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The Maternal Plasma Proteome Changes as a Function of Gestational Age in Normal Pregnancy: a Longitudinal Study

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Abstract

Objective—Pregnancy is accompanied by dramatic physiologic changes in maternal plasma proteins. Characterization of the maternal plasma proteome in normal pregnancy is an essential step for understanding changes to predict pregnancy outcome. The objective of this study was to describe maternal plasma proteins that change in abundance with advancing gestational age, and determine biological processes that are perturbed in normal pregnancy.

Materials and methods—A longitudinal study included 43 normal pregnancies that had a term delivery of an infant who was appropriate for gestational age (AGA) without maternal or neonatal complications. For each pregnancy, 3 to 6 maternal plasma samples (median=5,) were profiled to measure the abundance of 1,125 proteins using multiplex assays. Linear mixed effects models with polynomial splines were used to model protein abundance as a function of gestational age, and significance of the association was inferred via likelihood ratio tests. Proteins considered to be significantly changed were defined as having: 1) more than 1.5 fold change between 8 and 40 weeks of gestation; and 2) a false discovery rate (FDR) adjusted p-value <0.1. Gene ontology

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enrichment analysis was employed to identify biological processes over-represented among the proteins that changed with advancing gestation.

Results—1) Ten percent (112/1,125) of the profiled proteins changed in abundance as a function of gestational age; 2) of the 1,125 proteins analyzed Glypican-3, sialic acid-binding immunoglobulin-type lectins (Siglec)-6, placental growth factor (PlGF), C-C motif (CCL)-28, carbonic anhydrase 6, Prolactin (PRL), interleukin-1 receptor 4 (IL-1 R4), dual specificity mitogen-activated protein kinase 4 (MP2K4) and pregnancy-associated plasma protein-A (PAPP-A) had more than 5 fold change in abundance across gestation. These 9 proteins are known to be involved in a wide range of both physiologic and pathologic processes, such as growth regulation, embryogenesis, angiogenesis immunoregulation, inflammation etc.; and 3) biological processes associated with protein changes in normal pregnancy included defense response, defense response to bacteria, proteolysis and leukocyte migration (FDR=10%).

Conclusions—The plasma proteome of normal pregnancy demonstrates dramatic changes in both magnitude of changes and the fraction of the proteins involved. Such information is important to understand the physiology of pregnancy, development of biomarkers to differentiate normal vs. abnormal pregnancy, and determine the response to interventions.

Keywords

aptamer; biomarker; C-C motif (CCL)-28; carbonic anhydrase 6; dual specificity mitogen-activated protein kinase 4 (MP2K4); high-throughput biology; glypican-3; placental growth factor (PlGF); prolactin (PRL); interleukin-1 receptor 4 (IL-1 R4); pregnancy-associated plasma protein A (PAPP-A); proteins; sialic acid-binding immunoglobulin-type lectins (Siglec)-6

Introduction

Viviparity requires major adaptations in the mother to sustain the establishment, development, growth, and eventual separation of a fetal semi-allograft at the time of parturition. Pregnancy in placental mammals is a unique biological phenomenon, perhaps unmatched in the history of evolutionary biology. Reproductive success depends on an intensive and rich dialogue among mother, placenta, and fetus. The adaptations required for pregnancy appear to involve virtually all maternal organs/systems, including the metabolic/endocrine (1–6), cardiovascular (7–12), respiratory (13), gastrointestinal (12, 14–21), hematologic (22, 23), and central nervous systems (24–26).

The study of the physiology of pregnancy has spanned decades, and has largely depended upon available technological capabilities to study parameters that change with gestational age. Such parameters have been studied with relatively simple methods, such as hormonal determinations (20, 21, 27), concentrations of nutrients/fuels (glucose(17–19), lipids(28–33), proteins(34–40), amino acids(41–43)), blood pressure (8, 44), cardiovascular function (9, 11), spirometry (13, 16), immunological assays (14, 24, 45), and different tests of central nervous system function (25, 26). These studies have been essential to understand changes in body composition (4, 18), physiologic adaptation (10, 13), pathophysiology of selected pregnancy complications (17, 46–48). One of the domains of interest that has proven to be extraordinarily successful is the study of changes in plasma protein concentrations in maternal blood. For example, the detection of human chorionic gonadotrophin (hCG) in

human blood has allowed the early detection of pregnancy, even before the first signs of amenorrhea(56–58). Monitoring early pregnancy with serial determinations of hCG has also allowed identification of patients at risk for ectopic gestation(59–70), and other forms of pregnancy failure (60, 62, 63, 65, 67). In the case of ectopic pregnancy, this has allowed not only earlier diagnosis, but even the introduction of minimally invasive surgical techniques (e.g. laparoscopic resection and medical treatment) (71–79). The monitoring of gestational trophoblastic disease has also been dramatically changed with the use of serial hCG determinations in maternal serum/plasma (80, 81). However, these examples only represent the first of many diagnostic advances made possible by monitoring concentrations of a single protein during pregnancy.

The observation that a fetus with a neural tube defect had been born to a mother with an idiopathic elevation of maternal serum alpha fetoprotein eventually led to the discovery that such elevations could be used to screen for the presence of neural tube defects in the mid-trimester of pregnancy(56, 82–86), and continue to be the basis – more than 20 years later – for the biochemical screening of these congenital anomalies(84, 87–93). Further advances occurred with the introduction of the triple (followed by the quadruple) biochemical screening, including three proteins (alpha fetoprotein, hCG, inhibin), which were subsequently combined with a steroid hormone, estriol, to assess the likelihood of trisomies 18 and 21 at the end of the first trimester (88, 89, 93–100). Collectively, this evidence, which is now in routine clinical practice, provides compelling evidence that examination of the plasma/serum composition can provide important insight into the biology of pregnancy, fetal health and disease, and has changed the practice of obstetrics and medicine.

The most recent entry into the protein biomarker discovery panel is the determination of angiogenic/anti-angiogenic factors for the early prediction of preterm preeclampsia(47, 101–110), fetal death(111, 112), late preeclampsia(47, 101–110), small-for-gestational-age (SGA) (113), and maternal floor infarction(114). This set of biomarkers can now be readily determined using commercially-available tests, and has the potential to identify patients at risk for pregnancy complications in the long subclinical phase of the “great obstetrical syndromes”, and open the door for prevention, which has been a challenge in obstetrics for decades(105, 115–124).

High-dimensional biology techniques allow characterization of the genome (54, 55, 125, 126), transcriptome(55, 127–137), proteome(55, 125, 127, 138–148), lipidome(149–155), glucome(156, 157), metabolome(6, 55, 128, 158–163), and cytome(164–169). Major thrust of the new biology and medicine has been to gather the information derived from these platforms to optimize diagnosis, prognosis, and treatment (170, 171). Although each of these techniques has a particular informational domain (DNA, RNA, proteins, metabolites, lipids, etc.), they can be used independently or in combination (172, 173). Proteins are considered to be important executors of biological functions, as they include enzymes (80), structural components of tissues/cells (174), the coagulation cascade (175, 176), and the inflammatory network (177).

There have been substantial attempts to characterize the human plasma proteome in non-pregnant subjects, which have been made possible by the development of sophisticated

mass-spectrometry techniques, using a top-down approach (81, 140, 178). These efforts have been extended to the maternal plasma proteome and amniotic fluid(138–140, 145, 147, 148, 179–203); however, technological complexities continue to challenge the goal of developing a comprehensive map of the entire human plasma proteome. The total estimated number of proteins in the human body ranges from 20,000 to one million(78) – of these, plasma proteome studies have been able to detect and semi-quantify a number between 16,500–20,000 (79, 204–206). Immunoassays and related methods continue to be the “gold standard” for the sensitive determination of proteins in peripheral plasma, guide diagnosis, monitoring of disease, and treatment; in addition, they are more sensitive than 2D gels or mass spectrometry, and can detect analytes in very small quantities (below nM range). In addition, technologies like enzyme-linked immunosorbent assay (ELISA) require two antibodies to the same protein to elicit a signal. Such immunoassays cannot be multiplexed above a few tens of simultaneous measurement, largely due to the cross-reactivity of the secondary antibodies to surface-immobilized proteins (207–210).

To enlarge the number of proteins that can be detected simultaneously with a high degree of sensitivity and dynamic range, a new technology has been developed which is not based on conventional antigen/antibody reaction. The aptamer-based method uses single-strand DNA or RNA molecules that bind, with high affinity and specificity, to proteins, peptides, or other pre-defined molecules. Recent publications have emphasized the extraordinary potential of aptamer technology in biomarker discovery for cardiovascular disease (211),and other important biomedical disorders (212–218).

The objective of this study was to use aptamer-based technology to characterize the maternal plasma proteome of normal pregnancy as a function of gestational age. This study is important for the description of the simultaneous changes in plasma protein composition, and will serve as the basis to detect departures of abnormalities, before and during the time of diagnosis of major obstetrical complications.

Methods

Study design

We conducted a prospective longitudinal study that enrolled normal pregnant women attending the Center for Advanced Obstetrical Care and Research of the Perinatology Research Branch, NICHD, and the Detroit Medical Center / Wayne State University. A retrospective cohort study was conducted to include 43 who delivered at term, and each one of them had 3 to 6 plasma samples obtained during pregnancy, before the spontaneous onset of labor (median number of samples=5),]. Plasma samples were collected at the time of a prenatal visit, scheduled at four-week intervals from the first or early second trimester until delivery. Each patient had at least three samples collected during the following gestational age intervals (8-<16 weeks, 16-<24 weeks, 24-<28 weeks, 28-<32 weeks, 32-<37 weeks and >37 weeks). All patients had the placenta collected at the time of delivery, transported to the laboratory, and sectioned for histological examination, following criteria of the Society for Perinatal Pathology. Lesions were diagnosed using previously established criteria(71–73). Only patients without acute inflammatory lesions of the placenta were included in this study because of the potential to confound the relative abundance of the maternal plasma

proteome. All patients provided written informed consent and the use of biological specimens, as well as clinical and ultrasound data for research purposes were approved by the Wayne State University and Institutional Review Boards of NICHD.

Proteomics technique

Maternal plasma protein abundance was determined using the SOMAmer (Slow Off-rate Modified Aptamers) platform and its reagents. This platform allows measurement of over 1,125 proteins in maternal plasma samples (210, 219, 220). Proteomics profiling was performed by Somalogic, Inc. (Boulder, CO).

The serum samples were diluted and then incubated with the respective SOMAmer mixes pre-immobilized onto streptavidin-coated beads. The beads were washed in order to remove all non-specifically bound proteins and other matrix constituents. Proteins that remained specifically bound to their cognate SOMAmer reagents were tagged using an NHS-biotin reagent. After the labeling reaction, the beads were exposed to an anionic competitor solution that prevents non-specific interactions from reforming after disruption.

Using this approach, pure cognate-SOMAmer complexes and unbound (free) SOMAmer reagents are released from the streptavidin beads using ultraviolet light that cleaves the photo-cleavable linker used to quantitate protein. The photo-cleavage eluate, which contains all SOMAmer reagents (some bound to a biotin-labeled protein and some free), was separated from the beads and then incubated with a second streptavidin-coated bead that binds the biotin-labeled proteins and the biotin-labeled protein-SOMAmer complexes. The free SOMAmer reagents were then removed during subsequent washing steps. In the final elution step, protein-bound SOMAmer reagents were released from their cognate proteins using denaturing conditions. These SOMAmer reagents were then quantified by hybridization to custom DNA microarrays. The Cyanine-3 signal from the SOMAmer reagent was detected on microarrays (210, 219, 220).

Statistical analysis

Demographics data analysis—Clinical characteristics of the patient population were summarized as median and inter-quartile ranges (IQR) for continuous variables, or percentages for categorical variables, using SPSS software (version 19; IBM Corporation, Armonk, NY)

Differential abundance analysis—Protein abundance expressed as fluorescence units was log (base 2) transformed to improve normality. Linear mixed-effects models with cubic splines (number of knots = 3) were used to model protein abundance as a function of gestational age using *lme4* package (221) under the R statistical language and environment (www.r-project.org). Inference about statistical significance of associations was calculated using likelihood ratio tests between a model that included the gestational age terms (fixed and corresponding random effects) and a simpler random intercept linear mixed-effects model without gestational age terms.

Protein abundance was considered to have changed significantly with gestational age if it met the following criteria: 1) the magnitude of abundance of change was >1.5 fold between

8 and 40 weeks of gestation; and 2) false discovery rate (FDR) (222) adjusted p-values (q-values) <0.1. Similar or less stringent criteria have been extensively used in high-dimensional biology and have shown good validation by alternative techniques and/or in independent sets of samples(223–226).

Fold change was defined as the ratio of protein abundance (in relative fluorescence units) between the highest and the lowest mean value across gestational age. The median (50th quantile) and 10th and 90th quantiles of the protein abundance were also determined using quantile regression modeling (227, 228). In these models, the relationship between protein abundance was assumed to be linear within a narrow moving window of gestational age, and this allowed obtaining a non-linear smooth estimate of the quantiles as previously described (107).

Clustering proteins by average profile—To identify groups of proteins based on their pattern of change across gestation, we have used unsupervised hierarchical clustering. The input in this analysis was the mean protein abundance across gestation (longitudinal patterns) computed from linear mixed-effects models for each gestational week from 8 to 40 weeks. Average profiles were scaled between 0 and 1 prior to applying hierarchical clustering with Euclidean distance, so that proteins with similarity longitudinal patterns (e.g. monotonically increasing) are grouped together despite eventual differences in the magnitude of change (e.g. rate of increase) or overall protein abundance. With hierarchical clustering, each protein is considered a cluster by itself and iteratively, clusters are merged so that the distance between the farthest apart members of the clusters (complete linkage) is minimized. To determine the optimal number of clusters, we have used a goodness of clustering measure (the gap statistic) which compares the change in within-cluster dispersion (sum of squared distances between cluster members) with that expected under the null distribution (simulated by bootstrap)(229).

Gene ontology enrichment analysis—Having identified proteins which change in abundance as a function of gestational age, the next step was to gain an understanding of the potential functional roles of these proteins in human pregnancy. To accomplish this, we relied on the information deposited for the genes encoding for each protein, and which have been organized in publicly-available databases (i.e. gene ontology). We focused on the biological processes in which these proteins have been implicated. Each protein was mapped to an identifier in the Entrez gene database.(230) based on Somalogic, Inc. protein annotation system, and then to gene ontology (231). Biological processes over-represented among the proteins that changing in abundance with advancing gestational age. We used a Fisher's exact test and odds ratios to estimate enrichment. Gene ontology terms with three or more hits and an adjusted p-value <0.1 were considered significantly enriched in gestational age modulated proteins.

Protein-protein interaction network analysis—To explore the potential impact of gestation on human plasma proteins not profiled in this study, we conducted an in-silico analysis for which we retrieved the known protein-protein map interactions from the publicly available Protein Reference Database (HPRD, release 9) (232) using the *NCBI2R* package. For each of the 1,125 proteins profiled, we determined the number of protein-

protein interactions documented in the database. For visualization purposes, a graph was constructed linking proteins with known interactions with the 112 proteins changing with gestational age.

Results

Clinical characteristic of the study population

Forty-three women with normal pregnancies met the criteria for inclusion in this study. The median (interquartile range) maternal age was 25 (21–28) years old, and 88.4% of patients were of African-American origin by self-reporting. All patients delivered at term without any obstetrical complications and had neonates with an appropriate weight for gestational age(233). The median gestational age at delivery was 39.4 [interquartile range (IQR) 39.0–40.1].

Maternal Plasma Proteome in Normal Pregnancy Characterized by SomaSCAN

Ten percent (112/1,125) of the proteins profiled changed in abundance as a function of gestational age (fold change >1.5 and q-value <0.1) (see Table 2). Figure 1 shows longitudinal protein abundance for two selected proteins together with the fitted mean (by linear-mixed effects models) and median (by quantile regression) as a function of gestation. Similar plots for all 112 significant proteins are displayed in supp. File 1

Thirty-six percent (41/112) of proteins decrease in abundance and 64% (71/112) increase with gestational age. Hierarchical cluster analysis of average protein profiles across gestation (see Figure 2) demonstrated among the increasing abundant proteins three patterns in the change of the relative fluorescence reading (increasing rate: n=21, constant rate: n=23, and decreasing rate: n=27). Similar patterns were observed among proteins with decreasing abundance during gestation (increasing rate: n=8, constant rate: n=16, and decreasing rate: n=17).

The most highly modulated proteins (highest fold change) among the significant ones were: 1) placental growth factor (PlGF); 2) pregnancy-associated plasma protein A (PAPP-A) (>5 fold change in abundance across gestation,; 3) sialic acid-binding immunoglobulin-type lectins (Siglec)-6; 4) glypican-3; 5) C-C motif (CCL)-28; 6) carbonic anhydrase 6; 7) prolactin (PRL); 8) interleukin-1 receptor 4 (IL-1 R4); and 9) dual specificity mitogen-activated protein kinase kinase 4 (MP2K4)(see Figure 3).

Biological Processes Modulated During Gestation

Gene ontology analysis of the corresponding proteins that changed with gestational age revealed fourteen biological processes that are impacted with advancing gestation. These biological processes included: general defense response, defense response to bacteria, defense response to fungi, germ cell migration, proteolysis and leukocyte migration (FDR=10%) (see Table 3). Out of the fourteen processes, defense response to fungus, germ cell migration, and defense response to bacterium had all decreased abundance of the protein associated with these biological processes with advancing gestation. In contrast, only the

biological process of smooth muscle cell migration has an increase abundance of the proteins involved in it.

Protein-protein Interaction network

An analysis was performed to retrieve the known protein-protein interactions from the Human Protein Reference Database to assess the connections with proteins changing with gestational age of this study (see Figure 4). Proto-oncogene tyrosine-protein kinase Src (SRCN1) and Tyrosine-protein kinase Fyn (FYN) had the largest number of documented interactions (260 and 196, respectively) of all proteins changing during pregnancy suggesting that they have important roles in the interactome. Other well-known proteins such as MMP-9, VEGF and PIGF had 38, 26, and 5 documented interactions, respectively.

Discussion

Principal findings of the study

I) Ten percent (112/1,125) of the 1,125 proteins assessed in this study in maternal plasma change with advancing gestational age; II) the concentration of nine proteins [1) placental growth factor (PIGF); 2) pregnancy-associated plasma protein A (PAPP-A) 3) sialic acid-binding immunoglobulin-type lectins (Siglec)-6; 4) glypican-3; 5) C-C motif (CCL)-28; 6) carbonic anhydrase 6; 7) prolactin (PRL); 8) interleukin-1 receptor 4 (IL-1 R4); and 9) dual specificity mitogen-activated protein kinase kinase 4 (MP2K4)] increased dramatically in abundance (fold change >5); III) proteins demonstrated either increased or decreased in abundance with advancing gestational age following at least 3 distinct patterns of change (increasing rate, constant rate, and decreasing rate of change in abundance); and IV) functional analysis revealed that the proteins that were identified as changing with gestational age belonged to the following biological processes (as determined by gene ontology-derived analysis methods): a) general defense response, b) defense response to bacteria, c) defense response to fungi, d) germ cell migration, e) proteolysis, and f) leukocyte migration. This communication reports changes in a large number of proteins in the maternal plasma proteome in normal pregnancy using a state-of-the-art proteomic multiplex platform. The results in normal pregnancy reported herein can serve as the basis for the identification of biomarkers for the prediction, monitoring of disease, and diagnosis of obstetrical disorders.

Meaning of the Study

The reasons to characterize the maternal plasma proteome in normal pregnancy have been outlined in the introduction of this manuscript, and the information derived from measuring protein concentrations has had great clinical value for the care of pregnant women.

We found nine proteins which showed a dramatic increase in concentration, defined as more than five-fold. The magnitude of change of Placental growth factor (PIGF) was 14.5 fold, and this protein plays an important role in the control of angiogenesis, which is a key process in placental development. Low concentrations of PIGF have already been reported in patients who subsequently developed early onset preeclampsia(104–107, 234–237), fetal death of unknown origin(111, 112), small-for-gestational-age infants (with and without

Doppler abnormalities) (104–107), maternal floor infarction(109, 238, 239), mirror syndrome(114, 123, 240–244), and some forms of twin-to-twin transfusion syndrome(74). The identification of PIGF as a protein that undergoes dramatic changes in maternal plasma concentration in this study (and using current technologies) is reassuring, given its physiologic importance, as well as the prognostic value in measuring this concentration in maternal plasma to identify patients at risk for adverse pregnancy outcome.

The same applies to Pappalysin-1 (PAPP-A), one of the top nine proteins whose concentration increased more than five-fold in this study. PAPP-A is mainly produced by the placenta, and its concentration is low in the first trimester of pregnancies complicated by either chromosomal abnormalities (Trisomies 21, 18 and 13, and monosomy X) (93, 97–100, 245–248) or a subset destined to develop placenta-mediated obstetrical syndromes such as SGA and preeclampsia (119, 249–261) and preterm birth (262). In this study, we also report the longitudinal changes in the plasma concentrations of PAPP-A as a function of gestational age. The concentration of PAPP-A increased steadily until about 20 weeks of gestation, when it plateaued and remained relatively stable until term. Our observations are consistent with those of a previous report, and provide further strength to the validity of our findings (263).

Maternal plasma Siglec-6 and Glypican-3 were also among the top-ranked proteins which increase in concentration with advancing gestational age 17 and 26 fold, respectively (Table 2). Although these proteins were previously described in *in vitro* studies and non-pregnant subjects, there is no systematic study describing the changes in the concentrations of these proteins in maternal plasma in normal or abnormal pregnancy.

Sialic-acid-binding immunoglobulin-like lectins (Siglec)-6 is a CD33rSiglec that has been implicated in the regulation of two major biological functions: cell-to-cell interactions and regulation, through glycan recognition, of the innate and adaptive immune systems (264–267). In addition, this molecule can also serve as a leptin receptor (OB-BP1), which has high specificity and affinity to this molecule. Importantly, Siglec-6 is expressed only in cyto- and syncytiotrophoblasts of the human placenta (268–270), and this may explain how it gains access to the maternal circulation and increases with gestational age as the volume of the villous tree increases (270). A recent report has documented an increase in Siglec-6 expression in the placenta following spontaneous labor and delivery in comparison to those following elective cesarean section without labor; therefore, it has been proposed that this molecule may play a role in the process of parturition (270, 271). In addition, increased Siglec-6 trophoblast expression was reported in women with gestational trophoblastic disease and those with preterm preeclampsia (124, 269, 272–274). The findings in Siglec-6 reported herein provide further support that an increase in abundance of this protein, detected with current technology in the maternal circulation, may have biological and clinical implications.

There is a paucity of information about Glypican-3 in pregnancy. This protein is a heparan-sulfate proteoglycan which acts as a co-receptor for heparin-binding growth factors, such as insulin-like growth factor (275–281), which is expressed in the syncytiotrophoblast of term placentas, and has been reported to be downregulated in trophoblasts of patients with

preeclampsia (282, 283). One study reported a link between Glypican-3 and one of the major anticoagulation proteins of the trophoblast-placenta protein 5/tissue factor pathway inhibitor 2: this anticoagulation protein is specific to pregnancy and has been implicated in the maintenance of placenta hemostasis; the placental expression of the latter is reduced in preeclampsia(282). Glypican-3 has been proposed to serve as the anchoring protein of placenta protein 5/tissue factor pathway inhibitor 2; and that the decrease in Glypican-3 in preeclampsia leads to the release of placenta protein 5/tissue factor pathway inhibitor 2 into the maternal circulation, promoting a higher concentration in this obstetrical syndrome. Our study reports the first changes in the concentrations of Glypican-3 in the maternal circulation, and it is noteworthy that this protein increases 26-fold during pregnancy in a pattern of decreasing slope (Figure 3) with advancing gestational age.

Several of the findings reported herein are consistent with those described in maternal plasma/serum for other proteins: this lends reassurance to the validity of our findings derived with the use of a novel aptamer-based technology. Specific examples include plasminogen activator inhibitor type 1 (PAI-1) (284), insulin-like growth factor binding protein (IGFBP)-1 (285–290), hepcidin (291) and thyroid stimulating hormone (292). The current study is the first to examine and analyze longitudinally the profile of the maternal plasma proteome of more than 1,000 proteins simultaneously using a high-dimensional biology platform.

Biological processes modulated during gestation

Gene ontology analysis revealed that the defense response, proteolysis and cellular response to hormone stimulus were the most enriched biological processes among proteins that changed with gestational age. The host defense response is a protective mechanism against pathogens and “danger signals” such as alarmins, and involves activation of both the innate and adaptive immune response (293–300). Tolerance of a semi-allograft (fetus and placenta) represents a major biological challenge imposed by viviparity. While the fundamental mechanisms responsible for this remain to be elucidated, a general proposal is that there is a down-regulation of the specific limb of the adaptive immune response aimed at paternal antigens, with an up-regulation of the innate immune response (116–118, 149–154, 301, 302). Down-regulation of specific immune responses includes not only paternal/fetal antigens, but also microbial products; therefore, the physiologic modulation of the immune response to enhance tolerance of the semi-allograft could expose the mother to infection, and the infectious process may be more severe (165, 169). Evidence in support of this is that patients with pyelonephritis during pregnancy are more likely to develop acute respiratory distress syndrome and other complications,(155–157, 166–168) and those with viral diseases during pregnancy (e.g. influenza, varicella, H1N1, SARS) are more likely to develop serious complications, and even die during pregnancy ((179–186, 188, 189). The production of antimicrobial peptides (AMP) is a mechanism to enhance host immunoprotection, and indeed, the production of a broad range of antimicrobial peptides (antibacterial and antiviral) is enhanced during pregnancy (303–308). Such products have been detected in both the amniotic cavity and systemic circulation ((187, 190, 309, 310).

The amniotic fluid is known to have anti-microbial properties (310–316) and this could be due to the presence of naturally occurring AMPs, such as bactericidal/permeability-

increasing protein (307, 309), lysozyme (141, 317–320) lactoferrin (320–322), calprotectin (MRP8/14) (309), LL37 (319) and neutrophil defensins (305, 309, 310, 319, 323, 324). Moreover, we reported that increased AMP concentrations are associated with pregnancy complications such as intra-amniotic infection, preterm labor and preterm prelabor rupture of membranes (309, 310). The nature of the host immune response to microorganisms during pregnancy may not be uniform, and may be context-dependent. For example, there is some evidence that the host defense against fungi is not as robust as that against bacteria, and this may explain the increased predisposition to vaginal candidiasis during pregnancy ((191, 192, 325–327). In addition, patients who conceived with an intrauterine contraceptive device are particularly susceptible to infections with fungi in the amniotic cavity, and this may reflect unique features of the complex immune response to different microorganisms during pregnancy(193–202, 328).

One of the findings of this study is that proteins related to smooth muscle cell migration are increased in abundance in maternal plasma with advancing gestational age – this finding is entirely consistent with the fact that the uterus must grow during pregnancy to accommodate the increased size of the fetus, placenta, and amniotic fluid. Importantly, there has not been a good biomarker to monitor smooth muscle function in maternal plasma, and the findings in this study open the door for the identification of such proteins.

Protein-protein interaction network

Proteins function in concert as a part of larger protein complexes within a cell; therefore, an important aspect of proteomic analysis lies in the elucidation of interacting proteins and mapping the corresponding binding sites (329, 330). By identifying proteins interacting with those modulated during normal pregnancy, we can hypothesize on the importance of the change in protein abundance with gestation. These inferences rely on the basis of their degree (number of direct protein-protein interactions) in the *interactome*. Of note, the average number of interacting proteins in the Human Protein Reference Database is ~3.7 per protein (330). Proto-oncogene tyrosine-protein kinase Src (SRCN1) and Tyrosine-protein kinase Fyn (FYN) had 260 and 196 documented interactions in the Human Protein Reference Database; thus, these two proteins appear to play a central role in the interactome.

SRCN1 is part of the Src signaling system involved in cellular signaling of proteinase-activated receptors (PAR) 2, that is, a G-protein coupled receptor that modulates activation induces vascular endothelial growth factor receptor (VEGFR)-1 promoter activity and sVEGFR-1 release from endothelial cells. Given the importance of VEGFR-1 in the regulation of endothelial function during pregnancy and its pathogenesis in preeclampsia, SGA, fetal death, maternal floor infarction, and some forms of spontaneous preterm labor, our findings strengthen the case for the importance of discovery techniques in the elucidation of fundamental mechanisms of disease in obstetrics.

Tyrosine-protein kinase Fyn (FYN) is also a member of the Src family. In contrast to SRCN1, FYN is involved in immune system activity, especially in T-cell signaling and animal models, suggesting that it is associated with decreased fetal maternal tolerance through the regulation of Th17. In addition, animal experimentation has demonstrated that

this protein is also involved in neuronal signaling, migration, and cortical development cell physiology (331, 332).

Strengths and Limitations

The major strength of this study is the characterization of the maternal plasma proteome in longitudinal samples of patients who had a normal pregnancy outcome defined by clinical, neonatal, and pathologic examination of the placenta. We have examined a large number of proteins simultaneously (over 1,000), using sensitive techniques which have been rigorously validated. This study represents the largest examination of the maternal plasma proteome during pregnancy. Another strength of this study is that we have identified proteins that have been found previously to be dramatically up-regulated during pregnancy, such as PlGF and PAPP-A, but also discovered novel proteins which were not known to be drastically changed in concentration. The identification of three broad patterns of protein changes with a large number of proteins is also important, as these observations were not known with specificity prior to this study.

One limitation of this study is that the concentrations are expressed in relative fluorescence units, rather than absolute concentrations, and hence batch effects do not allow a direct comparison of the normal pregnancy reference intervals estimated in this study with data obtained in future studies. However, departures of longitudinal patterns across gestation from the reference intervals we have determined can enable discovery of biomarkers unhindered by possible experimental biases. Such discoveries can be followed by quantification by alternative protein measurement techniques such as immunoassays or mass-spectrometry-based assays. In addition, the large majority of the patients included in this study were of African American descent, and future studies will be required to determine whether the changes reported herein occur in populations of other ethnic groups.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Summary

This is the first comprehensive study to characterize the longitudinal maternal plasma proteome in pregnancy with the use of novel technology. Since the proteomics technique used in this study provided protein abundance measurements expressed in relative fluorescence units, we could not derive reference ranges of protein concentrations so that one can compare future data directly against these references. However, the patterns of change with gestation that we describe can still be useful in discovering disease markers in future studies provided that they deviate from the expected trajectory, regardless of the baseline concentration, which may be subject to experimental batch effects.

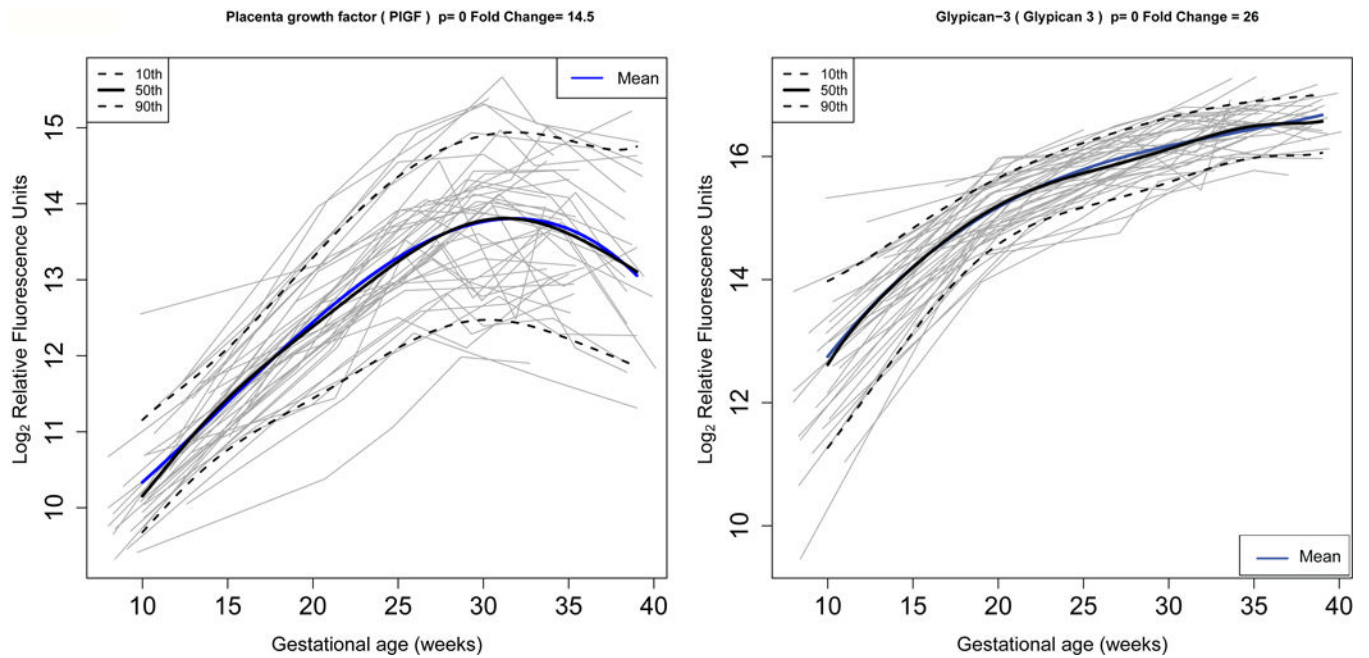


Figure 1.

Longitudinal profiles of placenta growth factor (left) and glypican-3 (right) in normal pregnancy. Protein abundance in (log, base 2, of) relative fluorescence units is shown for each of the 43 patients (grey lines). Mean protein abundance estimated by linear mixed-effects models with cubic splines (thick blue line) as well as median level (thick black line) and 10th / 90th centiles computed by quantile regression are also shown. Fold change (FC) is computed as the ratio in abundance between the highest and lowest value of the mean abundance over gestation.

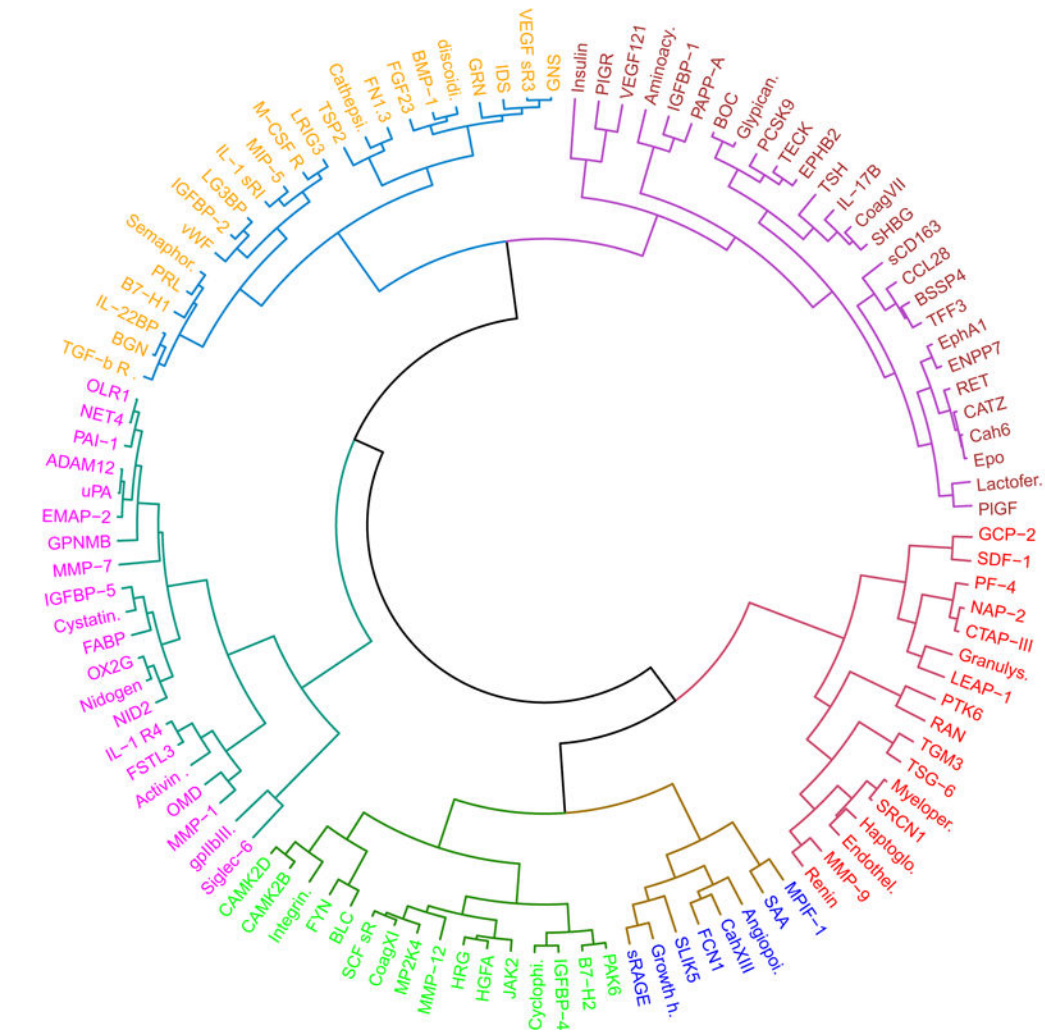
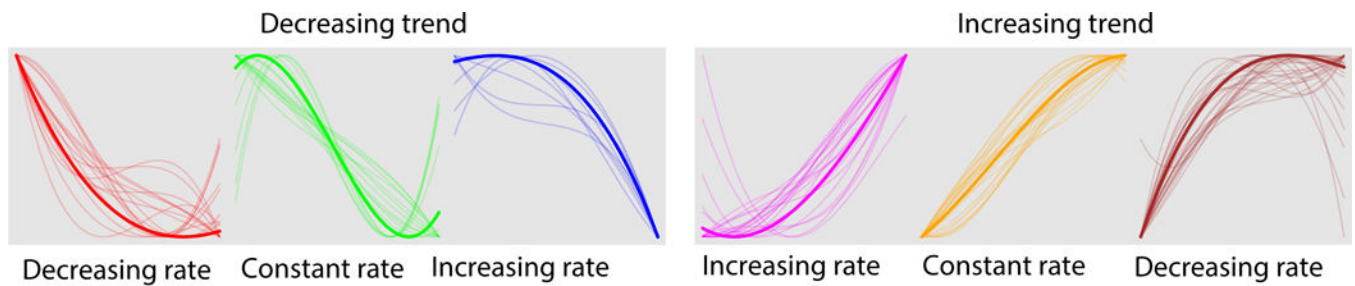


Figure 2. Clustering of maternal plasma average protein profiles. The figure shows three clusters of proteins with increasing overall trends (increasing rate: n=21, constant rate: n=23, and decreasing rate: n=27) and three clusters with decreasing overall trends (increasing rate: n=8, constant rate: n=16, and increasing rate: n=17).

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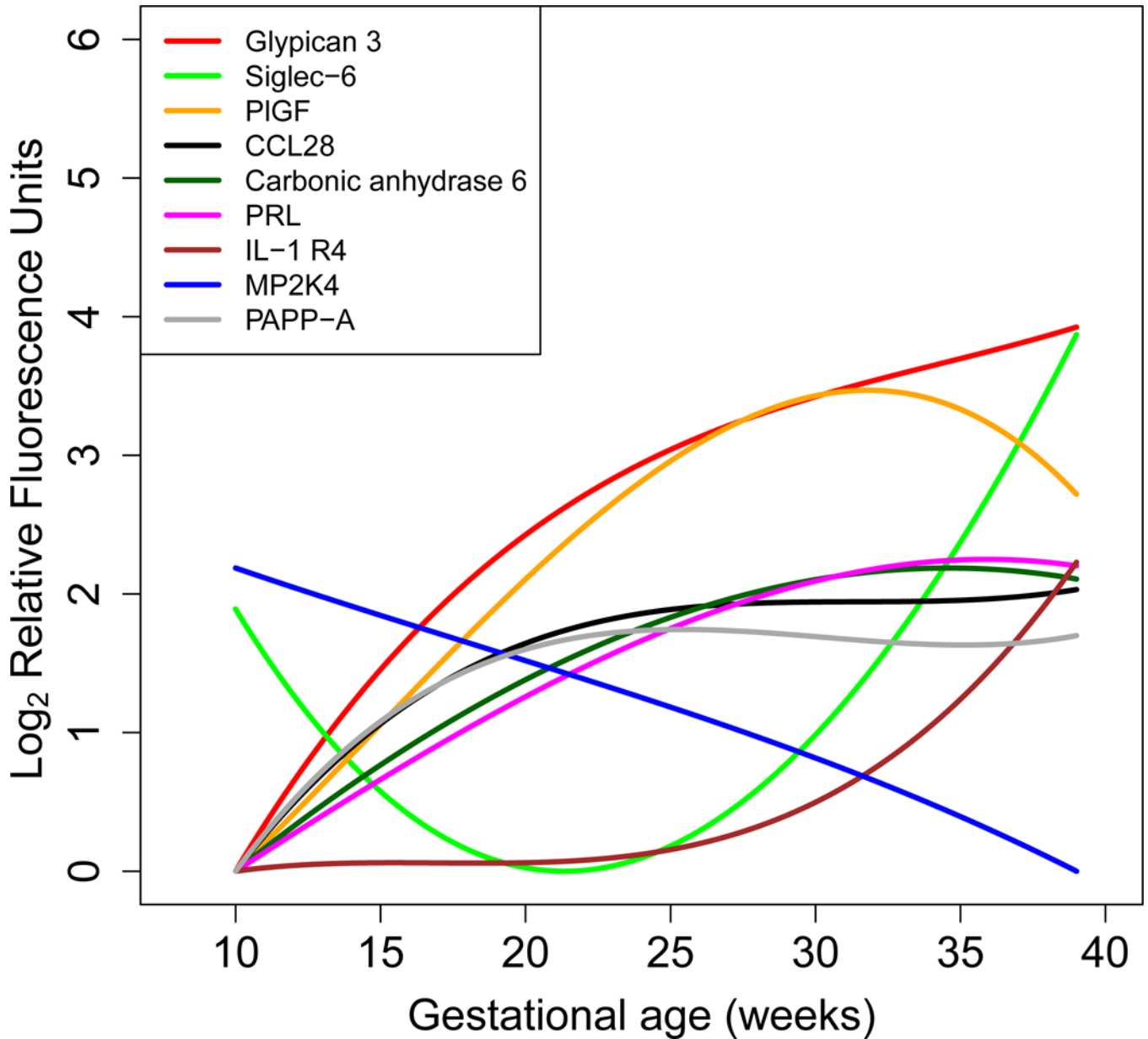


Figure 3.

Maternal plasma average protein abundance for nine highest modulated proteins. The figure shows protein abundance in log (base 2) relative fluorescence units computed from linear mixed-effects models with cubic splines. Average profiles were shifted so that minimum expression corresponds to 0 for all proteins. Most changing nine proteins were (decreasing fold change order): Glypican-3, Siglec-6: Sialic acid-binding immunoglobulin-type lectins 6, PIGF: placental growth factor, CCL28: C-C motif 28, Carbonic anhydrase 6, PRL: Prolactin, IL-1 R4: Interleukin-1 receptor 4, MP2K4: Dual specificity mitogen-activated protein kinase 4, PAPP-A: pregnancy-associated plasma protein A.

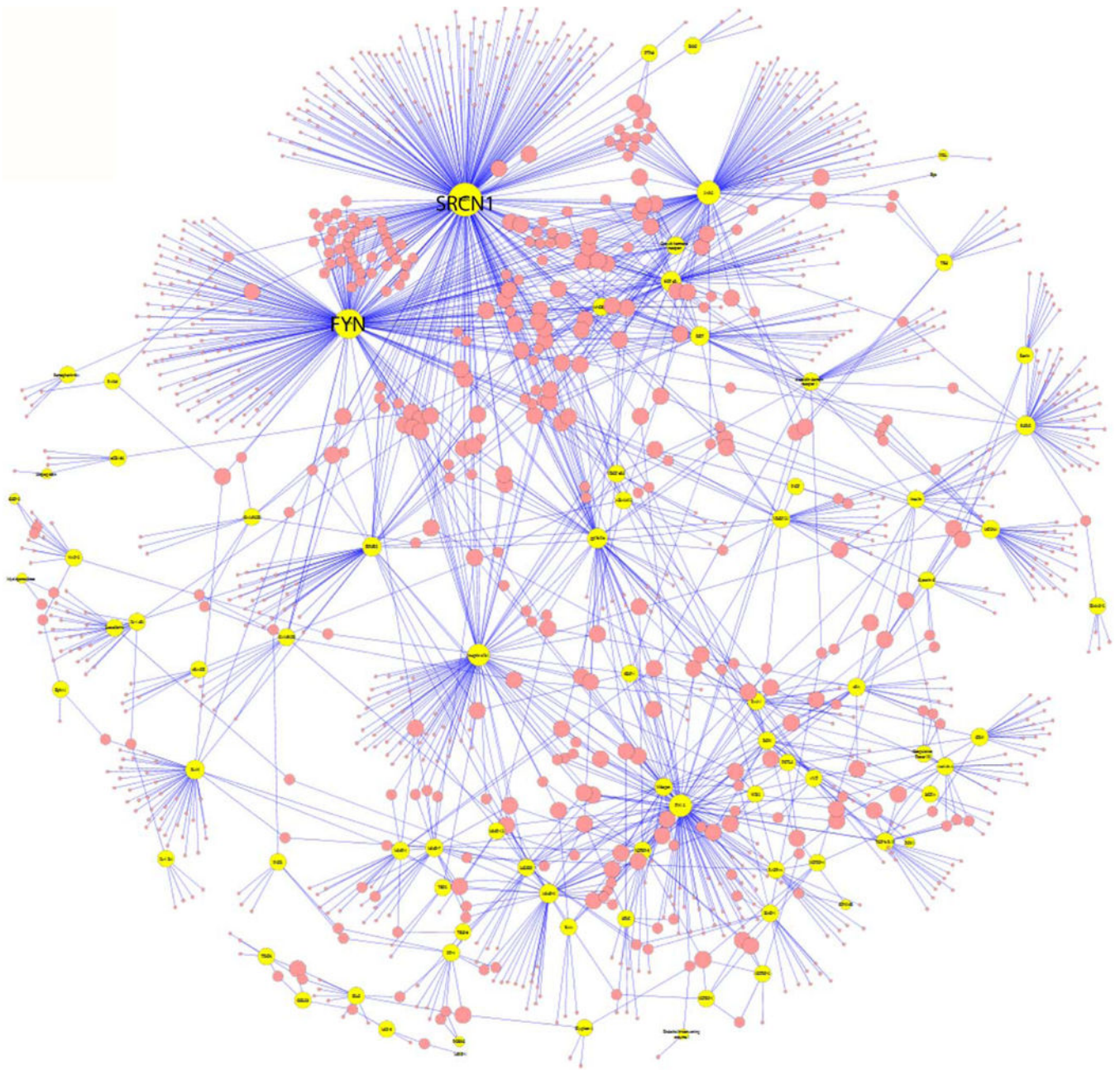


Figure 4. Protein-protein interaction network in normal pregnancy. Yellow circles represent proteins profiled that change with gestation while red circles represent proteins from the Human Protein Reference Database known to interact with these. The size of the circles is proportional with the number of interactions. Proto-oncogene tyrosine-protein kinase Src (SRCN1) and Tyrosine-protein kinase Fyn (FYN) had 260 and 196 interactions, respectively.

Table 1**Clinical characteristics**

Demographic characteristics of the study population. Data is presented as number (%percentage) for categorical variables or median/Inter quartile Range (IQR) for continuous variables.

Characteristics of the study population (n=43)	Median (IQR) or % (n)
Age (years)	25 (21–28)
Prepregnant BMI (kg/m ²)	25.2 (21.3–30.6)
Nulliparity (%)	27.9% (12)
Race (%) <ul style="list-style-type: none"> • African American • White • Other 	88.4% (38) 4.7% (2) 7.0% (3)
Gestational age at delivery (weeks)	39.4 (39.0–40.1)
Route of delivery <ul style="list-style-type: none"> • Vaginal delivery • Cesarean delivery 	67.4% (29) 32.6% (14)
Birthweight (grams)	3330 (3120–3545)

List of proteins that change with gestational age in normal pregnancy. Somalogic identifiers and protein symbols and names are provided together with corresponding UniProt database identifiers and gene symbols. Fold change represents the ratio in protein abundance between the maximum and minimum average value across gestation. The protein trend types correspond to the clusters defined in Figure 1.

Table 2

Target	Target Full Name	UniProt	Gene Symbol	FC	p	q	Direction	Trend Type
B7-H2	ICOS ligand	O75144	ICOSLG	1.84	0.0000	0.000	Decreasing	Constant rate
BLC	C-X-C motif chemokine 13	O43927	CXCL13	1.70	0.0000	0.000	Decreasing	Constant rate
CAMK2B	Calcium/calmodulin-dependent protein kinase type II subunit beta	Q13554	CAMK2B	1.53	0.0172	0.024	Decreasing	Constant rate
CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit delta	Q13557	CAMK2D	1.56	0.0183	0.025	Decreasing	Constant rate
Coagulation Factor XI	Coagulation Factor XI	P03951	F11	1.72	0.0000	0.000	Decreasing	Constant rate
Cyclophilin F	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	P30405	PP1F	1.56	0.0471	0.059	Decreasing	Constant rate
FYN	Tyrosine-protein kinase Fyn	P06241	FYN	1.70	0.0029	0.005	Decreasing	Constant rate
HGFA	Hepatocyte growth factor activator	Q04756	HGFAC	1.91	0.0000	0.000	Decreasing	Constant rate
HRG	Histidine-rich glycoprotein	P04196	HRG	3.26	0.0000	0.000	Decreasing	Constant rate
IGFBP-4	Insulin-like growth factor-binding protein 4	P22692	IGFBP4	1.61	0.0000	0.000	Decreasing	Constant rate
Integrin α 1b1	Integrin α 1b1: beta-1 complex	P56199, P05556	ITGAI1TGFB1	1.60	0.0012	0.002	Decreasing	Constant rate
JAK2	Tyrosine-protein kinase JAK2	O60674	JAK2	1.55	0.0004	0.001	Decreasing	Constant rate
MMP-12	Macrophage metalloelastase	P39900	MMP12	3.38	0.0000	0.000	Decreasing	Constant rate
MP2K4	Dual specificity mitogen-activated protein kinase kinase 4	P45985	MAP2K4	5.23	0.0000	0.000	Decreasing	Constant rate
PAK6	Serine/threonine-protein kinase PAK 6	Q9NQU5	PAK6	1.54	0.0000	0.000	Decreasing	Constant rate
SCF sR	Mast/stem cell growth factor receptor Kit	P10721	KIT	2.09	0.0000	0.000	Decreasing	Constant rate
CTAP-III	Connective tissue-activating peptide III	P02775	PPBP	1.52	0.0000	0.000	Decreasing	Decreasing rate
Endothelin-converting enzyme 1	Endothelin-converting enzyme 1	P42892	ECE1	2.21	0.0000	0.000	Decreasing	Decreasing rate
GCP-2	C-X-C motif chemokine 6	P80162	CXCL6	1.55	0.0000	0.000	Decreasing	Decreasing rate
Granulysin	Granulysin	P22749	GNLY	1.53	0.0000	0.000	Decreasing	Decreasing rate
Haptoglobin, Mixed Type	Haptoglobin	P00738	HP	2.11	0.0004	0.001	Decreasing	Decreasing rate
LEAP-1	Hepcidin	P81172	HAMP	4.32	0.0000	0.000	Decreasing	Decreasing rate
MMP-9	Matrix metalloproteinase-9	P14780	MMP9	1.56	0.0652	0.079	Decreasing	Decreasing rate
Myeloperoxidase	Myeloperoxidase	P05164	MPO	1.99	0.0000	0.000	Decreasing	Decreasing rate
NAP-2	Neutrophil-activating peptide 2	P02775	PPBP	1.59	0.0000	0.000	Decreasing	Decreasing rate

Target	Target Full Name	UniProt	Gene Symbol	FC	p	q	Direction	Trend Type
PF-4	Platelet factor 4	P02776	PF4	2.09	0.0000	0.000	Decreasing	Decreasing rate
PTK6	Protein-tyrosine kinase 6	Q13882	PTK6	1.55	0.0000	0.000	Decreasing	Decreasing rate
RAN	GTP-binding nuclear protein Ran	P62826	RAN	2.45	0.0002	0.000	Decreasing	Decreasing rate
Renin	Renin	P00797	REN	1.69	0.0000	0.000	Decreasing	Decreasing rate
SDF-1	Stromal cell-derived factor 1	P48061	CXCL12	1.54	0.0000	0.000	Decreasing	Decreasing rate
SRCN1	Proto-oncogene tyrosine-protein kinase Src	P12931	SRC	1.54	0.0000	0.000	Decreasing	Decreasing rate
TGM3	Protein-glutamine gamma-glutamyltransferase E	Q08188	TGM3	1.67	0.0000	0.000	Decreasing	Decreasing rate
TSG-6	Tumor necrosis factor-inducible gene 6 protein	P98066	TNFAIP6	1.61	0.0000	0.000	Decreasing	Decreasing rate
Angiopoietin-2	Angiopoietin-2	O15123	ANGPT2	2.27	0.0000	0.000	Decreasing	Increasing rate
Carbonic anhydrase XIII	Carbonic anhydrase 13	Q8N1Q1	CA13	1.83	0.0000	0.000	Decreasing	Increasing rate
FCN1	Ficolin-1	O00602	FCN1	1.71	0.0000	0.000	Decreasing	Increasing rate
Growth hormone receptor	Growth hormone receptor	P10912	GHR	1.89	0.0000	0.000	Decreasing	Increasing rate
MPIF-1	C-C motif chemokine 23	P55773	CCL23	1.57	0.0000	0.000	Decreasing	Increasing rate
SAA	Serum amyloid A-1 protein	PODJ18	SAA1	2.04	0.0166	0.023	Decreasing	Increasing rate
SLIK5	SLIT and NTRK-like protein 5	O94991	SLITRK5	2.20	0.0000	0.000	Decreasing	Increasing rate
sRAGE	Advanced glycosylation end product-specific receptor, soluble	Q15109	AGER	1.54	0.0000	0.000	Decreasing	Increasing rate
B7-H1	Programmed cell death 1 ligand 1	Q9NZQ7	CD274	3.12	0.0000	0.000	Increasing	Constant rate
BGN	Biglycan	P21810	BGN	2.62	0.0000	0.000	Increasing	Constant rate
BMP-1	Bone morphogenetic protein 1	P13497	BMP1	3.78	0.0000	0.000	Increasing	Constant rate
Cathepsin A	Lysosomal protective protein	P10619	CTSA	1.66	0.0000	0.000	Increasing	Constant rate
discoidin domain receptor 1	Epithelial discoidin domain-containing receptor 1	Q08345	DDR1	3.48	0.0000	0.000	Increasing	Constant rate
FGF23	Fibroblast growth factor 23	Q9GZV9	FGF23	2.86	0.0000	0.000	Increasing	Constant rate
FN1.3	Fibronectin Fragment 3	P02751	FN1	1.66	0.0000	0.000	Increasing	Constant rate
GNS	N-acetylglucosamine-6-sulfatase	P15586	GNS	1.74	0.0000	0.000	Increasing	Constant rate
GRN	Granulins	P28799	GRN	2.69	0.0000	0.000	Increasing	Constant rate
IDS	Iduronate 2-sulfatase	P22304	IDS	2.31	0.0000	0.000	Increasing	Constant rate
IGFBP-2	Insulin-like growth factor-binding protein 2	P18065	IGFBP2	2.01	0.0000	0.000	Increasing	Constant rate
IL-1 sRI	Interleukin-1 receptor type 1	P14778	IL1R1	1.66	0.0000	0.000	Increasing	Constant rate
IL-22BP	Interleukin-22 receptor subunit alpha-2	Q96915	IL22RA2	2.04	0.0000	0.000	Increasing	Constant rate
LG3BP	Galectin-3-binding protein	Q08380	LGALS3BP	1.61	0.0000	0.000	Increasing	Constant rate
LRIG3	Leucine-rich repeats and immunoglobulin-like domains protein 3	Q6UXM1	LRIG3	2.10	0.0000	0.000	Increasing	Constant rate

Target	Target Full Name	UniProt	Gene Symbol	FC	p	q	Direction	Trend Type
M-CSFR	Macrophage colony-stimulating factor 1 receptor	P07333	CSF1R	3.40	0.0000	0.000	Increasing	Constant rate
MIP-5	C-C motif chemokine 15	Q16663	CCL15	2.01	0.0000	0.000	Increasing	Constant rate
PRL	Prolactin	P01236	PRL	5.75	0.0000	0.000	Increasing	Constant rate
Semaphorin-6A	Semaphorin-6A	Q9H2E6	SEMA6A	2.52	0.0000	0.000	Increasing	Constant rate
TGF- β R III	Transforming growth factor beta receptor type 3	Q03167	TGFBR3	1.59	0.0000	0.000	Increasing	Constant rate
TSP2	Thrombospondin-2	P35442	THBS2	2.00	0.0000	0.000	Increasing	Constant rate
VEGF sR3	Vascular endothelial growth factor receptor 3	P35916	FLT4	1.75	0.0000	0.000	Increasing	Constant rate
vWF	von Willebrand factor	P04275	VWF	2.49	0.0000	0.000	Increasing	Constant rate
Aminoacylase-1	Aminoacylase-1	Q03154	ACY1	1.67	0.0001	0.000	Increasing	Decreasing rate
BOC	Brother of CDO	Q9BWW1	BOC	1.64	0.0000	0.000	Increasing	Decreasing rate
BSSP4	Brain-specific serine protease 4	Q9GZM4	PRSS22	2.18	0.0000	0.000	Increasing	Decreasing rate
Carbonic anhydrase 6	Carbonic anhydrase 6	P23280	CA6	5.79	0.0000	0.000	Increasing	Decreasing rate
CATZ	Cathepsin Z	Q9UBR2	CTSZ	1.60	0.0000	0.000	Increasing	Decreasing rate
CCL28	C-C motif chemokine 28	Q9NRJ3	CCL28	6.25	0.0000	0.000	Increasing	Decreasing rate
Coagulation Factor VII	Coagulation Factor VII	P08709	F7	1.59	0.0000	0.000	Increasing	Decreasing rate
ENPP7	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	Q6UWV6	ENPP7	1.84	0.0000	0.000	Increasing	Decreasing rate
EphA1	Ephrin type-A receptor 1	P21709	EPHA1	2.12	0.0000	0.000	Increasing	Decreasing rate
EPHB2	Ephrin type-B receptor 2	P29323	EPHB2	1.53	0.0000	0.000	Increasing	Decreasing rate
Epo	Erythropoietin	P01588	EPO	1.59	0.0000	0.000	Increasing	Decreasing rate
Glypican 3	Glypican-3	P51654	GPC3	26.04	0.0000	0.000	Increasing	Decreasing rate
IGFBP-1	Insulin-like growth factor-binding protein 1	P08833	IGFBP1	2.92	0.0000	0.000	Increasing	Decreasing rate
IL-17B	Interleukin-17B	Q9UHF5	IL17B	1.56	0.0000	0.000	Increasing	Decreasing rate
Insulin	Insulin	P01308	INS	1.54	0.0274	0.037	Increasing	Decreasing rate
Lactoferrin	Lactoferrin	P02788	LTF	1.50	0.0000	0.000	Increasing	Decreasing rate
PAPP-A	Pappalysin-1	Q13219	PAPPA	5.18	0.0000	0.000	Increasing	Decreasing rate
PCSK9	Proprotein convertase subtilisin/kexin type 9	Q8NBP7	PCSK9	1.89	0.0000	0.000	Increasing	Decreasing rate
PIGR	Polymeric immunoglobulin receptor	P01833	PIGR	1.86	0.0000	0.000	Increasing	Decreasing rate
PIGF	Placenta growth factor	P49763	PGF	14.46	0.0000	0.000	Increasing	Decreasing rate
RET	Proto-oncogene tyrosine-protein kinase receptor Ret	P07949	RET	4.15	0.0000	0.000	Increasing	Decreasing rate
sCD163	Scavenger receptor cysteine-rich type 1 protein M130	Q86VB7	CD163	1.57	0.0000	0.000	Increasing	Decreasing rate
SHBG	Sex hormone-binding globulin	P04278	SHBG	2.38	0.0000	0.000	Increasing	Decreasing rate

Target	Target Full Name	UniProt	Gene Symbol	FC	p	q	Direction	Trend Type
TECK	C-C motif chemokine 25	O15444	CCL25	2.02	0.0000	0.000	Increasing	Decreasing rate
TFF3	Trefoil factor 3	Q07654	TFF3	4.31	0.0000	0.000	Increasing	Decreasing rate
TSH	Thyroid Stimulating Hormone	P01215	CGA TSHB	2.63	0.0000	0.000	Increasing	Decreasing rate
VEGF121	Vascular endothelial growth factor A, isoform 121	P15692	VEGFA	2.02	0.0000	0.000	Increasing	Decreasing rate
Activin A	Inhibin beta A chain	P08476	INHBA	3.21	0.0000	0.000	Increasing	Increasing rate
ADAM12	Disintegrin and metalloproteinase domain-containing protein 12	O43184	ADAM12	1.74	0.0000	0.000	Increasing	Increasing rate
Cystatin C	Cystatin-C	P01034	CST3	1.98	0.0000	0.000	Increasing	Increasing rate
EMAP-2	Endothelial monocyte-activating polypeptide 2	Q12904	AIMP1	1.85	0.0000	0.000	Increasing	Increasing rate
FABP	Fatty acid-binding protein, heart	P05413	FABP3	1.58	0.0000	0.000	Increasing	Increasing rate
FSTL3	Follistatin-related protein 3	O95633	FSTL3	1.56	0.0000	0.000	Increasing	Increasing rate
gp11b/IIa	Integrin alpha-IIb: beta-3 complex	P08514	ITGA2B ITGB3	1.79	0.0696	0.084	Increasing	Increasing rate
GPNNMB	Transmembrane glycoprotein NMB	Q14956	GPNNMB	1.52	0.0000	0.000	Increasing	Increasing rate
IGFBP-5	Insulin-like growth factor-binding protein 5	P24593	IGFBP5	1.51	0.0000	0.000	Increasing	Increasing rate
IL-1R4	Interleukin-1 receptor-like 1	Q01638	IL1RL1	5.49	0.0000	0.000	Increasing	Increasing rate
MMP-1	Interstitial collagenase	P03956	MMP1	1.58	0.0000	0.000	Increasing	Increasing rate
MMP-7	Matrilysin	P09237	MMP7	1.53	0.0000	0.000	Increasing	Increasing rate
NET4	Netrin-4	Q9HB63	NTN4	1.50	0.0000	0.000	Increasing	Increasing rate
NID2	Nidogen-2	Q14112	NID2	1.51	0.0000	0.000	Increasing	Increasing rate
Nidogen	Nidogen-1	P14543	NID1	1.79	0.0000	0.000	Increasing	Increasing rate
OLR1	Oxidized low-density lipoprotein receptor 1	P78380	OLR1	2.65	0.0000	0.000	Increasing	Increasing rate
OMD	Osteomodulin	Q99983	OMD	1.79	0.0000	0.000	Increasing	Increasing rate
OX2G	OX-2 membrane glycoprotein	P41217	CD200	2.60	0.0000	0.000	Increasing	Increasing rate
PAI-1	Plasminogen activator inhibitor 1	P05121	SERPINE1	2.00	0.0000	0.000	Increasing	Increasing rate
Siglec-6	Sialic acid-binding Ig-like lectin 6	O43699	SIGLEC6	16.92	0.0000	0.000	Increasing	Increasing rate
uPA	Urokinase-type plasminogen activator	P00749	PLAU	2.18	0.0000	0.000	Increasing	Increasing rate

Table 3

Biological processes enriched in proteins that change with gestational age. Odds ratios from a Fisher's exact test and p-values are provided for all biological processes that had 3 or more significant proteins.

Biological process	No. of Proteins	Corresponding Genes Symbols	Odds Ratio	p	Decreasing	Increasing
defense response to fungus	4	MPO;GNLY;HAMP;HRG	12.4	0.003	MPO;GNLY;HAMP;HRG	
defense response	6	MPO; CST3; INHBA; HP; TFF3; ICOSLG	5.7	0.003	MPO;HP;ICOSLG	CST3;INHBA;TFF3
germ cell migration	3	KIT;ITGA1 ITGB1;CXCL12	27.7	0.004	KIT;ITGA1 ITGB1;CXCL12	
smooth muscle cell migration	3	ITGA2B ITGB3;DDR1;PLAU	27.7	0.004		ITGA2B ITGB3;DDR1;PLAU
regulation of bone resorption	3	CSF1R;ITGA2B ITGB3;SRC	27.7	0.004	SRC	CSF1R;ITGA2B ITGB3
negative regulation of leukocyte tethering or rolling	3	CCL25;CCL28;CXCL12	27.7	0.004	CXCL12	CCL25;CCL28
proteolysis	20	F11;MMP9;LTF;MMP7;CTSA;F7;ACY1;BMP1;REN;ECE1;HGFAC;OLR1;PAPPA;PLAU;ADAMI2;MMP12;PRSS22;MMP1;CTS;PCSK9	2.1	0.006	F11;MMP9;REN;ECE1;HGF AC;MMP12	LTF;MMP7;CTSA;F7;ACY1;BMP1;OLR1;PAPPA;PLAU;ADAMI2;PRSS22;MMP1;CTS Z;PCSK9
cell chemotaxis	8	KIT;CCL25;PPBP;CCL28;CXCL6;CCL15;CXCL12;PPBP	3.5	0.007	KIT;PPBP;CXCL6;CXCL12;PP BP	CCL25;CCL28;CCL15
leukocyte migration	11	MMP9;ANGPT2; CCL25;AIMP1;FN1;ITGA1 ITGB1;OLR1;ITGA2B ITGB3;FYN;MMP1;SRC	2.7	0.008	MMP9;ANGPT2;ITGA1 ITGB1;FYN;SRC	CCL25;AIMP1;FN1;OLR1;IT GA2B ITGB3;MMP1
cellular response to hormone stimulus	4	IGFBP2;GHR;PGF;CGA TSHB	7.4	0.008	GHR	IGFBP2;PGF;CGA TSHB
macrophage differentiation	3	MMP9;CSF1R; VEGFA	13.8	0.008	MMP9	CSF1R; VEGFA
cell-substrate adhesion	3	VWF;ITGA1 ITGB1;ITGA2B ITGB3	13.8	0.008	ITGA1 ITGB1	VWF;ITGA2B ITGB3
mesodermal cell differentiation	3	INHBA;ITGA1 ITGB1;ITGA2B ITGB3	13.8	0.008	ITGA1 ITGB1	INHBA;ITGA2B ITGB3
defense response to bacterium	7	PPBP;HP;GNLY;CXCL13;CXCL6;H AMP;PPBP	3.7	0.008	PPBP;HP;GNLY;CXCL13;CXCL6;HAMP;PPBP	