Supplementary material 3: CLUSTAL multiple sequence alignment of intracellular TcSOD a) and extracellular TcSods b) with respective SODs from other metazoan species.

A)

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Tribolium castaneum SODa      MPTKAVCVL--NGEVKGTIFFTQENGKAPVQVTGEVSGLKKGLHGFHIHEFGDNTNGCIS
Xenopus laevis IC-SOD         M-VKAVCVLAGSGDVKGVVHFEQQDE-GAVSVEGKIEGLTDGLHGFHIHVFGDNTNGCMS
Homo sapiens IC-SOD           MATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKGLTEGLHGFHVHEFGDNTAGCTS
Bos taurus IC-SOD             MATKAVCVLKGDGPVQGTIHFEAKGD--TVVVTGSITGLTEGDHGFHVHQFGDNTQGCTS
                              * .******  .* *:* : *  :    .* * *.: **..* ****:* ***** ** *

Tribolium castaneum SODa      AGAHFNPHGKDHGGPTHDVRHVGDLGNIEAGGDGVAKVGITDKFISLEGEHSIIGRTLVV
Xenopus laevis IC-SOD         AGSHFNPENKNHGAPGDTDRHVGDLGNVTAEG-GVAQFKITDSLISLKGPNSIIGRTAVV
Homo sapiens IC-SOD           AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVV
Bos taurus IC-SOD             AGPHFNPLSKKHGGPKDEERHVGDLGNVTADKNGVAIVDIVDPLISLSGEYSIIGRTMVV
                              **.**** ...**.*    ********: *   *** . * * .***.*  .***** **

Tribolium castaneum SODa      HADPDDLGQGGHELSKTTGNAGARLACGVVGITKA
Xenopus laevis IC-SOD         HEKADDLGKGGNDESLKTGNAGGRLACGVIGYSP-
Homo sapiens IC-SOD           HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ-
Bos taurus IC-SOD             HEKPDDLGRGGNEESTKTGNAGSRLACGVIGIAK-
                              * ..****.**:: * .*****.******:* :
```

bold = upper & lower rim

grey highlight = beta sheet, 3/10 helix & alpha helix

dark grey highlight = conserved region for ion binding

B)

```
TcSODb1                  MFKLFVLALCATATLATVEKA---------------------------------------
TcSODb2                  MFKLFVLALCATATLATVEKA---------------------------------------
TcSODc                   MFKSVVF-LCTLVTIKNVQSASMQTLAVRNALYQVPGLGNRPLIIKMYPGVENYQSDLYE
Homo_sapiens_EC-SOD      MLAL----LCSCLLLAAGASD-----AWTGEDSAEPNSDSAEWIRDMYAKVTEIWQEVMQ
                         *:      **:   :    .

TcSODb1                  ----------------IVCLKSGD--IDGKITFTQTAEG------VQVEGVINGLPKGKH
TcSODb2                  ----------------IVCLKSGD--IDGKITFTQTAEG------VQVEGVINGLPKGKH
TcSODc                   VYAEPYTFDLRAASAVALIQGEGESAAKGEIVFFQRHPP---NGPILVRGNLTDLPPGKH
Homo_sapiens_EC-SOD      RRDDDGTLHAACQVQPSATLDAAQPRVTGVVLFRQLAPRAKLDAFFALEGFPTEPNSSSR
                                               .:    * : * *          . : *  .    ...

TcSODb1                  GFHIHEKGALGDSCKDAGGHFNPDKKDHGAPEDAVRHVGDLGNIIADDKKVAHVNISDKI
TcSODb2                  GFHIHEKGALGDSCKDAGGHFNPDKKDHGAPEDAVRHVGDLGNIIADDKKVAHVNISDKI
TcSODc                   GLHIHQSGDLRQGCDKLGPHFNPYLLQHGGPSDPVRHVGDLGNIEVEEDGSVEFNIADPL
Homo_sapiens_EC-SOD      AIHVHQFGDLSQGCESTGPHYNPLAVPH------PQHPGDFGNFAVRDGSLWRYRAG--L
                         .:*:*: * * :.*.. * *:**    *      ::*:**:**: . :      . .  :

TcSODb1                  IS-LNGEHSIIGRAVVVHEGEDDLGKGNFNDSKTTGHAGARLVCGVIGIASDGTETCPEG
TcSODb2                  IS-LNGEHSIIGRAVVVHEGEDDLGKGNFNDSKTTGHAGARLVCGVIGIA----------
TcSODc                   LSLMGGPRGIVGRSIVISGNPDDLGRGGTAESLVNGDSGKPIACGVIAYIK---------
Homo_sapiens_EC-SOD      AASLAGPHSIVGRAVVVHAGEDDLGRGGNQASVENGNAGRRLACCVVGVCGPGLWERQAR
                          : : * ..*:**::*:  . ****.*.   *  .* :*  :.* *:.

TcSODb1                  PGNIAISTTGNYFLLFTGLYTLFLNLRF
TcSODb2                  ----------------------------
TcSODc                   ----------------------------
Homo_sapiens_EC-SOD      EHSERKKRRRESECKAA-----------
```

underlined = cleavage site predicted by signalP4.0
bold = upper & lower rim
grey highlight = beta sheet, 3/10 helix & alpha helix
dark grey highlight = conserved region for ion binding