

Table S1. Mass spectrometry-based protein identifications and scores for epaulette shark cerebellum proteins that were regulated in response to episodic anoxia or hypoxia. Data from both post-source decay (PSD) and collision-induced dissociation (CID) MS/MS peptide fragmentation modes were searched against the NCBI non-redundant sequence database (chordates). Sequence coverage for peptide mass fingerprint spectra (% of overall sequence) are shown in parentheses for Mascot matches. The numbers of de novo sequences from MS/MS spectra that matched the protein in PEAKS Studio v4.5 searches are shown in parentheses after PEAKS scores.

Spot	VIP	VIP score	Protein identification	Abbrev.	Mascot Scores		PEAKS Scores		
					PSD	CID	PSD	CID	
a) Energy producing processes									
i) Glycolysis									
1.5-66			Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (<i>Paralichthys olivaceus</i>)	GAPDH	66 (8)	42 (8)	29 (4)	26 (2)	
ii) Oxidative phosphorylation/electron transport chain									
1.5-33	VIP06	1.69	mitochondrial ATP synthase alpha-subunit (<i>Cyprinus carpio</i>)	ATP5A1	94 (3)		85 (3)	30 (2)	
1.5-36	VIP08	1.68	ATP synthase subunit alpha (<i>Larus ridibundus</i>)	ATP5A1	72 (20)		40 (4)	29 (2)	
1.5-38			mitochondrial ATP synthase, H+ transporting F1 complex beta subunit (<i>Mus musculus</i>)	ATP5B	154 (8)	165 (12)	99 (4)	95 (4)	
	VIP16	1.59	NADH dehydrogenase flavoprotein 2, 24 kDa subunit	NDUFV2	88 (9)		98 (3)		
iii) Oxidative substrate switching									
1.5-64			3-oxoacid CoA transferase 1 precursor (<i>Homo sapiens</i>)	OXCT1	66 (6)	47 (6)	67 (2)	13 (1)	
1.5-26			methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (<i>Homo sapiens</i>)	MCCC2		80 (4)	11 (2)	99 (2)	
1.5-31			propionyl-CoA carboxylase (<i>Xenopus laevis</i>)	PCCA	145 (5)	142 (12)	96 (3)	99 (3)	
iv) Intracellular movement of energetic equivalents									
	VIP04	1.73	Voltage-dependent anion-selective channel protein 2 (<i>Xenopus laevis</i>)	VDAC2	49 (8)	36 (2)		85 (2)	
	VIP23	1.56	Voltage-dependent anion-selective channel protein 2 (<i>Squalus acanthias</i>)	VDAC2	87 (8)	49 (2)	97 (3)	90 (3)	
b) Energy consuming processes									
i) Proteolysis in proteasome									
1.5-39			proteasome 26S ATPase subunit 2 (<i>Homo sapiens</i>)	PSMC2	302 (19)	502 (24)	99 (10)	99 (10)	
1.5-40	VIP19	1.56	proteasome 26S non-ATPase subunit 11	PSMD11		362 (20)	48 (2)	99 (7)	

Spot	VIP	VIP score	Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
					PSD	CID	PSD	CID
ii) Lysosome								
1.5-29			H ⁺ -ATPase beta 1 subunit, lysosomal	ATP6VIB1	44 (3)	44 (2)	19 (2)	
iii) Transcription and mRNA processing								
2-7			splicing factor, arginine/serine-rich 5a (<i>Danio rerio</i>)	SFRS5	40 (5)	93 (2)		
1.5-62			RNA binding motif protein 8A (<i>Danio rerio</i>)	RBM8A	90 (22)	134 (28)	95 (6)	
iv) Translation								
1.5-30			seryl tRNA synthetase (<i>Danio rerio</i>)	SARS	32 (2)	94 (2)	97 (3)	
1.5-48			acidic ribosomal phosphoprotein PO (<i>Bos taurus</i>)	RPLP0	62 (3)	382 (17)	99 (3)	99 (6)
VIP43	1.48		elongation factor 1-delta (<i>Tetraodon nigroviridis</i>)	EEF1D	34 (4)	64 (2)		
c) Apoptosis and cell cycle								
1.5-14			far upstream element-binding protein (<i>Homo sapiens</i>)	FUBP1	178 (5)	87 (3)	99 (4)	93 (3)
1.5-23	VIP28	1.53	ubiquitin-conjugating enzyme E2D 2 isoform 1 (<i>Homo sapiens</i>)	UBE2D2	94 (18)	108 (16)	93 (4)	84 (4)
1.5-45			Protein phosphatase 1 alpha (<i>Danio rerio</i>)	PPP1CA		102 (14)	74 (4)	68 (4)
1.5-58			Ras-related nuclear protein (<i>Ictalurus punctatus</i>)	RAN	45 (10)	30 (8)	97 (3)	
VIP26	1.54		high mobility group box 2 (<i>Mus musculus</i>)	HMGB2		39 (3)		75 (2)
d) Neurotransmitters								
i) Glutamate synthesis/degradation								
1.5-27			glutaminase (<i>Rattus norvegicus</i>)	GLS	99 (5)	95 (5)		
ii) Receptor processing, vesicle fusion (exo- and endocytosis)								
1.5-15			N-ethylmaleimide sensitive fusion protein (<i>Cricetulus longicaudatus</i>)	NSF	160 (7)	38 (3)	99 (6)	53 (3)
VIP01	1.92		N-ethylmaleimide sensitive fusion protein attachment protein beta (<i>Mus musculus</i>)	NAPB		35 (2)	90 (1)	84 (1)
1.5-44			SH3 domain-containing Grb-2-like protein (<i>Xenopus tropicalis</i>)	SH3GL1	120 (8)	207 (11)	45 (1)	99 (5)
1.5-51	VIP09	1.67	clathrin light-chain B isoform 1 (<i>Monodelphis domestica</i>)	CLTA	83 (7)	95 (7)	41 (3)	88 (4)
VIP34	1.51		dihydropyrimidinase-like 2 (<i>Danio rerio</i>)/collapsin response mediator protein-1A	DPYSL2	53 (1)	60 (4)	41 (2)	90 (1)
1.5-52			toll interacting protein (<i>Xenopus tropicalis</i>)	TOLLIP		45 (5)		52 (2)

Spot	VIP	VIP score	Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
					PSD	CID	PSD	CID
e) Ca²⁺ binding								
2-14			novel protein similar to vertebrate EF hand calcium binding protein 2 (<i>Danio rerio</i>)	NECAB2	97 (4)	110 (6)	93 (4)	99 (3)
1.5-18	VIP31	1.52	calmodulin (<i>Clemmys japonica</i>)	CALM1	85 (39)	87 (22)	86 (3)	54 (2)
f) Molecular chaperones								
1.5-20			heat shock 70kDa protein 4-like (unnamed protein product, <i>Tetraodon nigroviridis</i>)	HSPA4L	60 (2)	47 (3)	93 (3)	
	VIP03	1.74	Chain A, dimerization and U-box domains of zebrafish c-terminal of HSP70 interacting protein	HSPBP1	119 (9)	136 (9)		95 (3)
1.5-56			prohibitin (<i>Equus caballus</i>)	PHB	36 (8)		76 (2)	20 (2)
g) Cytoskeleton								
i) Microtubular skeleton								
2-4	VIP47	1.47	alpha tubulin (<i>Gillichthys mirabilis</i>)	TUBA1A	248 (15)	266 (15)	98 (5)	99 (5)
2-5			alpha tubulin (<i>Gillichthys mirabilis</i>)	TUBA1A	201 (18)		99 (5)	
1.5-12			alpha tubulin	TUBA1A	151 (15)	245 (20)	99 (7)	99 (6)
1.5-13	VIP27	1.54	alpha tubulin subunit (<i>Oncorhynchus nerka</i>)	TUBA1A	262 (16)	279 (20)	99 (6)	99 (6)
1.5-28			alpha tubulin	TUBA1A	52 (3)		72 (2)	
1.5-32			alpha tubulin	TUBA1A	563 (28)	616 (31)	99 (11)	99 (11)
1.5-34			alpha tubulin	TUBA1A	83 (14)	43 (3)	76 (2)	
1.5-70			tubulin alpha	TUBA1A	73 (5)	137 (5)	63 (1)	97 (4)
1.5-50			alpha 4 tubulin	TUBA4A	164 (16)		83 (6)	
2-9			tubulin folding cofactor B (Cytoskeleton-associated protein 1) (LOC735205, <i>Xenopus laevis</i>)	TBCB		56 (4)		55 (1)
ii) Actin cytoskeleton and dendrite morphology								
1.5-42			beta actin	ACTB	31 (5)		66 (4)	27 (3)
1.5-11			marcks (myristoylated alanine-rich C-kinase substrate) calmodulin binding domain protein	MARCKS	48 (2)	29 (2)	89 (1)	55 (1)
1.5-10			dynammin 3	DNM3	93 (5)	52 (3)		79 (4)
iii) Intermediate filaments								
1.5-41			glial fibrillary acidic protein (<i>Mus musculus</i>)	GFAP		49 (1)	76 (3)	85 (2)

Spot	VIP	VIP score	Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
					PSD	CID	PSD	CID
iv) Cytoskeleton anchoring								
1.5-25	VIP35	1.51	ezrin	EZR	127 (3)	136 (7)	79 (3)	
1.5-54			nebulette (<i>Homo sapiens</i>)	NEBL	36 (5)		87 (1)	99 (2)
1.5-43			Ribosomal protein SA (laminin-binding protein) (<i>Homo sapiens</i>)	RPSA	183 (17)	184 (13)	99 (3)	99 (4)
h) Signalling pathways								
i) cAMP dependent protein kinase (PKA)								
2-6			cAMP-dependent protein kinase type II-beta regulatory subunit isoform 1 (<i>Canis familiaris</i>)	PRKAR2B	38 (6)		76 (2)	
1.5-37			cAMP-dependent protein kinase type I-alpha regulatory subunit (<i>Mus musculus</i>)	PRKAR1A	86 (3)	27 (3)		
ii) 14-3-3 mediated phosphoprotein adapter signalling								
1.5-55	VIP15	1.60	14-3-3 theta (<i>Danio rerio</i>)	YWHAQ	117 (11)	149 (11)	96 (4)	98 (4)
	VIP21	1.56	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (14-3-3 gamma) (<i>Danio rerio</i>)	YWHAG	215 (21)	139 (19)	99 (7)	94 (5)
	VIP46	1.47	14-3-3 beta (<i>Tetraodon nigroviridis</i>)	YWHAB	48 (4)		91 (2)	90 (1)
iii) G protein coupled receptors								
1.5-47			guanine nucleotide binding protein G(o), alpha subunit (<i>Salmo salar</i>)	GNAO1	31 (13)	76 (9)	86 (2)	63 (3)
i) ROS/oxidative stress								
1.5-35			Aldehyde dehydrogenase 7 family, member A1 (<i>Monodelphis domestica</i>)	ALDH7A1	100 (4)	55 (3)	81 (2)	66 (2)
j) Unannotated								
2-2	VIP29	1.53	novel protein (zgc:92871) (<i>Danio rerio</i>)		90 (15)	82 (15)	91 (2)	

Table S2. Significantly overrepresented pathways in the epaulette shark cerebellum and rectal gland proteomics datasets, identified with Ingenuity Pathways Analysis software. The *p* values were corrected for multiple testing using the method of Benjamini and Hochberg (3). Abbreviations as in Tables 4 and 5.

Treatment	Ingenuity Canonical Pathway	p _{BH}	Molecules
Cerebellum			
A1+24	Mitochondrial Dysfunction	0.044	ATP5A1
	Oxidative Phosphorylation	0.044	ATP5A1
H1+24	Melatonin Signaling	0.010	PRKAR2B, GNAO1, CALM1
	Synaptic Long Term Potentiation	0.010	PRKAR2B, PPP1CA, CALM1
	14-3-3-mediated Signaling	0.010	YWHAQ, TUBA4A, GFAP
	Corticotropin Releasing Hormone Signaling	0.010	PRKAR2B, GNAO1, CALM1
	Androgen Signaling	0.010	PRKAR2B, GNAO1, CALM1
	cAMP-mediated Signaling	0.017	PRKAR2B, GNAO1, CALM1
	CREB Signaling in Neurons	0.018	PRKAR2B, GNAO1, CALM1
	ERK/MAPK Signaling	0.019	YWHAQ, PRKAR2B, PPP1CA
	Cardiac Hypertrophy Signaling	0.030	PRKAR2B, GNAO1, CALM1
	Valine, Leucine and Isoleucine Degradation	0.030	OXCT1, MCCC2
	Nitric Oxide Signaling in the Cardiovascular System	0.030	PRKAR2B, CALM1
	Dopamine Receptor Signaling	0.030	PRKAR2B, PPP1CA
	Chemokine Signaling	0.030	PPP1CA, CALM1
	CDK5 Signaling	0.037	PRKAR2B, PPP1CA
	IGF-1 Signaling	0.037	YWHAQ, PRKAR2B
α-Adrenergic Signaling	0.037	PRKAR2B, CALM1	
H1+H2+24	Valine, Leucine and Isoleucine Degradation	0.007	PCCA, ALDH7A1, MCCC2
	Huntington's Disease Signaling	0.047	NSF, GLS, DNM3
	Glutamate Receptor Signaling	0.047	GLS, CALM1
	Propanoate Metabolism	0.047	PCCA, ALDH7A1
	Melatonin Signaling	0.049	CALM1, PRKAR1A
	Nitric Oxide Signaling in the Cardiovascular System	0.049	CALM1, PRKAR1A
Rectal gland			
A1+24	Glycolysis/Gluconeogenesis	0.000	PGAM1, GAPDH, PDHB
	Alanine and Aspartate Metabolism	0.002	GOT2, PDHB
	Valine, Leucine and Isoleucine Biosynthesis	0.033	PDHB
	Phenylalanine, Tyrosine and Tryptophan Biosynthesis	0.044	GOT2
	Pentose Phosphate Pathway	0.048	PDHB
	Glutamate Metabolism	0.048	GOT2
	Phenylalanine Metabolism	0.048	GOT2
	Cysteine Metabolism	0.049	GOT2
	Butanoate Metabolism	0.049	PDHB
	Tyrosine Metabolism	0.049	GOT2
	Ubiquinone Biosynthesis	0.049	NDUFS3
	Pyruvate Metabolism	0.049	PDHB
	IRF Activ. by Cytosolic Pattern Recognition Receptors	0.049	PPIB
Arginine and Proline Metabolism	0.050	GOT2	
H1+24	Butanoate Metabolism	0.000	ALDH4A1, SDHB, OXCT1, ACADS
	Valine, Leucine and Isoleucine Degradation	0.006	ALDH4A1, OXCT1, ACADS
	Mitochondrial Dysfunction	0.027	SDHB, NDUFS1, PARK7

	Calcium Signaling	0.036	TPM1, TPM4, PRKAR1A
	NRF2-mediated Oxidative Stress Response	0.036	PPIB, DNAJB11, FTH1
	β -alanine Metabolism	0.036	ALDH4A1, ACADS
	Huntington's Disease Signaling	0.036	HSPA8, SDHB, HSPA9
	Propanoate Metabolism	0.036	ALDH4A1, ACADS
	Arginine and Proline Metabolism	0.045	CKB, ALDH4A1
H1+H2+24	Butanoate Metabolism	0.000	OXCT1, DBT, PDHB, ALDH7A1
	Valine, Leucine and Isoleucine Degradation	0.000	OXCT1, DBT, ALDH7A1
	Histidine Metabolism	0.001	DBT, ALDH7A1
	Pyruvate Metabolism	0.002	PDHB, ALDH7A1
	Glycolysis/Gluconeogenesis	0.002	PDHB, ALDH7A1
	Lysine Degradation	0.005	DBT, ALDH7A1
	Valine, Leucine and Isoleucine Biosynthesis	0.014	PDHB
	Synthesis and Degradation of Ketone Bodies	0.017	OXCT1
	Ascorbate and Aldarate Metabolism	0.028	ALDH7A1
	Glycosphingolipid Biosynthesis - Ganglioseries	0.029	DBT
	Pentose Phosphate Pathway	0.030	PDHB
	Phenylalanine Metabolism	0.032	DBT
	Alanine and Aspartate Metabolism	0.032	PDHB
	Bile Acid Biosynthesis	0.036	ALDH7A1
	β -alanine Metabolism	0.039	ALDH7A1
	Propanoate Metabolism	0.039	ALDH7A1
	Tyrosine Metabolism	0.039	DBT
	Glycine, Serine and Threonine Metabolism	0.039	DBT
	Arginine and Proline Metabolism	0.041	ALDH7A1
	Aldosterone Signaling in Epithelial Cells	0.044	HSPA8
	Glycerolipid Metabolism	0.046	ALDH7A1

Table S3. Mass spectrometry-based protein identifications and scores for epaulette shark rectal gland proteins that were regulated in response to episodic anoxia or hypoxia. Data from both post-source decay (PSD) and collision-induced dissociation (CID) MS/MS peptide fragmentation modes were searched against the NCBI non-redundant sequence database (chordates). Sequence coverage for peptide mass fingerprint spectra (% of overall sequence) are shown in parentheses for Mascot matches. The numbers of de novo sequences from MS/MS spectra that matched the protein in PEAKS Studio v4.5 searches are shown in parentheses after PEAKS scores.

Spot	VIP	VIP score	Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
					PSD	CID	PSD	CID
a) Energy producing processes								
i) Glycolysis								
	VIP22	1.46	aldolase B (<i>Equus caballus</i>)	ALDOB	32 (1)		55 (2)	
	VIP11	1.57	triose phosphate isomerase (<i>Xiphophorus maculatus</i>)	TPH1	95 (52)			
1.5-47			glyceraldehyde-3-phosphate dehydrogenase (<i>Paralichthys olivaceus</i>)	GAPDH	34 (4)		22 (4)	47 (1)
1.5-60			phosphoglycerate mutase 1 (<i>Gallus gallus</i>)	PGAMI	100 (8)	150 (8)	96 (3)	99 (2)
ii) Pyruvate dehydrogenase complex								
2-12	VIP13	1.54	pyruvate dehydrogenase (lipoamide) beta (<i>Danio rerio</i>)	PDHB	107 (8)		93 (4)	
1.5-48	VIP17	1.51	pyruvate dehydrogenase (lipoamide) beta (<i>Danio rerio</i>)	PDHB	95 (4)	60 (6)	98 (3)	95 (3)
1.5-28			dihydrolipoamide branched chain transacylase E2 (<i>Taeniopygia guttata</i>)	DBT	76 (4)	133 (5)	99 (4)	89 (9)
iii) TCA cycle								
2-14			isocitrate dehydrogenase 2 (NADP+), mitochondrial	IDH2		76 (7)		81 (3)
iv) Oxidative phosphorylation/electron transport chain								
2-6			ATP synthase subunit alpha, mitochondrial precursor (<i>Salmo salar</i>)	ATP5A1	57 (4)	498 (23)	49 (4)	99 (9)
1.5-27			mitochondrial ATP synthase alpha subunit (<i>Scyliorhinus canicula</i>)	ATP5A1	281 (19)	201 (10)	99 (9)	99 (5)
	VIP23	1.44	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit (<i>Danio rerio</i>)	ATP5A1	586 (23)	374 (18)	99 (9)	99 (9)
1.5-10			NADH dehydrogenase (ubiquinone) Fe-S protein 1 (<i>Danio rerio</i>)	NDUFS1	24 (2)	33 (1)	78 (2)	22 (2)
1.5-11			NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (<i>Gallus gallus</i>)	NDUFS1	191 (5)	102 (2)	99 (5)	90 (2)
1.5-14			NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (<i>Gallus gallus</i>)	NDUFS1	99 (4)	85 (2)	93 (3)	99 (4)
1.5-54	VIP10	1.57	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NDUFS3	175 (9)	277 (16)	99 (3)	99 (7)
1.5-55			succinate dehydrogenase complex, subunit B, iron sulfur (lp) (<i>Danio rerio</i>)	SDHB	75 (4)	156 (16)	58 (3)	98 (4)

Spot	VIP score	VIP Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
				PSD	CID	PSD	CID
v) Intracellular movement of energetic equivalents (Malate aspartate shuttle, phosphocreatine circuit)							
1.5-35		mitochondrial aspartate aminotransferase	GOT2	35 (4)	68 (3)	11 (2)	
1.5-52	VIP02 1.67	voltage-dependent anion channel 2 (<i>Squalus acanthias</i>)	VDAC2	89 (5)	76 (5)	97 (2)	95 (3)
1.5-37		creatine kinase (<i>Scyltorhinus canicula</i>)	CKB	111 (10)	42 (7)	63 (3)	66 (1)
1.5-41		creatine kinase (<i>Scyltorhinus canicula</i>)	CKB	123 (12)	162 (20)	95 (7)	88 (7)
vi) Oxidative substrate switching							
1.5-24	VIP38 1.39	3-oxoacid CoA transferase (oxct1) (<i>Xenopus tropicalis</i>)	OXCT1	90 (1)	115 (4)	77 (2)	98 (3)
	VIP37 1.40	3-hydroxyacyl-CoA dehydrogenase	HADH	73 (6)	87 (8)	89 (2)	88 (3)
2-11		acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-specific	ACADS	29 (3)	33 (2)		71 (2)
b) Energy consuming processes							
i) Proteolysis							
1.5-53		ubiquitin carboxyl-terminal esterase L3 (thioesterase)	UCHL3		51 (5)		90 (2)
c) Apoptosis and cell cycle							
	VIP07 1.60	similar to Cytidylylase kinase (UMP-CMP kinase), partial (<i>Ornithorhynchus anatinus</i>)	CMPK1	53 (5)	78 (8)	67 (1)	90 (2)
	VIP05 1.63	Annexin VII	ANXA7	71 (3)	31 (3)	81 (2)	66 (1)
d) Vesicles, endocytosis, intracellular trafficking							
1.5-58		RAB37, member RAS oncogene family (<i>Homo sapiens</i>)	RAB37	31 (8)	62 (8)		99 (2)
2-16	VIP29 1.42	glioblastoma amplified sequence (NipSnap2)	GBAS	84 (6)	90 (8)	88 (3)	79 (3)
	VIP27 1.42	sorting nexin 4 (<i>Homo sapiens</i>)	SNX4	54 (6)	44 (3)	81 (4)	19 (1)
e) Molecular chaperones							
2-17		peptidylprolyl isomerase B (<i>Danio rerio</i>)	PPIB	45 (10)	135 (25)	85 (4)	81 (5)
1.5-18	VIP26 1.43	heat shock 70kDa protein 9B (75kDa glucose-regulated protein) (<i>Gallus gallus</i>)	HSPA9	68 (6)	73 (6)	79 (4)	80 (3)
1.5-19		heat shock cognate 70 kDa (<i>Carassius auratus</i>)	HSPA8	252 (18)	231 (13)	99 (5)	99 (8)
1.5-40		DnaJ (Hsp40) homolog, subfamily B, member 11 (<i>Homo sapiens</i>)	DNAJB11	77 (6)	34 (2)	93 (4)	
f) Cytoskeleton							
i) Microtubular skeleton							
	VIP14 1.54	tubulin beta-1 chain (<i>Gadus morhua</i>)	TUBB1	295 (17)	436 (26)	99 (11)	99 (12)

Spot	VIP score	VIP Protein identification	Abbrev.	Mascot Scores		PEAKS Scores	
				PSD	CID	PSD	CID
ii) Actin cytoskeleton							
2-26		tropomyosin (<i>Takifugu rubripes</i>)	TPM1	232 (14)	286 (28)	99 (6)	99 (9)
1.5-43		fast tropomyosin (<i>Scyllorhinus retifer</i>)	TPM1	71 (16)		54 (3)	
1.5-49		cytoskeletal tropomyosin 4 (<i>Coturnix coturnix</i>)	TPM4	61 (4)	180 (24)	91 (2)	87 (7)
1.5-36		tropomodulin 2 (<i>Danio rerio</i>)	TMOD2	138 (9)	174 (10)	94 (4)	97 (4)
iii) Intermediate filaments							
1.5-34		type II keratin K8 (<i>Scyllorhinus stellaris</i>)	KRT8		55 (6)	99 (4)	99 (2)
iv) Cytoskeleton anchoring							
1.5-9		radixin	RDX	51 (1)	120 (4)	92 (2)	97 (4)
1.5-12		moesin/radixin	MSN	64 (2)	71 (3)	48 (1)	92 (4)
1.5-13		similar to Moesin (Membrane-organizing extension spike protein)	MSN	33 (1)	99 (6)		
v) mitochondrial cristae structure							
1.5-6		mitofilin (mitochondrial inner membrane protein) (<i>Homo sapiens</i>)	IMMT	52 (1)	70 (1)	91 (2)	90 (2)
g) Signalling pathways							
i) cAMP dependent protein kinase (PKA)							
1.5-31		cAMP-dependent protein kinase, regulatory subunit alpha 1 (<i>Homo sapiens</i>)	PRKARIA	212 (15)		99 (6)	
ii) 14-3-3 mediated phosphoprotein adapter signalling							
2-15		14-3-3 epsilon	YWHAE		46 (7)		44 (2)
1.5-51		14-3-3 epsilon (tyrosine 3/tryptophan 5 -monoxygenase activation protein, epsilon polypeptide)	YWHAE	378 (33)	138 (15)	99 (9)	99 (8)
iii) Oxygen sensing							
VIP25	1.43	cystathionase (<i>Danio rerio</i>)	CTH	70 (3)	65 (3)	93 (2)	90 (1)
h) ROS/oxidative stress							
2-21	VIP01	2.02 glyoxalase domain containing 5	GLOD5	62 (3)	69 (3)		96 (2)
1.5-23		aldehyde dehydrogenase 4 family, member A1 (<i>Danio rerio</i>)	ALDH4A1		59 (2)		87 (2)
1.5-26		aldehyde dehydrogenase 7 family, member A1	ALDH7A1	25 (1)	32 (1)	83 (3)	
1.5-71		ferritin, heavy polypeptide	FTH1	23 (7)	30 (7)	73 (2)	
1.5-64		Parkinson disease 7 (DJ-1)	PARK7	76 (7)	93 (7)	98 (3)	79 (3)
VIP20	1.47	Ubiquinone biosynthesis methyltransferase COQ5 (unnamed protein product, <i>Tetraodon nigroviridis</i>)	COQ5	35 (4)	71 (4)		93 (3)

Table S4. Expression ratios for epaulette shark cerebellum proteins that were regulated by episodic anoxia (A1+24) or hypoxia (H1+24; H1+H2+24) but that were not identified using mass spectrometry. Values in bold font met the statistical ($p < 0.05$) and expression ratio (< 0.67 or > 1.5) criteria for mass spectrometry analysis in that treatment. Variable importance in the projection ranks (VIP) based on a partial least squares discriminant analysis are also presented.

Spot	VIP	A1+24	p	H1+24	p	H1+H2+24	p
2-1	VIP02	0.55	0.006	0.46	0.001	0.69	0.037
2-3		0.92	0.798	0.79	0.484	0.35	0.031
2-8	VIP37	0.41	0.029	0.54	0.088	0.70	0.260
2-10		0.97	0.744	0.47	0.004	0.65	0.053
2-11		0.56	0.111	0.68	0.387	0.41	0.026
2-12		1.29	0.269	1.81	0.015	2.21	0.006
2-13		0.92	0.812	0.51	0.236	0.30	0.041
1.5-16		0.87	0.352	1.28	0.153	1.67	0.019
1.5-17		0.51	0.033	0.85	0.478	0.85	0.580
1.5-19		1.10	0.718	1.75	0.012	1.77	0.066
1.5-21		1.04	0.893	1.25	0.461	0.53	0.047
1.5-22	VIP30	1.98	0.029	1.46	0.256	1.16	0.469
1.5-24		1.68	0.148	1.74	0.022	1.48	0.086
1.5-46		1.17	0.588	0.58	0.045	0.75	0.331
1.5-49		0.83	0.107	0.67	0.031	0.68	0.019
1.5-53		0.91	0.570	0.64	0.040	0.90	0.567
1.5-57	VIP13	1.50	0.025	1.48	0.049	1.16	0.406
1.5-59		1.09	0.696	0.57	0.015	1.70	0.461
1.5-60		0.79	0.261	0.61	0.044	0.61	0.051
1.5-61	VIP14	0.56	0.021	0.62	0.011	0.75	0.061
1.5-63		0.93	0.677	0.70	0.013	0.55	0.004
1.5-65		1.01	0.957	0.88	0.570	0.50	0.007
1.5-67		0.67	0.269	0.52	0.026	0.57	0.012
1.5-68		1.26	0.492	1.46	0.051	1.65	0.020
1.5-69		0.88	0.322	1.33	0.028	1.72	0.023
	VIP05	1.16	0.398	1.29	0.022	0.70	0.113
	VIP07	0.79	0.073	0.69	0.032	1.02	0.766
	VIP10	0.83	0.048	0.84	0.062	0.78	0.006
	VIP11	0.71	0.001	0.82	0.163	0.82	0.023
	VIP12	0.84	0.219	1.25	0.188	0.81	0.130
	VIP17	0.81	0.094	0.83	0.329	1.20	0.081
	VIP18	0.84	0.048	0.64	0.000	0.81	0.061
	VIP20	0.85	0.023	0.75	0.006	0.82	0.031
	VIP22	0.83	0.046	0.77	0.028	0.93	0.481
	VIP24	1.15	0.035	0.95	0.616	1.18	0.182
	VIP25	0.88	0.632	1.37	0.114	0.84	0.461
	VIP32	1.40	0.030	0.96	0.721	0.90	0.437

Spot	VIP	A1+24	p	H1+24	p	H1+H2+24	p
VIP33	0.70	0.058	1.21	0.239	0.89	0.562	
VIP36	1.04	0.588	0.99	0.823	0.85	0.002	
VIP38	1.05	0.775	1.27	0.099	0.87	0.357	
VIP39	1.25	0.173	1.52	0.077	0.99	0.928	
VIP40	0.99	0.865	0.90	0.021	0.80	0.009	
VIP41	1.09	0.723	0.71	0.303	2.90	0.108	
VIP42	1.07	0.651	1.10	0.384	0.72	0.054	
VIP44	1.12	0.279	1.27	0.198	0.87	0.295	
VIP45	1.39	0.060	0.99	0.915	0.91	0.471	
VIP48	1.60	0.066	0.81	0.202	1.04	0.881	
VIP49	1.15	0.163	1.37	0.055	1.02	0.867	

Table S5. Expression ratios for epaulette shark rectal gland proteins that were regulated by episodic anoxia (A1+24) or hypoxia (H1+24; H1+H2+24) but that were not identified using mass spectrometry. Values in bold font met the statistical ($p < 0.05$) and expression ratio (< 0.67 or > 1.5) criteria for mass spectrometry analysis in that treatment. Variable importance in the projection ranks (VIP) based on a partial least squares discriminant analysis are also presented.

Spot	VIP	A1+24	p	H1+24	p	H1+H2+24	p
2-1		1.56	0.358	2.49	0.014	1.93	0.037
2-2		0.65	0.015	0.45	0.002	0.90	0.757
2-3		0.71	0.056	0.40	0.000	1.03	0.954
2-4		1.11	0.722	0.49	0.023	0.79	0.317
2-5		1.05	0.875	0.37	0.001	0.69	0.072
2-7		2.09	0.101	2.18	0.010	1.96	0.049
2-8		0.99	0.976	2.33	0.039	1.55	0.326
2-9		0.84	0.624	2.07	0.042	1.59	0.079
2-10		1.02	0.960	2.44	0.001	1.64	0.125
2-13		1.97	0.070	2.21	0.006	1.41	0.417
2-18		1.07	0.841	2.02	0.003	1.33	0.222
2-19		1.06	0.906	2.23	0.016	1.86	0.141
2-20		1.38	0.292	2.12	0.006	1.48	0.170
2-22	VIP12	0.74	0.513	2.84	0.001	1.84	0.061
2-23		0.98	0.967	3.60	0.001	3.07	0.008
2-24		1.64	0.163	2.58	0.009	3.14	0.014
2-25		0.86	0.564	0.49	0.048	0.97	0.959
2-27	VIP33	3.21	0.045	2.01	0.080	1.44	0.455
1.5-1		1.43	0.500	1.87	0.001	1.37	0.041
1.5-2		1.23	0.447	1.88	0.023	1.58	0.004
1.5-3		0.89	0.649	1.64	0.040	1.60	0.105
1.5-4		1.06	0.882	1.52	0.023	1.30	0.079
1.5-5		1.23	0.402	1.25	0.387	1.88	0.046
1.5-7		0.81	0.201	0.61	0.027	0.88	0.590
1.5-8		0.85	0.335	0.63	0.041	0.93	0.756
1.5-15		0.79	0.312	0.57	0.048	0.78	0.305
1.5-16		1.00	0.987	0.65	0.048	0.92	0.734
1.5-17		0.99	0.945	0.65	0.028	0.97	0.890
1.5-20		1.44	0.216	1.56	0.223	1.95	0.041
1.5-21		0.83	0.379	0.59	0.041	0.80	0.286
1.5-22		0.85	0.347	0.56	0.009	0.83	0.258
1.5-25	VIP19	0.72	0.134	0.57	0.001	0.51	0.000
1.5-29		1.00	0.997	1.52	0.005	1.35	0.059
1.5-30		0.99	0.945	0.59	0.032	0.92	0.657
1.5-32		1.11	0.745	1.17	0.514	1.52	0.037

Spot	VIP	A1+24	p	H1+24	p	H1+H2+24	p
1.5-33		0.87	0.594	0.53	0.006	0.80	0.231
1.5-38		0.66	0.038	1.01	0.969	1.33	0.293
1.5-39		0.07	0.015	1.74	0.466	0.26	0.012
1.5-42		0.90	0.708	1.56	0.001	1.32	0.139
1.5-44		0.60	0.014	0.75	0.115	0.81	0.258
1.5-45		1.05	0.851	1.61	0.015	1.23	0.120
1.5-46		1.18	0.388	2.00	0.029	1.61	0.193
1.5-50		1.11	0.672	1.90	0.005	1.87	0.096
1.5-56	VIP32	1.00	0.983	1.59	0.001	1.57	0.001
1.5-57		0.99	0.952	0.63	0.049	0.84	0.261
1.5-59	VIP31	0.89	0.543	1.56	0.011	1.03	0.852
1.5-61		1.10	0.700	1.51	0.220	1.74	0.021
1.5-62	VIP35	0.82	0.187	0.66	0.018	0.92	0.474
1.5-63		1.00	0.972	0.59	0.036	1.01	0.969
1.5-65		0.84	0.284	0.62	0.005	0.64	0.003
1.5-66		0.72	0.136	2.67	0.391	0.64	0.038
1.5-67		1.40	0.130	1.89	0.022	1.25	0.364
1.5-68		1.05	0.869	1.85	0.035	1.35	0.206
1.5-69		1.42	0.159	1.67	0.011	1.28	0.302
1.5-70		1.00	0.981	1.75	0.019	1.39	0.051
1.5-72		0.50	0.043	1.67	0.016	1.40	0.422
1.5-73		1.00	0.990	1.81	0.027	1.39	0.271
1.5-74		2.74	0.032	5.72	0.033	2.82	0.048
	VIP03	0.92	0.642	1.37	0.031	0.95	0.768
	VIP04	0.67	0.006	0.73	0.002	0.74	0.028
	VIP06	1.23	0.008	1.24	0.001	1.15	0.032
	VIP08	0.74	0.009	0.72	0.003	0.72	0.001
	VIP09	0.58	0.059	0.92	0.454	0.73	0.027
	VIP15	0.79	0.021	1.05	0.488	1.05	0.536
	VIP16	0.79	0.031	0.82	0.018	0.89	0.108
	VIP18	0.99	0.770	0.73	0.000	0.85	0.067
	VIP21	0.71	0.040	0.97	0.870	1.07	0.507
	VIP24	0.97	0.912	1.29	0.451	1.04	0.891
	VIP28	0.78	0.289	0.85	0.297	0.68	0.067
	VIP30	1.01	0.944	0.89	0.155	1.06	0.523
	VIP34	1.09	0.323	0.74	0.002	0.76	0.012
	VIP36	0.75	0.016	0.82	0.065	0.82	0.081