# iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting

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**Supplementary Information 2**

## Experimental results obtained using different values of the hyper parameter h of clustered sampling as balancing methods for different datasets

## Dataset: Enzymes

| Value of h | auROC | AUPR |
|---|---|---|
| 25% | 0.9478 | 0.66 |
| 50% | 0.9598 | 0.68 |
| 75% | 0.9398 | 0.65 |

## Dataset: GPCRs

| Value of h | auROC | AUPR |
|---|---|---|
| 25% | 0.9187 | 0.46 |
| 50% | 0.9322 | 0.48 |
| 75% | 0.9299 | 0.45 |

## Dataset: Ion Channels

| Value of h | auROC | AUPR |
|---|---|---|
| 25% | 0.9398 | 0.41 |
| 50% | 0.9369 | 0.48 |
| 75% | 0.9123 | 0.42 |

## Dataset: Nuclear Receptors

| Value of h | auROC | AUPR |
|---|---|---|
| 25% | 0.9012 | 0.71 |
| 50% | 0.9285 | 0.79 |
| 75% | 0.8942 | 0.74 |