28836	431.68	861.35	860.46	39.18	0.15	KKEEEAK
					701.73	1401.45	1399.71	64.74	0.00035	HVSVEALDFIDR
					763.17	1524.32	1523.73	49.92	0.0097	SDSGVYYLHLENK
					787.63	1573.25	1572.78	78.62	1.40E-05	FGQSGPSEPSGPVVTK
					802.58	1603.15	1602.86	37.57	0.18	YGVSEPLVSQNVIAK
					823.16	1644.31	1642.77	62.59	0.00054	VHGLIEDHEYEFR
					878.68	1755.35	1752.99	47.59	0.016	EAEILKPLASVEVVEK
					885.70	1769.38	1768.91	59.08	0.0011	SSVTLTWVKPAHDGGSK
					894.79	1787.56	1787.83	38.15	0.15	GENKVDVEYDEHINK
					920.77	1839.53	1838.93	62.48	0.00051	STVSLAWEKPLHDGGSR
					923.72	1845.43	1845.01	63.56	0.0004	VQILDKPGPPAGHIEFK
					928.68	1855.35	1854.92	75.30	2.60E-05	TSVSLSWEKPIHDGGSR
					940.54	1879.06	1877.90	56.82	0.0018	VLNYDEEVDDTRPVSK
					950.74	1899.47	1898.91	53.37	0.004	TTVTLSWEKPEHDGGSR
					988.99	1975.96	1976.14	61.35	0.00062	SQLERPGAPLKPVVSGITK
					1002.79	2003.56	2002.96	75.42	2.40E-05	KDNTSDDIGWVTVTSTHK
					1028.44	2054.86	2055.07	95.10	2.60E-07	LKGDVLSASPDVEIIEDGAK
					1033.83	2065.64	2064.06	76.98	1.70E-05	VISGVQDLEYTVTDVIEGK
					1047.32	2092.62	2092.08	64.74	0.00028	INVSALNSEGVGEAAPVPGSPK
					1073.03	2144.05	2142.23	51.74	0.0055	SFHVQVITLGPPSKPIGPIR
					757.52	2269.52	2270.33	62.36	0.00047	KSFHVQVITLGPPSKPIGPIR
					1258.48	2514.94	2514.23	83.61	3.10E-06	HTLPVDSDISSSDTTSVVTIPES
					1326.96	2651.91	2651.51	61.01	0.00053	KKPTLPATILTKPQSLTVSEGES
					902.92	2705.72	2706.41	50.47	0.0061	TPVLAVDPVEKPGEPENFQITEI
					966.81	2897.40	2895.47	44.42	0.022	RLDIIDTTDTSVTLAWLKPEHDG
26	gi|189523699	PREDICTED: titin a [Danio rerio]	47.9	32757	824.59	823.58	822.50	52.54	0.0049	VHIVIDK
					511.18	1020.34	1019.54	37.43	0.21	ITDQYRPK
					567.76	1133.51	1133.57	64.96	0.00036	KGDVTLSDSGR
					705.08	1408.14	1407.69	57.46	0.0017	TDDKFEVLQEGK
					749.20	1496.39	1495.81	47.75	0.016	KFDNLFFIEVPK
					781.54	1561.07	1560.75	40.14	0.095	EHSEVIPHTQQEK
					819.76	1637.51	1636.89	41.42	0.068	VEIPDIELPDELKK
					878.68	1755.35	1752.99	47.59	0.016	EAEILKPLASVEVVEK
					907.31	1812.60	1811.95	45.44	0.026	IGVGETADIPGSVIIEDK
					908.46	1814.91	1812.91	55.97	0.0023	ASQAPSAPDDLIVTDVSK
					926.82	1851.63	1850.96	67.65	0.00015	STVILGWEKPLHDGGSR
					623.27	1866.79	1866.98	62.77	0.00048	RRDEEAPTQIVPDITK
					940.78	1879.54	1878.92	96.56	1.90E-07	TPLHDGGAEVSHYIVER
					947.81	1893.61	1892.90	71.72	5.80E-05	HTVTLSWEKPDHDGGSK
					962.72	1923.43	1922.99	53.01	0.0043	AVNAAGVGEPGEVADVIEVK
					976.57	1951.13	1950.02	85.98	2.10E-06	SSDIVQISSTPTSSTLSIK
					1029.44	2056.87	2056.09	59.01	0.001	ELPISFVTPLADVHVYEK
					1052.34	2102.66	2102.05	88.77	1.10E-06	EQVTHQAALLQSHEVQER

					1060.46	2118.90	2118.12	44.96	0.027	ASIEITPSFTTLLIENVDR
					1062.63	2123.25	2122.13	56.57	0.0018	VLDRPGPSSGPLDITGLTAEK
					1080.01	2158.01	2157.24	74.26	3.10E-05	KVPAKPVEAITVPTEEPPKK
					734.17	2199.49	2199.29	49.32	0.01	KEPKPESILQVISTPVPLPK
					1114.26	2226.51	2226.10	51.16	0.0064	EHVIIEWFKPENDGGSEIK
					1133.89	2265.77	2265.23	56.10	0.002	KEQHKPVVLSVNETTQTLSK
					1137.55	2273.09	2271.31	36.90	0.16	VEIQDKPLLPEGPVVVDALLK
					1151.39	2300.76	2300.07	97.12	1.50E-07	EVTSNSVTLSWEKPDHDGGSR
					890.21	2667.59	2665.41	37.44	0.12	KPLNPSENVIIENTESYTHLVIR
					1682.58	5044.72	5042.61	49.40	0.0026	HQLQADQSSLIPGLDSAISVQPL
27	gi|38707983	aconitase 2, mitochondrial [Danio rerio]	59	782	854.52	853.51	853.47	42.30	0.051	IHETNLK
					1160.53	1159.52	1159.57	47.24	0.022	GEIATLADENK
					1362.65	1361.64	1361.61	50.84	0.0084	FEPSSYINYDK
					786.32	1570.62	1568.82	42.98	0.051	FKLEPPTGDELPAR
					1695.86	1694.85	1694.78	63.98	0.00039	FNPETDYLTAPNGEK
					878.21	1754.41	1752.88	63.36	0.00043	IVYGHLDDPAGQEIAR
					890.24	1778.47	1777.89	41.25	0.074	QGLLPLTFSNPADYDK
					1041.78	2081.55	2080.94	106.96	1.70E-08	NNISWVVVGDENYGEGSSR
					1080.47	2158.92	2157.96	40.01	0.084	DFDPGQDTYQHPPADGSALK
					1267.12	2532.23	2532.29	157.81	1.20E-13	GHLDNISNNLLIGAVNIENDGVN
					908.79	2723.34	2721.43	56.50	0.0015	NDANPATHAFVTSPEIVTALAIA
28	gi|66792936	tropomyosin 4 isoform 1 [Danio rerio]	62.7	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENAIDR
					586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					628.87	1255.73	1256.66	64.85	0.00035	QLDDELVGLQK
					637.15	1272.29	1271.61	72.43	6.20E-05	AADAEGDVAALNR
					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
					700.72	1399.42	1399.71	107.10	1.90E-08	KAADAEGDVAALNR
					770.15	1538.28	1537.71	100.31	8.70E-08	SIDDLEDELYAQK
					700.72	2099.13	2099.09	80.39	7.70E-06	LELSEKKAADAEGDVAALNR
					747.65	2239.92	2239.05	56.88	0.0017	QTEDELDKYSEALKDAQEK
					770.15	2307.42	2307.18	54.59	0.0027	TVAKLEKSIDDLEDELYAQK
29	gi|189537429	PREDICTED: hypothetical protein [Danio rerio]	51.2	377	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1129.54	50.00	0.012	GYSFVTTAER
					1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
					977.46	1952.91	1953.06	79.89	8.60E-06	VAPEEHPVLLTEAPLNPK
30	gi|18858961	lactate dehydrogenase B4 [Danio rerio]	55.4	334	474.55	947.09	946.60	38.80	0.16	HIIPQIVK
					1205.61	1204.60	1204.61	48.45	0.016	SSADTLWGIQK
					628.45	1254.88	1252.64	54.64	0.0036	MVVDSAYEVIK
					769.60	1537.18	1537.77	108.51	1.30E-08	IVADKDYSVTANSR
					844.16	1686.31	1684.85	113.65	4.30E-09	ELADELALVDVVEDR
					857.97	1713.92	1714.82	40.76	0.079	LNPDIGTDKDAENWK
					1075.64	2149.27	2150.13	38.31	0.12	GYTNWAIGLSVADLTETLVK
31	gi|125829449	PREDICTED: similar to myosin heavy chain [Danio rerio]	43.2	1945	538.17	1074.32	1073.54	42.91	0.063	ADIAESQVNK
					609.71	1217.41	1215.63	70.03	0.00011	AGLLGQLEEMR
					623.38	1244.75	1244.65	82.73	6.20E-06	DIDDLEITLAK
					687.67	1373.32	1372.74	51.55	0.0072	KDIDDLEITLAK
					504.06	1509.15	1507.70	37.65	0.16	SDSSKELEELSER
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					825.52	1649.02	1647.78	50.84	0.0082	LEEAGGATSAQIEMNK

					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
					1107.99	2213.97	2213.03	64.44	0.00029	TEIQAALEEAEGTLEHEESK
32	gi|41054651	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Dan	57.9	449	588.63	1175.24	1174.60	50.29	0.011	ATDFVVNQPGK
					677.67	1353.33	1354.68	79.89	9.80E-06	TIEAEAAHGTVTR
					716.14	1430.27	1428.73	81.19	7.70E-06	FKDIFQDIFEK
					861.03	1720.05	1719.82	124.78	3.30E-10	DQTDDQVTIDSAIATK
					947.29	1892.57	1891.93	67.72	0.00015	LNEHYVNTTDFLDAIK
33	gi|41053595	nucleoside diphosphate kinase-Z2 [Danio rerio]	90.2	153	1099.60	1098.59	1098.53	48.38	0.016	NLIHGSDSEK
					1100.63	1099.62	1098.53	52.09	0.0074	NLIHGSDSEK
					974.87	1947.73	1949.07	126.73	1.80E-10	GFRLVAAKFVQASEDLAK
					1106.96	2211.90	2211.12	85.26	2.40E-06	SAATEVSLWFKPEELVSYR
34	gi|47085883	hypothetical protein LOC406405 [Danio rerio]	88.7	337	465.05	928.09	927.46	41.82	0.074	HGVYNPNK
					537.92	1073.83	1072.58	43.90	0.05	IQEAGTEVVK
					661.60	1321.18	1319.67	86.06	2.50E-06	GYIGADQLGDALK
					728.21	1454.40	1453.70	37.29	0.18	AGAGSATLSMAYAGAR
					751.99	1501.97	1502.77	100.04	1.00E-07	VEFPADQLSALTGR
					1544.85	3087.69	3088.58	95.05	1.90E-07	NSPLVSELSLFDIAHTPGVAADL
35	gi|41054601	voltage-dependent anion channel 2 [Danio rerio]	62.2	283	588.19	1174.36	1173.56	42.41	0.068	SEYGLTFTEK
					665.84	1329.67	1329.66	41.35	0.077	RSEYGLTFTEK
					779.53	1557.05	1555.79	43.02	0.05	LTFDTTFSPNTGKK
					1051.96	2101.91	2102.15	84.24	3.20E-06	VNNTSLVGVGYTQSLRPGIK
					1088.43	2174.84	2174.05	117.04	1.60E-09	WNTDNTLGTEINIEDQIAK
36	gi|148596963	spectrin alpha 2 [Danio rerio]	45.1	2480	625.55	1249.08	1246.55	45.75	0.029	GEIDAHEDSFK
					773.69	1545.36	1544.77	82.66	5.60E-06	HALLEADVAAHQDR
					787.68	1573.34	1571.78	67.18	0.0002	HQALQAEISGHEPR
					537.25	1608.71	1607.74	39.91	0.098	HQAFEAELHANADR
					851.20	1700.38	1699.88	108.80	1.20E-08	KHQALQAEISGHEPR
					862.42	1722.82	1720.86	58.01	0.0015	LIQSHPEAVDDIQEK
					925.80	1849.59	1848.86	86.05	2.20E-06	KFEEFQTDLAAHEER
					1010.84	2019.66	2018.99	60.19	0.00082	LQIASDENYKDPSNLQGK
					1077.78	2153.55	2153.10	88.67	1.10E-06	ALINADELANDVAGAEALLDR
					1108.81	2215.60	2215.12	41.10	0.063	RDELITNWEQIQTLATER
					740.44	2218.30	2219.18	48.35	0.012	LEAELGAHEPAIQSVLETGKK
					1110.70	2219.39	2219.03	79.75	8.50E-06	STDEAGQALLNTGHYASEEVK
					792.49	2374.44	2375.28	66.34	0.00018	RLEAELGAHEPAIQSVLETGKK
					1246.00	2489.99	2489.22	66.52	0.00016	EKEPIVGSPDYGKDEDSAEALL
37	gi|18858335	bactin1 [Danio rerio]	55.5	375	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1131.52	37.35	0.22	GYSFTTTAER
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					895.41	1788.80	1789.88	109.38	1.10E-08	SYELPDGQVITIGNER
38	gi|189535893	PREDICTED: similar to myosin heavy chain [Danio rerio]	39	1938	612.98	1223.95	1223.61	40.18	0.093	TKYETDAIQR
					623.38	1244.75	1244.65	82.73	6.20E-06	DLDDLEITLAK
					687.67	1373.32	1372.74	51.55	0.0072	KDLDDLEITLAK
					761.65	1521.28	1520.76	81.03	7.70E-06	AITDAAMMAEELKK
					931.71	1861.40	1858.88	102.14	5.50E-08	LEQQVDDLEGSLEQEK
					994.44	1986.87	1986.97	82.62	4.70E-06	LEQQVDDLEGSLEQEKK
39	gi|18858587	elongation factor 1-alpha [Danio rerio]	53.5	462	766.50	765.49	765.39	39.76	0.091	FEEITK
					794.93	1587.84	1587.87	74.02	4.00E-05	THINIVVIGHVDSGK
					974.39	2920.14	2917.55	69.01	7.70E-05	EGNASGTTLLDALDAILPPSRPT
					1016.88	3047.61	3045.65	53.55	0.0026	KEGNASGTTLLDALDAILPPSRP
40	gi|47086807	acyl-Coenzyme A dehydrogenase, very long chain [Dani	50.7	659	837.23	1672.45	1671.94	109.89	9.80E-09	AIEQFGAVIEELLLK

41	gi|162287365	hemopexin [Danio rerio]	43.8	447	1211.60	1210.59	1210.61	42.67	0.054	GHHFLSITGDK
					1339.66	1338.65	1338.61	63.11	0.00047	FHSDTIESEFK
					900.94	1799.87	1800.00	65.94	0.00024	VGKPHTHLEGYPKPLK
					721.15	2160.41	2159.07	59.48	0.00093	GKPGGEGHKHELHHGAQLDR
42	gi|40786398	pyruvate kinase, muscle, a [Danio rerio]	49.6	532	587.69	1173.36	1170.61	37.35	0.22	GDLGIEIPTEK
					820.11	1638.21	1635.88	86.12	2.30E-06	GVNLPGAAVDLPAVSEK
					882.32	1762.62	1763.98	104.58	3.40E-08	KGVNLPGAAVDLPAVSEK
					1286.58	2571.15	2569.21	90.02	7.00E-07	GIFPIYYNSPSNDVWAEDVDLR
43	gi|47085773	glutamic-oxaloacetic transaminase 1, soluble [Danio reric	51.2	410	538.75	1075.48	1075.61	66.82	0.00025	KVNLGVGAYR
					1113.61	1112.60	1112.61	43.19	0.053	IALGEDSPAIK
					845.28	1688.54	1687.84	84.95	3.20E-06	NIDYVAESIHEAVTK
					1114.87	2227.73	2226.03	124.06	3.30E-10	NLFAFFDSAYQGFASGDLEK
					861.05	2580.13	2579.28	45.87	0.018	MIADDHSLNHEYLPILGLPEFR
44	gi|189529246	PREDICTED: hypothetical protein [Danio rerio]	71.4	119	529.66	1057.30	1056.56	77.57	2.10E-05	VAENVQELR
					599.58	1197.14	1195.75	45.88	0.027	AKLEPVVLSLK
					1050.75	2099.49	2100.09	79.52	9.40E-06	ELTELGEQVKPHFEGIFK
					743.41	2227.20	2228.18	62.96	0.00042	KELTELGEQVKPHFEGIFK
45	gi|48762657	enolase 1, (alpha) [Danio rerio]	67.6	432	573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					1504.37	3006.73	3006.57	90.04	6.00E-07	HIADLAGNPDVILPVPAFNVING(
46	gi|18858427	creatine kinase, muscle a [Danio rerio]	37	381	589.71	1177.41	1175.58	37.81	0.19	DLFDPVISDR
					755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
					836.18	1670.35	1670.77	59.49	0.001	LNYSVDEEYPDLSK
					999.00	1995.98	1993.93	93.47	3.80E-07	GTGGVDTASVGGVFDISNADR
					1077.13	2152.25	2150.04	41.65	0.058	RGTGGVDTASVGGVFDISNADF
47	gi|66773050	myosin, heavy polypeptide 11, smooth muscle [Danio rer	43.3	1974	864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
					586.03	1755.05	1753.87	55.57	0.0026	KQELEEILHEMEAR
					1000.03	1998.04	1997.92	75.62	2.30E-05	ELEGHISDLQEDLESER
					1007.31	2012.60	2012.04	100.39	7.70E-08	TLEAELLQLQEDLAAAER
					1066.77	2131.52	2131.00	43.65	0.037	QVEAERDELADELASNASGK
					1131.02	2260.02	2259.10	76.40	1.90E-05	KQVEAERDELADELASNASGK
					895.73	2684.15	2682.37	52.91	0.0034	KLEAESNDLQEQIADLQAQIADL
48	gi|41054435	hypothetical protein LOC324244 [Danio rerio]	28.6	248	586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					638.09	1274.16	1271.65	65.71	0.00029	EKAEGDVAALNR
					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
49	gi|189517521	PREDICTED: hypothetical protein [Danio rerio]	64.3	143	589.05	1176.08	1173.64	42.73	0.061	IVMGAITDAVGK
					767.47	1532.93	1532.73	89.40	1.10E-06	IASQADSIGQEAMGR
					1869.06	1868.05	1867.99	101.03	7.00E-08	IDDLLGALSSLSDLHATK
					978.64	1955.26	1954.97	58.28	0.0013	IYFAHWPDHSLGSAQVK
50	gi|31044489	heat shock 60 kD protein 1 [Danio rerio]	54.4	575	602.58	1203.14	1200.63	46.52	0.025	NAGVEGSLVVEK
					984.90	1967.78	1967.90	75.41	2.50E-05	VNEIAEQLESTNSDYEK
					943.10	2826.27	2825.53	118.08	9.90E-10	TALLDAAGVASLLSTAEAVVTEII
51	gi|38488731	natriuretic peptide precursor A [Danio rerio]	93.4	106	1026.57	2051.12	2049.99	90.71	7.10E-07	SLLQQFEEALATEEASER
					1182.38	2362.75	2362.99	76.85	1.60E-05	DREEAAAPGEDSNPSDGFDTQI
					1248.96	2495.90	2495.11	43.62	0.03	AVDYEDSNTVLEQSPPSTSWDF
52	gi|50344894	tropomyosin 2 (beta) [Danio rerio]	50.7	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENAIDR
					586.09	1170.17	1169.67	73.35	5.00E-05	LVILEGELER
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					651.07	1300.13	1297.76	59.34	0.0012	KLVILEGELER
					708.64	1415.26	1415.73	37.18	0.2	DAQEKLEQAEKK
53	gi|157787181	creatine kinase CKM3 [Danio rerio]	46.1	380	755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
					999.00	1995.98	1993.93	93.47	3.80E-07	GTGGVDTASVGGVFDISNADR

					1077.13	2152.25	2150.04	41.65	0.058	RGTGGVDTASVGGVFDISNADF
54	gi|47086021	aldolase a, fructose-bisphosphate, b [Danio rerio]	48.6	364	660.17	1318.33	1317.68	104.23	4.00E-08	GILAADESTGSVAK
					776.51	1551.00	1550.70	71.66	6.60E-05	FQSINAENTEENR
					932.72	1863.42	1862.90	38.48	0.13	RFQSINAENTEENRR
					1055.50	2108.98	2107.16	65.57	0.00023	ITPTTPSNLAIIENANVLAR
					1175.04	2348.06	2347.17	73.65	3.30E-05	GVVPLAGTNGETTTQGLDGLYE
55	gi|117606264	sarcalumenin [Danio rerio]	45.2	482	869.43	1736.85	1735.95	50.99	0.0076	AITHELPSLLGSINSGK
					1036.37	2070.72	2069.08	87.62	1.50E-06	REEISLLEDLNQVIENR
56	gi|47086523	ictacalcin [Danio rerio]	62.1	95	696.65	1391.29	1390.73	90.39	9.70E-07	ELLSAELGDIFGK
57	gi|50344790	hypothetical protein LOC415158 [Danio rerio]	61.5	104	608.49	1214.96	1214.66	57.95	0.0019	VGPNLWGLFGR
					744.56	1487.11	1487.65	83.55	4.50E-06	TGQAEGFSYTDANK
					808.82	1615.63	1615.75	107.78	1.60E-08	KTGQAEGFSYTDANK
					1061.98	2121.94	2121.05	45.63	0.022	GIVWGEDTLMEYLENPKK
58	gi|40538764	ceruloplasmin [Danio rerio]	30.7	1087	806.08	1610.15	1609.72	91.54	6.70E-07	SVNKEDADFQESNK
					828.99	1655.97	1654.78	85.47	2.70E-06	LVDDIVSDTFFDNR
					859.48	2575.40	2573.23	60.57	0.00061	VSWHLSGLGSETDIHGLYFEGN
59	gi|189535920	PREDICTED: similar to Filamin-A (Alpha-filamin) (Filamir	51.5	2523	823.47	1644.92	1645.89	81.60	6.80E-06	VHGPGLQSGITNKPNK
					886.49	1770.96	1770.93	63.28	0.00044	SGVELNKPTHFTVNTK
					901.26	1800.50	1799.96	62.58	0.00052	VAKPDITDNKDGTVTVK
					1115.87	2229.73	2228.05	63.53	0.00036	DGSSGVSYIVQEPGDYEVSIK
					1206.85	2411.68	2411.15	89.21	9.10E-07	EGPYSINVLYADEEIPQSPYK
60	gi|41282154	aldolase a, fructose-bisphosphate [Danio rerio]	45.3	364	660.17	1318.33	1317.68	104.23	4.00E-08	GILAADESTGSVAK
					1427.77	1426.76	1426.72	45.39	0.028	PHAYPFLTPEQK
					776.51	1551.00	1550.70	71.66	6.60E-05	FQSINAENTEENR
					932.72	1863.42	1862.90	38.48	0.13	RFQSINAENTEENRR
					1175.04	2348.06	2347.17	73.65	3.30E-05	GVVPLAGTNGETTTQGLDGLYE
61	gi|41393131	dihydrolipoamide S-succinyltransferase [Danio rerio]	38.4	458	1075.38	2148.75	2147.07	114.26	3.20E-09	AAAYALTDQPAVNAVIDDTTK
62	gi|41152342	creatine kinase, mitochondrial 2 (sarcomeric) [Danio reric	37.3	413	1040.87	2079.72	2079.97	91.39	6.20E-07	GTGGVDTAAVGDTFDISNLDR
					1119.31	2236.61	2236.07	52.22	0.0048	RGTGGVDTAAVGDTFDISNLDR
63	gi|41054193	hypothetical protein LOC327506 [Danio rerio]	51.1	178	1040.87	2079.72	2079.97	91.39	6.20E-07	GTGGVDTAAVGDTFDISNLDR
					1119.31	2236.61	2236.07	52.22	0.0048	RGTGGVDTAAVGDTFDISNLDR
64	gi|41053939	malate dehydrogenase 1a, NAD (soluble) [Danio rerio]	50.2	305	662.59	1323.17	1320.67	70.62	8.50E-05	VVDGLSINDFSR
					730.42	1458.82	1459.79	53.60	0.0044	EVIPTDKVEVGFK
					878.99	2633.93	2631.29	81.11	5.40E-06	NVTIWGNHSSTQYPDVHHAIVTI
65	gi|18858959	lactate dehydrogenase A4 [Danio rerio]	46.8	333	596.12	1190.22	1188.61	84.43	4.20E-06	VIGSGTNLDSAR
					628.45	1254.88	1252.64	54.64	0.0036	MVVDSAYEVIK
					756.18	1510.35	1509.77	73.74	4.00E-05	IVADKDYSVTANSK
66	gi|47086069	hypothetical protein LOC406529 [Danio rerio]	48.8	283	930.98	1859.95	1858.82	94.89	2.90E-07	SQSGVEFTTGGSSNTDTGK
					1030.85	2059.68	2058.12	82.00	5.30E-06	VNNASLVGVGYTQSLRPGVK
67	gi|50539808	hypothetical protein LOC436647 [Danio rerio]	48.4	525	908.92	1815.83	1815.92	76.41	2.10E-05	ENTLNQLVGAAFGAAGQR
					967.82	1933.62	1932.99	63.67	0.00037	VNAGDQPGADVGPLISPQAK
					1005.87	2009.73	2009.00	85.54	2.30E-06	SSQWLDIHNPATSEVIGR
68	gi|47087061	glutamic-oxaloacetic transaminase 2a, mitochondrial (asp	58.9	428	555.50	1108.99	1107.59	39.28	0.12	KMNLGVGAYR
					705.68	1409.35	1408.72	46.27	0.023	EYLPIGGLADFSK
					724.76	1447.51	1445.81	72.14	6.30E-05	IAATILNTPELYK
					946.71	1891.41	1893.02	95.60	2.50E-07	KLDKEYLPIGGLADFSK
					666.36	1996.04	1994.03	36.92	0.17	YFIEQGHNILLSQSFAK
					784.38	2350.11	2350.26	58.13	0.0012	ISVAGVTSANVEYLAHAIHAVTK
69	gi|68362804	PREDICTED: similar to Histone H4 replacement CG3379	68.9	103	1134.59	1133.58	1133.54	39.08	0.14	DAVTYTEHAK
					591.69	1181.36	1179.61	63.27	0.00048	ISGLIYEETR
					657.23	1312.44	1309.70	58.02	0.0016	TVTAMDVVYALK
					664.19	1326.36	1324.75	43.50	0.045	DNIQGITKPAIR

70	gi|41053873	succinate dehydrogenase complex, subunit A, flavoprotei	52.2	661	666.56	1331.11	1329.65	45.28	0.031	GEGGILINSEGER
					1474.80	1473.79	1473.75	85.53	2.80E-06	KHTLSYVDPETGK
					1055.70	2109.39	2109.13	43.11	0.041	DHVHLQLHHLPPQQLAAR
					861.14	2580.40	2582.14	47.38	0.013	DGQDHVVPGLYACGEAGCASV
					888.17	2661.47	2662.42	60.65	0.0006	GVGPDKDHVHLQLHHLPPQQL
71	gi|58801524	LIM domain containing preferred translocation partner in	51.4	556	1097.90	2193.79	2193.06	52.39	0.0047	AEPSHHPAPTPSQGYQPAPPK
					1397.62	2793.23	2793.39	108.68	9.10E-09	SSLDAEIDSLTSILADLESSSPYK
72	gi|23308625	fatty acid binding protein 3, muscle and heart [Danio reri	76.7	133	749.12	1496.23	1496.63	92.69	5.10E-07	LGEEFDETTADDR
					813.60	1625.18	1624.72	56.89	0.002	LGEEFDETTADDRK
					1081.42	2160.82	2160.13	62.50	0.00047	EVSDNNLTLTLTLGDIVSTR
73	gi|189516653	PREDICTED: myosin, heavy chain 9, non-muscle like-1,	39.2	1754	569.07	1136.13	1135.60	36.18	0.25	VLQEQGTHPK
					613.09	1224.17	1222.63	64.72	0.00033	AGVLAHLEEER
					575.27	1722.79	1721.89	60.94	0.00079	KQELEEILHDLEAR
					864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
					893.88	2678.62	2678.38	79.43	7.80E-06	KLEGDSTELHDQIAELQAQIAEL
74	gi|66773138	cytochrome c oxidase subunit Vaa [Danio rerio]	95	141	487.46	972.90	972.52	66.23	0.0003	LDDLASAIR
					487.46	1459.36	1458.77	41.65	0.069	ACRRLDDLASAIR
					1659.34	3316.67	3313.73	65.34	0.00016	EIYPYVIQELRPTLDELGIATPEE
					1694.78	3387.54	3384.77	59.62	0.00055	EIYPYVIQELRPTLDELGIATPEE
75	gi|189535578	PREDICTED: fetuin B [Danio rerio]	45	498	1053.80	2105.59	2104.92	74.74	2.90E-05	DETHEHDHEIVLDHDHK
					1117.31	2232.61	2233.01	77.52	1.40E-05	KDETHEHDHEIVLDHDHK
					797.00	2387.96	2389.01	42.38	0.043	AHEHGQDEWEHQHHQYGHK
76	gi|41055718	fumarate hydratase precursor [Danio rerio]	52.7	509	829.24	1656.46	1655.84	48.58	0.013	LGSKDPVHPNDHVNK
					719.09	2154.25	2153.18	65.75	0.00022	EVHEVLLPGLQTLHDALAAK
					1251.94	2501.87	2501.26	85.96	1.80E-06	THTQDAVPLSLGQEFGGYVQQ
77	gi|47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]	42.6	1079	1270.68	1269.67	1269.68	49.62	0.011	SLGAEPLEVDIK
					707.79	1413.56	1412.74	41.33	0.073	GVIHVGYTDIPSR
					789.81	1577.60	1577.77	66.87	0.0002	QGFNVVVESGAGESAK
					922.62	2764.83	2763.39	72.03	4.20E-05	DGSVVVDLAAEAGGNIETTVPG
78	gi|57222259	talin 1 [Danio rerio]	50.5	2538	1526.50	3050.98	3050.51	110.47	5.30E-09	GTEWVDPEDPTVIAENELLGAA
					1588.48	3174.95	3174.57	84.08	2.30E-06	EAVDDLGSTLAEVASAAGAVGG
79	gi|18858281	apolipoprotein A-I [Danio rerio]	54.2	262	585.45	1168.88	1166.55	57.61	0.0018	AFESNIEETK
					822.74	1643.47	1643.73	81.96	6.20E-06	ALDNLDGTDYEQYK
					912.03	1822.04	1821.93	58.57	0.0013	EKLEPVFQEYSALNR
					1580.96	3159.90	3159.53	45.88	0.015	LQEYAQTTSQALTPYAETISTQL
80	gi|56693297	hypothetical protein LOC494070 [Danio rerio]	66.5	182	952.64	1903.26	1902.91	92.17	5.30E-07	AKEELEQELADKEDEK
81	gi|56090150	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Dani	49.5	731	805.71	1609.40	1607.78	75.77	2.50E-05	FASEVAGVEDLGTTGR
					1571.20	3140.38	3139.56	89.52	6.30E-07	DSFIVYQGHHGDVGAPIADVILP
82	gi|189517523	PREDICTED: hypothetical protein [Danio rerio]	97.3	147	1060.96	1059.95	1060.52	40.46	0.11	LNVDPDNFK
					714.17	1426.32	1424.76	90.93	7.90E-07	INVDEIGPQTLAR
83	gi|47777298	inner membrane protein, mitochondrial (mitofilin) [Danio r	46.4	757	740.20	1478.39	1478.76	78.83	1.30E-05	IVSQYSELVNEAK
					978.64	1955.26	1955.09	67.25	0.00016	KPETVKPLQISSLSEATK
					1065.82	2129.63	2130.11	49.26	0.01	AELDALAALTAGLEETLGSSAK
84	gi|189522028	PREDICTED: similar to myomesin [Danio rerio]	64	923	1508.67	1507.66	1507.73	82.72	5.10E-06	FKGEFDESLPSPR
					1259.63	3775.87	3772.95	53.75	0.0018	GASAPWTGQIIVTEEEPVEGVV
					1301.49	3901.45	3901.05	67.56	7.10E-05	KGASAPWTGQIIVTEEEPVEGV
85	gi|41055728	ATPase, Ca++ transporting, cardiac muscle, slow twitch	45.5	996	1072.60	1071.59	1071.56	41.86	0.08	NAENAIEALK
					732.73	1463.44	1463.67	45.15	0.03	IRDEMASTEQER
					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
86	gi|71892474	ATPase, Ca++ transporting, cardiac muscle, slow twitch	41.4	1035	1072.60	1071.59	1071.56	41.86	0.08	NAENAIEALK
					732.73	1463.44	1463.67	45.15	0.03	IRDEMASTEQER

					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
87	gi|189530625	PREDICTED: similar to spectrin repeat containing, nucle	37.3	8621	550.57	1099.13	1097.66	68.83	0.00015	QLADAIAKLR
88	gi|113195582	hypothetical protein LOC556489 [Danio rerio]	54.4	226	724.23	1446.44	1445.78	47.73	0.017	VIFEAETEKPGVK
					881.46	2641.36	2641.29	69.67	7.40E-05	SPDPAAVEHKPEESKPEESKPE
					1421.57	2841.12	2840.42	49.82	0.0068	AKSPDPAAVEHKPEESKPEESK
89	gi|47271422	triosephosphate isomerase 1b [Danio rerio]	78.6	248	695.75	1389.49	1388.71	69.76	0.00011	SIEELANTLNSAK
					1458.82	1457.81	1457.72	75.26	3.00E-05	HVFGESDELIGQK
					808.43	1614.84	1613.82	57.16	0.0019	RHVFGESDELIGQK
					812.06	2433.15	2431.30	52.48	0.0041	DLDGFLVGGASLKPEFIDIINAK
90	gi|68433600	PREDICTED: similar to LOC495046 protein isoform 1 [Da	35.9	1056	1072.60	1071.59	1071.56	41.86	0.08	NAENAIEALK
					1525.55	1524.54	1524.80	83.44	4.30E-06	DIVPGDIVEVAVGDK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVLK
91	gi|50540358	hypothetical protein LOC436918 [Danio rerio]	51.5	357	1252.70	1251.69	1251.62	69.12	0.00012	LHAVNDAEVER
					1111.50	2220.99	2220.13	92.38	4.70E-07	NAITVEMYNELIEALELAGK
92	gi|41152400	peptidylprolyl isomerase A, like [Danio rerio]	70.7	164	686.63	1371.24	1370.73	82.70	5.50E-06	VVDGLDVVDAIEK
93	gi|52219194	fatty acid binding protein 11 [Danio rerio]	50	134	769.06	1536.10	1535.67	89.09	1.20E-06	LNEPFEETTADDR
					833.41	1664.80	1663.77	68.69	0.00013	LNEPFEETTADDRK
94	gi|114326248	elastin b [Danio rerio]	22.3	2054	880.55	1759.08	1759.92	38.98	0.12	SYGGAGSLGAGGILPGTGIR
					887.73	1773.45	1772.86	55.25	0.0029	SYGGAGALGGAGQGGIGGGPG
					1647.81	4940.40	4937.47	122.27	1.50E-10	LGVGPGGAGGIGGGLGVGPGG
95	gi|40254659	bactin2 [Danio rerio]	53.3	375	489.44	976.86	975.44	48.58	0.016	AGFAGDDAPR
					566.61	1131.20	1131.52	37.35	0.22	GYSFTTTAER
					600.12	1198.22	1197.70	43.75	0.045	AVFPSIVGRPR
					977.46	1952.91	1953.06	79.89	8.60E-06	VAPEEHPVLLTEAPLNPK
96	gi|51571925	hypothetical protein LOC445486 [Danio rerio]	42.3	194	902.32	1802.62	1800.95	39.68	0.1	INSELPVDEVFAIVEK
					966.43	1930.84	1929.05	82.64	4.70E-06	KINSELPVDEVFAIVEK
97	gi|71834286	hypothetical protein LOC321166 [Danio rerio]	40.3	3730	638.85	1275.69	1273.71	40.14	0.11	SKVEEILSELK
					967.82	1933.62	1931.96	84.94	2.80E-06	TLHLDDSIDSVHPIQDK
					1036.40	3106.17	3105.49	46.59	0.013	YDAEEIEAEVSSDVTTEIHNIITT
98	gi|50540008	zgc:92882 [Danio rerio]	45.2	334	474.55	947.09	946.60	38.80	0.16	HIIPQIVK
					596.12	1190.22	1188.61	84.43	4.20E-06	VIGSGTNLDSAR
99	gi|189537196	PREDICTED: similar to L-lactate dehydrogenase B chain	33.7	285	474.55	947.09	946.60	38.80	0.16	
					596.12	1190.22	1188.61	84.43	4.20E-06	
100	gi|189520789	PREDICTED: si:ch211-239j9.2 [Danio rerio]	68.4	76	675.31	1348.61	1348.63	71.30	7.50E-05	EAGIFESARPSGE
					787.29	1572.56	1571.68	64.31	0.00038	AYADFYTQYDSTK
101	gi|136429	Trypsin precursor	75.4	232	737.53	2209.57	2210.10	85.13	2.50E-06	LGEHNIDVLEGNEQFINAAK
102	gi|160333682	heat shock protein 8 [Danio rerio]	50.8	649	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
					847.03	1692.05	1690.72	44.48	0.035	STAGDTHLGGEDFDNR
					575.34	1722.98	1722.86	38.67	0.13	HWPFNVINDNSRPK
					887.36	1772.70	1772.81	39.80	0.1	NQTAEREEFEHQQK
					1131.58	2261.14	2259.14	47.52	0.014	SINPDEAVAYGAAVQAAILSGD
103	gi|166795887	vitellogenin 1 [Danio rerio]	42.6	1362	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					644.61	1287.21	1286.66	65.73	0.00029	AEAGVLGEFPAAR
					692.52	1383.03	1381.78	54.77	0.0034	ISDAPAQIVEVLK
104	gi|47086247	proto galectin Gal1-L2 [Danio rerio]	32.1	134	892.64	2674.90	2675.32	93.26	3.20E-07	ITFTNEEFLVTLPDGSEIHFPNR
105	gi|50345022	small muscle protein, X-linked [Danio rerio]	61.4	83	1037.75	2073.48	2072.97	83.71	3.70E-06	REDTVETEEVSPVTPEEK
					1115.86	2229.71	2229.08	60.21	0.00078	RREDTVETEEVSPVTPEEK
106	gi|8395615	cytochrome c oxidase subunit II [Danio rerio]	26.5	230	442.31	882.61	882.46	41.11	0.073	LLETDHR
					1068.52	2135.02	2133.18	60.00	0.00083	ILVSAEDVLHSWAVPSLGIK

107	gi|18859505	alpha-tropomyosin [Danio rerio]	44.4	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENALDR
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					770.15	2307.42	2307.18	51.55	0.0055	SVAKLEKTIDDLEDELYAQK
108	gi|41151982	major vault protein [Danio rerio]	45.3	863	1069.52	2137.03	2137.12	86.26	1.90E-06	IPPHHYIHVLDQNTNIAR
					1353.45	2704.89	2704.43	36.37	0.16	STLITDGSSPINLFTTANGLLGSL
109	gi|147906978	hypothetical protein LOC492719 [Danio rerio]	59.9	603	1359.62	1358.61	1358.64	59.74	0.0011	EEFAHDHPHIK
					1005.22	3012.64	3013.43	105.12	1.90E-08	HISDDIFLTTAEAISEMVTEEHLA
110	gi|18858299	ATPase, Na+/K+ transporting, alpha 1a.3 polypeptide [Da	44.2	1024	877.83	1753.65	1751.85	85.52	2.70E-06	DAFQNAYLELGGLGER
					906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
111	gi|18858295	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Dani	42.6	1028	877.83	1753.65	1751.85	85.52	2.70E-06	
					906.81	1811.60	1810.94	74.81	3.00E-05	
112	gi|32308153	annexin A2a [Danio rerio]	57.6	337	633.21	1264.40	1263.66	53.64	0.0044	SLHQTIAEHTK
					723.17	1444.33	1443.78	90.36	9.50E-07	GVDEQTIIDILTK
113	gi|189526598	PREDICTED: similar to COASTER [Danio rerio]	40.5	916	657.65	1313.29	1312.78	53.16	0.005	QAVALSLKEARK
114	gi|189540222	PREDICTED: similar to myosin, heavy polypeptide 2, fas	48.3	950	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
115	gi|189540214	PREDICTED: similar to myosin heavy chain, partial [Dani	51.2	809	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
					1183.60	2365.19	2366.12	87.76	1.30E-06	LQQFFNHHMFVLEQEEYK
116	gi|46358344	isocitrate dehydrogenase 3 (NAD+) alpha [Danio rerio]	45.8	365	1251.43	2500.84	2501.23	114.90	2.30E-09	ENTEGEYSGIEHVIVDGVVQSIK
117	gi|68448513	hypothetical protein LOC574004 [Danio rerio]	37.4	187	968.51	967.50	966.55	60.55	0.00083	HVLATLGEK
					757.12	1512.23	1511.69	84.28	3.60E-06	DQGTFEDFVEGLR
118	gi|156713467	vitellogenin 7 [Danio rerio]	56	1358	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					644.61	1287.21	1286.66	65.73	0.00029	AEAGVLGEFPAAR
119	gi|18859423	spectrin, beta, erythrocytic [Danio rerio]	31.3	2357	669.07	1336.13	1335.74	59.62	0.0011	HLLEVEDLLQK
					713.72	1425.42	1425.74	42.84	0.05	HRPDLVDYGNLK
					945.14	1888.27	1887.93	93.31	4.20E-07	KKHDAIETDIAAYEER
120	gi|119943123	apolipoprotein A-IV [Danio rerio]	57.3	255	903.92	1805.82	1802.94	78.36	1.40E-05	AQIVQQSLTPYAEDLK
121	gi|54400442	hypothetical protein LOC449795 [Danio rerio]	65.3	202	999.01	2993.99	2996.41	51.77	0.004	TLAAGSHAEHDGQPYCHKPCY
					1008.93	3023.75	3023.42	65.34	0.00017	TLNPGGHAEHDGKPYCHKPCY
122	gi|189531406	PREDICTED: similar to nicotinamide nucleotide transhyd	39.8	679	567.07	1132.13	1130.59	54.85	0.0038	SVAELEAEKR
					649.69	1297.36	1296.77	64.75	0.00033	VSVSPAGVELLVK
					1771.82	3541.62	3538.84	66.53	0.00011	VHEAELLSPGSTLVSFIYPAQNP
123	gi|45387763	hypothetical protein LOC402975 [Danio rerio]	59.5	284	623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
					770.15	2307.42	2307.18	51.55	0.0055	SVAKLEKTIDDLEDELYAQK
124	gi|189528827	PREDICTED: similar to LOC567732 protein [Danio rerio]	41.1	1368	1212.43	2422.84	2422.19	114.22	2.80E-09	GQNHLEEVELAFPQNVIEGSGR
125	gi|41055614	hypothetical protein LOC393478 [Danio rerio]	22.1	86	733.58	1465.15	1464.65	91.10	7.40E-07	WDSQIEDGSFPGK
126	gi|41055387	hypothetical protein LOC393586 [Danio rerio]	49.3	647	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
					847.03	1692.05	1690.72	44.48	0.035	STAGDTHLGGEDFDNR
127	gi|70778808	vesicle amine transport protein 1 [Danio rerio]	38	484	904.66	1807.30	1806.90	75.89	2.40E-05	HEVISQGGVTHPIDYR
128	gi|189529657	PREDICTED: similar to nonmuscle myosin heavy chain [	37.3	1962	613.09	1224.17	1222.63	64.72	0.00033	AGVLAHLEEER
					864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
129	gi|47086479	solute carrier family 25 (mitochondrial carrier, Aralar), me	39.1	682	1325.55	1324.54	1324.74	84.55	3.40E-06	TVHLLAGVADTTK
					677.29	1352.56	1352.69	36.67	0.2	SSGISTIHPETPK
					979.83	1957.64	1956.00	38.79	0.12	IAPLEEGSLPYNVAEAQR
130	gi|56118753	troponin C, slow [Danio rerio]	46.6	161	602.27	1202.52	1202.58	52.94	0.0057	AAAEQLTDEQK
					602.42	1202.83	1202.58	56.98	0.0022	AAAEQLTDEQK
					684.15	1366.28	1364.65	68.52	0.00013	NADGYIDLDELK
					726.33	1450.65	1448.65	60.34	0.0009	IDYDEFLEFMK
131	gi|41386743	eukaryotic translation elongation factor 2, like [Danio reri	56.1	858	703.70	1405.38	1404.80	59.08	0.0013	TFAQLILDPIFK
					1073.30	2144.58	2144.05	65.62	0.00023	ARPFPDGLAEDIDKGDVSSR

132	gi|148922875	hypothetical protein LOC567716 [Danio rerio]	26.3	331	969.85	1937.69	1936.93	109.86	9.00E-09	HLTTLVDDIWYYAGDR
133	gi|49274617	tropomyosin 1 alpha [Danio rerio]	21.5	284	537.56	1073.11	1072.55	55.86	0.0032	LDKENALDR
					623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
134	gi|55925387	carnitine palmitoyltransferase II [Danio rerio]	46.1	668	816.40	1630.78	1631.90	43.55	0.045	DGNLIKPAEVQAHLK
					1128.50	2254.98	2252.11	37.68	0.14	YLAAQRPLLNDEQYSNTEK
					1194.52	2387.02	2384.18	59.47	0.00084	DTTEKPLVGPGSQPASVDSSSA
135	gi|30410758	keratin 18 [Danio rerio]	41.5	431	843.64	1685.27	1683.84	107.62	1.70E-08	NQISQSGVQVDVDAPK
136	gi|41152346	hypothetical protein LOC393668 [Danio rerio]	57.3	433	573.42	1144.82	1142.61	42.17	0.07	IGAEVYHNLK
					1008.42	3022.23	3020.58	72.22	3.60E-05	HIADLAGNPEVILPVPAFNVING
137	gi|165972393	hypothetical protein LOC560210 [Danio rerio]	57.4	643	830.76	1659.50	1658.89	82.21	5.90E-06	IINEPTAAAIAYGLDK
139	gi|47085775	heat shock 70kDa protein 5 [Danio rerio]	45.2	650	830.76	1659.50	1658.89	82.21	5.90E-06	
140	gi|189517055	PREDICTED: similar to heat shock protein 8 [Danio rerio	51.3	698	830.76	1659.50	1658.89	82.21	5.90E-06	
141	gi|41053611	hypothetical protein LOC393828 [Danio rerio]	42.7	213	1602.92	3203.82	3202.41	103.90	2.40E-08	YTFESIQNEANALFNNENQANA
142	gi|47086533	2-peptidylprolyl isomerase A [Danio rerio]	63.4	164	820.21	1638.40	1637.91	103.88	3.90E-08	HVVFGQVVEGLDVIK
143	gi|160420306	hypothetical protein LOC678536 [Danio rerio]	58.9	1358	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
					692.52	1383.03	1381.78	54.77	0.0034	ISDAPAQIVEVLK
144	gi|189533701	PREDICTED: calpastatin [Danio rerio]	64.8	824	1343.80	1342.79	1342.74	71.34	7.60E-05	HGAGVPAGVPEKPK
					735.92	1469.83	1470.83	57.29	0.0018	KHGAGVPAGVPEKPK
145	gi|48762665	ubiquinol-cytochrome c reductase core protein II [Danio r	39.9	454	1245.76	1244.75	1244.68	78.80	1.50E-05	KVDFAAAGEPLK
					693.59	1385.16	1385.75	63.33	0.00049	INAVSSADVVNVAK
146	gi|52219050	hypothetical protein LOC447859 [Danio rerio]	66.6	617	701.31	1400.60	1400.70	64.79	0.00033	HSGSDYAQLKPAK
					928.87	2783.58	2782.39	77.52	1.20E-05	ITDENLQSQTTGLYIPEYEEALK
147	gi|70778734	ATPase, Na+/K+ transporting, alpha 3b polypeptide [Dan	52	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
					924.65	1847.29	1846.81	64.13	0.00035	YQLSIHETEDNNDNR
148	gi|148224245	hypothetical protein LOC793834 [Danio rerio]	59	763	653.21	1304.41	1303.71	61.87	0.00069	MQLLEIITTDK
					752.68	1503.34	1503.72	64.87	0.00033	TAEEVTGLSQEGQR
149	gi|47174755	myosin light chain alkali, smooth-muscle isoform [Danio r	74.2	151	757.12	1512.23	1511.69	84.28	3.60E-06	DQGTFEDFVEGLR
150	gi|189519111	PREDICTED: similar to ATPase, Ca++ transporting, fast	48.2	1005	1072.60	1071.59	1071.56	41.86	0.08	NAENAIEALK
					788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
151	gi|113678245	hypothetical protein LOC558738 [Danio rerio]	74.8	111	845.40	1688.79	1689.84	97.41	1.80E-07	IEFSPLDAWNSGVQK
152	gi|150378483	heat shock protein, alpha-crystallin-related, b11 [Danio re	28.8	205	1113.54	2225.06	2223.99	95.53	2.30E-07	NPALQNSEPENQAVEAEAAEN
153	gi|41393141	tropomyosin 3 [Danio rerio]	36.3	248	623.52	1245.02	1242.65	66.73	0.00025	IQLVEEELDR
154	gi|41055939	sorting and assembly machinery component 50 homolog	54.2	469	665.69	1994.04	1992.02	64.06	0.00033	TKEDILTYEIADVFHAK
155	gi|47085999	hypothetical protein LOC406484 [Danio rerio]	34.6	361	850.81	1699.60	1700.90	94.54	3.30E-07	EKGQAFLDDLILDPK
156	gi|55741944	wu:cegs655 [Danio rerio]	37.7	994	788.74	1575.47	1573.86	86.36	2.40E-06	VDQSILTGESVSVIK
157	gi|117606266	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	46.7	991	788.74	1575.47	1573.86	86.36	2.40E-06	
158	gi|189517144	PREDICTED: similar to adaptor-related protein complex	50.8	930	835.88	1669.75	1668.88	78.67	1.30E-05	KGPGAVSVNELEEGKR
159	gi|27545251	solute carrier family 25 alpha, member 5 [Danio rerio]	66.4	298	525.02	1048.03	1047.57	38.02	0.18	VFLDGVDKR
					589.21	1176.41	1175.67	69.50	0.00013	KVFLDGVDKR
					618.00	1233.99	1232.68	66.02	0.00027	DFLAGGIAAAISK
160	gi|24119234	triosephosphate isomerase 1a [Danio rerio]	46.8	248	1458.82	1457.81	1457.72	75.26	3.00E-05	HVFGESDELIGQK
					808.43	1614.84	1613.82	57.16	0.0019	RHVFGESDELIGQK
161	gi|154707842	methylmalonyl Coenzyme A mutase [Danio rerio]	37.3	757	595.61	1189.21	1188.61	47.59	0.02	AGLTIDEFAPR
					870.13	1738.25	1737.81	79.76	1.00E-05	SEFGEHEEIALAHNR
162	gi|47777306	Voltage-dependent anion channel 1 [Danio rerio]	57.6	283	660.08	1318.14	1317.64	60.19	0.001	WAEHGLTFTEK
					1045.44	2088.86	2088.16	70.82	6.90E-05	VNNSSLVGLGYTQTLKPGIK
163	gi|68379126	PREDICTED: hypothetical protein LOC767664 [Danio re	65.4	81	1494.75	1493.74	1493.82	56.01	0.0024	IFLEDNGLPVHIK
					748.64	1495.27	1493.82	76.25	2.20E-05	
164	gi|68448530	vitellogenin 5 [Danio rerio]	51.2	1360	481.12	960.22	959.47	36.63	0.28	LEVEWER
					587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR

					590.06	1178.11	1176.64	48.71	0.015	QTLAFVEIEK
165	gi|46559752	ATPase, Na+/K+ transporting, beta 1a polypeptide [Dani	40.8	306	659.22	1316.43	1315.59	65.54	0.0003	VYGENIDYSEK
					701.50	1400.99	1398.75	66.80	0.00022	REEEANLLGQIK
166	gi|50344731	fibrinogen alpha chain [Danio rerio]	57	684	676.59	1351.17	1350.70	72.52	5.30E-05	LGISDSEFLTAAK
					750.64	1499.26	1498.69	57.20	0.0018	FPTSGTGSTSQTSNK
167	gi|54262125	heat shock protein 9 [Danio rerio]	56.9	682	823.69	1645.37	1644.87	88.91	1.30E-06	VINEPTAAALAYGLDK
168	gi|189533438	PREDICTED: novel protein similar to vertebrate apolipop	37.7	2633	1037.68	2073.35	2075.28	38.73	0.12	LRLLLFFSLIILSICRR
					1230.28	2458.55	2458.19	81.11	5.50E-06	HAINQEINAYNTPAQFGLEGSG
169	gi|41056123	phosphoglycerate mutase 2 (muscle) [Danio rerio]	72.5	255	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					633.57	1265.13	1263.70	50.58	0.0088	NVIIAAHGNSLR
					672.48	1342.95	1342.57	41.92	0.067	HGESSWNQENR
					828.27	1654.52	1653.91	60.12	0.00091	ALPFWNEVIVPEIK
					1058.87	2115.72	2115.10	36.73	0.18	DLKPIKPMQFLGDEETVR
170	gi|54400698	hydroxysteroid (17-beta) dehydrogenase 10 [Danio rerio]	63.8	260	852.76	1703.51	1702.86	86.75	2.00E-06	HGASAVILDLPSSDGHK
171	gi|120952565	reticulon 4a isoform 4-l [Danio rerio]	31.1	322	843.32	1684.62	1684.83	86.64	2.10E-06	HQAQIDHYYGLVNK
172	gi|40254661	annexin A5 [Danio rerio]	42.3	317	530.21	1058.40	1058.56	40.72	0.1	SEVDLLDIR
					1144.59	2287.17	2284.98	86.60	1.80E-06	EHDKDLEEDVTGDTGGHFER
173	gi|41387146	peroxiredoxin 6 [Danio rerio]	45.5	222	1052.48	2102.95	2103.09	75.38	2.50E-05	PGILLGDVFPNFEADTTIGK
174	gi|157426949	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Co	60.8	761	653.21	1304.41	1303.71	61.87	0.00069	MQLLEIITTDK
					697.27	1392.52	1392.67	46.97	0.021	LSGQLDYHGFEK
					882.60	1763.19	1760.86	42.36	0.057	LTAPPAVSSDEDIQYR
175	gi|62955301	hypothetical protein LOC550355 [Danio rerio]	50.6	255	925.29	1848.57	1848.92	77.21	1.70E-05	VLPGVDVTVGHEEEQGGK
176	gi|47085765	hypothetical protein LOC406325 [Danio rerio]	59.7	397	1188.77	1187.76	1187.68	48.56	0.017	ITAHLVHELR
					932.43	1862.85	1861.98	75.84	2.40E-05	TNVNGGAIAIGHPLGASGTR
177	gi|189519965	PREDICTED: similar to nonmuscle myosin heavy chain [	40.3	1857	1093.83	2185.64	2184.99	76.48	1.90E-05	HAEQERDELADEISNSASGK
178	gi|189519969	PREDICTED: myosin, heavy polypeptide 10, non-muscle	37.5	1973	1093.83	2185.64	2184.99	76.48	1.90E-05	
179	gi|54400460	fibulin 5 [Danio rerio]	56	477	1111.23	2220.45	2220.00	85.10	2.50E-06	NSPLPYPEASYPEEPYPDR
180	gi|57526509	propionyl-Coenzyme A carboxylase, alpha polypeptide [D	55.6	709	1164.68	1163.67	1164.65	55.10	0.0032	HIEIQVLADK
					827.11	1652.21	1649.84	62.11	0.00057	TVAVHSDVDSSAVHVK
181	gi|68389723	PREDICTED: catechol-O-methyltransferase domain cont	61.8	238	1029.00	2055.99	2055.00	84.28	3.10E-06	SHEGDDPLLQYVVNNSLR
182	gi|41055748	integrin linked kinase [Danio rerio]	20.4	452	792.72	1583.43	1582.76	83.90	4.00E-06	GDDTPLHLAASHGHR
183	gi|113678344	BCL2-like 13 (apoptosis facilitator) [Danio rerio]	32.4	485	1030.15	3087.41	3085.41	61.28	0.00044	SLDSAEGVALAEEQSENNSSN
184	gi|61806484	hypothetical protein LOC541328 [Danio rerio]	58.6	116	1121.07	2240.13	2240.16	83.69	3.50E-06	INAGQIEEVIAQAEAELSLSR
185	gi|189521338	PREDICTED: hypothetical protein [Danio rerio]	56.2	523	790.68	1579.35	1577.76	83.48	4.30E-06	YDVQVQIENVEDK
					945.67	1889.33	1888.04	37.61	0.15	ASVNIQIVDVPGPPQNLK
186	gi|189520787	PREDICTED: tyrosine 3-monooxygenase/tryptophan 5-m	46.7	244	903.52	902.51	902.51	42.18	0.083	VISSIEQK
					1155.50	1154.49	1154.55	60.78	0.00087	YLSEVASGDSK
					587.18	1172.34	1170.56	41.88	0.075	AYQDAFEISK
					745.40	1488.78	1488.71	51.91	0.0066	AVTEGGVELSNEER
187	gi|67514531	ubiquitin specific protease 5 [Danio rerio]	33.7	834	602.99	1805.95	1804.92	67.29	0.00017	RREEAESSGAPPPVAPR
188	gi|47085905	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	40.1	242	903.52	902.51	902.51	42.18	0.083	VISSIEQK
					1155.50	1154.49	1154.55	60.78	0.00087	YLSEVASGDSK
					745.40	1488.78	1488.71	51.91	0.0066	AVTEGGVELSNEER
189	gi|58801526	SET translocation (myeloid leukemia-associated) B [Dani	24.7	275	1098.47	2194.92	2194.01	81.47	5.80E-06	EQQEAIEHIDEVQNEIDR
190	gi|58801528	SET translocation (myeloid leukemia-associated) A [Dani	17.5	269	1098.47	2194.92	2194.01	81.47	5.80E-06	
191	gi|47086189	propionyl Coenzyme A carboxylase, beta polypeptide [Da	70.4	557	838.80	1675.58	1675.79	55.44	0.0028	SVTNEDVTQEELGGAK
					872.59	1743.16	1744.85	63.94	0.00038	AYDMLDIVHGIVDER
192	gi|47085923	pyruvate dehydrogenase (lipoamide) beta [Danio rerio]	38.4	359	879.64	1757.27	1758.94	53.19	0.0045	SIRPLDADTIETSITK
					901.77	1801.52	1800.89	51.77	0.0062	VFLLGEEVAQYDGAYK
					967.33	1932.65	1932.85	44.87	0.028	DALNQAMDEELERDER
193	gi|50540382	hypothetical protein LOC436930 [Danio rerio]	47.4	460	735.25	1468.49	1467.79	63.52	0.00043	ALADQSPQIGVLEK
					832.57	1663.12	1662.89	52.80	0.0051	SAAPPVLQPQDVQVSK

194	gi|54606886	hexokinase 1 [Danio rerio]	48.1	918	864.33	1726.64	1723.83	79.77	9.90E-06	TKYDDAVDDLSLNAGK
195	gi|51010975	hypothetical protein LOC445053 [Danio rerio]	36.8	204	853.63	1705.25	1704.91	79.51	1.10E-05	GATYGKPVHHGVNQIK
196	gi|189518076	PREDICTED: filamin C, gamma b (actin binding protein 2	46.8	2732	805.13	1608.25	1607.78	36.13	0.23	VDVGKDEEFTVNTR
					1115.87	2229.73	2228.03	42.68	0.044	DGSCGVAYIVQEPGDYEVSIK
					1152.87	2303.73	2303.14	72.02	4.80E-05	GQHVPGSPFQFTVGPLGEGGA
197	gi|45356143	tumor protein D52-like 2 isoform 1 [Danio rerio]	55.7	201	737.80	1473.58	1473.69	79.41	1.20E-05	GLGSDSISDLPEER
198	gi|62955689	hypothetical protein LOC550556 [Danio rerio]	41.9	270	843.24	1684.46	1682.84	80.84	7.80E-06	AFAEFLTEEIKEEK
199	gi|51467909	ATP synthase, H+ transporting, mitochondrial F1 comple	80.4	209	637.34	1272.66	1272.67	64.58	0.00038	SLDKVEQELGR
					782.72	1563.43	1561.80	42.52	0.055	SDASILGGMIVSIGDK
200	gi|113678458	vitellogenin 2 isoform 1 [Danio rerio]	50.9	1631	587.65	1173.29	1172.62	56.41	0.0027	LEFEVQVGPR
201	gi|45387723	hypothetical protein LOC402952 [Danio rerio]	28.7	331	1181.36	3541.04	3539.71	57.14	0.00093	GEDYYPPPPPHYPPHPHDHPH
202	gi|27545305	laminin, gamma 1 [Danio rerio]	58.2	1593	559.44	1116.86	1115.56	37.28	0.22	DAENLINTAR
					665.17	1328.32	1327.68	63.97	0.00042	RAEAALGNAAADAK
					963.13	1924.24	1924.06	50.87	0.007	EVLNTINALLGQLGNIDK
203	gi|47085823	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight c	56.6	424	924.30	1846.58	1846.92	75.34	2.70E-05	AFTGFIVDADTPGVQPGR
204	gi|30017425	ATPase, Na+/K+ transporting, alpha 1a.5 polypeptide [D	37.7	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
205	gi|18858297	ATPase, Na+/K+ transporting, alpha 1a.2 polypeptide [D	40.7	1023	906.81	1811.60	1810.94	74.81	3.00E-05	
206	gi|18858303	ATPase, Na+/K+ transporting, alpha 1b polypeptide [Dan	41.5	1025	906.81	1811.60	1810.94	74.81	3.00E-05	
208	gi|18858305	ATPase, Na+/K+ transporting, alpha 2a polypeptide [Dan	24.7	1017	906.81	1811.60	1810.94	74.81	3.00E-05	
209	gi|66472494	phosphorylase, glycogen (muscle) A [Danio rerio]	40.6	842	594.42	1186.83	1184.64	74.74	4.00E-05	GLAGVENVADLK
210	gi|41054784	phosphorylase, glycogen (muscle) b [Danio rerio]	44.4	315	594.42	1186.83	1184.64	74.74	4.00E-05	
211	gi|41387136	hypothetical protein LOC393781 [Danio rerio]	45.3	128	902.80	1803.58	1801.94	74.18	3.60E-05	YHVSETPFAISAQKPK
212	gi|53933242	cytochrome c oxidase subunit VIa polypeptide 1 [Danio r	62	108	781.74	2342.19	2341.05	50.66	0.0068	TLFHNPHVNALPDGYEHHDE
213	gi|41282137	ATPase, Na+/K+ transporting, alpha 3a polypeptide [Dan	43.8	1023	906.81	1811.60	1810.94	74.81	3.00E-05	QGAIVAVTGDGVNDSPALK
214	gi|47085679	electron-transfer-flavoprotein, beta polypeptide [Danio re	61.4	254	924.89	923.88	924.50	63.43	0.00041	GIHVEVSGK
215	gi|61806580	hypothetical protein LOC541378 [Danio rerio]	49.6	448	919.52	1837.03	1836.96	73.38	4.20E-05	DKPHLNIGTIGHVDHGK
216	gi|35902900	aldolase c, fructose-bisphosphate [Danio rerio]	34.2	363	1136.95	2271.88	2271.13	72.97	4.10E-05	GVVPLAGTNGETTTQGLDGLSE
217	gi|57525836	hypothetical protein LOC445175 [Danio rerio]	37.9	697	652.16	1302.30	1301.66	63.04	0.00053	SHIDELYANIK
218	gi|66472480	NADH dehydrogenase (ubiquinone) Fe-S protein 5 [Dani	53.8	106	643.28	1284.55	1283.66	72.00	6.40E-05	WLLAQSGEQPR
219	gi|189536521	PREDICTED: similar to phosphofructokinase, platelet [D	60.5	789	699.53	1397.05	1395.70	71.84	6.30E-05	DLQANVEHLTEK
220	gi|189514551	PREDICTED: sorbin and SH3 domain containing 2a [Da	38.7	2115	643.71	1285.40	1284.76	57.60	0.0018	KSPTPVPLPPPR
221	gi|41152365	ATP synthase, H+ transporting, mitochondrial F1 comple	68.6	159	732.54	1463.06	1462.69	70.61	8.60E-05	AQSELVSASDEATR
					800.48	1598.94	1597.89	39.05	0.12	AEVLISIEANEAIVK
222	gi|51010955	hypothetical protein LOC445042 [Danio rerio]	40.4	104	609.53	1217.04	1215.65	71.12	8.90E-05	ALTAGSEASGKPK
223	gi|38488700	phosphoglycerate mutase 1 [Danio rerio]	57.5	254	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					835.57	1669.12	1668.89	60.67	0.0008	ALPFWNDEIVPQIK
224	gi|41053309	hydroxyacylglutathione hydrolase [Danio rerio]	40	260	970.67	1939.33	1938.91	70.11	8.40E-05	TVLTTHHHWDHAGGNEK
225	gi|47086009	ribosomal protein L19 [Danio rerio]	43.9	196	972.51	1943.00	1941.92	70.00	8.40E-05	VWLDPNETNEIANANSR
226	gi|18858873	heat shock protein 90-alpha 1 [Danio rerio]	33.7	726	868.56	1735.10	1734.74	69.58	0.00011	IEDLGADEDEDSKDGK
227	gi|189517212	PREDICTED: similar to myosin, heavy polypeptide 11, sr	35.1	1994	864.56	1727.10	1725.94	69.31	0.00011	QLLQANPILEAFGNAK
228	gi|116235424	hypothetical protein LOC572011 [Danio rerio]	35.1	823	715.67	1429.33	1429.70	69.18	0.00012	ELQEAQELANTGK
229	gi|189537447	PREDICTED: similar to Ndufa9 protein [Danio rerio]	39.5	380	690.97	1379.93	1379.71	69.07	0.00012	FFEAAVGEAKPSK
230	gi|47550733	SERPINE1 mRNA binding protein 1 [Danio rerio]	60.9	391	1118.80	2235.59	2235.08	68.31	0.00012	RFDKPADEKPAEGGEFSVEK
231	gi|189523865	PREDICTED: myosin 1b-like 2 [Danio rerio]	40.4	1078	752.67	2254.98	2255.13	50.39	0.0075	SLRHQDKDQCILITGESGAGK
232	gi|189527793	PREDICTED: wu:fb05a01 [Danio rerio]	47.6	6009	578.82	1155.63	1155.65	55.90	0.0028	LKGDVDVSVPK
					651.29	1300.57	1299.69	36.73	0.22	LMGSNVDLNLPK
233	gi|70887615	hypothetical protein LOC558711 [Danio rerio]	59.9	367	656.84	1311.67	1311.74	67.35	0.00018	VKVESQVAVPEK
234	gi|51467931	enolase 2 [Danio rerio]	45.2	434	1008.42	3022.23	3024.58	66.73	0.00013	HIADLAGNTELVLPVPAFNVING
235	gi|82658182	cytochrome c-1 [Danio rerio]	36.2	307	715.11	1428.21	1425.71	66.24	0.00024	NLVGVSHTEDEVK
236	gi|125832496	PREDICTED: similar to mCG2694 [Danio rerio]	54.5	308	550.57	1099.13	1098.61	50.09	0.011	QLADALKANR
237	gi|41054573	hydroxysteroid dehydrogenase like 2 [Danio rerio]	55.2	415	1588.03	3174.05	3171.54	58.77	0.00079	DFDVYAVEPGHPLLPDFFLDGQ
238	gi|189532432	PREDICTED: novel protein similar to vertebrate AT rich i	29	2113	651.79	1301.56	1299.71	37.15	0.2	EIGGLTQVNKNK

					653.21	1304.41	1303.77	60.26	0.001	RCLIEIFGILK
239	gi|189532434	PREDICTED: im:7160733 [Danio rerio]	30.8	1248	653.21	1304.41	1303.77	60.26	0.001	RCLIEIFGILK
240	gi|41056085	keratin 8 [Danio rerio]	42.7	520	1308.67	1307.66	1307.65	40.71	0.085	NKYEDEINKR
					744.60	1487.19	1485.71	65.58	0.00028	ANLENQIAEAEER
241	gi|38707985	electron-transfer-flavoprotein, alpha polypeptide [Danio re	43.8	333	713.78	1425.54	1424.81	70.23	9.20E-05	LDVAPISDIIEIK
242	gi|113681458	Ndrg4 [Danio rerio]	35.5	352	939.29	1876.56	1876.00	63.58	0.00039	GNKPAILTYHDVGLNHK
243	gi|113674619	hypothetical protein LOC692305 [Danio rerio]	34.9	352	939.29	1876.56	1876.00	63.58	0.00039	GNKPAILTYHDVGLNHK
244	gi|21426835	glucose phosphate isomerase a [Danio rerio]	32.5	553	717.59	1433.16	1432.70	63.47	0.00045	ELQASGLSGDSLEK
245	gi|54400554	cysteine and glycine-rich protein 3 (cardiac LIM protein) [	79.3	193	818.62	2452.82	2452.15	42.68	0.04	SLESTTVTDKDGELYCKVCYAK
					1251.74	2501.47	2503.17	53.78	0.003	KGLDSTTVAAHESEIYCKTCYG
246	gi|41152026	phosphoglycerate mutase 1 like b [Danio rerio]	40.2	254	530.30	1058.58	1058.55	50.79	0.011	HYGGLTGLNK
					1051.63	2101.25	2100.10	47.40	0.016	NLKPVKPMQFLGDEETVR
247	gi|116235416	hypothetical protein LOC553452 [Danio rerio]	33.2	316	1009.26	2016.51	2014.96	62.10	0.00052	HIDGAAVYNNETEVGEGIK
248	gi|189538466	PREDICTED: similar to alpha 2 actin [Danio rerio]	57.6	132	1161.09	1160.08	1160.61	45.99	0.029	EITALAPSTMK
					1115.18	2228.34	2227.06	49.56	0.0091	DLYANNVLSGGTTMYPGIADR
249	gi|51011113	hydroxyacyl-Coenzyme A dehydrogenase [Danio rerio]	84.5	309	819.15	1636.29	1636.85	49.33	0.011	DPDNPLFAPSPLLNK
					923.59	2767.73	2767.42	36.64	0.14	NVSTSTDAASVVHGTDLVVEAI
250	gi|47087077	phosphoglycerate kinase 1 [Danio rerio]	57.1	417	916.46	915.45	915.45	52.89	0.0064	FHVAEEGK
					817.60	1633.19	1633.78	36.82	0.21	LGDVYVNDAFGTAHR
251	gi|61651682	fibronectin 1b [Danio rerio]	41.9	2408	1070.65	3208.93	3208.44	59.70	0.00062	INTVGPTGHDSTDAHGQHVEYT
252	gi|41055823	hypothetical protein LOC393488 [Danio rerio]	17.2	186	968.51	967.50	966.55	60.55	0.00083	HVLATLGEK
253	gi|32308156	annexin A1a [Danio rerio]	40.6	340	783.03	1564.04	1563.83	59.90	0.00099	GVDEPTIIDTLVHR
254	gi|189536881	PREDICTED: hypothetical protein LOC402880 [Danio re	26.6	173	685.99	1369.96	1367.74	50.88	0.0081	LDTPLPDVPFVR
255	gi|40363541	S-adenosylhomocysteine hydrolase [Danio rerio]	33.5	433	480.61	1438.81	1437.75	58.91	0.0012	KLDEEVAAAHLDK
256	gi|50344812	ribosomal protein S13 [Danio rerio]	43	151	848.35	1694.68	1692.91	58.79	0.0013	GLAPDLPEDLYHLIK
257	gi|41054351	ribosomal protein L27 [Danio rerio]	22.8	136	752.58	2254.71	2255.09	58.76	0.0011	NIDDGTADRPYSHALVAGIDR
258	gi|50539832	lysyl-tRNA synthetase [Danio rerio]	34.9	602	1124.52	2247.02	2247.14	58.56	0.0011	YNHLQPGDHLTDVVLNLSGR
259	gi|57525624	malic enzyme 2, NAD(+)-dependent, mitochondrial [Dani	47.7	581	1093.30	2184.59	2184.23	58.56	0.0012	SFLDAVNVIKPTAIIGVSGAGR
260	gi|189518755	PREDICTED: similar to malic enzyme 2, NAD(+)-depend	46.3	581	1093.30	2184.59	2184.23	58.56	0.0012	
261	gi|47551341	adenylosuccinate synthase like 1 [Danio rerio]	46.9	456	643.44	1284.87	1284.72	56.83	0.0021	LDILDVLDEIK
262	gi|189526054	PREDICTED: hypothetical protein LOC335621, partial [D	52.3	530	721.66	1441.30	1439.87	56.81	0.0021	AKLAAQEVELKLK
263	gi|113678983	hypothetical protein LOC751707 [Danio rerio]	37.8	606	1090.85	2179.69	2179.07	56.63	0.0018	GGENIYPAEIEQFLHTHPK
264	gi|189530481	PREDICTED: similar to LIM domain-containing protein 1	52	490	843.76	1685.51	1684.80	56.53	0.0021	HHSTIIQHNDGPSSR
265	gi|189535572	PREDICTED: hypothetical protein [Danio rerio]	71.6	455	758.93	1515.84	1517.74	37.74	0.17	CPDCPGLLPLHEPK
					654.52	1960.54	1959.96	44.47	0.031	FHDHRPGSVHPLGPDHR
266	gi|41152375	mitochondrial ATP synthase gamma-subunit [Danio rerio	61.6	292	1097.58	1096.57	1095.60	55.25	0.003	HLIIGVSSDR
267	gi|47086943	ATP synthase, H+ transporting, mitochondrial F0 comple	63.4	112	905.44	904.43	904.45	39.81	0.14	NLAEETTK
					674.56	1347.10	1346.68	55.37	0.003	ASGGVVDAGPVYQK
268	gi|52219158	aquaporin 8 [Danio rerio]	20.8	260	1058.86	2115.71	2113.97	55.02	0.0027	SELFTVATGDGGDNHQNQPK
269	gi|68444185	PREDICTED: cytochrome c oxidase subunit Vab [Danio	76.2	172	487.46	972.90	971.54	40.97	0.1	LNDLASAIR
					1659.13	3316.24	3314.75	50.52	0.0047	EIYPYVIQELKPTLQELGISTPEE
271	gi|153945848	hypothetical protein LOC321053 [Danio rerio]	42.9	529	1059.44	1058.43	1058.47	54.82	0.004	EHDFSEAPK
272	gi|189516256	PREDICTED: similar to phosphofructokinase, platelet [D	42.6	782	706.78	1411.55	1411.69	54.77	0.0032	DLQSNVEHLTEK
273	gi|41152189	hypothetical protein LOC393720 [Danio rerio]	73.8	244	820.65	1639.28	1638.85	49.87	0.0098	RVEAIINNYPEGHK
274	gi|131888959	hypothetical protein LOC100034538 [Danio rerio]	27	448	710.05	1418.09	1415.74	54.44	0.0037	EALGAENIQSTKR
275	gi|47086817	bscv (C20orf3) homolog [Danio rerio]	19.8	415	1046.78	2091.54	2090.05	54.31	0.0031	LNRPHIITDETHEPQYK
276	gi|189524989	PREDICTED: neurobeachin-like 2 [Danio rerio]	46.4	1495	655.96	1309.91	1308.70	53.90	0.004	NNVAIEPLSAPGK
277	gi|168229163	cysteine-rich protein 2 [Danio rerio]	51	206	999.01	2993.99	2996.41	51.77	0.004	TLAAGSHAEHDGQPYCHKPCY
278	gi|52219190	hypothetical protein LOC447942 [Danio rerio]	69.9	103	1167.88	3500.62	3500.62	53.66	0.0021	TKPWPWGDGNHSLFHNPHTNA
279	gi|189527668	PREDICTED: similar to janus kinase and microtubule inte	43.4	807	773.19	1544.36	1543.91	52.30	0.006	FQLKIAELQSVIR
280	gi|46518516	interferon 1 [Danio rerio]	19	179	495.32	988.63	989.50	52.78	0.0065	MDIIASNAR
281	gi|55925377	peptidase (mitochondrial processing) alpha [Danio rerio]	35.6	517	1388.81	2775.60	2773.44	52.53	0.0038	SKPAVAALGDLTELPSYEDIQA

282	gi|189541652	PREDICTED: similar to Myosin-3 (Myosin heavy chain 3)	38.9	882	660.22	1318.42	1315.65	52.39	0.0061	ELELELDAEQK
283	gi|189546569	PREDICTED: complement component 3 [Danio rerio]	38.8	1648	652.15	1302.28	1301.65	52.01	0.0067	EGTDQVIEGQVK
284	gi|66773104	branched chain keto acid dehydrogenase E1, alpha poly	42.2	446	827.55	1653.08	1652.84	51.96	0.0059	QGQIINPSEDPQLSK
285	gi|189534068	PREDICTED: nuclear RNA export factor 1 [Danio rerio]	54	642	731.60	1461.18	1460.65	51.91	0.0065	FGGRGGGGGGGGGPSDGR
286	gi|18858379	carbonic anhydrase [Danio rerio]	50.4	260	502.52	1003.03	1000.54	37.51	0.22	VLDALDDIK
					824.69	2471.05	2471.13	51.80	0.0048	QFHFHWGSSDDKGSEHTIAGT
287	gi|56693302	heat shock protein, alpha-crystallin-related, 1 [Danio reri	9.5	199	668.10	1334.18	1332.69	51.50	0.0071	KYTLPPGVDSEK
288	gi|148229906	hypothetical protein LOC100037332 [Danio rerio]	32.8	302	550.58	1099.15	1098.64	46.82	0.024	LKQELAELR
289	gi|47271398	ribosomal protein L7 [Danio rerio]	47.2	246	680.91	1359.81	1359.62	51.36	0.0076	TTHFVEGGDAGNR
290	gi|125854185	PREDICTED: hypothetical protein [Danio rerio]	28.2	645	674.08	1346.15	1346.62	50.90	0.0086	EEEEEQLKADK
291	gi|41055997	hypothetical protein LOC393098 [Danio rerio]	54.5	343	863.60	1725.19	1724.92	50.74	0.0079	DSTVLAHVMKLLNER
292	gi|125833577	PREDICTED: similar to Galectin-3 (Galactose-specific le	16.6	368	670.63	1339.24	1337.66	50.69	0.0082	GHEVVFHFNPR
293	gi|41055658	3-hydroxyisobutyrate dehydrogenase b [Danio rerio]	67.2	329	867.36	1732.71	1729.95	50.68	0.0084	KGSLLIDSSTIDPAVSK
294	gi|41054603	actinin alpha 4 [Danio rerio]	27.1	901	762.20	1522.39	1520.71	50.51	0.0086	AGTQIENIEEDFR
295	gi|45387533	hypothetical protein LOC323320 [Danio rerio]	20.8	890	762.20	1522.39	1520.71	50.51	0.0086	
298	gi|153791915	hypothetical protein LOC100006671 [Danio rerio]	37.7	151	762.20	1522.39	1520.71	50.51	0.0086	
299	gi|66773056	proteasome (prosome, macropain) subunit, alpha type, 2	49.1	234	734.65	2200.92	2200.13	50.39	0.0077	YNEDLELEDAIHTAILTLK
300	gi|125845472	PREDICTED: si:rp71-45k5.4 [Danio rerio]	59	234	734.65	2200.92	2200.13	50.39	0.0077	
301	gi|189518402	PREDICTED: similar to NLR family, CARD domain conta	51	995	951.97	950.96	951.47	46.42	0.022	CFDDIVLK
302	gi|116875779	hypothetical protein LOC768287 [Danio rerio]	47.7	474	549.51	1097.01	1094.55	50.25	0.01	AELQHLNDR
303	gi|156616344	hypothetical protein LOC100124599 [Danio rerio]	55.4	278	745.59	1489.17	1488.74	49.21	0.012	ENQSVLITGESGAGK
304	gi|189522138	PREDICTED: similar to paxillin [Danio rerio]	31.7	527	1149.87	2297.72	2294.99	45.75	0.021	TWHPEHFVCTHCQEEIGSR
305	gi|125814831	PREDICTED: similar to zinc finger protein 585B [Danio re	59.4	298	837.97	1673.92	1672.88	46.67	0.021	EESEDVKIEEIIIK
306	gi|189524320	PREDICTED: similar to family with sequence similarity 8	55.7	174	533.18	1064.34	1063.51	49.33	0.013	SRVSDCLER
307	gi|148224341	hypothetical protein LOC100038781 [Danio rerio]	38.9	226	538.13	1074.25	1073.56	49.09	0.015	GGIHHISPEK
308	gi|55742519	vesicle-associated membrane protein 2 [Danio rerio]	69.1	110	833.77	1665.53	1664.80	48.94	0.012	ADALQAGASQFETSAAK
309	gi|50344800	vesicle-associated membrane protein 3 (cellubrevin) [Da	65.7	102	833.77	1665.53	1664.80	48.94	0.012	ADALQAGASQFETSAAK
310	gi|47085833	glyceraldehyde-3-phosphate dehydrogenase, spermatog	51.3	335	718.66	1435.30	1434.76	48.73	0.013	GAHQNIIPASTGAAK
311	gi|153791419	si:ch73-252g14.4 [Danio rerio]	22.8	386	829.77	2486.28	2486.30	48.59	0.0099	VQQLLHAHTFGPQHNPTVHGL
312	gi|189522849	PREDICTED: similar to oxoglutarate (alpha-ketoglutarate	26.2	961	1201.03	2400.04	2399.32	48.47	0.011	NITLSLVANPSHLEAVNPVVQG
313	gi|125814522	PREDICTED: si:dkey-261e22.2 [Danio rerio]	45.1	1868	653.21	1304.41	1303.69	48.31	0.016	DTSSDALELLIK
314	gi|47086525	ribosomal protein S15a [Danio rerio]	62.3	130	567.82	1700.43	1699.80	48.27	0.014	HGYIGEFEIIDDHR
315	gi|189518965	PREDICTED: similar to Acetyl-CoA carboxylase 2 (ACC-	39.4	2240	836.89	1671.76	1672.86	48.19	0.014	ESRGGVLEAEGTVEIK
316	gi|41055407	potassium channel, subfamily K, member 5 [Danio rerio]	18.3	448	609.35	1216.68	1216.64	47.76	0.02	KQEEELARSK
317	gi|189533166	PREDICTED: similar to G protein-coupled receptor 126 b	25.1	1236	581.81	1161.61	1161.64	47.63	0.019	LTSTVAWGLSK
318	gi|68448495	hypothetical protein LOC100003906 isoform 1 [Danio reri	38.4	915	911.39	1820.76	1820.84	47.56	0.016	SDASYDEIQGSQPPSLK
319	gi|125817349	PREDICTED: similar to CAP-GLY domain containing link	55.2	1041	686.11	1370.20	1368.68	47.37	0.018	HEIDAAVMAKER
320	gi|116004537	hypothetical protein LOC564694 [Danio rerio]	51.7	381	755.56	1509.10	1506.70	47.37	0.017	GGDDLDPNYVLSSR
321	gi|27545193	creatine kinase, brain [Danio rerio]	50.9	381	755.56	1509.10	1506.70	47.37	0.017	
322	gi|189527715	PREDICTED: similar to dentin sialophosphoprotein [Dani	29.6	998	729.47	1456.93	1457.71	47.26	0.019	SDNDPGSKINLGNK
323	gi|35902802	chromobox homolog 2 [Danio rerio]	51.4	510	609.35	1216.68	1215.67	47.20	0.022	EQEKELLISK
324	gi|41282163	protein disulfide isomerase-related protein (provisional) [	60.9	440	559.48	1116.95	1114.60	49.77	0.013	GSTATVGGGALPK
325	gi|41054003	Cap1 CAP, adenylate cyclase-associated protein 1 [Dani	58.5	463	994.76	1987.51	1985.99	46.71	0.018	VENQEGAQNLVISDTELK
326	gi|189530311	PREDICTED: hypothetical LOC555629 [Danio rerio]	65.8	401	796.88	1591.74	1591.82	46.57	0.021	QKMSLLSSNTEINK
327	gi|46309527	hypothetical protein LOC404610 [Danio rerio]	40.6	325	724.76	1447.51	1447.76	46.36	0.024	DALGILDELQAYK
328	gi|41152453	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	40	245	605.07	1208.12	1206.61	46.19	0.025	YLAEVAVGEEK
329	gi|125852544	PREDICTED: hypothetical protein [Danio rerio]	31.6	174	699.83	1397.64	1398.63	46.09	0.024	FTDEEVDELFR
330	gi|47550703	myosin, light polypeptide 9, like [Danio rerio]	25	172	699.83	1397.64	1398.63	46.09	0.024	
331	gi|189521867	PREDICTED: similar to histone cluster 2, H2ab [Danio re	69.4	144	1136.50	2270.98	2270.37	45.74	0.022	LLGGVTIAQGGVLPNIQAVLLPK
332	gi|73611922	histone 2, H2a [Danio rerio]	66.4	128	1136.50	2270.98	2270.37	45.74	0.022	
333	gi|157073897	ubiquinol-cytochrome c reductase, Rieske iron-sulfur poly	42.9	273	773.42	1544.82	1542.79	45.70	0.028	EIETEAGVNLAELR
334	gi|189525434	PREDICTED: im:7157373 [Danio rerio]	59.3	545	954.39	2860.13	2859.32	45.68	0.017	SAAAPPKEEAPPANAPDGDAP

335	gi|189523403	PREDICTED: NADH dehydrogenase (ubiquinone) flavop	31	516	994.20	1986.38	1983.93	45.62	0.024	TTDSPPADTAAADVAVEEPK
336	gi|189533816	PREDICTED: hypothetical protein [Danio rerio]	39.1	1020	493.60	985.18	983.60	45.55	0.032	QLIEQLLK
337	gi|189530783	PREDICTED: hypothetical protein isoform 2 [Danio rerio]	33.3	222	493.60	985.18	983.65	45.55	0.032	QILKKNLK
338	gi|50540198	hypothetical protein LOC436839 [Danio rerio]	34.8	201	721.18	1440.35	1439.63	45.52	0.027	NIDEHANEDVER
339	gi|116487349	carboxylesterase 2-like [Danio rerio]	43.6	555	1027.86	2053.71	2052.99	45.38	0.024	TGSPNPAPVPWPVYDQSNK
340	gi|125843378	PREDICTED: si:dkey-38l12.3 [Danio rerio]	39.5	549	1027.86	2053.71	2052.99	45.38	0.024	TGSPNPAPVPWPVYDQSNK
341	gi|189522914	PREDICTED: similar to RAS and EF-hand domain contai	37.6	551	506.72	1011.42	1012.59	45.19	0.031	IVLAGDAAVGK
342	gi|189523771	PREDICTED: wu:fa11e05 [Danio rerio]	44.1	715	664.43	1990.27	1988.96	45.09	0.026	HHTILSDMASVPNFQHR
343	gi|189523254	PREDICTED: similar to CD22 antigen [Danio rerio]	29.8	392	770.71	1539.41	1540.76	45.09	0.029	IFSISKISSDDSDK
344	gi|61806508	signal peptidase complex subunit 2 homolog [Danio rerio	56.2	201	650.84	1299.66	1299.73	44.33	0.037	AARNGKNSILEK
345	gi|68435369	PREDICTED: similar to Histone H1.5 (H1 VAR.5) (H1b) [	71.8	206	627.68	1253.35	1251.76	46.77	0.021	ALVLNGTLVQPK
346	gi|113679269	hypothetical protein LOC751661 [Danio rerio]	66.8	202	627.68	1253.35	1251.76	46.77	0.021	
347	gi|68383957	PREDICTED: apolipoprotein C-II isoform 1 [Danio rerio]	48	100	1014.03	2026.04	2024.92	44.92	0.027	SYYDQSVDTASGYVETIK
348	gi|189536629	PREDICTED: similar to DEP domain containing 2 [Danio	51.7	1600	611.27	1220.52	1218.70	44.63	0.037	FNTIAIIDGKK
349	gi|189517917	PREDICTED: similar to family with sequence similarity 4	29.7	789	589.21	1176.41	1177.49	44.53	0.04	VEMESDSPER
350	gi|47777321	ectodermal-neural cortex (with BTB-like domain) [Danio r	41.8	273	433.25	864.49	863.42	44.51	0.035	AVLASCSR
351	gi|90652819	hypothetical protein LOC664756 [Danio rerio]	66	462	766.50	765.49	765.39	39.76	0.091	FEEITK
					973.85	2918.52	2915.57	44.47	0.022	EGGANGVTLLEALDSILPPSRPT
352	gi|50233897	FLJ12716-like protein [Danio rerio]	25.9	1132	1188.77	1187.76	1187.63	44.42	0.043	TAYSLVHELR
353	gi|189529141	PREDICTED: similar to NLR family, pyrin domain contain	45.5	789	487.46	972.90	973.52	44.41	0.045	DSAALASALR
354	gi|153945891	hypothetical protein LOC100101652 [Danio rerio]	53.2	293	713.31	1424.60	1424.85	44.33	0.036	RALTIQEIAALAR
355	gi|189530012	PREDICTED: wu:fb94b04 [Danio rerio]	48.3	762	551.34	1100.67	1098.61	44.29	0.046	KLNEAQQLR
356	gi|41056221	hypothetical protein LOC393533 [Danio rerio]	29.8	617	566.38	1130.75	1129.72	44.21	0.045	SSLRLKVLSK
357	gi|47086263	phosphoglucomutase 2 [Danio rerio]	57.1	611	522.11	1042.20	1043.57	43.80	0.048	ELNRNTAVK
358	gi|123708080	hypothetical protein LOC791153 [Danio rerio]	29.9	304	916.46	915.45	914.55	43.74	0.053	IVATAKAGGK
359	gi|189530864	PREDICTED: similar to RIKEN cDNA 2810405J04 gene	46.3	516	581.62	1161.23	1160.63	43.73	0.047	LCAWLVSELK
360	gi|189525167	PREDICTED: hypothetical protein [Danio rerio]	43	1100	762.20	1522.39	1520.80	43.56	0.042	VQLLQDLQDFFR
361	gi|189533677	PREDICTED: hypothetical protein [Danio rerio]	55.5	128	531.01	1060.01	1058.51	43.41	0.057	MQNHFGAVR
362	gi|189530862	PREDICTED: wu:fb54a03 [Danio rerio]	32.2	727	401.07	800.12	800.46	43.33	0.056	ELEGLLK
363	gi|189520791	PREDICTED: family with sequence similarity 62 (C2 dom	32	1700	738.59	1475.17	1473.84	40.52	0.089	IDFGGKPMKVVGVK
					1094.98	3281.90	3280.56	43.09	0.027	QKPVVEDHSTGEEHEEKGPAT
364	gi|189528097	PREDICTED: similar to sushi-repeat-containing protein,	53.7	436	537.92	1073.83	1072.61	43.02	0.062	LKCPLSREK
					540.64	1079.26	1078.45	36.46	0.24	SSVQCMPNR
365	gi|45433520	hypothetical protein LOC327237 [Danio rerio]	34.4	157	707.70	1413.38	1413.81	42.98	0.05	ISREVIQMVLAR
366	gi|113678297	nudix (nucleoside diphosphate linked moiety X)-type moti	22.7	242	1056.28	2110.55	2110.04	42.84	0.044	SKPKPLQPAEEESESTEPK
367	gi|53292609	clathrin, heavy polypeptide a (Hc) [Danio rerio]	36.8	1680	472.54	943.07	942.49	42.73	0.063	HELIEFR
368	gi|189532250	PREDICTED: si:ch211-81a5.3 [Danio rerio]	49.7	2962	771.84	1541.67	1540.86	42.63	0.054	TDDPRSQLLQLKK
369	gi|32401408	annexin A11b [Danio rerio]	34.6	485	886.82	1771.62	1770.84	42.54	0.053	SLYTHISGDTSGDYKK
370	gi|47086993	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, ne	29.4	303	752.86	2255.55	2254.08	42.45	0.047	HLVQAQYWHDPLNDDLYK
371	gi|189522065	PREDICTED: similar to Histone H1.2 (H1 VAR.1) (H1c) [	75.5	200	456.60	1366.76	1365.83	44.67	0.032	AKKAGPGVGELIVK
372	gi|147905490	hypothetical protein LOC100037379 [Danio rerio]	90.4	115	456.60	1366.76	1365.83	44.67	0.032	
373	gi|82658210	protein phosphatase 1, regulatory (inhibitor) subunit 7 [D	40.9	345	1090.76	2179.50	2178.14	41.86	0.053	VIENLDSLSSLESLFLGTNK
374	gi|41053347	mitochondrial trifunctional protein, beta subunit [Danio re	39.3	471	561.67	1121.32	1119.56	36.12	0.26	LEQDEFALR
					1197.60	1196.59	1196.57	41.61	0.069	DFVYVSQDPK
375	gi|189531881	PREDICTED: solute carrier family 8 (sodium-calcium exc	23.6	967	770.74	1539.47	1536.85	41.54	0.066	RPSIGGELGGPRVSR
376	gi|52219178	high-mobility group box 2 [Danio rerio]	48.6	214	705.76	1409.50	1407.74	41.51	0.068	SEHPNLTIGEIAK
377	gi|47086505	fibrinogen, B beta polypeptide [Danio rerio]	65.2	485	1376.63	1375.62	1375.70	48.45	0.015	DTVDVTFPQNIK
378	gi|189526982	PREDICTED: similar to G protein-coupled receptor 103 [	36.7	422	500.54	999.06	998.59	41.05	0.09	IGIELWIR