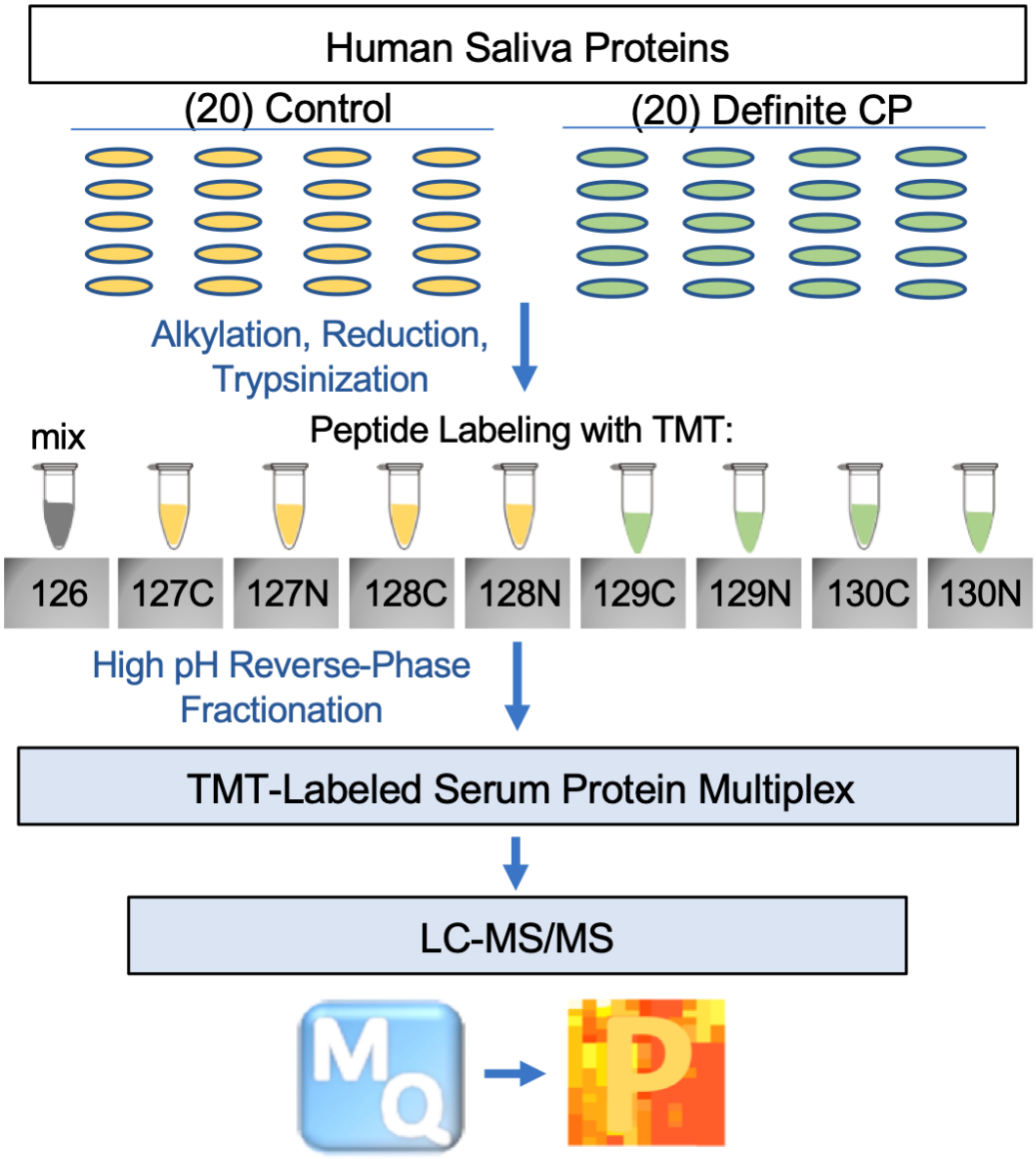
Salivary Biomarker Evaluation of Chronic Pancreatitis Patients Reveals Alterations in Human Proteins, Cytokines, Prostaglandin E_2 Levels, and Bacterial Diversity

SUPPLEMENTAL DIGITAL CONTENT



SUPPLEMENTAL FIGURE 1. Scheme depicting Proteomic Experiment with (40) Human Saliva Specimens (20 control and 20 chronic pancreatitis, CP) to Discover Novel Biomarkers of CP. Peptides were labeled with tandem mass tags (TMT) and subjected to liquid chromatography-tandem mass spectrometry (LC-MS/MS) as described in Materials and Methods.

SUPPLEMENTAL TABLE 1. Human Proteins Detected in Saliva Samples From Chronic Pancreatitis Patients and Healthy Controls

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P61604	10 kDa heat shock protein, mitochondrial	HSPE1	61	8	7	102	10.9	8.92
P31946	14-3-3 protein beta/alpha	YWHAB	45	23	4	246	28.1	4.83
P62258	14-3-3 protein epsilon	YWHAE	25	7	3	255	29.2	4.74
Q04917	14-3-3 protein eta	YWHAH	16	7	2	246	28.2	4.84
P61981	14-3-3 protein gamma	YWHAG	27	15	3	247	28.3	4.89
P31947	14-3-3 protein sigma	SFN	63	72	16	248	27.8	4.74
P63104	14-3-3 protein zeta/delta	YWHAZ	64	36	12	245	27.7	4.79
Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1	18	3	3	181	20.6	8.87
P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	5	2	2	494	53.8	5.87
P25398	40S ribosomal protein S12	RPS12	17	3	2	132	14.5	7.21
P63220	40S ribosomal protein S21	RPS21	30	3	2	83	9.1	8.5
P62857	40S ribosomal protein S28	RPS28	52	4	3	69	7.8	10.7
Q9BRK5	45 kDa calcium-binding protein	SDF4	14	5	5	362	41.8	4.86
P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD	21	15	9	483	53.1	7.23
P10809	60 kDa heat shock protein, mitochondrial	HSPD1	18	11	7	573	61	5.87
P05387	60S acidic ribosomal protein P2	RPLP2	43	4	2	115	11.7	4.54
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	9	2	2	249	28.6	4.09
P61160	Actin-related protein 2	ACTR2	8	2	2	394	44.7	6.74
P59998	Actin-related protein 2/3 complex subunit 4	ARPC4	11	3	2	168	19.7	8.43
P61158	Actin-related protein 3	ACTR3	12	3	3	418	47.3	5.88
P60709	Actin, cytoplasmic 1	ACTB	60	91	9	375	41.7	5.48
P63261	Actin, cytoplasmic 2	ACTG1	58	82	8	375	41.8	5.48
P07108	Acyl-CoA-binding protein	DBI	63	12	4	87	10	6.57
P54819	Adenylate kinase 2, mitochondrial	AK2	13	5	3	239	26.5	7.81
Q01518	Adenylyl cyclase-associated protein 1	CAP1	25	13	11	475	51.9	8.06
Q15847	Adipogenesis regulatory factor	ADIRF	80	7	4	76	7.9	5.31
P43652	Afamin	AFM	11	7	6	599	69	5.9
P40394	Alcohol dehydrogenase class 4 mu/sigma chain	ADH7	6	2	2	386	41.5	7.85
P30838	Aldehyde dehydrogenase, dimeric NADP-preferring	ALDH3A1	4	2	2	453	50.4	6.54
O60218	Aldo-keto reductase family 1 member B10	AKR1B10	8	2	2	316	36	7.84
P02763	Alpha-1-acid glycoprotein 1	ORM1	24	8	4	201	23.5	5.02
P19652	Alpha-1-acid glycoprotein 2	ORM2	6	5	2	201	23.6	5.11
P01011	Alpha-1-antichymotrypsin	SERPINA3	16	8	5	423	47.6	5.52
P01009	Alpha-1-antitrypsin	SERPINA1	48	28	15	418	46.7	5.59
P04217	Alpha-1B-glycoprotein	A1BG	10	4	4	495	54.2	5.86
P02765	Alpha-2-HS-glycoprotein	AHSG	22	10	7	367	39.3	5.72
A8K2U0	Alpha-2-macroglobulin-like protein 1	A2ML1	12	20	16	1454	161	5.73
P12814	Alpha-actinin-1	ACTN1	11	14	4	892	103	5.41
O43707	Alpha-actinin-4	ACTN4	24	20	14	911	104.8	5.44
P04745	Alpha-amylase 1	AMY1A	46	91	23	511	57.7	6.93
P19961	Alpha-amylase 2B	AMY2B	24	63	13	511	57.7	7.09
O43768	Alpha-endosulfine	ENSA	19	2	2	121	13.4	7.24
P06733	Alpha-enolase	ENO1	62	51	23	434	47.1	7.39
P04083	Annexin A1	ANXA1	49	34	18	346	38.7	7.02
P07355	Annexin A2	ANXA2	15	5	4	339	38.6	7.75
P12429	Annexin A3	ANXA3	17	4	4	323	36.4	5.92
P08758	Annexin A5	ANXA5	12	3	3	320	35.9	5.05
P03973	Antileukoproteinase	SLPI	45	14	7	132	14.3	8.75
P01008	Antithrombin-III	SERPINC1	7	3	3	464	52.6	6.71
P02647	Apolipoprotein A-I	APOA1	60	39	20	267	30.8	5.76

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P02652	Apolipoprotein A-II	APOA2	22	5	4	100	11.2	6.62
P06727	Apolipoprotein A-IV	APOA4	26	9	9	396	45.4	5.38
Q0VD83	Apolipoprotein B receptor	APOBR	8	7	6	1088	114.8	4.4
P05090	Apolipoprotein D	APOD	17	3	3	189	21.3	5.15
P02649	Apolipoprotein E	APOE	8	2	2	317	36.1	5.73
Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD	PYCARD	16	4	4	195	21.6	6.34
P25705	ATP synthase subunit alpha, mitochondrial	ATP5F1A	8	5	3	553	59.7	9.13
P06576	ATP synthase subunit beta, mitochondrial	ATP5F1B	17	6	6	529	56.5	5.4
O95817	BAG family molecular chaperone regulator 3	BAG3	4	3	2	575	61.6	6.95
P02812	Basic salivary proline-rich protein 2	PRB2	49	13	2	416	40.8	11.63
P02749	Beta-2-glycoprotein 1	APOH	26	8	7	345	38.3	7.97
P61769	Beta-2-microglobulin	B2M	34	25	6	119	13.7	6.52
P13929	Beta-enolase	ENO3	11	6	3	434	47	7.71
P08118	Beta-microseminoprotein	MSMB	17	3	2	114	12.9	5.5
P52848	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	NDST1	2	2	2	882	100.8	7.97
Q9NP55	BPI fold-containing family A member 1	BPIFA1	23	4	4	256	26.7	5.76
Q96DR5	BPI fold-containing family A member 2	BPIFA2	39	21	12	249	27	5.59
Q8TDL5	BPI fold-containing family B member 1	BPIFB1	25	13	9	484	52.4	7.23
Q8N4F0	BPI fold-containing family B member 2	BPIFB2	25	14	9	458	49.1	8.72
P80723	Brain acid soluble protein 1	BASP1	57	8	7	227	22.7	4.63
P12830	Cadherin-1	CDH1	3	2	2	882	97.4	4.73
Q14CN2	Calcium-activated chloride channel regulator 4	CLCA4	2	2	2	919	101.2	5.47
P0DP25	Calmodulin-3	CALM3	27	5	2	149	16.8	4.22
P27482	Calmodulin-like protein 3	CALML3	68	23	8	149	16.9	4.42
Q9NZT1	Calmodulin-like protein 5	CALML5	65	18	8	146	15.9	4.44
P20810	Calpastatin	CAST	34	34	22	708	76.5	5.07
P27797	Calreticulin	CALR	9	4	4	417	48.1	4.44
O43852	Calumenin	CALU	13	3	3	315	37.1	4.64
Q6JBY9	CapZ-interacting protein	RCSD1	6	2	2	416	44.5	5.4
P23280	Carbonic anhydrase 6	CA6	25	15	7	308	35.3	7.02
P16870	Carboxypeptidase E	CPE	9	3	3	476	53.1	5.14
P06731	Carcinoembryonic antigen-related cell adhesion molecule 5	CEACAM5	7	6	3	702	76.7	5.92
P31997	Carcinoembryonic antigen-related cell adhesion molecule 8	CEACAM8	11	3	2	349	38.1	7.39
P49913	Cathelicidin antimicrobial peptide	CAMP	26	9	5	170	19.3	9.41
P08311	Cathepsin G	CTSG	11	4	3	255	28.8	11.19
P16070	CD44 antigen	CD44	3	2	2	742	81.5	5.33
O43866	CD5 antigen-like	CD5L	7	2	2	347	38.1	5.47
P13987	CD59 glycoprotein	CD59	26	4	4	128	14.2	6.48
B4E1Z4	cDNA FLJ55673, highly similar to Complement factor B (EC 3.4.21.47)	cDNA	1	4	2	1266	140.9	7.18
Q99674	Cell growth regulator with EF hand domain protein 1	CGREF1	22	6	5	301	31.9	4.42
P29373	Cellular retinoic acid-binding protein 2	CRABP2	56	7	5	138	15.7	5.4
P00450	Ceruloplasmin	CP	3	2	2	1065	122.1	5.72

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
O43633	Charged multivesicular body protein 2a	CHMP2A	9	2	2	222	25.1	5.97
Q9H444	Charged multivesicular body protein 4b	CHMP4B	17	3	3	224	24.9	4.82
O00299	Chloride intracellular channel protein 1	CLIC1	36	7	5	241	26.9	5.17
Q13185	Chromobox protein homolog 3	CBX3	15	3	3	183	20.8	5.33
P09497	Clathrin light chain B	CLTB	14	4	3	229	25.2	4.64
P10909	Clusterin	CLU	28	27	13	449	52.5	6.27
P23528	Cofilin-1	CFL1	49	13	8	166	18.5	8.09
P02452	Collagen alpha-1(I) chain	COL1A1	3	9	5	1464	138.9	5.8
P12109	Collagen alpha-1(VI) chain	COL6A1	4	2	2	1028	108.5	5.43
P08123	Collagen alpha-2(I) chain	COL1A2	3	10	5	1366	129.2	8.95
P01024	Complement C3	C3	6	7	7	1663	187	6.4
P0C0L4	Complement C4-A	C4A	1	2	2	1744	192.7	7.08
P08603	Complement factor H	CFH	5	6	5	1231	139	6.61
P05156	Complement factor I	CFI	13	5	5	583	65.7	7.5
O75367	Core histone macro-H2A.1	H2AFY	5	2	2	372	39.6	9.79
Q15517	Corneodesmosin	CDSN	8	3	3	529	51.5	8.35
P35321	Cornifin-A	SPRR1A	79	16	2	89	9.9	8.48
P22528	Cornifin-B	SPRR1B	71	22	2	89	9.9	8.48
Q9UBG3	Cornulin	CRNN	79	209	33	495	53.5	6.1
P31146	Coronin-1A	CORO1A	11	6	5	461	51	6.68
P12532	Creatine kinase U-type, mitochondrial	CKMT1A	7	2	2	417	47	8.34
P01040	Cystatin-A	CSTA	87	15	7	98	11	5.5
P04080	Cystatin-B	CSTB	69	15	6	98	11.1	7.56
P01034	Cystatin-C	CST3	38	29	6	146	15.8	8.75
P28325	Cystatin-D	CST5	31	24	3	142	16.1	7.17
Q15828	Cystatin-M	CST6	14	2	2	149	16.5	8.09
P01036	Cystatin-S	CST4	79	153	6	141	16.2	5.02
P09228	Cystatin-SA	CST2	60	170	5	141	16.4	4.93
P01037	Cystatin-SN	CST1	70	170	7	141	16.4	7.21
P54108	Cysteine-rich secretory protein 3	CRISP3	36	21	9	245	27.6	7.8
P32320	Cytidine deaminase	CDA	25	2	2	146	16.2	6.92
P04839	Cytochrome b-245 heavy chain	CYBB	4	3	2	570	65.3	8.63
P99999	Cytochrome c	CYCS	22	3	3	105	11.7	9.57
Q9UGM3	Deleted in malignant brain tumors 1 protein	DMBT1	30	61	20	2413	260.6	5.44
Q8NFT8	Delta and Notch-like epidermal growth factor-related receptor	DNER	5	2	2	737	78.4	5.17
P81605	Dermcidin	DCD	20	3	2	110	11.3	6.54
Q6E0U4	Dermokine	DMKN	10	8	5	476	47.1	7.28
P17661	Desmin	DES	7	10	5	470	53.5	5.27
Q02487	Desmocollin-2	DSC2	24	22	13	901	99.9	5.34
Q02413	Desmoglein-1	DSG1	9	9	6	1049	113.7	5.03
P32926	Desmoglein-3	DSG3	25	38	19	999	107.5	5
P15924	Desmoplakin	DSP	7	21	18	2871	331.6	6.81
Q9UJU6	Drebrin-like protein	DBNL	13	6	4	430	48.2	5.05
Q13561	Dynactin subunit 2	DCTN2	10	4	4	401	44.2	5.21
Q14118	Dystroglycan	DAG1	5	2	2	895	97.4	8.56
Q96C19	EF-hand domain-containing protein D2	EFHD2	10	2	2	240	26.7	5.2
P19957	Elafin	PI3	43	8	7	117	12.3	8.82
P68104	Elongation factor 1-alpha 1	EEF1A1	7	3	2	462	50.1	9.01
P29692	Elongation factor 1-delta	EEF1D	11	2	2	281	31.1	5.01
P13639	Elongation factor 2	EEF2	3	2	2	858	95.3	6.83
O94919	Endonuclease domain-containing 1 protein	ENDOD1	5	2	2	500	55	5.71

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P11021	Endoplasmic reticulum chaperone BiP	HSPA5	33	32	17	654	72.3	5.16
P30040	Endoplasmic reticulum resident protein 29	ERP29	23	7	5	261	29	7.31
Q9BS26	Endoplasmic reticulum resident protein 44	ERP44	9	3	3	406	46.9	5.26
Q96HE7	ERO1-like protein alpha	ERO1A	15	6	5	468	54.4	5.68
P23588	Eukaryotic translation initiation factor 4B	EIF4B	6	2	2	611	69.1	5.73
P63241	Eukaryotic translation initiation factor 5A-1	EIF5A	18	3	3	154	16.8	5.24
Q6IS14	Eukaryotic translation initiation factor 5A-1-like	EIF5AL1	13	2	2	154	16.8	5
Q9GZV4	Eukaryotic translation initiation factor 5A-2	EIF5A2	13	2	2	153	16.8	5.58
Q9GZZ8	Extracellular glycoprotein lacritin	LACRT	24	3	3	138	14.2	5.5
Q16610	Extracellular matrix protein 1	ECM1	29	23	13	540	60.6	6.71
P15311	Ezrin	EZR	29	34	13	586	69.4	6.27
P52907	F-actin-capping protein subunit alpha-1	CAPZA1	12	4	3	286	32.9	5.69
P47756	F-actin-capping protein subunit beta	CAPZB	10	2	2	277	31.3	5.59
Q01469	Fatty acid-binding protein, epidermal	FABP5	78	42	11	135	15.2	7.01
P02671	Fibrinogen alpha chain	FGA	21	28	16	866	94.9	6.01
P02675	Fibrinogen beta chain	FGB	9	6	5	491	55.9	8.27
P02679	Fibrinogen gamma chain	FGG	10	3	3	453	51.5	5.62
P20930	Filaggrin	FLG	43	232	90	4061	434.9	9.25
Q5D862	Filaggrin-2	FLG2	4	7	6	2391	247.9	8.31
P21333	Filamin-A	FLNA	5	9	8	2647	280.6	6.06
P15328	Folate receptor alpha	FOLR1	7	3	2	257	29.8	7.97
Q12841	Follistatin-related protein 1	FSTL1	15	5	4	308	35	5.52
P04075	Fructose-bisphosphate aldolase A	ALDOA	47	30	13	364	39.4	8.09
P09972	Fructose-bisphosphate aldolase C	ALDOC	12	7	3	364	39.4	6.87
P17931	Galectin-3	LGALS3	22	5	5	250	26.1	8.56
Q08380	Galectin-3-binding protein	LGALS3BP	14	10	5	585	65.3	5.27
P47929	Galectin-7	LGALS7	49	6	5	136	15.1	7.62
P09104	Gamma-enolase	ENO2	8	5	2	434	47.2	5.03
P17900	Ganglioside GM2 activator	GM2A	10	2	2	193	20.8	5.31
P06396	Gelsolin	GSN	20	13	11	782	85.6	6.28
O60234	Glia maturation factor gamma	GMFG	34	5	4	142	16.8	5.26
P14314	Glucosidase 2 subunit beta	PRKCSH	20	12	9	528	59.4	4.41
P35754	Glutaredoxin-1	GLRX	42	4	3	106	11.8	8.09
P78417	Glutathione S-transferase omega-1	GSTO1	14	3	3	241	27.5	6.6
P09211	Glutathione S-transferase P	GSTP1	51	33	8	210	23.3	5.64
P04406	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	57	27	19	335	36	8.46
P06737	Glycogen phosphorylase, liver form	PYGL	2	2	2	847	97.1	7.17
Q9HC38	Glyoxalase domain-containing protein 4	GLOD4	7	2	2	313	34.8	5.6
Q92896	Golgi apparatus protein 1	GLG1	7	8	7	1179	134.5	6.9
Q8NBJ4	Golgi membrane protein 1	GOLM1	38	30	17	401	45.3	4.97
P28799	Granulins	GRN	17	12	9	593	63.5	6.83
P62993	Growth factor receptor-bound protein 2	GRB2	15	3	3	217	25.2	6.32
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	7	2	2	355	40.4	5.54
Q6ZN66	Guanylate-binding protein 6	GBP6	4	2	2	633	72.4	6.37
P00738	Haptoglobin	HP	55	67	24	406	45.2	6.58
P34931	Heat shock 70 kDa protein 1-like	HSPA1L	11	9	3	641	70.3	6.02
P0DMV9	Heat shock 70 kDa protein 1B	HSPA1B	22	19	11	641	70	5.66
P34932	Heat shock 70 kDa protein 4	HSPA4	4	4	3	840	94.3	5.19

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P17066	Heat shock 70 kDa protein 6	HSPA6	12	10	3	643	71	6.14
P11142	Heat shock cognate 71 kDa protein	HSPA8	12	7	4	646	70.9	5.52
P04792	Heat shock protein beta-1	HSPB1	56	27	14	205	22.8	6.4
P07900	Heat shock protein HSP 90-alpha	HSP90AA1	3	2	2	732	84.6	5.02
P08238	Heat shock protein HSP 90-beta	HSP90AB1	7	4	4	724	83.2	5.03
P14317	Hematopoietic lineage cell-specific protein	HCLS1	11	7	5	486	54	4.81
Q9Y5Z4	Heme-binding protein 2	HEBP2	25	5	5	205	22.9	4.63
P69905	Hemoglobin subunit alpha	HBA1	49	8	4	142	15.2	8.68
P68871	Hemoglobin subunit beta	HBB	79	24	5	147	16	7.28
P02042	Hemoglobin subunit delta	HBD	51	16	2	147	16	8.05
P02790	Hemopexin	HPX	17	6	5	462	51.6	7.02
P51858	Hepatoma-derived growth factor	HDGF	26	7	4	240	26.8	4.73
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	5	2	2	372	38.7	9.13
Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	10	4	3	355	38.4	7.81
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	16	6	6	463	50.9	5.54
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	15	7	5	353	37.4	8.95
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	10	3	3	306	33.7	5.08
P52790	Hexokinase-3	HK3	3	2	2	923	99	5.4
P26583	High mobility group protein B2	HMGB2	22	8	7	209	24	7.81
P04196	Histidine-rich glycoprotein	HRG	10	6	4	525	59.5	7.5
Q02539	Histone H1.1	HIST1H1A	11	4	2	215	21.8	10.99
P16403	Histone H1.2	HIST1H1C	36	14	2	213	21.4	10.93
P16402	Histone H1.3	HIST1H1D	21	8	5	221	22.3	11.02
P10412	Histone H1.4	HIST1H1E	26	12	6	219	21.9	11.03
P16401	Histone H1.5	HIST1H1B	37	13	8	226	22.6	10.92
P22492	Histone H1t	HIST1H1T	12	4	2	207	22	11.71
A0A0U1RRH7	Histone H2A	H2AC1	27	7	5	170	18.5	11.52
P62807	Histone H2B type 1-C/E/F/G/I	HIST1H2BC	48	19	2	126	13.9	10.32
P58876	Histone H2B type 1-D	HIST1H2BD	48	19	2	126	13.9	10.32
Q93079	Histone H2B type 1-H	HIST1H2BH	48	19	2	126	13.9	10.32
P06899	Histone H2B type 1-J	HIST1H2BJ	52	14	2	126	13.9	10.32
O60814	Histone H2B type 1-K	HIST1H2BK	49	17	7	126	13.9	10.32
Q99880	Histone H2B type 1-L	HIST1H2BL	63	27	3	126	13.9	10.32
Q99879	Histone H2B type 1-M	HIST1H2BM	48	19	2	126	14	10.32
Q99877	Histone H2B type 1-N	HIST1H2BN	48	19	2	126	13.9	10.32
Q5QNW6	Histone H2B type 2-F	HIST2H2BF	48	19	2	126	13.9	10.32
Q8N257	Histone H2B type 3-B	HIST3H2BB	57	26	2	126	13.9	10.32
P57053	Histone H2B type F-S	H2BFS	48	19	2	126	13.9	10.37
P68431	Histone H3.1	HIST1H3A	20	4	4	136	15.4	11.12
Q16695	Histone H3.1t	HIST3H3	13	4	2	136	15.5	11.12
Q71DI3	Histone H3.2	HIST2H3A	13	4	2	136	15.4	11.27
P84243	Histone H3.3	H3F3A	13	4	2	136	15.3	11.27
P62805	Histone H4	HIST1H4A	52	14	6	103	11.4	11.36
Q9BPY8	Homeodomain-only protein	HOPX	49	4	3	73	8.3	4.81
Q86YZ3	Hornerin	HRNR	18	24	13	2850	282.2	10.04
P50502	Hsc70-interacting protein	ST13	9	3	3	369	41.3	5.27
S4R3N1	HSPE1-MOB4 readthrough	HSPE1-MOB4	11	3	3	261	29.7	6.16
Q9Y4L1	Hypoxia up-regulated protein 1	HYOU1	3	2	2	999	111.3	5.22
Q9Y6R7	IgGFc-binding protein	FCGBP	5	15	12	5405	571.6	5.34
Q9GZP8	Immortalization up-regulated protein	IMUP	17	3	2	106	10.9	9.73
P01876	Immunoglobulin heavy constant alpha 1	IGHA1	49	52	9	353	37.6	6.51

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P01877	Immunoglobulin heavy constant alpha 2	IGHA2	31	36	3	340	36.6	6.27
P01857	Immunoglobulin heavy constant gamma 1	IGHG1	31	8	5	330	36.1	8.19
P01859	Immunoglobulin heavy constant gamma 2	IGHG2	23	10	4	326	35.9	7.59
P01860	Immunoglobulin heavy constant gamma 3	IGHG3	21	6	2	377	41.3	7.9
P01871	Immunoglobulin heavy constant mu	IGHM	10	6	4	453	49.4	6.77
P01764	Immunoglobulin heavy variable 3-23	IGHV3-23	19	3	2	117	12.6	8.28
P0DP03	Immunoglobulin heavy variable 3-30-5	IGHV3-30-5	19	3	2	117	12.9	8.92
A0A0B4J1X5	Immunoglobulin heavy variable 3-74	IGHV3-74	15	2	2	117	12.8	8.66
A0A0B4J2B5	Immunoglobulin heavy variable 3/OR16-9 (non-functional) (Fragment)	IGHV3OR16-9	29	13	2	98	10.7	8.46
A0A0J9YVY3	Immunoglobulin heavy variable 7-4-1	IGHV7-4-1	15	2	2	117	12.8	8.63
P01591	Immunoglobulin J chain	JCHAIN	79	57	14	159	18.1	5.24
P01834	Immunoglobulin kappa constant	IGKC	86	86	9	107	11.8	6.52
A0A075B6P5	Immunoglobulin kappa variable 2-28	IGKV2-28	17	3	2	120	12.9	5.94
A0A087WW87	Immunoglobulin kappa variable 2-40	IGKV2-40	17	4	2	121	13.3	4.61
A0A075B6R9	Immunoglobulin kappa variable 2D-24 (non-functional) (Fragment)	IGKV2D-24	17	4	3	120	13.1	8.87
A0A075B6H7	Immunoglobulin kappa variable 3-7 (non-functional) (Fragment)	IGKV3-7	23	3	2	116	12.8	5.25
P0CG04	Immunoglobulin lambda constant 1	IGLC1	68	39	2	106	11.3	7.87
P0DOY2	Immunoglobulin lambda constant 2	IGLC2	77	42	4	106	11.3	7.24
P0DOY3	Immunoglobulin lambda constant 3	IGLC3	77	40	4	106	11.3	7.24
A0M8Q6	Immunoglobulin lambda constant 7	IGLC7	62	20	3	106	11.2	8.29
P01700	Immunoglobulin lambda variable 1-47	IGLV1-47	25	2	2	117	12.3	5.91
A0A075B6K4	Immunoglobulin lambda variable 3-10	IGLV3-10	21	2	2	115	12.4	4.83
P01714	Immunoglobulin lambda variable 3-19	IGLV3-19	17	4	2	112	12	4.96
P80748	Immunoglobulin lambda variable 3-21	IGLV3-21	23	4	2	117	12.4	5.29
P01717	Immunoglobulin lambda variable 3-25	IGLV3-25	19	4	2	112	12	4.5
A0A075B6K5	Immunoglobulin lambda variable 3-9	IGLV3-9	23	7	2	115	12.3	7.39
A0A075B6I0	Immunoglobulin lambda variable 8-61	IGLV8-61	13	2	2	122	12.8	4.55
B9A064	Immunoglobulin lambda-like polypeptide 5	IGLL5	42	32	4	214	23	8.84
P05107	Integrin beta-2	ITGB2	3	2	2	769	84.7	6.95
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	3	2	2	930	103.3	6.98
P18510	Interleukin-1 receptor antagonist protein	IL1RN	38	26	7	177	20	6.19
Q14116	Interleukin-18	IL18	9	3	2	193	22.3	4.67
Q9UHA7	Interleukin-36 alpha	IL36A	49	6	5	158	17.7	6.3
Q9NZH8	Interleukin-36 gamma	IL36G	21	4	3	169	18.7	5.14
P07476	Involucrin	IVL	55	83	28	585	68.4	4.61
P06870	Kallikrein-1	KLK1	23	28	6	262	28.9	4.83
Q9UBX7	Kallikrein-11	KLK11	7	2	2	282	31	8.94
Q9UKR3	Kallikrein-13	KLK13	7	2	2	277	30.6	8.46
Q92876	Kallikrein-6	KLK6	27	7	4	244	26.8	7.44
P13645	Keratin, type I cytoskeletal 10	KRT10	17	12	6	584	58.8	5.21
P13646	Keratin, type I cytoskeletal 13	KRT13	52	50	19	458	49.6	4.96

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P02533	Keratin, type I cytoskeletal 14	KRT14	26	29	6	472	51.5	5.16
P08779	Keratin, type I cytoskeletal 16	KRT16	27	22	5	473	51.2	5.05
Q04695	Keratin, type I cytoskeletal 17	KRT17	16	20	4	432	48.1	5.02
P08727	Keratin, type I cytoskeletal 19	KRT19	15	13	2	400	44.1	5.14
P35527	Keratin, type I cytoskeletal 9	KRT9	40	58	19	623	62	5.24
P04264	Keratin, type II cytoskeletal 1	KRT1	37	54	23	644	66	8.12
P35908	Keratin, type II cytoskeletal 2 epidermal	KRT2	12	12	2	639	65.4	8
P19013	Keratin, type II cytoskeletal 4	KRT4	43	47	22	534	57.3	6.61
P13647	Keratin, type II cytoskeletal 5	KRT5	16	17	3	590	62.3	7.74
P02538	Keratin, type II cytoskeletal 6A	KRT6A	36	28	14	564	60	8
P48668	Keratin, type II cytoskeletal 6C	KRT6C	29	21	8	564	60	8
Q8N1N4	Keratin, type II cytoskeletal 78	KRT78	5	4	2	520	56.8	6.02
P01042	Kininogen-1	KNG1	12	9	6	644	71.9	6.81
O43278	Kunitz-type protease inhibitor 1	SPINT1	5	2	2	529	58.4	6.29
P00338	L-lactate dehydrogenase A chain	LDHA	17	8	6	332	36.7	8.27
P22079	Lactoperoxidase	LPO	12	13	7	712	80.2	8.62
P02788	Lactotransferrin	LTF	46	44	30	710	78.1	8.12
O00515	Ladinin-1	LAD1	9	5	5	517	57.1	9.67
P20700	Lamin-B1	LMNB1	19	14	9	586	66.4	5.16
P02750	Leucine-rich alpha-2-glycoprotein	LRG1	22	13	7	347	38.2	6.95
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	5	4	2	808	89.2	4.65
P30740	Leukocyte elastase inhibitor	SERPINB1	22	13	9	379	42.7	6.28
P09960	Leukotriene A-4 hydrolase	LTA4H	8	3	3	611	69.2	6.18
Q14847	LIM and SH3 domain protein 1	LASP1	26	7	6	261	29.7	7.05
P31025	Lipocalin-1	LCN1	72	190	17	176	19.2	5.58
Q86X29	Lipolysis-stimulated lipoprotein receptor	LSR	3	2	2	649	71.4	7.97
P08637	Low affinity immunoglobulin gamma Fc region receptor III-A	FCGR3A	7	2	2	254	29.1	8.07
O95274	Ly6/PLAUR domain-containing protein 3	LYPD3	23	10	6	346	35.9	7.75
P33241	Lymphocyte-specific protein 1	LSP1	28	12	7	339	37.2	4.74
P61626	Lysozyme C	LYZ	63	29	8	148	16.5	9.16
P14174	Macrophage migration inhibitory factor	MIF	14	2	2	115	12.5	7.88
P40121	Macrophage-capping protein	CAPG	17	5	4	348	38.5	6.19
P40925	Malate dehydrogenase, cytoplasmic	MDH1	10	2	2	334	36.4	7.36
P40926	Malate dehydrogenase, mitochondrial	MDH2	17	4	4	338	35.5	8.68
O75556	Mammaglobin-B	SCGB2A1	40	3	3	95	10.9	5.78
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	MAN1A1	4	3	2	653	72.9	6.47
P08493	Matrix Gla protein	MGP	39	5	4	103	12.3	9.67
P14780	Matrix metalloproteinase-9	MMP9	15	13	9	707	78.4	6.06
P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF	36	8	6	182	20.7	8.69
Q13421	Mesothelin	MSLN	10	4	4	630	68.9	6.38
P01033	Metalloproteinase inhibitor 1	TIMP1	15	2	2	207	23.2	8.1
P26038	Moesin	MSN	20	16	11	577	67.8	6.4
P08571	Monocyte differentiation antigen CD14	CD14	15	6	4	375	40.1	6.23
P98088	Mucin-5AC	MUC5AC	1	4	4	5654	585.2	7.02
Q9HC84	Mucin-5B	MUC5B	17	270	75	5762	596	6.64
Q8TAX7	Mucin-7	MUC7	9	21	4	377	39.1	8.78
P41218	Myeloid cell nuclear differentiation antigen	MNDA	19	12	7	407	45.8	9.76
P05164	Myeloperoxidase	MPO	18	22	15	745	83.8	8.97
P14649	Myosin light chain 6B	MYL6B	12	3	2	208	22.8	5.73

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P60660	Myosin light polypeptide 6	MYL6	52	14	7	151	16.9	4.65
P19105	Myosin regulatory light chain 12A	MYL12A	13	2	2	171	19.8	4.81
O14950	Myosin regulatory light chain 12B	MYL12B	13	2	2	172	19.8	4.84
P11055	Myosin-3	MYH3	1	2	2	1940	223.8	5.81
P35579	Myosin-9	MYH9	24	66	40	1960	226.4	5.6
P58546	Myotrophin	MTPN	31	4	2	118	12.9	5.52
O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	15	2	2	285	29.6	6.01
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	42	12	10	358	38.8	5.77
E9PAV3	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	1	3	2	2078	205.3	9.58
Q15843	NEDD8	NEDD8	23	6	2	81	9.1	8.43
E9PL57	NEDD8-MDP1 readthrough (Fragment)	NEDD8-MDP1	11	5	2	170	19.5	7.43
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	21	46	31	5890	628.7	6.15
P22894	Neutrophil collagenase	MMP8	4	2	2	467	53.4	6.87
P59665	Neutrophil defensin 1	DEFA1	20	10	4	94	10.2	6.99
P59666	Neutrophil defensin 3	DEFA3	20	7	3	94	10.2	5.99
P80188	Neutrophil gelatinase-associated lipocalin	LCN2	47	13	7	198	22.6	8.91
P05204	Non-histone chromosomal protein HMG-17	HMGN2	27	3	3	90	9.4	9.99
P10153	Non-secretory ribonuclease	RNASE2	20	7	3	161	18.3	8.73
P22307	Non-specific lipid-transfer protein	SCP2	3	2	2	547	59	6.89
P61916	NPC intracellular cholesterol transporter 2	NPC2	39	4	4	151	16.6	7.65
Q9UNZ2	NSFL1 cofactor p47	NSFL1C	11	3	3	370	40.5	5.1
P67809	Nuclease-sensitive element-binding protein 1	YBX1	19	4	2	324	35.9	9.88
Q02818	Nucleobindin-1	NUCB1	36	24	18	461	53.8	5.25
P80303	Nucleobindin-2	NUCB2	51	51	23	420	50.2	5.12
P22392	Nucleoside diphosphate kinase B	NME2	38	6	6	152	17.3	8.41
P04746	Pancreatic alpha-amylase	AMY2A	24	63	13	511	57.7	7.05
P20962	Parathymosin	PTMS	23	3	2	102	11.5	4.16
P62937	Peptidyl-prolyl cis-trans isomerase A	PPIA	55	24	13	165	18	7.81
Q9Y536	Peptidyl-prolyl cis-trans isomerase A-like 4A	PPIAL4A	17	4	3	164	18.2	9.22
A0A0B4J2A2	Peptidyl-prolyl cis-trans isomerase A-like 4C	PPIAL4C	9	3	2	164	18.1	9.22
F5H284	Peptidyl-prolyl cis-trans isomerase A-like 4D	PPIAL4D	9	3	2	164	18.2	9.35
P0DN26	Peptidyl-prolyl cis-trans isomerase A-like 4F	PPIAL4F	9	3	2	164	18.2	9.35
P0DN37	Peptidyl-prolyl cis-trans isomerase A-like 4G	PPIAL4G	9	3	2	164	18.2	9.06
P23284	Peptidyl-prolyl cis-trans isomerase B	PPIB	23	6	5	216	23.7	9.41
A0A075B767	Peptidyl-prolyl cis-trans isomerase	LOC105371242	9	3	2	164	18.2	9.06
O60664	Perilipin-3	PLIN3	34	17	11	434	47	5.44
P41219	Peripherin	PRPH	6	5	4	470	53.6	5.47
O60437	Periplakin	PPL	13	24	21	1756	204.6	5.6
Q06830	Peroxiredoxin-1	PRDX1	53	21	10	199	22.1	8.13
P32119	Peroxiredoxin-2	PRDX2	38	11	7	198	21.9	5.97
Q13162	Peroxiredoxin-4	PRDX4	7	2	2	271	30.5	6.29
P30044	Peroxiredoxin-5, mitochondrial	PRDX5	55	14	8	214	22.1	8.7
P30041	Peroxiredoxin-6	PRDX6	26	5	5	224	25	6.38

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
P30086	Phosphatidylethanolamine-binding protein 1	PEBP1	29	8	4	187	21	7.53
P00558	Phosphoglycerate kinase 1	PGK1	46	24	17	417	44.6	8.1
P07205	Phosphoglycerate kinase 2	PGK2	6	2	2	417	44.8	8.54
P18669	Phosphoglycerate mutase 1	PGAM1	38	14	7	254	28.8	7.18
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	11	3	3	408	44.9	8.65
P00747	Plasminogen	PLG	6	6	5	810	90.5	7.24
P13796	Plastin-2	LCP1	23	16	9	627	70.2	5.43
P13797	Plastin-3	PLS3	8	8	2	630	70.8	5.6
Q15149	Plectin	PLEC	2	9	9	4684	531.5	5.96
P21246	Pleiotrophin	PTN	10	3	2	168	18.9	9.6
Q15365	Poly(rC)-binding protein 1	PCBP1	12	3	3	356	37.5	7.09
P21128	Poly(U)-specific endoribonuclease	ENDOU	10	3	3	410	46.8	5.43
P01833	Polymeric immunoglobulin receptor	PIGR	44	145	38	764	83.2	5.74
Q6S8J3	POTE ankyrin domain family member E	POTEE	7	34	3	1075	121.3	6.2
A5A3E0	POTE ankyrin domain family member F	POTEF	5	29	2	1075	121.4	6.2
P0CG38	POTE ankyrin domain family member I	POTEI	3	12	2	1075	121.2	6.21
P0CG39	POTE ankyrin domain family member J	POTEJ	2	11	2	1038	117.3	5.97
P02545	Prelamin-A/C	LMNA	27	17	14	664	74.1	7.02
P07737	Profilin-1	PFN1	79	27	14	140	15	8.27
Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP	4	3	3	868	96	6.52
O14737	Programmed cell death protein 5	PDCD5	19	2	2	125	14.3	6.04
P12273	Prolactin-inducible protein	PIP	71	71	12	146	16.6	8.05
Q6MZM9	Proline-rich protein 27	PRR27	11	3	2	219	22.7	4.87
Q16378	Proline-rich protein 4	PRR4	22	4	2	134	15.1	7.06
P07602	Prosaposin	PSAP	34	26	16	524	58.1	5.17
Q06323	Proteasome activator complex subunit 1	PSME1	18	8	4	249	28.7	6.02
Q9UL46	Proteasome activator complex subunit 2	PSME2	9	2	2	239	27.4	5.73
Q8IVF2	Protein AHNAK2	AHNAK2	2	3	3	5795	616.2	5.36
P02760	Protein AMBP	AMBP	7	2	2	352	39	6.25
Q9Y2B0	Protein canopy homolog 2	CNPY2	14	2	2	182	20.6	4.92
O60888	Protein CutA	CUTA	16	2	2	179	19.1	5.5
P30101	Protein disulfide-isomerase A3	PDIA3	15	8	6	505	56.7	6.35
Q15084	Protein disulfide-isomerase A6	PDIA6	10	5	5	440	48.1	5.08
P07237	Protein disulfide-isomerase	P4HB	50	59	29	508	57.1	4.87
B3EWG6	Protein FAM25G	FAM25G	54	9	6	89	9.3	6.15
Q96BQ1	Protein FAM3D	FAM3D	25	9	6	224	24.9	9.33
Q9NUQ9	Protein FAM49B	FAM49B	6	2	2	324	36.7	6.06
Q6P5S2	Protein LEG1 homolog	LEG1	10	5	3	330	37.9	6.15
P31949	Protein S100-A11	S100A11	46	8	5	105	11.7	7.12
P80511	Protein S100-A12	S100A12	42	9	7	92	10.6	6.25
Q9HCY8	Protein S100-A14	S100A14	21	3	2	104	11.7	5.24
P29034	Protein S100-A2	S100A2	17	3	3	98	11.1	4.78
P26447	Protein S100-A4	S100A4	28	6	4	101	11.7	6.11
P06703	Protein S100-A6	S100A6	33	5	4	90	10.2	5.48
P31151	Protein S100-A7	S100A7	49	14	6	101	11.5	6.77
Q86SG5	Protein S100-A7A	S100A7A	31	6	3	101	11.3	7.44
P05109	Protein S100-A8	S100A8	72	68	15	93	10.8	7.03
P06702	Protein S100-A9	S100A9	89	108	14	114	13.2	6.13
P25815	Protein S100-P	S100P	28	2	2	95	10.4	4.88
P0DME0	Protein SETSIP	SETSIP	6	2	2	302	34.9	4.31

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
Q92734	Protein TFG	TFG	4	3	2	400	43.4	5.1
Q08188	Protein-glutamine gamma-glutamyltransferase E	TGM3	12	7	7	693	76.6	5.86
Q99497	Protein/nucleic acid deglycase DJ-1	PARK7	46	10	6	189	19.9	6.79
P00734	Prothrombin	F2	6	4	3	622	70	5.9
P06454	Prothymosin alpha	PTMA	15	5	4	111	12.2	3.78
P00491	Purine nucleoside phosphorylase	PNP	7	2	2	289	32.1	6.95
P55786	Puromycin-sensitive aminopeptidase	NPEPPS	3	2	2	919	103.2	5.72
A6NMY6	Putative annexin A2-like protein	ANXA2P2	13	4	3	339	38.6	6.95
Q9BYX7	Putative beta-actin-like protein 3	POTEKP	8	24	2	375	42	6.33
A8MUU1	Putative fatty acid-binding protein 5-like protein 3	FABP5P3	32	3	2	101	11.3	7.8
P48741	Putative heat shock 70 kDa protein 7	HSPA7	14	7	2	367	40.2	7.87
Q5VSP4	Putative lipocalin 1-like protein 1	LCN1P1	17	7	4	162	17.9	5
A6NI72	Putative neutrophil cytosol factor 1B	NCF1B	10	3	3	391	44.8	9.13
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10	SLC38A10	3	3	3	1119	119.7	5.73
Q5JXB2	Putative ubiquitin-conjugating enzyme E2 N-like	UBE2NL	12	2	2	153	17.4	5.92
Q9H6N6	Putative uncharacterized protein MYH16	MYH16	2	2	2	1097	128.2	5.49
P14618	Pyruvate kinase PKM	PKM	34	33	17	531	57.9	7.84
P50395	Rab GDP dissociation inhibitor beta	GDI2	5	2	2	445	50.6	6.47
P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1	2	3	3	1657	189.1	6.48
P15153	Ras-related C3 botulinum toxin substrate 2	RAC2	18	4	3	192	21.4	7.61
Q15907	Ras-related protein Rab-11B	RAB11B	10	2	2	218	24.5	5.94
P51159	Ras-related protein Rab-27A	RAB27A	10	2	2	221	24.9	5.22
Q6XPR3	Repetin	RPTN	20	9	8	784	90.7	6.92
Q9HD89	Resistin	RETN	59	6	5	108	11.4	6.86
Q15293	Reticulocalbin-1	RCN1	8	2	2	331	38.9	5
P52565	Rho GDP-dissociation inhibitor 1	ARHGDIA	23	8	4	204	23.2	5.11
P52566	Rho GDP-dissociation inhibitor 2	ARHGDIB	38	15	7	201	23	5.21
P42331	Rho GTPase-activating protein 25	ARHGAP25	3	2	2	645	73.4	6.37
P08134	Rho-related GTP-binding protein RhoC	RHOC	12	2	2	193	22	6.58
P34096	Ribonuclease 4	RNASE4	21	3	3	147	16.8	9.03
P13489	Ribonuclease inhibitor	RNH1	12	4	4	461	49.9	4.82
O00584	Ribonuclease T2	RNASET2	23	5	5	256	29.5	7.08
Q9P2E9	Ribosome-binding protein 1	RRBP1	12	3	3	1410	152.4	8.6
Q96E39	RNA binding motif protein, X-linked-like-1	RBMXL1	9	3	3	390	42.1	9.89
P38159	RNA-binding motif protein, X chromosome	RBMX	10	4	4	391	42.3	10.05
A0A096LPE2	SAA2-SAA4 readthrough	SAA2-SAA4	10	3	2	208	23.3	8.98
O95171	Sciellin	SCEL	13	10	8	688	77.5	9.38
P0DP57	Secreted Ly-6/uPAR domain-containing protein 2	SLURP2	25	3	2	97	10.2	6.62
P49908	Selenoprotein P	SELENOP	6	3	2	381	43.2	7.87
Q9NQ38	Serine protease inhibitor Kazal-type 5	SPINK5	31	51	27	1064	120.6	8.06
P58062	Serine protease inhibitor Kazal-type 7	SPINK7	26	7	4	85	9.2	7.58
P02787	Serotransferrin	TF	54	86	42	698	77	7.12
Q9UIV8	Serpin B13	SERPINB13	9	2	2	391	44.2	5.71
P29508	Serpin B3	SERPINB3	23	11	5	390	44.5	6.81
P48594	Serpin B4	SERPINB4	22	10	3	390	44.8	6.21
P36952	Serpin B5	SERPINB5	27	13	11	375	42.1	6.05
P02768	Serum albumin	ALB	84	409	69	609	69.3	6.28

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3BGRL3	51	11	5	93	10.4	4.93
O75368	SH3 domain-binding glutamic acid-rich-like protein	SH3BGRL	42	4	4	114	12.8	5.25
P35326	Small proline-rich protein 2A	SPRR2A	85	9	3	72	8	8.43
P35325	Small proline-rich protein 2B	SPRR2B	61	4	4	72	8	8.43
P22532	Small proline-rich protein 2D	SPRR2D	49	3	3	72	7.9	8.37
P22531	Small proline-rich protein 2E	SPRR2E	79	6	5	72	7.9	8.31
Q96RM1	Small proline-rich protein 2F	SPRR2F	43	5	2	72	7.8	8.31
Q9BYE4	Small proline-rich protein 2G	SPRR2G	30	2	2	73	8.2	7.96
Q9UBC9	Small proline-rich protein 3	SPRR3	93	46	26	169	18.1	8.57
Q14515	SPARC-like protein 1	SPARCL1	20	8	8	664	75.2	4.81
Q9BW04	Specifically androgen-regulated gene protein	SARG	4	2	2	601	63.9	8.62
Q13813	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	2	4	4	2472	284.4	5.35
Q01082	Spectrin beta chain, non-erythrocytic 1	SPTBN1	1	2	2	2364	274.4	5.57
Q14247	Src substrate cortactin	CTTN	3	2	2	550	61.5	5.4
P16949	Stathmin	STMN1	42	12	7	149	17.3	5.97
Q93045	Stathmin-2	STMN2	15	7	4	179	20.8	8.32
P31948	Stress-induced-phosphoprotein 1	STIP1	6	3	3	543	62.6	6.8
P02814	Submaxillary gland androgen-regulated protein 3B	SMR3B	66	121	2	79	8.2	9.57
P00441	Superoxide dismutase [Cu-Zn]	SOD1	76	16	11	154	15.9	6.13
Q6UWP8	Suprabasin	SBSN	67	63	30	590	60.5	7.01
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1	15	3	2	393	41.9	6.29
Q9Y490	Talin-1	TLN1	6	11	11	2541	269.6	6.07
O95881	Thioredoxin domain-containing protein 12	TXNDC12	14	4	2	172	19.2	5.4
Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17	41	6	4	123	13.9	5.52
Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	4	2	2	432	47.6	5.97
P10599	Thioredoxin	TXN	74	28	9	105	11.7	4.92
P07996	Thrombospondin-1	THBS1	4	5	3	1170	129.3	4.94
P19971	Thymidine phosphorylase	TYMP	7	2	2	482	49.9	5.53
P63313	Thymosin beta-10	TMSB10	48	5	2	44	5	5.36
P62328	Thymosin beta-4	TMSB4X	57	8	4	44	5.1	5.06
P37837	Transaldolase	TALDO1	27	14	9	337	37.5	6.81
P20061	Transcobalamin-1	TCN1	20	15	8	433	48.2	5.03
P37802	Transgelin-2	TAGLN2	35	11	8	199	22.4	8.25
P55072	Transitional endoplasmic reticulum ATPase	VCP	5	3	3	806	89.3	5.26
P29401	Transketolase	TKT	17	12	8	623	67.8	7.66
P13693	Translationally-controlled tumor protein	TPT1	33	11	6	172	19.6	4.93
P02766	Transthyretin	TTR	53	7	6	147	15.9	5.76
P04155	Trefoil factor 1	TFF1	30	3	2	84	9.1	4.35
Q07654	Trefoil factor 3	TFF3	40	10	4	94	10.2	6.92
P60174	Triosephosphate isomerase	TPI1	63	22	14	286	30.8	5.92
Q14134	Tripartite motif-containing protein 29	TRIM29	7	9	4	588	65.8	7.15
Q9NYL9	Tropomodulin-3	TMOD3	18	10	6	352	39.6	5.19
P06753	Tropomyosin alpha-3 chain	TPM3	45	37	8	285	32.9	4.72
P67936	Tropomyosin alpha-4 chain	TPM4	60	44	10	248	28.5	4.69
P07951	Tropomyosin beta chain	TPM2	24	23	3	284	32.8	4.7
Q71U36	Tubulin alpha-1A chain	TUBA1A	5	2	2	451	50.1	5.06
P68363	Tubulin alpha-1B chain	TUBA1B	8	4	2	451	50.1	5.06

(Continued on next page)

SUPPLEMENTAL TABLE 1. *(Continued)*

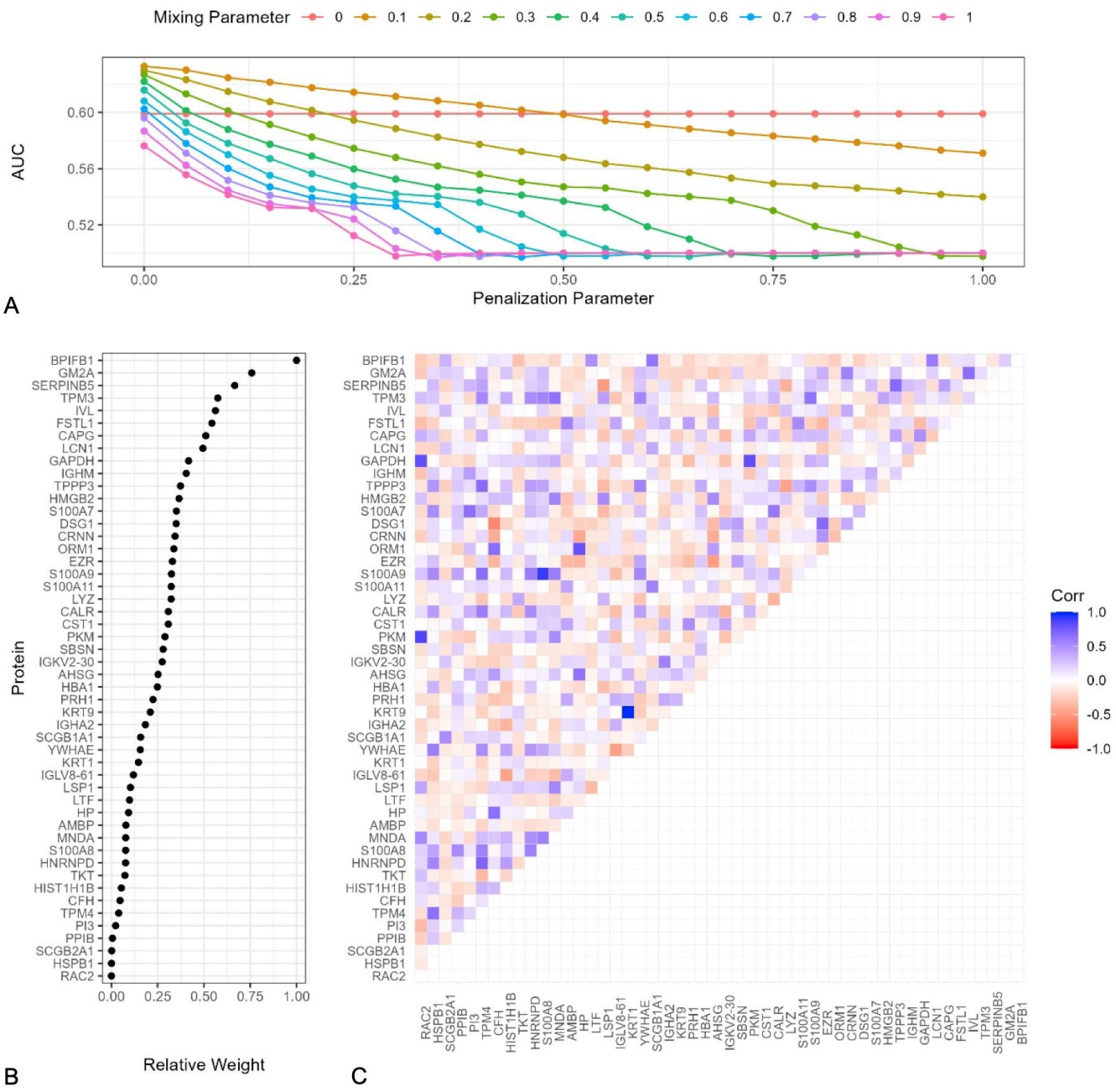
Accession	Description	Gene Name	Coverage, %	# PSMs	# Unique Peptides	# AAs	MW, kDa	Calc. pI
Q9BQE3	Tubulin alpha-1C chain	TUBA1C	5	2	2	449	49.9	5.1
P68371	Tubulin beta-4B chain	TUBB4B	6	2	2	445	49.8	4.89
Q9BW30	Tubulin polymerization-promoting protein family member 3	TPPP3	32	6	6	176	19	9.13
O75347	Tubulin-specific chaperone A	TBCA	64	16	8	108	12.8	5.29
O43399	Tumor protein D54	TPD52L2	15	2	2	206	22.2	5.36
P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1	2	2	2	1058	117.8	5.76
P30085	UMP-CMP kinase	CMPK1	22	4	3	196	22.2	5.57
F8W031	Uncharacterized protein (Fragment)	Uncharacterized	10	3	2	263	29.2	7.01
A0A0J9YY99	Uncharacterized protein (Fragment)	Uncharacterized	19	3	2	117	13	8.92
H0YAE9	Uncharacterized protein (Fragment)	Uncharacterized	14	2	2	185	21.9	5.77
A0A1B0GU03	Uncharacterized protein	Uncharacterized	6	3	3	582	62.7	7.77
H0YC42	Uncharacterized protein	Uncharacterized	13	3	3	278	31.2	6.19
P11684	Uteroglobin	SCGB1A1	29	6	4	91	10	5.06
Q86VR7	V-set and immunoglobulin domain-containing protein 10-like	VSIG10L	3	3	2	867	91.6	7.78
P50552	Vasodilator-stimulated phosphoprotein	VASP	14	8	6	380	39.8	8.94
Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA	11	4	2	249	27.9	8.62
P08670	Vimentin	VIM	64	64	32	466	53.6	5.12
P18206	Vinculin	VCL	3	2	2	1134	123.7	5.66
P02774	Vitamin D-binding protein	GC	50	27	19	474	52.9	5.54
P04004	Vitronectin	VTN	4	2	2	478	54.3	5.8
Q8WWY7	WAP four-disulfide core domain protein 12	WFDC12	23	6	2	111	12	5.5
Q14508	WAP four-disulfide core domain protein 2	WFDC2	39	14	3	124	13	4.84
P16989	Y-box-binding protein 3	YBX3	10	2	2	372	40.1	9.77
P25311	Zinc-alpha-2-glycoprotein	AZGP1	60	97	26	298	34.2	6.05
Q96DA0	Zymogen granule protein 16 homolog B	ZG16B	30	11	5	208	22.7	7.39

PSM indicates peptide spectra matched; AA, amino acid; MW, molecular weight; Calc. pI, calculated pI.

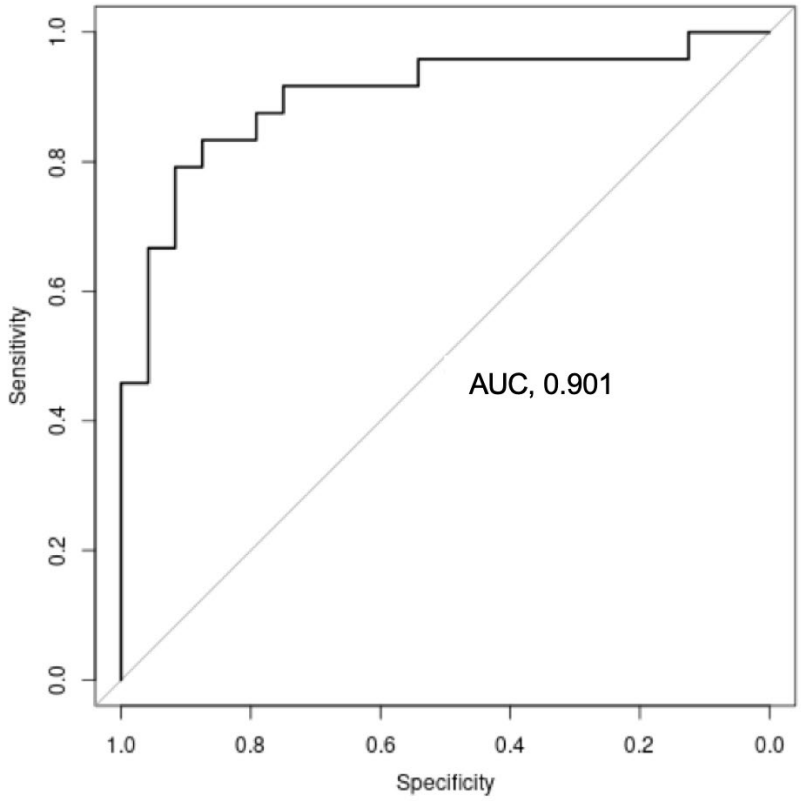
SUPPLEMENTAL TABLE 2. Proteins With Differential Expression in Saliva of CP Patients Compared to Healthy Controls

Accession	Description	Gene Name	*P*	Log2 (Fold Change)	Fold Change
P61626	Lysozyme C	LYZ	0.017	0.941	1.919
P16401	Histone H1.5	HIST1H1B	0.017	0.877	1.837
P26583	High mobility group protein B2	HMGB2	0.006	0.856	1.810
P10412	**Histone H1.4**	**HIST1H1E**	**0.053**	0.670	**1.591**
P33241	Lymphocyte-specific protein 1	LSP1	0.004	0.619	1.536
P00738	Haptoglobin	HP	0.029	0.589	1.504
P80511	Protein S100-A12	S100A12	0.073	0.583	1.498
P07910	**Heterogeneous nuclear ribonucleoproteins C1/C2**	**HNRNPC**	**0.033**	0.559	**1.473**
P35754	**Glutaredoxin-1**	**GLRX**	**0.016**	0.535	**1.449**
P35579	Myosin-9	MYH9	0.092	0.527	1.441
P02671	Fibrinogen alpha chain	FGA	0.038	0.469	1.384
P08670	Vimentin	VIM	0.100	0.371	1.293
P16949	Stathmin	STMN1	0.089	0.353	1.277
P06753	Tropomyosin alpha-3 chain	TPM3	0.040	0.349	1.274
P30086	Phosphatidylethanolamine-binding protein 1	PEBP1	0.072	-0.330	0.795
Q9UBG3	Cornulin	CRNN	0.075	-0.393	0.761
P17931	Galectin-3	LGALS3	0.056	-0.411	0.752
Q02487	Desmocollin-2	DSC2	0.073	-0.413	0.751
P36952	Serpin B5	SERPINB5	0.026	-0.463	0.725
P01871	Immunoglobulin heavy constant mu	IGHM	0.067	-0.466	0.724
P01860	**Immunoglobulin heavy constant gamma 3**	**IGHG3**	**0.090**	-0.474	**0.720**
Q02413	Desmoglein-1	DSG1	0.086	-0.570	0.674
A8K2U0	Alpha-2-macroglobulin-like protein 1	A2ML1	0.029	-0.603	0.658
Q8TDL5	BPI fold-containing family B member 1	BPIFB1	0.047	-0.605	0.657
P40121	Macrophage-capping protein	CAPG	0.076	-0.637	0.643
Q96HE7	ERO1-like protein alpha	ERO1A	0.076	-0.741	0.598
Q9Y6R7	IgGFc-binding protein	FCGBP	0.049	-0.951	0.517
P04196	Histidine-rich glycoprotein	HRG	0.060	-1.283	0.411

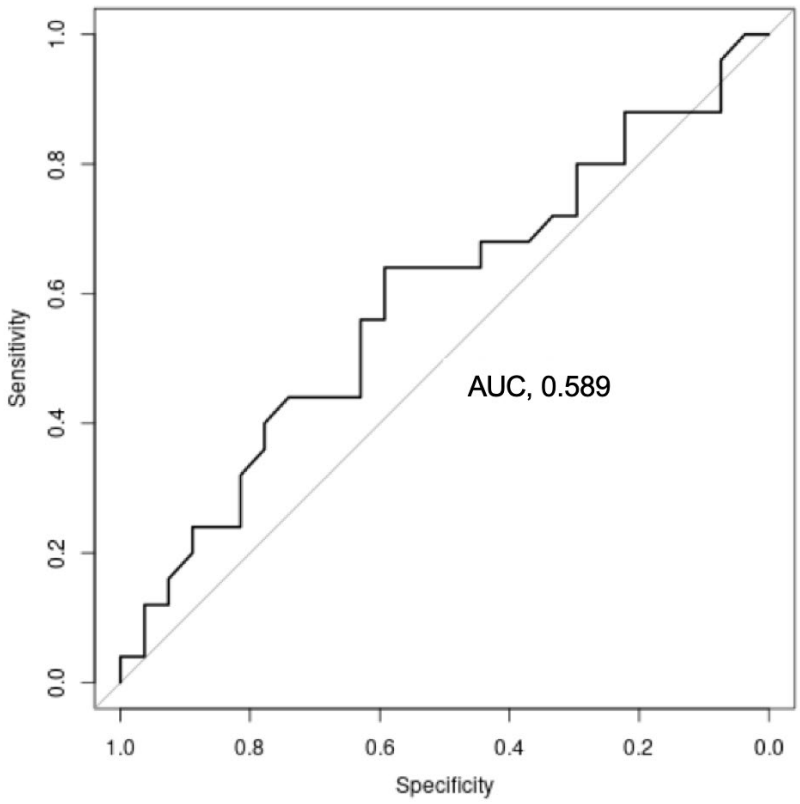
Regular font indicates proteins detected in all 20 sample ratios. Bold font indicates proteins detected in 16 of the 20 sample ratios.



SUPPLEMENTAL FIGURE 2. Predictive regression modeling of proteome AUC values. A, Diagram with our predictive model for the proteome. B, Plot of the weights associated with each of the 50 proteins. C, Correlogram indicating Pearson correlation coefficients (corr) between each set of proteins.



SUPPLEMENTAL FIGURE 3. AUC analysis for Luminex data.



SUPPLEMENTAL FIGURE 4. AUC analysis for PGE2 data.