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Summary

KNOWLEDGE DISCOVERY IN DATASETS: DRUGGABLE TARGETS FOR PANCREATIC DUCTAL ADENOCARCINOMA

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Pancreas

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Multimodal proteomics analysis identified 32 druggable protein targets in pancreatic ductal adenocarcinoma using knowledge discovery in datasets and computational molecular docking with repurposed drugs.

KEY POINTS

- A total of 1,975 proteins were identified across mouse and human PDAC models and patient samples, with 32 proteins confirmed by immunohistochemistry in patients at the Human Protein Atlas.
- Computational docking identified high-affinity binding between EIF2A and Padnarsertib, STAMBP and Bemcentinib, and ANXA2 and AHNAK2 with Zavegepant, suggesting targets on endocytosis and CGRP signaling pathways.
- The 32 proteins cluster in SNARE formation pathway for membrane fusion (60% associated genes), MAPK pathway regulation (67%), and ERK/MAPK signaling pathway (100%).
- Survival analysis of 176 PDAC patients showed that high expression of EIF2A, STAMBP, ANXA2, and AHNAK2 was associated with low survival probability ($p<0.001$), identifying these as strong prognostic biomarkers.
- This computational study may interest researchers working on drug repurposing and target discovery in pancreatic cancer.

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