

# **Supplementary Materials: One-Step Affinity Purification of Leucine-Rich $\alpha$ 2-Glycoproteins from Snake Sera and Characterization of Their Phospholipase A2-Inhibitory Activities as $\beta$ -Type Phospholipase A2 Inhibitors**

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1	AGTGTCCAAAAGGCTGGCAGGAGTGAGGTTTGGACAGAGTTCCAGGATGAAGTCT	55
(-23)		M K S (-21)
56	TCGGTTCTAGCACTTCTGATCATCTGCCTTGTGATGTCTTCAACAGCTACACCCAGCAGGTTCTT	121
(-20)	S V L A L L I I C L V M S F N S Y T Q Q <u>V L</u>	(2)
122	TATTGCCCAACCGATCCTGCTCCAGAAAATATCACTGAGTTTGGCTGCAACTCCCCATCTCTCCAT	187
(3)	<u>Y C P P D P A P E N I T E F G C N S P S L H</u>	(24)
188	GAATTTCCCACTGGCTTCCCTGTACGAACCAAACTTATCTCCATTGAGTTCACCCAGCTCTCCAGC	253
(25)	E F P T G F P V R T K L I S I E F T Q L S S	(46)
254	CTTGGCGTGGAAGCCCTCCAAGATCTTCAAACCTCCAGGAACCTTCACTCTCCAACAACAGGCTG	319
(47)	L G V E A L Q D L P N L Q E L H L S N N R L	(68)
320	AAGACCTTCCCACTGGCCTCTTCCGTAACCTCCAGAAATTGCACACCTGGATCTGTCCACCAAT	385
(69)	K T L P S G L F R N L P E L H T L D L S T N	(90)
386	CTCCTGGAAGATCTACCCCCAGAGATCTTACCAACGCAACCAACCTGATGCTTTTATCCATCAGT	451
(91)	L L E D L P P E I F T <b>N</b> A T N L M L L S I S	(112)
452	GAAAACCGACTGGCTGAGCTGCGGGCATCCTGGTTCGAAAACCTGAAGGAACTTAAGATCCTGAGC	517
(113)	E N R L A E L R A S W F E T L K E L K I L S	(134)
518	CTTGACCAAAACAGCTGAAGGAGGTCCCCATTTCTTGTTTCTCCAAGCTGAAGAAGTTGACCTTT	583
(135)	L D Q N Q L K E V P I S C F S K L K K L T F	(156)
584	CTAGATCTCTCCTCCAATCGCCTCCATCATCTCTCTCCAGACATGTTACGCGCCTAGAAAATTTG	649
(157)	L D L S S N R L H H L S P D M F S G L E N L	(178)
650	GAGAGTTGACCTTGGAATAACCAATCCGATGCATTGCCCGAGATCCTTCCATTGGGGACCC	715
(179)	E R L T L E N N P I R C I A P R S F H W G P	(200)
716	AAGCTGAGCATGATCTCCCTGAGGAACTGCAGCCTGACCGATATCACCTTTGGGGAATTTAGCCG	781
(201)	K L S M I S L R <b>N</b> C S L T D I T F G E F Q P	(222)
782	TTGGACCAACTGGTGCTGCTGGATCTCTCCGCCAATGAGCTCACCAGGCTGGATCCTCCAGCCGGC	847
(223)	L D Q L V L L D L S A N E L T R L D P P A G	(244)
848	ATCCTGTCTGCCAATCTCAGCCTGGATCTTGCAAGAAATCCTTGGGTGTGTGACTGCCGCTGGAC	913
(245)	I L S A <b>N</b> L S L D L A G N P W V C D C R L D	(266)
914	AATCTTCTAACCTGGGTCAAGGAGCACAAGATCCATTTATTTTCCAAGCAGGAAATTTGTCTGTGCT	979
(267)	N L L T W V K E H K I H L F S K Q E I V C A	(288)
980	TTCCCCAAGAATTTCAAAGGCGAAGAGGCAACCTCACTTCATCGATCCCAAATTTGTCCCTGCTAA	1045
(289)	F P K N F K G E E A T S L H R S Q I C P C	(309)
1046	ACCTTTAAATAGATCCTTTTCTTTCCACCCTGCTTCGCGAACAGCGAGATTTCCAGTTTGGAGAC	1111
1112	AATTTCCAGTTGAATTGGACTTCAACTCCCAGAAATCTCAGCAACAGCCATGCTGCCTGGGGAATT	1177
1178	CTGGGAGTTGGAGTCCACATAGCTGGATTTAAAGAGAAGAGACAGAACAGGATTGGGAAAAAAT	1243
1244	ACGAAATACTGATTTTAGGGAAGAAATAGCTGCTCAGGAAGAGATGCTCAAAAAAATCAACAATA	1309
1310	TAGGTAGTCCTTCACTTACAACCGTTCAGTTAGTGACTTTTTGAAGTATTAAGAGCCCTGAAGAAA	1375
1376	GTGACCGATGAGTGGATCAGAATCAGAATAGAGCTGCAAGGGACCTTGAGGTCTTCTAGTCCAAC	1441
1442	CCCTGCTCAAGCAGGAGACCTCTGCCATTTAGCAAGCAACTGTCAGTCTCTTCTTGAAAACT	1507
1508	GATGGAGCACCACAACCTTCTGGTGGCAAGCTGTTCCACTGATTAATTGTTCCCTGTCAGGAAGTTT	1573
1574	CTCCTTAGTTCTAGGTTGCTTCCCTCCTTGATTAATTTCCATCCTTTGCTTCTTGCTCCTGCCCTCA	1639
1640	GGTGCTTTGAAGAAATAGCTTGACTCCCTCTTCTTTGTGGCAGCCCTCAAATATTGGAAGACTGAT	1705
1706	ATCATGTACCCCTTAGTGCTTCTCAGAGCTGACTGTTTTGCTGTTTTCTATTATTATTAGTGTAGGG	1771
1772	TGCTGTTACATTAGCCAGGAGTCTGCAATGCTACTGAAGCGTAGTACTTTGCCTGCAATCTACTA	1837
1838	GCTCTGTTATGGTACATGCTCAGCACATCCCAAGGTGCACCACAGGAGAGCGAGCTAGCTTTGCA	1903
1904	ACAGAAAGAAAGACAAGCAGCTTTTCTGAGCATTAGCCAAGCCCTTTCCCTCCCTCCACCGTG	1969
1970	ACCACCTCGCAAGCGGGCATCGCAATGGGAAGGTTCAAAGCGGACAGAAATTTGACTGCCTGCAC	2035
2036	AGAGCACCAAGTCGTCTCCCCCTCAAAGTGGTACCTATTTGTCTACAGGCGGTATATATGATTTTG	2101
2102	AGCTGCTAGGTGGGCAGAAGCTGAGGCAAGTTGGGAGCTCATCCTGTACGCAGTGCTAGGGCTC	2167
2168	GAACCACTGGAGCAGAGACCAACTCCAGCATCATTAAGCCACTGAGCCAATGTACTTCTCTGTTTC	2233
2234	GCTGTTGAATAAACCTTATTTCCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2290

**Supplementary Figure S1. The nucleotide and deduced amino acid sequences of *Laticauda semifasciata* LRG.** The N-terminal sequence elucidated by sequencing the purified *L. semifasciata* LRG is underlined. Potential N-glycosylation sites are indicated in bold.

PfLRG-A	1	GTCTTTTACTGCCACCCACCCCTGCTCCAGAAAGTGTACCGAGTTCGTCTGCAACTCTCCATCTCTACGTGAATTTCCACCG	85
cDNA1	1	.....	85
cDNA2	1	.....	85
PfLRG-B	1	.....	85
cDNA3	1	.....	85
cDNA4	1	.....C...A...C.....	85
PfLRG-A	86	GCTTCCCCACACGAGCCAAGATGATCTCCGTTGAGTTACCCCAAGTCTCCAGCCTTGGCGTGGAGGCCCTCCAAGATCTTCCAAA	170
cDNA1	86	.....	170
cDNA2	86	.....	170
PfLRG-B	86	.....TG.....G.....G..T.....G.....C..	170
cDNA3	86	.....TG.....G.....G..T.....G.....C..	170
cDNA4	86	.....G.....G..T.....G.....C..	170
PfLRG-A	171	CTCCAGGAACCTCACCTCTCCAACAACAGGTTAAAACTCTTCCAAGTGGCCTCTCCGTAACCTCCCACAACCTGCACACCTTG	255
cDNA1	171	.....	255
cDNA2	171	.....	255
PfLRG-B	171	.....	255
cDNA3	171	.....	255
cDNA4	171	.....	255
PfLRG-A	256	GATCTCTCCACAAATCATCTAGAAGATCTACCTCCAGAGATCTTTACAAATGCAAGTAGCCTAACTCATTATCCCTCAGTGAAA	340
cDNA1	256	.....	340
cDNA2	256	.....	340
PfLRG-B	256	.....G....TC.....C.....	340
cDNA3	256	.....G....TC.....C.....	340
cDNA4	256	.....G....TC.....C.....	340
PfLRG-A	341	ATCAACTAGCTGAACTGCGCCATCCTGGTTCCAACTCTTGAAGGACTCAGGATCCTAGGCCTTGATCACAATCAGGTGAAGGA	425
cDNA1	341	.....	425
cDNA2	341	.....	425
PfLRG-B	341	.....G.....TG....C..G..G.A.....	425
cDNA3	341	.....G.....TG....C..G..G.A.....	425
cDNA4	341	.....G.....TG....C..G..G.A.....	425
PfLRG-A	426	GATCCCAATTCTTGTTTIGATAAGCTGAAGGAGTTGACATCTCTAGATCTCTCATTCAACCTCCTCCATCGCCTCGCTCCAGAG	510
cDNA1	426	.....	510
cDNA2	426	.....	510
PfLRG-B	426	.....T...A.....A..A..G..	510
cDNA3	426	.....T...A.....A..A..G..	510
cDNA4	426	.....T...A.....A..A..G..	510
PfLRG-A	511	ATGTTCAAGTGGCTTAGATAAATTGGAGAGGTTAGTGCTGGAAGCAACCCCATCCAGTGCAATGTCAGGAAGACCTTCCATTGGC	595
cDNA1	511	.....	595
cDNA2	511	.....C..T.....	595
PfLRG-B	511	.....C.....T.....T..A.....T...A.GG...G.....	595
cDNA3	511	.....C.....T.....T..A.....T...A.GG...G.....	595
cDNA4	511	.....C.....T.....T..A.....T...A.GG...G.....	595
PfLRG-A	596	ATCCCAAGCTGAGTGTGCTGCTGCCGAAGAACAGCAGCCTGACCCACATCTTAAGGGGAGTCTTTGACCCATTGCAACAACCTGGT	680
cDNA1	596	.....	680
cDNA2	596	.....C.....	680
PfLRG-B	596	G.....A.....TG..A...T...G.....C.G--...G.C.....	677
cDNA3	596	G.....A.....TG..A...T...G.....C.G--...G.C.....	677
cDNA4	596	G.....A.....TG..A...T...G.....C.G--...G.C.....	677
PfLRG-A	681	GCTGCTGGACCTCTCTGACAATGAGCTCAGCACAAATGGATGATCCAGTCTACAAGCCGTCTGCCAATCTCAGTCTTGATCTTTCA	765
cDNA1	681	.....	765
cDNA2	681	.....C.....	765
PfLRG-B	678	.....T...C...C...CC...G...C..G...A.....T.....	762
cDNA3	678	.....T...C...C...CC...G...C..G...A.....T.....	762
cDNA4	678	.....T...C...C...CC...G...C..G...A.....T.....	762
PfLRG-A	766	GGAACCCCTTGGGCGTGTGACTGCCGCTGGAGAATCTTCTAAGATGGCTCAATGATCACAACATCCATTTATATTCTAAGGAGG	850
cDNA1	766	.....A...	850
cDNA2	766	.....	850
PfLRG-B	763	.....G...T.....G.....C.....	847
cDNA3	763	.....G...T.....G.....C.....	847
cDNA4	763	.....G...T.....G.....C.....	847
PfLRG-A	851	AATTTGTCTGTGCTTCCCCCAAGCATTTCAAGGGTGAACATGCAATTTCACTTCAACCATACCAAATTTGTCCCTGCTAA	930
cDNA1	851	.....	930
cDNA2	851	.....	930
PfLRG-B	848	.....G.....G.....	927
cDNA3	848	.....G.....G.....	927
cDNA4	848	.....G.....G.....	927

**Supplementary Figure S2. Comparison of the nucleotide sequences of *Protophthrops flavoviridis* LRGs.**

PfLRG-A and PfLRG-B were located on habu1\_scaffold2243:7438-6509 and habu1\_scaffold11684:3373-2447, respectively, in the draft genome sequence of the habu snake *P. flavoviridis*. Four cDNA clones 1–4 were obtained from the total liver RNA. Sequence identities have been represented by dots.