Supplementary table 3
Predicted intrinsic disorder in LXRs

RECEPTOR	SPECIES	ACCESSION NUMBER	DISORDER PROBABILTY IN DBD[a]	DISORDER PROBABILTY IN LBD[a]	DISORDER PROBABILTY IN FULL-LENGTH PROTEIN[a]
LXRα (NR1H3)	Human (*Homo sapiens*)	Genbank:NM_005693	0.647	0.231	0.519
LXRα (NR1H3)	Chimpanzee (*Pan troglodytes*)	Genbank:XM_521906	0.647	0.231	0.519
LXRα (NR1H3)	Rhesus monkey (*Macaca mulatta*)	Ensembl:ENSMMUT00000021881	0.662	0.291	0.599
LXRα (NR1H3)	Cow (*Bos taurus*)	Ensembl:ENSBTAT00000014131	0.662	0.223	0.528
LXRα (NR1H3)	Mouse (*Mus musculus*)	Genbank:NM_013839	0.662	0.219	0.503
LXRα (NR1H3)	Rat (*Rattus norvegicus*)	Genbank:NM_031627	0.676	0.244	0.515
LXRα (NR1H3)	Cat (*Felis catus*)	Ensembl:ENSFCAT00000002528	0.662	0.244	0.649
LXRα (NR1H3)	Platypus (*Ornithorhynchus anatinus*)	Ensembl:ENOANT00000010003	0.676	0.211	0.451
LXRα (NR1H3)	Chicken (*Gallus gallus*)	Genbank:AF492498	0.676	0.186	0.465
LXRα (NR1H3)	African clawed frog (*Xenopus laevis*)	Genbank:BC074169	0.706	0.240	0.537
LXRα (NR1H3)	Spotted green pufferfish (*Tetraodon nigriviridis*)	Ensembl:GSTENT00018165001	0.676	0.290	0.534
LXRα (NR1H3)	Zebrafish (*Danio rerio*)	Genbank:NM_001017545	0.696	0.227	0.493
LXR (NR1H2/3)	Sea squirt (*Ciona intestinalis*)	Ensembl:ENSCINT00000014778	**0.838**	**0.017**	0.416
LXR (NR1H2/3)	Purple sea urchin (*Strongylocentrotus purpuratus*)	Genbank:XM_774904	0.750	0.457	0.653
		Average (excluding *Ciona* and sea urchin LXRs)	0.671	0.236	0.526
		Standard deviation	0.018	0.030	0.054
LXRβ (NR1H3)	Human (*Homo sapiens*)	Genbank:NM_007121	0.700	0.279	0.573
LXRβ (NR1H3)	Rhesus monkey (*Macaca mulatta*)	Ensembl:ENSMMUT00000032951	0.700	0.279	0.573
LXRβ (NR1H3)	Cow (*Bos taurus*)	Ensembl:ENSBTAT00000004229	0.643	0.479	0.636

LXRβ (NR1H3)	Dog (*Canis familiaris*)	Ensembl:ENSCAFT00000005340	0.700	0.416	0.628
LXRβ (NR1H3)	Guinea pig (*Cavia porcellus*)	Ensembl:ENSCOPOT00000002871	0.643	0.237	0.541
LXRβ (NR1H3)	Mouse (*Mus musculus*)	Genbank:NM_009473	0.643	0.291	0.549
LXRβ (NR1H3)	Rat (*Rattus norvegicus*)	Genbank:NM_031626	0.643	0.270	0.542
		Average	0.667	0.322	0.577
		Standard deviation	0.030	0.090	0.040

[a] Proportion of amino acid residues in DNA-binding domain (DBD), ligand-binding domain (LBD), or full-length protein that have disorder probability greater than 0.50.

Disorder calculations were calculated as previously described [1,2]. Ensembl sequences can be found at http://www.ensembl.org.

References

[1] A.K. Dunker, M.S. Cortese, P. Romero, L.M. Iakoucheva, V.N. Uversky, Flexible nets: the roles of intrinsic disorder in protein interaction networks, FEBS Lett. 270 (2005) 5129-5148.
[2] K. Peng, S. Vucetic, P. Radivojac, C.J. Brown, A.K. Dunker, Z. Obradovic, Optimizing long intrinsic disorder predictors with protein evolutionary information, J. Bioinform. Comput. Biol. 3 (2005) 35-60.