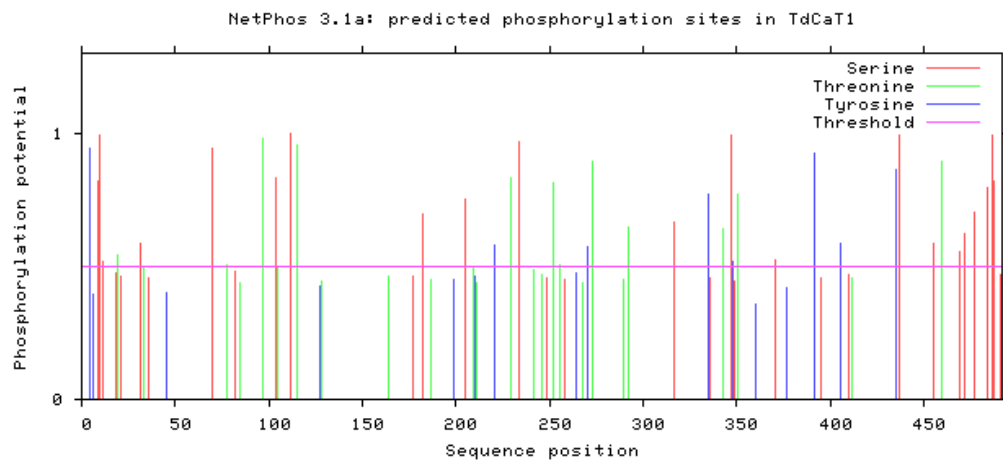**Supplementary Figure S1.** Comparison of the secondary structures of CAT1s. **(a)** *Triticum durum*, **(b)** *Brachypodiumdictyosum* (XP_003558892.1), **(c)** alpine snowbell (*Soldanella alpine*, O24339)*, **(d)** upland cotton *(Gossypium hirsutum*, P17598)*, **(e)** *Aegilops taushii (*XP_020164896.1*)* and *Triticum aestivum (*Q43206.1*)* as revealed by SOPMA. The helix, sheet, turn and coil are indicated in vertical lines in order from the longest to the shortest.

a)

```
#
    MDPYKYRPSSSFNAPMWSTNSGAPVWNNDNSLTVESRGPILLEDYHLVEK   #    50
    IADFDRERIPERVVHARGASAKGFFEVTHDVSHLTCADFLRAPGVQTPVI   #   100
    VRFSTVIHERGSPETLRDPRGFAIKFYTREGNWDLVGNNFPVFFIRDGMK   #   150
    FPDMVHALKPNPKTHIQENWRILDLFSHHPESLHMFTFLFDDIGVPADYR   #   200
    HMDGSGVNTYTLVNRAGKAHYVKFHWKPTCGVKSLLEEEAVTVGGTNHSH   #   250
    ATKDLTDSIAAGNYPEWTFYIQTIDPDHEERFDFDPLDVTKTWPEDVVPL   #   300
    QPVGRLVLNRNIDNFFSENEQLAFCPGIIVPGVDYSDDKLLQTRIFSYSE   #   350
    TQRHRLGANYLLLPANAPKWSHHNNHYDGLMNFMHRDEEVDYFPSRFDPA   #   400
    KHAPRYPIPSRTLNGRREKMVIEKENNFKQPGERYRSMDPARQERFINRW   #   450
    IDALSDPRLTHEIKAIWLSCWSQADKSLGQKLASRLSSKPSM           #   500
%1  ...Y....SSS.......T...........S..................   #    50
%1  ................S.......T....................T...   #   100
%1  ...S.......S..T.................................   #   150
%1  .............................S..................   #   200
%1  ....S..............Y.......T....S................   #   250
%1  .T...T............Y..T.....................T.....   #   300
%1  ..............S.................Y.......T...SY..   #   350
%1  T...............S...................Y...........   #   400
%1  .....Y.........................Y.S..............   #   450
%1  ....S....T.......S..S....S......S..SS....
```


b)

Position	Peptide	Score	Cutoff	Cluster
86	HDVSHLTCADFLRAP	2,011	0	Cluster B
230	KFHWKPTCGVKSLLE	19,226	0	Cluster C
325	ENEQLAFCPGIIVPG	1,163	0	Cluster B
470	IKAIWLSCWSQADKS	0,322	0	Cluster A

Supplementary Figure S2. Bio-informatics analysis of TdCAT1 protein. **(a)** Identification of phosphorylation sites in TdCAT1 protein using NetPhos database **(b)** Identification of Nitrosylation sites in TdCAT1 structure using GPS-NSO software.

Supplementary Table S1. List of primers used in PCR amplification of TdCAT1 and its truncated forms. The forward primer CF was used for the amplification of all forms with the use of reverse primers corresponding of each one.

Amplified fragments	Nucleotide sequences	Primers names
TdCAT1	TC<u>GAATTC</u>ATGGACCCCTACAAGTA	CF
TdCAT$_{200}$	AT<u>CTCGAG</u>TTACATGCTCGGCTTGG	CR1
TdCAT$_{295}$	AT<u>CTCGAG</u>GGCGGTAGTCGGCGGG	CR2
TdCAT$_{340}$	AT<u>CTCGAG</u>CCTCGGGCCACGTCTTG	CR3
TdCAT$_{400}$	AT<u>CTCGAG</u>GGTGAGGCGGGGGTCC	CR4
TdCAT$_{460}$	AT<u>CTCGAG</u>GGGTGAGGCGGGGGTC	CR5

Supplementary Table S2. Secondary structure analysis of plant catalase using SOPMA program (https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_sopma.html). 14 different catalase proteins were used to study the secondary structure of those proteins: [*Triticum turgidum*subsp durum]: TdCAT1 (GenBank: AKC00864.1); [*Triticum aestivum*]: TaCAT1 (GenBank: XP_044371531.1); [*Aegilops tauschii* subsp. *strangulata*] (GenBank: XP_020164896.1); [*Triticum monococcum*]: TmCAT1 (GenBank: QBZ38484.1); [*Brachypodiumdistachyon*]: BdCAT1 (GenBank: XP_003558892.1); [*Triticum dicoccoides*] (GenBank: XP_037426584.1); [*Panax ginseng*]: (GenBank: EU327037); [*Soldanellaalpina*)]: (GenBank: O24339); [*Gossypium hirsutum*] (GenBank: XP_016687939.1); [*Lotus japonicus*] (GenBank: AAR84578); [*Gossypium raimondii*] (GenBank: XP_012446280.1) and [*Arachis ipaensis*] (GenBank: XP_016167161.1).

Protein	α-helices	β-turns	random coils	extended strands
TdCat1	135	27	256	74
TaCat1	140	27	242	83
AetCAT1	127	30	258	77
TmCAT1	137	30	249	76
BdCat1	134	29	257	72
AtCat1	126	31	260	75
TdcCAT1	131	28	258	75
PgCAT1	138	29	250	75
SaCAT1	135	27	253	77
GhCAT1	139	29	249	75
LjCAT1	130	25	262	75
EsCAT1	137	28	255	72
GrCAT1	141	29	248	74
AiCAT1	134	32	247	79