MULTICOM

Protein Structure Prediction
Multi-COMbination
combine for better accuracy

MULTICOM

5x protein structure prediction server
1 x human predictor
CASP8 - Brenchmark (low/high-Res.)

CASP

Critical Assessment of Techniques for Protein Structure Prediction

First: Calculate/Predict 3D-Structure

Second: Predict with experimental

Classical Methods

Protein Tertiary Structure
X-Ray crystallography
NMR

genome sequencing?

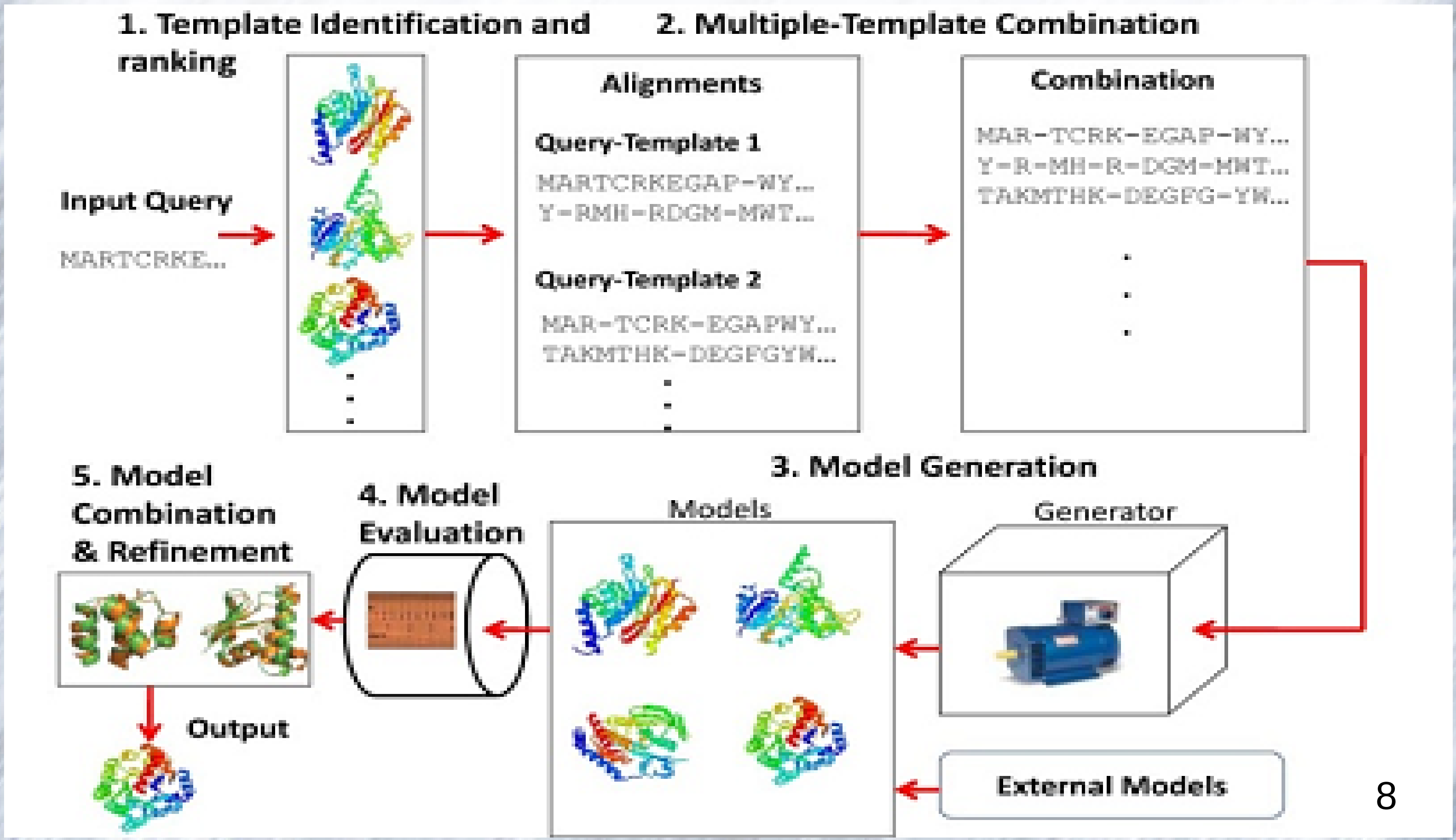
Templates

Template Based Modelling
Template Free Modelling

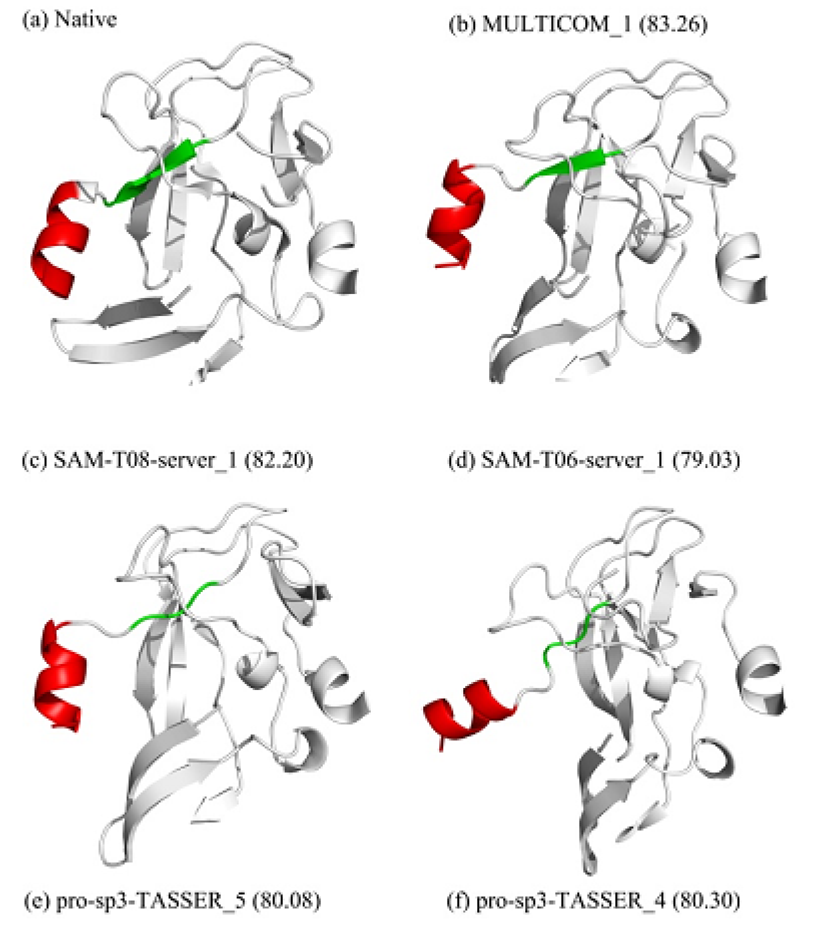
Steps

template identification and ranking
multi-template combination
model generation
model evaluation
model combination and refinement

Template identification and ranking

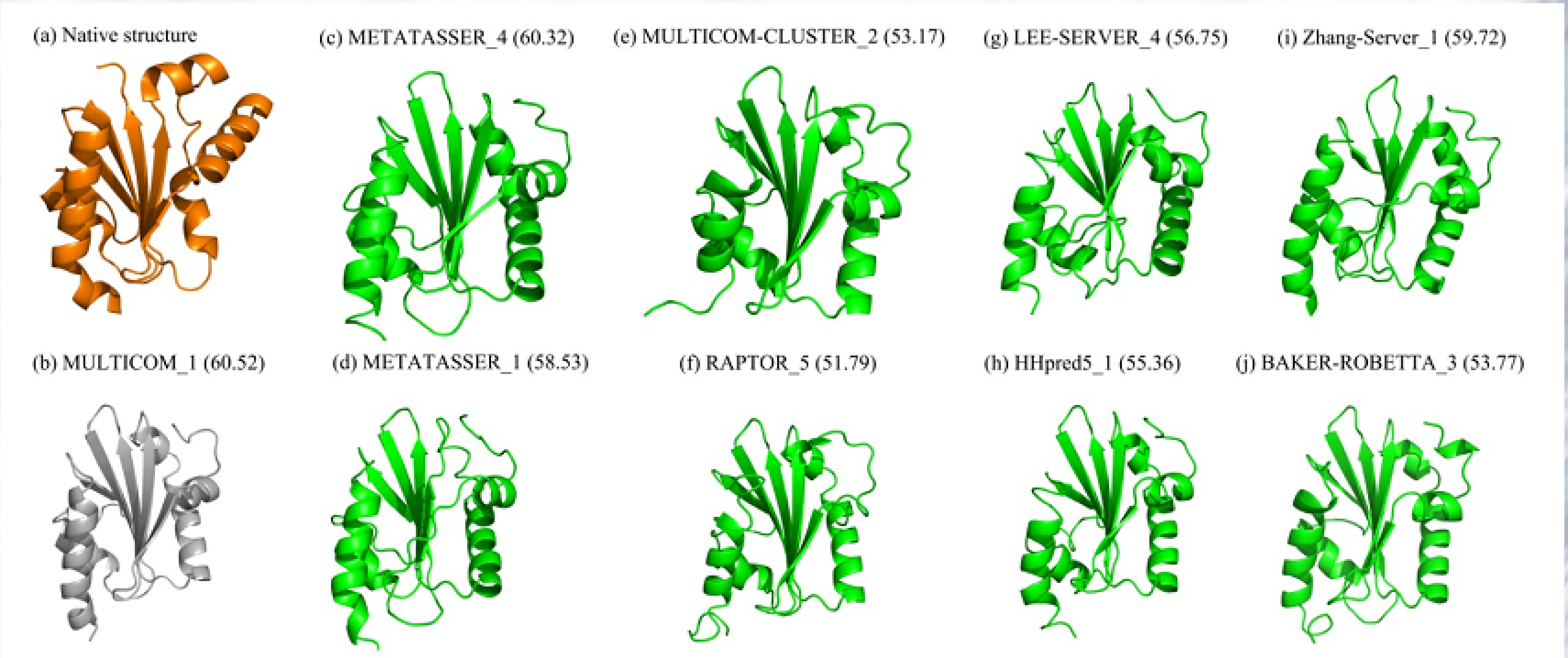


Comparisons



- Experimental Structure (a)
- Best model among all the server and human (b)
- Second best sever model (c)

Comparison



(a) Native structure

(c) METATASSER_4 (60.32)

(e) MULTICOM-CLUSTER_2 (53.17)

(g) LEE-SERVER_4 (56.75)

(i) Zhang-Server_1 (59.72)

(b) MULTICOM_1 (60.52)

(d) METATASSER_1 (58.53)

(f) RAPTOR_5 (51.79)

(h) HHpred5_1 (55.36)

(j) BAKER-ROBETTA_3 (53.77)

Conclusion

- Effective for the full spectrum of protein modeling
- Unique model combination step
- Improving System
- CASP-9