

Overview of the Matrisome—An Inventory of Extracellular Matrix Constituents and Functions

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Completion of genome sequences for many organisms allows a reasonably complete definition of the complement of extracellular matrix (ECM) proteins. In mammals this “core matrisome” comprises ~300 proteins. In addition there are large numbers of ECM-modifying enzymes, ECM-binding growth factors, and other ECM-associated proteins. These different categories of ECM and ECM-associated proteins cooperate to assemble and remodel extracellular matrices and bind to cells through ECM receptors. Together with receptors for ECM-bound growth factors, they provide multiple inputs into cells to control survival, proliferation, differentiation, shape, polarity, and motility of cells. The evolution of ECM proteins was key in the transition to multicellularity, the arrangement of cells into tissue layers, and the elaboration of novel structures during vertebrate evolution. This key role of ECM is reflected in the diversity of ECM proteins and the modular domain structures of ECM proteins both allow their multiple interactions and, during evolution, development of novel protein architectures.

The term extracellular matrix (ECM) means somewhat different things to different people (Hay 1981, 1991; Mecham 2011). Light and electron microscopy show that extracellular matrices are widespread in metazoa, underlying and surrounding many cells, and comprising distinct morphological arrangements. The initial biochemical studies on extracellular matrix concentrated on large, structural extracellular matrices such as cartilage and bone. In the 1980s, the availability of model systems such as the Engelbreth-Holm-Swarm (EHS) sarcoma opened the way to biochemical analyses of basement membranes and led to the discovery of the different group of ECM proteins that

make up basement membranes. Biochemistry of native ECM was, and still is, impeded by the fact that the ECM is, by its very nature, insoluble and is frequently cross-linked. Furthermore, ECM proteins tend to be large, and early work was frequently on proteolytic fragments. The application of molecular biology to studies of ECM proteins and their genes uncovered many previously unknown ECM molecules and defined their structures. The protein chemistry and molecular biology revealed that ECM proteins are typically made up of repeated domains, often encoded in the genome as separate exonic units. The completion of the sequences of many genomes now

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allows description of the entire list of proteins and, potentially, the definition of the complete repertoire of ECM proteins, based on homologies with known ECM proteins. Comparative analyses of the genomes of different organisms allow deductions about the evolution of this repertoire, which we term the matrisome. Newer methods such as mass spectrometry are also beginning to allow more detailed biochemical characterization of extracellular matrices. In this article, we will give an overview of the mammalian matrisome and briefly discuss certain aspects of the evolution of the matrisome and of the ECM.

DEFINITION OF THE MATRISOME

In analyzing the structure and functions of extracellular matrices, one would like to have a complete “parts list”—a list of all the proteins in any given matrix and a larger list of all the proteins that can contribute to matrices in different situations (the “matrisome”). As mentioned, the biochemistry of ECM is challenging because of the insolubility of most ECMs. However, the availability of complete genome sequences coupled with our accumulated knowledge about ECM proteins now makes it possible to come up with a reasonably complete list of ECM proteins. ECM proteins typically contain repeats of a characteristic set of domains (see figures and Table 1) (LamG, TSPN, FN3, VWA, Ig, EGF, collagen prodomains, etc.). Many of these domains are not unique to ECM proteins but their arrangements are highly characteristic. That is, the architecture of ECM proteins is diagnostic—they are built from assemblies of many ancient, and a few more recent, protein domains, each of which is typically encoded by one or a few exons in the genome. ECM proteins represent one of the earliest recognized and most elaborate examples of exon (domain) shuffling during evolution (Engel 1996; Patthy 1999; Hohenester and Engel 2002; Whittaker et al. 2006; Adams and Engel 2007). This characteristic of ECM proteins allows bioinformatic sweeps of the proteome encoded by any given genome, using a list of 50 or so domains to identify a list of

candidate ECM proteins. Negative sweeps of that list using domains from other protein families (e.g, tyrosine kinases, which share FN3 and Ig domains with ECM proteins) and screens for transmembrane domains allow refinement of the list. A very few known ECM proteins do not have readily recognizable domains (e.g., elastin, dermatopontin, and some dentin matrix proteins) although, increasingly, even those are now being incorporated into protein analysis sites such as SMART and InterPro, allowing their routine capture in the sweeps. Using such methods plus manual annotation, we have been able to define a robust list of the proteins defining the mammalian matrisome by analysis of the human and mouse genomes (Naba et al. 2011). We call this list of “core” ECM proteins the core matrisome. It comprises 1%–1.5% of the mammalian proteome (without considering the contribution of alternatively spliced isoforms (prevalent in transcripts of matrisome genes). This list comprises almost 300 proteins, including 43 collagen subunits, three dozen or so proteoglycans, and around 200 glycoproteins.

This core matrisome list does not include mucins, secreted C-type lectins, galectins, semaphorins, and plexins and certain other groups of proteins that plausibly do associate with the ECM but are not commonly viewed as ECM proteins; lists of these “ECM-affiliated” proteins are given in Naba et al. (2011). The core matrisome list also does not include ECM-modifying enzymes, such as proteases, or enzymes involved in cross-linking, or growth factors and cytokines, although these are well known to bind to ECMs (see below).

Two useful databases provide information on the expression and distribution of various ECM proteins (<http://www.matrixome.com/bm/Home/home/home.asp>, The Matrixome Project, maintained by Kiyotoshi Sekiguchi and <http://www.proteinatlas.org/>; Human Protein Atlas) (Ponten et al. 2008; Uhlen et al. 2010). A third database (MatrixDB, <http://matrixdb.ibcp.fr/>) (Chautard et al. 2009, 2010) collates information about interactions among ECM proteins.

COLLAGENS

Collagens are found in all metazoa and provide structural strength to all forms of extracellular matrices, including the strong fibers of tendons, the organic matrices of bones and cartilages, the laminar sheets of basement membranes, the viscous matrix of the vitreous humor, and the interstitial ECMs of the dermis and of capsules around organs. Collagens are typified by the presence of repeats of the triplet Gly-X-Y, where X is frequently proline and Y is frequently 4-hydroxyproline. This repeating structure forms stable, rodlike, trimeric, coiled coils, which can be of varying lengths. A primordial collagen exon encoded six of these triplets (18 amino acids) encoded in 54 base pairs and, during evolution, this original motif has been duplicated, modified, and incorporated into many genes (Fig. 1A). Collagen subunits assemble as homotrimers or as restricted sets of heterotrimers

and, in general, collagen subunits are very restricted in the partnerships they can form, although occasional promiscuity has been noted (for more details, see Ricard-Blum 2011; Yurchenco 2011).

Some of these genes are viewed as collagens, *sensu stricto*, whereas others that contain only short collagen segments are often referred to as “collagen-like” or “collagen-related.” The distinction is to some extent arbitrary because many proteins viewed as “true” collagens also contain significant portions made up of other domains. The original type I collagen of bones and tendons consists almost entirely of a long (~1000 amino acids) and rigid uninterrupted collagen triple helix (plus terminal noncollagenous prodomains that are removed during biosynthetic processing of the protein; Fig. 1A). The rodlike trimers assemble into higher-order oligomers and fibrils and become cross-linked by various enzymatic and nonenzymatic

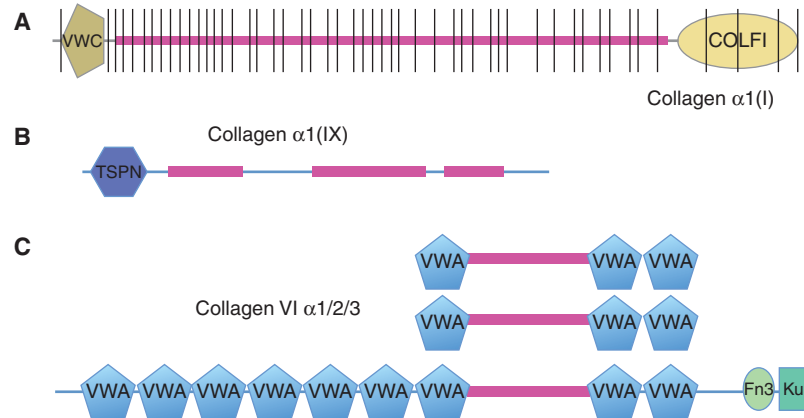


Figure 1. Examples of collagen structures. (A) Collagen I is a fibrillar collagen with a continuous collagen domain of around 1000 amino acids (fuchsia) comprising Gly-X-Y repeats that form a triple helix. It is encoded by multiple exons (note vertical lines) that are variants of a primordial exon encoding six such repeats. The collagen domain is flanked by amino- and carboxy-terminal noncollagenous domains that are removed by proteolysis to allow fibrillogenesis of the mature collagen. The VWC domain in this and other fibrillar collagens can be alternatively spliced and binds bone morphogenetic proteins (BMPs). (B) Collagen IX is a FACIT collagen (fibril-associated collagen with interrupted triple helix); the interruptions in the collagen domain allow bending. This and other FACIT collagens associate with fibrillar collagens and their amino-terminal domains extend out from the fibrils and presumably function as protein-binding domains. (C) Collagen VI is a heterotrimer of three related subunits, one of which is much longer and forms globular heads at each end. VWA domains are commonly protein-binding domains and probably allow interactions with other proteins during the formation of short fibrils by collagen VI.

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reactions conferring considerable structural strength. Several other collagens with similar fibrillar structure are found in various tissues. Many other collagen types have interruptions in the Gly-X-Y repeating structure, introducing flexibility into the molecules. All collagen genes also encode additional noncollagenous domains, some of which are the characteristic collagen N and C prodomains, whereas others are domains shared with other ECM proteins and retained in the mature proteins (Fig. 1B,C). These additional protein domains confer specific binding affinities, allowing collagen molecules to interact with each other and with other proteins to assemble the various structures. The diversity of collagen structures, genes, and assemblies is discussed by Ricard-Blum (2011) and the assembly of type IV collagen into the laminar structure of basement membranes is reviewed by Yurchenco (2011). Other reviews of the collagen family cover additional aspects (Eyre and Wu 2005; Robins 2007; Gordon and Hahn 2009).

Among the collagen-like or collagen-related proteins (see table in Ricard-Blum 2011), a few are membrane proteins; others, such as complement component C1q and related proteins are secreted but their main functions do not involve ECM and they are not considered as part of the ECM or matrisome; yet others, such as the collagen-like domain of acetylcholinesterase, serve to anchor other proteins into the ECM, and some, such as EMIDs, are true ECM proteins. It is worth keeping in mind the possibility that the presence of collagen-like domains could act to bind some of these non-ECM proteins to the ECM, at least part of the time; in that sense they are ECM-associated.

PROTEOGLYCANS

Proteoglycans are interspersed among the collagen fibrils in different ECMs. Rather than providing structural strength, they confer additional properties. Proteoglycans are glycoproteins with attached glycosaminoglycans (GAGs; repeating polymers of disaccharides with carboxyl and sulfate groups appended). The addition of GAGs confers on proteoglycans

a high negative charge, leading them to be extended in conformation and able to sequester both water and divalent cations such as calcium. These properties confer space-filling and lubrication functions. GAGs, especially heparan sulfates, also bind many secreted and growth factors into the ECM (see Sarrazin et al. 2011 for more details).

There are around three dozen extracellular matrix proteoglycans encoded in mammalian genomes; they fall into several families (Table 1) (see also Iozzo and Murdoch 1996). The two largest are those based on LRR repeats (Merline et al. 2009; Schaefer and Schaefer 2010) and those containing LINK and C-type lectin domains (hyalectans). Many of the LRR proteoglycans bind to various collagens and to growth factors and the hyalectan family members bind to various ECM glycoproteins such as tenascins, and through the LINK domain, to hyaluronic acid. These binding functions contribute to regulation of protein complexes in the ECM.

In addition, there are around a dozen proteoglycans that do not fall into these two families (e.g., lubricin/PRG4, endocan/ESM1, serglycin, and three testicans related to SPARC/osteonectin; see Table 1). Perhaps the most significant of all is perlecan (HSPG2), a multidomain protein that is a core proteoglycan of all basement membranes (see Table 1 and below). There are also many examples of proteins falling into other categories (e.g., some collagens, agrin, betaglycan, CD44, and other glycoproteins) that are sometimes or always modified by attachment of GAGs, which could lead one to consider them also as proteoglycans. The boundary between proteoglycans and glycoproteins is thus somewhat a matter of definition. The consensus view is to consider as proteoglycans those that have a significant fraction of their total mass made up by GAGs.

There are also two small families of integral membrane proteoglycans: glypicans (Filmus et al. 2008) and syndecans (Couchman 2010; Xian et al. 2010), both of which bear heparan sulfate side chains as does CD44, and there are a few additional transmembrane chondroitin sulfate proteoglycans. Further details of structure and functions of various heparan sulfate

Table 1. Extracellular matrix proteoglycans

GENE NAME	COMMON NAME(S)	DOMAINS	GAGs	
HSPG2	heparan sulfate proteoglycan 2/ perlecan	complex	HS/CS	
ASPN	asporin	LRR	maybe none	
BGN	biglycan	LRR	CS/DS	
DCN	decorin	LRR	CS/DS	
FMOD	fibromodulin	LRR	KS	
KERA	keratocan	LRR	KS	
LUM	lumican	LRR	KS	
OMD	osteo-modulin/osteo-adherin	LRR	KS	
PRELP	PRELP/prolargin (pro/arg-end/leu-rich repeat protein)	LRR	KS ??	
EPYC	epiphycean	LRR	CS/DS	
OGN	osteo-glycin/mimecan	LRR	KS	
OPTC	opticon	LRR	??	
CHAD	chondroadherin	LRR	maybe none	
CHADL	chondroadherin-like	LRR	maybe none	
NYX	nyctalopin (probably GPI-linked)	LRR	maybe none	
NEPNP	nephrocan (pseudogene in human)	LRR	maybe none	
PODN	podocan	LRR	maybe none	
PODNL1	podocan-like 1	LRR	maybe none	
ACAN	aggrecan	LINK/CLEC/CCP	CS/KS	
BCAN	brevican	LINK/CLEC/CCP	CS	
NCAN	neurocan	LINK/CLEC/CCP	CS	
VCAN	versican	LINK/CLEC/CCP	CS/DS	
HAPLN1	hyaluronan and proteoglycan link protein 1	LINK		
HAPLN2	hyaluronan and proteoglycan link protein 2	LINK		
HAPLN3	hyaluronan and proteoglycan link protein 3	LINK		
HAPLN4	hyaluronan and proteoglycan link protein 4	LINK		
PRG2	proteoglycan 2, bone marrow PG	CLEC		
PRG3	proteoglycan 3	CLEC		
SPOCK1	testican 1	SPARC, Kazal, TY	CS/KS	
SPOCK2	testican 2	SPARC, Kazal, TY	CS/KS	
SPOCK3	testican 3	SPARC, Kazal, TY	CS/KS	
PRG4	proteoglycan 4/lubricin	SO/HX	maybe none	
SRGN	serglycin		HS/CS	
IMP1	interphothoreceptor matrix proteoglycan 1	SEA domain	CS	
IMP2	interphothoreceptor matrix proteoglycan 2	SEA domain	CS	
ESM1	endocan/endothelial cell-specific molecule 1	IB domain	CS/DS	

Table lists known ECM proteoglycans and shows representative domain structures.

There are five subfamilies of small leucine-rich repeat (LRR) proteoglycans based on sequence homologies (Merline et al. 2009; Schaefer and Schaefer 2010)—A representative structure is shown for one member (bold) from each subfamily. LRR repeat regions in other proteins are involved in protein–protein interactions.

The hyalectans (aggrecan, brevican, neurocan, and versican) all share a similar structure with Ig-LINK-LINK at their amino terminus and EGF(1 or 2)-CLEC-CCP at their carboxyl terminus with variable lengths of sequence between these two sets of domains. The central intervening sequence bears the GAG side chains and is almost 2000 amino acids long in aggrecan, and in versican it varies from a few to almost 2700 amino acids through alternative splicing. The LINK domains in both hyalectans and in the four link proteins bind to hyaluronan with nanomolar affinity and the EGF-CLEC-CCP cluster, which is similar to that in selectins, binds carbohydrates.

The domain structures were extracted from the SMART database (<http://smart.embl-heidelberg.de>). The domain structure of perlecan, the major proteoglycan of basement membranes, includes multiple domains in N—C order (SEA, LDLa, Ig, LamB, EGF, Ig, LamG, EGF). The glycosaminoglycan (GAG) content of each proteoglycan is based on the reviews cited above (HS, heparan sulfate; CS, chondroitin sulfate; DS, dermatan sulfate; KS, keratan sulfate).

proteoglycans are discussed by Bishop et al. (2007) and Sarrazin et al. (2011).

GLYCOPROTEINS

In addition to the collagens and proteoglycans that provide strength and space-filling functions (among others), there are around 200 complex

glycoproteins in the mammalian matrisome (see Table 2 and Naba et al. 2011). These confer myriad functions including interactions allowing ECM assembly, domains and motifs promoting cell adhesion, and also signaling into cells and other domains that bind growth factors. The bound growth factors can serve as reservoirs that can be released (e.g., by proteolysis)



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Table 2. Extracellular matrix glycoproteins

Gene name	Protein names and synonyms
	Basement membrane components
Lama1-5	5 Laminin alpha subunits
Lamb1-4	3 Laminin beta subunits
Lamc1-3	3 Laminin gamma subunits
Nid1/2	2 Nidogens
Colq	Collagen-like tail subunit of asymmetric acetylcholinesterase
	Major known ECM glycoproteins
Eln	Elastin
Emilin1-3	3 Emilins, elastin microfibril interfacers
Emid1/2	2 EMI domain-containing proteins
Fbln1/2/5/7	4 Fibulins
Efemp 1/2	Fibulins 3 and 4
Fbn1/2	2 Fibrillins
Fn1	Fibronectin
Fras1	Fraser syndrome 1 homolog
Gldn	Gliomedin
Hmnc1/2	Hemicentins 1 and 2
Ibsp	Integrin-binding sialoprotein, BSP
Matn1-4	4 Matrilin proteins
Mfap1a/b - 5	6 Microfibrillar-associated proteins
Mmrn1 and 2	2 Multimerins
Npnt	Nephronectin
Papln	Papilin, proteoglycan-like sulfated glycoprotein
Postn	Periostin, osteoblast-specific factor
Sparc/Sparcl1	Secreted acidic cysteine-rich glycoproteins SPARC and SPARC-like
Spp1/SrpX	2 Secreted phosphoprotein 1, osteopontin
Tnc/n/r/x	4–5 Tenascins
Thbs1-4	4 Thrombospondins—see also COMP/TSP5
Comp/TSP5	Cartilage oligomeric matrix protein (thrombospondin 5)
	Nervous system-enriched ECM proteins
Agrn	Agrin
Coch	Cochlin
Ntn1-5	4 Netrins
Ntng1/g2	Netrins G1/G2
Reln	Reelin
Slit1-3	3 Slit homologs
Sspo	SCO-spondin
Tecta/b	Tectorins α and β
	Vascular ECM proteins
Fga/b/g	Fibrinogen $\alpha/\beta/\gamma$ chains
Vtn	Vitronectin
Vwf	von Willebrand factor
	ECM proteins of bones, cartilage, and teeth
Ambn	Ameloblastin
Amelx	Amelogenin X chromosome
Bglap2	Bone γ -carboxyglutamate protein 2
Bglap-rs1	Bone γ -carboxyglutamate protein-related sequence 1
Cilp	Cartilage intermediate-layer protein, nucleotide pyrophosphohydrolase
Cilp2	Cartilage intermediate-layer protein 2
Dmp1	Dentin matrix protein 1
Dpt	Dermatopontin
Dspp	Dentin sialophosphoprotein
Mgp	Matrix Gla protein
	CCN family proteins
Cyr61	Cysteine rich protein 61, CCN1
Ctgf	Connective tissue growth factor, CCN2
Nov	Nephroblastoma overexpressed gene, CCN3
Wisp1-3	3 WNT1 inducible signaling pathway proteins, CCN4-6
	Growth-factor-binding proteins
Bmper	BMP-binding endothelial regulator
Igfals	Insulin-like growth-factor-binding protein, acid labile subunit
Igfbp1-7	7 Insulin-like growth-factor-binding proteins
Igfbpl1	Insulin-like growth-factor-binding protein-like 1
Kcp	Kielin/chordin-like protein
Ltbp1-4	4 Latent transforming growth-factor β -binding proteins

Continued

Table 2. Continued

Gene name	Protein names and synonyms
	Other possible ECM proteins
Abi3bp	ABI gene family, member 3 (NESH)-binding protein
Adipoq	Adiponectin, C1Q, and collagen domain-containing protein
Aebp1	AE-binding protein 1
Bsph1	Binder of sperm protein homolog 1
Cdcp2	CUB domain-containing protein 2
Creld1/2	Cysteine-rich with EGF-like domains 1 and 2
Crim1	Cysteine-rich transmembrane BMP regulator 1 (chordin like)
Crispld1/2	Cysteine-rich secretory protein LCCL domain-containing 1 and 2
Cthrc1	Collagen triple helix repeat containing 1
Ddx26b	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B
Dmbt1	Deleted in malignant brain tumors 1
Ecm1	Extracellular matrix protein 1
Ecm2	Extracellular matrix protein 2, female organ, and adipocyte specific
Edil3	EGF-like repeats and discoidin I-like domains 3
Egflam	EGF-like, fibronectin type III, and laminin G domains
Fgl1/2	Fibrinogen-like proteins 1 and 2
Fndc1/7/8	3 Fibronectin type III domain-containing proteins
Gas6	Growth arrest specific 6
Igsf10	Immunoglobulin superfamily, member 10
Lgi1-4	4 Leucine-rich repeat LGI family proteins
Lrg1	Leucine-rich α -2-glycoprotein 1
Mepe	Matrix extracellular phosphoglycoprotein with ASARM motif
Mfge8	Milk fat globule-EGF factor 8 protein
Nell1/2	NEL-like 1 and 2
Oit3	Oncoprotein-induced transcript 3
Otog	Otogelin
Pcolce/Pcolce2	2 Procollagen C-endopeptidase enhancer proteins
Pxdn	Peroxidasin homolog
Rspo1-4	4 R-spondin homologs
Slamf6	SLAM family member 6
Smoc1	SPARC-related modular calcium-binding proteins 1 and 2
Sned1	Sushi, nidogen, and EGF-like domains 1
Spon1	Spondin 1, (f-spondin) extracellular matrix protein
Spon2	Spondin 2, extracellular matrix protein
Srpx2	Sushi-repeat-containing protein, X-linked 2
Svep1	Sushi, von Willebrand factor type A, EGF, and pentraxin domain-containing 1
Tgfb1	Transforming growth factor β -induced
Thsd4	Thrombospondin type 1 domain-containing 4
Tinag/Tinag1	Tubulointerstitial nephritis antigen/tubulointerstitial nephritis antigen-like 1
Tnfaip6	Tumor necrosis factor α -induced protein 6
Tsku	Tsukushin
Vit	Vitrin
Vwa1-5	5 von Willebrand factor A domain-containing proteins
Vwc2/21/e	3 von Willebrand factor C domain-containing proteins
Vwd/E	2 von Willebrand factor D and EGF domain proteins
Zp1-4	4 Zona pellucida glycoproteins
Zp3r	Zona pellucida 3 receptor
Zpld1	Zona pellucida-like domain-containing 1
	Novel predicted ECM proteins
2010321M09Rik	RIKEN cDNA 2010321M09 gene
5430419D17Rik	RIKEN cDNA 5430419D17 gene
6130401L20Rik	RIKEN cDNA 6130401L20 gene
9230107M04Rik	RIKEN cDNA 9230107M04 gene
A930038C07Rik	RIKEN cDNA A930038C07 gene
AW551984	Expressed sequence AW551984
C330046G03Rik	RIKEN cDNA C330046G03 gene
D17H6S56E-3	DNA segment, Chr 17, human D6S56E 3
Gm106	Predicted gene 106
Gm414	Predicted gene 414
Gm6924	Predicted gene 6924

Table lists known and predicted ECM glycoproteins other than collagens and proteoglycans, defined largely by their characteristic domain content. The table is split into rough categories—individual glycoproteins are listed in only a single category although many could be listed under more than one. The first page lists glycoproteins about which a significant amount is known; the second page lists glycoproteins about which relatively little to nothing has been reported concerning their role in the ECM.

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or can be presented as solid-phase ligands by the ECM proteins (Hynes 2009).

The best-studied ECM glycoproteins are the laminins (11 genes; 5 α , 3 β , 3 γ) and fibronectins (1 gene encoding multiple splice isoforms). These are reviewed in detail by Aumailley et al. (2005) and Yurchenco (2011) and by Schwarzbauer and DeSimone (2011), respectively. Also well studied are the thrombospondins and tenascins, reviewed by Bentley and Adams (2010) and Adams and Lawler (2011) and by Chiquet-Ehrismann and Turner (2011), respectively. The structures of these glycoproteins are well known and exemplify the typical multiple repeating domain structure and extended multimeric forms of ECM proteins (Fig. 2). The same is true for fibulins (de Vega et al. 2009) and nidogens (Ho et al. 2008; Yurchenco 2011) and many others. Two subgroups of ECM glycoproteins have been studied particularly in the context of the nervous system (netrins, slits, reelin, agrin, SCO-spondin—see article by Barros et al. [2011] and Fig. 3) and the hemostatic system (von Willebrand factor, vitronectin, and fibrinogen—a facultative ECM protein) (Bergmeier et al. 2008; Bergmeier and Hynes 2011). These two biological systems also involve roles for more widely distributed ECM proteins such as thrombospondins, fibronectins, laminins, collagens, proteoglycans, etc. Similarly, the matrices of other tissues typically contain both ubiquitous and tissue-restricted ECM glycoproteins. Another group of ECM glycoproteins that has been studied in the context of disease and the regulation of transforming growth factor beta (TGF- β) functions includes the fibrillins and LTBP (Ramirez and Dietz 2009; Ramirez and Rifkin 2009; see article by Munger and Sheppard 2011).

However, as can be seen in Table 2, there are multiple other ECM glycoproteins about which much less (in some cases, almost nothing) is known. These include some enormous glycoproteins with impressive arrays of domains, such as SCO-spondin (59 domains of seven types) and hemicentin-1, also known as fibulin-6 (61 domains of six types), and many that are affected in disease (Aszódi et al. 2006; Nelson and Bissell 2006; Bateman et al. 2009). It

will be of considerable interest to learn the distributions and functions of this diverse set of ECM glycoproteins and we can expect that the approaches that have been effective for the better-studied proteins will provide many insights into the roles of those less well known and novel.

ECM-BOUND GROWTH AND SECRETED FACTORS

As mentioned above and elsewhere (Hynes 2009; Ramirez and Rifkin 2009; Rozario and DeSimone 2010), many growth factors bind to ECM proteins and must be considered also as constituents of extracellular matrices. One popular idea is that growth and other secreted factors bind to GAGs, especially heparan sulfates. Although this is undoubtedly true, there are clear examples of growth factors binding to specific domains of ECM proteins. Fibronectin binds specifically to a variety of growth factors (VEGF, HGF, PDGF, etc.; Rahman et al. 2005; Wijelath et al. 2006; Lin et al. 2010) and the VWC/chordin and follistatin domains found in many ECM proteins (see Figs. 1–3) are known to bind BMPs (Wang et al. 2008; Banyai et al. 2010). TGF binds specifically to TB domains in LTBP, which bind in turn to fibrillins and to fibronectin-rich matrices (Ramirez and Rifkin 2009; Munger and Sheppard 2011). These ECM-TGF interactions have significant consequences for genetic diseases; mutations in fibrillins affect the regulation of TGF- β function in Marfan's syndrome and in other diseases (Ramirez and Dietz 2009).

It seems virtually certain that the known examples of growth factor binding to ECM, including directly to ECM proteins, presage many more such cases, and this aspect of ECM function is in great need of further investigation. The ECM can act as a reservoir or sink of such factors and there are many examples of this for chemokines and for many of the most important developmental signals (e.g., VEGFs, Wnts, Hhs, BMPs, and FGFs). Such factors form gradients that control pattern formation during developmental processes and it is clear that some of those gradients are markedly

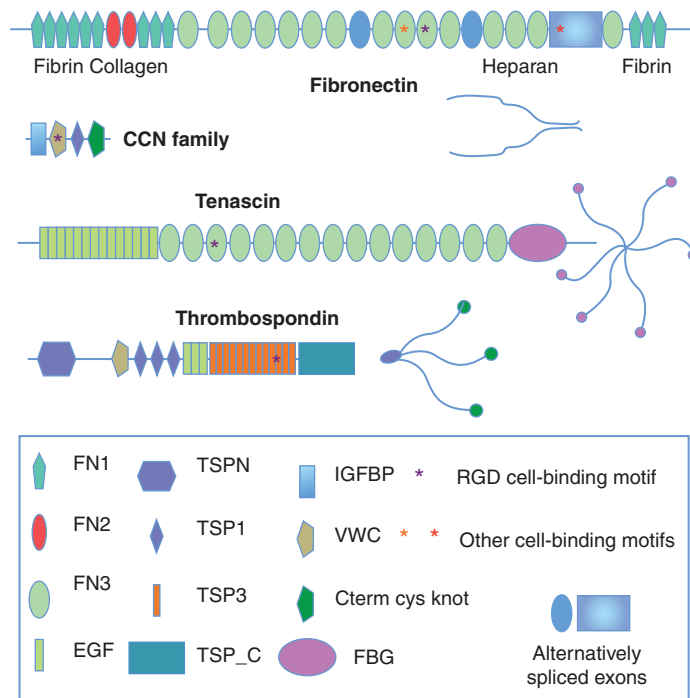


Figure 2. Examples of characteristic ECM glycoprotein structures. Note the multidomain structure of these ECM glycoproteins. Each domain is typically encoded by a single exon or a small set of exons. This has allowed shuffling of domains into different combinations during evolution. Individual domains are specialized for binding different proteins, as indicated for fibronectin. Some domains are alternatively spliced, as noted for fibronectin, and is also true for tenascin (not shown). Cell-binding motifs such as RGD and LGV are indicated by asterisks. Fibronectin dimerizes through disulfide bonding at the carboxyl terminus, whereas thrombospondin and tenascin form trimers and hexamers, respectively, through coiled coil domains and disulfide bonds near the amino terminus. The appearances of the intact protein multimers (as would be seen by electron microscopy) are diagrammed. Note that growth factor-binding domains (IGFBP, VWC, and others) are included in many ECM proteins. CYR61 is shown as a representative member of the CCN family (see Table 2), small ECM proteins that contain integrin-binding motifs and growth-factor-binding domains (IGFBP and VWC) and are known to regulate growth factor functions (Chen and Lau 2009) as are the larger proteins shown.

affected by ECM binding (Yan and Lin 2009). Indeed, it seems probable that many more gradients incorporate ECM binding as part of their regulation. Investigation of this concept will be greatly aided by our current fairly complete inventory of ECM proteins and their constituent domains.

MODIFIERS OF ECM STRUCTURE AND FUNCTION

Another aspect of ECM function is that ECM proteins and the fibrils into which they assemble are subsequently often significantly modified.

Collagens have long been known to become cross-linked by disulfide bonding, transglutaminase cross-linking, and through the action of lysyl oxidases and hydroxylases (Eyre and Wu 2005; Robins 2007; Ricard-Blum 2011). Laminins and other basement membrane proteins also become cross-linked by disulfide bonding (see Yurchenco 2011 for further details) and the same is true of fibronectin, which also undergoes further processing to a state characterized by insolubility in deoxycholate (DOC) (Choi and Hynes 1979; Schwarzbauer and DeSimone 2011). The exact basis for this insolubility is not known, but

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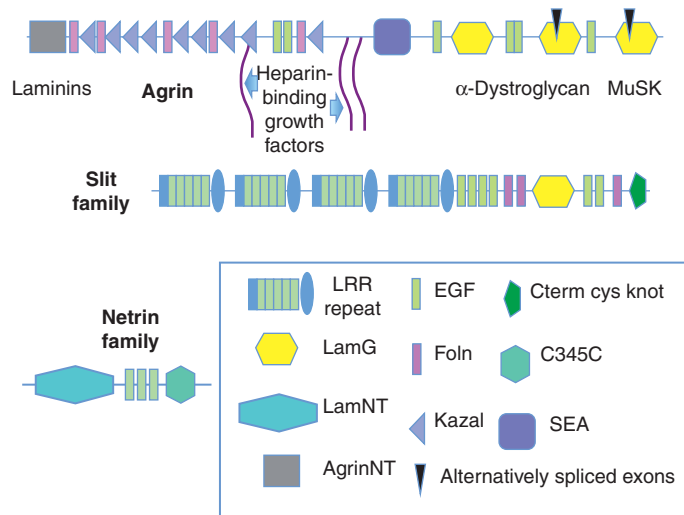


Figure 3. Glycoproteins with special roles in the nervous system. These three proteins are involved in synapse formation (Agrin) and in axonal guidance (Slits and Netrins). Sites for binding other ECM proteins (laminins), growth factors, and cell-surface receptors (α -dystroglycan and MuSK) are indicated for agrin. Slit also contains known GF-binding domains (Foln). Agrin has two small alternatively spliced exons that markedly affect its functions, a characteristic of many ECM proteins. Unlike many ECM proteins, the major receptors for these three proteins are not integrins. Slit family proteins bind to Robo receptors, whereas Netrins bind to Unc5 and DCC receptors. The functions of these ECM-receptor pairs in the CNS are discussed in Barros et al. (2011) but they also function in other aspects of cell and tissue pattern regulation during development. They are evolutionarily ancient and are conserved in all bilateral phyla.

fibronectin and other ECM proteins are also substrates for transglutaminase 2, which undoubtedly contributes to the insolubility of ECM (Lorand and Graham 2003; Iismaa et al. 2009).

Proteolytic enzymes also modify the ECM—indeed, procollagen propeptidases are necessary to process collagens so that they can polymerize. Collagens and other ECM proteins are also substrates for matrix metalloproteases (MMPs) (Page-McCaw et al. 2007; Cawston and Young 2010), ADAMs (Murphy 2008) and ADAMTS proteases (Porter et al. 2005; Apte 2009), and many other proteolytic enzymes (elastases, cathepsins, various serine esterase proteases, etc.) can also act on many ECM proteins (see article by Lu et al. 2011). These various proteolytic processes play roles in ECM turnover and are thought to release ECM-bound growth factors and also to expose cryptic activities in the ECM (Mott and Werb 2004; Ricard-Blum 2011), including the release

of antiangiogenic inhibitors (Bix and Iozzo 2005; Nyberg et al. 2005; Hynes 2007). Similarly, enzymes that degrade GAGs, such as heparanases and sulfatases, can also alter the properties of ECM proteoglycans (see articles by Lu et al. 2011; Sarrazin et al. 2011). The remodeling of ECM by these various processes has major effects on development and pathology (Daley et al. 2008; Kessenbrock et al. 2010; Lu et al. 2011). Lists of these ECM-modifying enzymes can be found in the reviews cited and in Naba et al. (2011).

CELLULAR RECEPTORS FOR EXTRACELLULAR MATRIX

For the ECM to affect cellular functions, it is obvious that there must be receptors for ECM proteins. The major receptors are the integrin family, comprising 24 $\alpha\beta$ heterodimers (Fig. 4). These have been extensively reviewed elsewhere and specific aspects are covered in

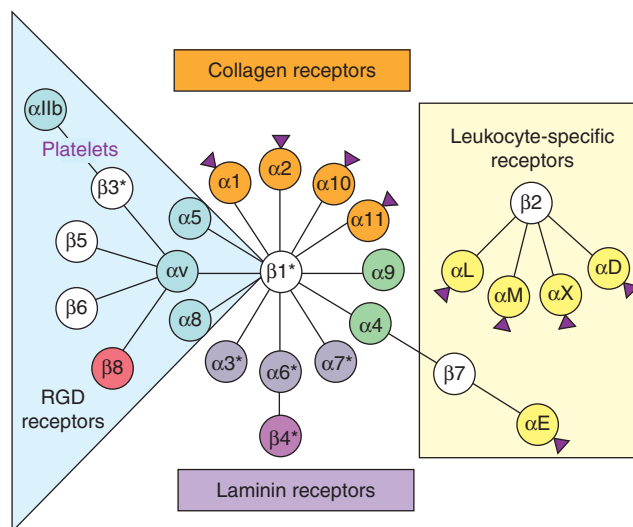


Figure 4. Integrin receptors for ECM proteins. The diversity of integrin subunits and their interactions. Shown are the mammalian integrins, separated by color coding into subsets of closely related subunits. The RGD-binding (blue) and laminin-binding (purple) subclasses are evolutionarily very ancient and found in all metazoan phyla, but they have diverged into clades in the vertebrate lineage. The $\alpha 4/\alpha 9$ clade (green) is vertebrate-specific. Two subclasses of chordate α subunits have inserted I domains (purple arrowheads); they include collagen-specific integrins (orange) and a set of α subunits confined to leukocytes (yellow). Some subunits show alternatively spliced isoforms (*). The leukocyte integrins bind predominantly to cell-surface counter-receptors, whereas integrins containing either the $\beta 1$ or αv subunits bind predominantly to extracellular matrix (ECM) proteins, although within each class there are exceptions to these generalizations and it is worth noting that most integrins are capable of binding multiple ligands, and there are many others beyond those shown here (Humphries et al. 2006). Many, if not all, αv integrins are also capable of activating TGF- β . Most β subunits are highly related (white) and bind to talin and related proteins (Campbell and Humphries 2011; Wickström et al. 2011), whereas the $\beta 4$ subunit instead binds to intermediate filaments through specific linker proteins and the $\beta 8$ subunit binds to band 4.1 proteins instead of to talin. (figure modified from Hynes 2002).

other articles in this collection (Schwartz 2010; Campbell and Humphries 2011; Geiger and Yamada 2011; Huttenlocher and Horwitz 2011; Watt and Fujimura 2011; Wickström et al. 2011). Another receptor for ECM proteins is dystroglycan, which binds to laminin, agrin, and perlecan in basement membranes as well as to the transmembrane neuroligins (Barresi and Campbell 2006). Each of these dystroglycan ligands contains LamG domains, which bind to dystroglycan in a glycosylation-dependent manner (see Fig. 3), probably by binding carbohydrate side chains on dystroglycan. Mutations in dystroglycan or its associated proteins in the membrane or the cytoskeleton (or in laminin) can all produce various forms of muscular dystrophy, because of the loss of the

transmembrane connection to the basement membrane surrounding the muscle cells. Other cellular receptors for ECM include GPVI on platelets and the DDR (discoidin domain receptor) tyrosine-kinases, all of which are receptors for collagens (Leitinger and Hohenester 2007), the GPIb/V/IX complex, which forms a receptor for von Willebrand factor on platelets (Bergmeier et al. 2008; Bergmeier and Hynes 2011), and CD44, which binds to hyaluronan and is expressed on many cells. As noted in Figure 3, Slits bind to Robo receptors of the Ig superfamily and netrins bind to Unc5-related tyrosine-kinase receptors or to DCC, an Ig superfamily receptor, whereas agrin binds to the MuSK tyrosine-kinase receptor. Thus, although integrins comprise the dominant class of ECM

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receptors and are present on most cells, numerous other receptors for ECM proteins are expressed on specific cell types.

In addition to binding extracellular ligands, these ECM receptors provide transmembrane links to the cytoskeleton and to signal transduction pathways. The cytoplasmic domains of ECM receptors assemble large and dynamic complexes of proteins, which regulate cytoskeletal assembly and activate many signaling cascades within cells (Geiger and Yamada 2011). In the case of integrins, these submembranous complexes also regulate the extracellular affinity of the receptors (so-called “inside-out” signaling) and the same may be true of other classes of ECM receptors. It has become clear that the signaling functions of ECM adhesion receptors are at least as complicated as those of canonical growth factor receptors and that engagement of ECM receptors provides signals regulating cellular survival, proliferation, and differentiation as well as adhesive and physical connections involved in cell shape, organization, polarity, and motility.

EVOLUTION OF THE MATRISOME AND THE EXTRACELLULAR MATRIX

The ~300 proteins that make up the core matrisome in mammals are a mixture of very ancient proteins and some much newer ones (Fig. 5). Comparative analyses of the genomes of different taxa have revealed that some ECM proteins are shared by almost all metazoa, even simple organisms such as sponges, coelenterates, and cnidaria (Huxley-Jones et al. 2007; Ozbek et al. 2010). Most notable are the proteins that make up the core of basement membranes—type IV collagens (2 subunits), laminin (4 genes, 2 α , 1 β , and 1 γ), nidogen, and perlecan (1 gene each)—see Yurchenco 2011. We call this set of genes the basement membrane toolkit and it is found in all protostome and deuterostome genomes and must therefore have been present in the common ancestor of all bilateria (Hynes and Zhao 2000; Whittaker et al. 2006). Many, but not all, of these genes are also found in more primitive metazoan organisms such as cnidaria and sponges (Putnam et al. 2007;

Chapman et al. 2010; Srivasatava et al. 2010). It is plausible to argue that the evolution of multilayered organisms with their different cell layers separated by basement membranes was dependent on this basement membrane toolkit that has been maintained ever since. Fibrillar collagens are also found in early metazoa, including *Hydra* and sponges. Interestingly, another collagen, the paralog of collagens XV and XVIII is also ancient, being found in both protostomes and deuterostomes, although the key functions of this class of collagens are not fully understood. Most other collagens are later evolutionary developments, for example the cuticular collagens of *Caenorhabditis elegans* (Hutter et al. 2000) and the complex collagens with VWA and FN3 domains (see Fig. 1C and Ricard-Blum 2011) found in vertebrates. Also found in all bilateria are the neuronal guidance ECM proteins, netrins, slits, and agrin (Fig. 3).

One characteristic feature of the evolution of ECM proteins, as for other genes, is an increase in numbers of homologous genes as one ascends the tree of life (Fig. 5). Thus, mammals have six type IV collagen genes (see Ricard-Blum 2011), two nidogen genes, and 11 laminin genes (see Yurchenco 2011) that have arisen by gene duplications and subsequent divergence without altering the basic structures of the proteins. This diversification accompanies the diversification of basement membranes in vertebrates. Similar evolution by duplication and diversification from a primordial gene shared by all bilateria is seen in the case of thrombospondins (see Adams and Lawler 2011), although in this case the diversification has involved more extensive evolution of the domain architecture than is the case for the basement membrane toolkit. This suggests that thrombospondins have evolved to fulfill a more diverse set of functions, whereas basement membranes have retained many of their basic structure-function requirements during the more than half a billion years of their evolution.

Other ECM proteins, in contrast, are more recent developments. Two clear examples are tenascins and fibronectins (Tucker and Chiquet-Ehrismann 2009; Chiquet-Ehrismann and Tucker 2011). Both are restricted to chordates,

The Matrisome—An Overview of ECM Constituents

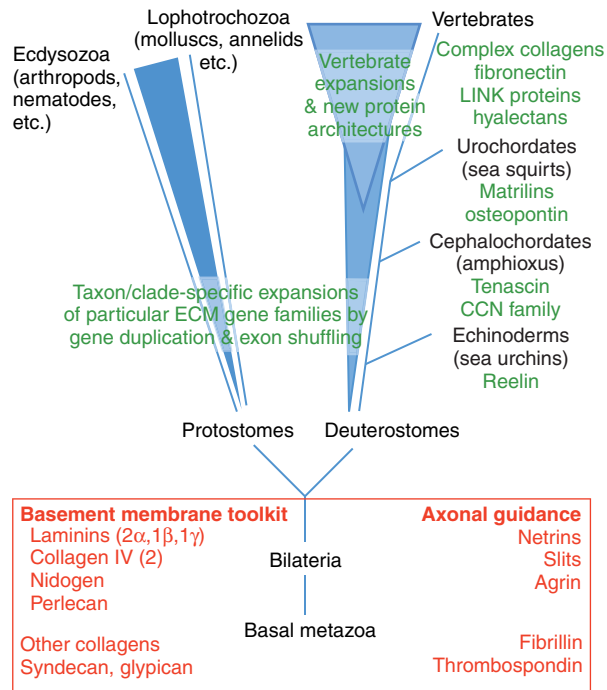


Figure 5. Evolution of ECM proteins. The figure outlines the main phylogenetic lineages (although the branch lengths are not drawn to scale), and illustrates the evolution of complexity of the matrisome and ECM during evolution. The inferred basal bilaterian had a core of ECM proteins including the basement membrane toolkit and some other ECM proteins (not all of which are shown) that have been retained in later-developing taxa, including the two main branches of metazoa (protostomes and deuterostomes). More primitive taxa had some, but not all, of these ECM proteins. During evolution of protostomes, there was modest expansion of the number of ECM genes/proteins mostly comprising taxon-specific expansions of ECM protein families by gene duplication and divergence, with some exon shuffling. A similar modest expansion occurred during evolution of the deuterostome lineage—first known acquisitions of novel ECM proteins of interest are noted in green. During evolution of the vertebrate subphylum, there was a major increase in ECM protein diversity, probably related to two whole genome duplications that occurred in that lineage. This expansion included expansion and diversification of preexisting ECM protein families, and also the development of novel protein architectures by shuffling of domains and the inclusion of novel domains (e.g., FN1, FN2, LINK). Some examples of such novel ECM proteins are indicated. As discussed in the text, this large expansion and diversification of the matrisome in vertebrates is presumably linked to novel structures such as neural crest and endothelial-lined vasculature as well as connective tissues such as cartilage, bones, and teeth, and also the development of more complex nervous and immune systems.

as are many of the more complex collagen genes. A tenascin gene is found in all the chordate genomes that have been sequenced and vertebrates have expanded the tenascin family. Tenascins represent a novel architectural assembly of preexisting domains (EGF and FN3; see Fig. 2). In contrast, fibronectin contains domains that do not appear until quite late in evolution; whereas FN3 domains are ancient, being found in cell-surface receptors in all

metazoa, FN1 and FN2 domains are restricted to chordates. The earliest fibronectin-like gene so far reported (although lacking the precise, characteristic domain organization of vertebrate fibronectin) appears in urochordates (ascidians, sea squirts) whereas vertebrates all have the canonical structure found in mammals (see Fig. 2) (Hynes 1990; Schwarzbauer and DeSimone 2011). Once assembled, this gene appears to have been strongly selected (it is

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essential for life) and has remained unchanged. Reelin, a protein that controls aspects of brain development in mammals also appears to be a deuterostome-specific gene (Whittaker et al. 2006), using one old domain (EGF) and two new ones (Reeler and BNR). Analyses of proteoglycans reveal a similar story. Whereas perlecan is ancient (as are the transmembrane proteoglycans, syndecan and glypican), proteoglycans containing the LINK domain are confined to deuterostomes, indeed largely to vertebrates (there are two genes containing that domain in sea urchins) (Whittaker et al. 2006).

In general, it seems clear that the fraction of the proteome that is ECM proteins has expanded disproportionately during the evolution of the deuterostome lineage, both by duplication and divergence of existing genes and by the appearance of novel gene architectures and even some new domains. It is interesting to speculate on the reasons for this. One obvious explanation is the development of cartilage, bones, and teeth in vertebrates and that undoubtedly accounts for some of the elaboration of novel collagens, proteoglycans, and ECM glycoproteins. However, proteins such as tenascins, fibronectin, and reelin (as well as other neural ECM proteins) have no obvious strong connections to the development of structural ECMs and it is tempting to hypothesize that their emergence was more closely tied to the emergence of novel structures such as the neural crest, endothelial-lined vasculature, and more complex nervous systems. Consonant with this model of key roles for ECM proteins in evolution, the matrisome is one of the most plastic and rapidly evolving compartments of the proteome.

CONCLUDING REMARKS

We now have a reasonably complete inventory of ECM proteins and their associated modifiers. Some ECM proteins have been well studied and we have a good picture of their basic functions—other ECM proteins are virtually unstudied. Even in the case of the well studied proteins, many of the constituent domains, all of which are well conserved and must, therefore,

have important functions, still lack assigned functions. Presumably, many of them, like those that we do understand, serve to bind other proteins in ways that contribute to ECM assembly, binding, and presentation of growth factors and interactions with cells to influence their behavior. There is now a pressing need to describe the changes in ECM composition in development and pathology, to better understand the interactions of individual domains, and to probe the cooperation of these multiprotein assemblies in modulating the functions of cells and tissues. The techniques for such analyses (biophysical, imaging, etc.) continue to advance and there is every prospect that studies of ECM structure and function will yield important insights into the crucial roles played by this vital component of metazoan organization, and genetic analyses and studies of human disease are revealing the biological relevance of individual ECM proteins and of specific interactions.

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Overview of the Matrisome—An Inventory of Extracellular Matrix Constituents and Functions

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