Table S1. Vertebrate, non-zebrafish sequences producing significant alignments to DICP D1-D2 domains.[*]

Query	Subject GenBank Accession #	Description of subject	Query coverage	E value	Max ident
Dicp3b D1-D2	AB098477.1	*Cyprinus carpio* NITR mRNA for novel immune type receptor, complete cds	99%	1e-52	48%
	XM_003458344.1	PREDICTED: *Oreochromis niloticus* hypothetical protein LOC100707140 (LOC100707140), mRNA	48%	4e-16	40%
	CR727116.2	*Tetraodon nigroviridis* full-length cDNA	73%	3e-10	38%
	CR726974.2	*Tetraodon nigroviridis* full-length cDNA	54%	7e-09	39%
	BT072793.1	*Salmo salar* clone ssal-rgf-541-015 unknown large open reading frame mRNA, novel cds	95%	9e-09	26%
	CR720133.2	*Tetraodon nigroviridis* full-length cDNA	59%	4e-08	33%
	CR732854.2	*Tetraodon nigroviridis* full-length cDNA	92%	5e-08	29%
	CR716578.2	*Tetraodon nigroviridis* full-length cDNA	51%	3e-06	36%
	NM_001124539.1	*Oncorhynchus mykiss* CD4 (LOC100136285), mRNA	91%	5e-06	27%
Dicp14a D1-D2	AB098477.1	*Cyprinus carpio* NITR mRNA for novel immune type receptor, complete cds	98%	3e-61	52%
	BT072793.1	*Salmo salar* clone ssal-rgf-541-015 unknown large open reading frame mRNA, novel cds	98%	1e-13	30%
	XM_003458344.1	PREDICTED: *Oreochromis niloticus* hypothetical protein LOC100707140 (LOC100707140), mRNA	37%	1e-09	36%
	CR690772.2	*Tetraodon nigroviridis* full-length cDNA	71%	1e-08	25%
Dicp16a D1-D2	AB098477.1	*Cyprinus carpio* NITR mRNA for novel immune type receptor, complete cds	95%	7e-55	54%
	BT072793.1	*Salmo salar* clone ssal-rgf-541-015 unknown large open reading frame mRNA, novel cds	96%	3e-16	28%
	XM_003458344.1	PREDICTED: *Oreochromis niloticus* hypothetical protein LOC100707140 (LOC100707140), mRNA	55%	3e-14	41%
	CR726974.2	*Tetraodon nigroviridis* full-length cDNA	53%	5e-09	34%
	CR690772.2	*Tetraodon nigroviridis* full-length cDNA	57%	8e-09	26%
	CR720133.2	*Tetraodon nigroviridis* full-length cDNA	60%	1e-08	31%
	CR727116.2	*Tetraodon nigroviridis* full-length cDNA	59%	2e-07	33%
	AJ506968.1	*Takifugu rubripes* aif1, csnk2B, cyp21A2, c4, tnx and rxrbeta genes	92%	2e-07	24%
	CR716578.2	*Tetraodon nigroviridis* full-length cDNA	39%	5e-07	35%
	XM_003457735.1	PREDICTED: *Oreochromis niloticus* neural cell adhesion molecule 2-like (LOC100711789), mRNA	55%	5e-07	26%
	CR732854.2	*Tetraodon nigroviridis* full-length cDNA	92%	8e-07	29%
	XM_003219306.1	PREDICTED: *Anolis carolinensis* contactin 5 (cntn5), mRNA	63%	2e-06	26%
	XM_001499430.1	PREDICTED: *Equus caballus* contactin 5, transcript variant 3 (CNTN5), mRNA	63%	3e-06	25%

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[*] Results from tBLASTn searches of the "nr" nucleotide database using DICP D1-D2 domains as queries. Alignments with E values less than 1e-06 are shown.