

# Highly effective proximate labeling in *Drosophila*

Bo Zhang<sup>1,2,3,5</sup>, Yuanbing Zhang<sup>1,2,3,5</sup>, and Ji-Long Liu<sup>1,4,\*</sup>

<sup>1</sup>School of Life Science and Technology, ShanghaiTech University, Shanghai, 201210, China

<sup>2</sup>Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, 200031, China

<sup>3</sup>University of Chinese Academy of Sciences, Beijing, 100049, China

<sup>4</sup>Department of Physiology, Anatomy and Genetics, University of Oxford, Oxford, OX1 3PT, UK

<sup>5</sup>These authors contributed equally to this work.

ORCID IDs: 0000-0002-7805-1786 (B.Z.); 0000-0002-4569-2798 (Y.Z.); 0000-0002-4834-8554 (J.L.L.)

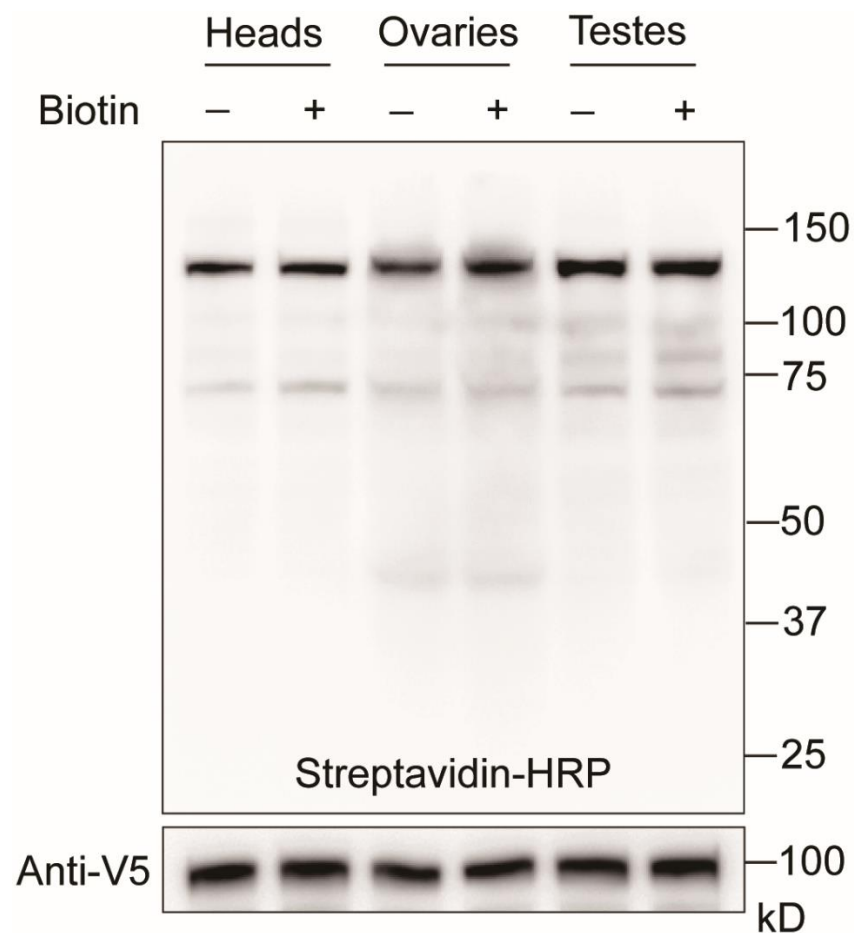
\*Corresponding author: liuji3@shanghaitech.edu.cn; jilong.liu@dpag.ox.ac.uk

## Supplementary materials

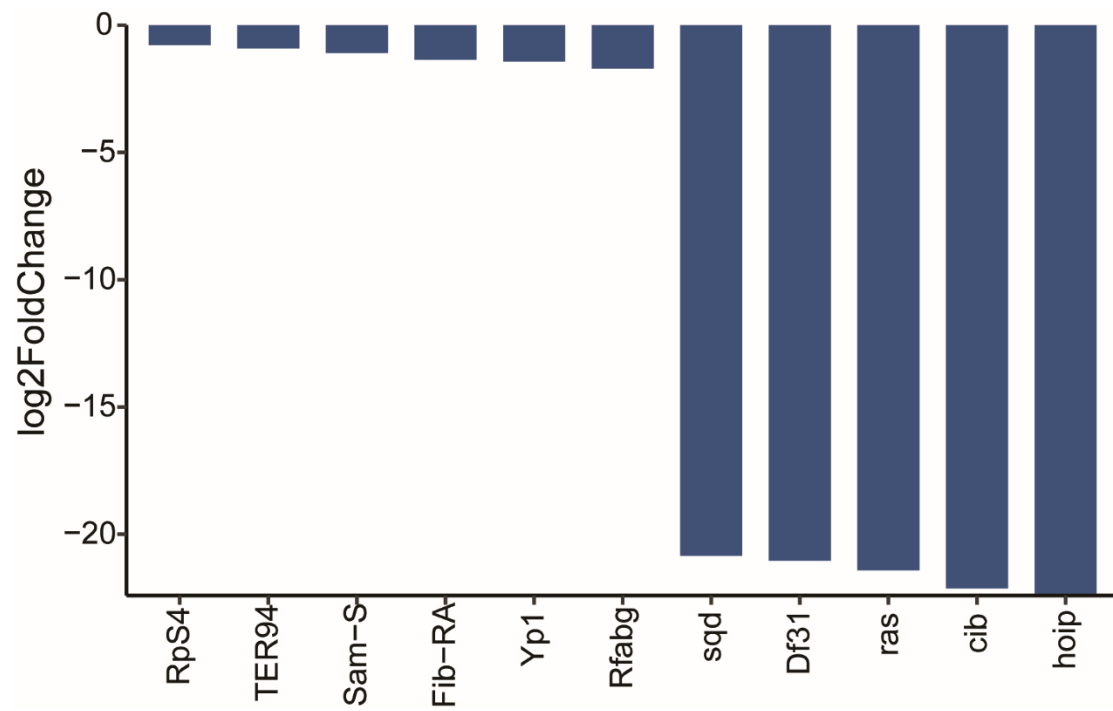
**Table S1**

**Figures S1-S4**

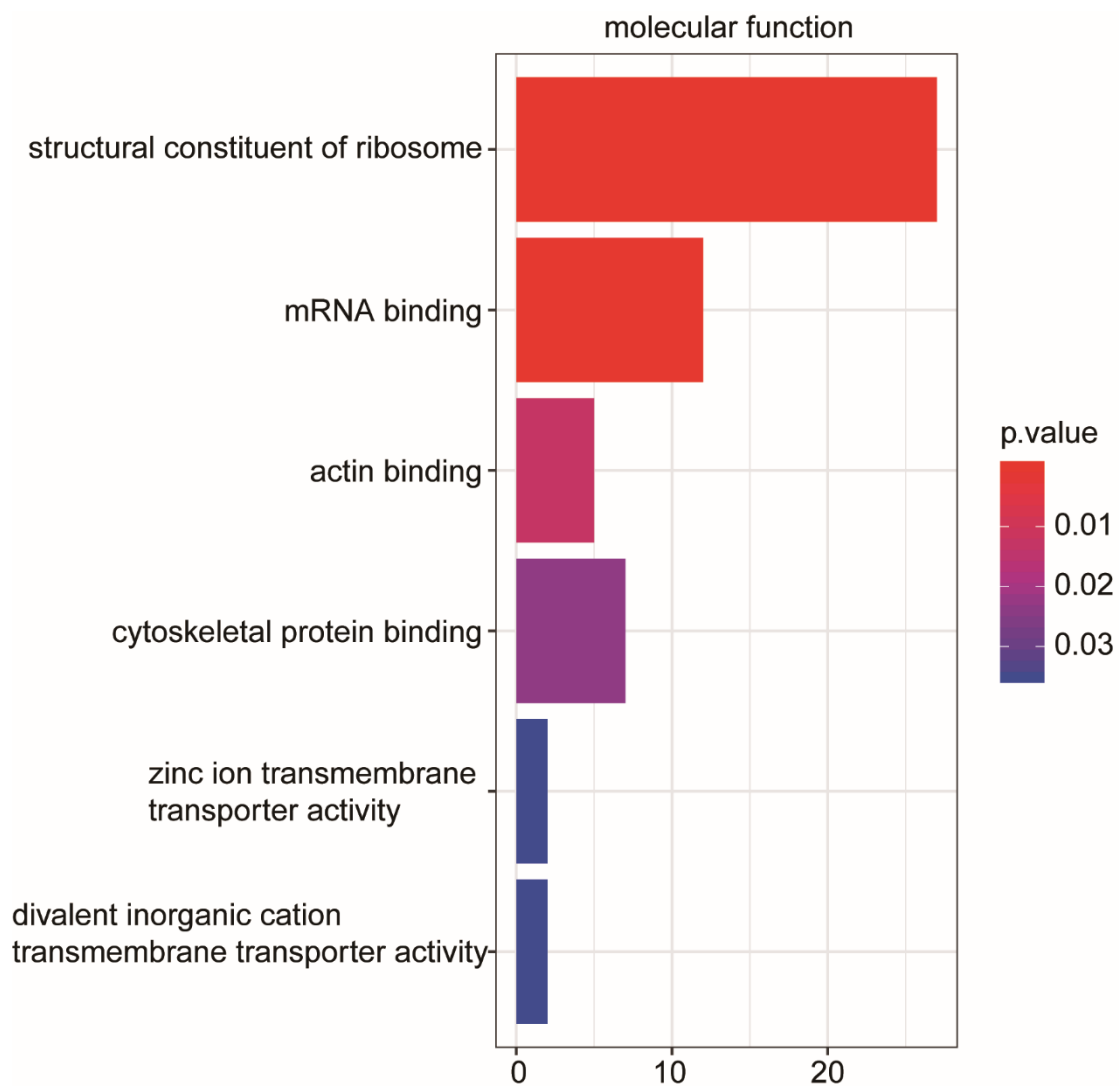
**Table S1. List of proximate proteome of CTPS cytoophidium and disrupted cytoophidium.**  
(in separated excel file)



**Figure S1. CTPS-mCherry was expressed ubiquitously via da-GAL4 driver.** Western blotting visualizing biotinylated proteins in different tissues from adult flies with streptavidin-HRP. CTPS-mCherry expression was detected by anti-V5 blotting.



**Figure S2. List of 11 enriched proteins residing adjacently to mutant CTPS.** Bar blot list of 11 enriched proteins of mutant CTPS compared to wild type CTPS.



**Figure S3. Enriched proximate proteins of CTPS classification based on molecular functions.** The single-item enrichment of p-value lower 0.05 is shown and ranked by p-value.

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hCTPS1 : MKYILVTGGVISGIGKGIASSVGTILKSCGLEVTSIKIDPYINILAGTFSPIYEHGEVFLDDGGEVDLDLGNVERFLIRITKDNNTTGKIYQYVINK : 100
mCTPS1 : MKYILVTGGVISGIGKGIASSVGTILKSCGLEVTSIKIDPYINILAGTFSPIYEHGEVFLDDGGEVDLDLGNVERFLIRITKDNNTTGKIYQYVINK : 100
dCTPS  : MKYILVTGGVISGIGKGIASSVGTILKSCGLEVTSIKIDPYINILAGTFSPIYEHGEVFLDDGGEVDLDLGNVERFLIRITKDNNTTGKIYQYVINK : 100

hCTPS1 : ERKGDVLGKTVQVVPHTTALIQEWMRCALIPVDEDGLEPQVQVIELGTVGDIESMPFIEAFRQFQFKVKRENFCNIHVSIVPQPSSTGEQKTKPTQNS : 200
mCTPS1 : ERKGDVLGKTVQVVPHTTALIQEWMRCALIPVDEDGLEPQVQVIELGTVGDIESMPFIEAFRQFQFKVKRENFCNIHVSIVPQPSSTGEQKTKPTQNS : 200
dCTPS  : ERKGDVLGKTVQVVPHTTALIQEWMRCALIPVDEDGLEPQVQVIELGTVGDIESMPFIEAFRQFQFKVKRENFCNIHVSIVPQPSSTGEQKTKPTQNS : 200

hCTPS1 : VRELRLGLSPDLIVCRCSNPLDTSVKEKISMFCHEVEPQVICVHDVSIYRVFILLLEEQGVVDYFIRLRLDLPIERQPRMIMRKEMADRYDRLLETCS : 300
mCTPS1 : VRELRLGLSPDLIVCRCSNPLDTSVKEKISMFCHEVEPQVICVHDVSIYRVFILLLEEQGVVDYFIRLRLDLPIERQPRMIMRKEMADRYDRLLETCS : 300
dCTPS  : RELRGCLSPDLIVCRSEKPIGLEVKEKISNFCVGPDPQVICIHDLNSIYHVPILMEQNGVIEYLNERLQLNIDMSKRTKQCCQRDLARFTETVRREVC : 300

hCTPS1 : IAVVGKYTKESDSYASVIRKALFESALAINHKLEIKYIDSDLEPPIISQEEVVRVYHEAWQKLGSAHGVLPVGGFVRCITEGKIQAIAANQKKFELVCL : 400
mCTPS1 : IAVVGKYTKESDSYASVIRKALFESALAINHKLEIKYIDSDLEPPIISQEEVVRVYHEAWQKLGSAHGVLPVGGFVRCITEGKIQAIAANQKKFELVCL : 400
dCTPS  : IAVVGKYTKESDSYASVIRKALFESALAINHKLEIKYIDSDLEPPIISQEEVVRVYHEAWQKLGSAHGVLPVGGFVRCITEGKIQAIAANQKKFELVCL : 400

hCTPS1 : GMLAVVEFSRNVLGWCLANSTEFDDTSHPVVVMPEHNFGCMGGTMRLGKRRTIRQTKNSVMRKLYGADYLEERHRRHEVNFVWKKOLEEQGLKFF : 500
mCTPS1 : GMLAVVEFSRNVLGWCLANSTEFDDTSHPVVVMPEHNFGCMGGTMRLGKRRTIRQTKNSVMRKLYGADYLEERHRRHEVNFVWKKOLEEQGLKFF : 500
dCTPS  : GLAPAVIEFARNKILGLKANTTIDENANALVICMPEHTGCLGGTMRLGKRRTIRSDGESVIRQLYGNPKSVQERHRRHEVNFVWKKOLEEQGLKFF : 500

hCTPS1 : GQVEGERMEIVELEIDHFFVGVQYHPPFLSRFHKPSPFYFGLILASVGRVSHFLKGCRLSPRDTYSDRSGSSSPDSEITELKFPSINH..... : 591
mCTPS1 : GQVEGERMEIVELEIDHFFVGVQYHPPFLSRFHKPSPFYFGLILASVGRVSHFLKGCRLSPRDTYSDRSGSSSPDSEITELKFPSISQD..... : 591
dCTPS  : GTDVKTRMEIIEISGHFYFVATQYHPPFLSRFHKPSPFYFGLILASVGRVSHFLKGCRLSPRQLSLASDEEDSVVGLAGATKSLSSLKIPITPTNGI : 600

hCTPS1 : ..... : -
mCTPS1 : ..... : -
dCTPS  : SKSCNGSISTSDSEGACGGVDPTNGHK : 627

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**Figure S4. Sequence alignment result of hCTPS1, mCTPS1, and dCTPS. Conserved amino acids were indicated in black.**