

### Na<sup>+</sup>/H<sup>+</sup>-exchanger 3 regulator

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	121 bits(304)	5e-31	Compositional matrix adjust.	57/72(79%)	61/72(84%)	0/72(0%)
A.F.	28	PRLCSLSKGTGGYGFNLHGEKKGKHFQFIRAVDPGSPADLAGVKPGDRVIEVSGTNIERET			87	
		PRLC L +G YGFFNLHGEKG HGQFIRAVD SPA+ AG+KPGDRVIEV+ TNIERE				
S.K.	10	PRLCHLVRGDKGYGFNLHGEKGGHGFQFIRAVDKDSPAEAGLKPGRVIEVNNNTNIERN			69	
A.F.	88	HSQVVARIRADG			99	
		HSQVVARIRA G				
S.K.	70	HSQVVARIRAGG			81	

### Aspartate aminotransferase

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	203 bits(517)	4e-61	Compositional matrix adjust.	92/117(79%)	105/117(89%)	0/117(0%)
A.F.	1	QSFAKNMGLYGERVGFSLICQDADEAKRCESQLKIIIRPMYSNPPVNGARIASTIMNTP			60	
		QSFAKNMGLYGERVG F+++C A+EAKR ESQ+KI+IRPMYSNPP+NGARIASTI+NTP				
S.P.	276	QSFAKNMGLYGERVGGFTVLCSSAAEEAKRVESQIKILIRPMYSNPPVNGARIASTIILNTP			335	
A.F.	61	DLNTVWLDELKVMMSGRIITMREQLVANLQKEGSTRNQWQHITDQIGMFCFTGIGPDQV			117	
		+L +WL EL+ MSGRII+MREQLVANLQKEGST NWQHITDQIGMFCFTG+ QV				
S.P.	336	ELYELWLGLRQMSGRIISMREQLVANLQKEGSTHNWQHITDQIGMFCFTGLNXXQV			392	

### Glutamate dehydrogenase 1

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	191 bits(485)	1e-59	Compositional matrix adjust.	91/102(89%)	96/102(94%)	0/102(0%)
A.F.	1	YFEWLKLNHNHVSYGRITFKYERDSNTFLESVQESLERKFGRHGGRIPIVPESEKQARIS			60	
		YFEWLKLNHNHVSYGRITFKYERDSN LL SVQESLERKFG+HGG IPIV+ +FQ RIS				
M.M	47	YFEWLKLNHNHVSYGRITFKYERDSNYHLLMSVQESLERKFGKHGGTIPIVPTAEFQDRIS			106	
A.F.	61	GATEKDIVNSGLAYTMERSARQIMRTAMKYNLGLDLRТАAYV			102	
		GA+EKDIV+SGLAYTMERSARQIMRTAMKYNLGLDLRТАAYV				
M.M.	107	GASEKDIVHNSGLAYTMERSARQIMRTAMKYNLGLDLRТАAYV			148	

### Succinate dehydrogenase

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	86.3 bits(212)	7e-19	Compositional matrix adjust.	48/113(42%)	71/113(62%)	10/113(8%)
A.F.	3	MATNSLLRANRVLSLAPSLMGKTCL--PCCSRTPLVVGSTKLHTSPQRHSGDGHGMMGS			60	
		MA N +LR+ R L +P LM L P + P ++ + LHT+ H+ G++ S				
S.P.	1	MAMN-ILRS-RALLTS PRLMTSAFLKSPYQANYPAMLNT--LHTTHNNHTA----GLLPS			52	
A.F.	61	THWNIERAVIIGMGLTPAALITHHPALDVALSAAFVVGHWGLENIFTDYVY			113	
		HWN ER + IG++G+ PAA + +PALD AL+A+ V+HGHWG+E +F DYV+				
S.P.	53	KHWNAERVLSIGLIGIIPAAFLIQNPALDYALAASLVLHGHWGMEQVFLDYVH			105	

### D-lactate dehydrogenase

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	113 bits(283)	4e-28	Composition-based stats.	55/74(74%)	59/74(79%)	0/74(0%)
A.F.	2	VQPGVTRNALNDYL RDQGLCFPIDPGADASLCGMAATSASGTNAVRYGTTWENVMLLEV				61
		VQPGVTR LN YLRDQGL FPIDPGADAS+CGM ATASGTNAVRYGT ENVMNL+VV				
S.K.	148	VQPGVTRKMLNKYL RDQGLWFPIIDPGADASICGMCATSASGTNAVRYGTMRENVMLQVV				207
A.F.	62	LSRWNINRYCWQ GK	75			
		L+ I +GK				
S.K.	208	LADGTIINTAGEGK	221			

### Na<sup>+</sup>/HCO<sub>3</sub><sup>-</sup> cotransporter

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	72.8 bits(177)	7e-13	Composition-based stats.	36/77(47%)	48/77(62%)	0/77(0%)
A.F.	1	ESGSTRRKTQVVGCREQRVTGFVVFLLI GLAVLMTNYYWLFQCQYYMAYSSSVGISSXKG				60
		E + + ++VGCREQRVTG +VF++IGLA LMT			+GI+S KG	
S.P.	915	ECKAPGERPKIVGCREQRVTGVMVFVMIGLATLMTKILSYVPMPLYGVFLFMGIASLKG				974
A.F.	61	VQFVNRLNLLFMPXKHH	77			
		VQFV+RL+L FMP K+				
S.P.	975	VQFVDRLSLFFMPLKYQ	991			

### V-type proton ATPase subunit d 1-like isoform 1

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	115 bits(288)	1e-29	Composition-based stats.	48/55(87%)	54/55(98%)	0/55(0%)
A.F.	1	HEVKLVNNGFMQQFHYGVFYSYVKLKEQECRNIVWIAECVAQRQRGKIDNYIPIL				55
		HEV+LN+N F+QQFH+GVFY+YVKLKEQECRNIVWIAECVAQRQRGKIDNYIPI+				
S.P.	294	HEVRLNINAF LQQFHFVGFYAYVKLKEQECRNIVWIAECVAQRQRGKIDNYIPIM				348

### sodium/potassium ATPase alpha subunit

	<b>Score</b>	<b>Expect</b>	<b>Method</b>	<b>Identities</b>	<b>Positives</b>	<b>Gaps</b>
	96.3 bits(238)	1e-21	Composition-based stats.	41/47(87%)	44/47(93%)	0/47(0%)
A.F.	1	YAQRKVLEYTCHTAFFVSIVVVQWADVIIICKTRKNSLIHQGMHNWVL				47
		+ QRK LEYTCHTAFF SIVVVQWADVIIICKTR+NSLIHQGM+NWVL				
S.P.	918	FYQRKQLEYTCHTAFFASIVVVQWADVIIICKTRRNSLIHQGMNNWVL				964

glucose-6-phosphate 1-dehydrogenase -like

Score	Expect	Method	Identities	Positives	Gaps
98.2 bits(243)	7e-23	Composition-based stats.	45/66(68%)	51/66(77%)	0/66(0%)
A.F.	1	KPATTNAEDIRNEKVKVLKTI EALELKDVVLGQYVGD PDGEGDAKEGYLEDPTVP	55		
		KPA+T AEDIRNEKVKVLK I L + D+VLGQY GDPDGE GDAKEGYL+D TVP			+G
S.P.	232	KPASTGAEDIRNEKVKVLK AISPLTVDDMVLGQYEGDPDGE GDAKEGYLDDSTVP	286		
A.F.	66	RGICHPNLCYG 66			
		+G+G P +			
S.P.	298	KGSTTPTFAFA 297			

alanine aminotransferase 2-like

Score	Expect	Method	Identities	Positives	Gaps
60.8 bits(146)	2e-09	Composition-based stats.	23/37(62%)	31/37(83%)	0/37(0%)
A.F.	1	DEESGWSLQIPELKRAIDEARKHCKPVAMVVINPGQP 37			
		DE++ WSL + EL+R+I+EARKHC P A+V+INPG P			
S.P.	239	DEDNAWSLDM AELQRSINEARKHCTPRAIVIINPGNP 275			

**Figure S1** Deduced amino acid alignments of gene sequences used for gene expression analyses. Sequences of *Amphiura filiformis* (A.F.) are aligned with related sequences from *Strongylocentrotus purpuratus* (S.P.), *Saccoglossus kowalevskii* (S.K.) *Macaca mulatta* (M.M.).

**Table S1** Biometric data (long-term experiment n = 4). Growth of body parts (disc, arms) during exposure to three pH levels (pH 8.1, pH 7.3 and pH 7.0), wet mass (WM), dry mass (DM), ash-free dry mass (AFDM) and ash dry mass (ADM) along the experimental time of 4 weeks. Values are given as means  $\pm$  SE. No statistical differences were measured (Two way ANOVA see table S2).

	day 7			day 14		
	pH 8.1	pH 7.3	pH 7.0	pH 8.1	pH 7.3	pH 7.0
<u>WM</u>						
total	287.23 $\pm$ 12.57	301.13 $\pm$ 29.92	282.50 $\pm$ 9.13	274.82 $\pm$ 12.93	260.34 $\pm$ 7.31	268.77 $\pm$ 20.21
disc	69.48 $\pm$ 2.46	69.86 $\pm$ 5.94	68.13 $\pm$ 4.49	64.48 $\pm$ 3.02	66.25 $\pm$ 2.79	65.91 $\pm$ 5.18
arms	217.75 $\pm$ 11.99	231.27 $\pm$ 24.18	214.37 $\pm$ 8.04	210.34 $\pm$ 12.01	194.09 $\pm$ 4.67	202.86 $\pm$ 16.47
<u>DM</u>						
total	104.97 $\pm$ 3.83	108.82 $\pm$ 10.39	106.89 $\pm$ 3.87	108.31 $\pm$ 4.35	100.23 $\pm$ 1.79	104.87 $\pm$ 6.89
disc	24.44 $\pm$ 0.69	24.88 $\pm$ 1.96	24.40 $\pm$ 1.53	24.16 $\pm$ 1.06	23.54 $\pm$ 0.52	24.54 $\pm$ 1.80
arms	80.53 $\pm$ 3.98	83.93 $\pm$ 8.49	82.49 $\pm$ 3.18	84.15 $\pm$ 4.12	76.68 $\pm$ 1.39	80.32 $\pm$ 5.29
<u>AFDM</u>						
total	54.57 $\pm$ 2.01	51.70 $\pm$ 3.89	51.64 $\pm$ 6.23	60.32 $\pm$ 2.38	54.61 $\pm$ 0.17	56.91 $\pm$ 2.66
disc	14.62 $\pm$ 0.40	14.06 $\pm$ 0.94	13.95 $\pm$ 1.56	15.25 $\pm$ 0.66	14.60 $\pm$ 0.25	15.72 $\pm$ 1.02
arms	39.95 $\pm$ 2.06	37.64 $\pm$ 2.98	37.70 $\pm$ 4.84	45.07 $\pm$ 2.17	40.01 $\pm$ 0.40	41.18 $\pm$ 1.92
<u>ADM</u>						
total	50.40 $\pm$ 1.93	57.12 $\pm$ 8.34	55.25 $\pm$ 3.33	48.00 $\pm$ 2.03	45.62 $\pm$ 1.77	47.96 $\pm$ 4.40
disc	9.82 $\pm$ 0.42	10.82 $\pm$ 1.35	10.46 $\pm$ 0.86	8.92 $\pm$ 0.43	8.95 $\pm$ 0.37	8.82 $\pm$ 0.80
arms	40.58 $\pm$ 2.12	46.29 $\pm$ 7.02	44.79 $\pm$ 2.77	39.08 $\pm$ 1.96	36.67 $\pm$ 1.44	39.14 $\pm$ 3.69
<u>Ratio ADM/DM</u>						
total	480.12 $\pm$ 4.54	515.31 $\pm$ 31.05	522.73 $\pm$ 46.92	443.02 $\pm$ 3.24	454.39 $\pm$ 9.29	454.02 $\pm$ 12.51
disc	401.49 $\pm$ 9.09	429.81 $\pm$ 24.65	433.22 $\pm$ 41.52	368.85 $\pm$ 5.33	379.41 $\pm$ 8.99	357.23 $\pm$ 9.58
arms	503.90 $\pm$ 8.55	540.68 $\pm$ 32.45	548.88 $\pm$ 48.67	464.30 $\pm$ 2.49	477.47 $\pm$ 10.27	483.67 $\pm$ 15.24
<hr/>						
	day 21			day 28		
	pH 8.1	pH 7.3	pH 7.0	pH 8.1	pH 7.3	pH 7.0
<u>WM</u>						
total	258.66 $\pm$ 25.57	253.49 $\pm$ 15.77	236.13 $\pm$ 25.80	247.15 $\pm$ 6.73	216.24 $\pm$ 31.94	226.44 $\pm$ 16.90
disc	64.88 $\pm$ 4.62	71.57 $\pm$ 3.33	62.26 $\pm$ 5.68	62.71 $\pm$ 2.61	58.78 $\pm$ 9.33	59.07 $\pm$ 3.10
arms	193.78 $\pm$ 21.08	181.92 $\pm$ 13.00	173.87 $\pm$ 20.12	184.44 $\pm$ 4.18	157.46 $\pm$ 22.99	167.37 $\pm$ 13.96
<u>DM</u>						
total	104.73 $\pm$ 11.69	102.07 $\pm$ 6.45	96.82 $\pm$ 11.09	100.27 $\pm$ 2.68	88.04 $\pm$ 13.18	91.16 $\pm$ 5.95
disc	23.92 $\pm$ 1.80	25.83 $\pm$ 1.07	22.88 $\pm$ 1.72	23.13 $\pm$ 0.89	20.21 $\pm$ 2.55	21.65 $\pm$ 0.92
arms	80.81 $\pm$ 9.94	76.25 $\pm$ 5.42	73.94 $\pm$ 9.39	77.14 $\pm$ 1.84	67.83 $\pm$ 10.65	69.51 $\pm$ 5.08
<u>AFDM</u>						
total	55.07 $\pm$ 6.35	54.49 $\pm$ 3.51	51.72 $\pm$ 6.32	56.62 $\pm$ 1.70	49.45 $\pm$ 7.60	51.41 $\pm$ 3.60
disc	14.00 $\pm$ 1.07	15.21 $\pm$ 0.76	13.64 $\pm$ 1.19	14.49 $\pm$ 0.58	12.57 $\pm$ 1.72	13.47 $\pm$ 0.80
arms	41.07 $\pm$ 5.28	39.28 $\pm$ 2.86	38.09 $\pm$ 5.14	42.13 $\pm$ 1.18	36.88 $\pm$ 5.91	37.94 $\pm$ 2.84
<u>ADM</u>						
total	49.66 $\pm$ 5.35	47.58 $\pm$ 2.99	45.10 $\pm$ 4.77	43.65 $\pm$ 1.00	38.59 $\pm$ 5.58	39.75 $\pm$ 2.35
disc	9.92 $\pm$ 0.77	10.62 $\pm$ 0.45	9.25 $\pm$ 0.53	8.64 $\pm$ 0.34	7.65 $\pm$ 0.84	8.18 $\pm$ 0.12
arms	39.75 $\pm$ 4.66	36.97 $\pm$ 2.56	35.85 $\pm$ 4.26	35.01 $\pm$ 0.67	30.95 $\pm$ 4.75	31.57 $\pm$ 2.24
<u>Ratio ADM/DM</u>						
total	475.13 $\pm$ 2.64	466.34 $\pm$ 4.10	468.09 $\pm$ 4.53	435.56 $\pm$ 2.34	439.90 $\pm$ 2.62	436.92 $\pm$ 3.00
disc	414.23 $\pm$ 8.59	411.76 $\pm$ 11.15	406.81 $\pm$ 8.11	373.60 $\pm$ 4.60	381.47 $\pm$ 6.98	379.87 $\pm$ 10.66
arms	493.62 $\pm$ 3.63	485.07 $\pm$ 1.69	487.41 $\pm$ 4.55	454.13 $\pm$ 2.46	457.79 $\pm$ 2.42	454.57 $\pm$ 1.23

**Table S2** Statistical information to the biometric data presented in table S1. Two way ANOVA was performed to test for differences between pH treatments and time factor (n = 4).

	disc		arms		total	
	F (2;3;6)	p	F (2;3;6)	p	F (2;3;6)	p
<u>WM</u>						
pH	0.226	0.799	0.452	0.64	0.3	0.742
time	1.228	0.314	4.045	0.014	495.552	<0.001
pH x time	0.213	0.97	0.235	0.962	0.195	0.976
<u>DM</u>						
pH	0.0879	0.916	0.392	0.679	0.326	0.724
time	1.581	0.211	1.072	0.373	1.187	0.328
pH x time	0.437	0.849	0.154	0.987	0.174	0.982
<u>AFDM</u>						
pH	0.172	0.842	0.845	0.438	0.689	0.509
time	0.939	0.432	0.415	0.743	0.504	0.682
pH x time	0.393	0.879	0.0461	1	0.0856	0.997
<u>ADM</u>						
pH	0.157	0.855	0.0475	0.954	0.035	0.966
time	4.274	0.011	3.353	0.029	3.535	0.024
pH x time	0.412	0.866	0.32	0.922	0.322	0.921
<u>Ratio ADM/DM</u>						
pH	0.325	0.725	0.489	0.617	0.393	0.678
time	5.144	0.005	6.192	0.002	0.023	0.002
pH x time	0.292	0.937	0.319	0.923	0.319	0.923