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Supporting information for article:

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Is dimerization a common feature in thioredoxins?: the case of thioredoxin from *Litopenaeus vannamei*

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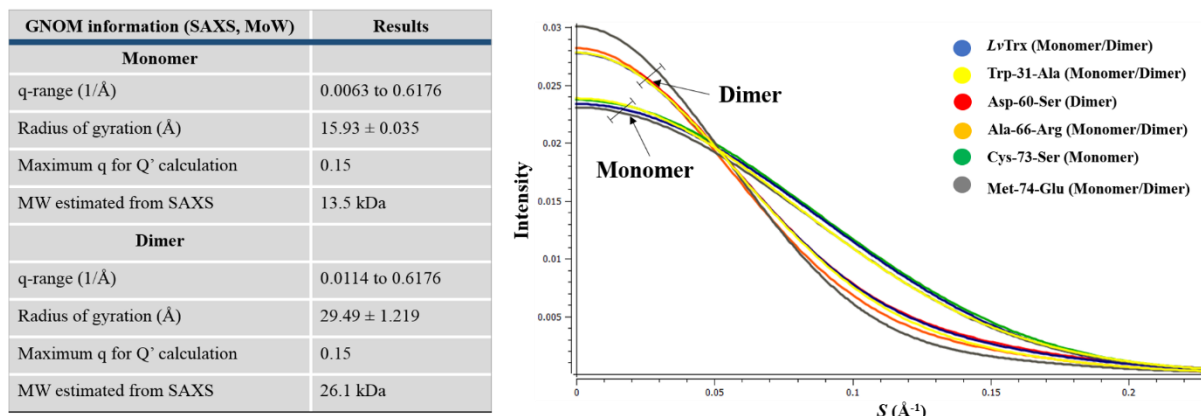
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GNOM information (SAXS, MoW)	Results
Monomer	
q-range (1/Å)	0.0063 to 0.6176
Radius of gyration (Å)	15.93 ± 0.035
Maximum q for Q' calculation	0.15
MW estimated from SAXS	13.5 kDa
Dimer	
q-range (1/Å)	0.0114 to 0.6176
Radius of gyration (Å)	29.49 ± 1.219
Maximum q for Q' calculation	0.15
MW estimated from SAXS	26.1 kDa

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12   **Figure S1** Molecular mass calculations for the monomer and dimer populations of *Lv*Trx wild type

13   were 13 kDa and 26 kDa, respectively. Additionally, the SAXS correlation functions of all the *Lv*Trx

14   mutants are analyzed here. The molecular weight was calculated with the SAXS MoW webserver

15   http://saxs.ifsc.usp.br/ (Fischer et al., 2010).
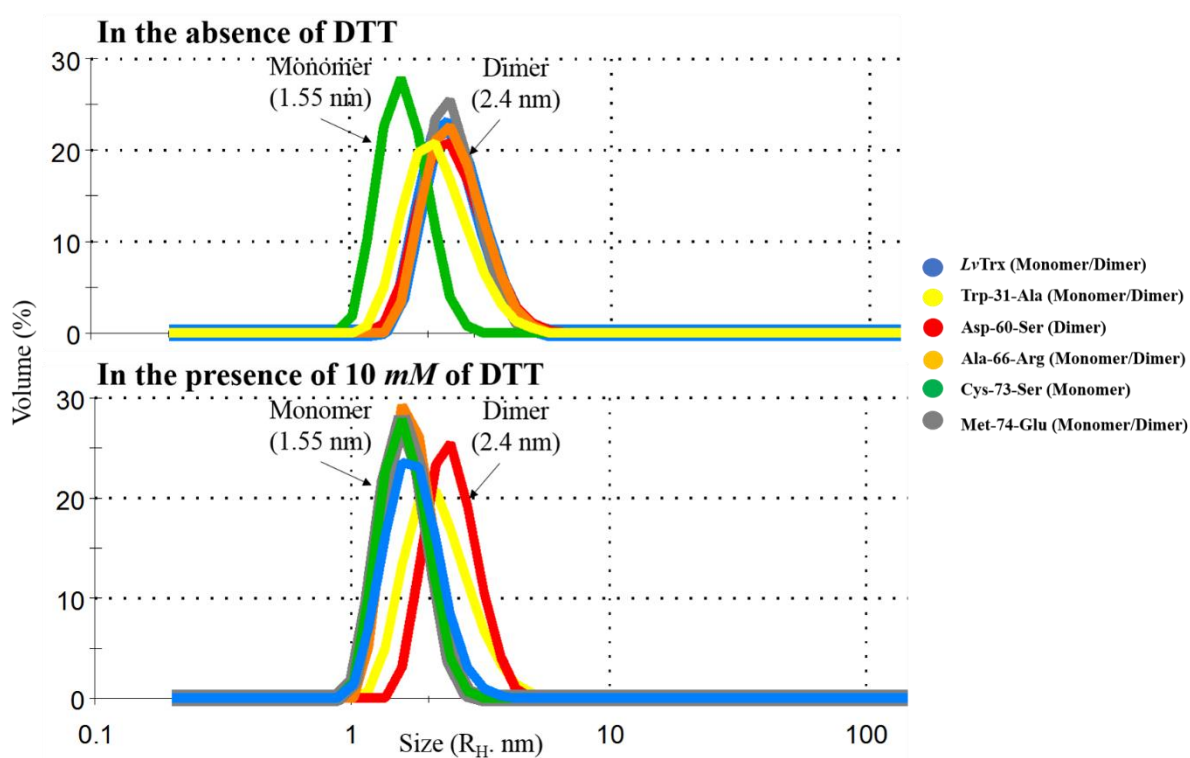
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17   **Figure S2** DLS results for all mutants and the *Lv*Trx wild type were analyzed under the absence and

18   the presence condition of DTT.

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Figure S3 Sequence alignment showed that shrimp thioredoxin reductase (Ghaffari et al., 2014) and rat thioredoxin reductase (rat-Uniprot entry O89049) share 64 % identity of their sequences, suggesting that rat TrxR can also reduce *Lv*Trx. The figure was made using the ESPript 3.0 webserver http://espript.ibcp.fr/ESPript/cgi-bin/ESPript.cgi (Robert & Gouet, 2014).