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(54) **Title**: PREDICTING AND TREATING DIABETIC COMPLICATIONS

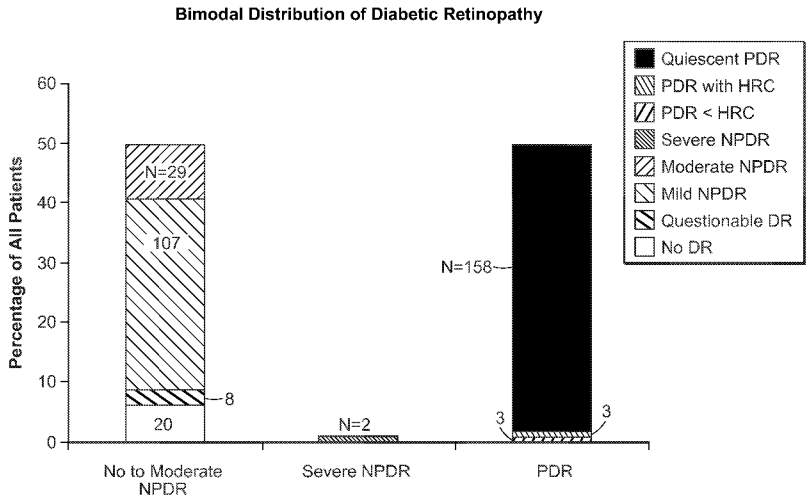


FIG. 1

(57) **Abstract**: Compositions and methods for diagnosing, predicting risk of, and/or treating diabetic retinopathy and/or diabetic nephropathy.

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PREDICTING AND TREATING DIABETIC COMPLICATIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional application No. 61/420,686, filed December 7, 2010, and PCT/US11/46672, filed August 4, 2011, the contents of both of which are specifically incorporated by reference herein.

TECHNICAL FIELD

This invention relates to compositions and methods for diagnosing or predicting risk of diabetic retinopathy (DR) and/or diabetic nephropathy (DN), and to compositions and methods for treating DR and/or DN.

BACKGROUND

Common complications of diabetes (e.g., long-term diabetes) include DR and DN. Moreover, the majority of diabetics develop DR and/or DN.

SUMMARY

The present invention is based, at least in part, on the discovery of an association between certain biological factors and the incidence, risk, or development of a microvascular complication, e.g., DR (e.g., PDR) and/or DN. Accordingly, the present disclosure provides that certain of the factors disclosed herein can be used, e.g., as biomarkers to diagnose predict risk of developing a microvascular complication, e.g., DR and/or DN. The present disclosure also provides that certain of the factors disclosed herein can be used in the treatment or therapy of a microvascular complication, e.g., DR and/or DN.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present invention; other, suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Other features and advantages of the invention will be apparent from the following detailed description and figures, and from the claims.

DESCRIPTION OF DRAWINGS

FIG. 1 is a bar graph showing the bimodal distribution of diabetic retinopathy in the Medalist subject population.

FIG. 2 is a line graph showing the rate of DR worsening in eyes with and without PDR at the final visit.

FIG. 3 is a scatter plot showing the correlation of plasma GPX3 Level to estimated GFR in a subset of 50 year medalist subjects. GFR was estimated using equation from Stevens et al, Am J Kidney Dis 2008; 51: 395-40.

FIG. 4 is a bar graph showing the prevalence of DR status (no DR or mild DR, moderate to severe DR, and proliferative DR ((PDR) advanced disease)) among the subjects described in Examples 4-.

FIG. 5 is a chart showing microvascular and macrovascular complications in the subjects disclosed in Examples 4-5.

FIG. 6 is a Table summarizing the clinical characteristics of the subjects disclosed in Examples 4-5.

FIG. 7 is a Table showing factors identified as being protective against PDR. (n= 5 for no or mild to moderate DR. n=7 for PDR. Data was analyzed using the Kruskal Wallis test.)

FIG. 8 is a Table showing factors identified as being protective against DN. (n=9 for ACR less than 30 and with a histology class of 1. N= 3 for ACR of greater than 30 and with a histology class greater than 1. Data was analyzed using the Kruskal Wallis test.)

FIG. 9 shows the amino acid sequence (SEQ ID NO: 2) of full length precursor of human RBP3 (SEQ ID NO: 2).

FIG. 10 shows the nucleotide sequence (SEQ ID NO: 1) of a cDNA encoding the full length precursor of human RBP3 (SEQ ID NO: 2).

FIG. 11 shows histograms with the values of RBP3, PTGDS and Cystatin C protein levels in vitreous of Medalists without PDR versus in vitreous from Medalists with PDR, as measured via Western blots. "M" refers to Mild-NPDR and "P" refers to PDR.

FIG. 12 is a histogram with the values of RBP3 protein levels in vitreous of Medalists without PDR versus in vitreous from Medalists with active PDR or quiescent PDR, as measured via Western blots.

FIG. 13 represents a Western blot (A) and a diagram (B) showing the levels of RBP3 in vitreous of Medalists with no to mild NPDR ("N") and Medalists with PDR ("PDR").

FIG. 14 represents a Western blot (A) and a diagram (B) showing the levels of RBP3 in retina of Medalists with mild NPDR ("N") and Medalists with PDR ("P").

FIG. 15 is a Western blot showing the presence of RBP3 in human plasma.

FIG. 16 is a diagram showing the number of endothelial cells that have migrated in the migration assay, following exposure to low or high glucose concentrations and no treatment, treatment with vehicle alone and treatment with RBP3.

FIG 17 shows the nucleotide and amino acid sequence of human PEBP1 (SEQ ID NOs: 3 and 4, respectively).

DETAILED DESCRIPTION

DR is damage that occurs to the retina of the eye in diabetics. Symptoms of DR range from blurred vision to loss of vision. Moreover, DR is a major cause of vision loss in developed countries. Understanding the causal role of vascular endothelial growth factor (VEGF) in the development of the proliferative DR (PDR) and vascular permeability has identified inhibitors of VEGF (e.g., AVASTIN and LUCENTIS) as effective treatments for diabetic neovascularization and macular edema. However, mechanisms by which hyperglycemia propagates the progression of DR are still not fully established. The only proven way to help prevent the initiation and progression of DR is good glycemic control. Several reasons may be responsible for the difficulty in identifying causal factors and effective treatments for the early stages of DR. These include challenges in obtaining retinal tissues in various stages of DR, lack of validated biomarkers and the absence of a salient rodent model. Recent therapeutic advances using inhibitors of VEGF for diabetic macular edema and neovascular lesions of DR are substantial. However, there remains a critical need to evaluate retinal tissue at all stages of DR to identify potential therapeutic targets and to validate potential markers of incidence and progression of DR in diabetic individuals.

DR is the result of microvascular retinal changes. The early stage of DR is referred to as non-proliferative diabetic retinopathy (NPDR), which is a stage during which blood vessels do not proliferate. NPDR can be separated out into mild NPDR, moderate NPDR, and severe NPDR. As DR progresses, blood vessels start to proliferate (i.e. grow) and new blood vessels form. This stage is referred to as proliferative diabetic neuropathy (PDR). These new blood vessels can bleed, cloud vision, and destroy the retina. Late stages may also involve retinal detachment and/or neovascular glaucoma. PDR can further be subdivided into two forms: (i) active PDR, wherein the blood vessels continue to develop and form; and (ii) quiescent PDR,

which is described as PDR that is no longer active and is seen, e.g., in subjects having been treated with laser therapy.

Diabetic retinopathy severity grading is described in the following two references: 1: Grading diabetic retinopathy from stereoscopic color fundus photographs--an extension of the modified Airlie House classification. ETDRS report number 10. Early Treatment Diabetic Retinopathy Study Research Group. Ophthalmology. 1991 May;98(5 Suppl):786-806. PubMed PMID: 2062513; and 2: Fundus photographic risk factors for progression of diabetic retinopathy. ETDRS report number 12. Early Treatment Diabetic Retinopathy Study Research Group. Ophthalmology. 1991 May;98(5 Suppl):823-33. PubMed PMID: 2062515. It is defined as follows:

1) Mild nonproliferative retinopathy (NPDR); At least one microaneurysm, and definition not met for moderate nonproliferative retinopathy, severe nonproliferative retinopathy, early proliferative retinopathy, or high-risk proliferative retinopathy (see below). ETDRS levels below 35. Level between 10 and 20 is very mild NPDR;
2) Moderate NPDR: Hemorrhages and/or microaneurysms ≥ standard photograph 2A*; and/or soft exudates, venous beading, or intraretinal microvascular abnormalities definitely present; and definition not met for severe nonproliferative retinopathy, early proliferative retinopathy, or high-risk proliferative retinopathy (see below). ETDRS levels 35, 43: moderate NPDR less than 4:2:1;
3) Severe NPDR: Soft exudates, venous beading, and intraretinal microvascular abnormalities all definitely present in at least two of fields four through seven; or two of the preceding three lesions present in at least two of fields four through seven and hemorrhages and microaneurysms present in these four fields, equaling or exceeding standard photo 2A in at least one of them; or intraretinal microvascular abnormalities present in each of fields four through seven and equaling or exceeding standard photograph 8A in at least two of them; and definition not met for early proliferative retinopathy or high-risk proliferative retinopathy (see below). ETDRS levels 53A-E: severe to very severe NPDR, 4:2:1 rule;
4) Early proliferative retinopathy (i.e., proliferative retinopathy without Diabetic Retinopathy Study high-risk characteristics): New vessels; and definition not met for high-risk proliferative retinopathy (see below); and
5) High-risk proliferative retinopathy (proliferative retinopathy with Diabetic Retinopathy Study high-risk characteristics): New vessels on or within one disc diameter of the optic

disc (NVD) ≥ standard photograph 10A* (about one-quarter to one-third disc area), with or without vitreous or preretinal hemorrhage; or vitreous and/or preretinal hemorrhage accompanied by new vessels, either NVD < standard photograph 10A or new vessels elsewhere (NVE) ≥ one-quarter disc area. ETDRS levels 61, 65, 71, 75, 81, 85: PDR, high-risk PDR, very severe or advanced PDR.

* Early Treatment Diabetic Retinopathy Study Research Group. Grading diabetic retinopathy from stereoscopic color fundus photographs--an extension of the modified Airlie House classification. ETDRS report number 10. Ophthalmology 1991;98:786-806. Adapted from the Early Treatment Diabetic Retinopathy Study Research Group. Early Treatment Diabetic Retinopathy Study design and baseline patient characteristics. ETDRS report number 7. Ophthalmology 1991;98:742.

DN is kidney disease or damage that occurs in diabetics. DN is a major cause of sickness and death in persons with diabetes. It is the leading cause of long-term kidney failure and end-stage kidney disease in the United States, and often leads to the need for dialysis or kidney transplantation.

As further described in the Examples, it has been shown herein that specific factors (e.g., proteins) are expressed at higher levels (e.g., at least 1.5 fold higher level) in type 1 diabetic individuals without a diabetic microvascular complication (DMC), such as diabetic retinopathy (DR) and diabetic nephropathy (DN), relative to type 1 diabetic individuals with DR or DN, respectively. Such factors are referred to as "protective factors." It has also been shown herein that specific factors (e.g., proteins) are expressed at lower levels in type 1 diabetic individuals without DN, relative to type 1 diabetic individuals with DN. Such factors are referred to herein as "risk factors."

Tables 2, 4 and Figure 7 provide examples of factors that are expressed at higher levels in type 1 diabetic individuals without DR relative to those with DR. Table 6 provides factors with a statistically significant difference in expression (e.g., at least 1.5 fold) between type 1 diabetic individuals without DR and those with DR (see Examples 1 and 4), wherein individuals without DR have a higher level of the factors. These factors are DR protective factors.

Table 6: DR protective factors, exemplary accession numbers and fold increase in type 1 diabetes individuals without DR relative to those with DR

	Name of DR protective factor	**Accession Nos.**	**Fold**

			increase
1	B3GNT1 N-acetyllactosaminide beta-1,3-Nacetylglucosaminyltransferase	IPI00009997 IPI00009997.1	∞
2	LRP2 Low-density lipoprotein receptor-related protein 2 precursor	IPI00024292 IPI00024292.2	∞
3	CD14 Monocyte differentiation antigen CD14 precursor	IPI00029260 IPI00029260.2	∞
4	TNR Isoform 2 of Tenascin-R precursor	IPI00554760, IPI00554760.1, IPI00554760.2, IPI00554760.3	∞
5	BTD Uncharacterized protein BTD (Fragment)	IPI00744685 IPI00744685.3	∞
6	CHL1 Isoform 1 of Neural cell adhesion molecule L1-like protein precursor	IPI00783390 IPI00783390.2	∞
7	IGLV1-40 V1-13 protein (Fragment)	IPI00789259 and EMBL CDS accession number AAF62890.1	∞
8	COL18A1 Isoform 2 of Collagen alpha-1(XVIII) chain precursor	Protein COPa ID IPI00022822	16.80
9	SEZ6 Isoform 3 of Seizure protein 6 homolog precursor	UniProt accession no. IPI00748395	10.73
10	HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein precursor	EMBI-EBI accession no. IPI00024284 and IPI00024284.5	9.10
11	APLP1 amyloid precursor-like protein 1 isoform 1 precursor	UniProt accession no. IPI00607600 and IPI00607600.3	9.10
12	FCGBP IgGFc-binding protein precursor	IPI00242956 and NP_003881.2	7.55

13	APLP2 Isoform 1 of Amyloid-like protein 2 precursor	EMBL-EBI accession no. IPI00031030 and IPI00031030.1	6.75
14	TAGLN Transgelin	EMBL-EBI accession no. IPI00216138 and IPI00216138.6	4.20
15	AGT Angiotensinogen precursor	EMBL-EBI accession no. IPI00032220 and IPI00032220.28	3.39
16	C9 Complement component C9 precursor	EMBL-EBI IPI00022395 and IPI00022395.1	3.27
17	Autotaxin isoform gamma	EMBI-EBL IPI00878576 and UniProt accession no. Q13822.3	2.84
18	RBP3 Interphotoreceptor retinoid-binding protein precursor	IPI00022337 and IPI00022337.1	2.71
19	Transthyretin	EMBL-EBI accession no. IPI00855916 and UniProt accession no. A6XGL1.1	2.68
20	CST3;CST2 Cystatin-C precursor	EMBL-EBI accession no. IPI00032293 and IPI00032293.1	2.45
21	A2M Alpha-2-macroglobulin precursor	EMBL-EBI accession no. IPI00478003 and	2.10

		IPI00478003.1	
22	CP Ceruloplasmin precursor	EMBL-EBI accession no. IPI00017601 and IPI00017601.1	1.58

Table 4 lists three factors that are expressed at lower levels in type 1 diabetic individuals without DR relative to those with DR. Table 7 provides factors with a statistically significant difference in expression (e.g., at least 1.5 fold) between type 1 diabetic individuals without DR and those with DR (see Examples 1 and 4), wherein individuals without DR have a lower level of the factors. These factors are DR risk factors. A fold decrease of "0" indicates essentially undetectable levels of the factor in a subject without DR (i.e., absence of the risk factor).

Table 7: DR protective factors, exemplary accession numbers and fold decrease in type 1 diabetes individuals without DR relative to those with DR

	Name of DR risk factor	**Accession Nos.**	**Fold decrease**
1	CLEC3B Putative uncharacterized protein DKFZp686H17246	EBML-EBI accession no. IPI00792115 and IPI00792115.1),	0.11
2	AFM Afamin precursor	IPI00019943	0
3	CFD Complement factor D preproprotein	IPI00165972	0

Tables 3, 5 and Figure 8 provide examples of factors that are expressed at higher levels in type 1 diabetic individuals without DN relative to those with DN. Table 8 provides factors with a statistically significant difference in expression (e.g., at least 1.5 fold) between type 1 diabetic individuals without DN and those with DN (see Examples 2 and 5), wherein individuals without DN have a higher level of the factors. These factors are DN protective factors.

Table 8: DN protective factors, exemplary accession numbers and fold increase in type 1 diabetes individuals without DN relative to those with DN

	Name of DN protective factor	Accession Nos.	Fold increase
1	HDDC3 Isoform 1 of HD domain-containing protein 3	IPI00789618 IPI00789618.3	∞
2	IGJ immunoglobulin J chain	IPI00178926 IPI00178926.3	23.63
3	Rheumatoid factor D5 light chain (Fragment)	IPI00816799 IPI00816799.1	11.00
4	BPNT1 Isoform 2 of 3(2),5-bisphosphate nucleotidase 1	IPI00410215 and UniProt O95861.85	8.00
5	GNPDA1 Glucosamine-6-phosphate isomerase	IPI00009305 and UniProt P46926.107	6.60
6	HPRT1 Uncharacterized protein HPRT1	IPI00873466 and NP_003881.2	4.09
7	GSTT1 Glutathione S-transferase theta 1	IPI00893316 and UniProt C9JA47.9	3.48
8	BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101 and UniProt Q93088.2	3.22
9	APOA1BP Isoform 2 of Apolipoprotein A-I-binding protein precursor	IPI00848298 and EMBL-EBI accession no.IPI00848298.1	2.69
10	HPX Hemopexin precursor	IPI00022488 EMBL-EBI accession no. IPI00022488.1	2.44
11	ALDOB Fructose-bisphosphate aldolase B	IPI00218407 and UniProt Q8NHT3.51	2.36
12	AGMAT Agmatinase, mitochondrial precursor	IPI00305360 and UniProt Q9BSE5.88	2.35

13	GATM Glycine amidinotransferase (L-arginine:glycine amidinotransferase) variant	IPI00792191	2.13
14	PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446 and EMBL-EBI accession no. IPI00219446.5	2.11
15	CS Citrate synthase, mitochondrial precursor	IPI00025366 IPI00025366.4	2.06

The bottom half of Table 5 provides examples of factors that are expressed at lower levels in type 1 diabetic individuals without DN relative to those with DN. Table 9 provides factors with a statistically significant difference in expression between type 1 diabetic individuals without DN and those with DN (see Example 5), wherein individuals without DN have a lower level of the factors. These factors are DN risk factors.

Table 9: DN risk factors, exemplary accession numbers and fold decrease in type 1 diabetes individuals without DN relative to those with DN

	Name of DN risk factor	**Accession Nos.**	**1/Fold decrease**	**Fold decrease**
1	TTLL3;ARPC4 Actin-related protein 2/3 complex subunit 4	IPI00554811 IPI00554811.2	1/0.48=2.08	0.48
2	CTNNA1 Isoform 1 of Catenin alpha-1	IPI00215948 IPI00215948.4	1/0.42=2.38	0.42
3	P4HB Protein disulfide-isomerase precursor	IPI00010796 IPI00010796.1	1/0.42=2.38	0.42
4	RAB14 20 kDa protein	IPI00646415 and EMBL-EBI accession no. IPI00646415.1	1/0.35=2.86	0.35
5	EEF1A1 Elongation factor 1-alpha	IPI00025447 and EMBL-EBI accession no. IPI00025447.8	1/0.32=3.13	0.32

6	AP1B1 Isoform B of AP-1 complex subunit beta-1	IPI00413947 and IPI00413947.2	1/0.31=3.23	0.31
7	PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904 and IPI00009904.1	1/0.31=3.23	0.31
8	CALR Calreticulin precursor	IPI00020599 and IPI00020599.1	1/0.28=3.57	0.28
9	ACSL1 Isoform 2 of Long-chain-fatty-acid--CoA ligase 1	IPI00401448 and IPI00401448.1	1/0.27=3.70	0.27
10	PRKCSH protein kinase C substrate 80K-H isoform 2	IPI00792916 and UniProt accession no. A8K318.8	1/0.23=4.35	0.23
11	PDIA3 Protein disulfide-isomerase A3 precursor	IPI00025252 and IPI00025252.1	1/0.2=5.0	0.20
12	CAP1 Adenylyl cyclase-associated protein 1	IPI00008274 and UniProt accession no. Q01518.110	1/0.19=5.26	0.19
13	KTN1 kinectin 1 isoform b	IPI00783726 UniProt accession no. Q17RZ5.32	1/0.17=5.88	0.17
14	NDUFS2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor	IPI00025239 IPI00025239.2	1/0.14=7.14	0.14
15	RAB6A Isoform 2 of Ras-related protein Rab-6A	IPI00217943 and UniProt accession no. P20340.131	1/0.12=8.33	0.12
16	AP2A2 Adaptor-related protein complex 2, alpha 2 subunit variant (Fragment)	IPI00016621 and UniProt AP2A2.2	∞	0.00
17	RPN1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	IPI00025874 and IPI00025874.2	∞	0.00

In this table, Table 9, the fold changes were calculated from the following: the peptide numbers from individuals without DN were numerators, and the peptide numbers from

individuals with DN were denominators. A fold number of "0.00" indicates that theses proteins were not detected in individuals without DN (therefore, decreased "infinitely").

The second to last column of the Table indicates the fold "decrease" as calculated by using 1 as numerators and using the numbers of the last column as denominators.

Methods of Diagnosis and Prognosis

The present disclosure provides, *inter alia*, methods and compositions for diagnosing and predicting risk of developing diabetic microvascular complications (DMCs), e.g., diabetic retinopathy (DR) and or diabetic nephropathy (DN), in a subject. The methods may also be used to determine the effectiveness of a therapy for a DMC or the prognosis of a subject. A method may comprise determining the level (e.g., protein or expression level) or activity of one or more protective or risk factors of a DMC, such as the factors described herein.

The methods include obtaining (or providing) a sample from a subject, e.g., a sample of an eye, such as vitreous, aqueous, or retinal tissue; tears; kidney tissue; plasma; or urine, and evaluating the presence and/or level of one or more biomarker described herein (e.g., in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8) in the sample, and comparing the presence and/or level with one or more reference values, e.g., a control reference value that represents a normal level of the protein, e.g., a level in an unaffected subject, and/or a disease reference that represents a level of the proteins associated with DR or DN, e.g., a level in a subject having DR or DN or an increased (high) likelihood of developing DR or DN. In a preferred embodiment, the biomarker is a DR protective factor listed in Table 6, a DN protective factor listed in Table 8, a DR risk factor listed in Table 7, or a DN risk factor listed in Table 9.

Certain methods may comprise providing a sample from a subject (e.g., a subject having diabetes, e.g., type 1 diabetes), such as plasma, a kidney sample or an eye sample, e.g., a vitreous sample; determining the level of at least one protein (factor) listed in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8, preferably a factor listed in Table 6, 8, 7, or 9, in the sample; and determining whether the at least one protein is present in the sample at levels at least 50%, 75% (i.e., 1 ½ fold), 100% (i.e., 2 fold), 2.5 fold, 3 fold, 4 fold, 5 fold, 10 fold, 15 fold or higher or lower than a control value (e.g., reference level), wherein the control value is, e.g., the level of the factor in a subject having type 1 diabetes for at least 10, 15, 20, 25, or more years and who has not developed a microvascular complication, and wherein (i) a level of one or more proteins of Table 6 that is lower by, e.g., at least 50%, 75% (i.e., 1 ½ fold), 100% (i.e., 2 fold), 2.5 fold, 3 fold, 4 fold, 5 fold, 10 fold, 15 fold or more relative to a control value, e.g., the level of the factor in a

subject having type 1 diabetes for at least 10, 15, 20, 25, or more years and who has not developed DR, indicates that the subject has or is likely to develop DR (or a form thereof, e.g., an advanced form of NPDR, e.g., moderate or severe NPDR; or PDR, such as active or quiescent PDR; (ii) a level of one or more proteins of Table 8 that is lower by, e.g., at least 50%, 75% (i.e., 1 ½ fold), 100% (i.e., 2 fold), 2.5 fold, 3 fold, 4 fold, 5 fold, 10 fold, 15 fold, 20 fold or higher relative to a control value, e.g., the level of the factor in a subject having type 1 diabetes for at least 10, 15, 20, 25, or more years and who has not developed DN, indicates that the subject has or is likely to develop DN; and (iii) a level of one or more proteins of Table 7 or 9 that is higher by, e.g., at least 50%, 75% (i.e., 1 ½ fold), 100% (i.e., 2 fold), 2.5 fold, 3 fold, 4 fold, 5 fold, 10 fold, 15 fold or higher relative to a control value, e.g., the level of the factor in a subject having type 1 diabetes for at least 10, 15, 20, 25, or more years and who has not developed DR or DN, respectively, indicates that the subject has or is likely to develop DR or DN, respectively.

Certain methods may comprise providing a sample from a subject (e.g., a subject having diabetes, e.g., type 1 diabetes), such as plasma, a kidney sample or an eye sample, e.g., a vitreous sample; determining the level of at least one protein (factor) listed in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8, preferably a factor listed in Table 6, 8, 7 or 9, in the sample; and determining whether the at least one protein is present in the sample at levels essentially identical (e.g., at most 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% higher or lower than) a control value (e.g., reference level), wherein the control value is, e.g., the level of the protein in a subject who has developed a microvascular complication (such as PDR, e.g., active or quiescent PDR; or NPDR, e.g., mild, moderate or severe NPDR), and wherein (i) a level of one or more proteins of Table 6 that is essentially identical to a control value, indicates that the subject has or is likely to develop DR (or a form thereof, e.g., advanced forms of NPDR, e.g., moderate or severe NPDR; or PDR, such as active or quiescent PDR); (ii) a level of one or more proteins of Table 8 that is essentially identical to a control value, e.g., the level of the factor in a subject having DN or a form thereof, indicates that the subject has or is likely to develop DN; and (iii) a level of one or more proteins of Table 7 or 9 that is essentially identical to a control value, e.g., the level of the factor in a subject having DR or DN, respectively, or a form thereof, indicates that the subject has or is likely to develop DR or DN, respectively.

In certain embodiments, the level of a DR protective factor in a subject is compared to both that in a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that in a subject who has developed DR, e.g., severe NPDR or PDR, wherein a level of the DR protective factor in the subject that is significantly closer to that in a

subject who is protected than to that in a subject having DR indicates that the subject is likely to be protected from developing DR, whereas a level of the DR protective factor in the subject that is significantly closer to that in a subject who has DR, e.g., severe NPDR or PDR, than to that in a subject that is protected indicates that the subject is likely to develop DR, e.g., severe NPDR or PDR.

In certain embodiments, the level of a risk factor in a subject is compared to both that in a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that in a subject who has developed DR, e.g., severe NPDR or PDR, wherein a level of the risk factor in the subject that is significantly closer to that in a subject who is protected than to that in a subject having DR indicates that the subject is likely to be protected from developing DR, whereas a level of the risk factor in the subject that is significantly closer to that in a subject who has DR, e.g., severe NPDR or PDR, than to that in a subject that is protected indicates that the subject is likely to develop DR, e.g., severe NPDR or PDR.

In certain embodiments, the level of a DN protective factor in a subject is compared to both that of a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that of a subject who has developed DN, wherein a level of the DN protective factor in the subject that is significantly closer to that in a subject who is protected than to that in a subject having DN indicates that the subject is likely to be protected from developing DN, whereas a level of the DN protective factor in the subject that is significantly closer to that in a subject who has DN, than to that of a subject that is protected indicates that the subject is likely to develop DN.

In certain embodiments, the level of a DN risk factor in a subject is compared to both that of a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that of a subject who has developed DN, wherein a level of the DN risk factor in the subject that is significantly closer to that in a subject who is protected than to that in a subject having DN indicates that the subject is likely to be protected from developing DN, whereas a level of the DN risk factor in the subject that is significantly closer to that in a subject who has DN, than to that of a subject that is protected indicates that the subject is likely to develop DN.

A control or reference value may also be a statistically significant value obtained by, e.g., averaging the level of a particular factor present in more than 5, 10, 15, 20, 30, 40, 50, 100 or more individuals with particular characteristic, e.g., diabetes, but no DR or DN, or only mild forms thereof, such as mild NPDR.

A control or reference value is generally factor specific, and may be the value of the factor, e.g., a statistically significant value of the factor, in (i) one or more subjects that are protected from a microvascular complication or (ii) one or more subjects that have a microvascular complication. These two types of control or reference values may be referred to "protected control value" (for the value found in protected subjects) and "disease control value" (for the value found in diseases subjects). A reference value may depend on the stage of the microvascular complication. For example, an "RBP3 control value" or "RBP3 reference value" is a control or reference value of RBP3, e.g., the value of RBP3 in one or more subjects that are protected (e.g., a subject having diabetes for over 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 years and not having developed DR; an "RBP3 protected control value") or the value of RBP3 in one or more subjects that are not protected and have or are likely to develop DR (an "RBP3 disease control value," such as "RBP3 severe NPDR control value" or "RBP3 PDR control value").

In one embodiment, the level of RBP3 is measured in a subject, e.g., a subject with type 1 or 2 diabetes, to determine the likelihood of the subject to develop a DR complication, e.g., severe NPDR and PDR. The level of RBP3 may be measured, e.g., in the vitreous, retina, plasma or urine of the subject. The level of RBP3 may also be predictive of the effectiveness of a treatment or determining the prognosis of a DR complication. A method may comprise obtaining a sample from a subject and determining the level of RBP3 in the sample. The presence of a lower level (e.g., 1.5 or 2 fold lower) of RBP3 relative to a reference value, e.g., the level of RBP3 in type 1 diabetes subjects who have not developed DR after at least 5, 10, 15, 20 or more years of disease is indicative of the likelihood of the subject to have or to develop an advanced stage of NPDR, e.g., severe, NPDR or PDR, or a poor prognostic of the DR. A method may also comprise comparing the level of RBP3 in a subject to a reference level that is the level of RBP3 (e.g., in the vitreous, retina, plasma or urine) that is present in a subject having NPDR, e.g., mild, moderate or severe NPDR, or having PDR. A subject that is found to have a similar level of RBP3 protein relative to that in a subject having severe NPDR or PDR is likely to develop a DR complication, e.g., severe NPDR or PDR. In certain embodiments, the level of RBP3 in a subject is compared to both that in a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that in a subject who has developed DR, e.g., severe NPDR or PDR, wherein a level of RBP3 in the subject that is significantly closer to that in a subject who is protected than to that in a subject having DR indicates that the subject is likely to be protected from developing DR, whereas a level of RBP3 in the subject that is significantly

closer to that in a subject who has DR, e.g., severe NPDR or PDR, than to that in a subject that is protected indicates that the subject is likely to develop DR, e.g., severe NPDR or PDR.

In one embodiment, the level of PEBP1 is measured in a subject, e.g., a subject with type 1 or 2 diabetes, to determine the likelihood of the subject from developing a kidney complication, e.g., DN. The level of PEBP1 may also be predictive of the effectiveness of a treatment or determining the prognosis of a kidney complication. A method may comprise obtaining a kidney sample (e.g., sample of glomeruli) from a subject and determining the level of PEBP1 in the sample. The presence of a lower level (e.g., 1.5 or 2 fold) of PEBP1 relative to a reference value, e.g., the level of PEBP1 in type 1 diabetes subjects who have not developed DN after at least 5, 10, 15, 20 or more years of disease is indicative of the likelihood of the subject to have or to develop DN or a poor prognostic of DN. A method may also comprise comparing the level of PEBP1 in a subject to a reference level that is the level of PEBP1 that is present in a subject having DN. A subject that is found to have a similar level of PEBP1 protein relative to that of a subject having DN is likely to develop a kidney complication, e.g., DN. In certain embodiments, the level of PEBP1 in a subject is compared to both that of a subject who is protected, i.e., has not developed DR after at least 5, 10, 15, 20 or more years of disease, and that of a subject who has developed DN, wherein a level of PEBP1 in the subject that is significantly closer to that in a subject who is protected than to that in a subject having DN indicates that the subject is likely to be protected from developing DN, whereas a level of RBP3 in the subject that is significantly closer to that in a subject who has DN, than to that of a subject that is protected indicates that the subject is likely to develop DN.

In certain embodiments, an increased level of a protective factor or reduced level of a risk factor is predictive of protection from a particular (or single) microvascular complication, such as DR, e.g., PDR, or DN. In certain embodiments, an increased level of a protective factor or reduced level of a risk factor is predictive of protection from more than one microvascular complication, e.g., both DR and DN. For example, an increased level of GPX3, e.g., in plasma indicates a reduced risk of a subject to develop DR or DN.

In certain embodiments, a method comprises determining the protein level of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30 or more protective or risk factors of Tables 6, 8, 7 or 9. In certain embodiments, a method comprises determining the protein level of 1-58, 1-50, 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10, 1-5, 1-4, 1-3 or 1-2 protective or risk factors set forth in Tables 6, 8, 7 or 9. Preferred combinations of protective factors to be measured for determining the likelihood of a subject to have or to develop DR include RBP3 and

or more other factors in Table 6. In certain embodiments, the level of PEDF is also measured, wherein an increased level of PEDF is protective against DR, e.g., PDR. In certain embodiments, the level of PEBP1 and that of at least one other factor, e.g., in Table 8 or 9 is measured.

The level or concentration of protective or risk factors may be determined in a tissue sample, such as a kidney sample (e.g., renal glomeruli sample), eye vitreous or retina, or bodily fluid sample, e.g., urine, blood, plasma, or intraocular fluid. Protective or risk factors for DR may be measured in an eye sample, e.g., a sample of the vitreous, retina or intraocular fluid, of a subject. Protective or risk factors for DN may be measured in a kidney sample, e.g., a renal glomerulus sample.

A "level of a factor" refers to the quantity or concentration of the protein or RNA (e.g., RNA) of the factor, and may also refer to the measurement of any other factor that results in the determination of the level of the factor (e.g., the measurement of the level of a metabolite of an enzyme may be a measurement of the level of the enzyme). Similarly, measurements of upstream products may also be measurements of the level of a factor.

In certain embodiments, the level or concentration of one or more factor is measured in the blood or plasma of a subject. For example, the level of GPX3 may be measured in plasma, wherein an increased (or higher) level of GPX3 in plasma of a first subject relative to that in a second subject indicates that the first subject is less likely than the second subject to develop a kidney problem, such as DN; whereas reduced levels of GPX3 in plasma of a first subject relative to that in a second subject indicates that the first subject is more likely than the second subject to develop a kidney problem, e.g., DN (see Example 3). The level of RBP3 may be measured in plasma, wherein an increased (or higher) level of RBP3 in plasma of a first subject relative to that in a second subject indicates that the first subject is less likely than the second subject to develop a kidney problem, such as DN; whereas reduced levels of RBP3 in plasma of a first subject relative to that in a second subject indicates that the first subject is more likely than the second subject to develop a DR, e.g., PDR (see Example 6). In certain embodiments, the plasma level or concentration of both GPX3 and RBP3 is measured in a subject, e.g., to determine the likelihood of a subject to develop DR and/or DN. Any of the other factors described herein may also be measured in plasma, particularly if the factor is a soluble factor, e.g., a factor that is produced in a secreted form from a cell or a factor, e.g., a membrane bound factor, that is shed by a cell.

A higher level of a protective factor, e.g., RBP3, or reduced level of a risk factor can also be used as a measure of the success of a treatment. For example, a subject having type 1 diabetes who is responding positively to a diabetic treatment may have a higher level of a protective factor

and/or a lower level of a risk factor relative to a subject having type 1 diabetes who is not responding to a treatment or to the value of the factor at the beginning of the treatment of the subject. Thus, an increase in the level of a protective factor and/or a decrease in the level of a risk factor in a subject with type 1 diabetes who is being treated indicates that the subject responds positively to the treatment.

The presence and/or level of a protein can be evaluated using methods known in the art, e.g., using quantitative immunoassay methods. In some embodiments, high throughput methods, e.g., protein or gene chips as are known in the art (see, e.g., Ch. 12, Genomics, in Griffiths et al., Eds. Modern genetic Analysis, 1999,W. H. Freeman and Company; Ekins and Chu, Trends in Biotechnology, 1999, 17:217-218; MacBeath and Schreiber, Science 2000, 289(5485):1760-1763; Simpson, Proteins and Proteomics: A Laboratory Manual, Cold Spring Harbor Laboratory Press; 2002; Hardiman, Microarrays Methods and Applications: Nuts & Bolts, DNA Press, 2003), can be used to detect the presence and/or level of a biomarker listed herein (e.g., in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8, preferably Table 6, 8 or 9).

In some embodiments, once it has been determined that a person has DR or DN, or has an increased risk of developing DR or DN, then a treatment, e.g., as known in the art or as described herein, can be administered.

The compositions disclosed herein can include agents that detect or bind (e.g., that detect or bind specifically) to a biomarker described herein (e.g., in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8, preferably Table 6, 8, 7 or 9). Such agents can include, but are not limited to, for example, antibodies, antibody fragments, and peptides. In some instances, the compositions can be in the form of a kit. Such kits can include one or more agents that can detect or bind (e.g., that detect or bind specifically) to one or more biomarkers described herein (e.g., one or more of the biomarkers disclosed in Table 2, 3, 4, 5, 6, 8, 7, 9 or Figure 7 or 8, preferably Table 6, 8, 7 or 9) and instructions for use.

In certain embodiments, a method comprises determining the level of a protective or risk factor in a subject. The measurement may be performed in the subject, e.g., by imaging, or on a sample obtained from a subject. If the level of the factor is determined in a sample of a subject, a method may comprise first obtaining a sample from a subject, e.g., by using a needle or other apparatus to aspirate a sample. A sample may then be sent to a laboratory for determining the level of the factor, following the doctor's instructions. If the measuring is performed in the subject, the subject may be sent to a particular department in the hospital where they handle such matters, following the doctor's instructions. The level of the factor, as determined in the

laboratory or hospital is then sent back to the doctor who had ordered the measurement, or entered into a computer or data system that is accessible to the doctor. The doctor may then compare the value(s) received to reference values, which may, e.g., be present in a computer. For example, the doctor may enter the values into a computer, and the computer performs the comparison with one or more control values. The computer may also provide the conclusion regarding the likelihood of development of a microvascular complication by the subject. The doctor may then discuss the results with the subject, and choose a path forward, e.g., an appropriate treatment; the decision to re-evaluate the level of one or more factors at a later time; or to evaluate other criteria of the subjects, e.g., the presence or absence of certain symptoms.

Methods of Treatment

As used herein, "treatment" means any manner in which one or more of the symptoms of DR and/or DN are ameliorated or otherwise beneficially altered. As used herein, amelioration of the symptoms of the disorder refers to any lessening, whether permanent or temporary, lasting or transient that can be attributed to or associated with treatment by the compositions and methods of the present invention. For example, with DR, treatment can include lessening of any symptom associated with DR, including, but not limited to, blurred or distorted vision or difficulty reading, floaters, reduced vision, vision loss, pain, and/or bleeding in the eye. Similarly, with DN, treatment can include lessening of any symptom associated with DN, including, but not limited to, changes in appetite, change in sleep, protein in serum, weakness, and/or nausea.

In some embodiments, the present disclosure provides methods for treating a microvascular complication, e.g., DR and/or DN, in a subject (e.g., a subject with diabetes (e.g., type 1 and/or type 2 diabetes) by administering to the subject a therapeutically effective amount of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more, including all) agents that increase the level or activity of one or more of the DR protective factors disclosed in Table 6 for treating or preventing DR or increase the level or activity of one or more of the DN protective factors disclosed in Table 8 for treating or preventing DN. In certain embodiments, a treatment comprises administering to a subject in need thereof a therapeutically effective amount of an agent that reduces the level or activity of a DR or DN risk factor of Table 7 or 9, respectively. An agent may increase the level or activity of a protective factor or decrease the level or activity of a risk factor by at least 50%, 100% (1 fold), 1 ½ fold, 2 fold, 3 fold, 4 fold, 5 fold, 10 fold, 15 fold, 20 fold or more. In certain embodiments, a therapeutic method comprises bringing the level or activity of a protective or risk factor essentially to its level or activity in a

subject that is protected from the development of a microvascular complication. "Essentially within its level," refers to within less than 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of the control value. How close the level or activity can be brought to a control value depends on the particular factor, in particular on how different the level of the factor is in a protected subject versus a diseased subject.

An agent that increases the level or activity of a protective factor may be a small molecule, a protein comprising the protective factor or a biologically active variant (e.g., fragment) thereof, or a nucleic acid encoding a protein comprising the protective factor or a biologically active variant (e.g., fragment) thereof. An agent that reduces the level or activity of a risk factor may be a small molecule, an RNAi inhibitory molecule (e.g., an siRNA or hsRNA molecule), an antisense molecule, a ribozyme, or an aptamer.

Accordingly, the present disclosure includes treatments comprising administering one or more proteins, or nucleic acid(s) encoding the one or more proteins, consisting of, consisting essentially of, or comprising the amino acid sequences, or variants thereof, that are associated with any one or more of the accession numbers of the factors disclosed in Table 6 and/or 8. For example, useful amino acid sequences can have 50%, 60%, 70%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% sequence identity to any one or more of the accession numbers disclosed in Table 6 and/or 8, provided that they retain the necessary biological activity of the factor for its protective characteristics.

The present disclosure also contemplates use of nucleic acid sequences that encode amino acid sequences consisting of, consisting essentially of, or comprising the amino acid sequences associated with any one or more of the accession numbers disclosed in Table 6 and/or 8 or variants thereof. For example, useful nucleic acid sequences can encode an amino acid sequence with 50%, 60%, 70%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% sequence identity to any one or more of the accession numbers disclosed in Table 6 and/or 8.

To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 90%, or 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or

nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The determination of percent identity between two amino acid sequences is accomplished using the BLAST 2.0 program. Sequence comparison is performed using an ungapped alignment and using the default parameters (Blossom 62 matrix, gap existence cost of 11, per residue gapped cost of 1, and a lambda ratio of 0.85). The mathematical algorithm used in BLAST programs is described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997).

Useful proteins can also comprise amino acid sequences consisting of, consisting essentially of, or comprising the amino acid sequences associated with any one or more of the accession numbers disclosed in Table 6 and/or 8 with one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or any range between any of the afore listed integers, or more than 100) amino acid additions, deletions or substitutions, e.g., conservative amino acid substitutions, provided that the protein retains the necessary biological activity of the factor for its protective characteristics. Conservative amino acid substitutions are known in the art.

In some embodiments, useful proteins can include modified proteins that possess at least a portion of the activity (e.g., biological activity) of the unmodified proteins. For example, modified proteins can retain 50%, 60%, 70%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% of the activity (e.g., biological activity) of the unmodified proteins, e.g., the unmodified version of the amino acid sequences associated with any one or more of the accession numbers disclosed in Table 6 and/or 8.

In some embodiments, useful proteins include proteins that comprise a biologically active fragment of any one or more of the factors disclosed in Table 6 and/or 8.

In some embodiments, treatment of DR or prevention of DR can include administering one or more of the following proteins or biologically active variants thereof or nucleic acid encoding such to a subject in need of such treatment or prevention: B3GNT1 N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase (e.g, IPI00009997 and IPI00009997.1), LRP2 Low-density lipoprotein receptor-related protein 2 precursor (e.g., IPI00024292 and IPI00024292.2), CD14 Monocyte differentiation antigen CD14 precursor (e.g., IPI00029260 and IPI00029260.2), TNR Isoform 2 of Tenascin-R precursor (e.g., IPI00554760, IPI00554760.1, IPI00554760.2, and IPI00554760.3), BTD Uncharacterized protein BTD (Fragment) (e.g., IPI00744685 and IPI00744685.3), CHL1 Isoform 1 of Neural cell adhesion molecule L1-like protein precursor (e.g., IPI00783390 and IPI00783390.2), IGLV1-40 V1-13

protein (Fragment) (e.g., IPI00789259 and EMBL CDS accession number AAF62890.1), COL18A1 Isoform 2 of Collagen alpha-1(XVIII) chain precursor (e.g., Protein COPa ID IPI00022822), SEZ6 Isoform 3 of Seizure protein 6 homolog precursor (e.g., UniProt accession no. IPI00748395), HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein precursor (e.g., EMBI-EBI accession no. IPI00024284 and IPI00024284.5), APLP1 amyloid precursor-like protein 1 isoform 1 precursor (e.g., UniProt accession no. IPI00607600 and IPI00607600.3), FCGBP IgGFc-binding protein precursor (e.g., IPI00242956 and NP_003881.2), APLP2 Isoform 1 of Amyloid-like protein 2 precursor (e.g., EMBL-EBI accession no. IPI00031030 and IPI00031030.1), TAGLN Transgelin (e.g., EMBL-EBI accession no. IPI00216138 and IPI00216138.6), AGT Angiotensinogen precursor (e.g., EMBL-EBI accession no. IPI00032220 and IPI00032220.28), C9 Complement component C9 precursor (e.g., EMBL-EBI IPI00022395 and IPI00022395.1), - Autotaxin isoform gamma (e.g., EMBI-EBL IPI00878576 and UniProt accession no. Q13822.3), RBP3 Interphotoreceptor retinoid-binding protein precursor (e.g., IPI00022337 and IPI00022337.1), - Transthyretin (EMBL-EBI accession no. IPI00855916 and UniProt accession no. A6XGL1.1), CST3;CST2 Cystatin-C precursor (e.g., EMBL-EBI accession no. IPI00032293 and IPI00032293.1), A2M Alpha-2-macroglobulin precursor (e.g., EMBL-EBI accession no. IPI00478003 and IPI00478003.1), and CP Ceruloplasmin precursor (e.g., EMBL-EBI accession no. IPI00017601 and IPI00017601.1).

In some embodiments, treatment of DN or prevention of DN can include administering one or more of the following proteins or biologically active variants thereof or nucleic acid encoding such to a subject in need of such treatment or prevention: IPI00789618 (e.g., HDDC3 Isoform 1 of HD domain-containing protein 3, IPI00789618.3), IPI00178926 (IGJ immunoglobulin J chain and IPI00178926.3), IPI00816799 (Rheumatoid factor D5 light chain (Fragment) and IPI00816799.1), IPI00410215 (BPNT1 Isoform 2 of 3(2),5-bisphosphate nucleotidase 1 and UniProt O95861.85), IPI00009305 (GNPDA1 Glucosamine-6-phosphate isomerase and UniProt P46926.107), IPI00873466 (HPRT1 Uncharacterized protein HPRT1 and NP_003881.2), IPI00893316 (GSTT1 Glutathione S-transferase theta 1 and UniProt C9JA47.9), IPI00004101 (BHMT Betaine--homocysteine S-methyltransferase 1 and UniProt Q93088.2), IPI00848298 (APOA1BP Isoform 2 of Apolipoprotein A-I-binding protein precursor and EMBL-EBI accession no.IPI00848298.1), IPI00022488 (HPX Hemopexin precursor and EMBL-EBI accession no. IPI00022488.1), IPI00218407 (ALDOB Fructose-bisphosphate aldolase B and UniProt Q8NHT3.51), IPI00305360 (AGMAT Agmatinase, mitochondrial precursor and UniProt Q9BSE5.88), IPI00792191 (GATM Glycine amidinotransferase (L-arginine:glycine

amidinotransferase) variant), IPI00219446 (PEBP1 Phosphatidylethanolamine-binding protein 1 and EMBL-EBI accession no. IPI00219446.5), and IPI00025366 (CS Citrate synthase, mitochondrial precursor and IPI00025366.4).

In certain embodiments, treatment of DR or prevention of DR can include administering an agent that inhibits or reduces the expression or activity of one or more of: CLEC3B Putative uncharacterized protein DKFZp686H17246 (e.g., EBML-EBI accession no. IPI00792115 and IPI00792115.1), AFM Afamin precursor (e.g., IPI00019943), CFD Complement factor D preproprotein (e.g., IPI00165972), and PTGDS in a subject.

In some embodiments, treatment of DN or prevention of DN can include administering an agent that inhibits or reduces the expression or activity of one or more of: IPI00554811 (TTLL3;ARPC4 Actin-related protein 2/3 complex subunit 4 and IPI00554811.2), IPI00215948 (CTNNA1 Isoform 1 of Catenin alpha-1 and IPI00215948.4), IPI00010796 (P4HB Protein disulfide-isomerase precursor and IPI00010796.1), IPI00646415 (RAB14 20 kDa protein and EMBL-EBI accession no. IPI00646415.1), IPI00025447 (EEF1A1 Elongation factor 1-alpha and EMBL-EBI accession no. IPI00025447.8), IPI00413947 (AP1B1 Isoform B of AP-1 complex subunit beta-1 and IPI00413947.2), IPI00009904 (PDIA4 Protein disulfide-isomerase A4 precursor and IPI00009904.1), IPI00020599 (CALR Calreticulin precursor and IPI00020599.1), IPI00401448 (ACSL1 Isoform 2 of Long-chain-fatty-acid--CoA ligase 1 and IPI00401448.1), IPI00792916 (PRKCSH protein kinase C substrate 80K-H isoform 2 and UniProt accession no. A8K318.8), IPI00025252 (PDIA3 Protein disulfide-isomerase A3 precursor and IPI00025252.1), IPI00008274 (CAP1 Adenylyl cyclase-associated protein 1 and UniProt accession no. Q01518.110), IPI00783726 (KTN1 kinectin 1 isoform b and UniProt accession no. Q17RZ5.32), IPI00025239 (NDUFS2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor and IPI00025239.2), IPI00217943 (RAB6A Isoform 2 of Ras-related protein Rab-6A and UniProt accession no. P20340.131), IPI00016621 (AP2A2 Adaptor-related protein complex 2, alpha 2 subunit variant (Fragment) and UniProt AP2A2.2), and IPI00025874 (RPN1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit pre and IPI00025874.2) in a subject.

In certain embodiments, RBP3, e.g., human RBP3, or a biologically active variant thereof is administered to a subject having or likely to develop DR, e.g., PDR, or to protect the cells of a subject from high glucose exposure. "RBP3" refers to "retinol binding protein 3, interstitial," and is also referred to as interphotoreceptor retinoid-binding protein, IRBP, D10S64, D10S65, D10S66, and RBPI. As indicated in the NCBI Gene database, RBP3 is a large glycoprotein

known to bind retinoids and found primarily in the interphotoreceptor matrix of the retina between the retinal pigment epithelium and the photoreceptor cells. It is thought to transport retinoids between the retinal pigment epithelium and the photoreceptors, a critical role in the visual process. The amino acid sequence of human RBP3 can be divided into four contiguous homology domains with 33-38% identity. The precursor of the human RBP3 protein is 1247 aa long and has the amino acid sequence set forth in GenBank Accession No. NP_002891. The nucleotide and amino acid sequences of human RBP3 are set forth as SEQ ID NOs: 1 and 2, respectively, and shown in Figure 9. The signal peptide of human RBP3 corresponds to amino acids 1-17. The mature protein consists of amino acids 18-1247. The protein comprises four domains referred to as Peptidase_S41_IRBP regions. These domains are located at amino acids 27 to 318 of SEQ ID NO: 2, amino acids 329 to 626 of SEQ ID NO: 2, amino acids 639 to 931 of SEQ ID NO: 2, and amino acids 940 to 1226 of SEQ ID NO: 2. The xenopus RBP3 has been crystalized and its structure solved (Ghosh D et al, Mol Vis. 2007 Dec 13;13:2275-81), and from sequence homology some regions can be predicted. The authors conclude that the data may indicate that the retinol-binding site is restricted to one of the four modules, or to an intramodule site defined by multiple modules, consistent with the notion that not all four modules are functionally equivalent as the homology modeling results indicated.

A homozygous missense mutation (pAsp1080Asn) in human RBP3 has been reported to be associated with retinitis pigmentosa (den Hollander et al. Invest. Ophthalmol. Vis. Sci. April 2009 vol. 50 no. 4 1864-187), and the authors predict that this residue participates in the retinol binding domain of the human RBP3 protein.

The nucleotide sequence of a cDNA encoding full length human RBP3 precursor (SEQ ID NO: 1) consists of 4289 nucleotides, wherein nucleotides 115 to 3858 encode SEQ ID NO: 2. The signal peptide is encoded by nucleotides 115 to 165, and the mature protein is encoded by nucleotides 166 to 3855 of SEQ ID NO: 1.

Biologically active variants of the full length human RBP3 protein (having SEQ ID NO: 2 or the mature form thereof) that may be used in therapeutic methods for treating DR include those comprising an amino acid sequence that comprises fewer amino acids than SEQ ID NO: 2 or the mature form thereof, and contains, e.g., at most 5, 10, 20, 30, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more, fewer amino acids. A biologically active fragment of human RBP3 may comprise 1, 2, 3 or all 4 homology domains. Other biologically active fragments of human RBP3 include those that retain the ability to bind to retinol or other lipid, e.g., they comprise Asp1080.

Biologically active variants of human RBP3 also include full length immature and mature forms of human RBP3 or fragments thereof that comprise an amino acid sequence that differs from SEQ ID NO: 2 or fragment thereof in at most 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50 or 100 amino acid deletions, additions or substitutions, such as conservative amino acid substitutions. Biologically active variants of a human RBP3 protein may also include variants that are at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the full length mature or precursor human RBP3 protein or a fragment thereof.

Biologically active variants of human PEBP1 also include full length immature and mature forms of human PEBP1 or fragments thereof that comprise an amino acid sequence that differs from the naturally occurring sequence (e.g., SEQ ID NO: 4; GenBank Accession No. NP_002558; encoded by a nucleotide sequence having GenBank Accession No. NM_002567 and set forth herein as SEQ ID NO: 3; Figure 17) or fragment thereof in at most 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50 or 100 amino acid deletions, additions or substitutions, such as conservative amino acid substitutions. Biologically active variants of a human PEBP1 protein may also include variants that are at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the full length mature or precursor human PEBP1 protein or a fragment thereof.

The present disclosure also includes fusion proteins comprising any one or more amino acid sequence disclosed in Table 6 and/or 8 in combination with a moiety that increases the stability of the fusion protein *in vivo* (e.g., polyethelene glycol (PEG)) and/or that increases transport of the fusion protein to the therapeutic target (e.g., the eye and/or the kidney).

As further described herein, protein may be administered systemically or locally. For example, a protein for treating or preventing DR, e.g., human RBP3 or a biologically active variant thereof, may be administered directly into the eye, e.g., in the vitreous, e.g., by injection. For example, a protein may be injected into the eye using the same or a similar methodology as that used for administered LUCENTIS or AVASTIN to the eye of a subject. An agent for treating or preventing DR may also be administered to the eye in the form of drops or a periocular injection (peribulbar or subconjunctival).

In certain embodiments, a protein for treating DR, e.g., human RBP3 or a biologically active variant thereof, may be administered with another agent for treating or preventing DR, such as LUCENTIS or AVASTIN. Two or more pharmaceutical agents may be administered simultaneously or sequentially. They may be present in one pharmaceutical composition or more than one pharmaceutical composition.

Systemic administration is also expected to be functional, e.g., for treating DR, as the retinal blood barrier is leaky in diabetic subjects. In particular, regarding RBP3, as it does not appear to be expressed in any other tissues than the eye, systemic administration is not expected to cause significant toxicity.

Other methods of treatment comprise preventing the degradation of a factor listed in Table 6 or 8, such as RBP3. Yet other methods include administering an agent that increases the expression of a factor in Table 6 or 8 or that reduces the expression of a risk factor listed in Table 7 or 9. An agent may be a small molecule, e.g., a small molecule that activates the promoter of the factor. In certain embodiments, an agent for treating a subject as described herein is an agent that increases the activity of a factor in Table 6 or 8 or reduces the activity of a factor in Table 7 or 9.

The present disclosure also contemplates the use of gene therapy methods, e.g., to administer a nucleic acid encoding one or more of the factors (e.g., protective factors) or nucleic acids inhibiting the expression or activity of a DR or DN risk factor disclosed herein to a subject. For example, nucleic acids encoding a protein disclosed in Table 6 and/or 8, or a variant thereof, or a nucleic acid encoding the protein that increases the expression, level or activity, of one or more of the factors disclosed in Tables 6 and/or 8 can be incorporated into a gene construct to be used as a part of a gene therapy protocol.

The invention includes targeted expression vectors for in vivo transfection and expression of a polynucleotide that encodes a polypeptide disclosed in Table 6 and/or 8, or an active fragment thereof, in particular cell types, for cells of the eye and/or kidney. Expression constructs of such components can be administered in any effective carrier, e.g., any formulation or composition capable of effectively delivering the component gene to cells in vivo. Approaches include insertion of the gene in viral vectors, including recombinant retroviruses, adenovirus, adeno-associated virus, lentivirus, and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. Viral vectors transfect cells directly; plasmid DNA can be delivered naked or with the help of, for example, cationic liposomes (lipofectamine) or derivatized (e.g., antibody conjugated), polylysine conjugates, gramacidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or CaPO4 precipitation carried out in vivo.

A preferred approach for in vivo introduction of nucleic acid into a cell is by use of a viral vector containing nucleic acid, e.g., a cDNA. Infection of cells with a viral vector has the advantage that a large proportion of the targeted cells can receive the nucleic acid. Additionally,

molecules encoded within the viral vector, e.g., by a cDNA contained in the viral vector, are expressed efficiently in cells that have taken up viral vector nucleic acid.

Retrovirus vectors and adeno-associated virus vectors can be used as a recombinant gene delivery system for the transfer of exogenous genes *in vivo*, particularly into humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host. The development of specialized cell lines (termed "packaging cells") which produce only replication-defective retroviruses has increased the utility of retroviruses for gene therapy, and defective retroviruses are characterized for use in gene transfer for gene therapy purposes (for a review see Miller, *Blood* 76:271 (1990)). A replication defective retrovirus can be packaged into virions, which can be used to infect a target cell through the use of a helper virus by standard techniques. Protocols for producing recombinant retroviruses and for infecting cells in vitro or in vivo with such viruses can be found in Ausubel, et al., eds., Current Protocols in Molecular Biology, Greene Publishing Associates, (1989), Sections 9.10-9.14, and other standard laboratory manuals. Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are known to those skilled in the art. Examples of suitable packaging virus lines for preparing both ecotropic and amphotropic retroviral systems include ΨCrip, ΨCre, Ψ2 and ΨAm. Retroviruses have been used to introduce a variety of genes into many different cell types, including epithelial cells, in vitro and/or in vivo (see for example Eglitis, et al. (1985) Science 230:1395-1398; Danos and Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:6460-6464; Wilson et al. (1988) Proc. Natl. Acad. Sci. USA 85:3014-3018; Armentano et al. (1990) Proc. Natl. Acad. Sci. USA 87:6141-6145; Huber et al. (1991) Proc. Natl. Acad. Sci. USA 88:8039-8043; Ferry et al. (1991) Proc. Natl. Acad. Sci. USA 88:8377-8381; Chowdhury et al. (1991) Science 254:1802-1805; van Beusechem et al. (1992) Proc. Natl. Acad. Sci. USA 89:7640-7644; Kay et al. (1992) Human Gene Therapy 3:641-647; Dai et al. (1992) Proc. Natl. Acad. Sci. USA 89:10892-10895; Hwu et al. (1993) J. Immunol. 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573).

Another viral gene delivery system useful in the present methods utilizes adenovirus-derived vectors. The genome of an adenovirus can be manipulated, such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. See, for example, Berkner et al., BioTechniques 6:616 (1988); Rosenfeld et al., Science 252:431-434 (1991); and Rosenfeld et al., Cell 68:143-155 (1992).

Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, or Ad7 etc.) are known to those skilled in the art. Recombinant adenoviruses can be advantageous in certain circumstances, in that they are not capable of infecting non-dividing cells and can be used to infect a wide variety of cell types, including epithelial cells (Rosenfeld et al., (1992) supra). Furthermore, the virus particle is relatively stable and amenable to purification and concentration, and as above, can be modified so as to affect the spectrum of infectivity. Additionally, introduced adenoviral DNA (and foreign DNA contained therein) is not integrated into the genome of a host cell but remains episomal, thereby avoiding potential problems that can occur as a result of insertional mutagenesis in situ, where introduced DNA becomes integrated into the host genome (e.g., retroviral DNA). Moreover, the carrying capacity of the adenoviral genome for foreign DNA is large (up to 8 kilobases) relative to other gene delivery vectors (Berkner et al., supra; Haj-Ahmand and Graham, J. Virol. 57:267 (1986).

Yet another viral vector system useful for delivery of nucleic acids is the adeno-associated virus (AAV). Adeno-associated virus is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle. (For a review see Muzyczka et al., Curr. Topics in Micro. and Immunol.158:97-129 (1992). It is also one of the few viruses that may integrate its DNA into non-dividing cells, and exhibits a high frequency of stable integration (see for example Flotte et al., Am. J. Respir. Cell. Mol. Biol. 7:349-356 (1992); Samulski et al., J. Virol. 63:3822-3828 (1989); and McLaughlin et al., J. Virol. 62:1963-1973 (1989). Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate. Space for exogenous DNA is limited to about 4.5 kb. An AAV vector such as that described in Tratschin et al., Mol. Cell. Biol. 5:3251-3260 (1985) can be used to introduce DNA into cells. A variety of nucleic acids have been introduced into different cell types using AAV vectors (see for example Hermonat et al., Proc. Natl. Acad. Sci. USA 81:6466-6470 (1984); Tratschin et al., Mol. Cell. Biol. 4:2072-2081 (1985); Wondisford et al., Mol. Endocrinol. 2:32-39 (1988); Tratschin et al., J. Virol. 51:611-619 (1984); and Flotte et al., J. Biol. Chem. 268:3781-3790 (1993).

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of a nucleic acid compound described herein (e.g., a nucleic acid encoding a polypeptide disclosed in Table 6 or 8, or an active fragment thereof, and/or a nucleic acid that increases the expression and/or activity of a polynucleotide that encodes a polypeptide disclosed in Table 6 or 8 or a nucleic acid that inhibits a protein in Table 7 or 9) in the tissue of a subject. Typically non-viral methods of gene transfer rely on the normal

mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In some embodiments, non-viral gene delivery systems can rely on endocytic pathways for the uptake of the subject gene by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes. Other embodiments include plasmid injection systems such as are described in Meuli et al., J. Invest. Dermatol. 116(1):131-135 (2001); Cohen et al., Gene Ther. 7(22):1896-905 (2000); or Tam et al., Gene Ther. 7(21):1867-74 (2000).

In some embodiments, an agent, e.g., a gene encoding a factor described herein, e.g., a polynucleotide that encodes a polypeptide disclosed in Table 6 or 8, or an active fragment thereof, or an agent that inhibits the expression or activity of a factor in Table 7 or 9, is entrapped in liposomes bearing positive charges on their surface (e.g., lipofectins), which can be tagged with antibodies against cell surface antigens of the target tissue (Mizuno et al., No Shinkei Geka 20:547-551 (1992); PCT publication WO91/06309; Japanese patent application 1047381; and European patent publication EP-A-43075).

In clinical settings, the gene delivery systems for the therapeutic gene can be introduced into a subject by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g., by intravenous injection, and specific transduction of the protein in the target cells will occur predominantly from specificity of transfection, provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited, with introduction into the subject being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g., Chen et al., PNAS USA 91: 3054-3057 (1994)).

The pharmaceutical preparation of the gene therapy construct can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is embedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can comprise one or more cells, which produce the gene delivery system.

In some embodiments, the present disclosure includes the use of agonists of any one or more of the factors disclosed in Tables 6 and/or 8. In some embodiments, suitable agonists can increase the expression and/or activity of one or more of the factors disclosed in Tables 6 and/or 8, e.g., by about 2-fold, 3-fold, 4-fold, 5-fold, or more.

In some embodiments, the present disclosure includes the use of antagonists of any one or more of the factors disclosed in Tables 7 and/or 9. In some embodiments, suitable antagonists can decrease the expression and/or activity of one or more of the factors disclosed in Tables 7 and/or 9, e.g., by about 2-fold, 3-fold, 4-fold, 5-fold, or more.

Many of the factors disclosed herein are referenced by the International Protein Index (IPI) number assigned to them. The sequences associated with each of the disclosed IPI numbers are publically available and can be obtained and/or viewed, for example, using the European Institute for Bioinformatics website available at world wide web address ebi.ac.uk. Other suitable websites are also known in the art.

Subject Selection

The term "subject" is used throughout the specification to describe an animal, human or non-human, to whom treatment according to the methods of the present invention is provided.

The methods disclosed herein can include selecting a subject for treatment. For example, a subject can be selected if the subject has or is at risk for developing DR and/or DN, e.g., a subject having diabetes, e.g., type 1 or type 2 diabetes, or a subject who is prediabetic, e.g., having metabolic syndrome, insulin resistance, hyperglycemia, hyperlipidemia or a subject who is overweight or obese, e.g., having a BMI ≥ 25. In some instances, a subject can be selected if the subject has or is at risk for developing type 1 and/or type 2 diabetes. In some instances, a subject can be selected if the subject is taking or will take insulin, e.g., to treat diabetes.

Routes of Administration

One or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more, including all) of the agents, such as factors disclosed herein (e.g., disclosed in Tables 6 and/or 8) or agents inhibiting a factor of Table 7 or 9, can be administered alone or as a pharmaceutical composition (disclosed below) using any mode of administration, e.g., including any mode of administration that results in a therapeutically effective level in the eye (for DR) and/or the kidney (for DN). In some instances, a therapeutically effective level is an amount or level that results in one or more of the symptoms of DR and/or DN being ameliorated or otherwise beneficially altered. For the treatment of DR, an exemplary route of administration can include local administration into or onto the eye. For the treatment of DN, an exemplary route of administration can include local administration to the kidney. Other exemplary modes of administration suitable for either DR or DN include, but are not limited to, oral, parenteral,

inhalation (e.g., as a spray), topical, rectal, nasal, buccal, vaginal, and/or via an implanted reservoir.

The term parenteral as used herein includes subcutaneous, intracutaneous, intravenous, intramuscular, intra¬articular, intraarterial, intrasynovial, intrasternal, intrathecal, intralesional and intracranial injection or infusion techniques. Alternatively or in addition, the present invention may be administered according to any of the Food and Drug Administration approved methods, for example, as described in CDER Data Standards Manual, version number 004 (which is available at fda.give/cder/dsm/DRG/drg00301.htm). Where application over a period of time is advisable or desirable, the compositions of the invention can be placed in sustained released formulations (e.g., hydrogels) or implantable devices (e.g., implantable pumps).

Pharmaceutical Compositions

One or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more, including all) of the agents, e.g., factors disclosed herein (e.g., disclosed in Tables 6 and 8) or inhibitors of factors in Table 7 or 9, can be formulated in or as pharmaceutical compositions. Such pharmaceutical compositions can contain any conventional non-toxic pharmaceutically-acceptable carriers, adjuvants or vehicles. In some cases, the pH of the formulation may be adjusted with pharmaceutically acceptable acids, bases or buffers to enhance the stability of the formulated compound or its delivery form.

In some cases, pharmaceutical compositions containing one or more factors can be formulated according to the intended method of administration.

Pharmaceutical compositions containing one or more factors can be formulated in a conventional manner using one or more physiologically acceptable carriers or excipients. The nature of the pharmaceutical compositions for administration is dependent on the mode of administration and can readily be determined by one of ordinary skill in the art. In addition, methods for making such formulations are well known and can be found in, for example, Remington's Pharmaceutical Sciences, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, Pa., 1990. In some embodiments, the pharmaceutical composition is sterile or sterilizable.

Pharmaceutical compositions featured in the invention can contain carriers or excipients, many of which are known to skilled artisans. Excipients that can be used include buffers (for example, citrate buffer, phosphate buffer, acetate buffer, and bicarbonate buffer), amino acids, urea, alcohols, ascorbic acid, phospholipids, polypeptides (for example, serum albumin), EDTA, sodium chloride, liposomes, mannitol, sorbitol, water, and glycerol.

In some embodiments, pharmaceutical compositions can be presented in unit dosage form, for example, in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the composition may be in powder form for constitution with a suitable vehicle, for example, sterile pyrogen-free water, before use. Agents that enhance delivery into a cell can be used as well, e.g., liposomes or micelles.

In addition to the formulations described previously, the compositions can also be formulated as a depot preparation. Thus, for example, the compositions can be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Pharmaceutical compositions can also take the form of tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (for example, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (for example, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (for example, magnesium stearate, talc or silica); disintegrants (for example, potato starch or sodium starch glycolate); or wetting agents (for example, sodium lauryl sulphate). The tablets can be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (for example, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (for example, lecithin or acacia); non-aqueous vehicles (for example, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (for example, methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate. Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

The methods herein contemplate administration of an effective amount of compound or compound composition to achieve the desired or stated effect. Toxicity and therapeutic efficacy of the compounds and pharmaceutical compositions described herein can be determined by standard pharmaceutical procedures, using either cells in culture or experimental animals to determine the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose

therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and can be expressed as the ratio LD50/ED50. Polypeptides or other compounds that exhibit large therapeutic indices are preferred.

Data obtained from cell culture assays and further animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (that is, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans.

The formulations and routes of administration can be tailored to the disease or disorder being treated, and for the specific human being treated. A subject can receive a dose of the agent once or twice or more daily for one week, one month, six months, one year, or more. The treatment can continue indefinitely, such as throughout the lifetime of the human. Treatment can be administered at regular or irregular intervals (once every other day or twice per week), and the dosage and timing of the administration can be adjusted throughout the course of the treatment. The dosage can remain constant over the course of the treatment regimen, or it can be decreased or increased over the course of the treatment.

Generally the dosage facilitates an intended purpose for both prophylaxis and treatment without undesirable side effects, such as toxicity, irritation or allergic response. Although individual needs may vary, the determination of optimal ranges for effective amounts of formulations is within the skill of the art. Human doses can readily be extrapolated from animal studies (Katocs et al., Chapter 27 In: Remington's Pharmaceutical Sciences, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, Pa., 1990). Generally, the dosage required to provide an effective amount of a formulation, which can be adjusted by one skilled in the art, will vary depending on several factors, including the age, health, physical condition, weight, type and extent of the disease or disorder of the recipient, frequency of treatment, the nature of concurrent therapy, if required, and the nature and scope of the desired effect(s) (Nies et al., Chapter 3, In: Goodman & Gilman's "The Pharmacological Basis of Therapeutics", 9th Ed., Hardman et al., eds., McGraw-Hill, New York, N.Y., 1996).

Subject Evaluation

The methods can also include monitoring or evaluating the subject during and after treatment to determine the efficacy of the treatment, and, if necessary, adjusting treatment (e.g., by altering the composition, by increasing the dose of a single administration of the composition, by increasing the number of doses of the composition administered per day, and/or by increasing the number of days the composition is administered) to improve efficacy. Monitoring or evaluating the subject can include identifying a suitable marker of disease prior to commencing treatment and optionally recording the marker, and comparing the identified or recorded marker to the same marker during and/or after treatment. Suitable markers can include one or more symptoms of the subject's disease. Suitable markers also include one or more of the factors described in Tables 6, 8, 7 and 9. Adjustment of treatment would be recommended where the marker is a symptom of disease and comparison of the marker during or after treatment with the marker prior to treatment revealed either no change in the marker or an increase in the marker. Conversely, adjustment of treatment may not be required using the same markers where an increase in the marker is observed.

EXAMPLES

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

Example 1: <u>Identification of protective DR factors</u>

Evidence that diabetic retinal pathologies can be halted has been documented by the Joslin 50-Year Medalist Study (Keenan et al., Diabetes Care. 2007 Aug;30(8):1995-7. Epub 2007 May 16). Population characteristics for these subjects are shown in Table 1.

Table 1. Characteristics of Medalist Study participants.

	% (n); mean ± std dev
Male (%)	47.0% (192)
HbA1c (%)	7.3% ±1.1
Age (years)	67.2 ± 7.4
Age at diagnosis (years)	11.0 ± 6.5
Duration (years)	56.2 ± 5.8
BMI (kg/m^2)	26.0 ± 5.1
C-peptide (nmol/L)	0.07 ± 0.12
Cholesterol (mmol/L)	4.2 ± 0.9
HDLc (mmol/L)	1.6 ± 0.5
LDL (mmol/L)	2.2 ± 0.6
Triglycerides (mmol/L)	0.9 ± 0.5
Insulin dose (u/kg)	0.46 ± 0.2
Family History Any DM T1DM	29.7 (122) 12.9 (53)
DR3	38.8 (116)
DR4	52.0 (156)
DR3 or DR4	93.7 (295)
DR3/4	39.1 (118)
IA2 or GAD	29.7 (111)
IA2	14.9 (56)
GAD	18.4 (69)
PDR	55 (163)
Microalbuminuria (ACR<7.91)	13.1 (45)
Neuropathy (MNSI >2)	60.6 (183)
CVD	48.3 (160)

This study characterizes a number of individuals collectively referred to herein as 'Medalists' who have lived with for 50 or more years with type 1 diabetes (T1DM) by clinical exam, medical history and extensive chemistries.

Retinal pathology was documented by dilated fundus examination and fundus photography. The degree of renal disease was assessed through measurements of albumin, creatinine, cystatin C and estimated glomerular filtration rate (eGFR). After characterizing over 500 Medalists, a bimodal distribution of DR was observed with 50% of the Medalists having none to moderate nonproliferative DR and 50% having quiescent PDR (Fig. 1 and Table 1).

Surprisingly, standard risk factors, including duration of diabetes and HbA1C levels, were not associated with severity.

A subset of 97 Medalists has been followed with multiple ophthalmic examinations. Analysis of DR progression showed that 47.4% of eyes without proliferative DR (PDR) at baseline progressed to PDR, with a median time to progression to PDR of 38.4 years. The majority of Medalists who did not progress to PDR developed mild to moderate non-proliferative DR (NPDR) over a median follow-up of 20.6 years. Interestingly, of the eyes that did not develop PDR, all but one eye stopped progressing after 17 years of follow-up (Fig 2). Over the last two years we have been collaborating with the network for Pancreatic Organ Donors with Diabetes (nPOD) to procure tissues from Medalists after they have passed away. Organ donations have been obtained from 11 Medalists, including whole eyes, kidneys, pancreas and skin. During their initial study visit we obtained specimens of DNA, serum, plasma, and urine.

In the present experiments, samples were taken from eight eyes: three with no to moderate NPDR, four with PDR, and one ungradeable (due to scatter laser performed for non-diabetic pathology) as determined by grading of fundus photographs. Retinal pathology was assessed using standard methods. For proteomic analysis, retinal and vitreous specimens were isolated and isolated using mass spectrometry methods as previously described (Gao et al., J Proteome Res. 2008;7:2516-25; Gao et al., Nat Med. 2007;13:181-8). Initial analysis of these eight eyes by mass spectrometry identified over 450 proteins. Based on a minimum 1.5 fold increase and significance level of at least 0.1, 26 proteins were found to be higher in the vitreous of Medalists who have no to moderate NPDR compared to those with PDR. Interestingly, pathway analysis indicated that 6/26 of these proteins have anti-angiogenic actions, whereas, only 1/26 have anti-oxidative stress properties and 8/26 are adhesion proteins. (Table 2).

Table 2. Protective genes or proteins in Eye vitreous

G-Protein	
APLP2	amyloid beta (A4) precursor-like protein 2
	G-protein coupled receptor protein signaling pathway
Prostaglandin	
Enzyme	
PTGDS	prostaglandin D2 synthase 21kDa (brain)
	glutathione-independent prostaglandin D synthase, PGH2-> PGD2
	also fatty acid biosynthetic process
associate with	

Basement Membrane	
B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 type II transmembrane protein, integral to Golgi membrane
Complement	
C5	Complement C5
C6	Complement C6
A2M	Alpha-2-macroglobulin a protease inhibitor and cytokine transporter
Growth/ tumor suppressor gene	
DKK3	
WIF1	
Ig superfamily	
Rheumatoid factor C6 light chain	
IGLV1-40	
Ig kappa chain V-IV region Len	
IGHM	
Cytokine	
FAM3C	
SERPINF1(PEDF)	
A2M	
Adhesion protein	
CLSTN1	
SPARCL1	
CDH2	cadherin 2, type 1, N-cadherin
SPP1	secreted phosphoprotein 1 ECM-receptor interaction, Focal adhesion, Toll-like receptor signaling pathway, Signaling by PDGF, Integrin cell surface interactions, osteoblast differentiation
NRCAM	

APP	
Protease inhibition	
A2M	Alpha-2-macroglobulin
	a protease inhibitor and cytokine transporter
SERPINF1(PEDF)	
PCSK1N	
CST3	cystatin C
CPE	Carboxypeptidase E
APP	serine-type endopeptidase inhibitor activity
Lipid metabolism	
ASAH1	Acid ceramidase
APOE	
Oxidative Stress	
GPX3	
Not grouped	
ABI3BP	
CUTA	
SEZ	

Clinical characterization of the Medalists and histopathologic and proteomic analysis of their tissues has enabled us to identify new biomarkers for progression to PDR for diabetic patients with shorter duration disease. Furthermore, these protective factors against the progression of DR are potential therapeutic targets.

These potential "protective" and "risk" factors identified from the vitreous and retinas of Medalist patients are secondarily screened using (intraocular) aqueous fluid and plasma from a population of both type 1 and 2 diabetic patients who are having cataract extraction, to determine the levels of biomarkers in more readily accessible fluids such as plasma, and correlate the levels in plasma to those in intraocular fluids. There is also a small group of nondiabetic individuals that undergoes cataract surgery at BEI each year. It is standard procedure to discard aqueous fluid during cataract surgery; this discarded fluid is used to assess the presence of candidate protective/ risk factors. Additionally, we will obtain medical history, physical exam, and blood samples to characterize the non-Medalists in the same manner as the Medalist participants. Using

this case-control approach, the differential presence of candidates can be assessed in the aqueous, plasma and potentially urine across the stages of DR.

Example 2: Identification of protective DN factors

Nine kidney samples from the Medalists were analyzed by mass spectrometry as previously described (Gao et al., J Proteome Res. 2008;7:2516-25; Gao et al. Nat Med. 2007;13:181-8). Using the results from the proteomic analyses and correlated pathology derived from the renal glomeruli, we found that the expression of 14 proteins are significantly (1.5 fold) greater in kidneys without disease vs. those with class II and III levels of nephropathy. The proteins are listed in Table 3.

Table 3. Protective genes or proteins in Renal Glomeruli

Lipid Metabolism	
APOA1BP	Isoform 2 of Apolipoprotein A-I-binding protein precursor interacts with apolipoprotein A-I (apoA-I), the major apolipoprotein of high-density lipoproteins (HDLs)
Oxidation reduction/ Oxidative Stree	
MOSC2	Isoform 1 of MOSC domain-containing protein 2, mitochondrial precursor (mt)
HPX	Hemopexin precursor glycoprotein, binds heme
GPX3	Glutathione peroxidase 3 precursor detoxification of hydrogen peroxide
GSTT1	Glutathione S-transferase theta 1
PRDX1	peroxiredoxin 1 antioxidant enzymes, reduce hydrogen peroxide and alkyl hydroperoxides
HADH	Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor (mt) also fatty acid metabolism
SCCPDH	saccharopine dehydrogenase (putative) oxidoreductase activity (mt)
Purine metabolism	

HPRT1	hypoxanthine phosphoribosyltransferase 1
Basement membrane	
COL18A1	collagen, type XVIII, alpha 1
Mitochondrial metabolism/ enymes	
MOSC2	
HADH	
SCCPDH	
GATM	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)
	Metabolism of amino acids and derivatives
AGMAT	agmatine ureohydrolase (agmatinase)
	Metabolism of amino acids and derivatives
CS	citrate synthase
Glucose metabolism	
GNPDA1	glucosamine-6-phosphate deaminase 1
	Amino sugar and nucleotide sugar metabolism

Validation of the proteins identified through comparison of those with and without DN will be done using samples of urine, plasma and serum from the Joslin Natural History of Microalbuminuria Studies. The validation study is a case-control testing the hypothesis of a significantly lower level of the factor of interest being present in fast progressors, defined as those who have had a greater than 7% eGFR loss of per year over a 10 year period within 15 year duration compared to those with chronic kidney disease classifications 1, 2, or 3.

Example 3: Plasma levels of DN protective factor GPX3 correlate positively with the GFR

Candidates identified by our proteomic analysis of the vitreous and kidney are measured in the plasma of normal and type 1 diabetic patients to validate the relationship with protection against DR/DN, and to examine whether there is a temporal relationship with progression of DR/DN.

GPX3, which was identified as a biomarker in both the vitreous and kidney, a secreted enzyme and is involved in neutralizing hydroxides and preventing lipid peroxidation, was measured plasma GPX3 levels by ELISA method in 40 Medalists and a positive correlation was observed between the level of GPX3 and estimated GFR calculated by cystatin C (Fig. 3).

The results described herein are corroborated by reports in the literature. PEDF, an anti-angiogenic protein representing a major pathway of protective factors identified in the vitreous proteomic study (Table 2), has been assayed in plasma. Levels of PEDF in plasma among those with PDR have been found at 5.3 ± 5.1 ng/mL and among those without at 7.7 ± 6.1 ng/mL (Matsuyama et al., Mol Vis. 2008 May 28;14:992-6). A sample size of 100 cases and 100 controls yields a power of 83% with p ≤0.05). In aqueous Yoshida et al report a mean PEDF level of 1.8 ±0.2 ng/mL among those with DR and 6.4 ±0.8 ng/mL among those without (Br J Ophthalmol. 2007 Sep;91(9):1133-4).

Example 4: Identification of factors that protect against DR

The prevalence of DR in the Medalists evaluated is shown in FIG.4. Candidate factors that protect against DR were identified by comparing the levels or expression of factors in individuals with DR and those without DR. Factors with a statistically significant difference in expression between the individuals with DR and those without DR were selected. A total of 700 candidate factors were selected. Further statistical analysis was then applied to select protective factors from the candidate factors. After applying kruskal-wallis statistical analysis, a total of 22 protective factors (the first 22 factors in the Table, i.e., those above the black line) and 3 risk factors (the last three lines in the Table, i.e., those under the black line) were identified, as shown in Table 4 and FIG. 7. FIG.7 lists only the protective factors. The criteria of the selection for the protective factors was p value <0.05, and expression level increased > = 1.5 fold in individuals without DR (i.e. no to mild NPDR).

The analysis was performed essentially as follows. The protein analysis was done using a label-free quantitative analysis of 1D PAGE-LC/MS/MS-based proteomics. Soluble proteins from vitreous tissues of 50-Year Medalists were loaded onto 10% acrylamide protein gels for separations in 1-D gel electrophoresis. We loaded 50uL (micro liter) of vitreous fluid with sample buffer in each sample lane on the gel. Then the gel was stained with Coomassie Blue. Each lane of gel was then cut into 40 slices. The 40 slices were digested in separate tubes by trypsin. These digested protein gel slices were then loaded into an LC machine for the later MS/MS analysis.

The number of peptide hits was obtained from the "MS manager," software previously developed by Benbo Gao (Gao B et al. Mol Cell Proteomics 2008;7:2399-2409). MS manager is designed based on the PHP-MySQL-Apache platform. It compiles the search results from SEQUEST and X!Tandem of MS/MS data, and then parses these results into the MySQL database. After applying the algorithm for filtering proteins and combining the IPI identifier, a

final report of identified proteins is generated in a table with peptide hit numbers. The results are shown in Table 4 below.

Table 4: Protective Factors for DR

	DR grade	2	3	2	0	0	No-mild NPDR	8	8	8	8	8	8	8	PDR		
Name of DR protective factor	**Accession Nos.**	**262CD**	**600KS**	**600KD**	**269CS**	**269CD**	**Average**	**629TD**	**629TS**	**482SS**	**482SD**	**365LD**	**220WS**	**220WD**	**Average**	**Fold increase**	**P value**
B3GNT1 N-acetyllactosaminide beta-1,3-Nacetylglucosaminyl transferase	IPI00009997	7	7	13	6	0	6.6	0	0	0	0	0	0	0	0.0	∞	0.006687
CHL1 Isoform 1 of Neural cell adhesion molecule L1-like protein precursor	IPI00783390	3	4	3	5	0	3.0	0	0	0	0	0	0	0	0.0	∞	0.006687
LRP2 Low-density lipoprotein receptor-related protein 2 precursor	IPI00024292	9	5	6	2	0	4.4	0	0	0	0	0	0	0	0.0	∞	0.006824
CD14 Monocyte differentiation antigen CD14 precursor	IPI00029260	4	2	0	0	2	1.6	0	0	0	0	0	0	0	0.0	∞	0.024768
TNR Isoform 2 of Tenascin-R precursor	IPI00554760	11	2	0	3	0	3.2	0	0	0	0	0	0	0	0.0	∞	0.025207
BTD Uncharacterized protein BTD (Fragment)	IPI00744685	3	0	6	2	0	2.2	0	0	0	0	0	0	0	0.0	∞	0.025207
IGLV1-40 V1-13 protein (Fragment)	IPI00789259	3	9	6	0	0	3.6	0	0	0	0	0	0	0	0.0	∞	0.025207
COL18A1 Isoform 2 of Collagen alpha-1(XVIII) chain precursor	IPI00022822	12	0	3	4	5	4.8	0	0	0	2	0	0	0	0.3	16.80	0.014495
SEZ6 Isoform 3 of Seizure protein 6 homolog precursor	IPI00748395	9	4	6	4	0	4.6	0	0	0	0	0	3	0	0.4	10.73	0.014282
APLP1 amyloid precursor-like protein 1 isoform 1 precursor	IPI00607600	0	8	8	6	4	5.2	0	0	0	0	0	4	0	0.6	9.10	0.018053
HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein precursor	IPI00024284	15	4	5	2	0	5.2	0	0	2	2	0	0	0	0.6	9.10	0.035993
FCGBP IgGFc-binding protein precursor	IPI00242956	66	18	29	5	6	24.8	0	5	8	0	2	8	0	3.3	7.55	0.032868
APLP2 Isoform 1 of Amyloid-like protein 2 precursor	IPI00031030	47	43	42	18	14	32.8	0	4	6	18	0	6	0	4.9	6.75	0.008637

TAGLN Transgelin	IPI00216138	0	2	4	39	30	15.0	0	0	0	0	25	0	0	3.6	4.20	0.03 7289
AGT Angiotensinogen precursor	IPI00032220	5	17	19	15	19	15.0	7	3	8	7	0	4	2	4.4	3.39	0.01 8124
C9 Complement component C9 precursor	IPI00022395	6	12	8	18	12	11.2	5	4	0	6	0	9	0	3.4	3.27	0.01 3818
Autotaxin isoform gamma	IPI00878576	16	14	18	13	14	15.0	3	0	6	7	0	19	2	5.3	2.84	0.04 1637
RBP3 Interphotoreceptor retinoid-binding protein precursor	IPI00022337	560	583	474	609	611	567.4	62	57	155	269	286	401	235	209.3	2.71	0.00 4483
Transthyretin	IPI00855916	534	462	1238	234	199	533.4	173	111	200	134	256	363	155	198.9	2.68	0.04 2357
CST3;CST2 Cystatin-C precursor	IPI00032293	51	49	62	34	14	42.0	18	21	17	16	9	31	8	17.1	2.45	0.04 2357
A2M Alpha-2-macroglobulin precursor	IPI00478003	187	223	265	218	172	217.0	42	34	124	108	130	238	49	103.6	2.10	0.02 8351
CP Ceruloplasmin precursor	IPI00017601	424	264	271	363	317	327.8	276	200	87	207	243	234	203	207.1	1.58	0.01 1829
CLEC3B Putative uncharacterized protein DKFZp686H17246	IPI00792115	0	3	4	0	0	1.4	10	12	3	10	3	23	22	11.9	0.12	0.01 6723
AFM Afamin precursor	IPI00019943	0	0	0	0	0	0.0	0	3	3	6	0	13	13	5.4	0.00	0.02 2991
CFD Complement factor D preproprotein	IPI00165972	0	0	0	0	0	0.0	6	4	0	5	0	5	5	3.6	0.00	0.02 2394

The first column in Table 4 shows the names of DR protective factors. The second column shows the International Protein Index numbers (IPI numbers) of the protective factor proteins. These accession numbers were retrieved from mass spectrometry analysis result, mapped to EMBI-EBI IPI database. Columns 3-7 and columns 9-15 show the peptide hits of each factor (reflecting the expression level) from each vitreous sample. Columns 3-7 are hits in samples from subjects having no-mild NPDR, and columns 9-15 are hits from subjects having PDR. The first line of the Table refers to the grade of the DR from which each of the samples were obtained (e.g., "2," "3," and "0," refer to NPDR grades 2, 3 and 0, respectively). The line listing, e.g., "262C D," refers to the name of the samples. Column 8 is the average number of hits in no-mild NPDR samples, compiled from columns 3-7 for each factor. Column 16 is the average number of hits in PDR samples, complied from columns 9-15. Column 17 shows the fold difference between the average number of hits in the no-mild NPDR samples (column 8) to the average number of hits in the PDR samples (column 16) for each factor. The fold increase column shows that the factors are expressed at higher levels in type 1 diabetic individuals without DR compared to those with DR.

Example 5: Identification of factors that protect against DN or increase the risk of DN

Complications observed in Medalists are shown in FIG. 5 and a summary of clinical characteristics in Medalists is shown in FIG. 6. Candidate factors that protect against DN were identified by comparing the levels or expression of factors in individuals with DN and those without DN. Factors with a statistically significant difference in expression between the individuals with DN and those without DN were selected. A total of 1709 candidate factors were selected. Further statistical analysis was then applied to select protective factors from the candidate factors. After applying kruskal-wallis statistical analysis, a total of 15 protective factors (first 15 entries in Table 5, i.e., those above the line in the middle of the Table) and 17 risk factors (bottom 17 entries in Table 5, i.e., those below the line in the middle of the table) were identified, as shown in Table 5 and FIG. 8. FIG. 8 only lists the protective factors. The criteria of the selection for protective factors was p value <0.05, and expression level increased > = 1.5 fold in individuals without DN. The criteria of the selection for risk factors was p value <0.05, and expression level increased <= 0.67 fold in individuals without DN (i.e., decreased >=1.5 fold in individuals with DN).

The analysis was performed essentially as follows. The protein analysis was done using a label-free quantitative analysis of 1D PAGE-LC/MS/MS-based proteomics. Soluble proteins from vitreous tissues of 50-Year Medalists were loaded onto 10% acrylamide protein gels for separations in 1-D gel electrophoresis. We loaded 200ug (micro gram) of protein-prep (isolated by sieving, buffering, centrifuging, etc. several steps.) with sample buffer in each sample lane on the gel. Then the gel was stained with Coomassie Blue. Each lane of gel was then cut into 40 slices. The 40 slices were digested in separate tubes by trypsin. These digested protein gel slices were then loaded into an LC machine for the later MS/MS analysis.

The number of peptide hits was obtained from the "MS manager," software previously developed by Benbo Gao (Gao B et al. Mol Cell Proteomics 2008;7:2399-2409). MS manager is designed based on the PHP-MySQL-Apache platform. It compiles the search results from SEQUEST and X!Tandem of MS/MS data, and then parses these results into the MySQL database. After applying the algorithm for filtering proteins and combining the IPI identifier, a final report of identified proteins is generated in a table with peptide hit numbers. The results are shown in Table 5 below.

Table 5: Protective and Risk Factors for DN

Accession	Protein Name	G7	G4	G3	Clean Mean	G11	G8	G6	G2	G1	G12	G9	G10	G5	Dz mean	Fold	P_KW
IPI00789618	HDDC3 Isoform 1 of HD domain-containing protein 3	3	3	0	2.00	0	0	0	0	0	0	0	0	0	0.00	#DIV/0!	0.01
IPI00178926	IGJ immunoglobulin J chain	0	45	18	21.00	0	0	0	0	0	0	0	8	0	0.89	23.63	0.04
IPI00816799	Rheumatoid factor D5 light chain (Fragment)	7	4	0	3.67	0	3	0	0	0	0	0	0	0	0.33	11.00	0.04
IPI00410215	BPNT1 Isoform 2 of 3(2),5-bisphosphate nucleotidase 1	4	4	0	2.67	0	0	0	3	0	0	0	0	0	0.33	8.00	0.04
IPI00009305	GNPDA1 Glucosamine-6-phosphate isomerase	4	3	4	3.67	0	0	5	0	0	0	0	0	0	0.56	6.60	0.02
IPI00873466	HPRT1 Uncharacterized protein HPRT1	6	4	5	5.00	3	3	5	0	0	0	0	0	0	1.22	4.09	0.02
IPI00893316	GSTT1 Glutathione S-transferase theta 1	30	23	20	24.33	4	10	25	11	4	0	0	0	9	7.00	3.48	0.03
IPI00004101	BHMT Betaine-homocysteine S-methyltransferase 1	182	74	118	124.67	17	105	60	78	29	16	10	0	33	38.67	3.22	0.03
IPI00848298	APOA1BP Isoform 2 of Apolipoprotein A-I-binding protein precursor	8	8	10	8.67	0	3	4	4	5	0	4	3	6	3.22	2.69	0.01
IPI00022488	HPX Hemopexin precursor	20	24	25	23.00	10	8	19	12	10	0	0	5	21	9.44	2.44	0.02
IPI00218407	ALDOB Fructose-bisphosphate aldolase B	690	450	521	553.67	76	486	381	428	176	84	34	36	414	235.00	2.36	0.02
IPI00305360	AGMAT Agmatinase, mitochondrial precursor	54	38	57	49.67	4	54	23	35	20	8	19	18	9	21.11	2.35	0.03
IPI00792191	GATM Glycine amidinotransferase (L-arginine:glycine amidinotransferase) variant	213	177	222	204.00	32	207	111	149	64	60	74	108	57	95.78	2.13	0.02
IPI00219446	PEBP1 Phosphatidylethanolamine-binding protein 1	235	235	171	213.67	30	227	129	203	97	32	24	25	145	101.33	2.11	0.03
IPI00025366	CS Citrate synthase, mitochondrial precursor	30	17	21	22.67	7	11	10	19	8	8	12	10	14	11.00	2.06	0.02
IPI00554811	TTLL3;ARPC4 Actin-related protein 2/3 complex subunit 4	4	4	5	4.33	16	8	6	7	6	12	17	5	4	9.00	0.48	0.04
IPI00215948	CTNNA1 Isoform 1 of Catenin alpha-1	5	13	3	7.00	26	6	17	14	16	20	18	22	11	16.67	0.42	0.03
IPI00010796	P4HB Protein disulfide-isomerase precursor	26	8	23	19.00	65	29	39	26	48	74	52	57	22	45.78	0.42	0.04
IPI00646415	RAB14 20 kDa protein	7	4	6	5.67	7	11	23	11	7	8	36	23	19	16.11	0.35	0.02
IPI00025447	EEF1A1 Elongation factor 1-alpha	5	9	2	5.33	9	14	15	15	21	4	35	15	20	16.44	0.32	0.04
IPI00413947	AP1B1 Isoform B of AP-1 complex subunit beta-1	6	7	0	4.33	10	12	13	6	9	22	26	11	17	14.00	0.31	0.03
IPI00009904	PDIA4 Protein disulfide-isomerase A4 precursor	8	6	4	6.00	23	16	24	15	16	17	19	27	20	19.67	0.31	0.01
IPI00020599	CALR Calreticulin precursor	7	11	25	14.33	46	18	30	51	23	43	133	89	30	51.44	0.28	0.03
IPI00401448	ACSL1 Isoform 2 of Long-chain-fatty-acid—CoA ligase 1	3	2	3	2.67	22	11	4	6	0	11	28	4	4	10.00	0.27	0.05
IPI00792916	PRKCSH protein kinase C substrate 80K-H isoform 2	3	0	4	2.33	14	4	9	5	4	15	20	14	6	10.11	0.23	0.02
IPI00025252	PDIA3 Protein disulfide-isomerase A3 precursor	5	12	8	8.33	72	12	29	26	30	30	85	58	27	41.00	0.20	0.02
IPI00008274	CAP1 Adenylyl cyclase-associated protein 1	5	0	0	1.67	13	4	10	4	7	16	15	6	5	8.89	0.19	0.04
IPI00783726	KTN1 kinectin 1 isoform b	0	3	0	1.00	5	7	8	5	8	5	2	6	6	5.78	0.17	0.02
IPI00025239	NDUFS2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor	0	3	0	1.00	20	4	5	3	2	12	3	10	4	7.00	0.14	0.03
IPI00217943	RAB6A Isoform 2 of Ras-related protein Rab-6A	2	0	0	0.67	0	7	8	2	2	8	14	8	3	5.78	0.12	0.05
IPI00016621	AP2A2 Adaptor-related protein complex 2, alpha 2 subunit variant (Fragment)	0	0	0	0.00	13	2	4	2	3	13	21	12	3	8.11	0.00	0.01
IPI00025874	RPN1 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 67 kDa subunit pre	0	0	0	0.00	33	6	6	2	0	36	32	23	0	15.33	0.00	0.04

The first column in table 5 shows the International Protein Index numbers (IPI numbers) of the protective factor proteins. These accession numbers were retrieved from mass spectrometry analysis result, mapped to EMBI-EBI IPI database. The second column shows names of DN protective factors. Columns 3-5 and columns 7-15 show the peptide hits of each factor (reflecting the expression level) from each kidney sample. Columns 3-5 are hits in samples from subjects with no DN, and columns 7-15 are hits in samples from subjects with DN. The first line (listing, e.g., "G7") refers to the names of each sample. Column 6 ("Clean Mea") shows the average number of hits in the non-DN samples, compiled from columns 3-5 for each factor. Column 16 is the average number of hits in the DN samples, compiled from columns 9-15. Column 17 shows the fold difference between the average number of hits in the no-DN samples (column 6) to the average number of hits in the DN samples (column 16) for each factor. The fold column shows that the protective factors (factors 1-15, i.e., those above the line) are expressed at higher levels in type 1 diabetic individuals without DN compared to those with DR. It also shows that the risk factors (factors 16-32, i.e., those below the line) are expressed at lower levels in type 1 diabetic individuals without DN relative to those with DN.

Example 6: RBP3 protein levels are higher in vitreous of Medalists without PDR than in vitreous from Medalists with PDR

Vitreous from 6 eyes (4 Medalists) from the no to Mild-NPDR and 8 vitreous (5 Medalists) from the PDR groups. "No to mild NPDR" is characterized as Early Treatment Diabetic Retinopathy Study (ETDRS) severity levels 10-35, characterized by absent or less than severe hemorrhages/microaneurysms throughout the retina (Grading diabetic retinopathy from stereoscopic color fundus photographs--an extension of the modified Airlie House classification. ETDRS report number 10. Early Treatment Diabetic Retinopathy Study Research Group. Ophthalmology. 1991May;98(5 Suppl):786-806. PubMed PMID: 2062513; and Fundus photographic risk factors for progression of diabetic retinopathy. ETDRS report number 12. Early Treatment Diabetic Retinopathy Study Research Group. Ophthalmology. 1991 May;98(5 Suppl):823-33. PubMed PMID: 2062515). 10 microliters of sonicated and centrifuged vitreous from each sample were loaded onto a 4-20% gel (Biorad) and transferred to a PVDF membrane (Immobilon-P). CystatinC, RBP3 and PTGDS (Abcam, 1:2000), Endophilin and Tenascin R (Santa Cruz 1:1000) were used for immunodetection. More specifically, rabbit anti-RBP3 (Abcam 101456) was used and Santa Cruz HRP anti-Rabbit was used as the secondary antibody for detection. The band density was analyzed using Image J, and p values represent student t test.

Western Blot confirmed that RBP3 protein levels are significantly higher in vitreous of Medalists without PDR than in vitreous from Medalists with PDR (pval=0.01; Figure 11). Cystatin C protein levels showed a similar trend (pval=0.06). Although the difference in PTGDS levels between both groups was not statistically significant, we decided to pursue this protein as well, since it belongs to the lipocalin superfamily (as does RBP3), and can bind to the same substrates.

CST3 is universally expressed. We confirmed that CST3 is detected in mouse retina protein extracts by Western blot (data not shown). RBP3 is secreted by the retinal photoreceptor cells (RPE), and thus, it could play a role in retinal endothelial cells and pericytes even when those cells do not express RBP3.

RBP3 was also quantified in the vitreous of Medalists with no-mild NPDR, active PDR or quiescent PDR by proteomics analysis. No to mild NPDR is as described above. "Quiescent PDR" corresponds to ETDRS severity level > 60, characterized by the presence of neovascularization, fibrous proliferation, or panretinal laser photocoagulation scars.

The results, which are shown in Figure 12, indicate that the level of RBP3 is high in Medalists with no DR, low in Medalists with active PDR and present at an intermediary level in Medalists with quiescent PDR. This data shows that the Medalist patients without PDR have retained high levels of RBP3 despite a long duration of type1 diabetes.

The level of RBP3 was also determined in the vitreous of Medalists with no to mild NPDR and compared to that in Medalists with PDR using proteomics analysis. The results, which are shown in Figure 13, indicate that the level of RBP3 is higher in Medalists with no to mild NPDR relative to that in Medalists with PDR.

Example 7: RBP3 protein levels are higher in the retina of Medalists with mild NPDR relative to that in Medalists with PDR

The level of RBP3 was also determined in the retina of Medalists with mild NPDR and Medalists with PDR. The assay was conducted as follows: 10 ug of protein were loaded onto a 4-20% gel (Biorad) and transferred to a PVDF membrane (Immobilon-P) and immunoblotted as described above.

The results, which are shown in Figure 14, indicate that the level of RBP3 follows the same trend as the vitreous, i.e. higher RBP3 in the retina of Medalists with mild NPDR relative to that in Medalists with PDR.

Example 8: RBP3 is expressed in human plasma

This Example describes that plasma from healthy human subjects contain detectable levels of RBP3. This was surprising, as RBP3 was so far believed to be present only in the eye.

Human plasma was obtained from control subjects from the Medalist study at the Joslin Diabetes Center. A blood sample was extracted by venipuncture using standard CLIA protocol after patient consent was obtained using a 10mL EDTA tube by a trained phlebotomist. This was then centrifuged at 4 degrees centigrade for 10 mins at 4000 rpm. After this process the supernatant (plasma) was aliquotted off into 100 mL samples and stored at -80 centigrade. The human plasma was serum albumin and IgG depleted using Pierce kit (89875) following the manufacturers instructions. Equal volumes (20ul) were loaded on a gel and immunoblotted as described above.

The results, which are shown in Figure 15, indicate that RBP3 is present in human plasma.

Example 9: RBP3 protect cells from high glucose exposure

This Example describes that human RBP3 protects endothelial cells from being activated by high glucose exposure, as shown in an endothelial migration assay.

Human RBP3 was prepared as follows: hRBP3 ORF containing plasmid was purchased from Origene (RC08063), transfected into HEK 293 cells using Fugene HD (Promega), the cells lysed and RBP3 was bound to M2 resin (Sigma, Aldrich) and eluted using 1XFlag peptide (Sigma) following the manufacturer's instructions. The purified peptide was confirmed by immunoblotting against the DDK tag, and a 137 kDa band was confirmed.

The migration assays were performed as follows: bovine retinal endothelial cells (BREC) were isolated as previously described (King et al, *J Clin Invest.* 1983;71(4):974–979). 3 x 10^4 per well were plated in a 24 well plate. The following day, a scratch was made, the cells rinsed off with saline to remove floating cells, and incubated with different conditions (low glucose= 5.6 mM, high glucose=25.6 mM D-glucose, Vehicle =TBS buffer, RBP3= 1:100 dilution). The width of this gap was measured at 0 and 4 hours in the corresponding conditions, two pictures of each gap were taken at each time point and the average was used. Four wells were plated for each condition. Statistics were done with excel (student ttest).

The results, which are shown in Figure 16, indicate that RBP3 prevents the endothelial cells from migrating in response to the high glucose concentration, thereby indicating that RBP3 protects endothelial cells from the toxic effects of a high glucose environment.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

INCORPORATION BY REFERENCE

The disclosure of each and every publication, including US and foreign patent and pending patent applications, referred to herein is specifically incorporated by reference herein in its entirety.

WHAT IS CLAIMED IS:

1. A method of diagnosing or predicting risk of developing a microvascular complication in a subject having diabetes, the method comprising:

providing or obtaining a sample from the subject;
determining the level of a biomarker listed in Table 6, 8, 7 or 9 in the sample from the subject; and

comparing the level of the biomarker to one or more reference levels, wherein (i) a lower level of a biomarker of Table 6 or 8 in the sample as compared to a DR or DN reference level, respectively, wherein the reference level is the level of a biomarker in a subject who has had diabetes for over 25 years and has not developed a microvascular complication, indicates that the subject has, or has an increased risk of developing, a microvascular complication relative to a subject having an amount of biomarker that is equal to or higher than the DR or DN reference level; and (ii) a higher level of a biomarker of Table 7 or 9 in the sample as compared to a DR or DN reference level, respectively, wherein the reference level is the level of a biomarker in a subject who has had diabetes for over 25 years and has not developed a microvascular complication, indicates that the subject has, or has an increased risk of developing, DR or DN, respectively, relative to a subject having an amount of biomarker that is equal to or lower than the DR or DN reference level.

2. The method of claim 1, wherein (i) a lower level of a biomarker of Table 6 in the sample as compared to a DR reference level indicates that the subject has, or has an increased risk of developing, DR relative to a subject having an amount of biomarker that is equal to or higher than the DR reference level; (ii) a lower level of a biomarker of Table 8 in the sample as compared to a DN reference level indicates that the subject has, or has an increased risk of developing, DN relative to a subject having an amount of biomarker that is equal to or higher than the DN reference level; (iii) a higher level of a biomarker of Table 7 in the sample as compared to a DR reference level indicates that the subject has, or has an increased risk of developing, DR relative to a subject having an amount of biomarker that is equal to or lower than the DR reference level and (iv) a higher level of a biomarker of Table 9 in the sample as compared to a DN reference level indicates that the subject has, or has an increased risk of developing, DN relative to a subject having an amount of biomarker that is equal to or lower than the DN reference level.

3. The method of claim 2, wherein the DR and DN reference levels are statistically significant levels of the biomarker in subjects who do not have a microvascular complication.

4. The method claim 2, wherein the sample comprises plasma, urine, vitreous, aqueous, retinal tissue, lacrinal fluid, or kidney tissue.

5. The method of claim 4, wherein the sample is a plasma sample and the method comprises determining the level of Retinol Binding Protein 3 (RBP3) in the sample, wherein a lower level of RBP3 relative to an RBP3 reference level indicates that the subject has, or has an increased risk of developing, DR relative to a subject having an amount of RBP3 that is equal to or higher than the RBP3 reference level, and wherein a higher level of RBP3 relative to an RBP3 reference level indicates that the subject does not have, or has a lower risk of developing, DR relative to a subject having an amount of RPB3 that is equal to or lower than the RBP3 reference level.

6. The method of claim 5, wherein DR is severe NPDR or PDR.

7. The method of claim 2, wherein the subject has type 1 diabetes.

8. The method of claim 2, wherein the subject has type 2 diabetes.

9. The method of claim 2, further comprising treating the subject for DR or DN, or to reduce the risk of developing DR or DN.

10. The method of claim 9, wherein treating the subject for DR or DN includes administering to the subject a therapeutically effective amount of an agent that increases or decreases the level or activity of the factor of Table 6, 8 or 9 that is decreased or increased, respectively, in the subject.

11. A method for determining the prognosis of a microvascular complication in a subject having diabetes and a microvascular complication, comprising

providing or obtaining a sample from the subject;
determining the level of a biomarker listed in Table 6, 8, 7 or 9 in the sample from the subject; and

comparing the level of the biomarker to one or more reference levels, wherein a reference level of a biomarker is a level that is present in a subject having diabetes for at least 25 years and who has not developed microvascular complication, and wherein (i) a lower level of a biomarker of Table 6 or 8 in the sample as compared to a DR or DN reference level,

respectively, indicates that the subject has a poorer prognosis of the microvascular complication relative to a subject having an amount of biomarker that is equal to or higher than the DR or DN reference level, respectively; and (ii) a higher level of a biomarker of Table 7 or 9 in the sample as compared to a DN reference level indicates that the subject has a better prognosis of the microvacular complication relative to a subject having an amount of biomarker that is equal to or lower than the DN reference level.

12. The method of claim 11, wherein (i) a lower level of a biomarker of Table 6 in the sample as compared to a DR reference level indicates that the subject has a poorer prognosis of the DR relative to a subject having an amount of biomarker that is equal to or higher than the DR reference level; (ii) a lower level of a biomarker of Table 8 in the sample as compared to a DN reference level indicates that the subject has a poorer prognosis of DN relative to a subject having an amount of biomarker that is equal to or higher than the DN reference level; (iii) a higher level of a biomarker of Table 7 in the sample as compared to a DR reference level indicates that the subject has a poorer prognosis of DR relative to a subject having an amount of biomarker that is equal to or lower than the DR reference level and (iv) a higher level of a biomarker of Table 9 in the sample as compared to a DN reference level indicates that the subject has a poorer prognosis of DN relative to a subject having an amount of biomarker that is equal to or lower than the DN reference level.

13. A method of determining the effectiveness of a treatment to prevent or treat a microvascular complication in a subject having diabetes and being treated for diabetes and/or for the microvascular complication, the method comprising:

providing or obtaining a sample from the subject;
determining the level of a biomarker listed in Table 6, 8, 7 or 9 in the sample from the subject; and

comparing the level of the biomarker to a reference level, which reference level is the level of the biomarker at an earlier time during the treatment or prior to the treatment, wherein (i) a lower level of a biomarker of Table 6 or 8 in the sample as compared to a DR or DN reference level indicates that the treatment of the subject is not significantly effective; and (ii) a higher level of a biomarker of Table 9 in the sample as compared to a DN reference level indicates that the treatment of the subject is significantly effective.

14. The method of claim 13, wherein (i) a lower level of a biomarker of Table 6 in the sample as compared to a DR reference level, which DR reference level is the level of the biomarker at

an earlier time during the treatment or prior to the treatment, indicates that the treatment is not significantly effective; (ii) a lower level of a biomarker of Table 8 in the sample as compared to a DN reference level, which DN reference level is the level of the biomarker at an earlier time during the treatment or prior to the treatment, indicates that the treatment is not significantly effective; and (iii) a higher level of a biomarker of Table 9 in the sample as compared to a DN reference level, which DN reference level is the level of the biomarker at an earlier time during the treatment or prior to the treatment, indicates that the treatment is significantly effective.

15. A method for treating diabetic retinopathy (DR) in a subject, the method comprising selecting a subject with DR and administering to the subject a therapeutically effective amount of a therapeutic agent that increases the level or activity of a protective factor disclosed in Table 6 or a biologically active variant thereof.

16. The method of claim 15, wherein the protective factor is RBP3.

17. The method of claim 15, wherein the therapeutic agent comprises a protective factor disclosed in Table 6 or a biologically active fragment thereof.

18. The method of claim 15, wherein the therapeutic agent is a nucleic acid encoding a protective factor of Table 6 or a biologically active variant thereof.

19. The method of claim 15, wherein the therapeutic agent is administered systemically.

20. The method of claim 15, wherein the therapeutic agent is administered locally to the eye.

21. The method of claim 20, wherein the therapeutic agent is injected into the vitreous of the eye.

22. The method of claim 15, further determining the effectiveness of the treatment.

23. A method for treating diabetic nephropathy (DN) in a subject, the method comprising selecting a subject with DN and administering to the subject a therapeutically effective amount of an agent that increases the level or activity of a protective factor disclosed in Table 8 or a biologically active variant thereof.

24. The method of claim 23, wherein the therapeutic agent comprises a protective factor disclosed in Table 8 or a biologically active fragment thereof.

25. The method of claim 23, wherein the therapeutic agent is a nucleic acid encoding a protective factor disclosed in Table 8 or a biologically active fragment thereof.

26. The method of claim 23, wherein the therapeutic agent is administered systemically.

27. The method of claim 23, wherein the therapeutic agent is administered locally to the kidney.

28. A method for treating DN in a subject, the method comprising selecting a subject with DR and administering to the subject a therapeutically effective amount of an agent that reduces the level or activity of a risk factor disclosed in Table 7.

29. The method of claim 28, wherein the agent is selected from the group consisting of a small molecule, an RNAi inhibitory nucleic acid, an antisense nucleic acid, a ribozyme or an aptamer.

30. A method for treating DN in a subject, the method comprising selecting a subject with DN and administering to the subject a therapeutically effective amount of an agent that reduces the level or activity of a risk factor disclosed in Table 9.

31. The method of claim 30, wherein the agent is selected from the group consisting of a small molecule, an RNAi inhibitory nucleic acid, an antisense nucleic acid, a ribozyme or an aptamer.

32. A composition comprising (i) a therapeutic agent that increases the level or activity of a protective factor of Table 6 or 8 or (ii) a therapeutic agent that decreases the level or activity of a risk factor of Table 7 or 9; and a pharmaceutically acceptable excipient.

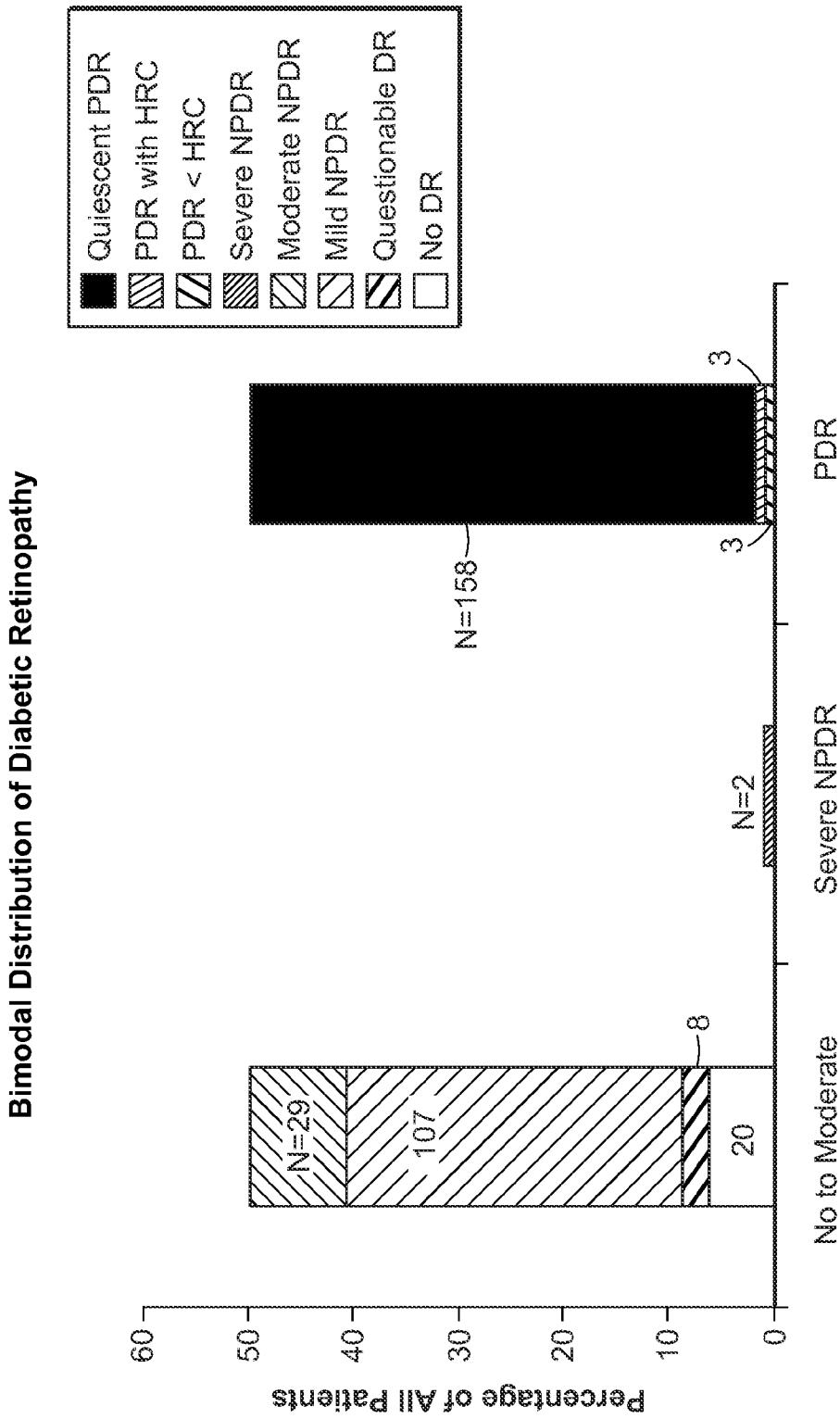

Bimodal Distribution of Diabetic Retinopathy
Quiescent PDR
PDR with HRC
PDR < HRC
Severe NPDR
Moderate NPDR
Mild NPDR
Questionable DR
No DR
Percentage of All Patients
0
10
20
30
40
50
60
N=29
107
8
20
N=2
N=158
3
3
No to Moderate NPDR
Severe NPDR
PDR

FIG. 1

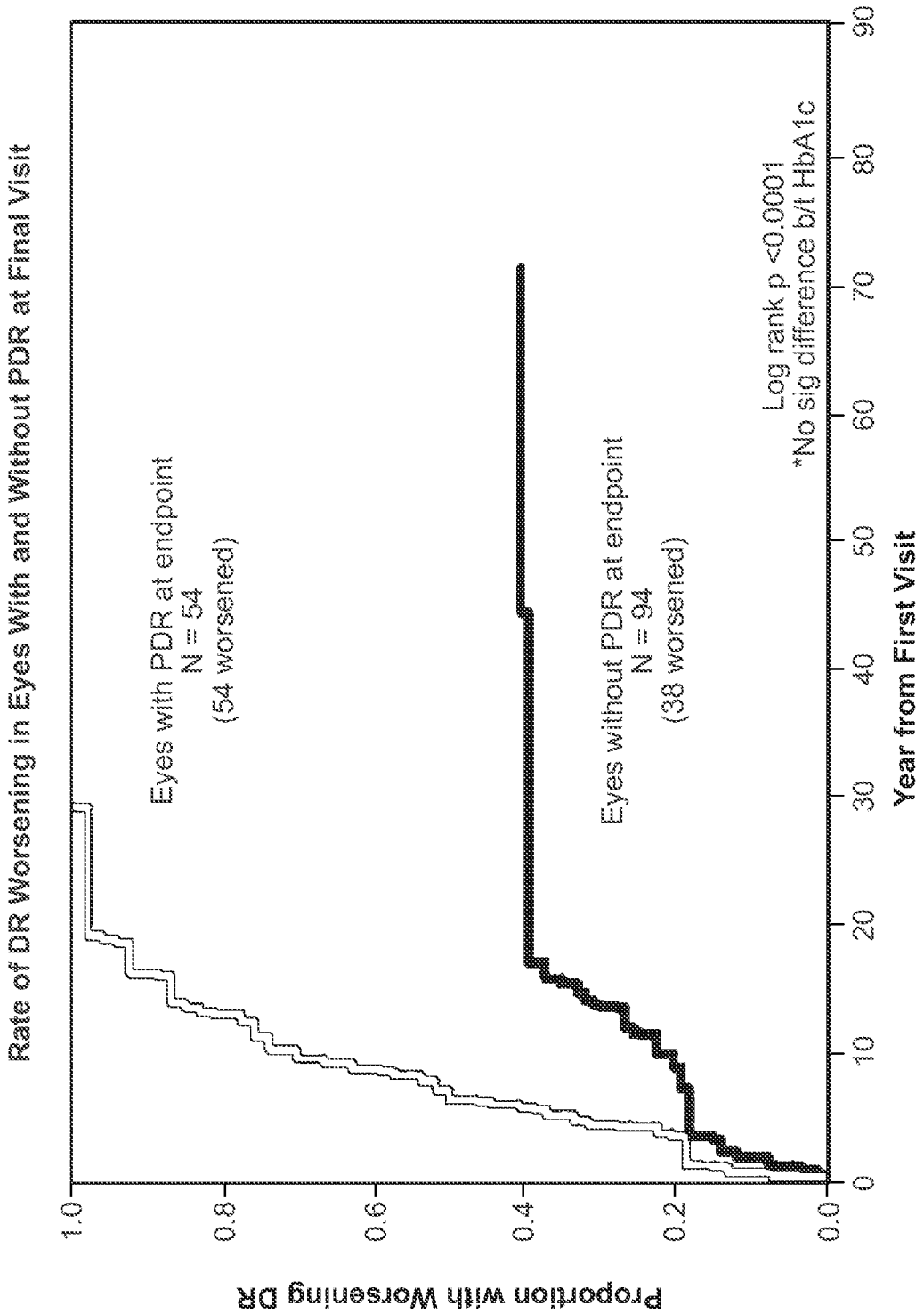

Rate of DR Worsening in Eyes With and Without PDR at Final Visit
Eyes with PDR at endpoint
N = 54
(54 worsened)
Eyes without PDR at endpoint
N = 94
(38 worsened)
Log rank p <0.0001
*No sig difference b/t HbA1c
Proportion with Worsening DR
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
60
70
80
90
Year from First Visit

FIG. 2

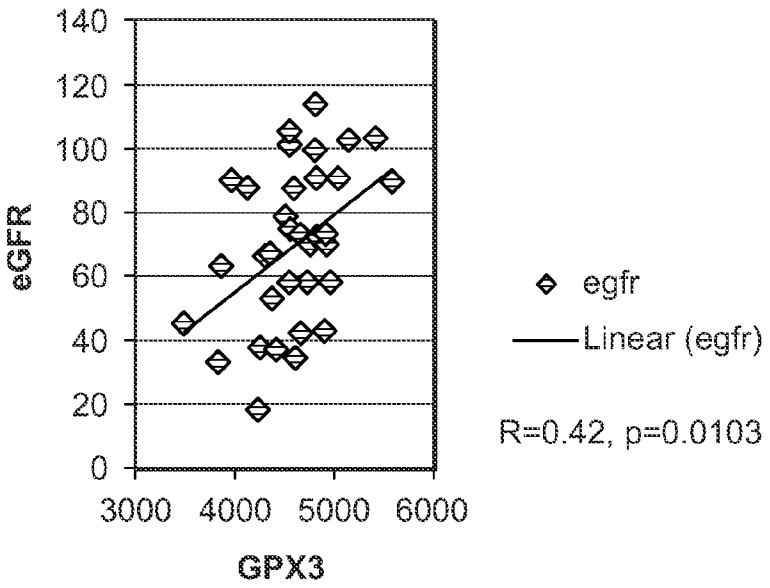

140
120
100
80
60
40
20
0
eGFR
3000
4000
5000
6000
GPX3
egfr
Linear (egfr)
R=0.42, p=0.0103

FIG. 3

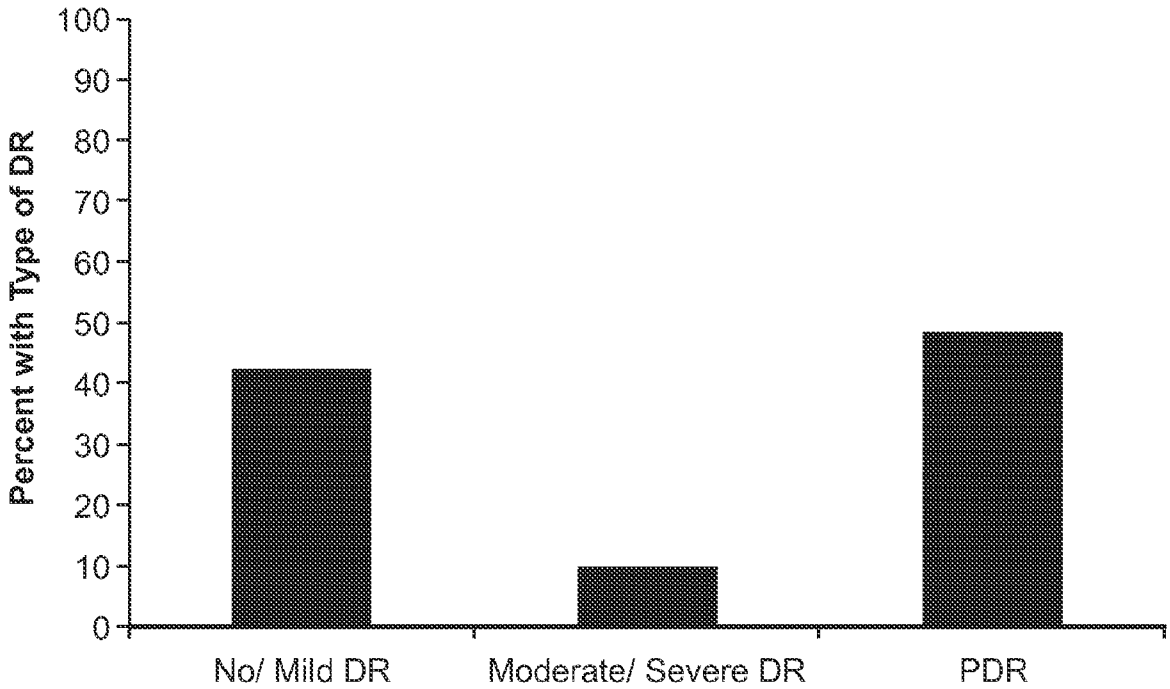

100
90
80
70
60
50
40
30
20
10
0
Percent with Type of DR
No/ Mild DR
Moderate/ Severe DR
PDR

FIG. 4

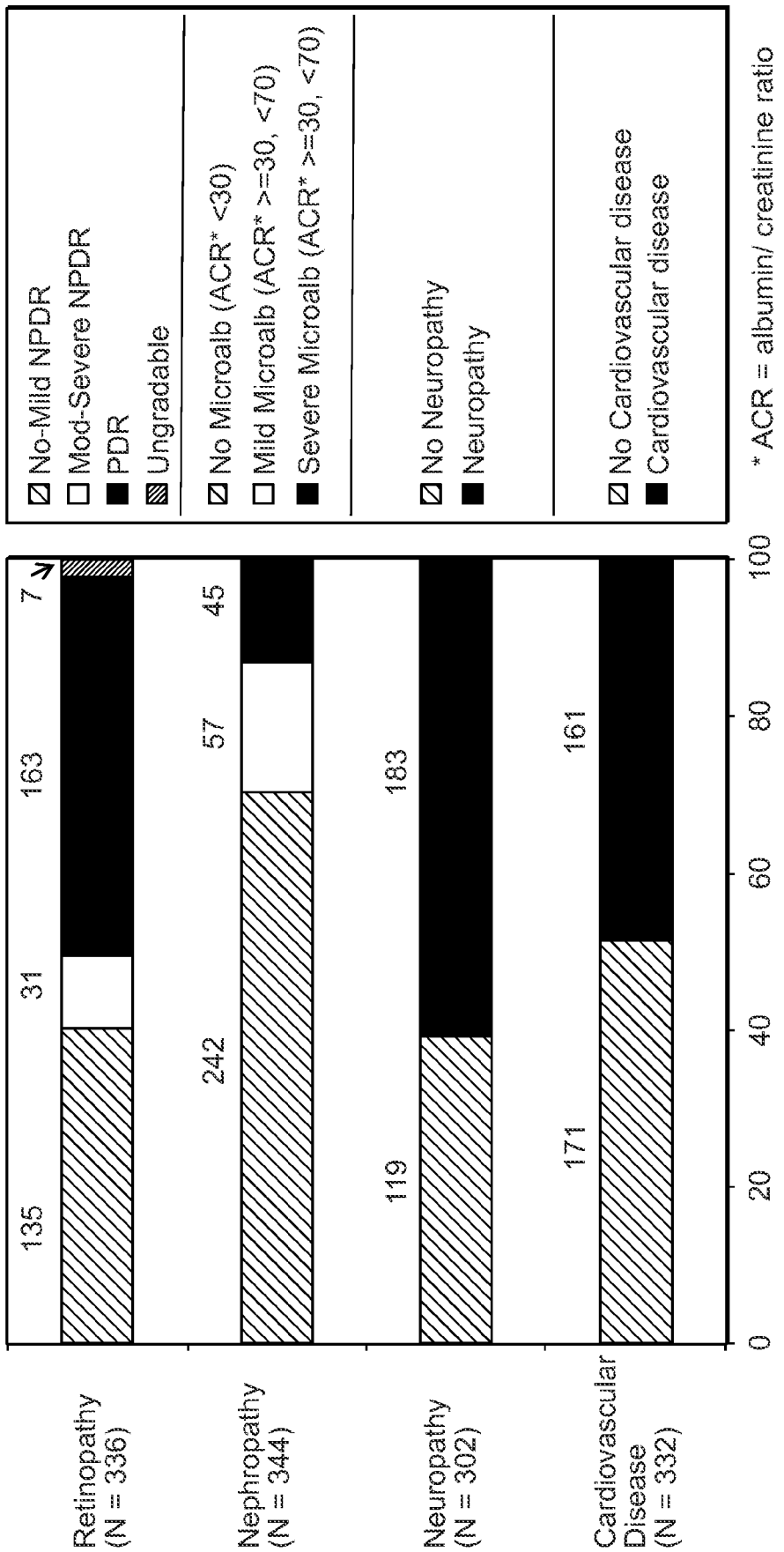

No-Mild NPDR
Mod-Severe NPDR
PDR
Ungradable
No Microalb (ACR* <30)
Mild Microalb (ACR* >=30, <70)
Severe Microalb (ACR* >=30, <70)
No Neuropathy
Neuropathy
No Cardiovascular disease
Cardiovascular disease
* ACR = albumin/ creatinine ratio
Retinopathy (N = 336)
Nephropathy (N = 344)
Neuropathy (N = 302)
Cardiovascular Disease (N = 332)
135
31
163
7
242
57
45
119
183
171
161
0
20
40
60
80
100
Percentage of all patients

FIG. 5

Nephro Class	PDR	Sex	A1c (%)	Agedx (years)	Dur (years)	Cause of Death	HTN	ACR (mcg/mg)	eGFR (ml/min/1.73 m²)
I	Mild	F	6.7	23	57	MI	Y	5.4	48.4
I	Mod	M	5.6	7	50	Cancer	N	4.3	82.0
I	PDR	M	6.6	4	72	Cardiac arrest	Y	3.5	47.2
IIA	No	M	7.2	16	72	Organ failure	N	18.3	67.9
IIA	No	M	7.1	27	51	Cancer	No	13.3	76.9
IIA	Mild	M	9.0	5	79	Cardiac arrest	Y	23.1	61.4
IIA	Mild	F	8.8	1	57	Stroke	Y	36.9	54.3
IIA	PDR	F	7.3	7	64	Intra-cranial hemorrhage	Y	39.3	44.9
IIB	PDR	M	7.3	10	75	CHF	Y	346.0	55.9
IIB	PDR	F	5.7	8	57	Cancer	Y	7.9	43.8
III	PDR	F	5.7	24	53	Cancer	Y	7.3	43.7
III	PDR	F	9.8	5	65	Renal Failure	Y	3619	26.2

FIG. 6

Accession	Protein Name	Fold	p
IPI00009997	B3GNT1: N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase	∞	0.0067
IPI00024292	LRP2: Low-density lipoprotein receptor-related protein 2 precursor	∞	0.0068
IPI00029260	CD14: Monocyte differentiation antigen CD14 precursor	∞	0.0248
IPI00554760	TNR: Isoform 2 of Tenascin-R precursor	∞	0.0252
IPI00744685	BTD: Uncharacterized protein BTD (Fragment)	∞	0.0252
IPI00783390	CHL1: Isoform 1 of Neural cell adhesion molecule L1-like protein precursor	∞	0.0067
IPI00789259	IGLV1: 40 V1-13 protein (Fragment)	∞	0.0252
IPI00022822	COL18A1: Isoform 2 of Collagen alpha-1(XVIII) chain precursor	16.80	0.0145
IPI00748395	SEZ6: Isoform 3 of Seizure protein 6 homolog precursor	10.73	0.0143
IPI00024284	HSPG2: Basement membrane-specific heparan sulfate proteoglycan core protein precursor	9.10	0.0360
IPI00607600	APLP1: amyloid precursor-like protein 1 isoform 1 precursor	9.10	0.0181
IPI00242956	FCGBP: IgGFc-binding protein precursor	7.55	0.0329
IPI00031030	APLP2: Isoform 1 of Amyloid-like protein 2 precursor	6.75	0.0086
IPI00216138	TAGLN: Transgelin	4.20	0.0373
IPI00032220	AGT: Angiotensinogen precursor	3.39	0.0181
IPI00022395	C9: Complement component C9 precursor	3.27	0.0138
IPI00878576	Autotaxin isoform gamma	2.84	0.0416
IPI00022337	RBP3: Interphotoreceptor retinoid-binding protein precursor	2.71	0.0045
IPI00855916	Transthyretin	2.68	0.0424
IPI00032293	CST3: CST2 Cystatin-C precursor	2.45	0.0424
IPI00478003	A2M: Alpha-2-macroglobulin precursor	2.10	0.0284
IPI00017601	CP: Ceruloplasmin precursor	1.58	0.0118

FIG. 7

Protein Name		Fold	p
IPI00789618	HDDC3: Isoform 1 of HD domain-containing protein 3	∞	0.0102
IPI00178926	IGJ: immunoglobulin J chain	23.63	0.0391
IPI00816799	Rheumatoid factor D5 light chain (Fragment)	11.00	0.0391
IPI00410215	BPNT1: Isoform 2 of 3(2),5-bisphosphate nucleotidase 1	8.00	0.0385
IPI00009305	GNPDA1: Glucosamine-6-phosphate isomerase	6.60	0.0206
IPI00873466	HPRT1: Uncharacterized protein HPRT1	4.09	0.0174
IPI00893316	GSTT1: Glutathione S-transferase theta 1	3.48	0.0319
IPI00004101	BHMT: Betaine--homocysteine S-methyltransferase 1	3.22	0.0335
IPI00848298	APOA1BP: Isoform 2 of Apolipoprotein A-I-binding protein precursor	2.69	0.0115
IPI00022488	HPX: Hemopexin precursor	2.44	0.0204
IPI00218407	ALDOB: Fructose-bisphosphate aldolase B	2.36	0.0208
IPI00305360	AGMAT: Agmatinase, mitochondrial precursor	2.35	0.0262
IPI00792191	GATM: Glycine amidinotransferase (L-arginine:glycine amidinotransferase) variant	2.13	0.0208
IPI00219446	PEBP1: Phosphatidylethanolamine-binding protein 1	2.11	0.0332
IPI00025366	CS: Citrate synthase, mitochondrial precursor	2.06	0.0204

FIG. 8

FIG. 9

```
   1 mmrewvllms vllcglagpt hlfqpslvld makvlldnyc fpenllgmqe aiqqaikshe
  61 ilsisdpqtl asvltagvqs slndprlvis yepstpeppp qvpaltslse eellawlqrg
 121 lrhevlegnv gylrvdsvpg qevlsmmgef lvahvwgnlm gtsalvldlr hctgggqvsgi
 181 pyiisylhpg ntilhvdtiy nrpsnttttei wtlpqvlger ygadkdvvvl tssqtrgvae
 241 diahilkqmr raivvgertg ggaldlrklr igesdffftv pvsrslgplg ggsqtwegsg
 301 vlpcvgtpae qalekalail tlrsalpgvv hclqevlkdy ytlvdrvptl lqhlasmdfs
 361 tvvseedlvt klnaglqaas edprllvrai gptetpswpa pdaaaedspg vapelpedea
 421 irqalvdsvf qvsvlpgnvg ylrfdsfada svlgvlapyv lrqvweplqd tehlimdlrh
 481 npggpssavp lllsyfqgpe agpvhlftty drrtnitqeh fshmelpgpr ystqrgvyll
 541 tshrtataae efaflmqslg watlvgeita gnllhtrtvp lldtpegsla ltvpvltfid
 601 nhgeawlggg vvpdaivlae ealdkaqevl efhqslgalv egtghlleah yarpevvgqt
 661 sallraklaq gayrtavdle slasqltadl qevsgdhrll vfhspgpelvv eeapppppav
 721 pspeeltyli ealfktevlp gqlgylrfda maeletvkav gpqlvrlvwq qlvdtaalvi
 781 dlrynpgsys taipllcsyf feaeprqhly svfdratskv tevwtlpqva gqrygshkdl
 841 yilmshtsgs aaeafahtmq dlqratvige ptaggalsvg iyqvqgssply asmptqmams
 901 attgkawdla gvepditvpm sealsiaqdi valrakvptv lqtagklvad nyasaelgak
 961 matklsglqs rysrvtseva laeilgadlq mlsgdphlka ahipenakdr ipgivpmqip
1021 spevfeelik fsfhtnvled nigylrfdmf gdgelltqvs rllvehiwkk imhtdamiid
1081 mrfnigqpts sipilcsyff degppvlldk iysrpddsvs elwthaqvvg erygsskksmv
1141 iltssvtagt aeeftyimkr lgralvigev tsggcqppqt yhvddtnlyl tiptarsvga
1201 sdgsswegvg vtphvvvpae ealarakeml qhnqlrvkrs pglqdhl   (SEQ ID NO: 2)
```

FIG. 10

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   1 tgtccaccag ctgagaagga caagggcgga aggcagctgc acagagcagg gccacgggcct
  61 tgcacacagt ccagggagct tttgtgcagg agccaggcct cccctgggt cccatgatg
 121 agagaatggg ttctgctcat gtccgtgctg ctctgtggcc tggctggccc cacacacctg
 181 ttccagccaa gcctggtgct ggacatggcc aaggtcctct tggataacta ctgcttcccg
 241 gagaacctgc tgggcatgca ggaagccatc cagcaggcca tcaagagccca tgagattctg
 301 agcatctcag acccgcagac gctggccagt gtgctgacag ccggggtgca gagctccctg
 361 aacgatcctc gcctggtcat ctcctatgag cccagcaccc ccgagcctcc cccacaagtc
 421 ccagcactca ccagcctctc agaagaggaa ctgcttgcct ggctgcaaag gggcctccgc
 481 catgaggttc tggagggtaa tgtgggctac ctgcgggtgg acagcgtccc gggccaggag
 541 gtgctgagca tgatgggggga gttcctgggtg gcccacgtgt gggggaatct catgggcacc
 601 tccgccttag tgctggatct ccggcactgc acaggaggcc aggtctctgg cattccctac
 661 atcatctcct acctgcaccc agggaacacc atcctgcacg tggacactat ctacaaccgc
 721 ccctccaaca ccaccacgga gatctggacc ttgccccagg tcctgggaga aaggtacggt
 781 gccgacaagg atgtggtggt cctcaccagc agccagacca ggggcgtggc cgagggacatc
 841 gcgcacatcc ttaagcagat gcgcaggggcc atcgtggtgg gcgagcgggac tgggggaggg
 901 gccctggacc tccggaagct gaggatagggc gagtctgact tcttcttcac ggtgcccgtg
 961 tccaggtccc tgggggcccct tggtggaggc agccagacgt gggagggcag cgggggtgctg
1021 ccctgtgtgg ggactccggc cgagcagggcc ctggagaaag ccctgggccat cctcactctg
1081 cgcagcgccc ttccagggggt agtccactgc ctccagggagg ctactacacg
1141 ctggtgggacc gtgtgcccac cctgctgcag cacttgggcca gcatgggactt ctccacgggtg
1201 gtctccgagg aagatctggt caccaagctc aatgccgggcc tgcagggctgc gtctgaggat
1261 cccaggctcc tggtgcgagc catcgggccc acagaaactc cttcttggcc cgcgcccgac
1321 gctgcagccg aagactcacc agggggtggcc ccagagttgc ctgaggacga ggctacctgg
1381 caagcactgg tggactctgt gttccagggtg tcggtgctgc cagggcaatgt gggctacctg
```

FIG. 10 (continued)

```
1441 cgcttcgata gttttgctga cgcctccgtc ctgggtgtgt tggccccata tgtcctgcgc
1501 caggtgtggg agccgctaca ggacacggag cacctcatca tggacctgcg ccacaaccct
1561 ggagggccat cctctgctgt gcccctgctc ctgtcctact tccagggccc tgagggccgg
1621 cccgtgcacc tcttcaccac ctatgatcgc cgcaccaaca tcacgcagga gcacttcagc
1681 cacatggagc tcccgggccc acgctacagc acccaacgtg gggtgtatct gctcaccagc
1741 caccgcaccg ccacgggccg ggaggagttc gccttcctta tgcagtcgct gggctgggcc
1801 acactggtag gtgagatcac cgcgggcaac ctgctgcaca cccgcacggt gccgctgctg
1861 gacacacccg aaggcagcct cgcgctcacc gtgccggtcc tcacctttcat cgacaatcac
1921 ggcgagggcct ggctgggtgg tggagtgggtg cccgatgcca tcgtgctggc cgaggaggcc
1981 ctggacaaag cccaggaagt gctggagttc caccaaaagcc tgggggcctt ggtggagggc
2041 acagggcacc tgctggaggc ccactatgct cggccagagg tcgtgggggca gaccagtgcc
2101 ctcctgcggg ccaagctggc ccagggcgcc taccgcacag ctgtggactt ggagtctctg
2161 gcctctcagc tcacagcaga cctccaggag gtgtctgggg accaccgctt gctagtgttc
2221 cacagccctg gcgagctggt ggtagagggaa gcacccccac cacccctgc tgtccctct
2281 ccagagggagc tcacctacct tattgagggcc ctgttcaaga cagaggtgct gcccggccag
2341 ctgggctacc tgcgttttga cgccatgggct gaactggaga cagtgaaggc cgtgggggcca
2401 cagctgggtgc ggctgggtatg gcaacagctg gtggacacgg ctgcgctggt gatcgacctg
2461 cgctacaacc ctggcagcta ctccacgggcc atcccgctgc tctgctccta ctctttgag
2521 gcagagcccc gccagcacct gtattctgtc ttgacagggg ccacctcaaa agtcacggag
2581 gtgtgggacct tgccccaggt cgccgggccag cgctacgggct cacacaagga cctctacatc
2641 ctgatgagcc acaccagtgg ctctgcgggcc gagggccttg cacacaccat gcaggacctg
2701 cagcgggcca cggtcattgg ggagcccacg gccggaggcg cactctctgt gggcatctac
2761 caggtgggca gcagcccctt atatgcatcc atgcccaccc agatgggccat gagtgccacc
2821 acagggcaagg cctgggacct ggctgggtgtg gagcccgaca tcactgtgcc catgagcgaa
```

FIG. 10 (continued)

```
2881 gcccttttcca tagcccaggga catagtggct ctgcgtgcca aggtgcccac ggtgctgcag
2941 acggccgggа agctggtggc tgataactat gcctctgccg agctgggggc caagatgggcc
3001 accaaactga gcggtctgca gagccgctac tccagggtga cctcagaagt ggccctagcc
3061 gagatcctgg gggctgacct gcagatgctc tccggagacc cacacctgaa ggcagcccat
3121 atccctgaga atgccaagga ccgcattccct ggaattgtgc ccatgcagat ccctttcccct
3181 gaagtatttg aagagctgat caagttttcc ttccacacta acgtgcttga ggacaacatt
3241 ggctacttga ggtttgacat gttggggac ggtgagctgc tcacccaggt ctccaggctg
3301 ctggtggagc acatctggaa gaagatcatg cacacggatg ccatgatcat cgacatgagg
3361 ttcaacatcg gtggcccccac atcctccatt cccatcttgt gctcctactt cttgatgaa
3421 ggccctccag ttctgctgga caagatctac agccggcctg atgactctgt cagtgaactc
3481 tggacacacg cccaggttgt aggtgaacgc tatggctcca agaagagcat ggtcattctg
3541 accagcagtg tgacggccgg caccgcgggag gagttcacct atatcatgaa gaggctgggc
3601 cgggccctgg tcattgggga ggtgaccagt ggggggctgcc agccaccaca gacctaccac
3661 gtggatgaca ccaacctcta cctcactatc cccacggccc gttctgtggg ggcctcggat
3721 ggcagctcct gggaaggggt ggggggtgaca ccccatgtgg ttgtccctgc agaagaggct
3781 ctcgccaggg ccaaggagat gctccagcac aaccagctga gggtgaagcg gagcccaggc
3841 ctgcaggacc acctgtaggg aagggccccca taggcagagc cccagggcag acagaacctc
3901 tgggacacac accaagggca ctcctgcagg tggcccgggcc tgagggttccc aggagcagca
3961 aagggggcctg ctgagctctg gttaggttac agctggaggt gtgtatatat acacacacac
4021 acatgtatat acacatatat atgtgtatgt atatatatgt ataatatatat ggctttccaa
4081 taaccaccta aattttaaca aagggttcctt ctaagtgggta gaacttgggg tggtatttttt
4141 acctttccttc ttcatacttt gctctttttc ttaaatactc attaatgtgc atatatcatt
4201 atttcagat gcagctatca ttatttccaaa atacaaaaata aagaagataa aataaattat
4261 atacccgagc cattaaaaaa aaaaaaaaaa  (SEQ ID NO: 1)
```

FIG. 11A

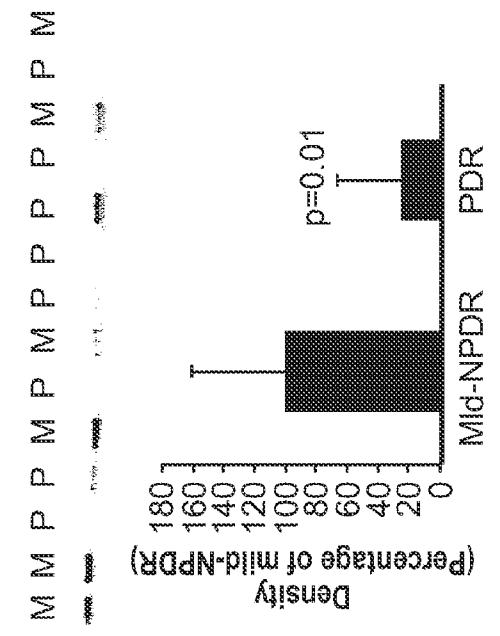


FIG. 11B

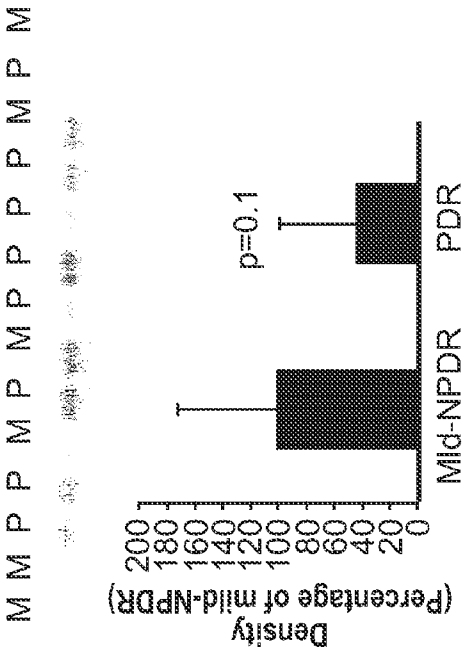
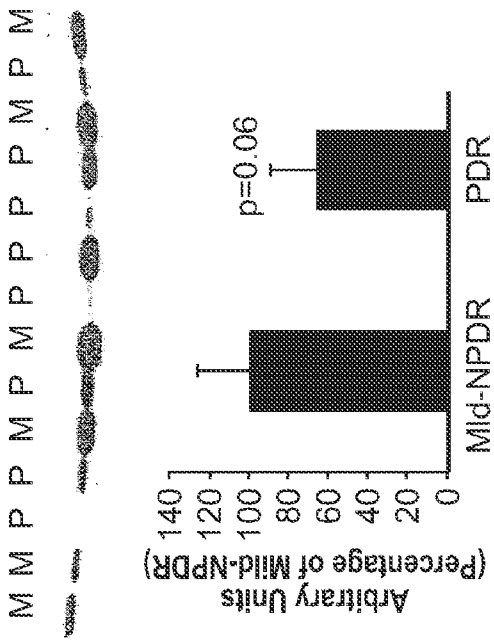


FIG. 11C



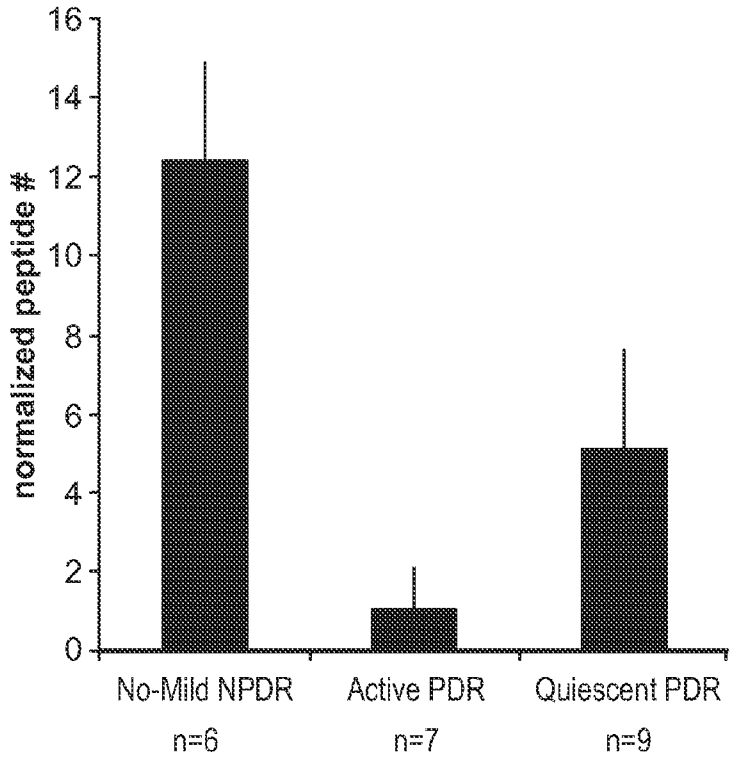
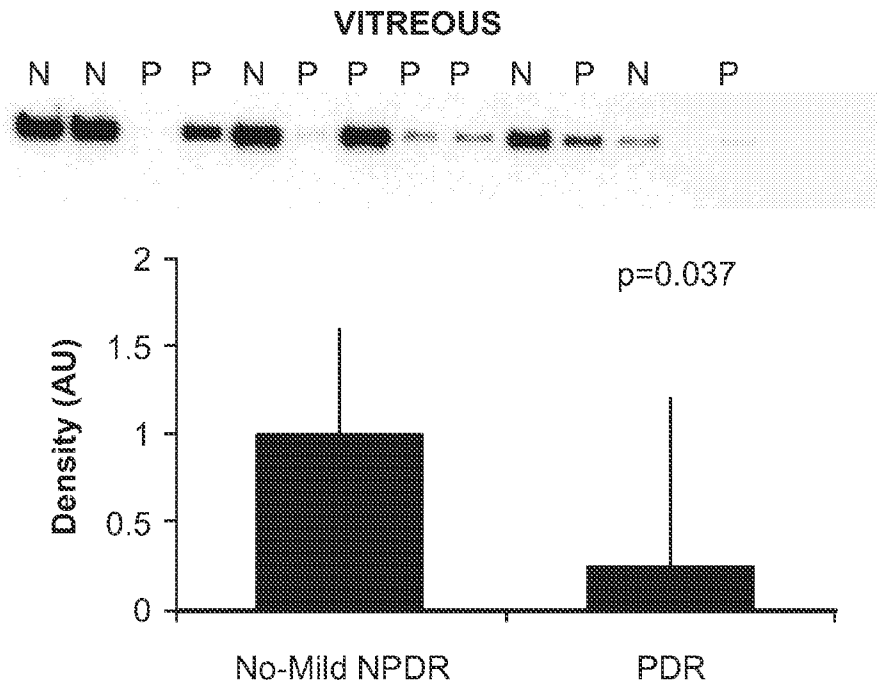


FIG. 12



No-Mild NPDR n=5 (from 4 Medalists)
PDR n=8 (from 5 Medalists)

FIG. 13

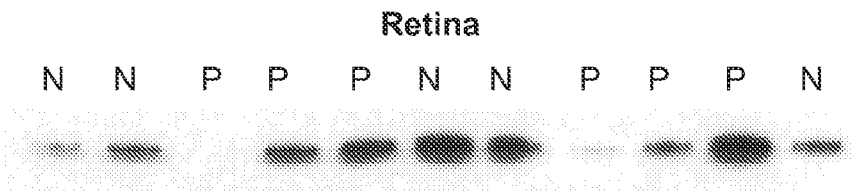


FIG. 14A

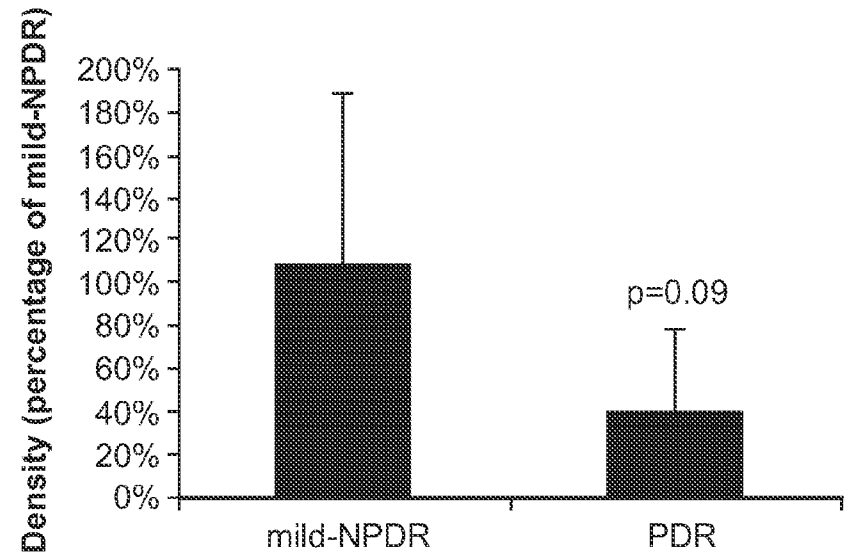


FIG. 14B

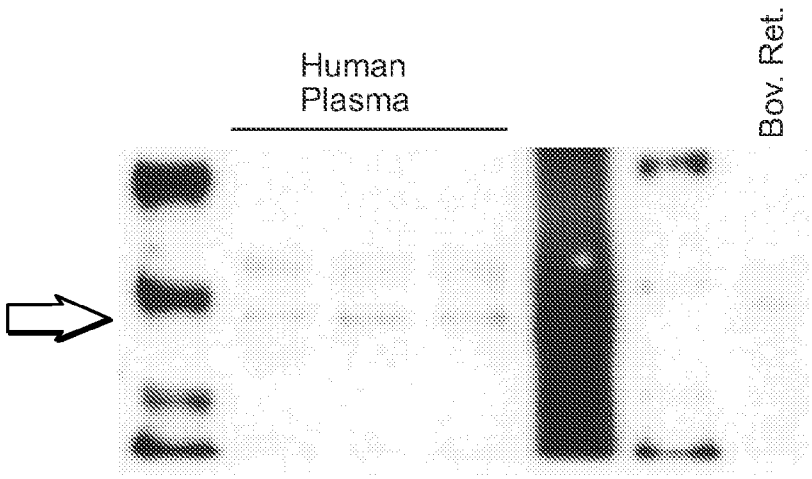


FIG. 15

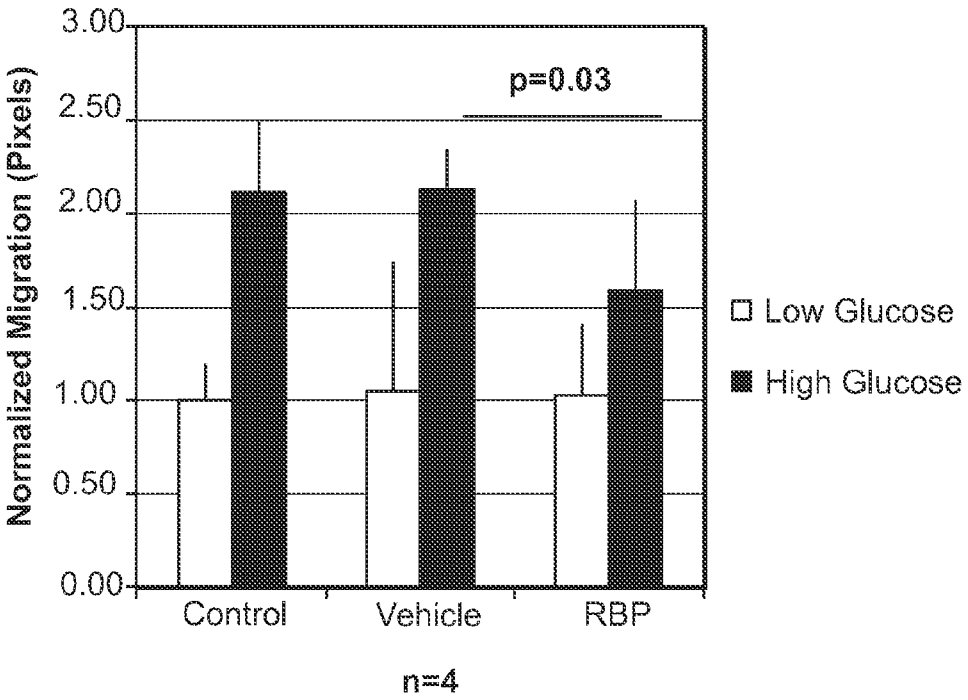

3.00
2.50
2.00
1.50
1.00
0.50
0.00
Normalized Migration (Pixels)
p=0.03
Low Glucose
High Glucose
Control
Vehicle
RBP
n=4

FIG. 16

FIG. 17

```
   1 tgggcgggcgg ctgagggcgcg tgctctcgcg tggtcgctgg gtctgcgtct tcccgagcca
  61 gtgtgctgag ctctccgcgt cgcctctgtc gcccgcgcct ggcctaccgc ggcactcccg
 121 gctgcacgct ctgcttggcc tcgccatgcc ggtggacctc agcaagtggt ccgggccctt
 181 gagcctgcaa gaagtgggacg agcagccgca gcacccgctg catgtcacct acgccgggc
 241 ggcggtgggac gagctgggca aagtgctgac gcccacccag gttaagaata gacccaccag
 301 catttcgtgg gatggtcttg attcagggaa gctctacacc ttggtcctga cagacccgga
 361 tgctcccagc aggaaggatc ccaaatacag agaatggcat cattcctgg tggtcaacat
 421 gaagggcaat gacatcagca gtggcacagt cctctccgat tatgtgggct cgggcctcc
 481 caagggcaca ggcctccacc gctatgtctg gctggtttac gagcaggaca ggccgctaaa
 541 gtgtgacgag cccatcctca gcaaccgatc tggagaccac cgtggcaaat tcaaggtggc
 601 gtcctttccgt aaaaagtatg agctcagggc cccggtggct ggcacgtgtt accaggccga
 661 gtgggatgac tatgtgccca aactgtacga gcagctgtct gggaagtagg gggttagctt
 721 ggggacctga actgtccctgg aggccccaag ccatgttccc cagttcagtg ttgcatgtat
 781 aatagatttc tcctcttcct gccccccttg gcatgggtga gacctgacca gtcagatggt
 841 agttgagggt gacttttcct gctgccctggc ctttataatt ttactcactc actctgattt
 901 atgttttgat caaatttgaa cttcattttg ggggtatttt tggtactgtg atgggtcat
 961 caaattatta atctgaaaat agcaacccag aatgtaaaaa agaaaaaact ggggggaaaa
1021 agaccaggtc tacagtgata gagcaaagca tcaaagaatc tttaagggag gtttaaaaaa
1081 aaaaaaaaaa aaaaagattg gttgcctctg cctttgtgat cctgagtcca gaatggtaca
1141 caatgtgatt ttatggtgat gtcactcacc tagacaacca gaggctgggca ttgaggctaa
1201 cctcccaacac agtgcatctc agatgcctca gtaggcatca gtatgtcact ctggtccctt
1261 taaagagcaa tcctggaaga agcagggagg agggtggctt tgctgttgtt gggacatggc
1321 aatctagacc ggtagcagcg ctcgctgaca gcttgggagg aaacctgaga tctgtgtttt
1381 ttaaattgat cgttcttcat ggggtaaga aaagctggtc tggagttgct gaatgttgca
```

FIG. 17 (continued)

```
1441 ttaattgtgc tgtttgcttg tagttgaata aaaatagaaa cctgaatgaa gaaaaaaaaa
1501 aaaaaaa  (SEQ ID NO: 3)

   1 mpvdlskwsg plslqevdeq pqhpplhvtya gaavdelgkv ltptqvknrp tsiswdglds
  61 gklytlvltd pdapsrkdpk yrewhhflvv nmkgndissg tvlsdyvgsg ppkgtglhry
 121 vwlvyeqdrp lkcdepilsn rsgdhrgkfk vasfrkkyel rapvagtcyq aewddyvpkl
 181 yeqlsgk  (SEQ ID NO: 4)
```