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An optimized method for protein extraction from OCT-embedded human kidney tissue for protein quantification by LC-MS/MS proteomics

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Table 1S.a: LC Method

Column	UPLC column (ACQUITY UPLC BEH C18 Column, 130Å, 1.7 Åµm, 3 mm X 150 mm)		
Guard column	Security Guard column (C18, 4 mm × 2.0 mm, Phenomenex)		
Run Time:	48 min		
Injection volume	5 µl		
Column oven temperature	25 °C		
Autosampler temperature	6 °C		
Gradient Table:			
Time	Flow rate	%A	%B
0	0.3	97	3
3	0.3	97	3
10	0.3	90	10
40	0.3	90	10
40.9	0.3	97	3
41	0.3	97	3
48	0.3	97	3
A = 0.1% formic acid water; B = 0.1% formic acid acetonitrile			

Table 1S.b: Optimized MRM parameters used for surrogate peptide quantification

Protein	Abbreviation	Accession#	Peptide sequence	Parent ion	Product ion	Collision energy	Cone voltage
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	729.89	318.18	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	729.89	389.21	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	729.89	488.28	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	729.89	887.5	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	733.9	326.19	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	733.9	397.22	35	31
Aldolase B	ALDOB	P05062	ELSEIAQSIVANGK	733.9	496.29	35	31
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	735.89	243.13	35	26
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	735.89	342.2	35	26
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	735.89	917.43	35	26
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	739.9	243.13	35	26
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	739.9	342.2	35	26
Aldolase B	ALDOB	P05062	ELVLTGSPDNQAK	739.9	925.44	35	26
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	216.1	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	272.17	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	444.21	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	472.29	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	600.35	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	631.85	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	697.4	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	493.26	784.43	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	496.6	282.18	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	496.6	482.3	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	496.6	707.41	35	16
Aquaporin 2	AQP2	P41181	QSVELHSPQSLPR	496.6	794.44	35	16
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	743.893	1103.5983	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	743.893	778.4345	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	743.893	536.3079	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	743.893	294.1812	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	747.9	1111.6125	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	747.9	786.4487	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	747.9	544.3221	38	28
Arginosuccinate synthase 1	ASS1	P00966	APNTPDILEIEFK	747.9	302.1954	38	28
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	714.355	790.4054	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	714.355	547.3198	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	714.355	476.2827	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	714.355	931.5045	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	717.3716	800.4136	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVSYDQATSLR	717.3716	557.3281	40	29

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Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVYDQATSLR	717.3716	486.291	40	29
Carbonic anhydrase 2	CA2	P00918	YDPSLKPLSVYDQATSLR	717.3716	936.5087	40	29
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	678.87	572.31	35	25
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	678.87	723.37	35	25
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	678.87	836.45	35	25
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	682.88	561.27	35	25
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	682.88	576.32	36	25
Cathepsin H	CTSH	P09668	VNHAVLAVGYGEK	682.88	943.53	35	25
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	756.04	804.37	35	26
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	756.04	935.42	35	26
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	756.04	991.96	35	26
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	758.71	808.38	35	26
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	758.71	939.43	35	26
CD34	CD34	P28906	LGILDFTEQDVASHQSYSQ K	758.71	995.97	35	26
CD34	CD34	P28906	SWSPPTGER	460.22	274.12	35	16
CD34	CD34	P28906	SWSPPTGER	460.22	559.28	35	16
CD34	CD34	P28906	SWSPPTGER	460.22	646.32	35	16
CD34	CD34	P28906	SWSPPTGER	465.22	274.12	35	16
CD34	CD34	P28906	SWSPPTGER	465.22	569.29	35	16
CD34	CD34	P28906	SWSPPTGER	465.22	656.33	35	16
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	421.24	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	555.21	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	558.33	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	657.39	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	838.36	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	841.48	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	956.51	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	698.34	1119.57	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	702.35	425.25	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	702.35	566.34	35	25
Claudin 5	CLDN5	O00501	EFYDPSVVPVSQK	702.35	849.49	35	25
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	861.46	730.39	35	26
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	861.46	748.39	35	26
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	861.46	1045.56	35	26
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	866.46	378.17	35	26
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	866.46	564.27	35	26
Claudin 5	CLDN5	O00501	VYDSVLALSTEVQAAR	866.46	871.45	35	26
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	559.296	230.1135	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	559.296	702.4145	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	559.296	589.3304	38	20

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Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	559.296	474.3035	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	564.3002	230.1135	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	564.3002	712.4227	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	564.3002	599.3387	38	20
Dicarbonyl/L-xylulose reductase	DCXR	Q7Z4W1	TQADLDSLVR	564.3002	484.3117	38	20
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	689.38	713.87	35	23
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	689.38	791.91	35	23
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	689.38	948.51	35	23
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	692.72	768.4	35	23
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	692.72	796.91	35	23
Dipeptidase 1	DPEP1	P16444	VASLIGVEGGHSIDSSLGVL R	692.72	953.51	35	23
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	544.29	303.18	35	16
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	544.29	418.2	35	16
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	544.29	758.42	35	16
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	549.29	313.19	35	16
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	549.29	428.21	35	16
Golgi membrane protein 1	GOLM1	Q8NBJ4	DTINLLDQR	549.29	768.43	35	16
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	622.34	333.19	35	23
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	622.34	904.42	35	23
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	622.34	1017.5	35	23
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	626.35	341.2	35	23
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	626.35	912.43	35	23
Intercell adhesion mol 2	ICAM2	P13598	ILLDEQAQWK	626.35	1025.51	35	23
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	725.41	456.32	35	26
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	725.41	642.4	35	26
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	725.41	981.55	35	26
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	729.42	469.28	35	26
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	729.42	650.41	35	26
Junction Plakoglobin	JUP	P14923	LLNQPNQWPLVK	729.42	989.56	35	26
Multidrug resistance protein 1	P-gp	P08183	NTTGALTTR	467.6	618.3	30	16
Multidrug resistance protein 1	P-gp	P08183	NTTGALTTR	467.6	719.4	30	16
Multidrug resistance protein 1	P-gp	P08183	NTTGALTTR	472.6	628.3	30	16
Multidrug resistance protein 1	P-gp	P08183	NTTGALTTR	472.6	729.5	30	16
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	290.15	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	419.19	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	490.23	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	564.25	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	619.27	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	845.36	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	942.42	35	26

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Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	706.82	999.44	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	952.424585	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	855.371821	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	758.319057	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	794.367909	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	923.410502	35	26
Podocalyxin-like	PODXL	Q9NZ53	LGDQGPPEEAEDR	711.822186	994.447616	35	26
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	211.14	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	282.18	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	437.23	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	574.29	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	703.34	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	838.94	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	873.44	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	597.32	1416.75	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	600.66	584.3	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	600.66	713.35	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	600.66	843.94	35	15
Podocin	NPHS2	Q9NP85	LPAGLQHS�AVEAEAQR	600.66	883.45	35	15
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	631.29	587.3173	35	21
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	631.29	709.3521	35	21
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	631.29	838.3947	35	21
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	633.96	591.32	35	21
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	633.96	713.36	35	21
SERPINA1	SERPINA1	P01009	DTEEDFHVDQVTTVK	633.96	842.4	35	21
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	471.79	671.41	35	15
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	471.79	742.45	35	15
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	475.8	272.16	35	15
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	475.8	679.42	35	15
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	475.8	750.46	35	15
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SPGVAELSLR	514.79	617.36	35	18
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SPGVAELSLR	514.79	688.4	35	18
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SPGVAELSLR	514.79	844.49	35	18
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SPGVAELSLR	519.79	627.37	35	18
SLAPAVVTGK	SLAPAVVTGK	SLAPAVVTGK	SPGVAELSLR	519.79	698.41	35	18
Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWAR	709.33	616.32	35	24
Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWAR	709.33	947.42	35	24
Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWAR	709.33	1175.5327	35	24
Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWAR	714.33	626.33	35	24

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Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWA <u>R</u>	714.33	741.36	35	24
Sodium/glucose cotransporter 2	SGLT2	P31639	LEDISEDPSWA <u>R</u>	714.33	957.43	35	24
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLVR	587.34	615.38	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLVR	587.34	762.45	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLVR	587.34	849.48	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLVR	587.34	946.54	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLV <u>R</u>	592.34	228.13	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLV <u>R</u>	592.34	284.2	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLV <u>R</u>	592.34	397.28	35	18
Solute carrier family 22 member 2	OCT2	O15244	LNPSFLDLV <u>R</u>	592.34	512.31	35	18
Solute carrier family 22 member 6	OAT1	Q4U2R8	TSLAVLGK	394.75	416.29	35	16
Solute carrier family 22 member 6	OAT1	Q4U2R8	TSLAVLGK	394.75	487.32	35	16
Solute carrier family 22 member 6	OAT1	Q4U2R8	TSLAVLGK	394.75	600.41	35	16
Solute carrier family 22 member 6	OAT1	Q4U2R8	TSLAVLG <u>K</u>	398.76	495.33	35	16
Solute carrier family 22 member 6	OAT1	Q4U2R8	TSLAVLG <u>K</u>	398.76	608.42	35	16
Solute carrier family 22 member 8	OAT3	Q8TCC7	TVLAVFGK	417.76	450.27	35	15
Solute carrier family 22 member 8	OAT3	Q8TCC7	TVLAVFGK	417.76	521.31	35	15
Solute carrier family 22 member 8	OAT3	Q8TCC7	TVLAVFGK	417.76	634.39	35	15
Solute carrier family 22 member 8	OAT3	Q8TCC7	TVLAVFG <u>K</u>	421.77	458.28	35	15
Solute carrier family 22 member 8	OAT3	Q8TCC7	TVLAVFG <u>K</u>	421.77	642.4	35	15
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	302.11	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	729.43	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	828.49	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	302.11	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	729.43	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPAR	565.3	828.49	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	454.27	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	739.44	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	838.5	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	454.27	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	739.44	35	21
Tamm-Horsfall Protein	THP	P07911	DWVSVVTPA <u>R</u>	570.3	838.5	35	21
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	696.02	657.29	35	18
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	696.02	674.41	35	18
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	696.02	773.48	35	18
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	698.69	569.33	35	18
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	698.69	682.42	35	18
Tight Junction protein 1	ZO1	Q07157	DNPHFQSGETSIVISDV <u>LK</u>	698.69	781.49	35	18

K and **R** shown in bold and italic are the labeled [13C615N2]-lysine and [13C615N4]-arginine residues, respectively in the heavy peptides.

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