Lo Piparo et al.:

Bisphenol A Binding Promiscuity: A Virtual Journey through the Universe of Proteins

Supplementary Data

BioGPS score against ESR1 and ESR2 binding sites

To establish a reasonable threshold for discriminating proteins that bind BPA/EST from proteins that do not bind BPA/EST, we first calculated the complementarity score obtained between the two ligands among all estrogen receptor binding sites (both α and β).

We first collected all ERα and ERβ x-ray structures from Protein Data Bank (October 2014). Then, by using BioGPS algorithm, we detected cavities on these structures. We then selected only binding sites (cavities known to bind BPA), ending up with 126 ERα and 41 ERβ binding sites.

We screened BPA and EST against all binding sites. Then for one ligand (i.e., BPA) we computed the mean and the standard deviation of all scores obtained against one receptor (i.e., ERα).

Figure S1 reports all data for all combinations of BPA/EST against ERα/ERβ. Known interactions between BPA/EST and ERα/ERβ are defined by a score around 0.6; thus, we established a score equal to 0.6 as a relevant threshold for screening putative targets for BPA/EST.

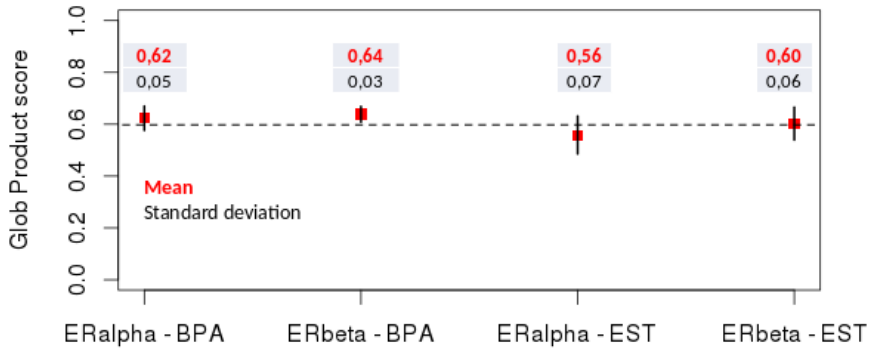

Fig. S1: Distribution of BioGPS score for BPA/EST versus ERα/ERβ

Tab. S1: Performance metrics for BPA and EST screening

BPA		prediction	
		active	inactive
in vitro	active	TP=23	FN=1
	inactive	FP=56	TN=26
		sensitivity	0.957
		specificity	0.317

EST		prediction	
		active	inactive
in vitro	active	TP=22	FN=3
	inactive	FP=42	TN=50
		sensitivity	0.880
		specificity	0.543

TP, true positives; FN, false negatives; FP, false positives; TN, true negatives
in vitro = data collected from PubChemBioassay and CTD
prediction = *in silico* BioGPS classification as active/inactive
sensitivity = TP/(TP+FN); specificity = TN/(TN+FP)

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