

Supplementary Table 2. Proteins that showed a significant change in abundance in activated sperm compared to immobilized sperm of rainbow trout.

No	Protein	Gene name	NCBI accession	Mass /pI	Score	No unique peptides (ion score ≥ 30)	Sequence Cov	Ion score	Peptide sequence
<i>Cytoskeleton, flagella and cell movement</i>									
1	Predicted: coiled-coil domain-containing protein 40 [Salmo salar]	CCDC40	XP_014032980.1	113599/5.92	243	2	23	0.005 0.010	R.VQQEFPQHGGALR.R R.TESEIQQEQR.E
2	Predicted: coiled-coil domain-containing protein 40 [Salmo salar]	CCDC40	XP_014032980.1	113599/5.92	219	2	20	0.005 0.015	R.VQQEFPQHGGALR.R R.TESEIQQEQR.E
23	PREDICTED: coiled-coil domain-containing protein 173 [Salmo salar]	CCDC173	gi 642131459	64775/9.16	163	3	25	0.02 0.025	K.TQQYYETDR.V K.DKEEEMFR.E
26	PREDICTED: cilia-and flagella-associated protein 53 [Salmo salar]	CFAP53	CDQ60305.1	63646/8.35	269	2	31	0.0055 0.04	R.SQTEQEHHQQGLVYQEYNR.K R.EFTGPTPHSVAVR.A
29	PREDICTED: coiled-coil domain-containing protein 183 isoform X2 [Salmo salar]	CCDC183	CDQ80245.1	34551/5.76	302	3	57	0.0011 0.02 0.03	R.EGLAEESAHIR.A K.FSAGPSSDRFER.L K.GVNNLFFR.M
30	PREDICTED: coiled-coil domain-containing protein 183 isoform X2 [Salmo salar]	CCDC183	gi 642094391	34551/ 5.76	391	5	54	0.00032 0.03 0.019 0.029 0.0038	R.EGLAEESAHIR.A K.LVEDIDALR.E K.FSAGPSSDRFER.L K.GVNNLFFR.M R.SIQLIEVHQPK.K
60	PREDICTED: coiled-coil domain-containing protein 173 [Salmo salar]	CCDC173	gi 642131459	64775/9.16	272	32	16	2.9e-005 0.015	K.FWSNTIAGQR.Q R.TLQDVYIHQMAEK.R+ Oxidation (M)
8	cilia- and flagella-associated protein 58 [Salmo salar]	CFAP58	gi 929221592	103858/8.12	577	5	53	0.00011 0.003 0.027 0.00033	R.QTEDQKLEVEQQR.D K.QFIDNQEAER.K K.GEIYQNR.V R.SLAQVQSVLPQR.N
19	PREDICTED: cilia- and flagella-associated protein	CFAP45	XP_014070227.1	68270/8.64	242	2	33	0.032 0.037	R.EFTLESQR.R R.ALEAQEQIDELRK.H

	45-like [Salmo salar]								
20	PREDICTED: cilia- and flagella-associated protein 45-like [Salmo salar]	CFAP45	gi 642122481	68270/8.64	338	3	34	0.035 0.0031 0.012	R.EFTLESQR.R R.ALEAQEQIDELRK.H R.EAEYEAQR.R
22	PREDICTED: cilia- and flagella-associated protein 45-like [Salmo salar]	CFAP45	gi 642122481	68270/8.64	203	3	24	0.0087 0.00095	R.ALEAQEQIDELRK.H K.QLIINQIEER.L
25	PREDICTED: cilia- and flagella-associated protein 53 [Salmo salar]	CFAP53	CDQ60305.1	63646/8.35	349	4	33	0.015 0.013 7.3e-010	K.QAQLAEERDELNK.T R.EFTGPTPHSVAVR.A R.SQTEQEQHQQGLVYQEQYNR.K
9	dynein regulatory complex protein 1 [Salmo salar]	DRC1	gi 929249040	86743/5.40	253	3	32	0.0019 0.0013	R.VEEYEVLLQQLR.T R.EENQNLTDYTR.I
10	PREDICTED: dynein regulatory complex protein 1 [Salmo salar]	DRC1	XP_014000687.1	86743/5.40	208	2	28	0.04 2.6e-005	K.SQHQQVEQSEKR.M R.EENQNLTDYTR.I
15	dynein intermediate chain 3, ciliary-like [Salmo salar]	DNAI2	gi 929056610	67665/5.13	497	5	35	0.00051 1.2e-009 5.2e-005 0.037	R.GINHVEGGWPK.D K.DVNPQEMEQTIR.F K.IVCTYSGHHGPIYALQR.N K.NFLTVDWTAR.I K.VCDEALYSR.V
17	PREDICTED: radial spoke head protein 6 homolog A-like [Salmo salar]	RSPH6A	XP_014051759.1	59724/4.29	324	3	35	2.9e-005 0.030 4.9e-005	K.SNLNLYDHLSR.L R.STFKPPPVPK.E K.LPTVTPTQITAAR.H
31	leucine-rich repeat-containing protein 48 isoform X1 [Salmo salar]	DRC3	gi 929095036	61057/4.67	138	2	19	0.041 0.043	K.LEDLSLYNNR.I K.YQYAIEMR.H + Oxidation (M)
4	Predicted: WD repeat-containing protein 63 isoform X2 [Salmo salar]	WDR63	gi 929122470	89254/5.87	338	4	23	0.037 3e-005 0.00048 0.00019	R.EFGAPIFFSDR.N K.SSSTQQTQWYPR.S R.SEVAPEYALLR.V R.FIIHGDQVNTVR.R
36	PREDICTED: tektin-2 isoform X3	TEKT2	gi 642132208	50824/5.89	424	4	61	0.00055 3.3e-005 2.4e-005 0.04	K.TSLKPNPLR.I R.AQEEMQASLQLR.E + Oxidation (M) R.AQLQNELDAQR.I K.DALSLEQR.S
39	PREDICTED: tubulin beta-4B chain-like [Salmo salar]	TUBB4B	XP_014005633.1	55/ 4.79	186	2	21	0.012 0.044	R.INVYNEATGGK.Y R.FPGQLNADLR.K

50	actin, cytoplasmic 2 [Salmo salar]	ACTG1	gi 924442847	42053/5.24	521	5	58	0.026 0.001 7.4e-005 2.1e-010	R.AVFPSIVGRPR.H K.IWHHTFYNELR.V R.VAPEEHPVLLTEAPLNPK.T R.GYSFTTTAER.E K.SYELPDGQVITIGNER.F
51	actin, cytoplasmic 2 [Salmo salar]	ACTG1	gi 642077850	40789/4.95	120	2	10	0.009 0.03	K.GQDYQEEGSSVVR.N k.SSVQDMK.K
55	PREDICTED: outer dense fiber protein 3B [Salmo salar]	RSPH9	XP_013980502.1	28054/10.03	499	5	54	2.7e-005 0.00018 0.012 0.048 1.2e-007	K.APAFSFGTR.H K.SAYYSAPAYLSAR.S K.TSAPNFSLR.G K.HKPPHYSMTGR.N + Oxidation (M) R.KPGPGAHHPEQVTFTR.I
56	Predicted: radial spoke head protein 9 homolog [O. mykiss]	RSPH9	gi 642131999	31086/5.66	537	5	44	3.1e-008 1.7e-005 8.8e-009 0.0011 9.4e-006	R.FVGDPSHEYEHEIR.R R.FVGDPSHEYEHEIRR.Q R.LASTVHTIDKEVSVVPR.G K.SPHGLVQTNR.S K.LSYFLHFTEPQK.L
57	PREDICTED: outer dense fiber protein 3B [Salmo salar]	ODF3	XP_013980502.1	28054/10.03	563	6	57	0.0041 7e-005 1.4e-005 0.007 0.006 3.8e-005	R.GPIAALYSSPGPK.Y K.APAFSFGTR.H K.SAYYSAPAYLSAR.S K.TSAPNFSLR.G K.HKPPHYSMTGR.N + Oxidation (M) R.KPGPGAHHPEQVTFTR.I
45	sperm-associated antigen 6 [O. mykiss]	SPAG6	gi 642089502	58032/6.86	469	4	32	0.00011 4.7e-007 0.047 3.6e-005	R.QVLQVFEQYQK.S K.GDILPQLVYSLTEQNR.F K.EAAAWALGYIAR.H K.AATAWAFGQIGR.H
Metabolism and energy production									
5	2-oxoglutarate dehydrogenase, mitochondrial isoform X2 [Salmo salar]	OGDH	XP_014030343.1	116248/6.30	239	4	20	0.035 0.043	R.SSPYPTDVAR.V R.SNFDEMLPGTDFQR.L + Oxidation (M)
6	2-oxoglutarate dehydrogenase, mitochondrial isoform X1 [Salmo salar]	OGDH	gi 929305625	117908/6.30	582	6	28	0.012 0.002 0.023 8.3e-009	R.HHVLHDQNVDKR.V R.SNFDEMLPGTDFQR.L + Oxidation (M) K.NQGYDYVKPR.M R.AKPVWYAGRPPAAAPATGNK.K
12	Predicted:	ACO2	gi 642077361	80305/7.29	200	2	14	0.011	K.IVYGHLDQVPGQDIAR.G

	aconitate hydratase [O. mykiss]							0.042	K.AAFTITPGSEQIR.A
33	glutamate dehydrogenase [Salmo salar]	GLUD1	gi 30314696	60576/8.45	209	2	16	6.4e-005 0.029	K.HGGAIPVVPTSEFQAR.I R.TANKYNLGLDLR.T
34	glutamate dehydrogenase [Salmo salar]	GLUD1	gi 30314696	60576/8.45	152	2	11	4.4e-005 0.0064	K.HGGAIPVVPTSEFQAR.I R.TANKYNLGLDLR.T
18	Predicted:Propionyl-CoA carboxylase alpha chain, mitochondrial-like [Salmo salar]	PCCA	XP_014040128.1	45800/5.47	101	2	15	0.048 0.047	R.LSSQEAS K.SFGLPSIG
16	PREDICTED: methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial-like [Salmo salar]	MCCC1	XP_014024859.1	78442/5.79	116	2	12	0.042 0.044	K.IIEEAPGPGISEEVR.C K.LVVWGEDR.S
35	Methylmalonate-semialdehyde dehydrogenase [Salmo salar]	ALDH6A1	gi 218505653	57313/6.48	195	2	19	0.021 5.3e-007	K.TLADAEGDVFR.G R.VNAGDQPGADVGLISPEAR.A
37	PREDICTED: adenylate kinase 8 isoform X1 [Salmo salar]	AK8	CDQ66442.1	54510/5.80	414	3	35	3.7e-005 0.0029 2.2e-011	R.HCSVAPHTPR.V K.LQESNFIPSR.V R.YHSLYKPAPSPEVQTR.L
48	creatine kinase, testis isozyme [O. mykiss]	CKB	gi 185132569	43262/6.20	416	3	49	0.02 0.00019 0.04	R.HGGYKPTDK.H K.GGDDLDPNYVISSR.V R.GFCLPPHCSR.G
52	acetyl-CoA acetyltransferase, mitochondrial [Salmo salar]	ACAT1	gi 929084622	44399/9.03	545	5	44	1.1e-005 0.04 9.6e-009 0.00023 3.1e-008	K.EVYMGNVLQAGEGQAPTR.Q R.DTPSYGGVR.M R.EEQDAYAISSYSR.S K.EIVPVSIPQR.G R.GKPDVVVSEDEEWR.R
Ion binding									
13	EF-hand domain-containing family member C2 isoform X2 [Salmo salar]	EFHC2	gi 929285878	86530/6.35	276	2	28	0.038 0.01	K.NSGIPQGLIR.R R.LNPPTSTPLDPYSNLR.Q
14	EF-hand domain-containing family member	EFHC2	gi 929285878	86530/6.35	453	3	42	0.0004 4.8e-006	K.NSGIPQGLIR.R R.LNPPTSTPLDPYSNLR.Q

	C2 isoform X2 [Salmo salar]							0.03	R.EVIYPNSGR.D
59	PREDICTED: EF-hand domain-containing protein 1 isoform X1 [Salmo salar]	EFHC1	XP_013999371.1	65064/6.07	314	3	29	0.0074 0.0021	K.NSGIPQGTLLIR.R R.LNPPTSTPLDPYSNLR.Q
3	uncharacterized protein LOC106584254 isoform X1 [Salmo salar]	CABYR	XP_014024777.1	89043/5.63	168	2	10	0.035 0.038	K.VNVPPGLR.T K.AEEIEALR.S
Signal transduction									
40	PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit-like isoform X3 [O. mykiss]	PRKAR2A	gi 642078503	42170/4.89	332	3	41	0.027 3.1e-009 1.3e-007	K.GSFGELALMYNTPR.A R.AATIIATQEGALWGLDR.A R.GQYFGELALVTNKPR.A
46	PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit-like isoform X3 [O. mykiss]	PRKAR2A	gi 642078503	42170/4.89	275	2	49	4.8e-006 0.0028	R.AATIIATQEGALWGLDR.A R.GQYFGELALVTNKPR.A
53	serine/threonine-protein phosphatase 2A catalytic subunit beta [Clupea harengus]	PPP2CB	XP_012687205.1	36273/5.22	429	3	39	0.026 0.003 0.03	K.TLGTGSFGR.V R.FPSHFSSDLK.D R.GAGDTSNFDDYEEEEIR.V
Protein folding and turnover									
44	PREDICTED: protein disulfide-isomerase A6-like [O. mykiss]	PDIA6	CDQ62935.1	48237/5.21	155	2	24	0.04 0.038	K.NVVELTDDNFDR.L K.KGEEPEDYQGGR.T
47	protein disulfide-isomerase A6-like [O. mykiss]	PDIA6	gi 929098196	48229/4.88	125	2	12	0.04 0.032	K.NKPDDYQGGR.S K.KGEEPEDYQGGR.T
Protein changed in abundance after isosmotic activation									
44	PREDICTED: protein disulfide-isomerase A6-like [O. mykiss]	PDIA6	CDQ62935.1	48237/5.21	155	2	22	0.04 0.038	K.NVVELTDDNFDR.L K.KGEEPEDYQGGR.T
47	protein disulfide-isomerase A6-like [O. mykiss]	PDIA6	gi 929098196	48229/4.88	125	2	14	0.04 0.032	K.NKPDDYQGGR.S K.KGEEPEDYQGGR.T

<i>Oxidation-reduction process</i>									
61	thioredoxin domain-containing protein 12 precursor [Salmo salar]	TXNDC12	NP_001139851.1	19247/5.12	293	3	33	4.8e-007 0.044 8.4e-009	K.DEAYSPDGGYIPR.I K.YFYNSADQVVSAMK.Q K.YFYNSADQVVSAMK.Q+ Oxidation (M)
<i>Other pathways</i>									
42	PREDICTED: uncharacterized protein LOC105935932 [Fundulus heteroclitus]	HIST2H3A	XP_012732015.1	43965/11.41	359	4	26	0.0022 0.0098 7.5e-007 5.3e-006	R.AGLQFPVGR.V R.DNIQGITKPAIR.R R.ISGLIYEETR.G K.VFLENVIR.D
54	Predicted: Protein FAM166B [O. mykiss]	FAM166B	gi 642128870	33157/9.78	615	6	78	0.00017 0.034 0.0032 1e-009 0.027 1.1e-007	R.FPSTETDTGPR.D K.SQNYFSR.T R.EALSEFDR.D R.LASAIPLVSNTISEFKPR.R K.YFISGFTGYVPK.S K.LTHNALGLSGTQR.K
58	L-asparaginase-like [Salmo salar]	ASPG	gi 929085371	29538/4.98	253	3	36	0.019 1.1e005	K.QAGVSFNFADADGR.T R.DLFNNQPVDDAR.R