

# Scientific and Standardization Committee Communications: Inventory Of Exogenous Inhibitors of Platelet Aggregation From Animal Sources

On behalf of the Registry of Exogenous Hemostatic Factors of the Scientific and Standardization Committee of the International Society on Thrombosis and Haemostasis

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Several exogenous factors isolated from animal sources affect platelet function and aggregation; some of them induce, whereas others inhibit platelet aggregation. This inventory deals with inhibitors from animal sources that have appeared in the literature until mid-1999.

## Inhibitors of Platelet Aggregation

The initial inventory of platelet aggregation inhibitors (1) dealt with those isolated from snake venoms. This updated inventory includes in addition to several new inhibitors platelet aggregation from snake venoms, those that were isolated from other animal sources. They are proteins or glycoproteins with their molecular weight ranging from 5000 to several tens of thousands. These factors inhibit platelet aggregation by different mechanisms. A large number of these inhibitors do not exhibit any enzymatic activity. In contrast, some of them exhibit enzymatic activities, such as phospholipase A<sub>2</sub> (PLA<sub>2</sub>), proteinase and nucleotidase. In general, the mechanism of inhibition of platelet aggregation is well understood for several groups of nonenzymatic proteins. However, further research is required to delineate the mechanism of inhibition by some of the enzymes.

### Nonenzymatic inhibitors

Based on the mechanism of inhibition, we have classified the nonenzymatic factors into five classes.

**Class I:** *Antagonists of fibrinogen receptor glycoprotein IIb/IIIa complex (GPIIb/IIIa).* Interaction between fibrinogen and GPIIb/IIIa complex is the important final step to platelet aggregation. Since most platelet agonists go through this final step, these antagonists inhibit platelet aggregation with similar, if not identical, IC<sub>50</sub> values irrespective of the agonist used to initiate aggregation. Several different classes of proteins have been shown to interfere at this critical step. Disintegrins are the most well studied aggregation platelet inhibitors. Although initial studies of purification and characterization of this group of proteins from snake venoms were done in the mid-1980's (2, 3), it was the simultaneous determination of the complete amino acid sequences of

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echistatin and trigramin (4, 5) that triggered immense research interest in both academia and pharmaceutical industries. These polypeptides contained the RGD tripeptide sequence, the short segment involved in adhesive reactions. To date more than 40 disulfide-rich polypeptides, known as disintegrins because of their ability to interfere in the integrin activity, have been purified from snake venoms alone (Table 1; Figure 1). On a molar basis, these polypeptides are 1000 – 30,000 times more potent inhibitors of platelet aggregation than the linear RGDS peptide (6). They are most commonly found in crotalid and viperid snake venoms, but rarely found in elapid and hydrophid snake venoms. Disintegrins are classified into three distinct subfamilies based on their size (7) (Figure 1). Short chain disintegrins contain 47-51 amino acid residues and four disulfide bridges; medium chain disintegrins contain 68-75 amino acid residues and six disulfide bridges; and long chain disintegrins contain 83-84 amino acid residues and seven disulfide bridges. Based on the structural analysis of the sequences, we proposed that disintegrins are proteolytic products of longer precursor proteins (8, 9). Since then cDNA and amino acid sequences of several precursors have been determined (10-19). These results support the presence of common precursors for metalloproteinases, disintegrins and related proteins. The proteolytic processing to form various subfamilies of disintegrins is most likely determined by intradomain disulfide bridges and the accessibility of interdomain regions, along with glycosylation (9).

Disintegrins bind to GPIIb/IIIa on both resting and activated platelets with high affinities (Kd,  $10^{-7} \sim 10^{-8}$  M) in the presence of divalent cations. Irrespective of their length, they contain the RGD tripeptide sequence in a homologous position and it is described to be essential for their inhibitory properties. Only two disintegrins contain KGD in the homologous position (20, 21). The authors claim that this makes barbourin (20) a specific inhibitor of interaction between fibrinogen and GPIIa/IIIb and went on to develop several cyclic peptides with KGD sequence as potent inhibitors of platelet aggregation (22). Three-dimensional structures of four disintegrins have been determined by NMR techniques (23-27). The R/KGD segment is located on the tip of a hair-pin loop that is stabilized by disulfide bridges. The residues in the immediate neighborhood of this RGD segment appear to contribute significantly to the inhibitory potency of disintegrins (28, 29).

As mentioned above, there are some venom proteins that contain disintegrin/disintegrin-like domain and these may inhibit platelet aggregation. In some cases, they may also contain metalloproteinase domains that may proteolytically alter the functions of the target protein (see below).

Based on the structure of disintegrins, a variety of cyclic R/KGD peptide or peptide-mimetic derivatives have been developed that are under clinical trials and some of them are found to be effective in reducing ischemic complication, particularly the restenosis after percutaneous transluminal coronary angioplasty (PTCA) (30, 31). In addition to their role in the development of anti-thrombotic agents and treatment of cardiovascular diseases, they may also be useful in the treatment of cancer growth and tumor metastasis as well as osteoporosis. Disintegrins have been shown to inhibit the adhesion between tumor cell and extracellular matrices (32-35). They also inhibit experimental metastasis of melanoma (36-39). Some of them inhibit tumor cell-induced platelet aggregation (40). Further, disintegrins through the blockade of  $\alpha_v \beta_3$  integrin show potent antiangiogenic effects (41, 42). Disintegrins block the osteoclast-mediated bone resorption by

interfering in the  $\alpha_3\beta_3$  integrin activity (43, 44) and prevent bone loss in mice and rats (45, 46). Thus the study of disintegrins contributes significantly to both academic and clinical research.

Apart from disintegrins, there are other inhibitors of platelet aggregation, which contain the RGD tripeptide in their structure. These proteins are isolated from snake venom, leeches and ticks (Table 2). These polypeptides do not share any significant structural homology with disintegrins (Figures 2 and 3). For example, mambin (or dendroaspin), a platelet aggregation inhibitor isolated from *Dendroaspis j. kaimosae* snake venom (47), shows a striking resemblance to the short-chain postsynaptic neurotoxins (48) (Figure 2). Although ornatin and decorsin were isolated from leeches, they do not have significant similarity except for RGD containing carboxy terminal segment (49, 50) (Figure 3). Variabilin from the salivary glands of hard tick *Dermacentor variabilis*, despite the presence of RGD, has little homology to any other GPIIb/IIIa antagonists (51).

Disagregin, a potent inhibitor of platelet aggregation isolated from the soft tick *Ornithodoros moubata* (52) is a GPIIb/IIIa antagonist. Surprisingly, it does not contain the tripeptide RGD (Figure 2). The structure-function relationship of this polypeptide will be of great interest.

**Class II: Antagonists of von Willebrand factor receptor glycoprotein Ib (GPIb).** Binding of plasma von Willebrand Factor (vWF) to the platelet glycoprotein, GPIb is assumed to play a key role in the earliest stages of platelet aggregation (53, 54). So far this group of inhibitors has been purified only from snake venoms (Table 3). They are heterodimeric with the two subunits (  $\alpha$  and  $\beta$  subunits) linked through a disulfide bridge. Only flavocetin-B from *Trimeresurus flavoviridis* (55) has 3 subunits. All subunits are structurally similar to  $Ca^{2+}$ -dependent (C-type) lectins. These proteins prevent platelet aggregation by binding to the GPIb and thus blocking the interaction between vWF and its receptors. It has been shown that the GPIb binding site resides on the  $\alpha$ -chain subunit (56). Unlike other inhibitors in this group, echicetin isolated from *Echis carinatus* also inhibits platelet aggregation induced by  $\alpha$ -thrombin (56, 57).

**Class III: Antagonists of collagen-platelet interaction.** Subendothelial collagen serves as an anchorage for circulating platelets in the process of hemostasis and thrombosis (58). Platelets adhere to exposed subendothelial collagen through GPIa/IIa receptors, become activated and the activated platelets aggregate. Some of the platelet aggregation inhibitors interfere with the interaction of collagen with platelet receptors (Table 4). They have been isolated from snake venoms, leech, soft tick and triatome bug. The inhibitors from snake venoms, similar to disintegrins, are derived from large metalloproteinase/disintegrin precursor proteins. Catrocollastatin-C, atrolysin A/DC and jararhagin-C have the disintegrin-like and cysteine-rich domains (59-61). The former two proteins inhibit platelet aggregation; catrocollastatin-C specifically binds to collagen and inhibits only collagen-induced aggregation, whereas atrolysin A/DC also inhibits ADP-induced aggregation (59, 60). Their longer counterparts containing a metalloproteinase domain, namely catrocollastatin, atrolysin A and jararhagin, respectively, also inhibit collagen-induced platelet aggregation (60, 62, 63). Jararhagin, in contrast, binds to GPIa and cleaves GPIIa (64) (see below). Since jararhagin-C has identical sequence to the C-terminal region of jararhagin (61), and since catrocollastatin-C and atrolysin A/DC by themselves inhibit platelet aggregation, it is conceivable that jararhagin-C too acts as a collagen receptor antagonist. A similar situation may also be true in the case of crovidisin (65). The inhibitors from leech and soft tick bind specifically to collagen fibers and interfere in the interaction between collagen and its receptor GPIa/IIa (66-

71). Although pallidin specifically inhibits collagen-induced platelet aggregation similar to all the above proteins, the mechanism of inhibition by pallidin is not yet clear (72, 73).

**Class IV: Antagonists of thrombin-thrombin receptor interaction.** Thrombin is a key enzyme in thrombosis and hemostasis. In addition to its main role in the formation of the fibrin clot in blood coagulation, it activates different types of cells, particularly platelets and acts as a potent inducer of platelet aggregation. Three functional sites have been recognized in thrombin; the active site, anion-binding exosite I, and anion-binding exosite II. Anion-binding exosite I mediates thrombin binding to fibrinogen, the platelet receptor and thrombomodulin, whereas the anion-binding exosite II is the heparin-binding site (74). Some thrombin inhibitors are shown to be inhibitors of thrombin-induced platelet aggregation (Table 5). It has been suggested that bothrojaracin and bothroaltein from *Bothrops jararaca* and *B. alternatus* venoms, respectively (75, 76) and triabin from *Triatoma pallidipennis* (77-79) bind to the exosite of thrombin preventing the interaction between thrombin and its receptors and hence platelet aggregation.

**Class V: Other nonenzymatic inhibitors.** These inhibitors in this group inhibit platelet aggregation by currently unknown mechanism(s) (Table 6). Lebetins is a group of inhibitors isolated from *Vipera lebetina* snake venom (80). Lebetins 1 are shorter with 12 or 13 residues, whereas lebetins 2 have 37 or 38 residues. Lebetins 1 appear to be derived by proteolysis of their larger counterparts, lebetins 2. It would be interesting to determine whether lebetins, like disintegrins, are proteolytic products of a larger precursor protein. They inhibit platelet aggregation induced by thrombin, collagen and PAF-acether (80). They also inhibit fibrinogen-induced aggregation of chymotrypsin-treated platelets. Truncation of more than one residue at the amino terminal end results in the loss of activity (81). These short peptides strongly inhibit collagen-induced thrombocytopenia in rats (80, 81).

## Inhibitors with enzymatic activity

Several proteins with enzymatic activity inhibit platelet aggregation. Some of these enzymes inhibit aggregation by indirect mechanisms either by the formation of a product, which inhibits platelet aggregation or by physical destruction of the agonist or its receptor. In these cases, the mechanisms appear to be simple and are directly dependent on the respective enzymatic activity. The study of such factors may not significantly contribute to our understanding of platelet aggregation.

**Nucleotidases.** ADP is a potent inducer of platelet aggregation that is secreted from the platelets as dense granules by various agonists. Logically, hydrolysis of ADP should lead to inhibition. Thus ADPases and 5'-nucleotidases inhibit platelet aggregation (Table 7). Such inhibitors have been isolated from *Trimeresurus gramineus* (82), *Agkistrodon acutus* (83) and *Vipera aspis* (84). It was concluded that the removal of ADP and possibly the generation of adenosine was responsible for the inhibitory effect (82).

**Phospholipase A<sub>2</sub> enzymes.** Some PLA<sub>2</sub> enzymes induce platelet aggregation, whereas others inhibit it. In addition, there are a few PLA<sub>2</sub> enzymes that both initiate as well as inhibit platelet aggregation, though under different conditions. However, not all PLA<sub>2</sub> enzymes affect platelet

aggregation. PLA<sub>2</sub> enzymes that affect platelet aggregation are classified into three major classes (85). Some of the inhibitors (Table 8) inhibit aggregation by mechanism(s) dependent on the enzymatic activity, whereas others appear to inhibit by mechanism(s) that are independent of their phospholipolytic activity. In the former case, the inhibitory effect may be due to the formation of lysophospholipids (86, 87). However, PLA<sub>2</sub> enzymes from *Naja nigricollis* (88), *Ophiophagus hannah* (89), *Pseudechis papuanus* (90), *Agkistrodon acutus* (91) and *A. halys* (92) seem to affect platelet aggregation inhibition by mechanisms independent of their enzymatic activity. The mechanism of antiplatelet effects of this group of PLA<sub>2</sub> enzymes is not yet understood.

*Metalloproteinases.* Some of the snake venom metalloproteinases inhibit platelet aggregation (Table 9). Most of these were first identified as fibrinogenases, since they release peptides from the carboxy-terminal of fibrinogen. They are classified into  $\alpha$  and  $\beta$  fibrinogenases based on their specificity for the A or B chain of fibrinogen (93).  $\alpha$ -Fibrinogenase inhibits platelet aggregation but not  $\beta$ -fibrinogenase. Since fibrinogen binding to its receptor GPIIb/IIIa complex is the essential final step in the platelet aggregation, it was initially thought that  $\alpha$ -fibrinogenase inhibits platelet aggregation as a result of the depletion of fibrinogen or through the generation of plasma fibrinogen degradation products (94). However, direct testing of fibrinogen degradation products did not show significant inhibition (95). We showed that an  $\alpha$ -fibrinogenase from *Naja nigricollis* (96) inhibits platelet aggregation even in the absence of plasma fibrinogen. This was the first indication that fibrinogen may not be the primary target protein, which determines the antiplatelet effects, for these metalloproteinases. Several other studies also support this possibility. Kistomin, a novel  $\alpha$ -fibrinogenase specifically cleaves GPIIb resulting in the inhibition of platelet aggregation (97). Since metalloproteinases exist as large proteins, which are precursors of disintegrins and disintegrin-like polypeptides, these proteins could strongly inhibit platelet aggregation. Disintegrin/disintegrin-like domains in catrocollastatin, atrolysin A and atrolysin E inhibit platelet aggregation (60, 62, 98). Their precursors containing metalloproteinase domains also inhibit platelet aggregation. In catrocollastatin disintegrin-like domain determines its binding to collagen (62). Jararhagin, another metalloproteinase containing disintegrin-like domain, binds specifically to GPIa (64). Both these proteinases specifically inhibit collagen-induced platelet aggregation. Thus non-proteinase domains of metalloproteinases can significantly contribute to the recognition and binding to specific target proteins and hence their antiplatelet effects. The proteolytic activity of the metalloproteinase domain may also play an important role. For example, though jararhagin binds to GPIa, it cleaves the nearby GPIIa (64). The identification of new target proteins for the metalloproteinases and the structure-function relationships of these antiplatelet proteins could lead to development of novel antithrombotic agents.

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Source	Protein	Chain	1	45
<i>Bitis arietans</i>	Bitistatin	Long	SPPVCGNEIL EQGEDCDCGS PANCQDQCCN AATCKLTPGS QCNHG	
<i>Bitis arietans</i>	Bitan	Long	SPPVCGNKIL EQGEDCDCGS PANCQDRCCN AATCKLTPGS QCNYG	
<i>Trimeresurus gramineus</i>	Trigramin	Medium	EAGEDCDCGS PAN PCCD AATCKLIPGA QCGEG	
<i>Agkistrodon rhodostoma</i>	Kistrin	Medium	GKECDCSS PEN PCCD AATCKLRPGA QCGEG	
<i>Echis carinatus</i>	Echistatin	Short		<ECESG
<i>Eristocophis macmahoni</i>	Eristocophin	Short		<ERQEE PCATG

Source	Protein	Chain	46	***	80
<i>Bitis arietans</i>	Bitistatin	Long	ECCDQ CKFKKARTVC RIARGDWND YCTGKSSDCP WNH		
<i>Bitis arietans</i>	Bitan	Long	ECCDQ CRFKKAGTVC RIARGDWND YCTGKSSDCP WNH		
<i>Trimeresurus gramineus</i>	Trigramin	Medium	LCCDQ CSFIEEGTVC RIARGDDLDD YCNGRSAGCP RNPFFH		
<i>Agkistrodon rhodostoma</i>	Kistrin	Medium	LCCEQ CKFSRAGKIC RIPRGDMPDD RCTGQSADCP RYH		
<i>Echis carinatus</i>	Echistatin	Short	PCCRN CKFLKEGTIC KRARGDDMDD YCNGKTCDCP RNP HKGP		
<i>Eristocophis macmahoni</i>	Eristocophin	Short	PCCRR CKFKRAGKVC RVARGDWND YCTGKSCDCP RNPWNG		

**Figure 1.** Amino acid sequences of disintegrins. Only a few selected sequences are shown. The amino acid sequences are taken from the following references: Bitistatin (107), bitan (106), trigramin (5), kistrin (106), echistatin (4) and eristocophin (20). The one-letter notation of amino acids is used. Blank spaces indicate deletions. <E represents 5-pyrroolidone-2-carboxylic acid (pyroglutamyl residue). The RGD sequence in the binding site of disintegrins is shown by asterisk.

Species	Protein	Biological Activity	1	25
<i>D. j. kaimosae</i>	Mambin <sup>a</sup>	Aggregation Inhibitor	RICYNHLGTK	PPTTETCQED SCYKN
<i>D. p. polylepis</i>	Toxin	Postsynaptic Neurotoxin	RICYNHQSTT	RATTKSCEEN SCYKK
<i>D. j. kaimosae</i>	V <sub>n</sub> <sup>I</sup> 1	Postsynaptic Neurotoxin	RICYNHQSTT	PATTKSCGEN SCYKK
<i>D. p. polylepis</i>	Calciseptine	Ca <sup>2+</sup> Channel Blocker	RICYIHKASL	PRATKTCVEN TCYKM
<i>D. p. polylepis</i>	FS2	Ca <sup>2+</sup> Channel Blocker	RICYSHKASL	PRATKTCVEN TCYKM
<i>D. angusticeps</i>	Toxin C	Anti-acetylcholinesterase	TICYSHTTTS	RAILKDCGEN SCYRK
<i>D. p. polylepis</i>	Fasciculin	Anti-acetylcholinesterase	TMCYSHTTTS	RAILTNCGEN SCYRK

Species	Protein	26	62
<i>D. j. kaimosae</i>	Mambin <sup>a</sup>	IWTFD N IIRRGCG	CFTPRGDMPG PYCCES DKC NL
<i>D. p. polylepis</i>	Toxin	YWRDH RGTIIERGCG	CPKVKPGVGI H CCQS DKC NY
<i>D. j. kaimosae</i>	V <sub>n</sub> <sup>I</sup> 1	TWSDH RGTIIERGCG	CPKVKQGIHL H CCQS DKC NY
<i>D. p. polylepis</i>	Calciseptine	FIRTQ REYISERGCG	CPTAMWPYQT E CCKG DRC NK
<i>D. p. polylepis</i>	FS2	FIRTH REYISERGCG	CPTAMWPYQT E CCKG DRC NK
<i>D. angusticeps</i>	Toxin C	SRRHP PKMVLGRGCG	CPPGDDYLEV K CCTSPDKC NY
<i>D. p. polylepis</i>	Fasciculin	SRRHP PKMVLGRGCG	CPPGDDYLEV K CCTSPDKC NY

**Figure 2.** Structural comparison of mambin with related toxins from mamba venoms. The original references for each sequence are given in Kini et al. (158). \* Mambin and dendroaspin have identical amino acid sequences. The one-letter notation of amino acids is used. Blank spaces indicate deletions.

Protein	Species	
<b>(a) Platelet aggregation inhibitors from leeches</b>		
Decorsin	<i>Macrobdella decora</i>	APRLPQCQG DDQEKCLCNK DECPPGQCRF PRGDADPYCE
Ornatin B	<i>Placobdella ornata</i>	IYVRPTNDEL NYCGDFRELG QPDKKCRCDG KPCTVGRCKF ARGDNDDKCI SA
Ornatin C	<i>Placobdella ornata</i>	IYVRPTKDEL LYCGEFRELG QPDKKCRCDG KPCTVGRCKF ARGDADDKCT SA
Ornatin E	<i>Placobdella ornata</i>	IYVRPTKDEL LYCGEFRELG QPDKKCRCDG KPCTVGRCNF ARGDNDDKCI
<b>(b) Platelet aggregation inhibitors from ticks</b>		
Variabilin	<i>Dermacentor variabilis</i>	NTFSDENPGF PCDCTSADAK RACGIQCACW PRGDTPGGGR RIIDGQQ
Disagregin	<i>Ornithodoros moubata</i>	SDDKCQGRPM YGCREDDDSV FGWTYDSNHG QCWKGSYCKH RRQPSNYFAS QQECRNTCGA

*Figure 3.* Amino acid sequences of fibrinogen receptor antagonists isolated from leeches and ticks. The amino acid sequences are taken from the following references: Decorsin (49), ornatins (50), variabilin (51) and disagregin (52). The one-letter notation of amino acids is used.

**Table 1.** Class I. Disintegrins and related antagonists of fibrinogen receptor glycoprotein IIb/IIIa complex (GPIIb/IIIa)

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
Accutin	<i>Agkistrodon acutus</i>	5241 Da, 47aa	66-267 nM	99
Agkistrostatin	<i>Agkistrodon piscivorus</i>			7
Albolabrin	<i>Trimeresurus albolabris</i>	7574 Da, 73 aa, single chain, pI 4.27	220 nM	100
Applaggin	<i>Agkistrodon piscivorus piscivorus</i>	17 700 Da, 71 aa, a disulfide linked homodimer	12-128 nM	101, 102
Arietin /Bitistatin	<i>Bitis arietans</i>	8500 Da	130-270 nM	103, 104
Barbourin	<i>Sistrurus m. barbouri</i>	73 aa	309 nM	20
Batroxostatin	<i>Bothrops atrox</i>	71 aa	133 nM	105
Bitan _	<i>Bitis arietans</i>	8987 Da, 83aa	108 nM	106
Bitistatin	<i>Bitis arietans</i>	9022 Da, 83aa, single chain	237 nM	107
Carinatin	<i>Echis carinatus</i>	6 800 Da, acidic glycoprotein, 22.1 % neutral sugars, pI 4.8	1.47 nM	2, 3
Cerastatin	<i>Cerastes cerastes</i>	32 000 Da, pI 6.2, glycoprotein, oligometric structure	2.3 nM	108
Contortrostatin	<i>Agkistrodon contortrix contortrix</i>	15 000 Da, homodimer, 13 500 Da	49 – 1 150 nM for platelet of different species	14
Crotavirin	<i>Crotalus viridis</i>	9200 Da, single chain	110 nM	109
Echistatin 1	<i>Echis carinatus</i>	5400 Da, 49aa, pI 8.3	30 nM	106
Echistatin 2	<i>Echis carinatus</i>	5243 Da, 47aa	555 nM	4, 106
Elegantin	<i>Trimeresurus elegans</i>	7806 Da, 73 aa, pI 4.69, single chain	136 nM	100
Eristocophin	<i>Eristocophis macmahoni</i>			20
Eristostatin	<i>Eristocophis macmahoni</i>	5 400 Da, 49 aa	59 nM	110, 111
Flavoridin	<i>Trimeresurus flavoviridis</i>	70 aa	50 nM	7
Flavostatin	<i>Trimeresurus flavoviridis</i>	7 304 Da, 68 aa	59-111 nM	112, 113
Gabonin	<i>Bitis gabonica</i>	21 000 Da, 84 aa, disulfide-linked homodimer, pI 9.2	340– 1600 nM	114
Halysin	<i>Agkistrodon halys</i>	7500 Da, 71aa single chain	160-360 nM	115
Kistrin	<i>Calloselasma (Agkistrodon) rhodostoma</i>	7318 Da, 68aa	105-128 nM	106
Multisquamatin	<i>Echis multisquamatus</i>	5700 Da	97-333 nM for platelet of different species	116
Rhodostomin	<i>Calloselasma (Agkistrodon) rhodostoma</i>			7, 12
Salmosin 1	<i>Agkistrodon halys brevicandus</i>	7474 Da, 73 aa, single chain	131 nM	117, 118
Salmosin 2		73 aa (by cDNA)		
Salmosin 3		80 aa (by cDNA)		
Tergeminin	<i>Sistrurus c. tergeminus</i>			20
Triflavin	<i>Trimeresurus flavoviridis</i>			119, 120

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
Trigramin Trigramin <sub>1</sub> Trigramin <sub>2</sub> Trigramin	<i>Trimeresurus gramineus</i>	7 500 Da, 72 aa, pI 5.61 7 551 Da, 72 aa 7 623 Da, 73 aa 7 563 Da, 73 aa	300 nM 170 nM 240 nM	5, 106, 121
Trimucrin	<i>Trimeresurus mucrosquamatus</i>	71 aa (by cDNA)		122
Ussuristatin 1 Ussuristatin 2	<i>Agkistrodon ussuriensis</i>	7 458 Da, 71 aa, single chain 7 385 Da, 71 aa, disulfide-linked homodimer	17-33 nM 140-290 nM	21
Venom inhibitor	<i>Calloselasma (Agkistrodon) rhodostoma</i>	31 000 Da, 266 aa dimer, glycoprotein, 8.3 % neutral sugars	160-320 nM	123

*Table 2.* Class I. Antagonists of fibrinogen receptor glycoprotein IIb/IIIa complex (GPIIb/IIIa) that are unrelated to disintegrins

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
Mambin	<i>Dendroaspis jamesonii</i>	6 744 da, 59 aa	172 nM	47
Decorsin	<i>Macrobdella decora</i>	4379 Da, 39 aa, pI 4.45	500 nM	49
Ornatins A2 A3 B C D E	<i>Placobdella ornata</i>	4449.6 Da, 41 aa, pI 9.8 5868.2 Da, 52 aa, pI 8.75 5839.5 Da, 52 aa, pI 9.45 5721.6 Da, 44 aa 5722.5 Da, 50 aa, pI 8.75	133 nM   279 nM  438 nM	50
Variabilin	<i>Dermacentor variabilis</i>	4 969 Da, 47 aa	157 nM	51
Salivary gland extract of deerfly	<i>Chrysops</i>			124
Disagregin	<i>Ornithodoros moubata</i>	6 987 Da, 60 aa, pI 7.35	104 nM	52

*Table 3. Class II. Antagonists of von Willebrand factor receptor glycoprotein Ib (GPIb)*

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
Agkicetin	<i>Agkistrodon acutus</i>	26 000 Da, disulfide-linked heterodimer	12.5 nM	125
CHH-A CHH-B	<i>Crotalus horridus</i> <i>horridus</i>	23 000 Da, disulfide-linked heterodimer 25 000 Da, disulfide-linked heterodimer ( = 15 000, =12 000 Da)		126
Echicetin	<i>Echis carinatus</i>	26 000 Da, disulfide-linked heterodimer, 16 000 , 14 000 Da, C-type lectin	5.77-42.3 nM	56, 57
Flavocetin-A  Flavocetin-B	<i>Trimeresurus flavoviridis</i>	149 000 Da, subunits =17 000 Da, =14 000 Da 139 000 Da, subunits =17 000, =15 000 Da, =14 000 Da	1.0-3.3 nM  1.80-4.00 nM	55
Jararaca GPIb-BP	<i>Bothrops jararaca</i>	30 000 Da, disulfide-linked heterodimer, = 142 aa (17 457 Da), =123 aa (15,035 Da)	28-42 nM	127, 128
Tokaracetin	<i>Trimeresurus tokarensis</i>	28 900 Da, disulfide linked heterodimer (16 100, 15 400 Da)	8.65-20 nM	129

**Table 4. Class III. Antagonists of collagen-platelet interaction**

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
Calin	<i>Hirudo medicinalis</i>	65 000 Da		66
Leech antiplatelet protein (LAPP)	<i>Haementeria officinalis</i>	16 000 Da, 126 aa	60 nM	67, 68
Moubatin	<i>Ornithodoros moubata</i>	17 000 Da	50 nM	69, 70
Tick adhesion inhibitor (TAI)	<i>Ornithodoros moubata</i>	15 000 Da		71
Pallidipin	<i>Triatoma pallidipennis</i>	19 000 Da	50-200 nM	72
Catrocollastatin-C	<i>Crotalus atrox</i>	23 600 Da	66 nM	59, 62
Crovidisin	<i>Crotalus viridis</i>	53 000 Da, single chain	0.17 $\mu$ M	65
Jararhagin-C	<i>Bothrops jararaca</i>	28 000 Da, 212 aa	N. D.	61



Table 5. Class IV. Antagonists of thrombin-thrombin receptor interaction

<b><u>Name</u></b>	<b><u>Species</u></b>	<b><u>Physical Properties</u></b>	<b><u>IC<sub>50</sub></u></b>	<b><u>References</u></b>
Bothroaltermin	<i>Bothrops alternatus</i>	27 000 Da, disulfide-linked homodimers (14 000 Da), C-type lectin	7 nM	76
Bothrojaracin	<i>Bothrops jararaca</i>	27 000 Da, pI 4.2, disulfide-linked heterodimer (15 000, 13 000 Da)	2.2 nM	75
Triabin	<i>Triatoma pallidipennis</i>	17 000 Da, 142 aa	2.6 nM	77-79

*Table 6.* Class V. Other nonenzymatic inhibitors which inhibit platelet aggregation through unknown mechanism

<b><u>Name</u></b>	<b><u>Species</u></b>	<b><u>Physical properties</u></b>	<b><u>IC<sub>50</sub></u></b>	<b><u>References</u></b>
Lebetin 1	<i>Vipera lebetina</i>	1 306 Da, 13 aa	27-125 nM	80, 81
Lebetin 1		1 249 Da, 12 aa		
Lebetin 2		3 944 Da, 38 aa	5-48 nM	
Lebetin 2		3 886 Da, 37 aa		

Table 7. Nucleotidases that inhibit platelet aggregation

<b>Name</b>	<b>Species</b>	<b>Physical Properties</b>	<b>IC<sub>50</sub></b>	<b>References</b>
5'-nucleotidase	<i>Trimeresurus gramineus</i>	74 000 Da, single glycoprotein chain, 589 aa, 22% neutral sugars, Hydrolysis: AMP: 15.8 μmol Pi/min per mg ADP: 3.2 μmol Pi/min per mg	0.68 μM	82
ADPase	<i>Agkistrodon acutus</i>	94 000 Da, 852 aa		83
ADPase/5'-nucleotidase	<i>Vipera aspis</i>	Hydrolysis: AMP: 1.03 μmol Pi/min per mg ADP: 2.03 μmol Pi/min per mg		84

Table 8. Phospholipase A<sub>2</sub> enzymes that inhibit platelet aggregation

<u>Species</u>	<u>Name</u>	<u>Physical Properties</u>	<u>IC<sub>50</sub></u>	<u>References</u>
<i>Acanthophis antarcticus</i>	Acanthin I	12 845 Da, 119 aa, pI 10.2	7 nM	130
	Acanthin II	12 896 Da, 118 aa, pI 10.4	4 nM	
<i>Acanthophis praelongus</i>	Praelongin 2bIII	12 783Da, pI 10.3	650 nM	131
	Praelongin 2cII	12 971 Da, pI 9.4	180 μM	
	Praelongin 2cIV	12 972 Da, pI 9.6	55 μM	
<i>Agkistrodon acutus</i>	Phospholipase A <sub>2</sub>	16 4000 Da, pI 4.9		91
<i>Agkistrodon halys</i>	Phospholipase A <sub>2</sub>	14 000 Da, 130 aa, single chain, <1% carbohydrate	0.78 μM	92, 132
<i>Agkistrodon halys pallas</i>	Phospholipase A <sub>2</sub>	124 aa, pI 4.5 single chain		133
<i>Austrelaps superba</i>	Phospholipase A <sub>2</sub>	15 000 Da	0.33 μM	87, 134
<i>Austrelaps superbus</i>	Superbin I	13 252 Da		135
	Superbin II	13 235, 13212.9 Da		
<i>Echis carinatus</i>	EC-I-PLA <sub>2</sub>	16 000 Da	~ 2 μM	136
<i>Lachesis muta</i>	LM-PLA <sub>2</sub>	17 000 Da, pI 4.7, single chain	25-125 nM	137
<i>Naja naja atra</i>	phospholipase A <sub>2</sub>			86
<i>Naja nigricollis</i>	CM-I	15 000 Da		88
	CM-II	15 000 Da		
	CM-IV	15 000 Da		
<i>Ophiophagus hannah</i>	OHV A-PLA <sub>2</sub>	13 719 Da, 124 aa, single chain	4-1530 nM	89, 138
<i>Pseudechis papuanus</i>	PPV	15 000 Da		90
<i>Trimeresurus graminues</i>	Platelet aggregation inhibitor	12 400 Da, 109aa, pI 3.6, single chain	0.2-0.4 μM	139, 140
<i>Vipera russelli</i>	VRV-PL-IIIb	14-15 000 Da, pI 7.3-7.7		141
<i>Vipera russelli formosensis</i>	Phospholipase A <sub>2</sub>			142
<i>Vipera russelli siamensis</i>	Venom inhibitor	13 800, 123 aa, pI 10.4	26.8-82.6 μM	143, 144
<i>Apis mellifera</i>	Phospholipase A <sub>2</sub>			145
<i>Heloderma horridum</i>	HHV-PLA	19 000 Da, 163 aa, single chain		146

**Table 9.** Metalloproteinases and their related domains that inhibit platelet aggregation

<b><u>Name</u></b>	<b><u>Species</u></b>	<b><u>Physical Properties</u></b>	<b><u>IC<sub>50</sub></u></b>	<b><u>References</u></b>
-Fibrogenase	<i>Calloselasma rhodostoma</i>	25 400 Da, 226 aa, single chain, pI >10, <1% carbohydrate		147, 148
-Fibrogenase	<i>Trimeresurus mucrosquamatus</i>	22 400 Da, 203 aa, pI 8.1, 2% carbohydrate		95, 149, 150
Fibrogenase	<i>Vipera lebetina</i>	26 000 Da, pI 5.9, glycoprotein, 5% carbohydrate		151, 152
Jararhagin	<i>Bothrops jararaca</i>	52 000 Da	40 nM	63, 64, 153
Kistomin	<i>Calloselasma rhodostoma</i>	21 800 Da, 202 aa, single chain	0.37 μM	97, 154
Protease L4	<i>Agkistrodon halys brevicaudus</i>	22 000 Da, 173 aa		155
Proteinase F1	<i>Naja nigricollis</i>	58 000 Da, pI >10, single chain	2μM	96, 156
Atrolysin A and Atrolysin A/DC	<i>Crotalus atrox</i>	24 479 Da, probably glycosylated	320-470 nM	60
Atrolysin E/D	<i>Crotalus atrox</i>	7 400 Da, 68 aa	4-8 nM	98
Catrocollastatin	<i>Crotalus atrox</i>			157