(a)

```
EsCAT1    DYQLVEIIANFDRERIPERVVHARGASAKGFFEVTHD
PgCAT1    DYQLVEKIANFDRERIPERVVHARGASAKGFFEVTHD
AtCat1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
SaCAT1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
GhCAT1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
LjCAT1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
GrCAT1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
AiCAT1    DYHLVEKLANFDRERIPERVVHARGASAKGFFEVTHD
BdCat1    DYHLVEKIANFDRERIPERVVHARGASAKGFFEVTHD
TtCAT1    DYHLVEKIADFDRERIPERVVHARGATAKGFFEVTHD
TaCAT1    DYHLVEKIADFDRERIPERVVHARGATAKGFFEVTHD
HvCAT1:   DYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHD
TdCat1    DYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHD
AetCAT1   DYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHD
TmCAT1    DYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHD
TdcCAT1   DYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHD
          **:*** :*:*************:*********
```

(b)

```
LjCAT1    YSDDKMLQTRIFSYADSQRHRLGPNYLQ-
TdCat1    YSDDKLLQTRIFSYSETQRHRLGANYLLL
TtCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
TaCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
AetCAT1   YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
TmCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
HvCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
BdCat1    YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
TdcCAT1   YSDDKLLQTRIFSYSDTQRHRLGPNYLL-
GhCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLQ-
GrCAT1    YSDDKLLQTRIFSYSDTQRHRLGPNYLQ-
PgCAT1    YSDDKLLQSRIFSYADTQRHRLGPNYLQ-
AtCat1    YSDDKLLQTRVFSYADTQRHRLGPNYLQ-
SaCAT1    YSDDKLLQTRIFSYADTQRHRLGPNYLQ-
EsCAT1    YSDDKLLQTRIFSYADTQRHRLGPNYLQ-
AiCAT1    YSDDKLLQTRIFSYADTQRHRLGPNYLQ-
          *****:**:*:***:::****** ***
```

Figure S1: Protein sequence alignment of Catalase proximal active site signature domain (a) and Catalase proximal heme-ligand signature (b) of TtCAT1 with other plant catalase proteins using clusterW database.
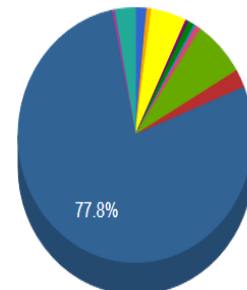
SeqID: HvCAT1:

CELLO predictor:

Localization Prediction

Localization	Score
Extracellular	0.079
Plasmamembrane	0.032
Cytoplasmic	0.243
Cytoskeletal	0.021
ER	0.042
Golgi	0.013
Lysosomal	0.037
Mitochondrial	0.362
Chloroplast	0.115
Peroxisomal	3.893
Vacuole	0.021
Nuclear	0.143

Localization Probability

- Chloroplast
- Peroxisomal
- Vacuole
- Nuclear

▲ 2/2 ▼

77.8%

SeqID: TtCAT1

CELLO predictor:

Localization Prediction

Localization	Score
Extracellular	0.080
Plasmamembrane	0.057
Cytoplasmic	0.348
Cytoskeletal	0.022
ER	0.062
Golgi	0.014
Lysosomal	0.043
Mitochondrial	0.348
Chloroplast	0.129
Peroxisomal	3.735
Vacuole	0.024
Nuclear	0.136

Localization Probability

- Chloroplast
- Peroxisomal
- Vacuole
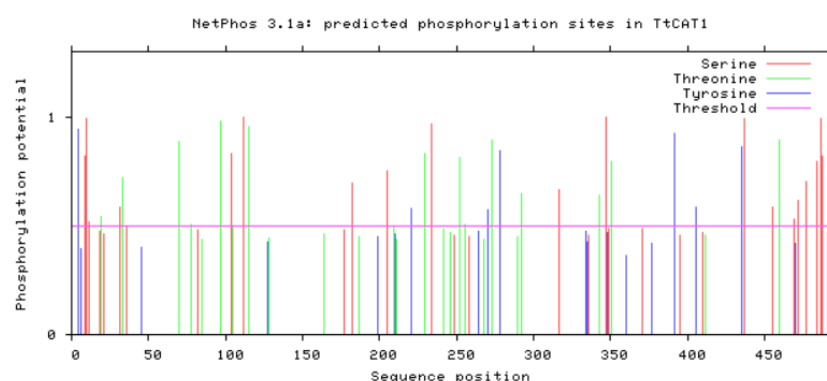- Nuclear

▲ 2/2 ▼

7%
7%
74.7%
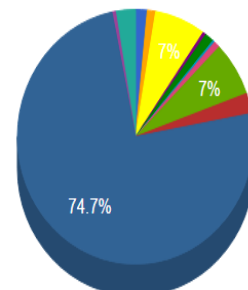
Figure S2: In silico localization of (a) HvCAT1 and (b) TtCAT1 proteins.

(a)

```
      MDPYKYRPSSSFNAPMWSTNSGAPVWNNDNSLTVGSRGPILLEDYHLVEK    #      50
      IADFDRERIPERVVHARGATAKGFFEVTHDVSHLTCADFLRAPGVQTPVI    #     100
      VRFSTVIHERGSPETLRDPRGFAIKFYTREGNWDLVGNNFPVFFIRDGMK    #     150
      FPDMVHALKPNPKTHIQENWRILDFFSHHPESLHMFTFLFDDIGVPADYR    #     200
      HMDGSGVNTYTLVNRAGKAHYVKFHWKPTCGVKSLLEEEAVTVGGTNHSH    #     250
      ATKDLTDSIAAGNYPEWTFYIQTIDPDYEERFDFDPLDVTKTWPEDVVPL    #     300
      QPVGRLVLNRNIDNFFSENEQLAFCPGIIVPGVYYSDDKLLQTRIFSYSD    #     350
      TQRHRLGPNYLLLPANAPKCSHHNNHYDGLMNFMHRDEEVDYFPSRFDPA    #     400
      KHAPRYPIPSRTLNGRREKMVIEKENNFKQPGERYRSMDPARQERFINRW    #     450
      IDALSDPRLTHEIKAIWLSYWSQADKSLGQKLASRLSSKPSM           #     500
%1    ...Y....SSS.......T...........S.T.................    #      50
%1    ..................T.......T...................T...    #     100
%1    ...S.......S..T...................................    #     150
%1    .............................S...................    #     200
%1    ....S..............Y.......T....S.................    #     250
%1    .T...T...........Y..T....Y..............T.........    #     300
%1    ...............S.........................T...S....    #     350
%1    T.................................Y..............    #     400
%1    .....Y...........................Y.S.............    #     450
%1    ....S....T.........S..S....S......S..SS....
```


(b)

```
      MDPYKHRPSSSFNSPMWSTNSGAPVWNNDNSLTVGSRGPILLEDYHLVEK    #      50
      IADFDRERIPERVVHARGASAKGFFEVTHDVSHLTCADFLRAPGVQTPVI    #     100
      VRFSTVIHERGSPETLRDPRGFAIKFYTREGNWDLVGNNFPVFFIRDGMK    #     150
      FPDMVHALKPNPKTHIQENWRVLDFFSHHPESLHMFTFLFDDIGVPADYR    #     200
      HMDGSGVNTYTLVNRAGKAHYVKFHWKPTCGVKSLLEDEAVTVGGTNHSH    #     250
      ATKDLTDSIAAGNYPEWTFYIQTIDPDHEDRFDFDPLDVTKTWPEDVVPL    #     300
      QPVGRLVLNRNIDNFFAENEQLAFCPGIIVPGVYYSDDKLLQTRIFSYSD    #     350
      TQRHRLGPNYLLLPANAPKCSHHNNHYDGLMNFMHRDEEVDYFPSRFDPA    #     400
      KHAPRYPIPARALNGRREKACIDKENNFKQPGERYRSMDPARQERFINRW    #     450
      IDALSDPRLTHEIKAIWLSYWSQADKSLGQKLASRLSAKPSM           #     500
%1    ...Y....SS...S...............S.T.................     #      50
%1    ....................S.......T...................T...  #     100
%1    ...S.......S..T...................................    #     150
%1    .............................S...................    #     200
%1    ....S..............Y.......T....S.......T.........    #     250
%1    .T...T...........Y..T...................T.........    #     300
%1    ...................................T...S....         #     350
%1    T.................................Y..............    #     400
%1    .....Y...........................Y.S.............    #     450
%1    ....S....T.........S..S....S......S..S.....
```
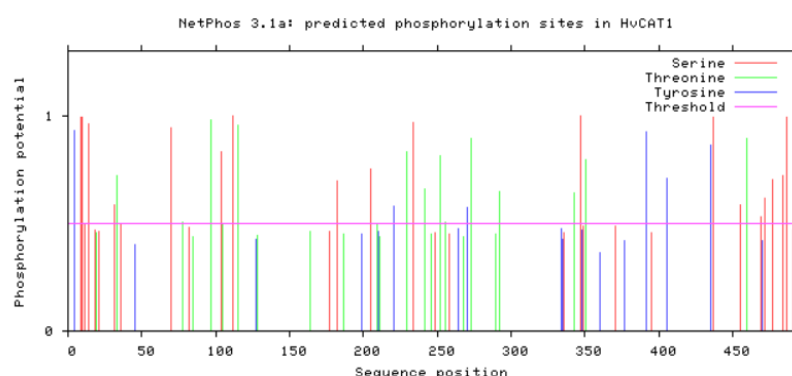

Figure S3: Identification of potential phosphorylation sites in (a) TtCAT1 and (b) HvCAT1 proteins using Netphos 3.1 database.

(a)

File Tools Help

Predicted Sites

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
370	LPANAPKCSHHNNHY	1,033	0	Cluster B

Enter sequence(s) in FASTA format

>TtCAT1
MDPYKYRPSSSFNAPMWSTNSGAPVWNNDNSLTVGSRGPILLEDYHLVEKIADFDRERIPERVVHARGATAKGFFEVTHDVSHLTCADFLRAPGVQT
PVIVRFSTVIHERGSPETLRDPRGFAIKFYTREGNWDLVGNNFPVFFIRDGMKFPDMVHALKPNPKTHIQENWRILDFFSHHPESLHMFTFLFDDIGVP
ADYRHMDGSGVNTYTLVNRAGKAHYVKFHWKPTCGVKSLLEEEAVTVGGTNHSHATKDLTDSIAAGNYPEWTFYIQTIDPDYEERFDFDPLDVTKTWP
EDVVPLQPVGRLVLNRNIDNFFSENEQLAFCPGIIVPGVYYSDDKLLQTRIFSYSDTQRHRLGPNYLLLPANAPKCSHHNNHYDGLMNFMHRDEEVD
YFPSRFDPAKHAPRYPIPSRTLNGRREKMVIEKENNFKQPGERYRSMDPARQERFINRWIDALSDPRLTHEIKAIWLSYWSQADKSLGQKLASRLSSK
PSM

(b)

File Tools Help

Predicted Sites

Position	Peptide	Score	Cutoff	Cluster
86	HDVSHLTCADFLRAP	2,011	0	Cluster B
230	KFHWKPTCGVKSLLE	19,226	0	Cluster C
325	ENEQLAFCPGIIVPG	1,152	0	Cluster B
370	LPANAPKCSHHNNHY	1,033	0	Cluster B
421	NGRREKACIDKENNF	0,224	0	Cluster A

Enter sequence(s) in FASTA format

>HvCAT1:
MDPYKHRPSSSFNSPMWSTNSGAPVWNNDNSLTVGSRGPILLEDYHLVEKIADFDRERIPERVVHARGASAKGFFEVTHDVSHLTCADFLRAPGV
QTPVIVRFSTVIHERGSPETLRDPRGFAIKFYTREGNWDLVGNNFPVFFIRDGMKFPDMVHALKPNPKTHIQENWRVLDFFSHHPESLHMFTFLFD
DIGVPADYRHMDGSGVNTYTLVNRAGKAHYVKFHWKPTCGVKSLLEDEAVTVGGTNHSHATKDLTDSIAAGNYPEWTFYIQTIDPDHEDRFDFDPL
DVTKTWPEDVVPLQPVGRLVLNRNIDNFFAENEQLAFCPGIIVPGVYYSDDKLLQTRIFSYSDTQRHRLGPNYLLLPANAPKCSHHNNHYDGLMNF
MHRDEEVDYFPSRFDPAKHAPRYPIPARALNGRREKACIDKENNFKQPGERYRSMDPARQERFINRWIDALSDPRLTHEIKAIWLSYWSQADKSL
GQKLASRLSAKPSM

Figure S4: Identification of putative S-nitrosylation sites in TtCAT1 (a) and HvCAT1 (b) proteins using GPS-NSO.1 database.