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# Muscle Proteomic Dataset of A Threatened Indian walking catfish, *Clarias magur* (Hamilton 1822) Exposed to Thermal Stress

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**This Data Descriptor presents a comprehensive LC–MS/MS-based muscle proteome dataset for *Clarias magur* subjected to sustained sub-lethal thermal stress. Fish were maintained at a control temperature of 26 °C or gradually warmed at a rate of 1 °C per day until reaching 37 °C, which was sustained for 60 days. Muscle samples were collected, proteins were extracted, digested with trypsin, and analyzed using a Waters SYNAPT G2-Si Q-TOF mass spectrometer. Resulting peptide spectra were searched against the *Danio rerio* Swiss-Prot UniProt database due to limited proteome resources for *C. magur*. The dataset includes raw mass spectral files, protein and peptide tables, sample metadata, water-quality logs, and processing files. These records are publicly available via PRIDE and are intended to support future studies on thermal tolerance in aquaculture species here the sole objective is to provide a transparent and reusable thermal proteome resource.**

## Background & Summary

Climate-related temperature fluctuations impose significant physiological challenges on aquaculture species. Warm-water fishes such as *Clarias magur* are economically important in South Asia due to resilience in variable aquatic environments; however, systematic proteome-level data documenting long-term heat exposure responses remain limited[1]. To address this gap, we generated a muscle proteomic dataset for *C. magur* exposed to chronic sub-lethal heat stress. The experiment captures the muscle protein landscape under stable control temperature and sustained elevated temperature conditions[2,3], providing a foundational resource for stress-physiology and aquaculture resilience studies[4]. The study does not aim to interpret or infer biological mechanisms; instead, it offers a rigorously documented dataset (Poonam Jayant Singh, Arpita Batta, Satish Kumar Srivastava. PRIDE. https://identifiers.org/pride.project:PXD029636 (2025))[5] with accompanying metadata, enabling independent re-analysis and reuse by the research community.

## Methods

All animal procedures followed CPCSEA guidelines[6] and were approved by the Institutional Animal Ethics Committee of ICAR-NBFGR (Approval No. NBFGR/IAEC/2020/037). Juvenile *C. magur* weighing 50–90 g were acclimated for 15 days at 26 °C in recirculating tanks. Two treatment groups were established: a control group maintained at 26 °C and a heat-stress group gradually heated at 1 °C per day to 37 °C, followed by maintenance at this temperature for 60 days. Each group consisted of ten fish, with three biological replicates processed for proteomics from each treatment. Fish were fed daily, and feed intake, body mass, and behavior were monitored throughout the trial. Water quality parameters, including pH (7.2–7.6), dissolved oxygen (5.8–6.5 mg $L^{-1}$), ammonia (<0.05 mg $L^{-1}$), and temperature, were recorded daily. No mortality occurred in control group but as sub lethal temperature mortality increased.

Fish were euthanized using clove oil at 0.10 mL $L^{-1}$, and muscle tissue samples were immediately collected and stored at −80 °C. For protein extraction, tissues were homogenized in 50 mM Tris buffer supplemented with PMSF and protease inhibitors. Protein concentration was determined by BCA assay. Samples were reduced using 100 mM DTT at 95 °C for one hour, alkylated using 250 mM IAA for 45 minutes in the dark, and digested

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overnight with trypsin at 37 °C. Peptides were separated on a Waters ACQUITY UPLC BEH C18 column[7] and analyzed on a SYNAPT G2-Si Q-TOF mass spectrometer in positive electrospray ionization mode, scanning m/z 50–1500.

Raw data were processed using PLGS v3.0.2. Protein identification[8] employed the *Danio rerio* Swiss-Prot UniProt database (downloaded March 2024) due to limited proteome resources for *C. magur*. A 1% false-discovery rate was applied at both peptide and protein levels, with carbamidomethylation of cysteine set as a fixed modification and oxidation of methionine and deamidation of asparagine/glutamine set as variable modifications. Technical quality checks included assessment of retention-time stability, total-ion chromatogram consistency, and calibration accuracy.

## Data Records

All data files are publicly archived in PRIDE[9] (https://doi.org/10.6019/PXD029636) accession number: PXD029636. Poonam Jayant Singh, Arpita Batta, Satish Kumar Srivastava. PRIDE. https://identifiers.org/pride.project:PXD029636 (2025)[5]. The repository includes raw LC-MS/MS data files, processed peptide and protein identification tables, instrument method files, search results, and experimental metadata. The accompanying metadata spreadsheet provides sample information, including fish identifiers, treatment groups, body weights, water-quality logs, and acquisition parameters. File names follow a transparent structure, indicating sample group and biological replicate. A README text file provides detailed instructions for data navigation and reuse.

A total of 2159 and 1880 unique proteins were identified in control and experimental groups, respectively. 581 proteins were commonly expressed in all control samples; 437 in all experimental samples. 1570 proteins were commonly expressed in both groups. 310 proteins were uniquely expressed in experimental and 589 in control groups.

## Technical Validation

Sample preparation and LC–MS/MS analyses were performed in biological triplicates to ensure reproducibility and analytical robustness. Protein identifications were accepted as high confidence based on stringent PLGS scoring thresholds, supported by consistent detection across replicates and low false-discovery rates. Only reproducibly identified proteins were retained for downstream quantitative and pathway analyses to minimize technical variability and enhance data reliability. The current dataset Poonam Jayant Singh, Arpita Batta, Satish Kumar Srivastava. PRIDE. https://identifiers.org/pride.project:PXD029636 (2025) thus provides a foundation for future research and practical applications in developing thermos-tolerant strains for sustainable aquaculture[10,11].

## Usage Notes

This dataset Poonam Jayant Singh, Arpita Batta, Satish Kumar Srivastava. PRIDE. https://identifiers.org/pride.project:PXD029636 (2025) may be used for spectral library generation, ortholog mapping, comparative proteomics, biomarker discovery pipelines, and future re-annotation as *C. magur* genomic resources expand. Users may reprocess raw data using alternative search databases, FDR cutoffs, or normalization strategies. The dataset is intended to serve as a reproducible reference resource rather than a hypothesis-driven experimental study. This dataset also provides valuable insights into the thermal stress response in fish, useful for researchers studying climate change impact on aquaculture. The data can be re-analysed for cross-species comparisons or functional genomic studies.

**Ethical Committee Clearance.** The proposal of the experiment has clearance from animal ethics committee of ICAR-NBFGR No. NBFGR/IAEC/2020/037

## Data availability

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier and **Project accession** is PXD029636 and the Data is available via ProteomeXchange with identifier PXD029636 (https://www.ebi.ac.uk/pride/archive/projects/PXD029636). Poonam Jayant Singh, Arpita Batta, Satish Kumar Srivastava. PRIDE. https://identifiers.org/pride.project:PXD029636 (2025).

## Code availability

No custom code was used for Data.

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## Author contributions

Poonam Jayant Singh: Paper writing, Draft preparation, Data Analysis, Data curation, Formal analysis, Investigation, Methodology, Writing original draft; Arpita Batta: Manuscript drafting, review; Satish Kumar Srivastava: Experiment conducting, coordination, paper writing.

## Competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Additional information

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