**Table S1. Biophysical parameters for PGC-1α RID isolated and in complex with ERRα LBD and ERRγ LBD**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  | **AUC** | |  | |
| **Sample** | **MW (Da)** a | **Vbar(cm3/g)a** | | **S20,w**b **(calc.**c**)** | | **f/fo**b **(calc.**c,d**)** |
| **PGC-1α RID1** | 14773 | 0.7118 | | 1.23 | | 2.12 (1.9d) |
| **PGC-1α RID2** | 20263 | 0.7151 | | 1.44 | | 2.03 (1.97d) |
| **PGC-1α NTD** | 33603 | 0.7143 | | 1.97 | | 2.08 (2.03d) |
| **ERRα LBD** | 51360 | 0.7495 | | 3.25 (3.73) | | 1.3 (1.2c) |
| **ERRγ LBD** | 52946 | 0.7493 | | 3.56 (3.79) | | 1.2 (1.19c) |
| **PGC-1α RID2/ERRα LBD** | 71623 | 0.7398 | | 3.69 | | 1.52 (1.61d) |
| **PGC-1α RID2/ERRγ LBD** | 73209 | 0.7399 | | 3.79 | | 1.55 (1.59d) |

a Molecular weights (MW) and partial specific volume (Vbar) at 20°Ccomputed using Ultrascan II; the molecular weights of ERRα and ERRγ are given for the dimer

b experimental value

c computed using SOMO hydrodynamics calculations [42-44] using the crystal structures of ERRα and ERRγ (pdb entries 3D24 and 1KV6, respectively), where the peptide coordinates were removed from the structures

d computed using the calculated molecular weight, the calculated partial specific volume and the measured sedimentation coefficient S20,w