

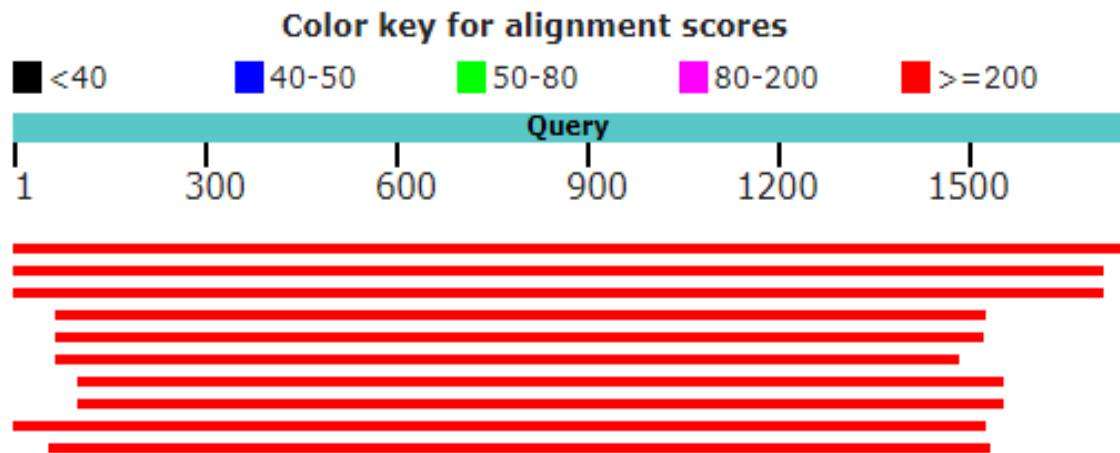
Supplementary Material

Characterization, Docking and Molecular Dynamics Simulation of Gonadotropin-Inhibitory Hormone Receptor (GnIHR2) in *Labeo Catla*

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	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	Catla catla GnIHR2 mRNA for gonadotropin-inhibitory hormone receptor, complete cds	3126	3126	100%	0.0	100.00%	LC380835.1
<input type="checkbox"/>	Carassius auratus G-protein couple receptor IHR2 mRNA, complete cds	2360	2360	98%	0.0	90.80%	JX946587.1
<input type="checkbox"/>	PREDICTED: Carassius auratus neuropeptide FF receptor 1-like (LOC113068965), mRNA	2346	2346	98%	0.0	90.62%	XM_026241930.1
<input type="checkbox"/>	PREDICTED: Sinocyclocheilus rhinoceros neuropeptide FF receptor 1-like (LOC107755826), mRNA	2195	2195	83%	0.0	93.47%	XM_016572747.1
<input type="checkbox"/>	PREDICTED: Sinocyclocheilus grahami neuropeptide FF receptor 1-like (LOC107599640), mRNA	2179	2179	83%	0.0	93.26%	XM_016291290.1
<input type="checkbox"/>	PREDICTED: Sinocyclocheilus anshuiensis neuropeptide FF receptor 1-like (LOC107668729), mRNA	2105	2105	81%	0.0	93.06%	XM_016460701.1
<input type="checkbox"/>	PREDICTED: Carassius auratus neuropeptide FF receptor 1-like (LOC113049997), mRNA	1810	1810	83%	0.0	87.57%	XM_026212720.1
<input type="checkbox"/>	PREDICTED: Carassius auratus neuropeptide FF receptor 1-like (LOC113049982), mRNA	1801	1801	83%	0.0	87.43%	XM_026212708.1
<input type="checkbox"/>	Danio rerio neuropeptide FF receptor 1 like 2 (npffr1l2), mRNA	1709	1709	87%	0.0	85.08%	NM_001171697.1
<input type="checkbox"/>	PREDICTED: Danio rerio neuropeptide FF receptor 1 like 2 (npffr1l2), transcript variant X1, mRNA	1709	1709	84%	0.0	85.81%	XM_021476303.1
<input type="checkbox"/>	Cyprinus carpio genome assembly common carp genome, scaffold: LG9, chromosome: 9	1666	2309	96%	0.0	91.13%	LN590718.1
<input type="checkbox"/>	PREDICTED: Sinocyclocheilus anshuiensis neuropeptide FF receptor 1-like (LOC107654224), mRNA	1590	1590	83%	0.0	84.17%	XM_016441217.1
<input type="checkbox"/>	Cyprinus carpio genome assembly common carp genome, scaffold: 000001513	1236	1594	72%	0.0	86.21%	LN598459.1

Supplementary Fig. 1. NCBI protein BLAST of GnIHR2 amino acid sequence