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Plasminogen Receptors: The First Quarter Century

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Abstract

The interaction of plasminogen with cell surfaces results in promotion of plasmin formation and retention on the cell surface. This results in arming cell surfaces with the broad spectrum proteolytic activity of plasmin. Over the past quarter century, key functional consequences of the association of plasmin with the cell surface have been elucidated. Physiologic and pathophysiologic processes with plasmin-dependent cell migration as a central feature include inflammation, wound healing, oncogenesis, metastasis, myogenesis, and muscle regeneration. Cell surface plasmin also participates in neurite outgrowth, and prohormone processing. Furthermore, plasmin-induced cell signaling also affects the functions of inflammatory cells, via production of cytokines, reactive oxygen species, and other mediators. Finally, plasminogen receptors regulate fibrinolysis. In this review we highlight emerging data that shed light on long-standing controversies and raise new issues in the field. We focus on 1) the impact of the recent X-ray crystal structures of plasminogen and the development of antibodies that recognize cell-induced conformational changes in plasminogen, on our understanding of the interaction of plasminogen with cells; 2) the relationship between apoptosis and plasminogen binding to cells; 3) the current status of our understanding of the molecular identity of plasminogen receptors and the discovery of a structurally unique novel plasminogen receptor, Plg-R_{KT}; 4) the determinants of the interplay between distinct plasminogen receptors and cellular functions; and 5) new insights into the role of co-localization of plasminogen and plasminogen activator receptors on the cell surface.

Keywords

α -enolase; actin; annexin A2; plasminogen receptors; Plg-R_{KT}; S100A10

Introduction

Over twenty-five years ago it was first recognized that plasminogen specifically interacts with the surfaces of cells. This interaction is analogous to the interaction of plasminogen with fibrin in that plasminogen bound to cells is more efficiently activated by plasminogen activators compared with plasminogen in solution (1–10). Furthermore, plasmin remains associated with the cell surface where it is relatively protected from inactivation by α_2 -antiplasmin (11;12). This results in association of the broad spectrum proteolytic activity of plasmin with the cell surface leading to a wide array of physiological and pathological sequelae. In this review we will highlight emerging data that shed light on long-standing

controversies and that raise new questions in the field. Plasminogen receptors are very broadly distributed on both prokaryotic and eukaryotic cells, including monocytes (13), monocytoïd cells (11), macrophages (14), endothelial cells (3;15), fibroblasts (16), platelets (1), adrenal medullary cells (17;18) and carcinoma cells (19;20) as well as on cell-derived microvesicles (21;22). The structure and function of plasminogen receptors on prokaryotic cells have been comprehensively reviewed recently (23;24). Here, we focus on the structure and function of eukaryotic plasminogen receptors.

Physiological and Pathological Consequences of Localization of Plasminogen on Cell Surfaces

When cells become armed with the broad-spectrum activity of plasmin, they acquire the ability to degrade extracellular matrices and activate other matrix-associated growth factors and proteolytic enzymes that facilitate cell migration. Physiologic and pathophysiologic processes with plasmin-dependent cell migration as a central feature include inflammation (25–27), wound healing (28;29), oncogenesis (30;31), metastasis (32;33), myogenesis, and muscle regeneration (34–36). Cell surface plasmin also participates in neurite outgrowth (37;38), and prohormone processing (17;18;39;40). Furthermore, plasmin-induced cell signaling also affects the functions of inflammatory cells, via production of cytokines, reactive oxygen species, and other mediators (41;42). Finally, plasminogen receptors regulate fibrinolysis (43–47).

Structural Determinants within Plasminogen that Mediate its Interaction with Cells

The recent X-ray crystal structures of full-length human Glu-plasminogen (the native circulating form of plasminogen with N-terminal Glutamic acid) (48;49) have provided new insights into the structural determinants in the plasminogen molecule that mediate its interaction with cells. The interactions of plasminogen with all cell types evaluated are blocked by lysine and lysine analogs, e.g. ϵ -aminocaproic acid (EACA), as well as peptides with carboxyl terminal lysines. This implies that the lysine binding sites within the disulfide-bonded kringle domains of plasminogen are required for the interaction with cells. Indeed, isolated kringle-containing plasminogen domains can specifically bind to cells with the following order of potency: The kringle 1–3 domain > the kringle 5-protease domain > kringle 2 (50). Nonetheless, the crystal structures of plasminogen reveal that only the lysine binding site of kringle 1 is available in the closed form of Glu-plasminogen, suggesting that Kringle 1 mediates the initial recruitment of plasminogen to the cell surface (48).

Conformational Changes Induced in Plasminogen upon Binding to Cells and Their Relationship to Plasminogen Activation

Glu-plasminogen exists in a closed tight (T) conformation in the presence of Cl^- ion (51). In the presence of lysine and lysine analogs, Glu-plasminogen adopts a more open relaxed (R) conformation that is much more readily activated by plasminogen activators (52). In addition, plasmin catalyzes hydrolysis of the N-terminal 77 amino acids of Glu-plasminogen, resulting in formation of a truncated form with an N-terminal lysine, Lys-plasminogen. Lys-plasminogen exists in an open conformation [relaxed (R) form] and is, consequently, more readily activated by plasminogen activators than Glu-plasminogen in the closed conformation (53–55).

When Glu-plasminogen binds to cells, its activation is markedly enhanced, compared with the reaction in solution due to a reduction in the K_m (by 11 to 60-fold) for the plasminogen

activation reaction in solution (1–10). This suggests that Glu-plasminogen on the cell surface adopts a conformation distinct from its conformation in solution. Direct evidence for such a conformational change was obtained recently using monoclonal anti-plasminogen antibodies that recognize receptor-induced binding sites (RIBS) in Glu-plasminogen upon its interaction with cells, but react poorly with soluble Glu-plasminogen (56–58). Previously, it has generally been accepted that Glu-plasminogen adopts a Lys-plasminogen-like open conformation when bound to the cell surface, to account for enhancement of activation of cell-associated Glu-plasminogen (59). However, soluble Lys-plasminogen did not compete for the interaction of anti-plasminogen RIBS mAbs with surface-associated Glu-plasminogen, suggesting that the conformation induced when Glu-plasminogen binds to cells is distinct from the conformation of Lys-plasminogen (56). Furthermore, conformational changes in Glu-plasminogen induced by lysine analogs were detected by an anti-plasminogen RIBS mAb, suggesting that the R form of Glu-plasminogen induced by its interaction with lysine analogs, is distinct from the conformation of Lys-plasminogen (56).

The crystal structure of full-length plasminogen has revealed that the plasmin cleavage site in the N-terminus (that produces Lys-plasminogen) is buried in the closed conformation of Glu-plasminogen, suggesting that a conformational rearrangement precedes the production of Lys-plasminogen (48). Plasmin proteolysis of Glu-plasminogen to Lys-plasminogen is promoted when Glu-plasminogen is bound to the cell surface (60–62). Taken together, these studies suggest that the conformation adopted by Glu-plasminogen when bound to cells is one that exposes the cleavage site for plasmin-mediated removal of the N-terminal 77 amino acids, as a mechanism for promoting the conversion of Glu-plasminogen to Lys-plasminogen on the cell surface. Analysis of the crystal structure of plasminogen (48) as well as earlier studies (38;63–65) suggest that this conformational rearrangement may be due to an interaction of the lysine binding site within plasminogen kringle 5 with plasminogen receptors on the cell surface.

Relationship Between Plasminogen Binding to Cells and Apoptosis

An evolving area of research strongly supports a role for plasminogen receptors and the plasminogen activation system in regulation of apoptosis. With adherent cells, plasmin promotes anoikis, depriving cells of a necessary survival signal due to the loss of cell/matrix interactions, leading to programmed cell death. For example, plasmin degrades the hippocampal extracellular matrix protein, laminin, in response to excitotoxin treatment, leading to neuronal cell detachment and cell death (66;67). Similarly, plasmin-dependent anoikis is observed with adherent smooth muscle cells (68;69), retinal cells (70) and fibroblast cell lines (71).

Plasminogen binding capacity is markedly enhanced on both early apoptotic and late apoptotic/necrotic monocytoid cells following treatment with either cycloheximide (72–74) or TNF α (74), consistent with a role for cell-associated plasminogen in regulation of apoptosis. In contrast to adherent cells, monocytoid cells do not depend on adherence for a survival signal. Interestingly, plasminogen has a cytoprotective effect on TNF α -induced apoptosis in monocytoid cells that is independent of anoikis and requires both plasmin activity and PAR1 (74). In addition, plasminogen has prosurvival effects on both spontaneous and Fas-induced neutrophil apoptosis and triggers Akt phosphorylation and ERK1/2 activation via an interaction of plasminogen with the integrin, $\alpha_M\beta_2$ (75). Thus, plasminogen receptors play a key role in the inflammatory responses of both monocytoid cells and neutrophils by regulating cellular apoptosis.

Plasminogen binding is also markedly higher on non-viable breast cancer cell lines compared with viable cancer cells (32). Cell-associated plasmin has recently been

demonstrated to cleave the CUB domain containing protein 1 (CDCP1), resulting in outside-in signaling involving activation of Akt-related cell survival and suppression of PARP1-induced apoptosis in cancer cells (76;77). This signaling cascade ultimately regulates the survival potential of tumor cells in the late stages of the metastatic cascade, namely during extravasation and early tissue colonization. The results also suggest that the original link of the uPA-plasmin system with cancer may not all be via protease-mediated invasive migration, but also via plasmin cleavage and activation of cell survival signaling molecules.

The observation that plasminogen binding capacity is markedly enhanced on both early apoptotic and late apoptotic/necrotic cells (32;72–74) was made possible by the use of fluorescence activated cell sorting (FACS) analysis in which plasminogen binding, separately, to live, apoptotic and necrotic cell populations could be evaluated. Thus, it became incumbent upon investigators studying plasminogen receptors to use this method and it has since replaced earlier methods in which tagged plasminogen binding to whole cell populations was quantified. In addition, kinetic constants can be derived using quantitative FACS analysis (78;79). The relationship between plasminogen binding and apoptosis also serves as an impetus for re-examination of the broad distribution as well as the number of plasminogen binding sites on numerous viable cell types, since these former analyses may have included apoptotic/necrotic cell types. For example, previously, the only cell type examined (in analysis of more than twenty cell types that were not separated into viable/apoptotic/necrotic populations) that did not appreciably bind plasminogen was the erythrocyte (13). However, using FACS analysis, we were able to identify the first viable nucleated cell type, the murine macrophage progenitor line, Hoxa9ER4 (80), which did not detectably bind plasminogen unless differentiated to macrophages (79).

Molecular Identity of Plasminogen Receptors

A key concept regarding the mechanism by which an interaction with the eukaryotic cell surface promotes plasminogen activation is that a subset of carboxypeptidase B (CpB)-sensitive plasminogen binding proteins is responsible for enhancing plasminogen activation. When cells are treated with CpB, the ability to stimulate plasminogen activation is lost (81). Furthermore, plasminogen-dependent macrophage recruitment in the inflammatory response *in vivo* is mediated by CpB-sensitive plasminogen binding sites (82). Since CpB removes C-terminal basic residues, these results imply that plasminogen binding proteins exposing C-terminal basic residues on cell surfaces are responsible for stimulation of plasminogen activation.

Several distinct plasminogen receptors have been identified over the past decades, consistent with the high number of receptors determined/cell [ranging from 37,000/platelet (1) to $> 10^7$ sites/endothelial cell (15)] and also consistent with the diversity of cell types that bind plasminogen.

Until recently, known CpB-sensitive cellular plasminogen receptors could be divided into two classes: 1) proteins synthesized with C-terminal basic residues and having well established intracellular functions, including α -enolase (83;84), cytokeratin 8 (20;85), S100A10 (in complex with annexin A2 within the annexin A2 heterotetramer) (46;86;87), TIP49a (88) and histone H2B (89) and; 2) proteins requiring proteolytic processing in order to reveal a C-terminal basic residue (lysine), including actin (90;91). It was initially proposed that the annexin A2 monomer functioned directly as a plasminogen receptor after a proteolytic cleavage event to liberate a new C-terminal lysine (92). However, recent data suggest that the profibrinolytic role of annexin A2 is to transport and localize the plasminogen regulatory protein, S100A10, to the cell surface within the annexin A2 heterotetramer [reviewed in (31;46)]. It should be noted that there is a CpB-insensitive

component of plasminogen binding to eukaryotic cells, as exemplified by tissue factor (93) and the non-proteinaceous gangliosides (94). However, this CpB-insensitive class of plasminogen receptors does not appreciably promote activation of cell-bound plasminogen (81). Integrins, including α IIb β ₃ (95;96), α _M β ₂ (47;97) and α ₅ β ₁ (97), as well as amphoterin (98) and GP330 (99;100) are plasminogen binding proteins not synthesized with C-terminal basic residues. Whether this group of proteins undergoes proteolysis to reveal C-terminal basic residues and/or are susceptible to CpB proteolysis has not been investigated.

Recently, we used a proteomics approach involving multidimensional protein identification technology (MudPIT) [reviewed in (101)] to probe the membrane proteome of differentiated, macrophage colony stimulating factor (M-CSF)-treated murine monocyte progenitor cells for the presence of integral membrane plasminogen receptor(s) exposing a C-terminal basic residue on the cell surface (79). Intact cells were biotinylated using a biotinylation reagent that reacts with carboxyl groups, rather than basic groups (thus, avoiding potential interference with the plasminogen-binding function of C-terminal basic residues). Because early apoptotic and non-viable/necrotic cells exhibit markedly enhanced plasminogen binding ability (72–74) we wished to focus on plasminogen receptors on viable cells and, therefore, passed the biotinylated cells over a dead cell removal column to enrich for live cells. The cells were then lysed and membrane fractions prepared and passed over a plasminogen-Sepharose affinity column and specifically eluted with EACA. Biotinylated cell surface proteins bound to the avidin column and were digested with trypsin while still on the column. The peptide digest was then subjected to MudPIT. In MudPIT, the peptide mixtures were first resolved by strong cation exchange liquid chromatography upstream of reversed phase liquid chromatography. The eluting peptides were electrosprayed onto an LTQ ion trap mass spectrometer and full MS spectra were recorded over a 400–1600 m/z range, followed by three tandem mass events. The resulting spectra were searched against a mouse protein database. Only one protein with a predicted transmembrane sequence and a C-terminal basic residue was identified: the hypothetical protein, C9orf46 homolog (IPI00136293), homologous to the protein predicted to be encoded by human chromosome 9, open reading frame 46. We have designated the protein, Plg-R_{KT}, to indicate a plasminogen receptor with a C-terminal lysine and having a transmembrane domain (see below).

The C9orf46 homolog/Plg-R_{KT} murine DNA sequence encodes a protein of 147 amino acids with a molecular mass of 17,261 Da and a C-terminal lysine (Figure 1, top line). We blasted the C9orf46 homolog/Plg-R_{KT} sequence against all species using NCBI Blast and obtained unique human, rat, dog, cow, dog, giant panda, gibbon, horse, pig, rabbit, and rhesus monkey predicted orthologs, which exhibited high identity (e.g. human vs. chimpanzee = 99% identity) and no gaps in the sequence. Of key importance, a C-terminal lysine was predicted for all of the mammalian orthologs obtained in the blast search. In a query of the Ensembl Gene Report, DNA sequences of all 10 other sequenced mammalian orthologs encoded a C-terminal lysine (102).

In addition to mammals, the DNA sequences of xenopus, the green lizard and zebrafish also encode a C-terminal lysine. The Plg-R_{KT} sequence also encodes a putative conserved DUF2368 domain (encompassing amino acids 1–135), an uncharacterized protein with unknown function conserved from nematodes to humans. Notably, the DNA sequences of Plg-R_{KT} orthologs of lower organisms (e.g. the sea urchin, *Strongylocentrotus purpuratus*, *Drosophila* and *Paramecium*) predicted proteins of different lengths and did not consistently predict C-terminal lysines. It is interesting to note that the evolutionary origin of plasminogen is currently believed to originate with protochordates (103), so that lower organisms without plasminogen would not need the C-terminal lysine of Plg-R_{KT} to bind plasminogen.

It is noteworthy that the primary sequence of C9orf46/Plg-R_{KT} is apparently tightly conserved in humans, with no validated coding polymorphisms (cSNPs) thus far identified within the 6 exons encoded by the gene (on chromosome 9p24.1) in the NCBI human genome sequence variation database (dbSNP, <http://www.ncbi.nlm.nih.gov/SNP>).

We analyzed the C9orf46 homolog/Plg-R_{KT} sequence in the TMpred site (www.ch.embnet.org/cgi-bin/TMPRED). The strongly preferred model included two transmembrane helices extending from F₅₃-L₇₃ (secondary helix, oriented from outside the cell to inside the cell) and P₇₈-Y₉₉ (primary helix, oriented from inside the cell to outside the cell) (Figure 1). Thus, a 52 amino acid N-terminal region and a 48 amino acid C-terminal tail with a C-terminal lysine were predicted to be exposed on the cell surface. The predictions of the topology model were supported using several experimental approaches. 1) In Triton X-114 phase separation experiments Plg-R_{KT} partitioned to the detergent phase, thus behaving as an integral membrane protein (79;104). 2) When we treated intact cells with CpB, prior to performing our proteomic analysis, Plg-R_{KT} was not recovered, consistent with cell surface exposure of the C-terminus of Plg-R_{KT} (79). 3) A mAb raised against the C-terminal peptide of Plg-R_{KT} reacted with the cell surface (79;104). 4) Extracellular exposure of both N- and C-termini of Plg-R_{KT} was supported by protease accessibility experiments (102;105).

Plg-R_{KT} exhibited key properties of a plasminogen receptor. First, plasminogen bound directly to the C-terminal peptide of Plg-R_{KT} and a mAb raised against the C-terminal peptide of Plg-R_{KT} recognized plasminogen binding sites on cells (79). Second, Plg-R_{KT} promoted plasminogen activation by both t-PA (79) and uPA (106). Third, over-expression of Plg-R_{KT} increased the ability of cells to promote plasminogen activation (104). In our first evaluations of potential physiological functions of Plg-R_{KT}, we found that Plg-R_{KT} regulated cellular invasion through an extracellular matrix, promoted chemotaxis/cell migration *in vitro* and regulated plasminogen-dependent macrophage recruitment in the inflammatory response *in vivo* (106). In addition, Plg-R_{KT} regulates plasmin-dependent modulation of catecholamine release from catecholaminergic cells (104).

Because the murine genome has been sequenced we searched for C9orf46 homolog/Plg-R_{KT} mRNA microarray expression data at <http://www.ebi.ac.uk/microarray-as/aew/>. Plg-R_{KT} mRNA is present in monocytes, leukocytes, NK cells, T cells, myeloid, dendritic, and plasmacytoid cells, breast cancer, acute lymphoblastic leukemia and Molt-4 acute lymphoblastic leukemia cells. These data are consistent with previous reports documenting expression of plasminogen binding sites on peripheral blood leukocytes (13), breast cancer cells (32;107) and other tissues [reviewed in (108)]. The broad distribution in tissues that express plasminogen binding sites, suggest that Plg-R_{KT} provides plasminogen receptor function that may serve to modulate plasmin proteolytic functions in these tissues, as well.

Interplay Among Plasminogen Receptors in Cellular Functions

The high number of plasminogen binding sites/cell taken together with the diversity of cell types that bind plasminogen (15) suggests that the plasminogen binding capacity of a given cell may be composed of contributions from a set of distinct cell surface proteins and that different cell types may utilize a different panel of plasminogen receptors [recently reviewed by Plow and colleagues in (109)]. The results of our proteomic analysis of differentiated monocyte progenitor cells were consistent with this concept: In addition to peptides corresponding to Plg-R_{KT}, peptides corresponding to other proteins previously identified as plasminogen binding proteins on monocytes were also detected in the membrane preparations: α -enolase, gamma actin, S100A10, annexin 2 (that most likely bound to the

plasminogen-Sepharose column via S100A10 in the annexin 2 heterotetramer), histone H2B, and β_2 integrin.

The thioglycollate-induced model of macrophage recruitment originally demonstrated the key role of plasminogen receptors with C-terminal lysines in cell migration in the inflammatory response *in vivo* (82). Recent studies utilizing this model illustrate the interplay among distinct plasminogen receptors *in vivo* because the sum of the effects of functional blockade of specific plasminogen receptors, is greater than a 100% reduction in plasminogen-dependent macrophage recruitment. Intravenous injection of specific antibodies to histone H2B results in 48% less macrophage recruitment (110), injection of specific antibodies to α -enolase results in 24% less recruitment (110) and injection of mice with anti-Plg-R_{KT} mAb results in 49% less macrophage recruitment (106) (compared to injection of nonimmune control). In S100A10^{-/-} mice, macrophage recruitment in response to thioglycollate is 53% less in S100A10^{-/-} mice, compared to wild type mice (111). Thus, it is likely that each specific plasminogen receptor may be required at different steps in the inflammatory response, for example chemotactic migration to the peritoneum, or, perhaps, crossing different layers of peritoneal tissue at which different contributions of direct plasmic cleavage of the extracellular matrix or activation of MMP-9 for collagen degradation (112) may predominate. It is noteworthy that a reduction in pro-MMP-9 activation has been demonstrated in S100A10^{-/-} peritoneal macrophages in culture (111) and by treatment of mice with anti-Plg-R_{KT} mAb *in vivo* and there may be overlap in this function, as well. Although each of these receptors regulates Matrigel invasion *in vitro* (106;110;111;113), only Plg-R_{KT} has been demonstrated to contribute to directed chemotaxis/chemokinesis (106). Thus, Plg-R_{KT} may be the predominant modulator of this component of macrophage recruitment.

It should also be recognized that the annexin A2/S100A10 complex binds to anionic phospholipids in a Ca⁺²-dependent manner (31;46;114;115) and it has recently been shown that histone H2B is tethered to the cell surface via an electrostatic interaction with phosphatidyl serine (116). Phosphatidyl serine exposure is a well established marker of apoptosis. When apoptosis is induced, cell surface expression of both histone H2B and S100A10 is increased (109;116). In addition, differentiation of monocytes to macrophages (117;118) and cellular activation (119) are associated with phosphatidyl serine exposure and when cells are induced to differentiate, phosphatidyl serine exposure is increased on non-apoptotic cells (116). Thus, differential exposure of phosphatidyl serine may play a role in determining which plasminogen receptors are utilized at a given stage in cell maturation and activation.

The contribution of distinct plasminogen receptors to macrophage recruitment may also be tissue- and stimulus- specific. For example in a model of monocyte recruitment to the alveolar compartment, α -enolase appears to play a predominant role (113). α -enolase also plays a role in inflammatory cell infiltration required for muscle repair after injury (120).

The Role of Co-localization of Plasminogen and Plasminogen Activators on the Cell Surface

Both Plg-R_{KT} and S100A1 co-localize with uPAR on the cell surface (46;79) and uPAR is also detected in immunoprecipitates of Plg-R_{KT}, of S100A10 and of $\alpha_M\beta_2$ (46;47;104;121). This physical association supports a mechanism for enhancement of plasminogen activation when plasminogen is bound to Plg-R_{KT} or S100A10 and uPA is bound to the uPAR. In addition, the group of Angles-Cano has recently suggested a new mechanism for cell surface plasmin generation, which bypasses the requirement for molecular coassembly of plasminogen and uPA on the same surface, via proteolytic crosstalk between plasminogen

and uPA bound to uPAR on adjacent cells, rather than simultaneously to the same cell (59). Alternatively, a uPAR-independent mechanism requiring simultaneous binding of both plasminogen and uPA (via its amino terminal domain) for stimulation of plasminogen activation has been demonstrated using leukemic cell lines (9). This involves a low affinity/high capacity interaction of uPA with the cell surface (9) and may be similar to the mechanism by which plasminogen activation by uPA is enhanced on the platelet surface (1;122) as platelets do not express the uPAR. Nonetheless, all of the foregoing mechanisms require that plasminogen be directly bound to the cell surface (5;9) and the relative importance of each mechanism may depend on the specific plasminogen receptor(s) utilized by a given cell type.

In contrast to the results with uPA, molecular cross-talk between t-PA and plasminogen bound to adjacent cells was not observed (59), and, thus, may require their simultaneous colocalization on the same cell surface. It is noteworthy that plasminogen and t-PA share binding sites on the cell surface, based on cross-competition studies (123). Both Plg-R_{KT} and S100A10 have been demonstrated to directly bind t-PA (79;124–126). Despite potentially sharing binding sites on Plg-R_{KT} and S10010, the relative concentrations of t-PA and plasminogen in the circulation should permit simultaneous binding of both ligands to the cell surface, and each t-PA molecule should be bound proximally to several plasminogen molecules (123).

Conclusions

Over the past 25 years, a broad spectrum of experimental approaches and areas of investigation have demonstrated the wide array of cellular events and functions that are mediated by the interaction of plasminogen with its cellular receptors. Plasminogen receptors play a fundamentally important role in physiological and pathological processes. Future studies *in vivo* with antibody blockade of specific receptors and with transgenic mice will further elucidate mechanisms by which these processes are regulated.

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Abbreviations

CpB	Carboxypeptidase B
EACA	ε-aminocaproic acid
FACS	fluorescence activated cell sorting
M-CSF	macrophage colony stimulating factor
MudPIT	multidimensional protein identification technology
RIBS	receptor-induced binding sites
t-PA	tissue type plasminogen activator
uPA	urokinase-type plasminogen activator
uPAR	urokinase plasminogen activator receptor

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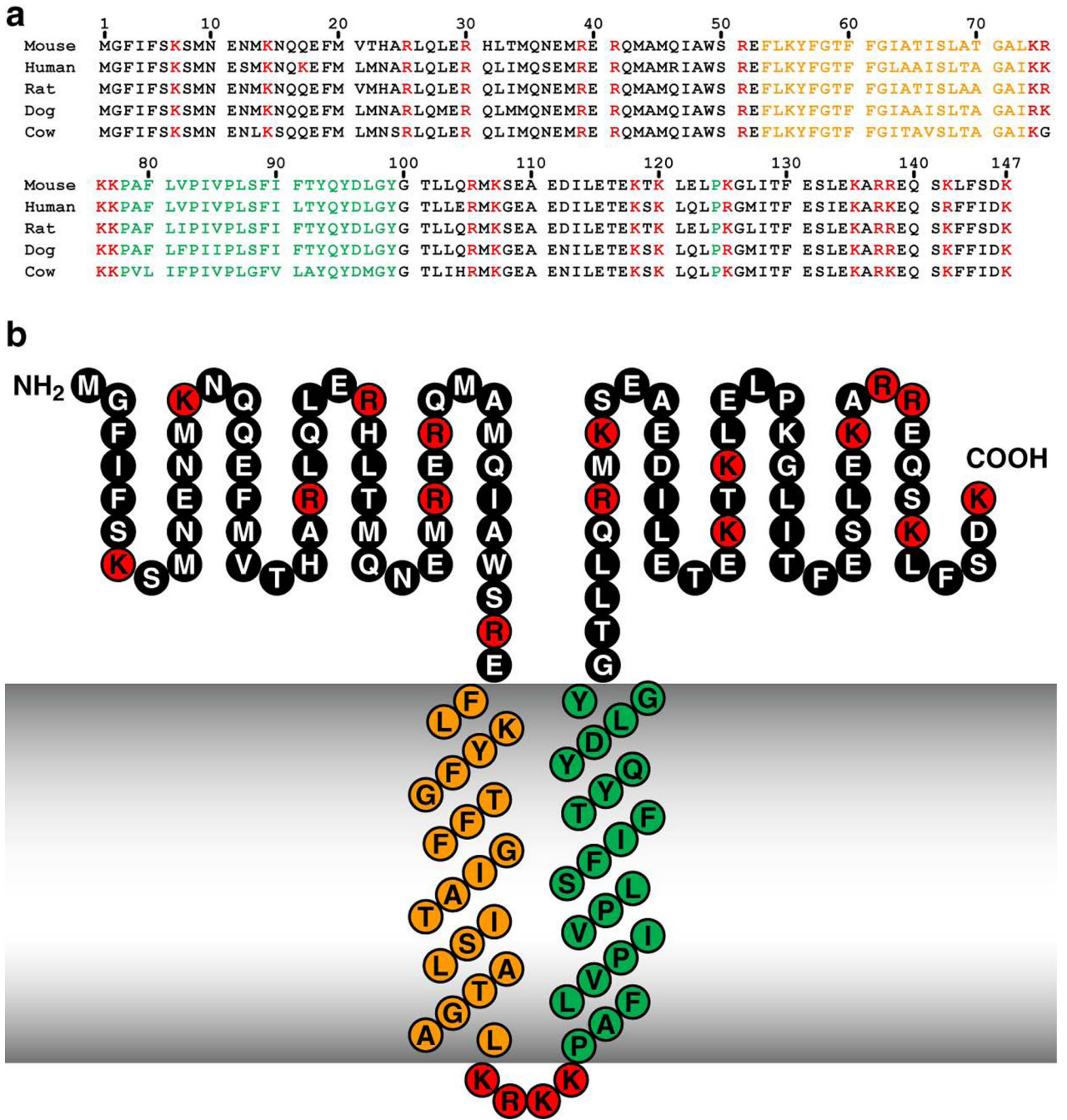


Figure 1. Alignment of predicted amino acid sequences of mouse, human, rat, dog and cow orthologs of Plg-R_{KT} (a) and the structural model of Plg-R_{KT} (b) show high interspecies sequence homology

Green indicates amino acids within the predicted primary transmembrane helix. Orange indicates amino acids within the predicted secondary transmembrane helix. Red indicates basic amino acids. This research was originally published in *Blood*, Andronicos, N.M., Chen, E.I., Baik, N., Bai, H., Parmer, C.M., Kiosses, W.B., Kamps, M.P., Yates, J.R., III, Parmer, R.J., Miles, L.A., Proteomics-based discovery of a novel, structurally unique, and developmentally regulated plasminogen receptor, Plg-R_{KT}, a major regulator of cell surface plasminogen activation, *Blood*. 2010, 115: 1319–30. © the American Society of Hematology.