

S2 Table. Listing of predicted non-immune *B. glabrata* plasma proteins eluted from Mem and LTP affinity columns identified in VectorBase.

Protein Identification	Unique Peptide Count				VectorBase Scaffold
	BS-90		NMRI		
	Mem	LTP	Mem	LTP	
hemoglobin type 1 [<i>Biomphalaria glabrata</i>] ; Sequence ID: CAJ44466.1; Identities: 100%	108	128	143	128	LGUN_random_Scaffold5741:1590-15334; minus strand
PREDICTED: uncharacterized protein LOC106051763 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013062423.1; Identities: 100% haemoglobin type 1 [<i>B. glabrata</i>]; Sequence ID: CAJ44466.1; Identities: 76%	12	11	6	7	LG17_random_Scaffold37: 105709-105474; 103671-103436; 101378-101137; 99539-99300; 91005-90767; 88372-88137; 23383-23148; 21154-20907; 19765-19530; 16554-16319; minus strand
PREDICTED: uncharacterized protein LOC106051722 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013062383.1 ; Identities: 100% haemoglobin type 1 [<i>B. glabrata</i>] Sequence ID: CAJ44466.1; Identities: 87%	10	5	3	5	LG17_random_Scaffold37:10,424-11,812; minus strand; BGLB000834-PA
PREDICTED: uncharacterized protein LOC106077292 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_010393514.1; Identities: 100% haemoglobin type 1 [<i>B. glabrata</i>]; Sequence ID: CAJ44466.1; Identities: 65%	4	6	6	5	LGUN_random_Scaffold558: 30767-30464; 24999-24708; 20689-20454; 16076-15841; 13539-13304; 10586-10351; 7603-7362; 2289-2054; 1556-590; minus strand
PREDICTED: uncharacterized protein LOC106078048 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013094243.1; Identities: 100% haemoglobin type 1 [<i>B. glabrata</i>]; Sequence ID: CAJ44466.1; Identities: 60%	3	6	8	8	LGUN_random_Scaffold5741: 12584-12495; 11353-11244; 9616-9322; 8037-7419; minus strand

PREDICTED: uncharacterized protein LOC106050210 , partial [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013060614.1; Identities: 100% haemoglobin type 1 [<i>B. glabrata</i>]; Sequence ID: CAJ44466.1 ; Identities: 58%	5	8	6	7	LGUN_random_Scaffold7018: 3821-3568; 371-76; minus strand
hemoglobin type 2 [<i>Biomphalaria glabrata</i>] Sequence ID: CAJ44467.1; Identities: 100%	81	102	108	108	LGUN__random_Scaffold 8143:20,982-37,676; minus strand. BGLB013430
PREDICTED: uncharacterized protein LOC106051916 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013062584.1; Identities: 100% haemoglobin type 2 [<i>B. glabrata</i>]; Sequence ID: CAJ44467.1; Identities: 98%	7	7	10	6	LGUN_random_Scaffold8143:20982:37676:-1 gene:BGLB013430; 97%; plus strand
PREDICTED: uncharacterized protein LOC106050211 , partial [<i>Biomphalaria glabrata</i>]; Sequence ID:XP_013060615.1 ; Identities: 100% haemoglobin type 2 [<i>B. glabrata</i>]; Sequence ID: CAJ44467.1; Identities: 96%	3	3	3	2	LGUN_random_Scaffold7018:4623:18026:1 gene:BGLB012730 87%; plus strand
PREDICTED: uncharacterized protein LOC106051747 , partial [<i>Biomphalaria glabrata</i>];Sequence ID: XP_013062404.1; Identities: 100% haemoglobin type 2 [<i>B. glabrata</i>]; Sequence ID: CAJ44467.1; Identities: 86%	6	7	6	4	LGUN_random_Scaffold8143:20982:37676:- 1 gene:BGLB013430; 86%; plus strand
Chain A, acetylcholine-binding protein Type 2 (Bgachbp2) [<i>Biomphalaria glabrata</i>]; Sequence ID: 4AOE_A ; Identities: 100%	10	15	9	17	LG29_random_Scaffold14:635533-635416; 634747-634508; 632875-632202; minus strand
PREDICTED: acetylcholine-binding protein-like isoform X1 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_ 013067426.1; Identities: 100%	4	10	4	9	LG29_random_Scaffold14:635533-635416; 634747-634508; 632875-632202; minus strand
PREDICTED: actin-2-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013083929.1; Identities: 100%	1	0	2	2	LGUN_random_Scaffold29:432435:441953:1 gene:BGLB008299; plus strand

<p>hypothetical protein LOTGIDRAFT_193218 [<i>Lottia gigantea</i>]; Sequence ID: XP_009060604.1; Identities: 100%</p> <p>PREDICTED: actin [<i>Crassostrea brasiliana</i>]; Sequence ID: ANB49595.1; Identities: 99%</p>	5	2	7	4	LGUN_random_Scaffold10528:12872:19460:1 gene:BGLB00391; plus strand
<p>PREDICTED: actin, alpha skeletal muscle [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013073050.1; Identities: 95%</p>	2	0	1	0	LGUN_random_Scaffold29:432435:441953:1 gene:BGLB008299 plus strand
<p>PREDICTED: tubulin alpha-1A chain-like, partial [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013091074.1; Expect: 0.0; Identities: 100%</p>	11	0	8	1	LGUN_random_Scaffold5085:5474-17809:1 gene:BGLB010861 (100%); plus strand
<p>PREDICTED: tubulin alpha-3 chain-like, partial [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013095645.1 ; Identities: 100%</p>	4	0	1	1	LGUN_random_Scaffold6191:6220-9108:-1 gene:BGLB012164; plus strand
<p>PREDICTED: tubulin beta-4B chain-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013097130.1; Identities: 100%</p>	2	0	1	0	LGUN_random_Scaffold6940:15330-18731:1 gene:BGLB012690 (100%); plus strand
<p>PREDICTED: tubulin beta-4B chain-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013085141.1; Identities: 100%</p>	16	0	13	0	LGUN_random_Scaffold3175:23130:28038:1 gene:BGLB008716 (100%); plus strand
<p>PREDICTED: collagen alpha-1(XII) chain-like, partial [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013088320.1 ; Identities: 100%</p>	6	0	5	2	LGUN_random_Scaffold409: 210568-210376; 208117-207998; 203161-202925; 200670-200506; 198286-198104; 195116 194857; minus strand
<p>PREDICTED: collagen alpha-5(VI) chain-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013079619.1 ; Identities: 100%</p>	0	0	4	7	LGUN_random_Scaffold2059:1: 17949-18112; 19250-19482; 21462-21627; 22126-22308; 31136-31259; 33936-34068; 36698-36930; 39753-39921; 41246-41428; plus strand
<p>PREDICTED: uncharacterized protein LOC106073418 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013089410.1; Identities: 100%</p> <p>PREDICTED: collagen alpha-1(IX) chain-like, partial [<i>B. glabrata</i>]; Sequence ID: XP_013071005.1; Identities: 70%</p>	0	2	0	2	LGUN_random_Scaffold105369: 585-5; minus strand

PREDICTED: balbiani ring protein 3-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013096729.1 ; Identities: 100%	8	10	9	13	LGUN_random_Scaffold675: 24344-21090; minus strand
PREDICTED: apolipoprotein-like isoform X1 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013082155.1 ; Identities: 100%	6	0	9	8	LG4_random_Scaffold2455: 41449-41188; 39683-39359; 36375-36110; 33330-33059; 32080-31815; 30252-25604; 18006-17780; 13866-13496; 6868-6117; minus strand
PREDICTED: alpha-amylase-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013062082.1 ; Identities: 100%	2	2	5	2	LGUN_random_Scaffold784:118162-121490:-1 gene:BGLB013250
PREDICTED: ATP synthase subunit alpha, mitochondrial-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013081788.1 ; Identities: 100%	4	0	3	0	LGUN_random_Scaffold2464:29420-32015:1 gene:BGLB007667
PREDICTED: ATP synthase subunit beta, mitochondrial-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013070512.1; Identities: 100%	6	0	6	0	LGUN_random_Scaffold10059:2817-7549:-1 gene:BGLB003755
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013071165.1; Identities: 100%	5	0	4	0	LGUN_random_Scaffold107:64347-71294:-1 gene:BGLB004031
PREDICTED: elongation factor 1-alpha [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013067348.1; Identities: 100%	2	0	3	2	LG28i_random_Scaffold9449:4199-6514:-1 gene:BGLB001639
PREDICTED: ubiquitin-40S ribosomal protein S27a [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013063486.1; Identities: 100%	3	1	1	1	LGUN_random_Scaffold868:32636:33553:-1 gene:BGLB013769 LGUN_random_Scaffold868:1:102120:135986-35764; 32796-32596
PREDICTED: tyrosine-protein phosphatase non-receptor type 23-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013069839.1; Identities: 100%	1	2	1	1	LG9i_random_Scaffold325:325130:325976:1 gene:BGLB003636 LG9i_random_Scaffold325: 326111-326271; 325799-325962; 337767-337976; 339268-339428; 343490-343683; 346069-348652; 351757-351981; 358275-358477; 358667-360177

Histone H4 [<i>Larimichthys crocea</i>]; Sequence ID: KKF20647.1 ; Identities: 100%	4	0	4	0	LGUN_random_Scaffold3683:39221:39397:1 gene:BGLB009366
PREDICTED: adenosine deaminase CECR1-like, partial [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013061189.1; Identities: 100%	0	0	3	0	LGUN_random_Scaffold7376:1:18597:1: 5703-5853; 6641-6818; 8965-9097; 13395-13527; 16836-16913 plus strand
PREDICTED: clathrin heavy chain 1 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013079752.1; Identities: 98%	3	0	0	0	LGUN_random_Scaffold2072:39208:58064:-1 gene:BGLB007033
PREDICTED: V-type proton ATPase catalytic subunit A-like [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013086122.1; Identities: 96%	2	0	0	0	LGUN_random_Scaffold3436:56868:63955:1 gene:BGLB009092
PREDICTED: V-type proton ATPase subunit B [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013087752.1; Identities: 99.8%	2	0	0	0	LG8_random_Scaffold135:164139:169688:1 gene:BGLB003477
PREDICTED: putative tyrosinase-like protein tyr-1 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013065893.1; Identities: 100%	2	0	0	0	LG20i_random_Scaffold3077:1:54679:1: 29371-29078; 27996-27830; 23386-23126; 22813-22597; 22259- 22108; 20827-20517; 19464-19267; 18992-18836; 18366-18277
PREDICTED: ovalbumin-like isoform X2 [<i>Biomphalaria glabrata</i>]; Sequence ID: XP_013088530.1; Identities: 100%	2	0	1	0	LGUN_random_Scaffold4153:1:27349:1: 18675-18513; 17521-17299; 5618-5480; 4454-4305; 2924-2702