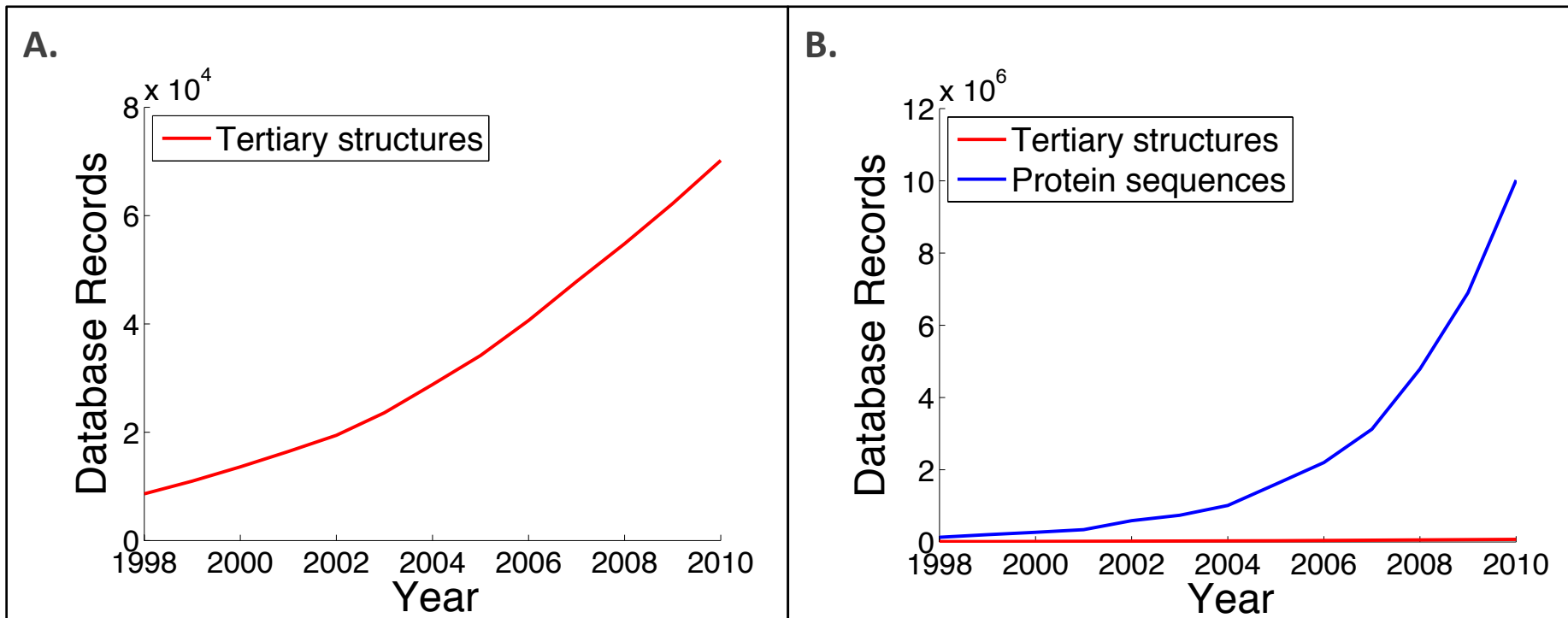
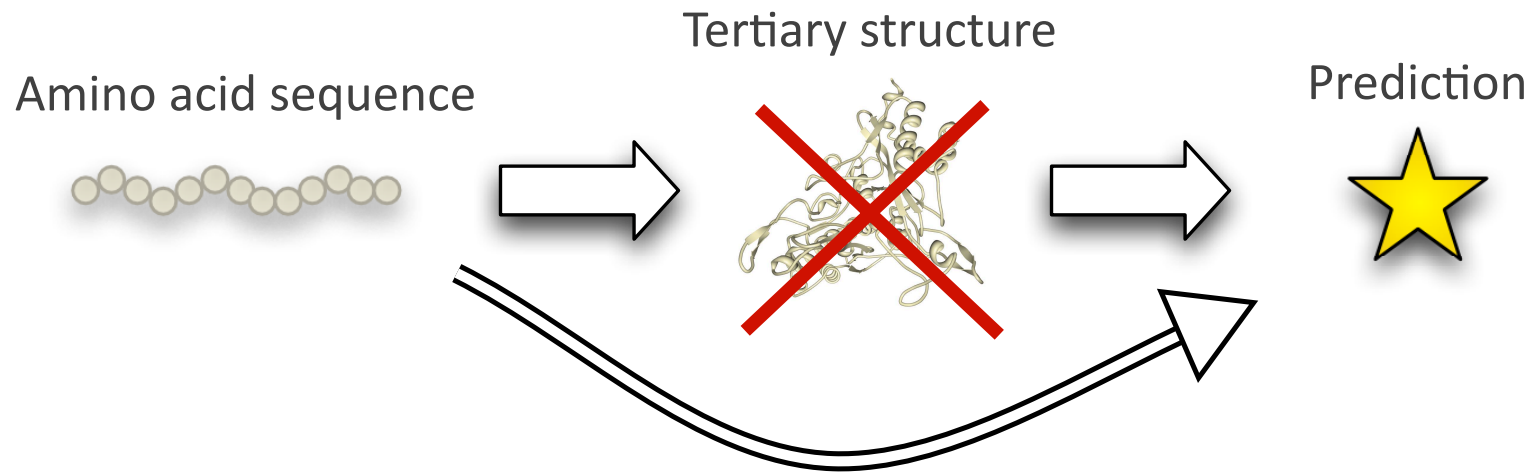




# Identification of DNA-binding Residues from Amino Acid Sequence Data

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# Sliding Window

Example:

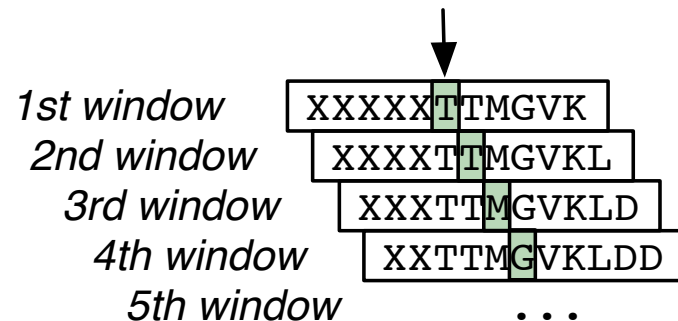
PDB entry 2RBF chain B

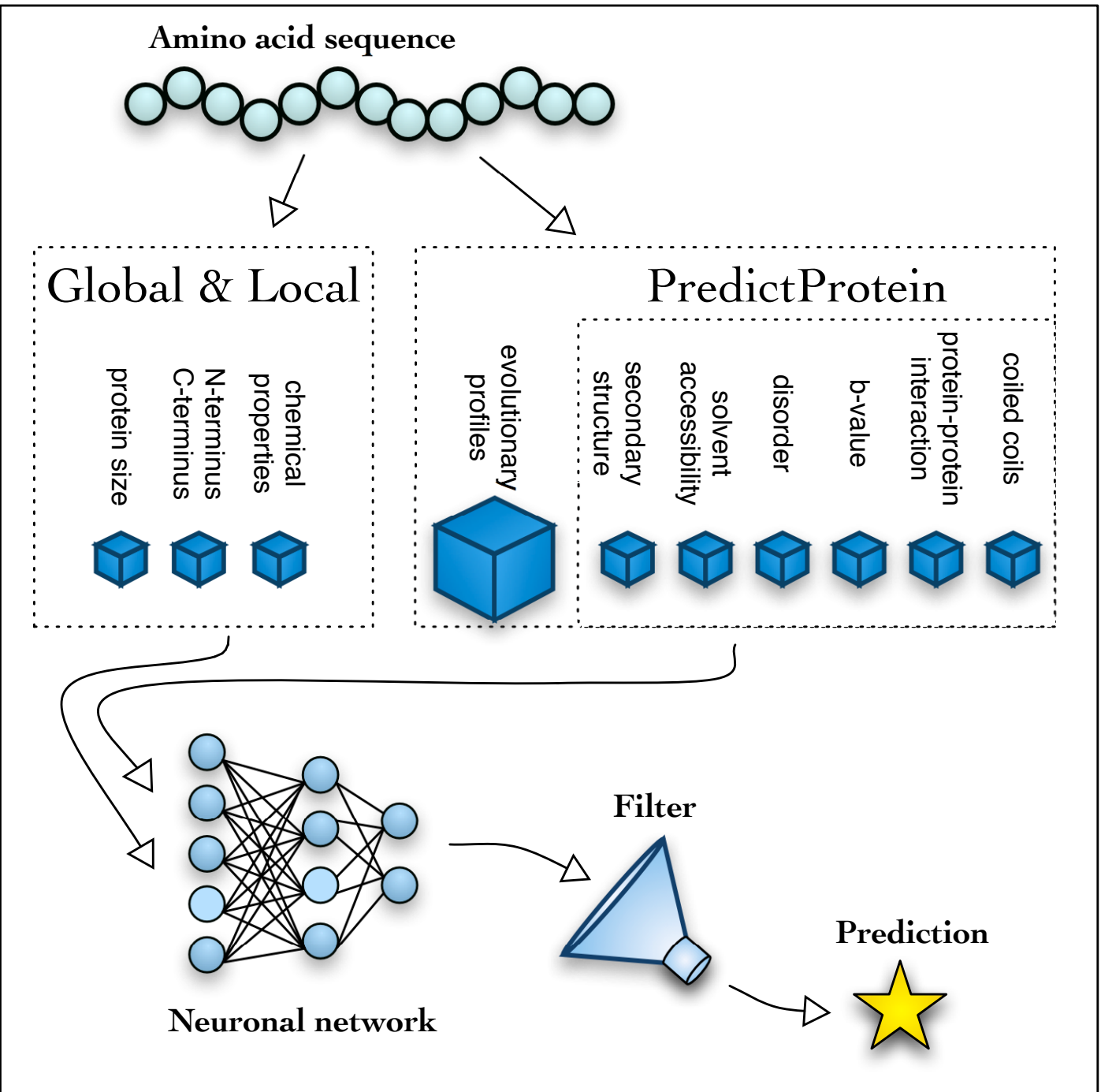
window size 11 ( $w = 11$ )

extend left = extend right =  $\text{floor}(11/2) = 5$



focus on the input amino acid





*Predict Protein: Rost et al., 2004*  
*Evolutionary profiles: Altschul et al., 1997*

# Feature Insights

FEATURE	$\mu$ AUC (%) $\pm \sigma$
Amino acid sequence (w=9)	72.2 $\pm$ 1.9
Amino acid sequence (w=11)	72.6 $\pm$ 1.7
Evolutionary profile (w=9)	80.6 $\pm$ 2.4
Evolutionary profile (w=11)	80.6 $\pm$ 1.9
Evolutionary profile (w=9) + global & local	81.2 $\pm$ 1.3
Evolutionary profile (w=11) + global & local	81.1 $\pm$ 1.8
Evolutionary profile (w=9) + global & local + PredictProtein (w=3)	81.7 $\pm$ 1.3
Evolutionary profile (w=11) + global & local + PredictProtein (w=3)	82.0 $\pm$ 1.7
Evolutionary profile (w=9) + global & local + PredictProtein (w=9)	82.1 $\pm$ 2.2
Evolutionary profile (w=11) + global & local + PredictProtein (w=11)	81.8 $\pm$ 2.0
Evolutionary profile (w=11) + global & local + PredictProtein (w=3) + refinement filter	82.2 $\pm$ 1.6

# Acknowledgment:

## Rost Lab:

**Burkhard Rost**

**Shaila C. Roessle**

Christian Schaefer

Marc Offman

Marco Punta

Arthur Dong

Esmeralda Vicedo

Laszlo Kajan

Tim Karl

Edda Kloppman

Guy Yachdav

Tobias Hamp

Markus Schmidberger

Andrea Schafferhans

Dedan Githae

Tatyana Goldberg

Maina Bitar

Marlena Drabik

## HSWT:

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