Supplemental Data



Figure S1. ¹H-¹⁵N HSQC NMR experiments AtBolA2 is alone (black) or with 1 equivalent of AtGrxS14 (A) and AtGrxS17 (B) (blue and green respectively) at pH 7.0 and 288K. AtGrxS14 is alone (black) or with 1 equivalent of AtBolA1 (C) and AtBolA2 (D) (red) at pH 7.0 and 288K.

		α_1	B1	C	X.Z.	B2
AtGrxS14	لالالال	llll	\rightarrow	للللا	eeeeee	→eee e.
	70	80	90	100	110	120
AtGrxS14	SALTPOLKD	TLEKLVNS	EKVVLFMKGTF	RDFPMCGFSNT	VVOILKNLNVI	PFEDVNILENE.
AtGrxS15	PDSTDŠLKD	IVENDVKD	NP VMIY MKGVE	PESPO <mark>C</mark> GFSSL Z	AVRVLQQYNV	PISSRN I LEDQ.
AtGrxS16	VELTVPLEE	LIDRLVKE	SK VVAF IKGSF	RSAPÕ <mark>C</mark> GFSOR V	v vg i lēšog v i	OYETVD V LDDÊY
AtGrxS17	VSTADALKS	RLEKLTNS	HP VMLF MKGIE	PEEPRCGFSRK	V VD I LKEVN V I	DFGSFDILSDN.
AtGrxC7	GMVADTGLL	RIESLASE	SAVVIFS	.VSTCCMCHAN	VKGLFRGMGV:	SPAVHELDLHPY
ScGrx3	EETEEOINA	RLTKLVNA	AP VMLF MKGSE	SEPKCGFSROI	LVGILREHOV	RFGFFD I LRDE.
ScGrx4	DETEEEINA	RLVKLVOA	AP VMLF MKGSF	SEPKCGFSROI	LVGILREHÕI	RFGFFD I LRDE.
		-		-	~	
	- 2		02	0.4		
	α3		β3	β4	α4	α5
AtGrxS14	α3 <u>000000</u> .		β3	β4	α4	α5 00000000
AtGrxS14	α3 <u>000000</u> .	<u>000</u> 130	β3 14 0	β4 150	α4 <u>0000000</u> 000 160	α5 2020202020 170
<i>AtGrxS14</i> AtGrxS14	α3 <u>000000</u> . M L RQG L .	<u>000</u> 130 KEY	$\frac{\beta 3}{140}$	$\beta 4$ $1 5 0$ $I G G E F F G G C D I 1$	α4 0000000 00 160 TLEAFKTGEL(α5 000000000 170 2EEVEKAMCS
At <i>GrxS14</i> AtGrxS14 AtGrxS15	α3 QQQQQQ. MLRQGL. ELKNAV.		β3 140 SNWPTFPQLY1 SHWPTFPQIF1	$\frac{\beta 4}{150}$	α4 0000000 001 160 TLEAFKTGEL(ILNMHKEGEL)	α5 000000000 170 2EEVEKAMCS EQKLKDVSGNQD
AtGrxS14 AtGrxS14 AtGrxS15 AtGrxS16	α3 <u>000000</u> . MLRQGL. ELKNA V . NHGLRETL.	<u>000</u> 130 KEY KSF	β3 140 SNWPTFPQLY1 SHWPTFPQIF1 SNWPTFPQIF1	β4 150 IGGEFFG GCDII IKGEFIG GSDII VKGELVG GCDII	α4 0000000 003 160 TLEAFKTGEL ILNMHKEGEL LTSMYENGEL	α5 000000000 170 2EEVEKAMCS EQKLKDVSGNQD ANILN
AtGrxS14 AtGrxS14 AtGrxS15 AtGrxS16 AtGrxS17	α3 <u>000000</u> . ml RQG L . el KNA V . NHGLRETL. eV REGL	<u>000</u> 130 KSF KSF KNY	β3 140 SNWPTFPQLY1 SHWPTFPQIFU SNWPTFPQIFU SNWPTFPQLY0	β4 150 IGGEFFG GCDII IKGEFIG GSDII VKGELVG GCDII CNGELLG GADIA	α4 <u>0000000</u> 00 160 TLEAFKTGEL(ILNMHKEGEL) LTSMYENGEL) AIAMHESGEL)	α5 200000000 170 2EEVEKAMCS 2EEVEKAMCS 2EEVEKAMCS 2ANILN KDAFKDLGITTV
AtGrxS14 AtGrxS15 AtGrxS15 AtGrxS16 AtGrxS17 AtGrxC7	α3 QQQQQQ MLRQGL. ELKNAV. NHGLRETL. EVREGL. GGDIQRALI		β3 140 SNWPTFPQLY1 SHWPTFPQIFY SNWPTFPQIFY SSNWPTFPQLY0 SSPGSLPVVF1	β4 150 IGCEFFGGCDII KCEFICGSDII KCELLGGADIA IGCKLVGAMDR	α4 <u>160</u> <u>150</u> <u>1LEAFKTGEL</u> <u>1LNMHKEGEL</u> <u>LTSMYENGEL</u> <u>AIAMHESGEL</u> VMASHINGSL	α5 200000000 170 2EEVEKAMCS EQKLKDVSGNQD ANILN KDAFKDLGITTV VPLLKDAGALWL
AtGrxS14 AtGrxS15 AtGrxS16 AtGrxS17 AtGrxC7 ScGrx3	α3 QQQQQQ MLRQGL. ELKNAV. NHGLRETL. EVREGL. GGDIQRALI SVRQNL.		β3 140 SNWPTFPQLY1 SHWPTFPQIFJ SNWPTFPQLY0 SSPGSLPVVFJ SEWPTFPQLY3 SEWPTFPQLY3	β4 150 IGEFFGGCDI KGEFIGGSDI KGELVGGCDI IGELLGGADI IGEKLVGAMDR IGEFQGGLDI	α4 160 1EAFKTGEL ILNMHKEGEL LTSMYENGEL AIAMHESGEL WASHINGSL IKESLEEDP.	α5 200000000 170 2EEVEKAMCS EQKLKDVSGNQD ANILN KDAFKDLGITTV VPLLKDAGALWL DFLQHALQS.

Figure S2. Glutaredoxin interacting areas with transcription factors

Multiple sequence alignment of AtGrxS14 with *S. cerevisiae* Grx3 and Grx4, *A. thaliana* GrxS15, S16, S17 and GrxC7 (with CCMC active site). Secondary structure annotation and numbering on top correspond to AtGrxS14. Conserved residues are in black box and residues potentially interacting with AtBolA2 (AtGrxS14), Aft1 (ScGrx3/4) and TGA (AtGrxC7) are colored in red.





Figure S3. ¹⁵N backbone relaxation measurements $R_1, R_2, and [^1H, ^{15}N]$ heteronuclear NOE plotted as function of the residue number for AtBolA2. The $[^1H, ^{15}N]$ heteronuclear NOE negative values observed for the 10 C-terminal residues indicate that this tail is totally unstructured which may have hampered crystallization. In fact, structural disorder in Nand C-terminal extensions can also be noticed in the NMR models of BolA1 from M. musculus and E. coli.