

Table S1. Primers used in the qRT-PCR analysis

Primers	Sequence (5' - 3')	Amplified gene
α Tub1	TGTCGTCCCCAAGGAT	α -tubulin
α Tub2	GTTCTCTTGGTCTTGATGGT	
β act1	CTCTCTTTCTACCTTCCAACT	β -actin
β act2	AGGACCAGATTCATCATATTC	
GPx1A	CTTGGGCTGAGTCTGAAA	<i>TtGPx1</i>
GPx1B	GAAAAGAGGGAATTCTACGT	
GPx3A	TAGCAAATAATACTCCTGGAT	<i>TtGPx3</i>
GPx3B	GGTTTTCCCTCAGCATT	
GPx9A	CCCGATGGTAAGGTTCA	<i>TtGPx9</i>
GPx9B	CAGCTATCATATCGTTAGGAT	
GPx10A	GTGATGGTACAGTTCATAGTT	<i>TtGPx10</i>
GPx10B	AGGTTCAATTTCTTTTGGTT	
GPx11A	AAGGTAGAGGTAAATGGTTCA	<i>TtGPx11</i>
GPx11B	AGAAGAATGTCTCTTCAAGAA	
GPx12A	CTAGTATACAAGATGATTCTG	<i>TtGPx12</i>
GPx12B	GTCTCTACTGAAAAGCTTAAT	

Table S2. Quantitative RT-PCR standard-curve parameters

Gene	Slope	Efficiency (%)	R ² ⁽¹⁾
α -tubulin	- 3.43	95.56	0.99
β -actin	- 3.35	98.98	0.99
<i>TtGPx1</i>	- 3.47	93.96	0.99
<i>TtGPx3</i>	- 3.58	90.16	0.99
<i>TtGPx9</i>	- 3.52	92.24	0.99
<i>TtGPx10</i>	- 3.50	92.92	0.99
<i>TtGPx11</i>	- 3.42	96.14	0.99
<i>TtGPx12</i>	- 3.33	99.77	0.99

⁽¹⁾ Correlation coefficient. Efficiency (E) is calculated from the slope value of the standard curve: $E = 10^{(-1/\text{slope})-1}$

Table S3. Characteristics of ciliate GPx SECIS elements.

GPx	Location ⁽¹⁾	Length (b)	DNA strand ⁽²⁾	Type ⁽³⁾	Score ⁽⁴⁾	Grade ⁽⁵⁾
TtGPx10	3'UTR (96 b -> Stop)	82	+	I	22.19 (C)	A
TbGPx6	3'UTR (63 b -> Stop)	77	+	I	14.89 (I)	A
					27.17 (C)	
TbGPx7	3'UTR (121 b -> Stop)	74	+	I	13.97 (I)	A
					21.84 (C)	
TmGPx9	3'UTR (48 b -> Stop)	74	+	I	13.54 (I)	A
					23.89 (C)	
TmGPx10	3'UTR (99 b -> Stop)	82	+	I	30.28 (C)	A
EocGPx1	3'UTR (29 b -> Stop)	71	+	I	14.49 (C)	A
TeGPx8	2 ^o intron	75	+	I	19.34 (I)	A
					29.61 (C)	
StyGPx5	ORF (337 b -> ATG)	59	-	I	13.89 (I)	B
					1.35 (C)	
StyGPx6	5'UTR (105 b -> Tel)	71	-	I	18.71 (I)	B
					14.89 (C)	

⁽¹⁾ Nine possible SECIS locations have been detected: in the 3'UTR region (the number of bases (b) from the stop codon to the SECIS element is indicated), within an intron (the intron number is indicated), in the ORF or coding region (the number of bases from the start codon to the SECIS element is indicated), or in the 5'UTR region (the number of bases from the telomere to the SECIS element is indicated). ⁽²⁾ Strand on which the SECIS element was found: (+): on the sequence as it was input, (-): on its reverse complement.

⁽³⁾ Eukaryotic SECIS Type-I or II. ⁽⁴⁾ The search method(s) predicted the SECIS element: by Covels (C) program and/or Infernal (I) program. ⁽⁵⁾ Marker for how good the SECIS prediction looks like. The SECIS grade can be A, B, C in decreasing order of goodness.

Table S4. Secondary structure characteristics of ciliate SECIS elements.

GPx	SECIS core ⁽¹⁾ (UGAN/KGAW)	Conserved A in Loop-II	Stem-I (bp)	Stem-II ⁽²⁾ (bp)	Loop-I (b)	Loop-II (b)	Mismatches bases (bp)	Non-canonical pairing (AG/GA)
TtGPx10	UGAA/UGAA	3	7	11	21	13	2	0
TbGPx6	UGAC/UGAA	3	6	11	11	16	1	0
TbGPx7	UGAC/UGAA	2	6	11	12	14	2	0
TmGPx9	UGAU/UGAA	3	11	11	6	15	2 + 1b	1
TmGPx10	UGAA/UGAA	3	7	11	19	15	2	0
EocGPx1	UGAU/UGAA	3	8	10	10	10	1 b	1
TeGPx8	UGAU/UGAA	3	11	12	6	15	1	1
StyGPx5	UGAU/UGAC	0	8	8	13	2	1	1
StyGPx6	UGAC/AGAU	3	9	11	6	13	2	1

⁽¹⁾ K: (U/G), W: (U/A), N: any nucleotide. ⁽²⁾ After removing the SECIS core.

Table S5. Relative-fold induction values $\pm$ SD of selected *TtGPx* genes, under different stressful conditions.

Treatment	TtGPx gene					
	<i>TtGPx1</i>	<i>TtGPx3</i>	<i>TtGPx9</i>	<i>TtGPx10</i>	<i>TtGPx11</i>	<i>TtGPx12</i>
H ₂ O ₂ (1h)	74.76 $\pm$ 1.45	9.09 $\pm$ 0.15	6.26 $\pm$ 0.89	5.77 $\pm$ 0.09	1.94 $\pm$ 0.06	4.9 $\pm$ 0.88
MD (1h)	733.34 $\pm$ 67.4	45.59 $\pm$ 2.91	3802 $\pm$ 296.17	40.62 $\pm$ 5.23	6.91 $\pm$ 0.55	3.24 $\pm$ 1.78
PQ (1h)	224.9 $\pm$ 6.93	7.42 $\pm$ 0.22	664.95 $\pm$ 16.9	52.14 $\pm$ 2.43	8.21 $\pm$ 0.28	26.21 $\pm$ 0.95
PQ (24h)	218.58 $\pm$ 80.31	33.19 $\pm$ 3.46	168.46 $\pm$ 58.79	58.34 $\pm$ 21.01	29.9 $\pm$ 3.72	113.92 $\pm$ 11.86
CAM (1h)	0.91 $\pm$ 0.09	9.22 $\pm$ 1.38	6.31 $\pm$ 0.63	9.17 $\pm$ 2.3	4.14 $\pm$ 0.58	13.71 $\pm$ 2.1
CAM (24h)	19.62 $\pm$ 0.72	561.87 $\pm$ 24.65	1996.27 $\pm$ 93.69	312.16 $\pm$ 84.8	25.11 $\pm$ 1.07	237.42 $\pm$ 15.36
Cd (1h)	949.11 $\pm$ 59.1	156.13 $\pm$ 26.67	2175.83 $\pm$ 656.27	216.16 $\pm$ 63.98	26.97 $\pm$ 8.34	81.01 $\pm$ 41.45
Cd (24h)	15.22 $\pm$ 1.05	17.87 $\pm$ 0.98	42.22 $\pm$ 2.57	29.64 $\pm$ 6.28	9.78 $\pm$ 0.75	318.12 $\pm$ 17.12
Pb (1h)	141.44 $\pm$ 3.94	73.04 $\pm$ 2.2	138.27 $\pm$ 5.65	41.79 $\pm$ 1.08	18.74 $\pm$ 0.56	45.25 $\pm$ 6.32
Pb (24h)	119.55 $\pm$ 7.25	52.06 $\pm$ 1.85	134.88 $\pm$ 7.07	126.84 $\pm$ 6.39	24.2 $\pm$ 1.2	158.88 $\pm$ 8.87
Cu (1h)	2.98 $\pm$ 0.61	47.67 $\pm$ 8.76	12.39 $\pm$ 2.22	36.98 $\pm$ 7.24	10.4 $\pm$ 1.97	71.2 $\pm$ 7.22
Cu (24h)	2.67 $\pm$ 0.42	33.85 $\pm$ 4.01	25.83 $\pm$ 3.39	64.79 $\pm$ 6.87	9.97 $\pm$ 2.14	35.9 $\pm$ 3.03

SD: Standard deviation. MD: menadione. PQ: paraquat. CAM: camptothecin.

Figure S1. Multiple-sequence alignment of 101 GPx from ciliates and other organisms. Only regions containing residues of the catalytic tetrad (U/C, Q, W, N) are shown, indicated by ▼. Highly conserved residues in the regions adjacent to the tetrad are indicated by grey shading and +. See Table 1 for species names.

	940	950	960		940	950	960
		+++ ▼				+++ ▼	
TtGPx1	K KAIIVNVAC	QCGLTSD---		OxyGPx1	- KVLLEFVNMSV	EDKQKLEESE	
TtGPx2	K KAIIVNVAC	KCGLTSG---		OxyGPx2	-	-----	
TtGPx3	K KAYLIVNVAS	KCGFTST---		OxyGPx3	P KATLIANVAS	NCGFTNN---	
TtGPx4	K KAIIVNVAC	KCGLTSD---		OxyGPx4	K KCTMVNVAS	QSKFAAT---	
TtGPx5	K KVIVNVAC	KCGLTSD---		OxyGPx5	P QVTMIVNVAS	KCGHTKK---	
TtGPx6	K KAIIVNVAC	KCGLTSD---		OxyGPx6	P KLAIVNVAT	KCGLTKG---	
TtGPx7	K KCILVNVAC	KCGLTSD---		OxyGPx7	K SCILVNVAS	-----	
TtGPx8	K KCILVNVAC	KCGLTSD---		OxyGPx8	P KLSLFNVAS	KCGLTDS---	
TtGPx9	R KCLLVNVAC	KCGLTSD---		OxyGPx9	K RCILVT	-----	
TtGPx10	Q KLLTLMEIYV	KCQSFKI---		EvGPx1	-	-----	
TtGPx11	N KYAIVVNTGS	QNPNEFKQ---		EvGPx2	Y KAILIVNVAS	KCGLTKG---	
TtGPx12	K KAIIVNVAC	KUGLTGD---		SteGPx1	- KVLIIIVNVAS	AUARTAR---	
TbGPx1	K KAIIVNVAC	KCGLTSD---		SteGPx2	- KALLIVNIAS	EURKTSS---	
TbGPx2	K KVILVNVAC	KCGLTSA---		SteGPx3	- KILLIVNIAC	KUHMSGK---	
TbGPx3	K KCILVNVAC	KCGLTSE---		SteGPx4	- KVLIVNVAS	EUGLTKK---	
TbGPx4	K KCILVNVAC	KCGLTSD---		SteGPx5	- HILLIVNVAS	QUELTKI---	
TbGPx5	K KAYLIVNVAS	KCGFTST---		SteGPx6	- KVLIVNIAC	KUQLSPK---	
TbGPx6	K KAIIVNVAC	-----		SteGPx7	- KVLIIIVNVAS	QUGKTRR---	
TbGPx7	R KAVIVNVVAL	-----		PtGPx1	Q KVIIVNVAT	DSPELND---	
TbGPx8	N KYAIVVNTGS	QNPNEFKQ---		PtGPx2	K KAYICNVAC	SCGLTSS---	
TeGPx1	K KAIIVNVAC	KCGLTSD---		PtGPx3	K KVIICNVAC	SCGLTSG---	
TeGPx2	K KAIIVNVAC	QCGLTSD---		PtGPx4	K KAYICNVAC	SCRLLTQ---	
TeGPx3	R KCLLVNVAC	KCGLTSD---		PtGPx5	K KAYICNVAC	SCGLTSS---	
TeGPx4	K KCILVNVAC	KCGLTSD---		McGPx1	K KCIMVNVAS	KUGLTKT---	
TeGPx5	K KCILVNVAC	KCGLTSD---		McGPx2	R KCTMVNVAS	KUGLTKT---	
TeGPx6	K KCILVNVAC	KCGLTSD---		McGPx3	R KCTMVNVAS	KUGLTKT---	
TeGPx7	K KAYLIVNVAS	KCGFTST---		PcpGPx1	Y KIIMIVNVAS	ACGTID---	
TeGPx8	K KAIIVNVAY	-----		PcpGPx2	S WGLFSPHPDA	FTPICT---S	
TeGPx9	Q KKIYVFNLNL	-----		PcpGPx3	K DVYLLVNVAS	EQD-----	
TeGPx10	N KYAIVVNTGS	QNPNEFKQ---		PcpGPx4	-	-----	
TmGPx1	K KVIVNVAC	KCGLTSD---		PcpGPx5	S WAILFSPHPAD	FTPVCT---T	
TmGPx2	K KAIIVNVAC	KCGLTSD---		PcpGPx6	-	-----	
TmGPx3	K KAIIVNVAC	KCGLTSD---		PcpGPx7	K -IILCTNVAS	RGSMMAKE---	
TmGPx4	R KCLLVNVAC	KCGLTSD---		EocGPx1	C KCIMVNVAS	KCSLTNK---	
TmGPx5	K KCILVNVAC	KCGLTSD---		EocGPx2	C KCMVNVAS	ECGLTKT---	
TmGPx6	K KCILVNVAC	KCGLTSD---		EocGPx3	-	-----	
TmGPx7	K KCILVNVAC	KCGLTSD---		EocGPx4	Y KCIMVNVAS	GCYTDGT---	
TmGPx8	K KAYLIVNVAS	KCGFTST---		EocGPx5	- QVTLYSNICH	NDKESKA---	
TmGPx9	-	-----		CrGPx5	- KAVLIVNVAS	KCGFTP---	
TmGPx10	R KALIVNVVAL	-----		CrGPx1	- RVVLVNVAS	KUGLTAA---	
TmGPx11	N KYAIVVNTGS	QNPNEFKQ---		ScGPx1	- KVLIVNVAS	KCGFTP---	
ImGPx1	-	-----		TcGPx1	- RVTVVVNTAS	LCSFANS---	
ImGPx2	N KVVIVVNLGS	QNNCYQE---		PfGPx1	- KVLIIIFNSAS	KCGLTKN---	
StyGPx1	-	-----MV		AtGPx6	- KVLIVNVAS	QCGLTNS---	
StyGPx2	P KLSIVNVAS	ECGLTES---		DmGPx1	- KVLIVNIAS	KCGLTKN---	
StyGPx3	K KCTIIVNVAS	KCGLSQK---		HsGPx1	- KVLIIENVAS	LUGTTVR---	
StyGPx4	P KLSIVNVAS	KCGLTDS---		HsGPx5	- KHILFNVAT	YCGLT-A---	
StyGPx5	- KVILFTNLSI	EESQKEEITE		HsGPx4	- FVCIVTNVAS	QUGKTEVNYT	
StyGPx6	K RCTLVS	-----					
StyGPx7	-	-----LV					
StyGPx8	K KCILVTNTAS	LSPHANM---					
StyGPx9	K RCILVTNVAS	-----					

```

.....|.....|.....|.....|.....|.....|
      1030      1040
      ++ ++   +++ ▼++   +
TtGPx1  SQGLEILGFP  CNQFGAQEPW  AESEILSYTQ
TtGPx2  SQGLEVLAFP  CNQFGEQEPW  AESEILSYTQ
TtGPx3  DKGLEILAFP  SNQFFNQEPF  DEPAIKKEFVK
TtGPx4  SQGLEILAFP  CNQFGQQEPW  AESEILSYTQ
TtGPx5  SQGLEVLAFP  CNQFGEQEPW  AESEILSYTQ
TtGPx6  SQGLEVLAFP  CNQFGEQEPW  AESEILSYTQ
TtGPx7  SRGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TtGPx8  SRGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TtGPx9  SRGFELAFP  ANQFMQEPW  DNAKIKEYVV
TtGPx10 HLTTLTSQWK  CIRNTNREVW  KFLHSLPINL
TtGPx11 KDKLEILAFP  CNQFYN-EPS  NFKTIKDSYS
TtGPx12 DSGLEILGFP  CNQFMSQEPW  AEPKIKDFIT
TbGPx1  AQGLEILGFP  CNQFGAQEPW  DEKEILSYTK
TbGPx2  DQGLEILGFP  CNQFLSQEPW  DEPKIQEFIK
TbGPx3  TQGFELAFP  ANQFMQEPW  DNKKIKEYIV
TbGPx4  NRGFELAFP  TNDFMQEPW  DSKKIKEYVQ
TbGPx5  DQGLEILAFP  SNQFMNQEPF  DEPOIKEFVK
TbGPx6  ---LEILGFP  CNQFLSQEPW  AEPKIKDFIT
TbGPx7  SRGLEILAFP  SNQFMQEPW  DPPQIKEFVV
TbGPx8  KDQLEVIAP  CNQFYN-EPS  NFKGIQENYA
TeGPx1  QQGLEILGFP  CNQFGAQEPW  SESEILSYTQ
TeGPx2  SQGLEILGFP  CNQFGSQEPW  AESEILSYTQ
TeGPx3  SQGFELAFP  ANQFMQEPW  DNKKIKEYTV
TeGPx4  SRGFELAFP  TNDFMEQEPW  DNQKIKEYVQ
TeGPx5  SKGFELAFP  TNDFMQEPW  DNKKIKEYVQ
TeGPx6  SKGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TeGPx7  DKGLEILAFP  SNQFLNQEPF  DEPAIKKEFVK
TeGPx8  -HGLEVLGFP  CNQFMSQEPW  AEPKIKEFIT
TeGPx9  SRGLEILAFP  SNQFMEQEPW  DPPQIKEFVV
TeGPx10 NDKLEILAFP  CNQFYN-EPS  NFKTIKEQYS
TmGPx1  SQGLEILGFP  CNQFGAQEPW  SESEILSYTQ
TmGPx2  SQGLEILAFP  CNQFGQQEPW  AESEILSYTQ
TmGPx3  TQGLEILAFP  CNQFGQQEPW  DESEILSYTQ
TmGPx4  SQGFELAFP  ANQFMQEPW  DNAKIKEYVV
TmGPx5  SRGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TmGPx6  SRGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TmGPx7  SRGFELAFP  TNDFMEQEPW  DNKKIKEYVQ
TmGPx8  DKGLEILAFP  SNQFLNQEPF  DEPAIKKEFVK
TmGPx9  DSGLEILGFP  CNQFMSQEPW  AEPKIKDFII
TmGPx10 SRGLEILAFP  SNQFMQEPW  DPPQIKEFVV
TmGPx11 KDKLEILAFP  CNQFYN-EPL  NFKNIKDSYS
ImGPx1  ---FTILAFP  ANQFMSQEPW  DPPQIKDFVI
ImGPx2  -----ANQ-----
StyGPx1  EQGFELAFP  VNQFFSQEPG  TNQQIKSLVR
StyGPx2  DQGFELAFP  CNQFGAQEPG  SNSQIFEFV
StyGPx3  DQGLEILAFP  CNQFMNQEPG  SNLQILEYAR
StyGPx4  PQGFVMAFP  CNQFGSQEPG  TNKQILDFV
StyGPx5  ERGFCVYGAL  PNDVAGGNPL  RNKEIANTLK
StyGPx6  DQGFELTFP  CNQFGGQEPG  TNQEVKQFIR

```

```

.....|.....|.....|.....|.....|.....|
      1030      1040
      ++ ++   +++ ▼++   +
StyGPx7  EKGFEILAFP  CNQFMKQEPK  TNQEIKTFLQ
StyGPx8  SKGLEILAFP  CNQFHKQEP  NDNEIKVNAQ
StyGPx9  DQGFELAFP  CNQFMSQEPG  SNQEIKQFVR
OxyGPx1  -----ESGNPL  RNRDLAILLK
OxyGPx2  DQGFELAFP  SNEFFSTEPG  DSKQIKSLVR
OxyGPx3  QHGLEIVGFP  CNQFFSQEPG  TNDEIFQFV
OxyGPx4  AQGFELAFP  CNQFNKEEPW  NDHEIKQHVI
OxyGPx5  DQGFELAFP  CNQFGSQEP  PNETIYEFV
OxyGPx6  SQGFDVLAFP  CNQFLFQEPG  SAEETQKFA
OxyGPx7  DKGFELAFP  CNQFMRQEP  SNQEIKYVI
OxyGPx8  EQGFELAFP  CNQFGSQEPD  SNASILDV
OxyGPx9  DQGFELAFP  CNQFMNQEPG  TPEEIKKFIK
EvGPx1  HKGFQILAFP  CNQFLGQESC  SNDDINEFVR
EvGPx2  DKGFQIFAFP  CNQFGAQEPG  TNEEIRAFQ
SteGPx1  SEGELILAFP  CNQFFHQEPG  TSNEIKDYIR
SteGPx2  DKEFEILGFP  CNQFNNREPG  TDEQIVAFK
SteGPx3  SRGLEILSFP  CNQFFWREYS  EQETIKSYLI
SteGPx4  SKGLEILAFP  CNQFLHQEPG  SDEEIEKFAR
SteGPx5  KEGLIILAFP  CNQFNNQEPG  TNAEIQEFIR
SteGPx6  SRGLEILAFP  CNQFFWREYS  THNEIKDYLS
SteGPx7  SRGLCILAFP  CNQFFYQEPG  TSDQIKDFIT
PtGPx1  -LPYQVLLFP  KCDH-----TF  TY-----KQ
PtGPx2  AQGLEILGFP  CNQFMGQEP  PEPEIKEFVL
PtGPx3  AQGLEILGFP  CNQFMNQEP  PEPEIKEFVI
PtGPx4  DQGLEILGFP  CNQFRNQEP  PEPEIKNYVT
PtGPx5  AQGLEILGFP  CNQFMGQEP  PEPEIKEFVI
McGPx1  DKGFELAFP  CNQFLSQEPG  SNEDIKKFAR
McGPx2  DQGFELAFP  CNQFMSQEPG  THEQIKKFAQ
McGPx3  DHGFELAFP  CNQFMSQEPG  THEQIKKFAQ
PcpGPx1  -----EIKQFLN
PcpGPx2  KREVKVVAIS  CNQVVKTHKW  IKD-IEHY--
PcpGPx3  -----EIQHVVR
PcpGPx4  DQGFELAFP  CNQFGKQEP  PNDQILEAAR
PcpGPx5  KKGVKVIALS  CNDADTHKEW  IKD-VDHY--
PcpGPx6  QKGLEIFAFP  CNQFGAQEP  PNNEILDAAR
PcpGPx7  NNGFEILCFP  SNQFYN-EPG  TFSNLKQIYL
EocGPx1  DKGFELAFP  CNQFLSQEP  SNEHIKNFVQ
EocGPx2  DKGFQIFAFP  CNQFMKQEPG  SNEDIKKFAQ
EocGPx3  -----
EocGPx4  DKGFQIFAFP  CNQFMGQEP  CNLDIKKYAQ
EocGPx5  DKGLRVGLP  TTDVLIGSTK  LTYD-----
CrGPx1  DRGLVILGFP  CNQFGGQEPG  DASAIGEF
CrGPx2  ATDLTIVAFP  CNQFGGQEPG  TNAEIKAFAS
ScGPx1  DEGFTIIGFP  CNQFGHQEPG  SDEETIAQF
TcGPx1  PRGFTILAFP  CAQFANQEPK  SNEETIAVWAQ
PfGPx1  ARGLEILAFP  TNQFLNQEPD  NTKDICTFNE
AtGPx6  GHGFELAFP  CNQFGNQEPG  TNEETIVQFA
DmGPx1  ERGLVILNFP  CNQFGSQEP  ADGEAMVCHL
HsGPx1  PRGLVVLGFP  CNQFGHQEP  KNEETILNSLK
HsGPx5  PYGLVVLGFP  CNQFGKQEPG  DNKEILPGLK
HsGPx4  EFAAGYNVAF  DMFSKITVNG  IDAHLWKKWM

```

```

      .|. .|. .|. .|. .|. .|.
      1140      1150
      + ▼ ▼+ +++
TtGPx1 AATKIPW NF-AKFLVDG
TtGPx2 SATKIPW NF-AKFLIDG
TtGPx3 FQGYIQW NF-AKFLVNA
TtGPx4 SATKIPW NF-AKFLIDG
TtGPx5 YATKIPW NF-AKFLIDG
TtGPx6 SATKIPW NF-AKFLIDG
TtGPx7 KTRQIPW NF-AKFLIDP
TtGPx8 KTRQIPW NF-AKFLINP
TtGPx9 KTRQIPW NF-AKFLIGP
TtGPx10 NLAQILF SL-VKQMLTE
TtGPx11 NGAKITE DF-SKFLINT
TtGPx12 KAKQIPW NF-SKFVVD R
TbGPx1 AAQKIPW NF-AKFLIDG
TbGPx2 KSKQIPW NF-GKFLIN K
TbGPx3 KTRQIPW NF-AKFLIGP
TbGPx4 KTRQIPW NF-AKFLIDP
TbGPx5 FQGYIQW NF-AKFLINS
TbGPx6 KAKQIPW NF-SKFLVNQ
TbGPx7 KAKQIPW NF-AKFLIQP
TbGPx8 NGEKITE DF-TKFLVNT
TeGPx1 AATKIPW NF-AKFLVDG
TeGPx2 AATKIPW NF-AKFLIDG
TeGPx3 KTRQIPW NF-AKFLIGP
TeGPx4 KTRQIPW NF-AKFLINP
TeGPx5 KTRQIPW NF-AKFLINP
TeGPx6 KTRQIPW NF-AKFLINP
TeGPx7 FQGYIQW NF-AKFLVDG
TeGPx8 KAKQIPW NF-SKFLIN R
TeGPx9 NSKQIPW NF-AKFLIQN
TeGPx10 GGIKITE DF-SKFLINN
TmGPx1 AATKIPW NF-AKFLIDG
TmGPx2 SATKIPW NF-AKFLIDG
TmGPx3 SATKIPW NF-AKFLIDG
TmGPx4 KTRQIPW NF-AKFLIGP
TmGPx5 KTRQIPW NF-AKFLIDP
TmGPx6 KTRQIPW NF-AKFLINP
TmGPx7 KTRQIPW NF-AKFLIDP
TmGPx8 FQGYIQW NF-AKFLVNA
TmGPx9 KAKQIPW NF-SKFVVD R
TmGPx10 NSKQIPW NF-AKFLIQS
TmGPx11 NGAKITE DF-SKFLINT
ImGPx1 KAKNIPW NF-GKFLIN K
ImGPx2 NGIKINE DF-CKFLVDQ
StyGPx1 QVKRIPW NF-SKFLVNK
StyGPx2 GLDQVTW NF-GKFLIDQ
StyGPx3 KVKALPW NF-CKFLIDQ
StyGPx4 RLARITW NF-GKFLVNQ
StyGPx5 KAIRVKE NY-SKLLCNR
StyGPx6 EVKEIPW NF-AKFLVNE
StyGPx7 DIRMIPW NF-SKFLVDS
StyGPx8 KIKDIPG NF-TKFLVDR
StyGPx9 EVKEIPW NF-AKFLVNE

```

```

      .|. .|. .|. .|. .|. .|.
      1140      1150
      + ▼ ▼+ +++
OxyGPx1 RAYRIKE SY-AKFLCNR
OxyGPx2 KVKQIPW NF-SKFLVDS
OxyGPx3 NFNKIGW NF-GKFLVNQ
OxyGPx4 NIKEIPG NF-AKFLVDR
OxyGPx5 KVGKIPW NF-AKFLGDQ
OxyGPx6 GITRIEW NF-GKFLVDS
OxyGPx7 GVKEVPW NF-SKFLVNK
OxyGPx8 RIAKITW NF-GKFLVNK
OxyGPx9 EVKEIPW NF-AKFLVDQ
EvGPx1 KLKSIPF NF-SKFLINS
EvGPx2 TTGDIPW NF-AKFLINS
SteGPx1 DGKRICW NF-GKFLVDR
SteGPx2 KSGSIDW NF-GKFLVDK
SteGPx3 NGRKIGM NF-CKFLVDR
SteGPx4 DGGKIGW NF-GKFLVSR
SteGPx5 KGREIGW NF-TKFLVNR
SteGPx6 NSTQIGL NF-GKFLVDK
SteGPx7 NRRKICW NF-GKFLID R
PtGPx1 NGRQIKQ DF-CKFLISE
PtGPx2 EAKEVPW NF-GKFLINS
PtGPx3 SARQVPW NF-GKFLIDS
PtGPx4 EVKYVPW NF-AKFLIDA
PtGPx5 EAKEVPW NF-GKFLINS
McGPx1 TIQNIPW NF-AKFLIDE
McGPx2 VVQNIPW NF-AKFLIDN
McGPx3 VVQNIPW NF-AKFLIDE
PcpGPx1 NTNNIPW NF-AKFVVYD
PcpGPx2 DPQGLPM TVRSVYVIGP
PcpGPx3 ENPNIA Y ----VTIKSN
PcpGPx4 KTKNILW NF-GKFLIDK
PcpGPx5 DAKGLPM TVRSVYIIGP
PcpGPx6 KCEDIKW NF-GKFLVDG
PcpGPx7 SAEPIVE DF-SKFLIDQ
EocGPx1 TMQSIPW NF-TKFLIDE
EocGPx2 TLQNIPW NF-AKFLIDE
EocGPx3 -----
EocGPx4 EIQSIPW NF-TKFLIND
EocGPx5 KSRRI NT HF-NKFLCD R
CrGPx5 MMEMIKW NF-EKFLVDK
CrGPx1 --SDIGW NF-GKFLVRP
ScGPx1 GLRGIKW NF-EKFLVDK
TcGPx1 --GPIRW NY-TKFLCD R
PfGPx1 TLKSIGW NF-GKFLVDK
AtGPx6 -GDGIKW NF-AKFLVDK
DmGPx1 -GSGIKW NF-TKFLVNK
HsGPx1 CRNDVAW NF-EKFLVGP
HsGPx5 KVHDIRW NF-EKFLVGP
HsGPx4 LGNAIKW NF-TKFLIDK

```

Figure S2. Phylogram of all *T. thermophila* GPx amino acid sequences. Catalytic tetrads are indicated. Numbers indicate bootstrap values from 2000 replicates. Branch lengths are drawn to scale as indicated by the scale bar.

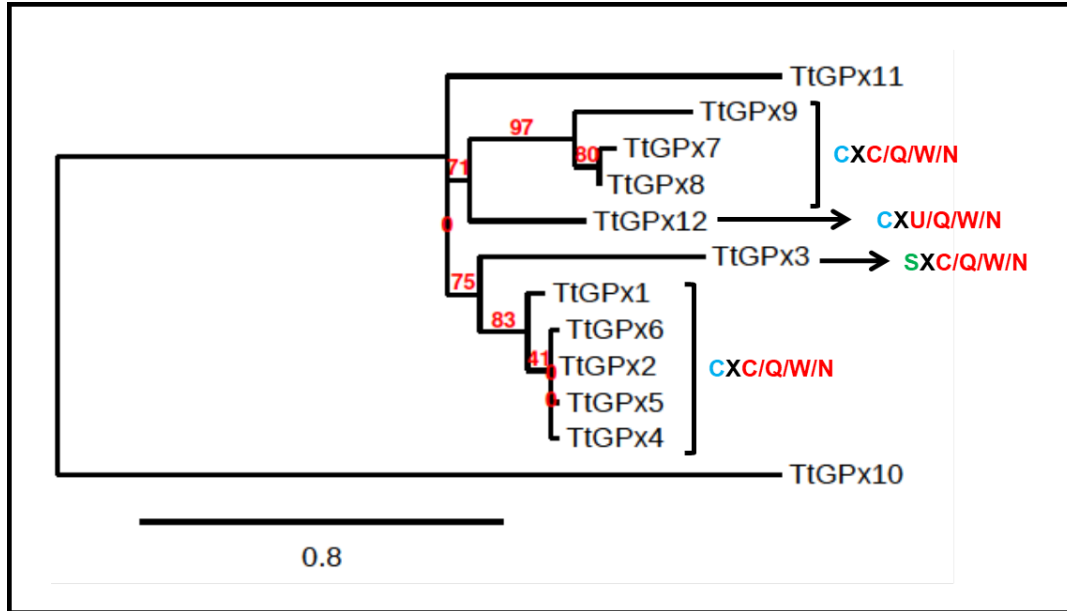


Figure S3. Phylogram of all ciliate putative GPx isoforms. Catalytic tetrads are indicated. No residue of the GPx catalytic tetrad are highlighted within a red square. Species with SECIS elements are indicated by a red star. Numbers indicate bootstrap values from 2000 replicates. Branch lengths are drawn to scale as indicated by the scale bar. See Table 1 for ciliate species identification.

