Supplementary Data 1

Table 1: A1

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q13007	Isoform 3 of Interleukin-24	MDA7, ST16	8.93	17.75	IL24					LLQQEVLQNVSDAESCYLVH TLLEFYLK
2	Q96RQ9	L-amino-acid oxidase	FIG1	8.79	62.881	IL4I1	Urinary bladder	56.32	1.59E-10	immunoregulator	ALLSSLSGLVLLNAPVVAMT QGPHDVHVQIETSPPAR
3	Q8WWZ1	Interleukin-1 family member 10	FIL1T, IL1HY2,IL38	4.94	16.943	IL1F10	Renal medulla	39.53	0.76	immunomodulatory activity	CLACVETEEGPSLQLEDVNI EELYK
4	Q12906	Interleukin enhancer-binding factor 3	DRBF, MPHOSPH4, NF90	8.86	95.338	ILF3	Renal medulla	92.83	0.002	Biogenesis of circular RNAs	GYNHGQGSYSYSNSYNSPGG GGGSDYNYESK
5	P29466	Caspase-1	IL1BC, IL1BCE	5.63	45.158	CASP1	kidney	76.33	<=1.00e-14	apoptosis, protease activity, inflammatory response	TGAEVDITGMTMLLQNLGYS VDVK
6	O43542	DNA repair protein XRCC3	XRCC3	8.81	37.849	XRCC3	kidney	73.34	1.21E-13	homologous recombination repair (HRR) pathway, DNA damage, DNA recombination, DNA repair	FGSQIFIEHVADVDTLLECV NK
7	O15287	Fanconi anemia group G protein	XRCC9	5.32	68.553	FANCG	kidney	72.69	1.61E-11	Post replication repair, DNA damage, DNA repair	APQFLIEVELLLPPPDLASP LHCGTQSQTK
8	P13010	X-ray repair cross-complementing protein 5	G22P2	5.55	82.704	XRCC5	kidney	96.17	<=1.00e-14	DNA non-homologous end joining (NHEJ), DNA damage, DNA recombination, DNA repair, Transcription regulation, immunity	ASFEEASNQLINHIEQFLDT NETPYFMK
9	Q9Y6H3	Mitochondrial inner membrane protease ATP23 homolog	KUB3, XRCC6BP1	8.3	28.08	ATP23	Cortex kidney	75.17	1.09E-09		HFSCEDCNGNVSGGFDASTS QIVLCQNNIHNQAHMNR
10	P31941	DNA dC->dU-editing enzyme APOBEC-3A	phorbolin-1	6.34	22.997	APOBEC3A	kidney	54.07	1.82E-07	Epigenetic regulation, Antiviral defence, immunity	VTWFISWSPCFSWGCAGEVR
11	Q4ZHG4	Fibronectin type III domain-containing protein 1	FNDC2, KIAA1866, MEL4B3	9.34	20.556	FNDC1	Cortex kidney	46.46	2.13E-04	Activator of G protein signaling	VQAQNPHGYGPISPSVSFVT

(*Continued*)

12	Q13216	DNA excision repair protein ERCC-8	CKN1,CSA	5.91	44.055	ERCC8	kidney	72.42	8.82E-10	DNA single-strand and double-strand breaks (DSSBs) repair, DNA damage, DNA repair, Ubl conjugation pathway	FTVSCGCSSEFVFVPYGSTI
13	O15446	DNA-directed RNA polymerase I subunit RPA34	ASE1, CAST, CD3EAP, PAF49	8.66	54.951	POLR1G	kidney	60.65	7.59E-07	Transcription of DNA into RNA, Transcription	GQMAMMEPGTEAMEPVEPEM
14	Q5T890	DNA excision repair protein ERCC-6-like 2	C9orf102, RAD26L	8.83	177.016	ERCC6L2	kidney epithelium	80.21	0.018	Early DNA damage response, DNA damage, DNA repair	EFNSTQDVNICLVSTMAGGL
15	Q9UF12	Hydroxyproline dehydrogenase	HSPOX1,HYPDH	8.94	58.87	PRODH2	Renal glomerulus	90.94	0.002	Proline metabolism	MWELGIPLDGTVCFGQLLGM
16	Q9NPH5	NADPH oxidase 4	RENOX	8.96	66.931	NOX4	Renal glomerulus	96.26	0.002	Regulating gene expression	TFHITCGVTICIFSGVHVAA HLVNALNFSVNYSEDFVELN AAR
17	O94925	Glutaminase kidney isoform, mitochondrial	GLS1,KIAA0838	7.85	73.461	GLS	kidney	97.1	<=1.00e-14	Acid-base homeostasis	ILQEYQVQYTPQGDSDNGK
18	Q7Z4W1	L-xylulose reductase	SDR20C1	8.33	25.913	DCXR	kidney	98.65	<=1.00e-14	Osmoregulation, Carbohydrate metabolism, Glucose metabolism, Xylose metabolism	ALGSVGPVDLLVNNAAVALL QPFLEVTK
19	Q5SVS4	Kidney mitochondrial carrier protein 1	KMCP1	9.49	32.474	SLC25A30	Renal medulla	92.33	0.002	Probable transporter, Transport	LFIERPEDETLPINVICGIL SGVISSTIANPTDVLK
20	P78540	Arginase-2, mitochondrial		6	38.577	ARG2	Renal medulla	94.92	0.002	Inflammatory response, Arginine metabolism, immunity, Urea cycle	AVSDGYSCVTLGGDHSLAIG TISGHAR
21	P11279	Lysosome-associated membrane glycoprotein 1	CD107a	9	44.882	LAMP1	Renal glomerulus	99.92	0.002	Lysosome biogenesis, autophagy, cholesterol homeostasis, Host-viral interaction	YSVQLMSFVYNLSDTHLFPN ASSK
22	P13498	Cytochrome b-245 light chain		9.58	21.012	CYBA	kidney	96.41	<=1.00e-14	Voltage gated proton channel, ion channel, transport	GQIEWAMWANEQALASGLIL ITGGIVATAGR
23	P15144	Aminopeptidase N	CD13	5.31	109.47	ANPEP	kidney	98.07	<=1.00e-14	Protease activity, Angiogenesis, differentiation, host-viral interaction	VVTVIAHELAHQWFGNLVTI
24	Q8TEU8	Kazal	WFIKKN2	5.85	63.941	GASP1, WFIKKNRP	Cortex of kidney	37.43	0.032	Protease-inhibitor	NLNHFETYEACMLACMSGPL AACSLPALQGPCK

(*Continued*)

(*Continued*)

25	Q86SU0	Immunoglobulin-like domain-containing receptor 1	ILDR1	9.12	62.814		Kidney epithelium	85.65	0.023	Maintains epithelial barrier function	LLIGVCWCQCCPQYCCCYIR
26	P11021	Endoplasmic reticulum chaperone BiP	HSPA5	5.07	72.332	GRP78	Renal medulla	99.08	0.002	Chaperone, apoptosis, cell proliferation	GINPDEAVAYGAAVQAGVLS
27	P38646	Stress-70 protein, mitochondrial	GRP75, HSPA9B, mt-HSP70	5.87	73.68	HSPA9	Renal glomerulus	95.39	0.002	Chaperone	STNGDTFLGGEDFDQALLR
28	Q9Y4L1	Hypoxia up-regulated protein 1	GRP170, ORP150	5.16	111.335	HYOU1	Kidney	94.29	<=1.00e-14	Cytoprotective, Chaperone, stress response	LIPEMDQIFTEVEMTTLEK
29	Q9Y2N7	Hypoxia-inducible factor 3-alpha	BHLHE17, MOP7, PASD7	5.67	72.432	HIF3A	Kidney	73.12	9.66E-11	Transcriptional regulator, Angiogenesis, stress response, apoptosis, transcription regulation	DTEAVETDLDIAQDADALDL
30	P80188	Neutrophil gelatinase-associated lipocalin	HNL, NGAL	9.02	22.588	LCN2	Kidney	75.41	<=1.00e-14	Renal development, Apoptosis, immunity, iron transport, ion transport	TFVPGCQPGEFTLGNIK
31	P04839	Cytochrome b-245 heavy chain	NOX2	8.9	65.335	CYBB	Kidney	68.72	1.58E-10	Inflammation, cellular homeostasis	SYFEVFWYTHHLFVIFFIGL AIHGAER
32	P30740	Leukocyte elastase inhibitor	ELANH2, MNEI, PI2	5.9	42.741	SERPINB1	Kidney	87.3	<=1.00e-14	Transcriptional regulator	TYGADLASVDFQHASEDAR
33	Q16665	Hypoxia-inducible factor 1-alpha	BHLHE78, MOP1, PASDB	5.17	92.67	HIF1A	Kidney	96.56	<=1.00e-14		SFDQLSPLESSSASPESASP
34	P49184	Deoxyribonuclease-1-like 1	DNAS1L1, DNL1L	5.45	33.892	DNASE1L1	kidney	85.35	2.70E-14	DNA damage, DNA repair, DNA replication	ELNALYDVFLEVSQHWQSK
35	P39748	Flap endonuclease 1	RAD2	8.8	42.592	FEN1	kidney	72.26	7.43E-10	DNA damage, DNA repair	EAHQLFLEPEVLDPESVELK
36	P78549	Endonuclease III-like protein 1	NTH1, OCTS3	9.72	34.389	NTHL1	kidney	74.88	6.06E-12	endonuclease	DAPVDHLGTEHCYDSSAPPK
37	Q14249	Endonuclease G, mitochondrial		9.53	32.62	ENDOG	renal medulla	85.96	0.004	Zinc phosphodiesterase, tRNA processing	TYVMPNAPVDEAIPLER
38	Q9BQ52	Zinc phosphodiesterase ELAC protein 2	HPC2	8.13	92.219	ELAC2	kidney	87.46	<=1.00e-14	Zinc phosphodiesterase, tRNA processing	GIELAVRPHSAPEYEDETMT VYQIPIHSEQR
39	Q9H777	Zinc phosphodiesterase ELAC protein 1	D29	6.32	40.019	ELAC1	kidney	71.6	1.14E-10		TMELSHTELVFHYVVHELVP TADQCPAEELK
40	Q92629	Delta-sarcoglycan	35DAG	9.24	32.071	SGCD	Cortex of kidney	58.41	0.001	binds heme and transports	LFLSQAGAGSTCQINTSVCL
41	P02790	Hemopexin		6.55	51.676	HPX	kidney	60.29	3.19E-07	vesicular protein trafficking, protein transport	DGWHSWPIAHQWPQGPSAVD AAFSWEEK

(*Continued*)

42	Q9BVK6	Transmembrane emp24 domain-containing protein 9	GP25L2	7.81	27.277	TMED9	renal glomerulus	98.34	0.002	Protein recruitment, mRNA transport, translocation,transport	VHLDIQVGEHANDYAEIAAK
43	P37198	Nuclear pore glycoprotein p62		5.19	53.254	NUP62	kidney	82.24	<=1.00e-14	Regulator of lysosomal function, inflammation, wound healing, cell proliferation	DIIEHLNTSGAPADTSDPLQ QICK
44	P28799	Progranulin	GP88, PCDGF, PEP	6.43	63.544	GRN	kidney	97.31	<=1.00e-14	integral membrane glycoprotein, Immunity	DVECGEGHFCHDNQTCCR
45	P10966	T-cell surface glycoprotein CD8 beta chain	CD8B1	10.03	23.722	CD8B	Cortex of kidney	49.59	1.17E-04	Involved in T-cell activation	QAPSSDSHHEFLALWDSAK
46	P10747	T-cell-specific surface glycoprotein CD28	TP44	9.46	25.066	CD28	Cortex of kidney	49.45	0.006	Inbitor of MAC	QSPMLVAYDNAVNLSCK
47	P13987	CD59 glycoprotein	MIC11, MIN1, MIN2, MIN3, MSK21	6.02	14.177	CD59	renal medulla	98.87	0.002	Transport, sorting, Protein transport	TAVNCSSDFDACLITK
48	Q12907	Vesicular integral-membrane protein VIP36	C5orf8	6.46	40.228	LMAN2	kidney	93.99	<=1.00e-14	Heparin binding	LFQLMVEHTPDEESIDWTK
49	P02749	Beta-2-glycoprotein 1	B2G1	8.34	38.298	APOH	renal glomerulus	86.47	0.002	Inhibitor of serine proteases, acute phase, blood coagulation, hemostasis	TFYEPGEEITYSCKPGYVSR
50	P01009	Alpha-1-antitrypsin	AAT,PI	5.37	46.736	SERPINA1	kidney	99.18	<=1.00e-14	SERPINE1/PAI1 mRNA binding	ADTHDEILEGLNFNLTEIPE AQIHEGFQELLR
51	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRBP1	8.66	44.965	SERBP1	renal glomerulus	97.75	0.002	Physiological function unclear	GEGGEFSVDRPIIDRPIR
52	P01011	Alpha-1-antichymotrypsin	AACT	5.33	47.65	SERPINA3	kidney	84.66	<=1.00e-14	Inhibitor of kallikrein-8, cathepsin G and thrombin	FNLTETSEAEIHQSFQHLLR
53	P35237	Serpin B6	PI6, PTI	5.18	42.594	SERPINB6	kidney	96.52	<=1.00e-14	Mitochondrial membrane ATP synthase (F1F0 ATP synthase of complex V), hydrogen ion transport	TYIGEIFTQILVLPYVGK
54	P30049	ATP synthase subunit delta	ATP5D	5.34	17.489	ATP5F1D	renal medulla	97.75	0.002	involved in muscular contraction/excitation, calcium transport	AQAELVGTADEATR

(*Continued*)

(*Continued*)

55	O14983	Sarcoplasmic/ endoplasmic reticulum calcium ATPase 1		5.07	110.252	ATP2A1	kidney	67.64	6.98E-09		MPPWVNIWLLGSICLSMSLH FLILYVDPLPMIFK
56	Q93084	Sarcoplasmic/ endoplasmic reticulum calcium ATPase 3		5.37	109.256	ATP2A3	kidney	74.81	4.50E-13	calcium transport	QWVVVLQISLPVILLDEALK
57	Q01814	Plasma membrane calcium-transporting ATPase 2	PMCA2	5.66	136.876	ATP2B2	cortex of kidney	57.7	5.75E-09	Calmodulin binding, calcium transport	NNSAIDSGINLTTDTSK
58	Q9UII2	ATPase inhibitor	ATPI, ATPIF1	9.34	12.248	ATP5IF1	cortex of kidney	98.9	<=1.00e-14	Endogenous F1F(o)-ATPase inhibitor	GSDQSENVDR
59	P05023	Sodium/potassium-transporting ATPase subunit alpha-1		5.33	112.896	ATP1A1	kidney	99.54	<=1.00e-14	Sodium/potassium transport	DAFQNAYLELGGLGER
60	P35670	Copper-transporting ATPase 2	PWD, WC1, WND	6.25	157.262	ATP7B	kidney	68.46	6.23E-10	copper transport	NGLTISSDVSDAMTDHEMK
61	Q9UN42	Protein ATP1B4		4.69	41.597	ATP1B4				transcriptional coregulator	LTHVNYTSPLVAMHFTDVVK
62	Q7Z5L7	Isoform 3 of Podocan	SLRR5A	8.47	74.141	PODN					EDFATTYFLEELNLSYNR
63	P08133	Annexin A6	ANX6	5.41	75.873	ANXA6	kidney	93.8	<=1.00e-14	Regulate the release of Ca2+	EDAQVAAEILEIADTPSGDK
64	Q92876	Kallikrein-6	PRSS18, PRSS9	7.15	26.855	KLK6	renal glomerulus	90.05	0.002	protease inhibitor	AVIHPDYDAASHDQDIMLLR
65	P02787	Serotransferrin	TF	6.81	77.049		kidney	67.23	<=1.00e-14	iron binding and transport	SAGWNIPIGLLYCDLPEPR
66	P35613	Basigin	BSG	5.39	42.2		kidney	97.71	<=1.00e-14	Angiogenesis	SELHIENLNMEADPGQYR
67	P08254	Stromelysin-1	MMP3	5.77	53.977	STMY1	kidney	49.86	1.52E-05	collagen degradation	LEPELHLISSFWPSLPSGVD AAYEVTSK
68	P16035	Metalloproteinase inhibitor 2	TIMP2	7.46	24.399		renal medulla	95.95	0.002	metalloprotease inhibitor	MHITLCDFIVPWDTLSTTQK
69	P25713	Metallothionein-3	MT3	4.79	6.926		kidney	75.07	2.70E-12	heavy metal binding	SCCSCCPAECEK
70	Q6DD87	Zinc finger protein 787		8.25	40.428	ZNF787	kidney	75.61	1.39E-12	Transcriptional regulation, DNA-binding	IHTGEKPYTCPDCGR
71	Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	ZNF744	8.69	80.926	ANKZF1	kidney	85.24	<=1.00e-14	cellular response to stress	LFCSTCDQTFQNHQEQR
72	O95201	Zinc finger protein 205	ZNF210	8.88	60.629	ZNF205	renal medulla	80.06	0.004	Transcriptional regulation	TPDAAPPDPSPTEPQEYR
73	Q9NQX6	Zinc finger protein 331	RITA, ZNF361, ZNF463	9.16	53.738	ZNF331	kidney epithelium	82.47	0.004	Transcriptional regulation	IHTGEKPYECQECGK
74	Q5SXM8	DNL-type zinc finger protein	C9orf151	9.88	19.203	DNLZ	kidney	66.55	3.97E-08	co-chaperone	SSEQGPGPAAALGR

(*Continued*)

75	Q6ZSS3	Zinc finger protein 621		9.16	49.204	ZNF621	kidney	76.91	1.59E-10	Transcriptional regulation	GEAPWGPDPWDTEILR
76	Q8NB15	Zinc finger protein 511		7.6	28.265	ZNF511	kidney epithelium	91.45	0.012	Transcriptional regulation	HLYLQDVIMQVADVPEKPR
77	Q06455	Protein CBFA2T1	AML1T1, CBFA2T1, CDR, ETO, MTG8, ZMYND2	8.15	67.566	RUNX1T1	renal glomerulus	64.46	0.01	Transcriptional corepressor	FLTTLQQFGNDISPEIGER
78	O75844	CAAX prenyl protease 1 homolog	FACE1, ATE24	7.11	54.812	ZMPSTE24	renal glomerulus	94.63	0.002	Transmembrane metalloprotease, metal -binding	TTTHVPPELGQIMDSETFEK
79	Q63HK5	Teashirt homolog 3	KIAA1474, TSH3, ZNF537	6.83	118.566	TSHZ3	kidney	63.79	3.25E-07	Developmental protein, transcriptional regulator, repressor	CMYCGHSFESLQDLSVHMIK
80	Q8IZ13	Protein ZBED8	Buster3, C5orf54	5.98	68.326	ZBED8	renal glomerulus	60.66	0.005		WILDPFLFNIDFVDDSYLMK
81	Q12778	Forkhead box protein O1	FKHR, FOXO1A	6.28	69.661	FOXO1	urethra	90.08	0.002	apoptosis, autophagy, transcription regulation	ASLQSGQEGAGDSPGSQFSK
82	P55316	Forkhead box protein G1	FKH2, FKHL1, FKHL2, FKHL3, FKHL4, FOXG1A, FOXG1B, FOXG1C	8.99	52.352	FOXG1	cortex of kidney	41.04	0.015	Transcription repression factor	AGSLYWPMSPFLSLHHPR
83	Q12951	Forkhead box protein I1	FKHL10, FREAC6	5.89	40.972	FOXI1	kidney	83.6	<=1.00e-14	transcription activator	LTLSQIYQYVADNFPFYNK
84	P20807	Calpain-3	CANP3, CANPL3, NCL1	5.81	94.253	CAPN3	kidney	93.66	<=1.00e-14	thiol protease, metal binding	VLYVDPEFPPDETSLFYSQK
85	O14773	Tripeptidyl-peptidase 1	CLN2	6.01	61.247	TPP1	renal glomerulus	97.09	0.002	tripeptidyl-peptidase I activity, metal binding	FLSSSPHLPPSSYFNASGR
86	P05067	Amyloid-beta precursor protein	A4, AD1	4.73	86.943	APP	kidney epithelium	98.63	0.002	heparin-binding, apoptosis, cell adhesion, endocytosis	LALENYITALQAVPPRPR
87	Q86UV5	Ubiquitin carboxyl-terminal hydrolase 48	USP31	5.75	119.032	USP48	renal glomerulus	86.81	0.003	Regulatory role at postsynaptic sites, Ubl conjugation pathway	WAETVRPEEVSQEHIETAYR
88	Q14790	Caspase-8	MCH5	4.99	55.391	CASP8	kidney	78.85	5.28E-12	apoptosis, thiol protease	VFFIQACQGDNYQK
89	P49662	Caspase-4	ICH2	5.69	43.262	CASP4	kidney	85.11	<=1.00e-14	inflammatory caspase	ELLEGLDYSVDVEENLTAR

(*Continued*)

(*Continued*)

90	P55211	Caspase-9	MCH6	5.73	46.28	CASP9	kidney	84.56	2.85E-13	apoptosis, thiol protease	SGSWYVETLDDIFEQWAHSE DLQSLLLR
91	P42574	Caspase-3	CPP32	6.09	31.607	CASP3	kidney	73.76	3.21E-11	apoptosis, thiol protease	MDYPEMGLCIIINNK
92	P23946	Chymase	CYH, CYM	9.44	27.324	CMA1	kidney	43.34	0.019	Serine protease	SITVTLGAHNITEEEDTWQK
93	P36776	Lon protease homolog	PRSS15	6.01	106.489	LONP1	kidney epithelium	85.64	0.003	ATP-binding	EIFDIAFPDEQAEALAVER
94	Q9Y4P1	Cysteine protease ATG4B	APG4B, AUTL1, KIAA0943	4.91	44.294	ATG4B	kidney	92.8	<=1.00e-14	Cysteine protease, autophagy, protein transport	DSYYSIHQIAQMGVGEGK
95	Q6UWY2	Serine protease 57	PRSSL1	9.56	30.333	PRSS57				Serine protease, heparin binding	TPDVYTQVSAFVAWIWDVVR
96	Q8N4E7	Ferritin		6.79	27.538	FTMT				iron homeostasis, iron storage	GDPHLCDFLETYYLNEQVK
97	P35579	Myosin-9		5.5	226.532	MYH9	kidney	95	<=1.00e-14	actin binding, calmodulin binding, cell adhesion	LQQLFNHTMFILEQEEYQR
98	Q06830	Peroxiredoxin-1	PAGA, PAGB, TDPX2	8.27	22.11	PRDX1	kidney	99.29	<=1.00e-14	antioxidant	YVVFFFYPLDFTFVCPTEII AFSDR
99	Q13162	Peroxiredoxin-4		5.86	30.539	PRDX4	renal glomerulus	93.48	0.002	antioxidant	YLVFFFYPLDFTFVCPTEII AFGDR
100	Q99719	Septin-5	PNUTL1, SEPT5	6.21	42.776	SEPTIN5	kidney	73.53	2.43E-11	platelet secretion, cell cycle, cell devision	FGIHVYQFPECDSDEDEDFK
101	O43236	Septin-4	C17orf47, PNUTL2, SEP4, SEPT4	5.77	55.098	SEPTIN4	kidney	81.69	<=1.00e-14	cell cycle, cell devision	LYPWGIVEVENPGHCDFVK
102	Q13515	Phakinin		5.41	45.879	BFSP2	kidney	46.28	0.001	sensory transduction	ASWASSCQQVGEAVLENAR
103	P31947	14-3-3 protein sigma	HME1	4.68	27.774	SFN	renal medulla	82.05	4.38E-04	regulates MDM2	LGLALNFSVFHYEIANSPEE AISLAK
104	O00299	Chloride intracellular channel protein 1	G6, NCC27	5.09	26.922	CLIC1	kidney	98.89	<=1.00e-14	voltage-gated channel,chloride channel	FLDGNELTLADCNLLPK
105	P07203	Glutathione peroxidase 1		6.15	22.088	GPX1	kidney	98.83	<=1.00e-14	protects hemoglobin from oxidative breakdown, lipid metabolism	GLVVLGFPCNQFGHQENAK
106	Q9H223	EH domain-containing protein 4	HCA10, HCA11, PAST4	6.32	61.175	EHD4	urethra	91.13	0.002	ATP- and membrane binding protein	LDGYELPSSLPPHLVPPSHR
107	Q16891	MICOS complex subunit MIC60	HMP, MIC60, MINOS2	6.08	83.677	IMMT	renal medulla	96.32	0.002	mitochondrial cristae morphology, host-viral interaction	LSQEQVDNFTLDINTAYAR

(*Continued*)

108	Q9NX95	Syntabulin	GOLSYN, KIAA1472	5.87	72.388	SYBU	renal medulla	70.75	0.008	part of kinesin motor-adapter complex	LESLLQSMEMAHSGSLR
109	Q9NRS6	Sorting nexin-15		5.09	38.291	SNX15	kidney	85.08	<=1.00e-14	Involved in intracellular trafficking, protein transport	DLHILPPPLIPTPPPDDPR
110	Q92543	Sorting nexin-19	KIAA0254	4.97	108.598	SNX19	kidney	87.16	<=1.00e-14	intracellular vesicle trafficking and exocytosis	HLIYCLGDIILEFLDLSASVEESAATTSASDTPGNSK
111	Q8NFK1	Gap junction gamma-3 protein	GJE1	9.35	31.299	GJC3	kidney	53.75	7.19E-07	cell signaling	FWVFQVILVAVPSALYMGFTLYHVIWHWELSGK
112	O15265	Ataxin-7	SCA7	9.89	95.451	ATXN7	kidney epithelium	74.47	0.005	transcription coactivator	NCVAHSGPPYPSTVTSSHSIGLNCVTNK
113	Q16595	Frataxin	FRDA, X25	8.8	23.135	FXN	kidney	76.59	3.60E-11	hema biosynthesis, ion transport	SGTLGHPGSLDETTYER
114	Q7Z2E3	Aprataxin	AXA1	9.27	40.74	APTX	renal medulla	83.35	0.002	DNA-binding, DNA damage, DNA repair	LGYHAIPSMSHVHLHVISQDFDSPCLK
115	Q9UBB4	Ataxin-10	SCA10	5.12	53.488	ATXN10	renal glomerulus	94.41	0.002	intracellular glycosylation, homeostasis	DPSQVENLASSLQLITECFR
116	P54252	Ataxin-3	ATX3, MJD, MJD1, SCA3	4.69	41.25	ATXN3	kidney	77.55	1.40E-12	protein homeastasis	VLEANDGSGMLDEDEEDLQR
117	P02790	Hemopexin		6.55	51.676	HPX	kidney	60.29	3.19E-07	heme binding, transport	DGWHSWPIAHQWPQGPSAVDAAFSWEEK
118	Q9NRS6	Sorting nexin-15		5.09	38.291	SNX15	kidney	85.08	<=1.00e-14	Intracellular trafficking, protein transport, lipid binding	DGVHVLLQGVPSDPLPAR
119	P29033	Gap junction beta-2 protein		9.11	26.215	GJB2	kidney epithelium	84.52	0.016	metal binding	EVWGDEQADFVCNTLQPGCK
120	O75712	Gap junction beta-3 protein	CX31	8.94	30.818	GJB3	urethra	69.44	0.003	cell signaling	QPGCTNVCYDNYFPISNIR
121	O75431	Metaxin-2		5.9	29.763	MTX2	renal medulla	89.6	0.002	protein transport	SLVAEAFVSQIAAAEPWPENATLYQQLK
122	P04083	Annexin A1	ANX1, LPC1	6.57	38.714	ANXA1	urethra	98.19	0.002	inflammatory response, calcium/phospholipid binding	QAWFIENEEQEYVQTVK
123	P09525	Annexin A4	ANX4	5.83	35.882	ANXA4	urethra	97.72	0.002	exocytosis. calcium/phospholipid binding	AASGFNAMEDAQTLR
124	P08758	Annexin A5	ANX5, ENX2, PP4	4.93	35.936	ANXA5	urethra	99.19	0.002	anticoagulant protein, hemostasis	DPDAGIDEAQVEQDAQALFQAGELK
125	P08133	Annexin A6	ANX6	5.41	75.873	ANXA6	urethra	96.47	0.002	regulate Ca2+ storage	EDAQVAAEILEIADTPSGDK
126	P50995	Annexin A11	ANX11	7.53	54.389	ANXA11	kidney	97.17	<=1.00e-14	cell division	GFGTDEQAIIDCLGSR

(*Continued*)

(*Continued*)

127	P12429	Annexin A3	ANX3	5.62	36.375	ANXA3	kidney	80.25	2.20E-14	anticoagulant, phospholipase A2 inhibitor	GELSGHFEDLLLAIVNCVR
128	Q9UJ72	Annexin A10	ANX14	5.13	37.277	ANXA10	kidney	44.08	1.37E-04		DVMAGLMYPPPLYDAHELWH AMK
129	P56962	Syntaxin-17		6.14	33.403	STX17	renal medulla	86.7	0.002	Autophagy, ER-golgi transport	IDSIADHVNSAAVNVEEGTK
130	P27824	Calnexin		4.46	67.568	CANX	cortex of kidney	98.64	<=1.00e-14	calcium binding protein, chaperone	WKPPMIDNPSYQGIWKPR
131	P35241	Radixin		6.03	68.563	RDX	urethra	94.32	0.002	actin binding	VTTMDAELEFAIQPNTTGK
132	Q86WW8	Cytochrome c oxidase assembly factor 5	C2orf64	8.97	8.375	COA5	kidney epithelium	91.43	0.029	Involved in the process of mitochondrial complex IV assembly	EDLGACLLQSDCVVQEGK
133	Q9UBK2	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha	LEM6, PGC1, PGC1A, PPARGC1	5.71	91.026	PPARGC1A	renal medulla	96.88	0.002	Transcriptional coactivator, Biological rhythms	SNYADLDSNSDDFDPASTK
134	P53420	Collagen alpha-4(IV) chain		8.9	164.037	COL4A4	renal medulla	87.51	0.002	structural component of glomerular basement membranes	GFGPGYLGGFLLVLHSQTDQ EPTCPLGMPR
135	P50461	Cysteine and glycine-rich protein 3	CLP.MLP	8.89	20.968	CSRP3	kidney	45.83	0.002	actin binding, myogenesis, transcription regulation	NFGPTGIGFGGLTQQVEK
136	P14210	Hepatocyte growth factor	HPTA	8.22	83.133	HGF	kidney	71.85	1.20E-11	acts as growth factor	NPDDDAHGPWCYTGNPLIPW DYCPISR
137	Q3KNW1	Zinc finger protein SNAI3	ZNF293	9.45	32.473	SNAI3	kidney	50.73	1.20E-04	transcriptional repressor, transcription regulation	APGGFECFHCHKPYHTLAGL AR
138	P02647	Apolipoprotein A-I		5.56	30.777	APOA1	kidney	62.63	2.96E-07	cholesterol metabolism, transport	EQLGPVTQEFWDNLEK

Table 2: A2

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	Expression	FDR	Function	Sequence
1	P13987	CD59 glycoprotein	MIC11, MIN1, MIN2, MIN3, MSK21	6.02	14.177	CD59	renal medulla	98.87	0.002	Transport, sorting, Protein transport	TAVNCSSDFDACLITK
2	P15144	Aminopeptidase N	CD13	5.31	109.47	ANPEP	kidney	98.07	<=1.00e-14	Protease activity, Angiogenesis, differentiation, host-viral interaction	VVTVIAHELAHQWFGNLVTI
3	P04083	Annexin A1	ANX1, LPC1	6.57	38.714	ANXA1	urethra	98.19	0.002	inflammatory response, calcium/phospholipid binding	QAWFIENEEQEYVQTVK
4	P28799	Progranulin	GP88, PCDGF, PEP	6.43	63.544	GRN	kidney	97.31	<=1.00e-14	integral membrane glycoprotein, Immunity	DVECGEGHFCHDNQTCCR
5	P08133	Annexin A6	ANX6	5.41	75.873	ANXA6	kidney	93.8	<=1.00e-14	Regulate the release of Ca2+	EDAQVAAEILEIADTPSGDK
6	P05023	Sodium/potassium-transporting ATPase subunit alpha-1		5.33	112.896	ATP1A1	kidney	99.54	<=1.00e-14	Sodium/potassium transport	DAFQNAYLELGGLGER
7	Q06830	Peroxiredoxin-1	PAGA, PAGB, TDPX2	8.27	22.11	PRDX1	kidney	99.29	<=1.00e-14	antioxidant	YVVFFFYPLDFTFVCPTEII AFSDR
8	O14773	Tripeptidyl-peptidase 1	CLN2	6.01	61.247	TPP1	renal glomerulus	97.09	0.002	tripeptidyl-peptidase I activity, metal binding	FLSSSPHLPPSSYFNASGR
9	P02749	Beta-2-glycoprotein 1	B2G1	8.34	38.298	APOH	renal glomerulus	86.47	0.002	Inhibitor of serine proteases, acute phase, blood coagulation, hemostasis	TFYEPGEEITYSCKPGYVSR
10	Q12907	Vesicular integral-membrane protein VIP36	C5orf8	6.46	40.228	LMAN2	kidney	93.99	<=1.00e-14	Heparin binding	LFQLMVEHTPDEESIDWTK
11	P02790	Hemopexin		6.55	51.676	HPX	kidney	60.29	3.19E-07	heme binding, transport	DGWHSWPIAHQWPQGPSAVD AAFSWEEK
12	P50995	Annexin A11	ANX11	7.53	54.389	ANXA11	kidney	97.17	<=1.00e-14	cell division	GFGTDEQAIIDCLGSR
13	P08758	Annexin A5	ANX5, ENX2, PP4	4.93	35.936	ANXA5	urethra	99.19	0.002	anticoagulant protein, hemostasis	DPDAGIDEAQVEQDAQALFQ AGELK
14	P09525	Annexin A4	ANX4	5.83	35.882	ANXA4	urethra	97.72	0.002	exocytosis. calcium/ phospholipid binding	AASGFNAMEDAQTLR
15	O94925	Glutaminase kidney isoform, mitochondrial	GLS1,KIAA0838	7.85	73.461	GLS	kidney	97.1	<=1.00e-14	Acid-base homeostasis	ILQEYQVQYTPQGDSDNGK
16	Q16891	MICOS complex subunit MIC60	HMP, MIC60, MINOS2	6.08	83.677	IMMT	renal medulla	96.32	0.002	mitochondrial cristae morphology, host-viral interaction	LSQEQVDNFTLDINTAYAR
17	P36776	Lon protease homolog	PRSS15	6.01	106.489	LONP1	kidney epithelium	85.64	0.003	ATP-binding	EIFDIAFPDEQAEALAVER

(*Continued*)

(*Continued*)

18	Q9Y2N7	Hypoxia-inducible factor 3-alpha	BHLHE17, MOP7, PASD7	5.67	72.432	HIF3A	Kidney	73.12	9.66E-11	Transcriptional regulator, Angiogenesis, stress response, apoptosis, transcription regulation	DTEAVETDLDIAQDADALDL
19	Q13162	Peroxiredoxin-4		5.86	30.539	PRDX4	renal glomerulus	93.48	0.002	antioxidant	YLVFFFYPLDFTFVCPTEII AFGDR
20	Q9Y4L1	Hypoxia up-regulated protein 1	GRP170, ORP150	5.16	111.335	HYOU1	Kidney	94.29	<=1.00e-14	Cytoprotective, Chaperone, stress response	LIPEMDQIFTEVEMTTLEK
21	O00299	Chloride intracellular channel protein 1	G6, NCC27	5.09	26.922	CLIC1	kidney	98.89	<=1.00e-14	voltage-gated channel,chloride channel	FLDGNELTLADCNLLPK
22	P11279	Lysosome-associated membrane glycoprotein 1	CD107a	9	44.882	LAMP1	Renal glomerulus	99.92	0.002	Lysosome biogenesis, autophagy, cholesterol homeostasis, Host-viral interaction	YSVQLMSFVYNLSDTHLFPN ASSK
23	Q7Z4W1	L-xylulose reductase	SDR20C1	8.33	25.913	DCXR	kidney	98.65	<=1.00e-14	Osmoregulation, Carbohydrate metabolism, Glucose metabolism, Xylose metabolism	ALGSVGPVDLLVNNAAVALL QPFLEVTK
24	P35241	Radixin		6.03	68.563	RDX	urethra	94.32	0.002	actin binding	VTTMDAELEFAIQPNTTGK
25	P35579	Myosin-9		5.5	226.532	MYH9	kidney	95	<=1.00e-14	actin binding, calmodulin binding, cell adhesion	LQQLFNHTMFILEQEEYQR
26	Q9H223	EH domain-containing protein 4	HCA10, HCA11, PAST4	6.32	61.175	EHD4	urethra	91.13	0.002	ATP- and membrane binding protein	LDGYELPSSLPPHLVPPSHR
27	P80188	Neutrophil gelatinase-associated lipocalin	HNL, NGAL	9.02	22.588	LCN2	Kidney	75.41	<=1.00e-14	Renal development, Apoptosis, immunity, iron transport, ion transport	TFVPGCQPGEFTLGNIK
28	P12429	Annexin A3	ANX3	5.62	36.375	ANXA3	kidney	80.25	2.20E-14	anticoagulant, phospholipase A2 inhibitor	GELSGHFEDLLLAIVNCVR
29	P35237	Serpin B6	PI6, PTI	5.18	42.594	SERPINB6	kidney	96.52	<=1.00e-14	Mitochondrial membrane ATP synthase (F1F0 ATP synthase of complex V), hydrogen ion transport	TYIGEIFTQILVLPYVGK
30	P27824	Calnexin		4.46	67.568	CANX	cortex of kidney	98.64	<=1.00e-14	calcium binding protein, chaperone	WKPPMIDNPSYQGIWKPR
31	P30740	Leukocyte elastase inhibitor	ELANH2, MNEI, PI2	5.9	42.741	SERPINB1	Kidney	87.3	<=1.00e-14	Transcriptional regulator	TYGADLASVDFQHASEDAR
32	P05067	Amyloid-beta precursor protein	A4, AD1	4.73	86.943	APP	kidney epithelium	98.63	0.002	heparin-binding, apoptosis, cell adhesion, endocytosis	LALENYITALQAVPPRPR
33	Q9BVK6	Transmembrane emp24 domain-containing protein 9	GP25L2	7.81	27.277	TMED9	renal glomerulus	98.34	0.002	Protein recruitment, mRNA transport, translocation,transport	VHLDIQVGEHANDYAEIAAK
34	P11021	Endoplasmic reticulum chaperone BiP	HSPA5	5.07	72.332	GRP78	Renal medulla	99.08	0.002	Chaperone, apoptosis, cell proliferation	GINPDEAVAYGAAVQAGVLS
35	P38646	Stress-70 protein, mitochondrial	GRP75, HSPA9B, mt-HSP70	5.87	73.68	HSPA9	Renal glomerulus	95.39	0.002	Chaperone	STNGDTFLGGEDFDQALLR

Table 3: B1

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q13007	Isoform 3 of Interleukin-24	MDA7, ST16	8.93	17.75	IL24					LLQQEVLQNVSDAESCYLVHTLLEFYLK
2	Q96RQ9	L-amino-acid oxidase	FIG1	8.79	62.881	IL4I1	Urinary bladder	56.32	1.59E-10	immunoregulator	ALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPAR
3	Q8WWZ1	Interleukin-1 family member 10	FIL1T, IL1HY2,IL38	4.94	16.943	IL1F10	Renal medulla	39.53	0.76	immunomodulatory activity	CLACVETEEGPSLQLEDVNIEELYK
4	Q12906	Interleukin enhancer-binding factor 3	DRBF, MPHOSPH4, NF90	8.86	95.338	ILF3	Renal medulla	92.83	0.002	Biogenesis of circular RNAs	GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK
5	P29466	Caspase-1	IL1BC, IL1BCE	5.63	45.158	CASP1	kidney	76.33	<=1.00e-14	apoptosis, protease activity, inflammatory response	TGAEVDITGMTMLLQNLGYSVDVK
6	P78540	Arginase-2, mitochondrial		6	38.577	ARG2	Renal medulla	94.92	0.002	Inflammatory response, Arginine metabolism, immunity, Urea cycle	AVSDGYSCVTLGGDHSLAIGTISGHAR
7	P04839	Cytochrome b-245 heavy chain	NOX2	8.9	65.335	CYBB	Kidney	68.72	1.58E-10	Inflammation, cellular homeostasis	SYFEVFWYTHHLFVIFFIGLAIHGAER

Table 4: B2

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	O43542	DNA repair protein XRCC3	XRCC3	8.81	37.849	XRCC3	kidney	73.34	1.21E-13	homologous recombination repair (HRR) pathway, DNA damage, DNA recombination, DNA repair	FGSQIFIEHVADVDTLLECV NK
2	O15287	Fanconi anemia group G protein	XRCC9	5.32	68.553	FANCG	kidney	72.69	1.61E-11	Post replication repair, DNA damage, DNA repair	APQFLIEVELLLPPPDLASP LHCGTQSQTK
3	P13010	X-ray repair cross-complementing protein 5	G22P2	5.55	82.704	XRCC5	kidney	96.17	<=1.00e-14	DNA non-homologous end joining (NHEJ), DNA damage, DNA recombination, DNA repair, Transcription regulation, immunity	ASFEEASNQLINHIEQFLDT NETPYFMK
4	Q9Y6H3	Mitochondrial inner membrane protease ATP23 homolog	KUB3, XRCC6BP1	8.3	28.08	ATP23	Cortex kidney	75.17	1.09E-09		HFSCEDCNGNVSGGFDASTS QIVLCQNNIHNQAHMNR
5	P31941	DNA dC->dU-editing enzyme APOBEC-3A	phorbolin-1	6.34	22.997	APOBEC3A	kidney	54.07	1.82E-07	Epigenetic regulation, Antiviral defence, immunity	VTWFISWSPCFSWGCAGEVR
6	Q13216	DNA excision repair protein ERCC-8	CKN1,CSA	5.91	44.055	ERCC8	kidney	72.42	8.82E-10	DNA single-strand and double-strand breaks (DSSBs) repair, DNA damage, DNA repair, Ubl conjugation pathway	FTVSCGCSSEFVFVPYGSTI
7	Q5T890	DNA excision repair protein ERCC-6-like 2	C9orf102, RAD26L	8.83	177.016	ERCC6L2	kidney epithelium	80.21	0.018	Early DNA damage response, DNA damage, DNA repair	EFNSTQDVNICLVSTMAGGL
8	P49184	Deoxyribonuclease-1-like 1	DNAS1L1, DNL1L	5.45	33.892	DNASE1L1	kidney	85.35	2.70E-14	DNA damage, DNA repair, DNA replication	ELNALYDVFLEVSQHWQSK
9	P39748	Flap endonuclease 1	RAD2	8.8	42.592	FEN1	kidney	72.26	7.43E-10	DNA damage, DNA repair	EAHQLFLEPEVLDPESVELK
10	Q7Z2E3	Aprataxin	AXA1	9.27	40.74	APTX	renal medulla	83.35	0.002	DNA-binding, DNA damage, DNA repair	LGYHAIPSMSHVHLHVISQD FDSPCLK
11	P31947	14-3-3 protein sigma	HME1	4.68	27.774	SFN	renal medulla	82.05	4.38E-04	regulates MDM2	LGLALNFSVFHYEIANSPEE AISLAK

Table 5: B3

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q92629	Delta-sarcoglycan	35DAG	9.24	32.071	SGCD	Cortex of kidney	58.41	0.001	binds heme and transports	LFLSQAGAGSTCQINTSVCL
2	P02790	Hemopexin		6.55	51.676	HPX	kidney	60.29	3.19E-07	vesicular protein trafficking, protein transport	DGWHSWPIAHQWPQGPSAVD AAFSWEEK
3	Q9BVK6	Transmembrane emp24 domain-containing protein 9	GP25L2	7.81	27.277	TMED9	renal glomerulus	98.34	0.002	Protein recruitment, mRNA transport, translocation,transport	VHLDIQVGEHANDYAEIAAK
4	P37198	Nuclear pore glycoprotein p62		5.19	53.254	NUP62	kidney	82.24	<=1.00e-14	Regulator of lysosomal function, inflammation, wound healing, cell proliferation	DIIEHLNTSGAPADTSDPLQ QICK
5	P28799	Progranulin	GP88, PCDGF, PEP	6.43	63.544	GRN	kidney	97.31	<=1.00e-14	integral membrane glycoprotein, Immunity	DVECGEGHFCHDNQTCCR
6	P10966	T-cell surface glycoprotein CD8 beta chain	CD8B1	10.03	23.722	CD8B	Cortex of kidney	49.59	1.17E-04	Involved in T-cell activation	QAPSSDSHHEFLALWDSAK
7	P10747	T-cell-specific surface glycoprotein CD28	TP44	9.46	25.066	CD28	Cortex of kidney	49.45	0.006	Inbitor of MAC	QSPMLVAYDNAVNLSCK
8	P13987	CD59 glycoprotein	MIC11, MIN1, MIN2, MIN3, MSK21	6.02	14.177	CD59	renal medulla	98.87	0.002	Transport, sorting, Protein transport	TAVNCSSDFDACLITK
9	Q12907	Vesicular integral-membrane protein VIP36	C5orf8	6.46	40.228	LMAN2	kidney	93.99	<=1.00e-14	Heparin binding	LFQLMVEHTPDEESIDWTK
10	P02749	Beta-2-glycoprotein 1	B2G1	8.34	38.298	APOH	renal glomerulus	86.47	0.002	Inhibitor of serine proteases, acute phase, blood coagulation, hemostasis	TFYEPGEEITYSCKPGYVSR

Table 6: B4

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	P15144	Aminopeptidase N	CD13	5.31	109.47	ANPEP	kidney	98.07	<=1.00e-14	Protease activity, Angiogenesis, differentiation, host-viral interaction	VVTVIAHELAHQWFGNLVTI
2	Q8TEU8	Kazal	WFIKKN2	5.85	63.941	GASP1, WFIKKNRP	Cortex of kidney	37.43	0.032	Protease-inhibitor	NLNHFETYEACMLACMSGPLAACSLPALQGPCK
3	P01009	Alpha-1-antitrypsin	AAT,PI	5.37	46.736	SERPINA1	kidney	99.18	<=1.00e-14	SERPINE1/PAI1 mRNA binding	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR
4	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRBP1	8.66	44.965	SERBP1	renal glomerulus	97.75	0.002	Physiological function unclear	GEGGEFSVDRPIIDRPIR
5	P01011	Alpha-1-antichymotrypsin	AACT	5.33	47.65	SERPINA3	kidney	84.66	<=1.00e-14	Inhibitor of kallikrein-8, cathepsin G and thrombin	FNLTETSEAEIHQSFQHLLR
6	P35237	Serpin B6	PI6, PTI	5.18	42.594	SERPINB6	kidney	96.52	<=1.00e-14	Mitochondrial membrane ATP synthase (F1F0 ATP synthase of complex V), hydrogen ion transport	TYIGEIFTQILVLPYVGK
7	Q92876	Kallikrein-6	PRSS18, PRSS9	7.15	26.855	KLK6	renal glomerulus	90.05	0.002	protease inhibitor	AVIHPDYDAASHDQDIMLLR
8	P16035	Metalloproteinase inhibitor 2	TIMP2	7.46	24.399		renal medulla	95.95	0.002	metalloprotease inhibitor	MHITLCDFIVPWDTLSTTQK
9	O75844	CAAX prenyl protease 1 homolog	FACE1, ATE24	7.11	54.812	ZMPSTE24	renal glomerulus	94.63	0.002	Transmembrane metalloprotease, metal-binding	TTTHVPPELGQIMDSETFEK
10	P20807	Calpain-3	CANP3, CANPL3, NCL1	5.81	94.253	CAPN3	kidney	93.66	<=1.00e-14	thiol protease, metal binding	VLYVDPEFPPDETSLFYSQK
11	O14773	Tripeptidyl-peptidase 1	CLN2	6.01	61.247	TPP1	renal glomerulus	97.09	0.002	tripeptidyl-peptidase I activity, metal binding	FLSSSPHLPPSSYFNASGR
12	Q14790	Caspase-8	MCH5	4.99	55.391	CASP8	kidney	78.85	5.28E-12	apoptosis, thiol protease	VFFIQACQGDNYQK
13	P49662	Caspase-4	ICH2	5.69	43.262	CASP4	kidney	85.11	<=1.00e-14	inflammatory caspase	ELLEGLDYSVDVEENLTAR
14	P55211	Caspase-9	MCH6	5.73	46.28	CASP9	kidney	84.56	2.85E-13	apoptosis, thiol protease	SGSWYVETLDDIFEQWAHSEDLQSLLLR
15	P42574	Caspase-3	CPP32	6.09	31.607	CASP3	kidney	73.76	3.21E-11	apoptosis, thiol protease	MDYPEMGLCIIINNK
16	P23946	Chymase	CYH, CYM	9.44	27.324	CMA1	kidney	43.34	0.019	Serine protease	SITVTLGAHNITEEEDTWQK
17	Q9Y4P1	Cysteine protease ATG4B	APG4B, AUTL1, KIAA0943	4.91	44.294	ATG4B	kidney	92.8	<=1.00e-14	Cysteine protease, autophagy, protein transport	DSYYSIHQIAQMGVGEGK
18	Q6UWY2	Serine protease 57	PRSSL1	9.56	30.333	PRSS57				Serine protease, heparin binding	TPDVYTQVSAFVAWIWDVVR

Table 7: B5

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q3KNW1	Zinc finger protein SNAI3	ZNF293	9.45	32.473	SNAI3	kidney	50.73	1.20E-04	transcriptional repressor, transcription regulation	APGGFECFHCHKPYHTLAGL AR
2	Q9UBK2	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha	LEM6, PGC1, PGC1A, PPARGC1	5.71	91.026	PPARGC1A	renal medulla	96.88	0.002	Transcriptional coactivator, Biological rhythms	SNYADLDSNSDDFDPASTK
3	P50461	Cysteine and glycine-rich protein 3	CLP.MLP	8.89	20.968	CSRP3	kidney	45.83	0.002	actin binding, myogenesis, transcription regulation	NFGPTGIGFGGLTQQVEK
4	O15265	Ataxin-7	SCA7	9.89	95.451	ATXN7	kidney epithelium	74.47	0.005	transcription coactivator	NCVAHSGPPYPSTVTSSHSI GLNCVTNK
5	Q63HK5	Teashirt homolog 3	KIAA1474, TSH3, ZNF537	6.83	118.566	TSHZ3	kidney	63.79	3.25E-07	Developmental protein, transcriptional regulator, repressor	CMYCGHSFESLQDLSVHMIK
6	Q8IZ13	Protein ZBED8	Buster3, C5orf54	5.98	68.326	ZBED8	renal glomerulus	60.66	0.005		WILDPFLFNIDFVDDSYLMK
7	Q12778	Forkhead box protein O1	FKHR, FOXO1A	6.28	69.661	FOXO1	urethra	90.08	0.002	apoptosis, autophagy, transcription regulation	ASLQSGQEGAGDSPGSQFSK
8	P55316	Forkhead box protein G1	FKH2, FKHL1, FKHL2, FKHL3, FKHL4, FOXG1A, FOXG1B, FOXG1C	8.99	52.352	FOXG1	cortex of kidney	41.04	0.015	Transcription repression factor	AGSLYWPMSPFLSLHHPR
9	Q12951	Forkhead box protein I1	FKHL10, FREAC6	5.89	40.972	FOXI1	kidney	83.6	<=1.00e-14	transcription activator	LTLSQIYQYVADNFPFYNK
10	Q06455	Protein CBFA2T1	AML1T1, CBFA2T1, CDR, ETO, MTG8, ZMYND2	8.15	67.566	RUNX1T1	renal glomerulus	64.46	0.01	Transcriptional corepressor	FLTTLQQFGNDISPEIGER
11	Q6ZSS3	Zinc finger protein 621		9.16	49.204	ZNF621	kidney	76.91	1.59E-10	Transcriptional regulation	GEAPWGPDPWDTEILR
12	Q8NB15	Zinc finger protein 511		7.6	28.265	ZNF511	kidney epithelium	91.45	0.012	Transcriptional regulation	HLYLQDVIMQVADVPEKPR
13	O95201	Zinc finger protein 205	ZNF210	8.88	60.629	ZNF205	renal medulla	80.06	0.004	Transcriptional regulation	TPDAAPPDPSPTEPQEYR

(*Continued*)

(*Continued*)

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
14	Q9NQX6	Zinc finger protein 331	RITA, ZNF361, ZNF463	9.16	53.738	ZNF331	kidney epithelium	82.47	0.004	Transcriptional regulation	IHTGEKPYECQECGK
15	Q6DD87	Zinc finger protein 787		8.25	40.428	ZNF787	kidney	75.61	1.39E-12	Transcriptional regulation, DNA-binding	IHTGEKPYTCPDCGR
16	Q9UN42	Protein ATP1B4		4.69	41.597	ATP1B4				transcriptional coregulator	LTHVNYTSPLVAMHFTDVVK
17	P30740	Leukocyte elastase inhibitor	ELANH2, MNEI, PI2	5.9	42.741	SERPINB1	Kidney	87.3	<=1.00e-14	Transcriptional regulator	TYGADLASVDFQHASEDAR
18	Q9Y2N7	Hypoxia-inducible factor 3-alpha	BHLHE17, MOP7, PASD7	5.67	72.432	HIF3A	Kidney	73.12	9.66E-11	Transcriptional regulator, Angiogenesis, stress response, apoptosis, transcription regulation	DTEAVETDLDIAQDADALDL
19	Q9NPH5	NADPH oxidase 4	RENOX	8.96	66.931	NOX4	Renal glomerulus	96.26	0.002	Regulating gene expression	TFHITCGVTICIFSGVHVAA HLVNALNFSVNYSEDFVELN AAR
20	O15446	DNA-directed RNA polymerase I subunit RPA34	ASE1, CAST, CD3EAP, PAF49	8.66	54.951	POLR1G	kidney	60.65	7.59E-07	Transcription of DNA into RNA, Transcription	GQMAMMEPGTEAMEPVEPEM
21	P11021	Endoplasmic reticulum chaperone BiP	HSPA5	5.07	72.332	GRP78	Renal medulla	99.08	0.002	Chaperone, apoptosis, cell proliferation	GINPDEAVAYGAAVQAGVLS
22	P38646	Stress-70 protein, mitochondrial	GRP75, HSPA9B, mt-HSP70	5.87	73.68	HSPA9	Renal glomerulus	95.39	0.002	Chaperone	STNGDTFLGGEDFDQALLR
23	Q9Y4L1	Hypoxia up-regulated protein 1	GRP170, ORP150	5.16	111.335	HYOU1	Kidney	94.29	<=1.00e-14	Cytoprotective, Chaperone, stress response	LIPEMDQIFTEVEMTTLEK
24	P78549	Endonuclease III-like protein 1	NTH1, OCTS3	9.72	34.389	NTHL1	kidney	74.88	6.06E-12	endonuclease	DAPVDHLGTEHCYDSSAPPK
25	Q14249	Endonuclease G, mitochondrial		9.53	32.62	ENDOG	renal medulla	85.96	0.004	Zinc phosphodiesterase, tRNA processing	TYVMPNAPVDEAIPLER
26	Q9BQ52	Zinc phosphodiesterase ELAC protein 2	HPC2	8.13	92.219	ELAC2	kidney	87.46	<=1.00e-14	Zinc phosphodiesterase, tRNA processing	GIELAVRPHSAPEYEDETMT VYQIPIHSEQR
27	Q9H777	Zinc phosphodiesterase ELAC protein 1	D29	6.32	40.019	ELAC1	kidney	71.6	1.14E-10		TMELSHTELVFHYVVHELVP TADQCPAEELK
28	Q5SXM8	DNL-type zinc finger protein	C9orf151	9.88	19.203	DNLZ	kidney	66.55	3.97E-08	co-chaperone	SSEQGPGPAAALGR
29	P35579	Myosin-9		5.5	226.532	MYH9	kidney	95	<=1.00e-14	actin binding, calmodulin binding, cell adhesion	LQQLFNHTMFILEQEEYQR

Table 8: B6

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q5SVS4	Kidney mitochondrial carrier protein 1	KMCP1	9.49	32.474	SLC25A30	Renal medulla	92.33	0.002	Probable transporter, Transport	LFIERPEDETLPINVICGILSGVISSTIANPTDVLK
2	P13498	Cytochrome b-245 light chain		9.58	21.012	CYBA	kidney	96.41	<=1.00e-14	Voltage gated proton channel, ion channel, transport	GQIEWAMWANEQALASGLILITGGIVATAGR
3	P80188	Neutrophil gelatinase-associated lipocalin	HNL, NGAL	9.02	22.588	LCN2	Kidney	75.41	<=1.00e-14	Renal development, Apoptosis, immunity, iron transport, ion transport	TFVPGCQPGEFTLGNIK
4	P30049	ATP synthase subunit delta	ATP5D	5.34	17.489	ATP5F1D	renal medulla	97.75	0.002	involved in muscular contraction/excitation, calcium transport	AQAELVGTADEATR
5	Q93084	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3		5.37	109.256	ATP2A3	kidney	74.81	4.50E-13	calcium transport	QWVVVLQISLPVILLDEALK
6	Q01814	Plasma membrane calcium-transporting ATPase 2	PMCA2	5.66	136.876	ATP2B2	cortex of kidney	57.7	5.75E-09	Calmodulin binding, calcium transport	NNSAIDSGINLTTDTSK
7	P05023	Sodium/potassium-transporting ATPase subunit alpha-1		5.33	112.896	ATP1A1	kidney	99.54	<=1.00e-14	Sodium/potassium transport	DAFQNAYLELGGLGER
8	P35670	Copper-transporting ATPase 2	PWD, WC1, WND	6.25	157.262	ATP7B	kidney	68.46	6.23E-10	copper transport	NGLTISSDVSDAMTDHEMK
9	P02787	Serotransferrin	TF	6.81	77.049		kidney	67.23	<=1.00e-14	iron binding and transport	SAGWNIPIGLLYCDLPEPR
10	Q8N4E7	Ferritin		6.79	27.538	FTMT				iron homeostasis, iron storage	GDPHLCDFLETYYLNEQVK
11	P07203	Glutathione peroxidase 1		6.15	22.088	GPX1	kidney	98.83	<=1.00e-14	protects hemoglobin from oxidative breakdown, lipid metabolism	GLVVLGFPCNQFGHQENAK
12	Q9NRS6	Sorting nexin-15		5.09	38.291	SNX15	kidney	85.08	<=1.00e-14	Involved in intracellular trafficking, protein transport	DLHILPPPLIPTPPPDDPR
13	Q92543	Sorting nexin-19	KIAA0254	4.97	108.598	SNX19	kidney	87.16	<=1.00e-14	intracellular vesicle trafficking and exocytosis	HLIYCLGDIILEFLDLSASVEESAATTSASDTPGNSK
14	Q8NFK1	Gap junction gamma-3 protein	GJE1	9.35	31.299	GJC3	kidney	53.75	7.19E-07	cell signaling	FWVFQVILVAVPSALYMGFTLYHVIWHWELSGK
16	Q16595	Frataxin	FRDA, X25	8.8	23.135	FXN	kidney	76.59	3.60E-11	hema biosynthesis, ion transport	SGTLGHPGSLDETTYER
17	Q9UBB4	Ataxin-10	SCA10	5.12	53.488	ATXN10	renal glomerulus	94.41	0.002	intracellular glycosylation, homeostasis	DPSQVENLASSLQLITECFR

(*Continued*)

(*Continued*)

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
18	P54252	Ataxin-3	ATX3, MJD, MJD1, SCA3	4.69	41.25	ATXN3	kidney	77.55	1.40E-12	protein homeastasis	VLEANDGSGMLDEDEEDLQR
19	P02790	Hemopexin		6.55	51.676	HPX	kidney	60.29	3.19E-07	heme binding, transport	DGWHSWPIAHQWPQGPSAVDAAFSWEEK
20	Q9NRS6	Sorting nexin-15		5.09	38.291	SNX15	kidney	85.08	<=1.00e-14	Intracellular trafficking, protein transport, lipid binding	DGVHVLLQGVPSDPLPAR
21	P29033	Gap junction beta-2 protein		9.11	26.215	GJB2	kidney epithelium	84.52	0.016	metal binding	EVWGDEQADFVCNTLQPGCK
22	O75712	Gap junction beta-3 protein	CX31	8.94	30.818	GJB3	urethra	69.44	0.003	cell signaling	QPGCTNVCYDNYFPISNIR
23	O75431	Metaxin-2		5.9	29.763	MTX2	renal medulla	89.6	0.002	protein transport	SLVAEAFVSQIAAAEPWPENATLYQQLK
24	P04083	Annexin A1	ANX1, LPC1	6.57	38.714	ANXA1	urethra	98.19	0.002	inflammatory response, calcium/phospholipid binding	QAWFIENEEQEYVQTVK
25	P09525	Annexin A4	ANX4	5.83	35.882	ANXA4	urethra	97.72	0.002	exocytosis. calcium/ phospholipid binding	AASGFNAMEDAQTLR
26	P08758	Annexin A5	ANX5, ENX2, PP4	4.93	35.936	ANXA5	urethra	99.19	0.002	anticoagulant protein, hemostasis	DPDAGIDEAQVEQDAQALFQAGELK
27	P08133	Annexin A6	ANX6	5.41	75.873	ANXA6	urethra	96.47	0.002	regulate Ca2+ storage	EDAQVAAEILEIADTPSGDK
28	P50995	Annexin A11	ANX11	7.53	54.389	ANXA11	kidney	97.17	<=1.00e-14	cell division	GFGTDEQAIIDCLGSR
29	P12429	Annexin A3	ANX3	5.62	36.375	ANXA3	kidney	80.25	2.20E-14	anticoagulant, phospholipase A2 inhibitor	GELSGHFEDLLLAIVNCVR
30	P08133	Annexin A6	ANX6	5.41	75.873	ANXA6	kidney	93.8	<=1.00e-14	Regulate the release of Ca2+	EDAQVAAEILEIADTPSGDK
31	Q9UJ72	Annexin A10	ANX14	5.13	37.277	ANXA10	kidney	44.08	1.37E-04		DVMAGLMYPPPLYDAHELWHAMK
32	P56962	Syntaxin-17		6.14	33.403	STX17	renal medulla	86.7	0.002	Autophagy, ER-golgi transport	IDSIADHVNSAAVNVEEGTK
33	P27824	Calnexin		4.46	67.568	CANX	cortex of kidney	98.64	<=1.00e-14	calcium binding protein, chaperone	WKPPMIDNPSYQGIWKPR
34	P35241	Radixin		6.03	68.563	RDX	urethra	94.32	0.002	actin binding	VTTMDAELEFAIQPNTTGK
35	Q86WW8	Cytochrome c oxidase assembly factor 5	C2orf64	8.97	8.375	COA5	kidney epithelium	91.43	0.029	Involved in the process of mitochondrial complex IV assembly	EDLGACLLQSDCVVQEGK

(*Continued*)

36	P53420	Collagen alpha-4(IV) chain		8.9	164.037	COL4A4	renal medulla	87.51	0.002	structural component of glomerular basement membranes	GFGPGYLGGFLLVLHSQTDQ EPTCPLGMPR
37	P14210	Hepatocyte growth factor	HPTA	8.22	83.133	HGF	kidney	71.85	1.20E-11	acts as growth factor	NPDDDAHGPWCYTGNPLIPW DYCPISR
38	P02647	Apolipoprotein A-I		5.56	30.777	APOA1	kidney	62.63	2.96E-07	cholesterol metabolism, transport	EQLGPVTQEFWDNLEK
39	O14983	Sarcoplasmic/ endoplasmic reticulum calcium ATPase 1		5.07	110.252	ATP2A1	kidney	67.64	6.98E-09		MPPWVNIWLLGSICLSMSLH FLILYVDPLPMIFK
40	Q9UII2	ATPase inhibitor	ATPI, ATPIF1	9.34	12.248	ATP5IF1	cortex of kidney	98.9	<=1.00e-14	Endogenous F1F(o)-ATPase inhibitor	GSDQSENVDR
41	O00299	Chloride intracellular channel protein 1	G6, NCC27	5.09	26.922	CLIC1	kidney	98.89	<=1.00e-14	voltage-gated channel,chloride channel	FLDGNELTLADCNLLPK
42	Q9H223	EH domain-containing protein 4	HCA10, HCA11, PAST4	6.32	61.175	EHD4	urethra	91.13	0.002	ATP- and membrane binding protein	LDGYELPSSLPPHLVPPSHR
43	Q16891	MICOS complex subunit MIC60	HMP, MIC60, MINOS2	6.08	83.677	IMMT	renal medulla	96.32	0.002	mitochondrial cristae morphology, host-viral interaction	LSQEQVDNFTLDINTAYAR
44	Q9NX95	Syntabulin	GOLSYN, KIAA1472	5.87	72.388	SYBU	renal medulla	70.75	0.008	part of kinesin motor-adapter complex	LESLLQSMEMAHSGSLR
45	Q13515	Phakinin		5.41	45.879	BFSP2	kidney	46.28	0.001	sensory transduction	ASWASSCQQVGEAVLENAR
46	P36776	Lon protease homolog	PRSS15	6.01	106.489	LONP1	kidney epithelium	85.64	0.003	ATP-binding	EIFDIAFPDEQAEALAVER
47	P05067	Amyloid-beta precursor protein	A4, AD1	4.73	86.943	APP	kidney epithelium	98.63	0.002	heparin-binding, apoptosis, cell adhesion, endocytosis	LALENYITALQAVPPRPR
48	Q86UV5	Ubiquitin carboxyl-terminal hydrolase 48	USP31	5.75	119.032	USP48	renal glomerulus	86.81	0.003	Regulatory role at postsynaptic sites, Ubl conjugation pathway	WAETVRPEEVSQEHIETAYR

Table 9: B7

Sl. No.	Uniprot ID	protein	synonym	pI	molecular weight	gene	Anatomical entity	expression	FDR	Function	sequence
1	Q4ZHG4	Fibronectin type III domain-containing protein 1	FNDC2, KIAA1866, MEL4B3	9.34	20.556	FNDC1	Cortex kidney	46.46	2.13E-04	Activator of G protein signaling	VQAQNPHGYGPISPSVSFVT
2	Q9UF12	Hydroxyproline dehydrogenase	HSPOX1,HYPDH	8.94	58.87	PRODH2	Renal glomerulus	90.94	0.002	Proline metabolism	MWELGIPLDGTVCFGQLLGM
3	O94925	Glutaminase kidney isoform, mitochondrial	GLS1,KIAA0838	7.85	73.461	GLS	kidney	97.1	<=1.00e-14	Acid-base homeostasis	ILQEYQVQYTPQGDSDNGK
4	Q7Z4W1	L-xylulose reductase	SDR20C1	8.33	25.913	DCXR	kidney	98.65	<=1.00e-14	Osmoregulation, Carbohydrate metabolism, Glucose metabolism, Xylose metabolism	ALGSVGPVDLLVNNAAVALL QPFLEVTK
5	P11279	Lysosome-associated membrane glycoprotein 1	CD107a	9	44.882	LAMP1	Renal glomerulus	99.92	0.002	Lysosome biogenesis, autophagy, cholesterol homeostasis, Host-viral interaction	YSVQLMSFVYNLSDTHLFPN ASSK
6	Q86SU0	Immunoglobulin-like domain-containing receptor 1	ILDR1	9.12	62.814		Kidney epithelium	85.65	0.023	Maintains epithelial barrier function	LLIGVCWCQCCPQYCCCYIR
7	Q16665	Hypoxia-inducible factor 1-alpha	BHLHE78, MOP1, PASDB	5.17	92.67	HIF1A	Kidney	96.56	<=1.00e-14		SFDQLSPLESSSASPESASP
8	Q7Z5L7	Isoform 3 of Podocan	SLRR5A	8.47	74.141	PODN					EDFATTYFLEELNLSYNR
9	P35613	Basigin	BSG	5.39	42.2		kidney	97.71	<=1.00e-14	Angiogenesis	SELHIENLNMEADPGQYR
10	P08254	Stromelysin-1	MMP3	5.77	53.977	STMY1	kidney	49.86	1.52E-05	collagen degradation	LEPELHLISSFWPSLPSGVD AAYEVTSK
12	P25713	Metallothionein-3	MT3	4.79	6.926		kidney	75.07	2.70E-12	heavy metal binding	SCCSCCPAECEK
13	Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	ZNF744	8.69	80.926	ANKZF1	kidney	85.24	<=1.00e-14	cellular response to stress	LFCSTCDQTFQNHQEQR
14	Q06830	Peroxiredoxin-1	PAGA, PAGB, TDPX2	8.27	22.11	PRDX1	kidney	99.29	<=1.00e-14	antioxidant	YVVFFFYPLDFTFVCPTEII AFSDR
15	Q13162	Peroxiredoxin-4		5.86	30.539	PRDX4	renal glomerulus	93.48	0.002	antioxidant	YLVFFFYPLDFTFVCPTEII AFGDR
16	Q99719	Septin-5	PNUTL1, SEPT5	6.21	42.776	SEPTIN5	kidney	73.53	2.43E-11	platelet secretion, cell cycle, cell devision	FGIHVYQFPECDSDEDEDFK
17	O43236	Septin-4	C17orf47, PNUTL2, SEP4, SEPT4	5.77	55.098	SEPTIN4	kidney	81.69	<=1.00e-14	cell cycle, cell devision	LYPWGIVEVENPGHCDFVK

Table 10: Algorithm of table from table 1:A1 to table 9: B7

Table No.	Code	Title
1	A1	List of 135 proteins
2	A2	List of 35 selected proteins
B1 to B7		The list of 135 proteins, segregated into different groups based on their functional role
3	B1	Proteins related to immune response identified in urine
4	B2	Endonucleases/DNAase identified in urine
5	B3	Glycoproteins identified in urine
6	B4	Proteases and antiproteases identified in urine
7	B5	Proteins related to regulation of transcription and translation identified in urine
8	B6	Transporters identified in urine (ATPases and intergral membrane proteins)
9	B7	Proteins involved in various other physiological pathways

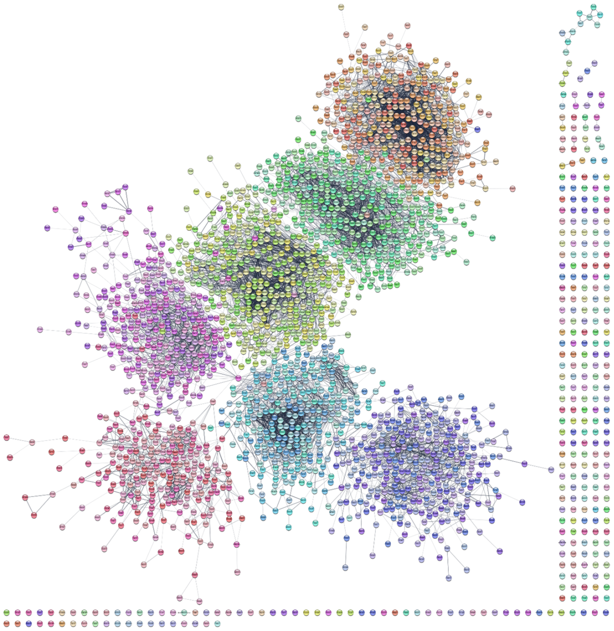

Figure S1: Protein interaction analysis of whole identified proteins in urine of patients with CKD stage V.

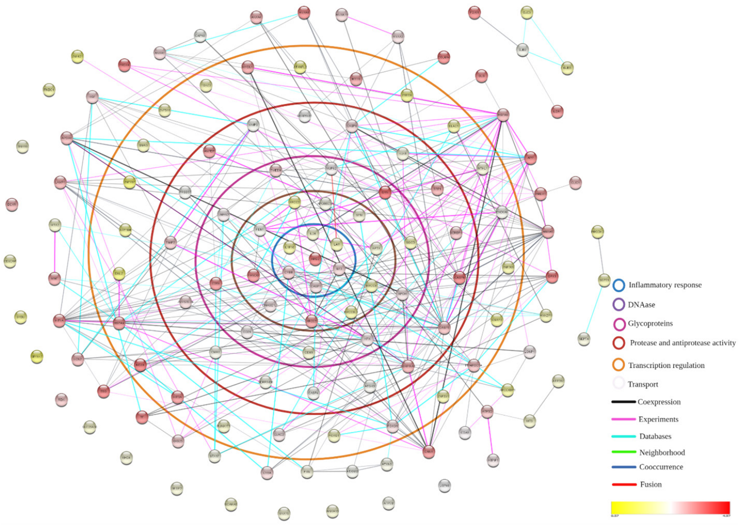

Figure S2: Protein interaction analysis of 135 proteins identified in urine categorized based on their functional role in kidney by colored circular ring.