

# PancreScan K-Fold Cross-Validation Report

Date: 2026-02-10

## Regularization Settings

- Early Stopping Patience: 2
- Dropout: 0.5
- Backbone Frozen: True
- Weight Decay: 0.0001

## Configuration

- Data directory: DATASET/train/train
- Model: efficientnet\_b0
- Folds: 2
- Epochs per fold: 1
- Batch size: 16
- Image size: 224
- Learning rate: 0.0003
- Augmentation preset: basic
- Sampler: shuffle
- Positive class: pancreatic\_tumor
- Positive threshold: 0.4
- Classes: normal, pancreatic\_tumor

## Fold Metrics (Validation)

Fold	Loss	Accuracy	Precision (macro)	Recall (macro)	F1 (macro)	Precision (pos)	Recall (pos)	F1 (pos)
1	0.348295	0.9060	0.9197	0.8925	0.9009	0.8735	0.9792	0.9233
2	0.274880	0.9840	0.9817	0.9862	0.9836	1.0000	0.9723	0.9860

## Summary (Mean ± Std)

Metric	Mean	Std
loss	0.311587	0.036708
accuracy	0.944984	0.038984
precision	0.950667	0.030984
recall	0.939311	0.046848
f1	0.942289	0.041348
pos_precision	0.936728	0.063272
pos_recall	0.975779	0.003460
pos_f1	0.954646	0.031319

## Notes

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- Metrics are computed on the validation split of each fold.
- Positive-class metrics use the selected threshold.