

# ERRATUM

To our dismay, two unfortunate formatting/typographical errors have slipped through our article *“A Unified Conformational Selection and Induced Fit Approach to Protein-Peptide Docking”*. They both relate to the description of our dataset and do not change in any regards the results and conclusions drawn from our observations.

Please find below the corrections:

- **Figure 1B** (page 3): The legend states that the darker the color, the less peptide residues are accessible to the solvent in the context of the complex. It should be the opposite; light colors correspond to buried peptides while dark colors mean exposed peptide. The correct legend of the figure is the following:
  - 0-20% of residue accessible -> **2** cases
  - 21-40% of residue accessible -> **13** cases
  - 41-60% of residue accessible -> **30** cases
  - 61-80% of residue accessible -> **34** cases
  - 81-100% of residue accessible -> **24** cases
- Section **“Material and Methods”**, paragraph **“Benchmark classification”** (page 11). The cutoffs reported here are wrong and the correct definition is:
  - Easy:  $\text{RMSD}_{\text{bound/extended}} \leq 2\text{\AA}$
  - Medium:  $2\text{\AA} < \text{RMSD}_{\text{bound/extended}} \leq 4\text{\AA}$
  - Difficult:  $\text{RMSD}_{\text{bound/extended}} > 4\text{\AA}$

All results and figures (e.g. **1A**) are based on the correct classification.