

## Publication

### Assessment of protein assembly prediction in CASP12

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We present the results of the first independent assessment of protein assemblies in CASP. A total of 1624 oligomeric models were submitted by 108 predictor groups for the 30 oligomeric targets in the CASP12 edition. We evaluated the accuracy of oligomeric predictions by comparison to their reference structures at the interface patch and residue contact levels. We find that interface patches are more reliably predicted than the specific residue contacts. Whereas none of the 15 hard oligomeric targets have successful predictions for the residue contacts at the interface, six have models with resemblance in the interface patch. Successful predictions of interface patch and contacts exist for all targets suitable for homology modeling, with at least one group improving over the best available template for each target. However, the participation in protein assembly prediction is low and uneven. Three human groups are closely ranked at the top by overall performance, but a server outperforms all other predictors for targets suitable for homology modeling. The state of the art of protein assembly prediction methods is in development and has apparent room for improvement, especially for assemblies without templates.

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