

Table S1. LRRTM protein accession numbers, pI values of LRR domains, and manually curated amino-acid sequences used for the alignment.

Protein	pI value*	Refseq	Ensembl	Elephant shark genome
HsLRRTM1	7.5	NP_849161.2		
GgLRRTM1	7.5	XP_004936330.1		
XtLRRTM1	7.8	XP_002935525.1		
LcLRRTM1	6.5	XP_006014691.1		
DrLRRTM1	5.4	XP_005160139.1		
LoLRRTM1	6.2		ENSLACP00000013386_1	
CmLRRTM1	(5.9)			AAVX01003276.1
HsLRRTM2	7.8	NP_056379.1		
GgLRRTM2	7.9	XP_004944826.1		
LcLRRTM2	7.2	XP_006003760.1		
DrLRRTM2	7.3	XP_003201382.1		
LoLRRTM2	6.8		ENSLOCP00000022413	
CmLRRTM2	(8.1)			AAVX01197253.1
HsLRRTM3	9.6	NP_821079.3		
GgLRRTM3	9.6		ENSGALP00000033454	
XtLRRTM3	9.8	XP_002936907.2		
LcLRRTM3	9.7	XP_006003251.1	ENSLACP00000012957	
LoLRRTM3	9.5		ENSLOCP00000014278	
CmLRRTM3	(7.9)			AAVX01197253.1
HsLRRTM4	9.5	NP_079269.4		
GgLRRTM4	9.6	XP_417690.3		
XtLRRTM4	9.6	XP_002932606.1		
LcLRRTM4	9.3	XP_006004503.1		
DrLRRTM4-1	9.7	XP_005172519.1	ENSDARP00000077281	
DrLRRTM4-2	9.2	XP_692159.4	ENSDARP00000097998	
DrLRRTM4-3	8.9	XP_697133.6	ENSDARP00000100212	
DrLRRTM4-4	8.2	XP_001340869.4	ENSDARP00000101739	
LoLRRTM4	8.9		ENSLOCP00000019846	
CmLRRTM4	(8.2)			AAVX01198974.1
PmLRRTM_A	9.2		ENSPMAP00000011013	
PmLRRTM_B	9.6		ENSPMAP00000007010	

*The pI values are for the extracellular parts without the signal sequence and hinge domains. (Values for the partial shark sequences are not comparable).

>HsLRRTM1

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HVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITLAGNLWDCGRNVCALASWLNQFGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCE
DGAEPSTGHLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLLIVVLVLYVSWKCFPA
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>GgLRRTM1

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DCRSLKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNLAHFPRILSLHSLCLRRNKVTIVVNTLDWIWQLEKLDLSGNEIEYIEP
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IRQLRQCFTVQRRKQKQKQTMHQMAAMSAQEYVVDYKPNHIEGALVINEYGSCTCHQQPARECEV

>XtLRRTM1

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HVFESLPHLESQLDNSRLTYVDRILDSWSSLTISLISGNIWNCNRNVCALASWLSAFKGRCDGNMLCTTPEYAQGEDVLDVAVYFRLCD
DPVDPTSANAISTALNNSDRIAIDSPTATSYNVQDTEGERTTNVQTATVANEHHEHTVQIHKVVTGTMALIFSFLIVVLMVLYVSWKCFPAS
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>LcLRRTM1

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DCRSLEVLDLGYNQLKSLARNSFAGLFKLTQLEHLEHNDLVKVNLAHFPRLLSLRSLTYMQRNKVTIIVNSLDTWVNFLEKMDLSNNEIEYIE
PHVFETVPLNKILQLDSNRLTYVDRILDSWSSLTISLISGNIWNCNRNVCALASWLSNFKGHDSLLCASPENVQGEDILDVAVYAFNLC
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>DrLRRTM1

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>LoLRRTM1

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>CmLRRTM1

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SPEHTQGEDVLDVAVHGFHICDDLDSTPATAGTTAATAAQRSVTAAGEALSSAAANTGDTTGEVPTAPVTVTSEEGSPEPRENTIQV
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SRECEV

>HsLRRTM2

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>GgLRRTM2

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>LcLRRTM2

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>DrLRRTM2

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>LoLRRTM2

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VVVTERSYPQAPRTPQRPVFIKPKPTVSKLESNQPTSVVPSSTDLPTPAVEPEYEHVSFHKIIAGSVALFSLVAMILLVIYVSWKRYPASMK
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>XtLRRTM4

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VLATERAYPTTKPPKPKPTIYKLESVSSPTTSSPSPALQTPMAEQEYEHVSFHKIIAGSVALFSLVAMILLVIYVSWKRYPASMK
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>LcLRRTM4

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VVVTRDRPQAPKASQKSTFILKPTIPEQESNPQVPTTSSPSPVLQTPGSEQEYEHVSFHKIIAGSVALFSLVAMILLVIYVSWKRYPASMK
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>DrLRRTM4_1

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>DrLRRTM4_2

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STIFVPSTPFVAFSQTPASSLVPTLKSQDSRRVHGTSLGEGTSSVPSQDPVPPQEQDFEPVVSFHKIIAGSVALFSLVAMILLVIYVSWKRY
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>DrLRRTM4_3

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>DrLRRTM4_4

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RECEV

>LoLRRTM4

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>CmLRRTM4

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>PmLRRTM_A

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>PmLRRTM_B

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