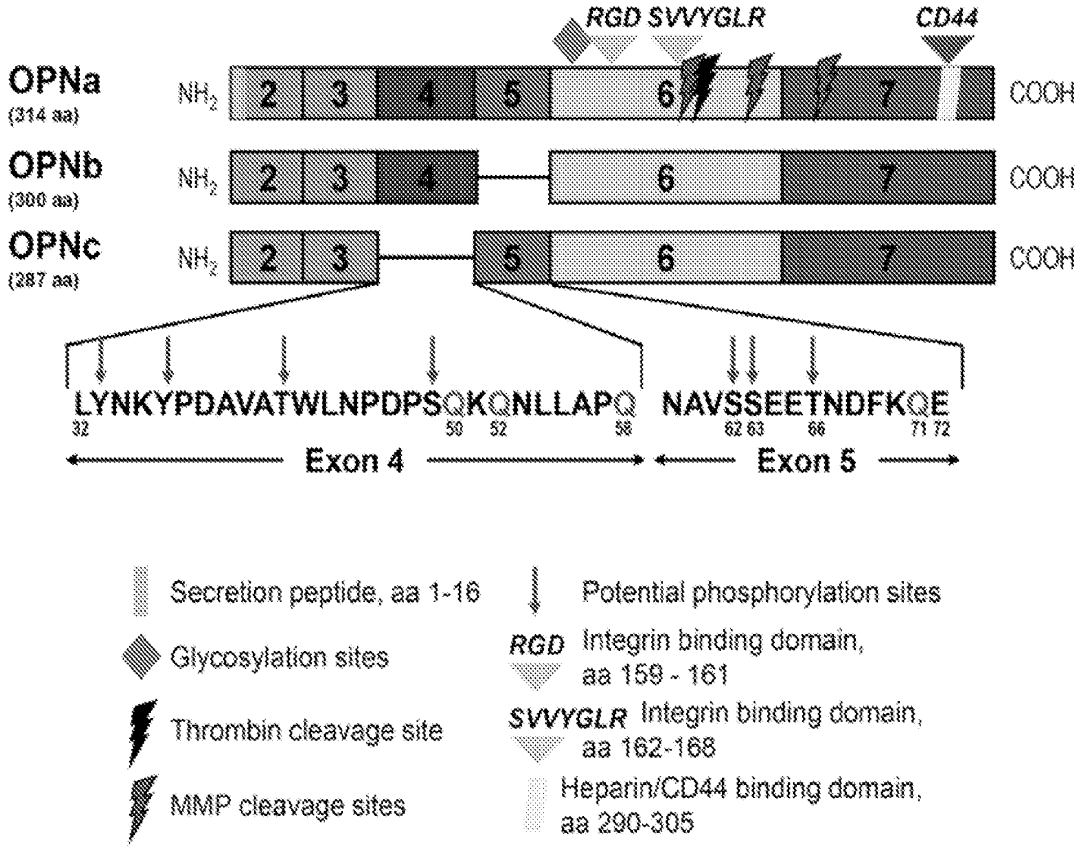

RGD SVVYGLR
CD44
OPNa
(314 aa)
OPNb
(300 aa)
OPNc
(287 aa)
NH2
COOH
2
3
4
5
6
7
LYNKYPDAVATWLNPDPSQKQNLLAPQ
NAVSSEETNDFKQE
32
50
52
58
62 63
66
71 72
Exon 4
Exon 5
Secretion peptide, aa 1-16
Potential phosphorylation sites
Glycosylation sites
RGD Integrin binding domain, aa 159 - 161
Thrombin cleavage site
SVVYGLR Integrin binding domain, aa 162-168
MMP cleavage sites
Heparin/CD44 binding domain, aa 290-305

Fig. 1

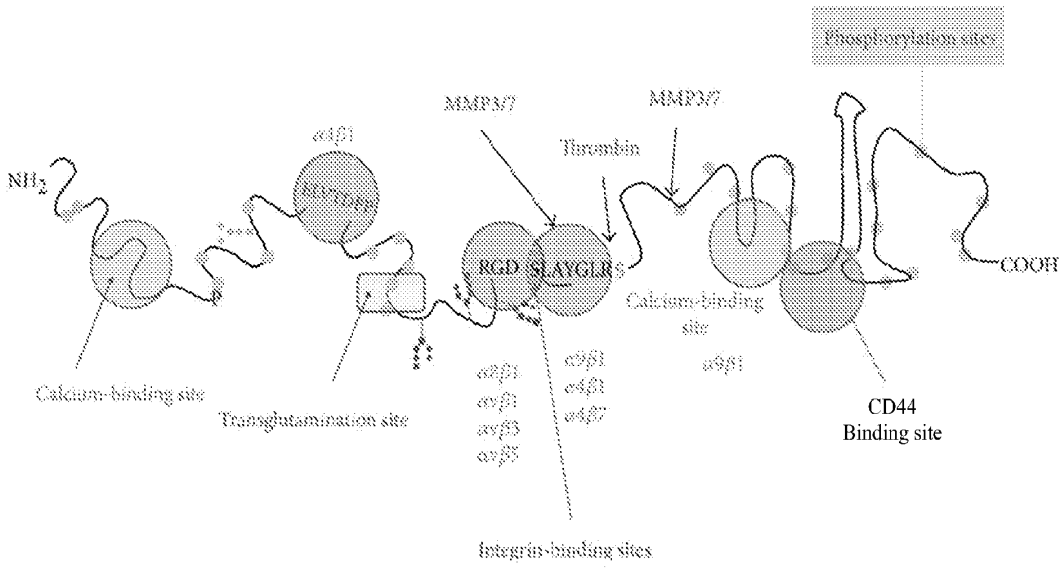

Phosphorylation site
MMP3/7
MMP3/7
Thrombin
$\alpha 4\beta 1$
NH_2
RGD SLAYGLR
COOH
Calcium-binding site
Calcium-binding site
$\alpha 9\beta 1$
$\alpha 4\beta 1$
$\alpha v\beta 1$
$\alpha v\beta 3$
$\alpha v\beta 5$
$\alpha 9\beta 1$
$\alpha 4\beta 1$
$\alpha 4\beta 7$
Transglutamination site
CD44
Binding site
Integrin-binding sites

Fig. 2

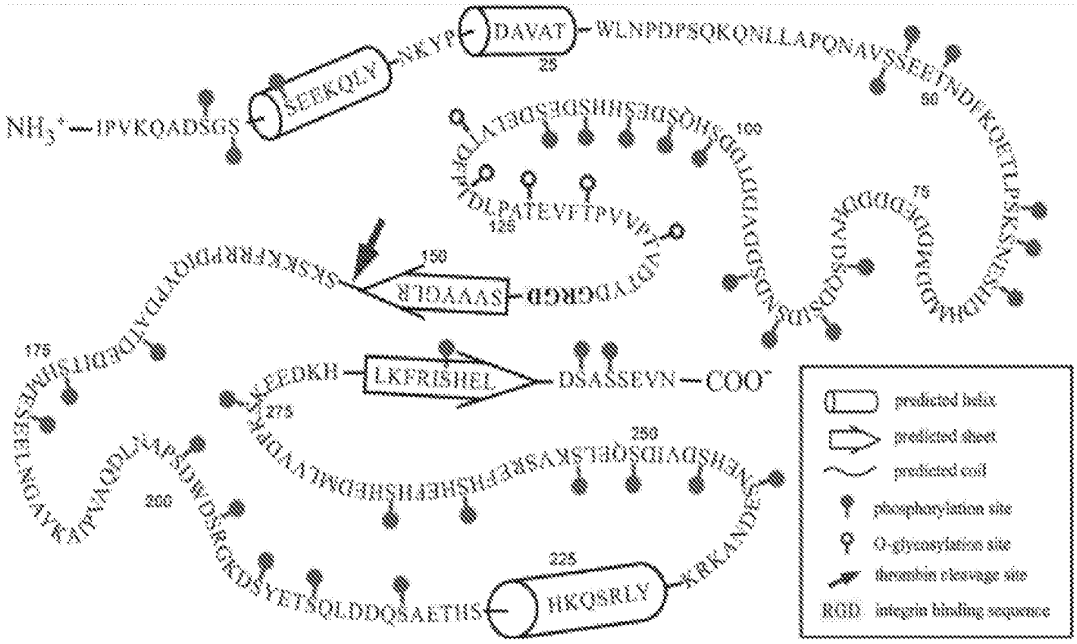

predicted helix
predicted sheet
predicted coil
phosphorylation site
O-glycosylation site
thrombin cleavage site
RGD integrin binding sequence

Fig. 3

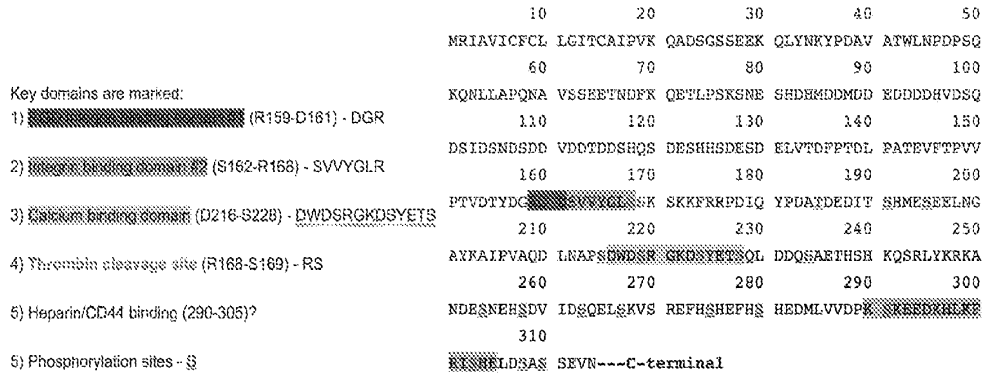

Key domains are marked:
1) (R159-D161) - DGR
2) (S162-R168) - SVVYGLR
3) Calcium binding domain (D216-S228) - DWDSRGKDSYETS
4) Thrombin cleavage site (R168-S169) - RS
5) Heparin/CD44 binding (290-305)?
5) Phosphorylation sites - S
10 20 30 40 50
MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYNKYPDAV ATWLNPDPSQ
60 70 80 90 100
KQNLLAPQNA VSSEETNDFK QETLPSKSNE SHDHMDDMDD EDDDDHVDSQ
110 120 130 140 150
DSIDSNDSDD VDDTDDSHQS DESHHSDESD ELVTDFPTDL PATEVFTPVV
160 170 180 190 200
PTVDTYDG EGVVHEVVNK SKKFRRPDIQ YPDATDEDIT SHMESEELNG
210 220 230 240 250
AYKAIPVAQD LNAPSDWDSR GKDSYETSQL DDQSAETHSH KQSRLYKRKA
260 270 280 290 300
NDESNEHSDV IDSQELSKVS REFHSHEFHS HEDMLVVDPK SKEEDKHLKF
310
FIHFLDSAS SEVN---C-terminal

Fig. 4

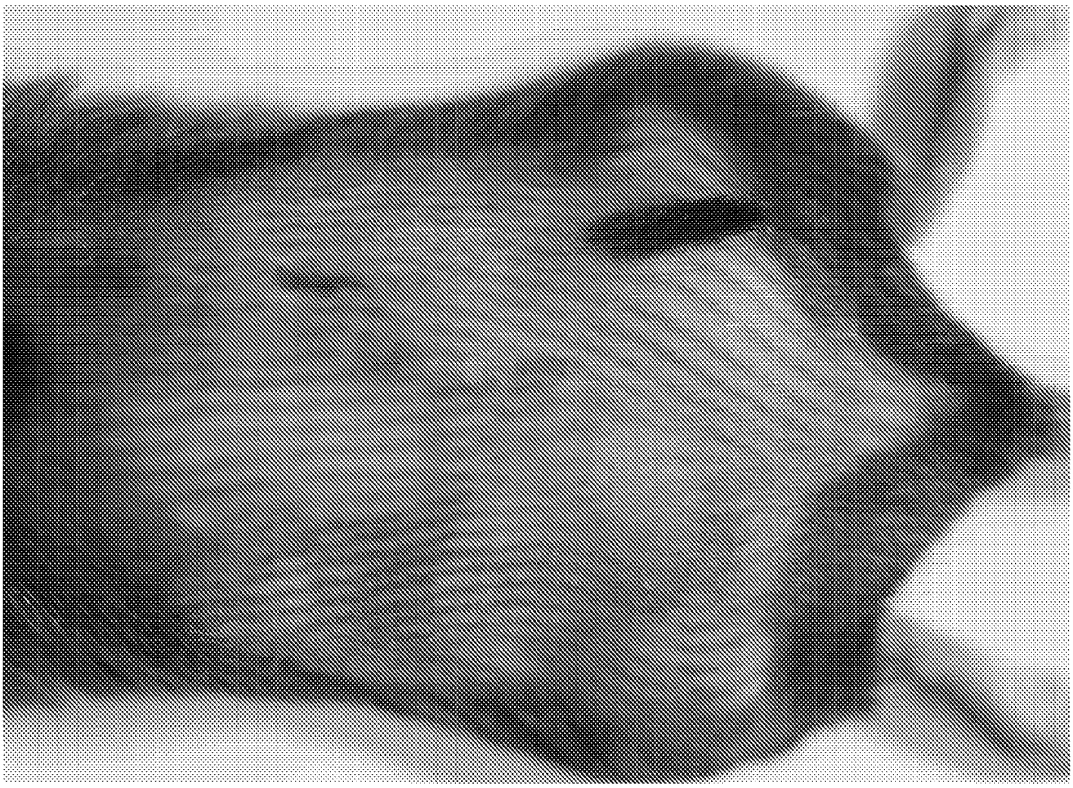


Fig. 5

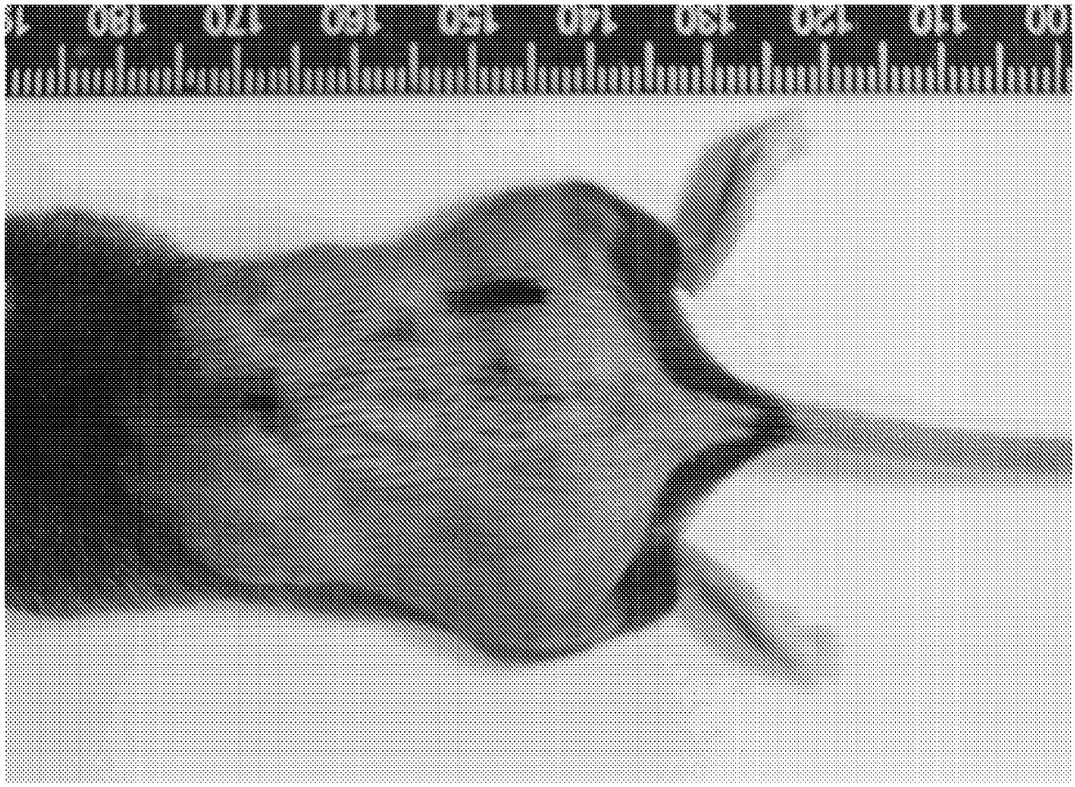


Fig. 6

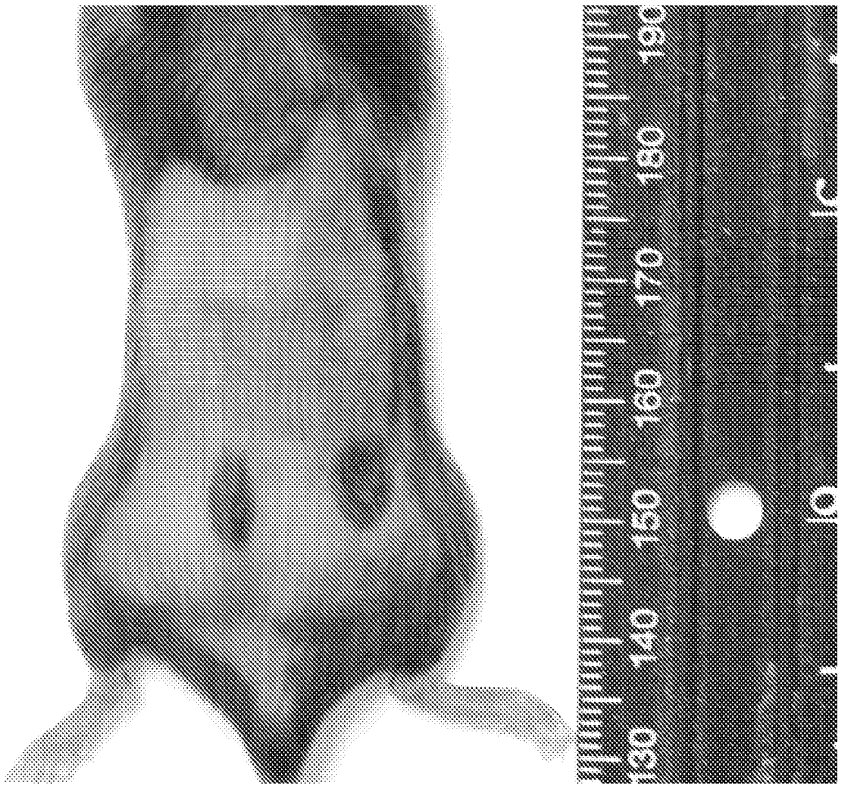


Fig. 7

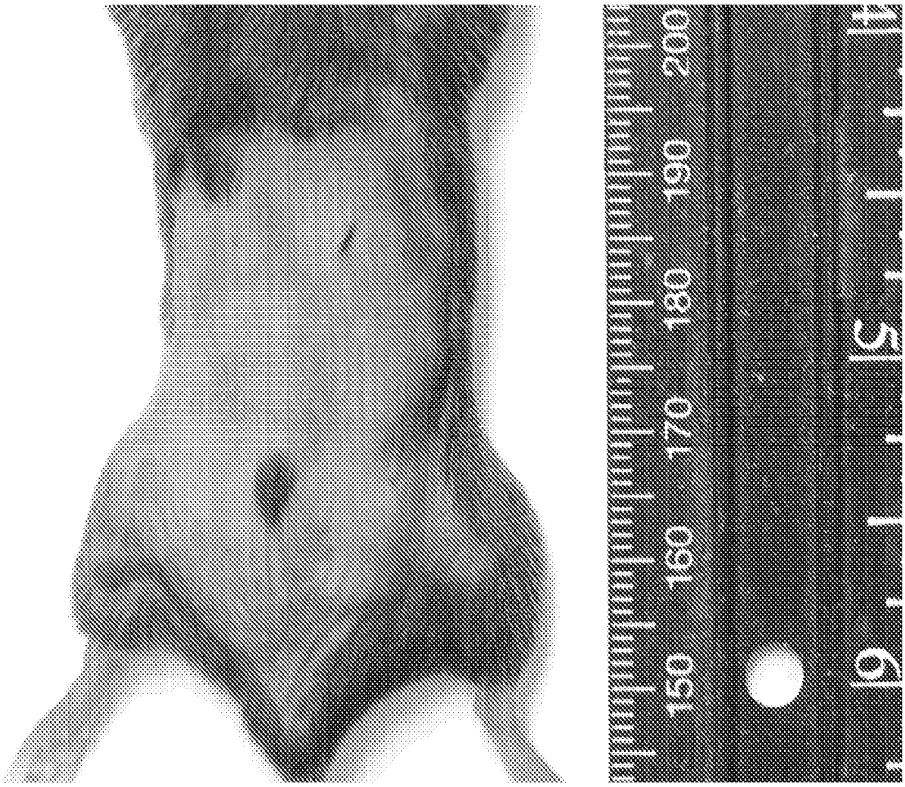


Fig. 8