Supporting Information Table S2

Table S2. Methodological differences between DISPLAR, our previous method and our present method (DBPSite).

Difference	**DISPLAR [1]**	**Our previous method [2]**	**Our present method (DBPSite)**
Features analyzed and used	PSSM, Solvent accessibility	PSSM, Solvent accessibility, Side chain pK_a, Packing density and B-factor	PSSM, Side chain ASA, Propensity and Betweenness centrality
Distance of neighboring residues	No	No	Yes
Global topological measure of the protein structure network	No	No	Yes
Side chain information	No	Yes (side chain pK_a)	Yes (side chain ASA)
Feature extraction method	Concatenated encoding of neighboring residues	Concatenated encoding of neighboring residues	Weighted average encoding of neighboring residues
Dimensionality of encoding vectors	315	253	43
Threshold-dependent evaluation measure	No	Yes (ROC-AUC)	Yes (PR-AUC)
Significance of the difference between methods for comparison	No	No	Yes

References

1. Tjong H, Zhou HX (2007) DISPLAR: an accurate method for predicting DNA-binding sites on protein surfaces. Nucleic Acids Res 35: 1465-1477.

2. Xiong Y, Liu J, Wei DQ (2011) An accurate feature-based method for identifying DNA-binding residues on protein surfaces. Proteins-Structure Function and Bioinformatics 79: 509-517.