

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e000028	PTGSGRPE	none	DAN domain family member 5	2.63	0.0	5.82	2.14	within
e000029	PGERGRP*	2xOxidation [P1; P7]	Collagen alpha-1(III) chain	3.0	0.09	6.56	3.26	within
e000031	KTLTSGGH	none	Cysteine-rich protein 1	4.18	1.38	10.45	4.4	within
e000039	MVLGTPSP	none	Mitogen-activated protein kinase 7	6.31	3.33	9.19	9.52	up
e209382	APGNDGAKG*	1xOxidation [P2]	Collagen alpha-1(I) chain	7.58	3.01	12.15	8.21	within
e000119	ASTREEN	none	Corticosteroid-binding globulin	3.86	0.84	7.29	6.73	within
e000149	AADFNR	none	Protein tyrosine phosphatase domain-containing protein 1	3.09	0.06	6.41	5.15	within
e000169	TGVFEK	none	Calmegein	6.82	5.07	9.9	9.76	within
e092835	REHGVGGV	none	182 kDa tankyrase-1-binding protein	6.91	3.31	11.0	5.98	within
e000203	PPGPEGGKG*	1xOxidation [P2]	Collagen alpha-1(III) chain	6.59	4.0	9.61	7.08	within
e000204	EGARGAPGP	none	Collagen alpha-1(VI) chain	7.49	4.54	9.64	9.2	within
e000226	DTASPEGH	none	L-amino-acid oxidase	6.96	4.2	10.17	6.68	within
e209462	PSDPNGNI	none	Insulin receptor	6.96	4.13	9.66	5.65	within
e000229	AAGGPAAGGGGA	none	Inward rectifier potassium channel 4	5.72	3.13	8.78	8.84	up
e209464	SHGSAQVK	none	Hemoglobin subunit alpha	6.1	3.83	9.21	6.85	within
e209470	GPPGREGP*	3xOxidation [P2; P3; P8]	Collagen alpha-1(XVIII) chain	5.23	2.36	8.22	7.63	within
e209478	SLSPGERA	none	Immunoglobulin kappa variable 3-20	5.22	1.17	12.62	6.27	within
e000317	GPASGGSGEV	none	Coatomer subunit epsilon	8.97	5.32	10.82	11.31	up
e209567	DPDSGTAPA	none	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	7.64	5.24	10.05	9.3	within
e000531	SGAEAVNAL	none	T-cell activation inhibitor, mitochondrial	7.73	4.96	10.4	10.73	up
e209590	SVKTHIF	none	Zinc finger protein 534	7.04	4.7	10.61	7.36	within
e209595	VKVPMMK	none	Alpha-1-antitrypsin	4.98	0.61	8.76	5.15	within

a: Distribution in healthy female

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e209596	KAIMEKL	none	Plasma protease C1 inhibitor	5.21	1.57	8.15	5.15	within
e000556	FDLSHGSA	none	Hemoglobin subunit alpha	6.93	4.35	10.12	6.83	within
e093058	TGRTGHGGP	none	Plasminogen activator inhibitor 2	6.61	4.7	8.6	6.94	within
e209655	NAGPAGPAGP*	2xOxidation [P7; P10]	Collagen alpha-2(I) chain	4.25	1.49	6.89	3.2	within
e209658	EEGPELAP	none	Rho guanine nucleotide exchange factor 40	9.0	5.49	11.31	11.1	within
e099800	PPGEAGKPG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	9.11	5.76	11.33	11.45	up
e200037	SHGTVQAAA	none	Probable oxidoreductase PXDNL	9.03	6.38	11.47	11.3	within
e099743	LGTSTSYL	none	Leucine-rich repeat- and IQ domain-containing protein 1	6.72	3.59	10.54	9.53	within
e209668	GARGSAGPPG*	1xOxidation [P8]	Collagen alpha-1(I) chain	7.3	3.19	10.16	9.68	within
e209670	PGEAGPQGD*	1xOxidation [P1]	Collagen alpha-1(VI) chain	8.54	5.42	10.69	10.07	within
e000772	IHSSDTTS	none	ATPase family AAA domain-containing protein 2B	5.91	4.92	9.0	7.54	within
e209715	PPDVPDHA	none	Inter-alpha-trypsin inhibitor heavy chain H4	7.88	4.58	10.15	9.23	within
e000786	SNTEERL	none	Semenogelin-1	7.22	3.31	10.25	11.42	up
e209723	PGGPGHAEAG	none	Zinc finger protein 839	7.68	5.17	9.95	10.27	up
e209726	VTHDAVHA	none	Small G protein signaling modulator 3	7.49	5.35	10.2	10.27	up
e000852	PRGDGQQP	none	Putative uncharacterized protein encoded by MAPKAPK5-AS1	6.6	2.9	8.97	8.83	within
e209746	KPGTHPMS	none	Ankyrin repeat domain-containing protein 13B	6.65	3.07	10.45	8.83	within
e209759	HVDPENF	none	Hemoglobin subunit delta	8.83	6.26	11.43	10.39	within
e209761	RTGPPGPSG*	2xOxidation [P4; P5]	Collagen alpha-2(I) chain	8.23	5.22	10.6	9.88	within
e200063	KYYRDL	none	P2X purinoceptor 4	7.1	4.81	9.79	7.63	within

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e209769	EAGGNPEGQ	none	Protein FAM83F	6.72	2.83	9.29	5.74	within
e000925	SATGPSGGQP	none	Serine/threonine-protein kinase LMTK1	6.25	2.59	9.74	6.94	within
e000931	SPGEAGRPG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	10.34	7.19	12.6	11.93	within
e101638	HAHKLRV	none	Hemoglobin subunit alpha	7.17	4.32	10.69	11.91	up
e097025	DDGEAGKPG*	1xOxidation [P8]	Collagen alpha-1(II) chain	12.02	8.13	14.22	12.02	within
e001089	GPPGPPGLQ*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XIII) chain	7.59	5.14	10.37	6.71	within
e001096	KGGPRQGPA	none	Telomere length regulation protein TEL2 homolog	7.8	4.58	9.86	9.49	within
e209827	PSLPDRSP	none	Synaptopodin	5.34	1.12	7.71	6.07	within
e001135	APGERGPPG*	2xOxidation [P2; P7]	Collagen alpha-1(III) chain	10.36	6.33	12.27	12.4	up
e209833	EPEPELR	none	Apolipoprotein E	10.39	7.07	12.18	12.29	up
e209834	RSSPASAPP	none	Kinesin-like protein KIF26A	10.13	6.62	11.93	12.32	up
e103225	TGPQGPGQP*	2xOxidation [P3; P6]	Collagen alpha-1(XXII) chain	8.22	3.32	10.95	10.57	within
e001179	DQPLSAEL	none	Son of sevenless homolog 1	4.01	1.81	10.19	6.07	within
e001256	PVGGESDSE	none	Microtubule cross-linking factor 1	8.34	3.82	11.37	10.98	within
e097039	GPPGEPGPPG*	1xOxidation [P9]	Collagen alpha-3(V) chain	10.69	6.75	14.04	8.54	within
e200100	FPQGSGASE	none	Protein transport protein Sec16A	5.0	3.72	6.83	4.72	within
e209901	FLRDTKT	none	Alpha-1-acid glycoprotein 2	9.41	5.44	11.9	9.88	within
e209902	GVANALAHK	none	Hemoglobin subunit delta	9.46	5.7	11.82	10.78	within
e209905	QRETGGFS	none	Ribosomal RNA processing protein 1 homolog B	6.81	4.65	9.26	7.71	within
e001355	RGETGPPGP*	1xOxidation [P7]	Collagen alpha-1(III) chain	8.11	5.76	10.33	10.99	up
e001356	TYVPKEF	none	Albumin	7.16	5.18	9.78	10.9	up
e001365	PPGENGKPG*	2xOxidation [P2; P8]	Collagen alpha-1(III) chain	9.54	6.01	11.45	12.0	up

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e209921	TMAMDGME	none	DDB1- and CUL4-associated factor 7	11.73	7.9	14.66	13.14	within
e207663	CDDYRLC*	2xDisulfide bridge [C1; C7]	Matrix Gla protein	11.82	8.0	14.6	13.14	within
e209922	PDSTYSES	none	Grainyhead-like protein 2 homolog	8.62	6.44	10.24	7.72	within
e209933	TSEEEAKT	none	Arginase-2, mitochondrial	4.74	1.97	7.48	3.49	within
e209946	NFYPREA	none	Immunoglobulin kappa constant	4.87	1.36	8.48	2.93	within
e001497	STFIGNSTA	none	Tubulin beta-3 chain	8.27	4.82	13.0	8.04	within
e001503	KSSDRPAH	none	Ly6/PLAUR domain-containing protein 6B	8.71	5.96	11.15	9.79	within
e200137	KSTSPPPSP	none	Dematin	5.18	3.29	9.57	5.17	within
e001521	EGSRPGGAAP	none	Ras-related protein Rab-34, isoform NARR	8.57	4.24	11.44	10.38	within
e001565	PGTWESQP	none	Nuclear factor of activated T-cells, cytoplasmic 4	7.94	5.29	10.07	8.92	within
e209975	KGSKGAPGPA*	2xOxidation [P7; P9]	Collagen alpha-1(XVIII) chain	8.21	5.12	11.18	9.91	within
e209976	KRSGSGVNP	none	Importin subunit alpha-7	8.25	5.4	11.15	9.81	within
e001602	PSAEGADGQA	none	Zinc fingers and homeoboxes protein 3	6.88	3.03	9.41	8.17	within
e001623	DPGKNGDKG*	1xOxidation [P2]	Collagen alpha-2(I) chain	12.31	8.91	14.05	13.16	within
e209986	HSPNPSKH	none	Zinc finger protein 195	12.19	8.01	13.89	13.12	within
e209987	TSSPQDRL	none	Nuclear pore complex protein Nup93	12.14	8.18	13.78	13.13	within
e210002	DAFTAPFH	none	Partner and localizer of BRCA2	8.32	5.78	11.93	6.77	within
e210003	ATAATAAGGTGG	none	Cyclin-dependent kinase 13	8.74	5.71	11.21	9.07	within
e210004	RLEPEDF	none	Immunoglobulin kappa variable 3-20	8.04	5.8	13.05	6.77	within
e210011	GPHDGGDRP	none	TBC1 domain family member 10B	8.75	6.6	10.78	11.51	up
e093417	HLPAEFTP	none	Hemoglobin subunit alpha	8.61	5.37	11.2	7.1	within
e207668	SGSDSDDDD	none	Pre-mRNA-processing factor 40 homolog A	14.05	9.34	16.06	15.15	within

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e210029	PERMNEH	none	Carbohydrate sulfotransferase 14	5.48	1.55	11.68	6.98	within
e001719	PGFGNPGPPG*	1xOxidation [P9]	Collagen alpha-5(IV) chain	6.81	2.46	9.37	8.49	within
e093421	DGKTGPPGPA*	1xOxidation [P7]	Collagen alpha-1(I) chain	12.11	7.38	14.21	12.43	within
e001759	PGADGPAGAPG*	3xOxidation [P1; P6; P10]	Collagen alpha-1(I) chain	7.21	3.55	9.75	7.37	within
e106027	GDRGFPGPP*	1xOxidation [P8]	Collagen alpha-5(IV) chain	9.52	6.11	11.71	11.37	within
e001788	STPGDTQPN	none	Chromodomain-helicase-DNA-binding protein 4	8.07	3.44	10.85	9.59	within
e200172	ATPSRSSAAA	none	Protein phosphatase 1 regulatory subunit 15A	5.75	3.51	8.32	8.06	within
e106744	KGNEENPH	none	Beta-1,4-galactosyltransferase 3	7.54	3.46	10.08	10.08	up
e001912	FDTASTGKT	none	Fibrinogen alpha chain	9.17	5.76	11.44	7.77	within
e001919	PGGAPSAWAD	none	NAC-alpha domain-containing protein 1	6.87	2.91	9.76	9.99	up
e210102	GEPGKQGAPG*	2xOxidation [P3; P9]	Collagen alpha-1(II) chain	10.0	6.5	12.46	9.19	within
e210103	GGLGAGAAGGGGAG	none	Autism susceptibility gene 2 protein	10.21	6.92	12.6	9.19	within
e001996	DKGESGPSGP	none	Collagen alpha-1(I) chain	8.3	4.13	13.0	6.59	within
e210119	SPGRDGSPGA*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	7.41	3.39	10.72	8.96	within
e210125	KGDRAGDASG	none	Scavenger receptor class A member 5	7.64	5.47	9.91	7.59	within
e099041	DGKTGPPGPA*	1xCation:Na [C-Term]; 1xOxidation [P7]	Collagen alpha-1(I) chain	8.1	3.92	11.66	9.48	within
e210143	KDDDHNGH	none	Ubiquitin-like modifier-activating enzyme 6	7.88	5.78	9.33	10.17	up
e101407	GNAVGAESPH	none	Laminin subunit alpha-1	6.9	3.44	10.86	10.23	within
e002111	QGEPEGAPGLP*	1xOxidation [P]	Collagen alpha-1(XVI) chain	8.89	5.67	11.26	9.63	within
e002114	PVQGQQQGP	none	Homeobox protein cut-like 1	9.05	5.81	11.05	9.74	within
e002129	SPGKDGP GP*	2xOxidation [P2; P7]	Collagen alpha-1(III) chain	7.11	3.19	10.59	8.25	within

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e093585	GPPGENGKPG*	2xOxidation [P3; P9]	Collagen alpha-1(III) chain	8.65	6.01	11.94	10.36	within
e103795	PPGERGGPGS*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	6.7	2.94	10.2	9.86	within
e210189	DPAGAGGAGAGGS	none	NADPH oxidase activator 1	7.11	3.94	9.77	6.98	within
e210190	GAGPGAEGMTP	none	PDZ domain-containing protein 2	7.4	4.06	9.86	6.99	within
e002225	SPGENGAPGQ*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	8.09	5.49	11.42	9.48	within
e002229	RYVGGQEH	none	Alpha-1-acid glycoprotein 1	7.12	4.66	9.33	7.56	within
e002235	TSPKGGRSR	none	Serine/arginine repetitive matrix protein 2	12.5	8.82	14.62	14.45	within
e002271	PGDKGESGPS*	1xOxidation [P1]	Collagen alpha-1(I) chain	10.04	6.7	12.0	9.21	within
e093627	SGDRGETGPA	none	Collagen alpha-1(I) chain	10.1	6.19	11.98	9.19	within
e210213	SPGGKGEMGP*	2xOxidation [P2; M8]	Collagen alpha-1(III) chain	5.25	2.56	9.73	5.6	within
e210214	SGSFLPVPE*	1xOxidation [P6]	Collagen alpha-1(VII) chain	10.21	5.13	13.0	10.5	within
e002299	SGSVIDQSR	none	Uromodulin	10.21	4.98	12.98	10.5	within
e002301	QQPPREPP	none	Protein-lysine 6-oxidase	10.04	3.88	12.96	10.5	within
e002418	SSPHGKDLL	none	Serotransferrin	6.62	4.1	11.29	7.29	within
e200241	DHV/KLVNE	none	Albumin	8.16	4.21	13.23	7.29	within
e002427	YDRSDIDA	none	Nidogen-1	6.84	3.24	9.46	4.74	within
e200243	KQDTSSSTT	none	Anillin	5.43	1.54	9.75	5.48	within
e106567	AYDGAKKMA	none	Unconventional myosin-XVIIIb	4.67	1.26	9.2	1.96	within
e002431	PSASTPLPQG	none	Collagen alpha-1(XXIV) chain	7.02	3.32	9.3	8.14	within
e002481	TSGPPGSAGPP*	2xOxidation [P5; P10]	Collagen alpha-2(V) chain	7.12	3.31	9.61	7.31	within
e002482	DKGDTGPPGP*	1xOxidation [P8]	Collagen alpha-1(III) chain	7.88	3.56	10.26	8.05	within
e093665	EHGPPGPPGP*	1xOxidation [P8]	Collagen alpha-2(XI) chain	7.84	5.58	10.18	8.5	within
e210258	GPPGPPGFQG*	3xOxidation [P3; P5; P6]	Collagen alpha-2(I) chain	7.0	3.33	9.85	8.01	within

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e002526	GAVGPPGFAGE	none	Collagen alpha-2(I) chain	6.72	3.57	9.64	6.81	within
e200261	GDPGKNGDKG*	1xOxidation [P3]	Collagen alpha-2(I) chain	7.98	4.18	10.23	10.09	within
e210269	ASGAGGAANGTGA	none	ATP-binding cassette sub-family A member 2	7.44	4.22	9.8	6.68	within
e002566	NRGERGSEG	none	Collagen alpha-1(III) chain	8.1	4.81	11.31	9.24	within
e002601	AGPGYGGRND	none	Lipoma-preferred partner	6.42	5.24	8.77	6.78	within
e002611	HLGEHDGSL	none	Transmembrane channel-like protein 5	5.94	3.4	9.66	4.6	within
e002653	TGPVGAAGPAGP*	1xOxidation [P3]	Collagen alpha-2(I) chain	6.24	4.35	9.31	8.57	within
e002662	AEPAGGEVAAP	none	Protein FAM181B	5.31	2.76	9.81	6.46	within
e002702	GPPGEKGPQG*	3xOxidation [P2; P3; P8]	Collagen alpha-1(XI) chain	9.9	6.18	12.4	11.13	within
e210306	PGNDGAKGDAG*	1xOxidation [P1]	Collagen alpha-1(I) chain	5.03	2.42	8.69	6.85	within
e210307	PNEPNFGSL	none	Tensin-1	5.9	2.39	10.72	4.96	within
e002802	STPPEGSDST	none	Tumor necrosis factor receptor superfamily member 16	8.4	5.9	10.68	7.54	within
e002821	DLGGSSAATEA	none	Mineralization regulator ANKH	7.31	4.14	9.56	6.3	within
e200314	SGSEETLQ	none	Autophagy-related protein 2 homolog B	10.01	6.64	12.4	11.53	within
e002858	SGVYITRGQ	none	Nucleus accumbens-associated protein 2	7.89	3.91	10.28	8.68	within
e207680	PGKDGPRGPT	none	Collagen alpha-1(III) chain	9.38	6.39	11.47	10.48	within
e002899	PPSLPLSSAL	none	Mitogen-activated protein kinase kinase kinase 21	8.98	6.43	10.68	10.95	up
e002905	HLPAEFTPA	none	Hemoglobin subunit alpha	8.46	4.26	11.12	11.31	up
e097069	QKPGQSPQL	none	Immunoglobulin kappa variable 2-28	8.3	5.55	11.33	11.31	within
e002910	VLNLGPITR	none	Uromodulin	11.98	8.25	14.82	12.23	within
e002918	AGAAAAGRPGAG	none	Alpha-protein kinase 3	6.64	4.27	9.21	8.33	within

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e002953	PKGGPGTGSGGGG	none	SKI family transcriptional corepressor 1	8.94	6.9	10.81	9.58	within
e002961	QGDWSPEAP	none	Complement receptor type 1	8.89	5.08	12.22	7.97	within
e003008	TGATGDKGPPG*	2xOxidation [P9; P10]	Collagen alpha-2(V) chain	6.91	5.1	9.61	7.83	within
e103129	RERAQAATS	none	Putative uncharacterized protein ADARB2-AS1	11.45	8.43	13.22	13.34	up
e210377	PSSTVEDAGQ	none	Titin	4.55	2.09	7.71	4.55	within
e101262	SQTEPTSAGD	none	Uncharacterized protein KIAA1671	4.79	1.52	7.83	5.07	within
e003088	LEEGDAGSSE	none	LON peptidase N-terminal domain and RING finger protein 2	8.75	6.93	10.42	10.52	up
e210388	SASSESSGAGGP	none	Centriole, cilia and spindle-associated protein	7.6	5.38	11.0	8.21	within
e003123	PSSESKSEGS	none	Disintegrin and metalloproteinase domain-containing protein 32	6.88	3.25	9.48	7.9	within
e210402	PSGPQGPGGPP*	3xOxidation [P1; P4; P7]	Collagen alpha-1(I) chain	8.85	6.14	11.35	11.09	within
e003164	DHLPENDR	none	Beta-1,4-galactosyltransferase 6	7.36	5.45	9.37	6.41	within
e003165	GPDGKTGPPGP*	1xOxidation [P9]	Collagen alpha-1(I) chain	8.51	5.95	11.27	11.68	up
e003197	SGDMHQHEG	none	E3 ubiquitin-protein ligase DTX3L	8.97	6.0	11.82	10.58	within
e200366	SVAPETKVNG	none	Ankyrin repeat domain-containing protein 24	7.44	5.24	10.4	8.72	within
e003352	SDGSSGGSSIGP	none	Inactive tyrosine-protein kinase PRAG1	8.94	6.53	11.13	11.2	up
e003370	YVSGFHPSD	none	Beta-2-microglobulin	6.82	3.62	9.24	9.49	up
e003416	SGVWNDDSM	none	F-box only protein 7	8.85	6.41	11.13	12.2	up
e003415	TEYEEDAGP	none	Patatin-like phospholipase domain-containing protein 6	9.01	6.04	11.29	12.2	up
e210461	NNFYPREA	none	Immunoglobulin kappa light chain	5.32	1.65	8.41	5.86	within
e210464	DSTSDEDRS	none	Retinitis pigmentosa 9 protein	8.08	6.45	10.86	11.34	up

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e003483	TNGLLSPAGSP	none	Transcription factor Sp7	9.98	7.08	12.33	11.53	within
e207689	CDDYRLCE*	2xDisulfide bridge [C1; C7]	Matrix Gla protein	14.41	11.47	17.16	15.07	within
e094089	DGEAGKGRP*	2xOxidation [P7; P10]	Collagen alpha-1(I) chain	7.97	5.53	10.39	5.86	within
e003552	TEAGETDSAHA	none	Anoctamin-2	7.55	4.96	10.22	5.96	within
e003556	PDFNGGAWGP	none	Arylsulfatase I	8.17	4.89	11.02	6.03	within
e003557	APGDKGESGPS*	1xOxidation [P2]	Collagen alpha-1(I) chain	13.85	11.13	15.3	14.35	within
e210495	KKENKNEK	none	Protein S100-A9	6.17	3.85	10.11	9.52	within
e103280	SHKQSRLY	none	Osteopontin	7.15	3.34	11.67	6.15	within
e210504	GGAVGAFGGAAGGA	none	Voltage-dependent calcium channel gamma-8 subunit	10.13	7.58	12.76	11.43	within
e003616	VEHSDLSFS	none	Beta-2-microglobulin	7.6	4.46	11.18	10.32	within
e207691	PSGASHSPLPA	none	Membrane frizzled-related protein	8.38	5.05	11.78	9.81	within
e210508	KGPPGPQGPPG*	2xOxidation [P3; P4]	Collagen alpha-1(XXIII) chain	8.5	5.77	11.63	9.81	within
e003664	EAGPGGPPGVPG*	2xOxidation [P7; P8]	Collagen alpha-2(VIII) chain	7.9	5.71	10.88	8.31	within
e003705	SSHESSHGTP	none	Interleukin-15 receptor subunit alpha	6.31	4.75	8.96	7.79	within
e003715	PGDRGEPGPP*	3xOxidation [P1; P7; P9]	Collagen alpha-1(I) chain	10.9	6.21	12.8	12.36	within
e003716	PPGSAGAPGKDG*	1xOxidation [P]	Collagen alpha-1(I) chain	10.9	6.59	12.81	12.38	within
e003736	FGDDPSDKF	none	Fibrinogen gamma chain	8.77	6.53	11.09	10.89	within
e003737	EDLRNDEH	none	Period circadian protein homolog 3	9.37	6.96	10.89	10.22	within
e003746	PPQVNVEVF	none	MAP7 domain-containing protein 3	5.24	3.58	7.27	4.52	within
e094099	IEQNTKSPL	none	Alpha-1-antitrypsin	9.13	6.43	12.22	9.97	within
e003794	TLSLSPGERA	none	Immunoglobulin kappa variable 3-20	7.45	4.46	13.01	8.59	within
e003837	SPASSQEGSPS	none	PAX-interacting protein 1	11.04	7.93	12.58	12.2	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e003841	SLGTSAAQAMP	none	Storkhead-box protein 2	7.59	5.25	11.61	9.3	within
e210552	EMLGQSQLQ	none	Unconventional myosin-XVB	13.32	9.09	15.09	14.12	within
e003840	GGPGLSTPGGHP	none	Splicing factor, proline- and glutamine-rich	13.36	9.36	15.12	14.15	within
e003843	RVAPEEHPV	none	Actin, cytoplasmic 1	12.79	7.51	15.04	14.06	within
e200469	KTGGSRSDDL	none	Voltage-gated potassium channel regulatory subunit KCNF1	9.64	6.71	12.39	11.52	within
e101203	PDISSGTSDTG	none	Thrombopoietin	8.67	5.09	11.24	10.56	within
e003937	VSHEDPEVK	none	Immunoglobulin gamma-1 heavy chain	8.79	6.06	11.62	11.74	up
e003953	DPGKNGDKGH*	1xOxidation [P2]	Collagen alpha-2(I) chain	6.59	3.02	11.62	5.94	within
e207696	PDGAPGERGGP*	2xOxidation [P1; P5]	Collagen alpha-1(VI) chain	9.15	6.57	11.7	11.49	within
e003980	TPVPDSGSAN	none	Mid1-interacting protein 1	9.09	6.52	11.18	11.49	up
e003981	SPGPDGKTGPP*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	10.89	7.48	13.13	12.92	within
e003989	PPGSAGAPGKDG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	9.27	5.16	12.57	12.07	within
e003988	AGTAGGPGAGAAAGG	none	Transcription initiation factor TFIID subunit 10	7.86	4.86	10.3	10.54	up
e210575	PGKDGKPGTPG*	2xOxidation [P7; P10]	Collagen alpha-3(IV) chain	9.22	5.5	12.65	12.0	within
e004000	PEGPAGNDGTP*	2xOxidation [P1; P4]	Collagen alpha-2(V) chain	9.11	6.76	11.43	10.33	within
e004062	DGKDGSPGEPG*	2xOxidation [P7; P10]	Collagen alpha-1(III) chain	9.45	6.94	11.46	10.19	within
e300003	GKWERPFE	none	Alpha-1-antitrypsin	7.69	4.37	10.39	6.8	within
e101469	GAPGQGGAPGPPG*	2xOxidation [P9; P11]	Collagen alpha-2(VIII) chain	12.42	8.98	14.15	13.12	within
e004128	QAHDPDAGANG	none	Protocadherin-16	8.11	3.48	11.88	8.12	within
e210609	GLPGSDGAPGPP*	2xOxidation [P9; P11]	Collagen alpha-2(XI) chain	8.4	6.74	11.42	6.9	within
e210613	GPGSDGKPGPPG*	2xOxidation [P2; P8]	Collagen alpha-1(III) chain	9.49	6.47	11.61	10.69	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e210614	QDAGRPLSN	none	Cadherin EGF LAG seven-pass G-type receptor 3	9.6	6.55	12.72	10.69	within
e004173	QGTGQGDPGPAA	none	Centrosomal protein of 152 kDa	7.6	5.87	11.33	7.94	within
e004198	SGGFGGGFGGGSGG	none	Keratin, type I cytoskeletal 9	8.3	5.92	11.95	10.17	within
e210616	SPGPTGENGPP*	3xOxidation [P2; P4; P10]	Collagen alpha-2(XI) chain	8.83	6.18	11.81	10.18	within
e200537	SGDNYPPNP	none	Protein lifeguard 1	8.14	5.95	10.84	9.1	within
e101782	FHPSDIEVD	none	Beta-2-microglobulin	7.57	4.48	10.31	8.4	within
e004224	SPGEAGRPGEA*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	8.46	5.93	15.54	8.33	within
e210627	RTHLAPYSD	none	Apolipoprotein A-I	7.93	5.79	11.25	7.5	within
e004238	DGSPGKDGVRG*	1xOxidation [P4]	Collagen alpha-1(I) chain	7.13	3.96	13.79	8.35	within
e004242	VESQREAGGK	none	Smoothelin-like protein 1	6.4	3.62	11.49	4.25	within
e210633	QGDDGDGPGMG*	1xOxidation [P]	Collagen alpha-1(XXVII) chain	9.74	5.96	12.91	6.33	within
e210634	PDSDDTEAP	none	Rho GTPase-activating protein 5	9.8	6.54	12.91	6.33	down
e004328	GPDKTGPPGPA*	1xOxidation [P9]	Collagen alpha-1(I) chain	9.47	6.01	11.93	8.62	within
e004333	QQQDGAAGPPGP*	1xOxidation [P10]	Collagen alpha-1(XXIII) chain	10.11	6.84	12.35	10.83	within
e004341	VAGPPGGSGPAGP*	3xOxidation [P4; P5; P10]	Collagen alpha-1(III) chain	8.45	5.34	11.4	8.94	within
e207699	NGADGPQGPPGS*	1xOxidation [P]	Collagen alpha-1(XI) chain	14.63	11.99	16.14	15.48	within
e100904	GEYKFQNAL	none	Albumin	11.78	8.72	13.39	13.61	up
e210649	GPGSDGKPGPPG*	3xOxidation [P2; P8; P10]	Collagen alpha-1(III) chain	13.99	10.36	15.48	15.29	within
e004375	SPGERGEVGPA*	1xOxidation [P2]	Collagen alpha-2(I) chain	11.73	8.95	13.45	13.4	within
e004380	DGEAGKPGRPG*	2xOxidation [P7; P10]	Collagen alpha-1(I) chain	9.49	5.73	11.9	11.31	within
e207701	DGAPGKNGERG*	1xOxidation [P4]	Collagen alpha-1(III) chain	9.74	6.93	11.86	9.58	within
e101016	ARGNDGARGSD	none	Collagen alpha-1(III) chain	9.5	7.06	11.43	10.24	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e300132	GGSPKGDVDPF	none	Sodium/potassium-transporting ATPase subunit gamma	8.49	6.61	14.1	8.65	within
e004436	ETFTSSTAFS	none	Paternally-expressed gene 3 protein	8.61	5.7	11.53	11.75	up
e004440	NTRENNSSR	none	AF4/FMR2 family member 2	8.85	5.88	11.54	11.85	up
e004438	GERGFPGERG*	1xOxidation [P6]	Collagen alpha-1(I) chain	9.0	6.19	11.66	11.94	up
e102047	GGGDAGDDDDAGG	none	B-cell lymphoma/leukemia 11B	8.93	2.81	12.25	12.45	up
e004457	HGDQGAPGSVGP	none	Collagen alpha-2(I) chain	8.22	4.52	11.49	11.84	up
e004502	DRGEPGPPGPA*	2xOxidation [P7; P]	Collagen alpha-1(I) chain	10.35	7.05	12.53	10.46	within
e004510	PSNTSAPHSQG	none	Synaptophysin-like protein 1	6.05	2.51	8.28	5.61	within
e004519	DGPQGPPEGVGN*	2xOxidation [P3; P6]	Collagen alpha-2(XI) chain	10.68	7.36	12.42	11.95	within
e004521	GPEGGKGAAGPPG*	2xOxidation [P2; P11]	Collagen alpha-1(III) chain	11.1	8.57	12.86	10.91	within
e004567	MAGSGMGQSME	none	B-cell CLL/lymphoma 9-like protein	14.19	10.62	16.35	14.94	within
e210684	DGPSGAEGPPGP*	3xOxidation [P3; P9; P10]	Collagen alpha-1(II) chain	14.38	11.16	16.22	15.14	within
e210688	TSKPEFEFT	none	Selenocysteine insertion sequence-binding protein 2	10.79	7.03	12.76	11.98	within
e004573	PGPPGPPGPPSP*	2xOxidation [P3; P4]	Collagen alpha-6(IV) chain	10.39	6.91	12.68	11.99	within
e004640	SISSGLNSDPD	none	Calmodulin-binding transcription activator 1	6.31	3.21	10.98	6.2	within
e004691	KEDEENTSAA	none	Transcription factor E2-alpha	8.2	5.33	11.19	9.08	within
e207708	GPSGNAGPPGPPG*	2xOxidation [P9; P11]	Collagen alpha-1(I) chain	8.95	6.37	11.62	9.08	within
e004710	EFTPTKDE	none	Beta-2-microglobulin	9.48	5.77	12.01	9.13	within
e004716	KDLDQVQLH	none	Ventricular zone-expressed PH domain-containing protein homolog 1	7.77	4.84	9.92	8.37	within
e102069	SERAHQVLR	none	Vitamin K-dependent protein C	7.81	5.29	10.04	8.7	within
e210750	APGDRGEPGPP*	3xOxidation [P2; P8; P10]	Collagen alpha-1(I) chain	15.69	11.91	16.74	16.55	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e004757	DPDAPSRKDP	none	Phosphatidylethanolamine-binding protein 1	9.2	6.26	11.65	8.28	within
e004769	GSPGPTGENGPP*	2xOxidation [P5; P11]	Collagen alpha-2(XI) chain	14.43	9.62	15.6	15.47	within
e004771	PPGEAGKPGEQ*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	14.5	11.67	15.53	15.47	within
e200669	PPGERGGPGSR*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	8.15	4.55	11.32	9.36	within
e004783	KGGDSPGQQEP	none	Spermatogenesis-associated protein 31E1	11.87	8.73	13.64	12.46	within
e210756	GAGGAAGAGTGAGPA	none	Serine/threonine-protein kinase SIK3	11.86	8.87	13.67	12.45	within
e004787	DGGGSPKGDVDP	none	Sodium/potassium-transporting ATPase subunit gamma	12.8	10.05	14.21	13.7	within
e004791	DGESGRPGRPG*	1xOxidation [P10]	Collagen alpha-1(III) chain	11.19	7.51	12.79	11.64	within
e004798	DTGAKGEPGPVG*	1xOxidation [P8]	Collagen alpha-1(I) chain	12.79	9.9	14.19	13.69	within
e004806	GLPGPPDVPDH	none	Inter-alpha-trypsin inhibitor heavy chain H4	12.68	9.09	14.12	13.69	within
e094161	PGPPGPPGPPSP*	3xOxidation [P4; P6; P7]	Collagen alpha-6(IV) chain	10.32	7.41	12.48	9.85	within
e210773	TQSPHGYPKS	none	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2	10.34	7.52	12.47	9.84	within
e004876	GGGAGGGSGEREGG	none	Microtubule cross-linking factor 3	7.35	4.44	10.1	6.54	within
e104910	HEGTHSTKRG	none	Fibrinogen alpha chain	7.05	4.13	11.62	6.02	within
e005022	NAEAEGSPGPGE	none	Sarcalumenin	11.06	7.04	12.98	11.36	within
e097139	IHEDSDSALQ	none	Inter-alpha-trypsin inhibitor heavy chain H4	11.06	7.27	13.05	12.0	within
e005043	KDGEAGAQQPPG*	2xOxidation [P10; P11]	Collagen alpha-1(I) chain	9.08	6.53	11.02	8.02	within
e005044	SPGERGETGPP*	2xOxidation [P2; P10]	Collagen alpha-1(III) chain	15.13	12.41	16.19	15.94	within
e005055	DEAGSEADHEG	none	Fibrinogen alpha chain	8.67	5.14	11.14	10.5	within
e005059	DGESGRPGRPG*	2xOxidation [P7; P10]	Collagen alpha-1(III) chain	11.18	6.28	13.16	6.05	down
e005060	SPGSNGAPGQRG*	2xOxidation [P2; P8]	Collagen alpha-1(III) chain	14.1	10.63	15.24	14.96	within
e005063	VSAANLNGEAGGG	none	E3 ubiquitin-protein ligase SH3RF3	10.99	4.51	13.0	5.9	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e207725	VEESTQVGGDP	none	Filamin-C	10.6	7.4	12.78	12.43	within
e005090	SPGRDGSPGAKG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	10.6	7.5	12.75	12.43	within
e005094	PGEQGPPGPPGP*	2xOxidation [P9; P10]	Collagen alpha-1(IX) chain	10.34	6.45	12.55	11.34	within
e210823	GPSGPIGPPGPPG*	2xOxidation [P9; P11]	Collagen alpha-1(V) chain	10.26	6.72	12.31	11.35	within
e100834	APGDRGEPGPP*	1xCation:Na [D4]; 3xOxidation [P2; P8; P10]	Collagen alpha-1(I) chain	11.15	7.6	14.0	9.99	within
e099048	DGRPGPPGPPGA*	3xOxidation [P6; P7; P9]	Collagen alpha-1(I) chain	9.11	5.65	11.73	10.01	within
e005181	GISPFHEHAE	none	Transthyretin	7.86	5.12	10.51	9.6	within
e005188	ETSTGPDAMSE	none	Neurobeachin	8.32	4.73	10.69	11.24	up
e101611	TQASASPDPRP	none	Isthmin-2	12.01	8.69	13.56	13.59	up
e005224	SGYSSGGASGSGGP	none	Protein FosB	11.53	8.26	13.29	12.88	within
e005227	GGPGSDGKPGPPG*	3xOxidation [P3; P9; P11]	Collagen alpha-1(III) chain	11.02	7.49	12.75	11.91	within
e106113	GEPGAGGGAAGAAGAG	none	La-related protein 1	11.45	7.09	13.51	11.06	within
e005237	QDGIDGEAGPPG*	1xOxidation [P11]	Collagen alpha-3(IX) chain	9.8	6.24	11.43	11.13	within
e005254	TDDSDNYGEN	none	Zinc finger protein 652	13.94	10.88	15.88	15.04	within
e005257	APGEAGRDGNPG*	2xOxidation [P2; P11]	Collagen alpha-2(I) chain	11.21	8.0	12.87	12.52	within
e210857	VSGPPGRDGQQ*	2xOxidation [P4; P5]	Collagen alpha-1(XVI) chain	8.41	6.11	10.52	7.9	within
e005261	SAEDADAPGSPN	none	Cadherin-16	11.5	7.61	13.33	13.29	within
e097148	KGEPGSPGENGA*	2xOxidation [P4; P7]	Collagen alpha-1(I) chain	10.31	7.42	12.1	12.68	up
e005283	TPPPSSGPTYQ	none	Plasminogen	8.64	6.44	11.21	8.69	within
e005328	TTGEEDEEEP	none	Voltage-dependent L-type calcium channel subunit alpha-1C	12.63	8.34	15.32	6.95	down
e005333	PIGQEGAPGRPG	none	Collagen alpha-2(IV) chain	11.73	8.51	13.56	12.11	within
e100951	YVVHTNYDE	none	Protein AMBP	9.42	6.49	12.93	9.21	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e200793	GPPGADGIAGAAGP*	2xOxidation [P3; P14]	Collagen alpha-1(XXII) chain	9.01	6.3	11.67	9.21	within
e210893	NGAESKNYEE	none	Nuclear GTPase SLIP-GC	7.85	4.4	12.93	8.69	within
e005441	PAEPEEPADW	none	Obscurin	11.3	7.67	12.99	12.49	within
e005443	NRGDSTFESK	none	Fibrinogen alpha chain	11.2	6.72	12.99	12.4	within
e005444	SPGSPHSGVQTS	none	Protein aurora borealis	7.76	4.72	12.3	8.56	within
e005465	PSGNDGSAGPPGP*	2xOxidation [P10; P11]	Collagen alpha-1(VII) chain	14.49	11.84	15.83	15.25	within
e005467	KGEPGEAGNPGP*	2xOxidation [P4; P10]	Collagen alpha-1(XI) chain	10.7	7.14	13.0	11.83	within
e200796	VGQPGAAGADGEP*	1xOxidation [P4]	Collagen alpha-2(XI) chain	14.35	10.22	15.76	15.32	within
e005471	TQVKESLSSY	none	Apolipoprotein C-II	9.31	6.83	12.23	8.33	within
e101656	KGAMGEPGPPGP*	3xOxidation [P7; P9; P10]	Collagen alpha-3(IV) chain	11.03	6.44	13.0	12.54	within
e097151	GPPGPPGPPGPPS*	2xOxidation [P5; P]	Collagen alpha-1(XVIII) chain	10.25	5.92	12.8	11.43	within
e005503	KGSEGPTGPQGL*	1xOxidation [P6]	Collagen alpha-1(XXVIII) chain	10.28	7.35	12.26	9.7	within
e105855	SPGLASGSVGQSP	none	Scavenger receptor class F member 1	10.54	7.06	12.73	12.47	within
e105075	SINQENG TANP	none	BMP-2-inducible protein kinase	7.96	4.28	10.85	8.17	within
e005511	GPPGEPGPPGPPG*	2xOxidation [P11; P]	Collagen alpha-2(V) chain	11.42	6.58	14.06	13.05	within
e005512	SGLKGEPGETGP*	1xOxidation [P]	Collagen alpha-1(VII) chain	11.52	6.94	14.0	13.05	within
e200809	GDPGPPGPPGPPG*	3xOxidation [P5; P9; P12]	Collagen alpha-1(XV) chain	7.77	4.46	11.99	8.19	within
e005579	PGNPGAPGSPGPAG*	1xOxidation [P4]	Collagen alpha-1(III) chain	10.14	6.44	12.75	11.75	within
e005593	GPPGPPGPAGKEG*	2xOxidation [P3; P5]	Collagen alpha-1(I) chain	9.71	7.02	13.12	9.77	within
e104788	GSSDAWEASDQ	none	Protein FAM131B	8.52	4.89	12.45	8.48	within
e005651	PPGPDGNKGEPPG*	2xOxidation [P4; P11]	Collagen alpha-2(I) chain	11.92	8.04	13.85	10.57	within
e102085	DENSMEDDAE	none	Sal-like protein 3	10.84	6.59	13.78	14.87	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e005667	MHESSQLEGH	none	S-adenosylmethionine sensor upstream of mTORC1	11.3	8.02	13.63	11.33	within
e105142	GNGAAGGGGPPASEG	none	Striatin-3	10.66	7.75	12.35	12.37	up
e005691	GPPGEAGKPGEQ*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	12.01	8.75	13.27	12.61	within
e105832	KSSDPTGRNHG	none	TOG array regulator of axonemal microtubules protein 1	9.44	6.33	12.04	12.63	up
e005698	SPGGENSPGGGGSP	none	Protein kintoun	10.92	7.41	12.71	12.24	within
e005699	QGLPGAPGDQQQ*	2xOxidation [P4; P7]	Collagen alpha-1(IX) chain	11.02	7.0	12.48	12.23	within
e005712	QGPPGFEGAPGQ*	1xOxidation [P3]	Collagen alpha-6(IV) chain	10.23	7.31	12.78	10.13	within
e210933	GPPGPPGPPGPPS*	3xOxidation [P5; P6; P8]	Collagen alpha-1(XVIII) chain	13.2	9.52	15.49	14.31	within
e210934	VNVDEVGGEALG	none	Hemoglobin subunit beta	13.2	9.69	15.39	14.31	within
e005719	LRREGDHEF	none	Alpha-1B-glycoprotein	5.95	2.72	10.95	5.38	within
e005752	KNGDDGEAGKPG*	1xOxidation [P11]	Collagen alpha-1(I) chain	6.6	3.49	11.59	6.88	within
e005756	SVPGPPGPPGPPG*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XVIII) chain	10.5	6.44	13.07	10.92	within
e207757	KIVLDPSGSMN	none	Complement factor B	11.8	7.42	15.52	8.76	within
e005767	SGSVIDQSRVL	none	Uromodulin	12.3	7.76	15.67	8.76	within
e005794	QEEPPGSQGPH	none	TRIO and F-actin-binding protein	7.35	3.6	10.26	10.2	within
e104649	GMPGPPGPPGPPG*	3xOxidation [P8; P9; P11]	Collagen alpha-1(XVIII) chain	9.7	5.6	12.65	12.47	within
e005795	VNALSNSTTAGQ	none	Aquaporin-2	6.98	3.24	9.41	8.1	within
e005803	AGGINGHADSPAP	none	DNA replication licensing factor MCM6	11.04	7.64	12.78	11.62	within
e200872	SFSKDWSFY	none	Beta-2-microglobulin	7.5	3.95	11.65	9.6	within
e005870	GGKGEGQPPGPPG*	2xOxidation [P9; P11]	Collagen alpha-2(I) chain	8.22	4.38	11.71	9.6	within
e005896	VGPQGEPPGPPGQ*	3xOxidation [P3; P7; P9]	Collagen alpha-1(V) chain	8.17	5.04	10.7	8.62	within
e210965	DEGPGHHHKPG	none	Protein S100-A9	8.95	4.32	12.1	10.24	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e005901	DHEGTHSTKR	none	Fibrinogen alpha chain	8.35	4.36	12.08	9.78	within
e005918	NPFPKERALP	none	B-cell lymphoma 6 protein	8.09	5.39	10.17	10.26	up
e102985	TAAHGDTAQDSP	none	FYVE, RhoGEF and PH domain-containing protein 3	6.93	2.96	12.55	5.66	within
e106215	PGAKGEPGDAGAK*	1xOxidation [P7]	Collagen alpha-1(I) chain	9.26	5.4	11.35	12.14	up
e005992	DGAKGDAGAPGAPG*	2xOxidation [P10; P13]	Collagen alpha-1(I) chain	8.47	4.9	10.77	10.22	within
e006011	SLGTKADTHDE	none	Alpha-1-antitrypsin	7.94	5.83	10.41	8.61	within
e102920	GPPGPPGPPGPPS*	4xOxidation [P5; P6; P8; P9]	Collagen alpha-1(XVIII) chain	10.13	5.68	13.13	12.04	within
e105308	SPGSPGSAGTAAES	none	Astrotactin-2	8.77	5.49	11.07	9.59	within
e210984	GPPGPPGPPGEQG*	2xOxidation [P3; P5]	Collagen alpha-3(V) chain	10.54	7.32	13.68	12.66	within
e210989	GPPGPPGPPQAV*	3xOxidation [P5; P6; P]	Collagen alpha-1(X) chain	10.91	7.69	13.25	12.66	within
e210987	PGPPGRAGPPGSP*	2xOxidation [P3; P4]	Collagen alpha-1(XVIII) chain	10.89	7.57	13.82	12.66	within
e006103	DTDDDEEEDPD	none	Centrosomal protein of 170 kDa protein B	10.54	7.19	12.78	12.95	up
e200914	QDGRPGPPGPPG*	3xOxidation [P7; P8; P10]	Collagen alpha-1(I) chain	10.72	7.28	12.52	9.78	within
e006108	PGPDGKTGPPGPA*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	10.22	7.29	12.56	9.36	within
e211002	SGPGSTGSWNSGS	none	Fibrinogen alpha chain	10.01	5.74	13.54	8.03	within
e211003	GPPGEPGDPGPMG*	1xOxidation [P3]	Collagen alpha-2(V) chain	10.14	6.09	13.61	8.01	within
e103380	GPPGPPGSSNQG*	2xOxidation [P3; P5]	Collagen alpha-6(IV) chain	10.42	6.23	13.59	8.15	within
e211006	PGDRGEPGPPGP*	3xOxidation [P1; P7; P9]	Collagen alpha-1(I) chain	12.66	9.21	13.91	12.67	within
e094244	PPGQQGNPQPQG*	3xOxidation [P2; P8; P10]	Collagen alpha-1(XI) chain	12.32	8.06	14.28	13.7	within
e006148	GPPGEPGKAGEPG*	2xOxidation [P2; P3]	Collagen alpha-1(XXII) chain	11.62	8.08	13.31	11.89	within
e006149	TVPYFAEGSGGP	none	Arrestin domain-containing protein 1	7.0	4.8	9.62	9.06	within
e207773	WKGDVDQDGY	none	WD repeat- and FYVE domain-containing protein 4	10.08	6.15	13.99	10.82	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e006168	QGPSGAPGPQGPT*	2xOxidation [P7; P9]	Collagen alpha-1(II) chain	8.0	4.99	10.63	11.08	up
e006169	QGPQGPKGDPGP*	3xOxidation [P3; P6; P10]	Collagen alpha-1(III) chain	10.23	6.14	12.31	10.75	within
e207775	APGQRGEPGPQG*	2xOxidation [P2; P8]	Collagen alpha-1(III) chain	10.29	6.37	12.37	10.75	within
e006195	LDGGPAGYFLSS	none	Nuclear factor of activated T-cells, cytoplasmic 1	10.08	7.37	12.33	10.71	within
e211023	SDSPKQSPPE	none	WD repeat-containing protein 62	6.14	2.92	7.91	6.97	within
e006240	DDGEAGKPGRPG*	2xOxidation [P8; P11]	Collagen alpha-1(I) chain	12.68	9.98	14.21	13.05	within
e006242	STVKDKFSEF	none	Apolipoprotein C-III	8.59	5.49	13.14	8.43	within
e211033	GGPPGMTGFPGAAG*	1xOxidation [P3]	Collagen alpha-2(I) chain	9.57	6.8	11.61	10.54	within
e102356	LGSPSDPSFSPV	none	Probable E3 ubiquitin-protein ligase HERC1	11.81	8.19	13.61	14.1	up
e211040	TSNEWSSPTSP	none	Transcriptional enhancer factor TEF-3	11.73	8.17	13.85	12.82	within
e106509	GLPGADGPPGHPG*	4xOxidation [P3; P8; P9; P12]	Collagen alpha-1(XI) chain	11.71	8.24	13.86	12.82	within
e006370	PHFDLSHGSAQ	none	Hemoglobin subunit alpha	8.96	5.68	11.56	9.52	within
e006372	SPGPDGKTGPPGP*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	14.46	12.17	15.24	14.12	within
e006374	EAGPTGARGPEGP	none	Collagen alpha-2(V) chain	14.45	12.38	15.24	14.12	within
e211057	PGADSVSMQAFS	none	RNA-binding protein 10	6.5	3.33	9.03	7.0	within
e211058	SISRDYNLND	none	Alpha-1-antichymotrypsin	12.25	7.72	14.18	10.94	within
e211059	QGQRGETGPPGP*	1xOxidation [P10]	Collagen alpha-2(V) chain	9.18	6.18	11.83	10.95	within
e211064	DDDEDDDDDD	none	Nucleolin	17.75	14.34	19.27	18.87	within
e207783	GSDDDDNDDDD	none	DmX-like protein 1	17.74	14.4	19.27	18.86	within
e207784	GSAAREEDEHP	none	Ankyrin repeat and SAM domain-containing protein 1A	11.19	7.86	13.18	12.2	within
e094258	SRPGSPGPPGSPG*	3xOxidation [P6; P8; P9]	Collagen alpha-1(XIV) chain	9.72	6.52	13.28	9.65	within
e006436	GSPGTSENHPDT	none	Chondroitin sulfate proteoglycan 5	13.12	10.4	14.44	13.83	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211071	SHLNPYSHDE	none	Membrane-associated phosphatidylinositol transfer protein 3	13.05	7.68	14.47	13.88	within
e006437	KGEPGPTGAPGQA*	2xOxidation [P4; P6]	Collagen alpha-1(VII) chain	9.52	5.59	13.82	9.09	within
e006441	VAPDHKYGSPQ	none	Glutamate receptor ionotropic, delta-2	5.58	2.14	11.12	6.45	within
e211077	GLPGSPGFPGPQG*	2xOxidation [P3; P6]	Collagen alpha-1(IV) chain	9.87	7.0	12.91	11.39	within
e094259	IPGEKGPA GERG*	2xOxidation [P2; P7]	Collagen alpha-1(III) chain	8.26	5.43	12.56	7.12	within
e006464	STAPPTFPALTP	none	Histone-lysine N-methyltransferase PRDM16	7.07	4.93	10.8	9.39	within
e006474	ETSVYEEGSSL	none	Protein Shroom4	7.74	3.95	10.53	9.06	within
e006473	LSSSPEPAYYS	none	Fibrous sheath-interacting protein 2	9.39	5.76	11.51	6.53	within
e006477	NFNSMFAIISG	none	Rap guanine nucleotide exchange factor 6	7.89	4.05	10.47	6.53	within
e006481	LFANSQDIRH	none	Pro-epidermal growth factor	11.4	7.61	13.21	13.29	up
e106777	KGDAGAPGAPGSQG*	2xOxidation [P7; P10]	Collagen alpha-1(I) chain	16.1	13.82	17.49	16.54	within
e211088	KGEQGFMGPPGP	none	Collagen alpha-1(IV) chain	16.13	13.81	17.53	16.47	within
e006525	GTVGAGGEDAGPSQ	none	Regulator of telomere elongation helicase 1	15.18	12.03	16.64	15.54	within
e006552	FPPSDEQLKSG	none	Immunoglobulin kappa constant	8.16	5.54	11.74	12.06	up
e211096	PSLLNVASYLQ	none	ATPase family AAA domain-containing protein 5	7.84	4.52	11.02	11.08	up
e006603	HAKATEHLSTL	none	Apolipoprotein A-I	7.43	4.32	11.07	5.7	within
e211112	PGQQGVAGERGH*	1xOxidation [P1]	Collagen alpha-1(XXVII) chain	8.67	4.55	13.07	11.18	within
e211117	YVGDEAQSKRG	none	Actin, gamma-enteric smooth muscle	8.18	4.81	12.51	10.22	within
e211125	PGPTGEPGSPGPP*	4xOxidation [P3; P7; P9; P12]	Collagen alpha-1(V) chain	11.69	7.04	13.62	11.9	within
e006665	DGPAGAPGTPGPQG*	2xOxidation [P7; P10]	Collagen alpha-1(I) chain	8.8	4.9	11.64	9.37	within
e094268	GPPGPPGPPGYPG*	4xOxidation [P3; P5; P6; P8]	Collagen alpha-2(IX) chain	11.88	8.61	13.76	11.9	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e006667	SGSTPLFSSSSPG	none	Teneurin-2	6.07	3.22	9.93	9.67	within
e006675	GKAGERGVPGPPG*	2xOxidation [P9; P11]	Collagen alpha-1(I) chain	8.81	4.35	14.9	6.46	within
e006687	SPGPTGENGPPGP*	3xOxidation [P4; P10; P11]	Collagen alpha-2(XI) chain	11.28	8.45	13.35	12.26	within
e100310	PGPDGAPGERGGP*	3xOxidation [P3; P7; P13]	Collagen alpha-1(VI) chain	10.7	6.81	12.59	12.78	up
e211130	SPGPDGKTGPPGP*	3xOxidation [P4; P10; P11]	Collagen alpha-1(I) chain	11.27	8.7	13.35	12.31	within
e211131	PGSTGSRGPPGPP*	3xOxidation [P9; P10; P12]	Collagen alpha-1(XII) chain	11.19	8.4	13.28	12.31	within
e006709	GPPGEAGKPGEQG*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	11.18	7.46	13.24	13.04	within
e006711	SMLAVTFSGGDK	none	Proprotein convertase subtilisin/kexin type 7	10.6	6.87	12.97	8.54	within
e006741	KEAAGAGAGPGGDVG	none	Forkhead box protein D3	8.83	4.98	11.11	11.24	up
e006774	KGDAGNPGDPGTP*	2xOxidation [P10; P13]	Collagen alpha-1(XVI) chain	8.23	4.78	10.52	9.48	within
e006777	PAGFPGAPGQNGE*	1xOxidation [P5]	Collagen alpha-1(III) chain	8.61	5.18	12.93	10.43	within
e006776	FPHFDLSHGSA	none	Hemoglobin subunit alpha	8.33	4.8	10.53	9.45	within
e006781	TPGAGVPSSGRDGG	none	Endothelial cell-specific chemotaxis regulator	7.14	1.34	9.63	3.19	within
e211157	PPYAGSGAGTDPA	none	Sterol regulatory element-binding protein 1	13.93	11.29	15.34	14.43	within
e006835	GEKGDSPSGAAGP*	2xOxidation [P8; P14]	Collagen alpha-3(V) chain	12.97	9.9	14.47	13.47	within
e101812	PGLPGMPGHGAP*	1xOxidation [P4]	Collagen alpha-5(IV) chain	14.42	9.75	16.48	15.61	within
e006853	PGENGVPVPGPP*	3xOxidation [P6; P9; P10]	Collagen alpha-1(XXII) chain	13.29	9.29	15.94	11.35	within
e211170	GQDGRPGPPGPPG*	2xOxidation [P9; P11]	Collagen alpha-1(I) chain	7.85	4.74	12.03	11.06	within
e211172	QGGAPGPPGLPGA*	3xOxidation [P5; P7; P8]	Collagen alpha-2(VIII) chain	8.09	5.14	12.92	9.79	within
e097197	PGDQGEPSGPP*	2xOxidation [P1; P7]	Collagen alpha-4(IV) chain	9.53	7.14	11.64	7.25	within
e094280	PGSRGDTGPPGPP*	2xOxidation [P10; P12]	Collagen alpha-1(IV) chain	9.56	6.97	11.61	10.45	within
e211181	PGPAGPAGPPGYGP*	2xOxidation [P6; P]	Collagen alpha-3(IV) chain	3.19	0.31	11.05	4.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e006908	TEIPEAQIHEG	none	Alpha-1-antitrypsin	9.09	6.51	11.22	10.45	within
e006920	GPGGDKGDTGPPGP*	1xOxidation [P12]	Collagen alpha-1(III) chain	9.28	5.37	11.79	11.66	within
e006925	DHEGTHSTKRG	none	Fibrinogen alpha chain	9.33	5.9	14.42	9.63	within
e006946	PGPSGADGEPGPR*	2xOxidation [P3; P10]	Collagen alpha-1(V) chain	8.31	5.92	10.61	9.8	within
e006947	TPAPPGVDTPPP*	5xOxidation [P2; P4; P5; P10; P11]	Collagen alpha-3(VI) chain	9.92	7.25	12.2	11.26	within
e006951	IQGTGSWGPEPP	none	Sentrin-specific protease 3	9.47	7.1	11.83	11.29	within
e006950	LDSAETTLFQ	none	Collagen alpha-3(VI) chain	8.04	4.76	10.61	9.8	within
e006958	GPPGKDGPNGPPG*	5xOxidation [P2; P3; P8; P11; P12]	Collagen alpha-1(XXII) chain	11.49	8.43	12.77	12.32	within
e211187	PAGDGEAGPQAE	none	Lethal(3)malignant brain tumor-like protein 1	7.23	4.13	10.6	7.39	within
e211188	PGLPGMPGSDGPP*	3xOxidation [P1; P4; M/P]	Collagen alpha-2(XI) chain	11.51	8.47	12.78	12.32	within
e211190	SPGPGGSNTAPSTP	none	Extended synaptotagmin-2	6.95	1.94	10.27	7.71	within
e201053	GQPGAKGEPGDAGA*	1xOxidation [P9]	Collagen alpha-1(I) chain	9.84	7.33	11.86	11.81	within
e211193	PAGSPGERGAAGSGG	none	Collagen alpha-2(XI) chain	11.72	7.56	13.9	10.13	within
e211195	GPPGPGSDQGASGP*	3xOxidation [P2; P3; P5]	Collagen alpha-1(II) chain	7.93	5.59	10.4	10.06	within
e211198	PGADGQPGAKGANG*	2xOxidation [P1; P7]	Collagen alpha-1(I) chain	8.12	5.29	10.97	10.08	within
e211199	PQGHQGPAGPPGP*	2xOxidation [P10; P11]	Collagen alpha-2(I) chain	10.78	6.81	12.96	8.78	within
e006992	FDTASTGKTFRG	none	Fibrinogen alpha chain	7.82	5.15	12.84	9.63	within
e007008	DAGAPGAPGGKGDAG*	2xOxidation [P5; P8]	Collagen alpha-1(III) chain	8.4	5.9	10.33	7.79	within
e007011	DDPRPPNPPKP	none	CD99 antigen	8.13	6.19	10.84	2.58	down
e007019	PSAGEQGGGEAGAAE	none	Transforming acidic coiled-coil-containing protein 2	8.38	5.13	10.26	8.01	within
e007020	DGQPGAKGEPGDA*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	7.73	4.04	10.3	9.3	within
e007034	WGKVGAHAGEYG	none	Hemoglobin subunit alpha	10.53	5.21	14.04	14.62	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e007047	GDTEEAQKQIN	none	Alpha-1-antitrypsin	9.17	5.57	12.81	11.11	within
e007069	MSGESGQPEAGPS	none	RPA-related protein RADX	11.76	7.67	13.95	9.34	within
e007073	NGNPGPPGPPGPSG*	2xOxidation [P7; P]	Collagen alpha-1(II) chain	10.55	7.15	12.76	11.63	within
e105022	PPGRDQGPQHGK*	2xOxidation [P2; P8]	Collagen alpha-2(I) chain	6.64	3.29	9.21	9.43	up
e007091	APGDRGEPGPPGP*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	13.11	10.77	14.2	12.27	within
e007094	VEVGEAGQGKDF	none	Basement membrane-specific heparan sulfate proteoglycan core protein	13.01	10.68	14.14	12.27	within
e007106	DEDDPDEGDDD	none	Scm-like with four MBT domains protein 1	12.48	8.43	14.34	14.6	up
e099711	QPGFDTMQSP	none	Protein phosphatase EYA4	8.49	4.77	10.94	7.57	within
e007115	GQDGRPGPPGPPG*	3xOxidation [P8; P9; P]	Collagen alpha-1(I) chain	14.68	12.41	15.96	14.93	within
e097208	GSPGPDGKTGPPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	14.66	12.37	15.95	14.93	within
e211226	GPPGSTGSRGPPGP*	1xOxidation [P12]	Collagen alpha-1(XII) chain	14.56	11.96	15.93	14.93	within
e211227	QQQDGAAGPPGPPG*	2xOxidation [P10; P12]	Collagen alpha-1(XXIII) chain	13.73	10.47	15.15	14.36	within
e007141	GGGLGSVPGGSHAGGA	none	Keratin, type I cytoskeletal 28	13.72	10.3	15.13	14.37	within
e007144	KTMYSVPNGKI	none	Unconventional myosin-IXb	8.18	5.21	11.58	6.25	within
e007149	PSGNDGSAGPPGPP*	2xOxidation [P11; P13]	Collagen alpha-1(VII) chain	12.09	7.13	13.79	13.39	within
e007150	TSTSLESASPG	none	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	12.48	8.82	13.89	13.3	within
e007152	TTTTVATGSMATP	none	Mucin-5B	12.47	8.86	13.85	13.39	within
e211232	GPPGDPGSPGSPGP*	4xOxidation [P3; P6; P9; P12]	Collagen alpha-3(IV) chain	10.56	6.79	12.99	11.73	within
e007175	PGTPGSPGPAGASGN*	1xOxidation [P1]	Collagen alpha-1(II) chain	11.21	7.4	12.92	11.65	within
e211233	GGGPGAGAPAGTGGGAAG	none	Doublesex- and mab-3-related transcription factor A2	12.51	9.49	14.22	11.94	within
e007192	KDGQDGAPGEGGP*	1xOxidation [P11]	Collagen alpha-3(IX) chain	9.33	5.03	11.77	8.69	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211242	GPGGDKGDTGPPGP*	2xOxidation [P2; P11]	Collagen alpha-1(III) chain	9.34	5.51	11.57	10.56	within
e211243	PGPKGETGPAGPAG*	3xOxidation [P1; P3; P9]	Collagen alpha-1(X) chain	9.21	5.47	11.67	9.96	within
e007209	APGEDGRPGPPGS*	3xOxidation [P2; P8; P10]	Collagen alpha-2(V) chain	10.82	7.22	12.34	10.88	within
e207812	GPPGPDGNKGEPG*	4xOxidation [P2; P3; P5; P12]	Collagen alpha-2(I) chain	10.01	6.62	11.93	11.7	within
e007218	GAGGGAGGAAGAEGGPE	none	Intercellular adhesion molecule 5	10.32	6.65	11.88	11.74	within
e007219	APGDKGESGPSGPA*	1xOxidation [P2]	Collagen alpha-1(I) chain	10.03	6.34	12.09	11.7	within
e007229	SPDPRWQSSSP	none	Integrator complex subunit 1	6.34	4.16	8.9	7.09	within
e211247	SGEKGERGAAGEP	none	Collagen alpha-1(XVII) chain	6.27	2.68	12.27	1.49	down
e099054	DHEGTHSTKRG*	1xCation:Na [E3]	Fibrinogen alpha chain	6.91	3.41	11.12	10.67	within
e007270	EGSPGRDGSPGAK*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	8.99	5.46	11.63	11.51	within
e007302	MSLTLGKNMPR	none	Inositol 1,4,5-triphosphate receptor associated 1	8.15	3.47	12.24	9.36	within
e007309	SGGSSEPSPTVD	none	F-box only protein 38	13.56	10.68	15.2	15.08	within
e094301	DKGETGEQGDRG	none	Collagen alpha-1(I) chain	13.57	10.57	15.2	15.08	within
e007365	YDQGYGNYNNA	none	Heterogeneous nuclear ribonucleoprotein D-like	6.53	4.18	8.74	6.17	within
e211266	APGDRGEPGPPGP*	3xOxidation [P2; P8; P10]	Collagen alpha-1(I) chain	18.34	16.82	18.83	18.16	within
e211267	RGDPGPSGPPGPP*	4xOxidation [P4; P6; P9; P10]	Collagen alpha-1(V) chain	18.32	16.81	18.82	18.13	within
e211268	PEKGGRGQPGPVG*	1xOxidation [P9]	Collagen alpha-2(IV) chain	10.27	6.92	12.44	11.37	within
e007393	EGAEPGPSGSGPGP	none	B box and SPRY domain-containing protein	6.31	3.21	10.63	5.15	within
e007397	QGEKEAGPPGPP*	2xOxidation [P10; P]	Collagen alpha-1(IV) chain	17.28	14.76	17.74	17.2	within
e211271	GSPGPDGKTGPPGP*	2xOxidation [P5; P11]	Collagen alpha-1(I) chain	17.31	15.68	17.77	17.23	within
e007404	DGVPGKDGRGPT	none	Collagen alpha-1(III) chain	11.35	6.35	12.95	7.63	within
e211276	SLASDFGKDDSL	none	Suppressor of cytokine signaling 6	8.86	5.45	10.88	1.43	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e007440	RFKDLGEENF	none	Albumin	8.45	4.35	11.5	7.07	within
e007451	HDTRPETRED	none	SH3 and multiple ankyrin repeat domains protein 3	8.58	5.97	11.29	10.64	within
e300875	EDGPAGEPGPPGP*	5xOxidation [P4; P8; P10; P11; P13]	Collagen alpha-1(XV) chain	6.92	3.45	12.14	5.12	within
e100937	RGPQGPTGSEGTP*	1xOxidation [P13]	Collagen alpha-3(V) chain	11.76	8.12	13.84	11.3	within
e007494	DAGAPGAGSQGAPG*	3xOxidation [P5; P8; P14]	Collagen alpha-1(I) chain	8.11	5.52	10.47	10.15	within
e007491	ETGDVQMGPPGP*	1xOxidation [P]	Collagen alpha-1(V) chain	9.91	6.84	12.13	9.32	within
e007495	DGGGSHRKEGEE	none	CD99 antigen	10.09	5.56	12.26	9.25	within
e201151	PGEPGPPGPPGPPG*	3xOxidation [P7; P10; P13]	Collagen alpha-2(V) chain	8.55	6.42	12.47	10.15	within
e007501	TDDSN DYGENE	none	Zinc finger protein 652	15.28	12.39	16.97	16.23	within
e102659	EFTPTEKDEY	none	Beta-2-microglobulin	9.42	5.84	12.78	8.08	within
e007514	DTGPAGPPGPPGAPA	none	Collagen alpha-3(V) chain	10.13	7.05	13.92	9.84	within
e007516	SPVTGRRSQSSP	none	Nik-related protein kinase	8.88	5.41	15.68	8.39	within
e211295	SPAAAAGDSPALMT	none	Stromal interaction molecule 2	8.85	6.06	10.93	11.35	up
e007543	KDDSPQLSEEL	none	Zinc finger protein 462	6.04	2.42	9.86	10.24	up
e007572	SGNPPLSSTSTLT	none	Cadherin-8	7.05	4.22	10.95	8.95	within
e007591	SPSGGGGSGGGSGSGTP	none	Dual specificity mitogen-activated protein kinase kinase 4	6.56	3.23	12.77	7.86	within
e094310	DGSPGAKGDRGET*	1xOxidation [P4]	Collagen alpha-1(I) chain	10.34	6.47	13.15	12.37	within
e007596	PEDEEEKKKM	none	Heat shock protein HSP 90-beta	6.75	3.05	10.35	5.7	within
e207825	VEHSDLSFSKD	none	Beta-2-microglobulin	11.22	7.89	13.41	11.73	within
e007623	HYSNGDESSDPG	none	Transmembrane prolyl 4-hydroxylase	7.64	4.63	11.45	5.38	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e007626	SGGGGSGSGTGGGDAAL	none	Ankyrin repeat and KH domain-containing protein 1	12.94	10.27	14.26	13.63	within
e007630	NRGSGAAGSSQTGD	none	Transcription factor 4	9.36	5.88	11.66	10.43	within
e207827	KEEEDKDDKE	none	Putative heat shock protein HSP 90-beta 4	12.89	10.2	14.23	13.63	within
e211310	EPPEPPQEAAEA	none	Palmitoyltransferase ZDHHC9	12.68	8.64	14.13	13.69	within
e007652	SPGPDGKTGPPGPA*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	15.32	12.86	16.93	15.29	within
e100759	PGPDGLPGSMGPPG*	2xOxidation [P7; P12]	Collagen alpha-1(IV) chain	10.01	6.88	11.96	10.41	within
e007666	AHHFGKEFTPP	none	Hemoglobin subunit beta	6.96	4.06	11.34	7.87	within
e211316	ETDESSVPELY	none	Fibronectin type-III domain-containing protein 3A	9.89	6.18	11.92	10.18	within
e007679	VAHVDDMPNALS	none	Hemoglobin subunit alpha	11.99	8.99	13.86	12.19	within
e207828	RNSSASYGDDPT	none	Protein diaphanous homolog 1	11.76	8.18	13.5	12.13	within
e007701	SPGERGETGPPGP*	2xOxidation [P2; P10]	Collagen alpha-1(III) chain	15.41	14.07	16.83	15.16	within
e211327	PGSAGPGGGGEEDSP	none	Doublesex- and mab-3-related transcription factor A2	10.66	6.42	12.62	11.58	within
e007731	DGQPGAKGEPGDAG*	1xOxidation [P10]	Collagen alpha-1(I) chain	11.19	8.02	12.84	10.66	within
e099055	APGDRGEPGPPGP*	1xCation:Na [C-Term]; 3xOxidation [P2; P8; P10]; 1xCation:Na [E7]	Collagen alpha-1(I) chain	14.28	9.67	16.4	12.25	within
e007778	PPGWEVGVYAAGA	none	Synaptotagmin-12	7.14	4.1	9.98	5.99	within
e007781	VVDPKSKEEDK	none	Osteopontin	6.79	3.89	10.29	7.7	within
e007792	HSAELPPPDQPS	none	Neuronal acetylcholine receptor subunit alpha-4	6.15	2.66	9.09	2.38	down
e201207	EAEDLSDSTPTL	none	Obscurin	8.31	6.07	10.95	7.18	within
e007836	ASATATDAVSSEAP	none	Nck-associated protein 5	8.25	5.93	10.6	7.18	within
e007845	QADSGSSEEKQL	none	Osteopontin	6.6	3.47	13.74	6.04	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e007869	PSRGIPSSPGAHT*	1xOxidation [P1]	Collagen alpha-1(XVIII) chain	7.5	4.66	12.09	10.84	within
e007879	IINSSDEDDVSS	none	FYVE, RhoGEF and PH domain-containing protein 6	8.3	4.65	11.57	8.89	within
e007884	APGAPGHGPPGPVG*	1xOxidation [P]	Collagen alpha-1(III) chain	9.08	4.2	12.89	12.47	within
e007899	TNTKESSSHHPG	none	Fibrinogen alpha chain	7.91	4.89	10.76	4.23	down
e007904	SPSGEVSHPRKT	none	Alpha-2-HS-glycoprotein	8.32	5.6	11.93	7.31	within
e007906	DNESLGGFSIED	none	PHD finger protein 6	8.48	4.03	11.17	10.62	within
e007907	GYHFSWTNDR	none	Carboxypeptidase A6	6.52	3.11	9.79	9.84	up
e007910	AGGDGEPRGQQG	none	Collagen alpha-1(XI) chain	10.18	5.26	12.41	11.42	within
e007913	QESQPVSGGPEAP	none	Sodium channel protein type 5 subunit alpha	9.76	5.28	12.37	11.24	within
e201227	KGYENGNFVGPT	none	Methylmalonate-semialdehyde/malonate-semialdehyde dehydrogenase [acylating], mitochondrial	7.05	3.49	10.82	8.17	within
e007914	APGKNGERGGPGGP*	2xOxidation [P2; P11]	Collagen alpha-1(III) chain	9.27	5.49	11.65	9.44	within
e211360	TNDYRVSGGVSE	none	Receptor-type tyrosine-protein phosphatase zeta	10.8	6.71	13.52	13.99	up
e007935	DDDEDDDDTDD	none	DDB1- and CUL4-associated factor 1	12.29	8.89	14.13	14.69	up
e007942	GSPGPTGENGPPGP*	4xOxidation [P3; P5; P11; P12]	Collagen alpha-2(XI) chain	9.87	4.83	12.36	11.6	within
e007969	SPGERGETGPPGP*	3xOxidation [P2; P10; P11]	Collagen alpha-1(III) chain	10.92	7.93	12.63	12.51	within
e007989	NDGAKGDAGAPGAPG*	2xOxidation [P11; P14]	Collagen alpha-1(I) chain	9.23	6.3	11.43	11.72	up
e211370	VNGMQNQDPVGQ	none	Transcriptional activator GLI3	6.97	3.79	11.5	8.17	within
e007997	ELAGNAARDNKK	none	Histone H2A type 1-D	7.91	3.13	12.97	7.31	within
e008005	DGQPGAKGEPGDAG*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	11.6	7.88	13.06	11.6	within
e008022	EPGEHLFPEHP	none	Zinc finger CCCH domain-containing protein 4	11.74	7.69	13.69	14.04	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e008029	LGPHAGDVEGHLS	none	Apolipoprotein A-IV	11.67	7.41	13.73	14.08	up
e008030	GGTLGPPSPPGAPSP	none	E3 ubiquitin-protein ligase RING1	10.81	6.03	13.27	10.9	within
e104231	SPEAQDPDGESEA	none	Zinc finger protein 785	15.51	11.82	17.71	12.0	within
e211385	TGSGPESSQTLPP*	2xOxidation [P5; P12]	Collagen alpha-1(VII) chain	7.57	5.1	10.4	6.5	within
e104161	TAGSGKASEAEAPD	none	CDKN2A-interacting protein	7.98	4.12	10.89	10.96	up
e008119	TSSGVSEESSTSH	none	Mucin-12	10.27	5.24	12.34	11.57	within
e008120	PGDPGSPGSPGAPG*	3xOxidation [P7; P10; P12]	Collagen alpha-3(IV) chain	10.28	6.38	12.43	11.75	within
e008122	GSNGNPGPPGSPGSP*	1xOxidation [P9]	Collagen alpha-1(III) chain	10.24	6.11	12.44	11.73	within
e211394	ADHEGTHSTKRG	none	Fibrinogen alpha chain	8.41	3.98	10.52	9.51	within
e211396	SDSGSSQHLEHI	none	Partner and localizer of BRCA2	8.86	5.28	11.0	9.21	within
e008197	PGGGGAGDQDSEPPG	none	Trafficking protein particle complex subunit 14	12.03	8.65	13.94	11.07	within
e008203	PGEQGPSGASGPAGP*	2xOxidation [P12; P15]	Collagen alpha-1(I) chain	12.2	8.7	13.95	10.79	within
e207844	DPGGAGASSGPGAPAE	none	Multiple epidermal growth factor-like domains protein 8	8.87	5.87	11.25	6.04	within
e008201	NEQNDFFPSVT	none	Ral GTPase-activating protein subunit beta	9.73	6.06	12.28	11.53	within
e201285	VSMGSMQPLHPGG	none	Protein polybromo-1	10.17	6.11	12.66	13.05	up
e008209	RGAPGEKGEGGPPG*	2xOxidation [P4; P12]	Collagen alpha-1(III) chain	9.01	5.59	11.87	9.14	within
e008210	DINYEETLSTL	none	Kinesin-like protein KIF1C	10.13	7.16	12.24	10.54	within
e008212	PVGPSGKDGANGIP*	2xOxidation [P4; P14]	Collagen alpha-1(II) chain	7.76	5.47	9.79	7.74	within
e008218	SPGSPGPDGKTGPP*	3xOxidation [P2; P5; P7]	Collagen alpha-1(I) chain	13.7	9.44	14.85	14.71	within
e211404	TYVPKEFNAET	none	Albumin	13.59	8.71	14.81	14.72	within
e008237	DDDDDDDTGMD	none	Nucleoprotein TPR	11.95	8.48	14.54	8.85	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211416	PEEPIDEDEDI	none	ATP-binding cassette sub-family A member 6	6.34	3.07	10.34	4.74	within
e008248	DGAPGKNGERGGPG*	2xOxidation [P4; P13]	Collagen alpha-1(III) chain	11.33	6.42	12.96	11.43	within
e008272	GEDGYPGGPGPPGP*	3xOxidation [P9; P11; P12]	Collagen alpha-4(IV) chain	9.15	6.69	11.5	9.8	within
e207846	NGDDGEAGKPGRP*	2xOxidation [P10; P13]	Collagen alpha-1(I) chain	10.61	6.89	12.78	12.06	within
e104817	VSGFHPSDIEVD	none	Beta-2-microglobulin	9.52	6.1	13.43	10.12	within
e008287	GSPAASDDGRRTL	none	Inter-alpha-trypsin inhibitor heavy chain H4	8.96	5.27	11.27	10.73	within
e097246	EGSPGRDGSPGAKG*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	8.76	5.99	11.15	7.22	within
e008301	EELTPPTTEAAP*	3xOxidation [P5; P7; P12]	Collagen alpha-1(V) chain	8.73	5.99	11.14	7.22	within
e201315	DELEDLPSPPPP	none	Gephyrin	10.05	6.2	12.79	13.12	up
e008332	FLGDQTINLPTS	none	Bridge-like lipid transfer protein family member 1	10.19	4.29	13.36	9.73	within
e008335	PFGDDGDEGLTSP	none	Inositol 1,4,5-trisphosphate-gated calcium channel ITPR2	10.26	6.65	13.58	7.23	within
e008337	APGDRGEPGPPGPA*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	8.71	4.52	12.26	7.1	within
e008338	LFNMNQLLANE	none	Beta-citrylglutamate synthase B	9.16	4.91	12.28	12.11	within
e211444	RQKLGPAGDVE	none	Apolipoprotein A-IV	6.0	2.53	11.92	7.1	within
e211446	EEEGASLGDGSGAE	none	Zinc finger and BTB domain-containing protein 10	13.16	7.85	15.33	3.55	down
e097248	GQDGRPGPPGPPGA*	3xOxidation [P8; P9; P11]	Collagen alpha-1(I) chain	12.51	7.89	14.32	12.87	within
e008356	DLRKESMATGSI	none	DNA replication licensing factor MCM2	7.94	4.87	10.23	8.06	within
e008371	ERGDAGDPGPPGAP*	1xOxidation [P11]	Collagen alpha-3(V) chain	11.96	7.6	13.71	12.1	within
e201332	VVENGESSQGRF	none	Uromodulin	11.31	7.32	13.28	12.1	within
e211454	ELQEGARQKLH	none	Apolipoprotein A-I	7.4	3.76	9.96	7.86	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211457	LPGTGGPPGENGKP*	2xOxidation [P2; P7]	Collagen alpha-1(III) chain	8.95	6.58	13.23	8.43	within
e201342	SPSGQEPAPSQEP	none	Regulator of G-protein signaling 3	8.88	5.59	11.08	8.09	within
e008423	EAIPMSIPPEVK	none	Alpha-1-antitrypsin	9.76	5.86	14.55	11.88	within
e097276	VIDQSRVLNLGP	none	Uromodulin	9.91	6.17	14.06	11.88	within
e104422	DEDDNDEDDDD	none	Transcription termination factor 4, mitochondrial	9.71	6.5	12.65	12.48	within
e008436	SPGGPGSDGKPGPPG*	3xOxidation [P5; P11; P13]	Collagen alpha-1(III) chain	10.79	7.98	12.58	8.64	within
e211462	PSGPPGDKGSPGSR*	1xOxidation [P1]	Collagen alpha-1(XXII) chain	9.5	6.93	11.85	8.17	within
e008443	VDPKSKEEDKH	none	Osteopontin	7.77	3.07	12.02	3.96	within
e211464	EAGGPEATGQAHST	none	BAH and coiled-coil domain-containing protein 1	9.77	6.52	12.09	8.1	within
e211465	PGSPGFPLQGPPG*	3xOxidation [P4; P7; P12]	Collagen alpha-5(IV) chain	9.21	6.35	12.04	8.13	within
e008502	KAEDSQFSESDA	none	Zinc finger protein 18	14.05	12.41	15.27	15.11	within
e100290	EVETVMSEVSGF	none	Bystin	9.2	4.56	12.07	8.03	within
e097278	VTDYGKDLMEK*	1xOxidation [M9]	Apolipoprotein A-II	11.88	8.37	13.62	12.34	within
e008518	EFTPAVHASLDK	none	Hemoglobin subunit alpha	11.77	8.05	13.47	12.34	within
e008539	SPGAKGDRGETGPA*	1xOxidation [P2]	Collagen alpha-1(I) chain	10.6	7.12	12.98	10.39	within
e008549	GKVGAHAGEYGAEA	none	Hemoglobin subunit alpha	9.06	5.54	11.73	8.48	within
e008575	YSNEKPFTGFE	none	Mannan-binding lectin serine protease 2	8.84	4.54	12.45	12.74	up
e300098	PGSRGSPGAPGPPGP*	2xOxidation [P10; P13]	Collagen alpha-3(IV) chain	9.53	5.8	11.69	10.93	within
e211481	ELNDTGSYFFQ	none	Interleukin-18 receptor 1	8.66	4.61	11.63	11.39	within
e008626	FAYYKAMAGSVL	none	Cytoplasmic FMR1-interacting protein 2	6.94	2.42	13.24	6.35	within
e103035	VTEEKDDAVTSAG	none	Biorientation of chromosomes in cell division protein 1-like 1	9.52	6.2	11.64	12.36	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e008638	APGDRGEPGPPGPA*	3xOxidation [P2; P8; P10]	Collagen alpha-1(I) chain	16.7	14.47	17.86	16.65	within
e201396	DEDDPDEGDDDS	none	Scm-like with four MBT domains protein 1	12.1	8.0	14.24	14.81	up
e008653	EAGVDGQVGPPGQP*	1xOxidation [P11]	Collagen alpha-1(XIII) chain	14.99	12.04	16.74	14.08	within
e008656	MIEQNTKSPLF*	1xOxidation [M1]	Alpha-1-antitrypsin	12.49	8.75	16.44	10.62	within
e008664	PGRDGEDGPTGPPG*	1xOxidation [P13]	Collagen alpha-2(I) chain	7.36	3.47	10.45	8.37	within
e211495	GPPGPPGTKGEPGE*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XXII) chain	5.76	2.51	11.14	6.11	within
e008666	SPGERGETGPPGPA*	1xOxidation [P11]	Collagen alpha-1(III) chain	14.15	11.57	15.32	14.49	within
e008692	RSQAQESNYEN	none	Sialic acid-binding Ig-like lectin 15	11.48	7.96	12.96	11.6	within
e008695	TGPGGDKGDTGPPGP*	1xOxidation [P13]	Collagen alpha-1(III) chain	12.65	9.62	14.17	12.77	within
e211503	PEPAPPSEAMDAD	none	Serine/threonine-protein phosphatase 1 regulatory subunit 10	11.58	8.21	13.13	12.22	within
e008706	KDENTISPYEM	none	E3 ubiquitin-protein ligase HECTD1	7.19	4.44	9.41	5.12	within
e008707	QKGDAGNPGDPGTP*	1xOxidation [P8]	Collagen alpha-1(XVI) chain	11.64	7.79	13.1	12.21	within
e102893	RGNDGATGAAGPPGP*	2xOxidation [P12; P13]	Collagen alpha-1(I) chain	12.19	8.82	13.37	12.5	within
e008726	NSGEGNTGAAESSF	none	Nucleoprotein TPR	10.54	7.45	12.59	12.65	up
e008729	SPGGPGSDGKPGPPG*	4xOxidation [P2; P5; P11; P13]	Collagen alpha-1(III) chain	13.11	10.7	14.18	14.01	within
e008731	YGGFTVQNEANK	none	Fibrinogen beta chain	12.36	8.68	13.87	12.57	within
e008739	VASGMGPSASSHGSP	none	Trinucleotide repeat-containing gene 18 protein	12.11	9.0	13.33	13.37	up
e008740	VPGGPGMRGMPGSP*	2xOxidation [P2; P5]	Collagen alpha-1(III) chain	8.88	5.44	10.88	10.45	within
e008753	CEEDEEFTCRA*	2xDisulfide bridge [C1; C9]	Plasminogen	10.06	6.97	14.0	12.18	within
e102497	RDGLPGPPGSPGPP*	2xOxidation [P5; P7]	Collagen alpha-1(IV) chain	6.5	3.91	13.57	5.81	within
e008807	TSNSSDTESNRH	none	Microtubule-associated serine/threonine-protein kinase 4	6.94	3.61	14.64	6.04	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e008862	GAPGPDGNNGAQQGP*	2xOxidation [P5; P14]	Collagen alpha-2(I) chain	10.34	6.51	12.62	11.02	within
e008863	PGAAGQDGPPGPMGP*	2xOxidation [P9; P10]	Collagen alpha-1(XI) chain	10.37	6.34	12.6	11.02	within
e099060	SPGAKGDRGETGPA*	1xCation:Na [C-Term]; 1xOxidation [P2]	Collagen alpha-1(I) chain	10.34	6.74	12.59	11.23	within
e008873	GPPGEPGPPGPPGPP*	2xOxidation [P11; P]	Collagen alpha-2(V) chain	9.91	5.48	12.68	11.12	within
e008878	EPPQSPWDRVK	none	Apolipoprotein A-I	7.36	3.28	14.39	6.72	within
e207875	IDEKGTEAAGAMF	none	Alpha-1-antitrypsin	8.31	5.63	12.72	8.12	within
e211525	SGERGPPGPMGPPG*	3xOxidation [P7; P9; P12]	Collagen alpha-1(I) chain	9.11	6.06	11.33	10.76	within
e008902	SPGERGETGPPGPA*	2xOxidation [P2; P10]	Collagen alpha-1(III) chain	9.11	5.75	11.44	10.75	within
e102299	GPAGKDGEAGAQQGP*	2xOxidation [P2; P14]	Collagen alpha-1(I) chain	7.37	3.85	10.36	6.78	within
e094371	TGPGGDKGDTGPPGP*	2xOxidation [P12; P13]	Collagen alpha-1(III) chain	10.39	7.11	12.21	11.37	within
e008947	FPHFDLSHGSAQ	none	Hemoglobin subunit alpha	9.65	4.79	14.75	13.45	within
e100071	SPGEAGRPEAGLP*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	8.81	5.65	11.67	10.47	within
e008949	GHPDTLNQGEFK	none	Protein S100-A9	8.65	4.21	14.59	12.82	within
e008956	MKVGEANPKLQK	none	Carbonic anhydrase 1	6.73	3.6	12.43	6.02	within
e211534	FPAAGGRGGSGGGPAA	none	Protein downstream neighbor of Son	7.7	4.55	14.75	10.62	within
e099061	APGDRGEPGPPGPA*	1xCation:Na [C-Term]; 3xOxidation [P2; P8; P10]; 1xCation:Na [E7]	Collagen alpha-1(I) chain	12.68	8.75	15.15	12.15	within
e211539	ISNHQNSNRYL	none	Serum amyloid A-4 protein	6.92	4.44	12.23	7.58	within
e099704	WEGADAGAAGGEAGGA	none	Serine/threonine-protein kinase LMTK3	11.27	6.65	13.61	7.6	within
e009021	KDPDAANSPIRY	none	Cadherin-11	6.43	2.82	10.97	4.98	within
e009032	NSMSYTSPYSPN	none	SLAIN motif-containing protein 2	7.05	4.59	10.28	8.07	within
e009035	HVTDHIHAGMET	none	Ceruloplasmin	7.73	4.34	10.52	8.12	within
e009065	DGPPGRDQGPGHK*	2xOxidation [P4; P10]	Collagen alpha-2(I) chain	8.92	5.06	11.65	4.42	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e009068	KPGRPGERGPPGP*	3xOxidation [P2; P5; P10]	Collagen alpha-1(I) chain	7.93	2.42	12.97	5.14	within
e009085	DINSQGEESMGNA	none	Retinoic acid-induced protein 2	9.27	6.39	11.59	11.86	up
e211565	SETDTDSEKDKP	none	Nuclear exosome regulator NRDE2	9.46	6.23	11.62	12.91	up
e009087	PAGAPGPQGFGNPG	none	Collagen alpha-1(II) chain	7.08	4.25	11.05	7.44	within
e009088	PPGEAGKPGEQGV*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	11.91	8.31	13.73	11.49	within
e009089	PGLAVGYDEFNAV	none	Thrombospondin-1	6.9	4.1	11.14	7.66	within
e009091	KQQGPGRDPLQQ	none	Protein piccolo	7.64	3.08	12.26	6.43	within
e102143	PPGTSGHPGSPGSPG*	4xOxidation [P2; P8; P11; P14]	Collagen alpha-1(III) chain	8.37	5.33	11.27	9.16	within
e009100	VYKSAEQGEVEN	none	Trafficking protein particle complex subunit 6B	6.08	3.26	10.55	4.47	within
e211568	PGEAGIPGRPDSAP*	2xOxidation [P1; P7]	Collagen alpha-4(IV) chain	11.26	7.33	12.97	10.98	within
e009101	EFGAPIKFSDQN	none	Dynein axonemal intermediate chain 3	5.93	2.88	11.11	4.34	within
e009102	PPGPPGPPGPPGPPS*	3xOxidation [P5; P7; P]	Collagen alpha-1(I) chain	10.25	6.2	12.97	10.79	within
e009104	SPGNIGPAGKEGPVG*	1xOxidation [P2]	Collagen alpha-2(I) chain	11.08	6.86	12.79	10.11	within
e009113	DSGSSEEQGGSSRA	none	Polymeric immunoglobulin receptor	10.09	7.1	12.13	11.59	within
e207891	QSRVLNLGPITR	none	Uromodulin	10.39	6.97	12.77	10.88	within
e009128	SMNPGPNMGQPQP	none	Histone acetyltransferase p300	10.4	6.46	12.71	12.56	within
e009129	EPSPPAAYDSSHP	none	Solute carrier family 12 member 3	8.29	4.43	10.58	7.85	within
e009131	PPGKNGDDGEAGKP*	1xOxidation [P]	Collagen alpha-1(I) chain	10.25	5.43	12.6	12.53	within
e009135	PVGPSGKD GANGIPG*	2xOxidation [P4; P14]	Collagen alpha-1(II) chain	11.39	6.7	13.03	11.79	within
e009133	MASSKNYGSPLIS	none	Mediator of RNA polymerase II transcription subunit 1	6.58	3.06	9.43	8.59	within
e009145	EVRDAAAGPDVGAAG	none	Diacylglycerol O-acyltransferase 1	10.69	7.49	12.46	10.91	within
e009162	FSDGASISFNGAPS	none	Trophinin	8.55	4.44	11.83	10.26	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e009170	PSAAGADREAASSPA	none	NAD-dependent protein deacetylase sirtuin-1	7.91	4.7	10.67	7.88	within
e009180	DGQPGAKGEPGDAGA*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	9.02	5.08	11.22	9.89	within
e009189	YSRHPAENGKSN	none	Beta-2-microglobulin	7.16	4.05	10.2	6.12	within
e211581	GGSGNTEPQKKGLS	none	Interleukin-17 receptor C	7.26	1.89	13.61	10.27	within
e009200	DGRNGEKGETGAPG*	1xOxidation [P13]	Collagen alpha-1(III) chain	10.33	6.22	12.74	5.73	down
e211584	GEPGAPGSKGDTGAK*	2xOxidation [P3; P6]	Collagen alpha-1(I) chain	9.21	5.42	12.45	5.73	within
e211587	GEPGPPGPPGPPGH*	7xOxidation [P3; P5; P6; P8; P9; P11; P12]	Collagen alpha-2(V) chain	13.01	8.43	15.49	10.74	within
e009222	AVADTRDQADGSR	none	Polymeric immunoglobulin receptor	9.67	6.57	12.33	6.44	down
e009229	NSGEPGAPGSKGDTG*	2xOxidation [P5; P8]	Collagen alpha-1(I) chain	12.14	7.39	14.4	11.09	within
e009235	GPGGGQARGPEPGEP	none	Helix-loop-helix protein 1	11.96	8.71	13.71	14.2	up
e009243	PPGRDQGPGHKGE*	2xOxidation [P2; P8]	Collagen alpha-2(I) chain	8.25	4.94	10.95	9.26	within
e100396	EDEDFYDSDDD	none	Kanadaplin	14.63	12.46	16.04	16.04	up
e009248	LNDAENLSSDSSL	none	POU domain, class 2, transcription factor 1	8.04	4.51	11.37	10.84	within
e211595	GGIKEDTEEHL	none	Heterogeneous nuclear ribonucleoproteins A2/B1	6.94	3.2	10.91	9.28	within
e009267	LLQAGLPLGQQDL	none	Actin-like protein 9	9.66	4.85	13.59	12.33	within
e009271	ARVQVVAGKKYF	none	Kininogen-1	8.33	4.45	13.57	12.32	within
e103998	GPAGERGSPGPAGPK*	2xOxidation [P11; P14]	Collagen alpha-1(I) chain	7.07	3.03	11.95	9.71	within
e211600	AHHFGKEFTPPV	none	Hemoglobin subunit beta	7.42	3.61	12.22	9.71	within
e009299	PPGEAGKPGEQGV*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	12.7	10.07	13.91	12.79	within
e009311	TADQDDSDGSTAA	none	Serine/threonine-protein kinase LMTK1	8.0	4.69	10.93	12.48	up
e099827	VGFPDGPDPGEGGP*	2xOxidation [P7; P9]	Collagen alpha-2(XI) chain	7.23	3.84	9.64	5.59	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e009328	GSPGPKGDKGEPGGP*	2xOxidation [P5; P12]	Collagen alpha-1(III) chain	6.69	1.33	11.09	4.77	within
e009330	PPGPPGPPGPPGPS*	4xOxidation [P5; P7; P8; P]	Collagen alpha-1(I) chain	12.24	7.64	14.55	12.44	within
e009332	PSLSDPSTPRGASP	none	Myb/SANT-like DNA-binding domain-containing protein 2	11.71	8.24	12.99	12.81	within
e009339	LDSEQEMAMAASS	none	Putative beta-actin-like protein 3	11.54	7.53	13.64	12.02	within
e097301	DKLHVDPENFR	none	Hemoglobin subunit delta	7.16	5.13	11.3	9.27	within
e009343	KAAEGQAAARRGSP	none	Myosin light chain kinase 2, skeletal/cardiac muscle	7.96	4.97	11.35	9.27	within
e211609	GHVLAKELEAFR	none	Insulin-like growth factor 2	7.88	4.77	12.46	9.27	within
e009354	EDSKRPSGIPER	none	Immunoglobulin lambda variable 3-10	7.43	4.32	10.47	4.62	within
e009371	DSFGSQASSAPSMT	none	AT-rich interactive domain-containing protein 1A	8.0	4.85	10.29	10.77	up
e009399	AGPPGPSPPGDKGSP	none	Collagen alpha-1(XXII) chain	7.04	2.42	12.62	5.91	within
e102161	PPGKAGEDGHPGKP*	2xOxidation [P2; P11]	Collagen alpha-2(I) chain	7.41	4.61	12.78	6.67	within
e009418	VTESWTAGTSSGGH	none	Mucin-19	9.71	5.53	12.07	9.14	within
e009419	TSPSSEQVGEATSP	none	Potassium voltage-gated channel subfamily KQT member 4	6.14	2.32	10.8	4.29	within
e211619	MDRGGFGGRRGGP	none	RNA-binding protein EWS	6.19	2.94	12.07	5.27	within
e105831	ELPGPPEPSGPVGP*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XV) chain	9.51	6.46	12.24	8.12	within
e009428	PPGPAGKEGGKGRG*	1xOxidation [P]	Collagen alpha-1(I) chain	9.8	5.87	15.43	7.68	within
e009435	EFTPPVQAAYQK	none	Hemoglobin subunit beta	8.77	3.47	13.59	7.24	within
e009438	APGEDGRPGPPGPQ*	3xOxidation [P2; P8; P10]	Collagen alpha-1(II) chain	14.8	13.07	15.78	14.24	within
e009445	EQGPKGEPGPAGPQ*	2xOxidation [P8; P10]	Collagen alpha-1(II) chain	14.03	12.21	14.94	13.77	within
e211630	PSGEAGTAGPPGTPGP*	2xOxidation [P11; P14]	Collagen alpha-2(I) chain	10.39	6.93	13.22	9.95	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211631	QSLDDNTFNLQS	none	Dynein axonemal heavy chain 10	6.63	4.08	9.61	6.31	within
e009460	DAGAPGAPGGKGDAGAP*	1xOxidation [P8]	Collagen alpha-1(III) chain	10.34	7.3	13.29	9.95	within
e100196	PGPAGPKGSPGEAGR*	3xOxidation [P3; P6; P10]	Collagen alpha-1(I) chain	7.99	4.66	10.76	10.95	up
e009484	GGSYETGDRDDGR	none	Myocyte-specific enhancer factor 2D	8.44	3.79	10.84	4.81	within
e104045	GSPGGPGSDGKPGPPG*	4xOxidation [P3; P6; P12; P14]	Collagen alpha-1(III) chain	10.76	7.5	12.56	11.77	within
e102676	GPSGASGERGPPGPM*	2xOxidation [P12; P]	Collagen alpha-1(I) chain	9.24	5.62	11.75	6.92	within
e211636	PPGPPGPPGPPGEKG*	3xOxidation [P4; P5; P7]	Collagen alpha-1(IV) chain	10.49	7.04	12.8	9.09	within
e211640	DTEEEEPGPEGTP	none	Caskin-2	7.37	3.45	11.04	2.32	down
e009501	AEGQQGQGQGQGQG	none	Mesoderm posterior protein 2	9.94	6.48	12.03	9.5	within
e009531	PGEDGQPGDPGPPGP*	1xOxidation [P13]	Collagen alpha-2(V) chain	9.43	5.92	12.12	9.74	within
e102825	KELMPDVGRSMQ	none	Probable E3 ubiquitin-protein ligase HERC4	8.75	5.42	11.64	7.1	within
e009562	VGTQGPRGPPGAPG*	3xOxidation [P10; P12; P15]	Collagen alpha-1(XIV) chain	5.72	0.0	10.38	4.81	within
e211655	SAAATGAGGAGAYGTGGP	none	T-cell leukemia homeobox protein 1	15.56	13.07	16.79	15.89	within
e009589	PGPEGPAGNDGTPGR*	1xOxidation [P13]	Collagen alpha-2(V) chain	14.55	12.11	15.81	14.9	within
e105121	TTIPEQSFQGPS*	1xOxidation [P12]	Collagen alpha-2(IV) chain	8.25	5.25	12.22	8.48	within
e211663	PAGAPGDKGESGPSGP*	1xOxidation [P1]	Collagen alpha-1(I) chain	8.25	4.47	11.1	7.08	within
e009639	EEEEDEDDDSAD	none	F-box only protein 3	11.01	7.28	13.59	14.61	up
e207918	AAGSGSGSGSGGPGPGGG	none	Neuralized-like protein 4	11.92	8.47	13.18	12.32	within
e009644	GPPGSEGFTGPPGPQ*	1xOxidation [P12]	Collagen alpha-2(IV) chain	11.88	8.76	13.17	12.32	within
e106519	GTGGPPGENGKPGEP*	3xOxidation [P5; P6; P12]	Collagen alpha-1(III) chain	11.39	7.58	12.59	12.1	within
e104141	SPGEAGRPGEAGLPG*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	11.16	7.56	12.82	8.56	within
e009681	TVTDYGKDLMEK	none	Apolipoprotein A-II	8.81	5.81	11.96	7.03	within
e009690	NGAPGNDGAKGDAGAP*	2xOxidation [P4; P16]	Collagen alpha-1(I) chain	10.22	6.46	11.7	11.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e009691	FDADTPGSRNSAY	none	Voltage-dependent L-type calcium channel subunit beta-1	6.76	2.88	9.89	1.32	down
e009693	RSDYSNEKPFTG	none	Mannan-binding lectin serine protease 2	7.77	4.26	12.13	4.12	down
e211669	PATAVPSASTPLPQ*	4xOxidation [P1; P6; P11; P13]	Collagen alpha-1(XXIV) chain	8.7	6.03	11.73	8.79	within
e207923	EGGGAGGGSGEREGGAP	none	Microtubule cross-linking factor 3	10.2	6.68	13.32	10.79	within
e102999	SPGENGAPGQMGP*	3xOxidation [P2; P8; M11]	Collagen alpha-1(I) chain	9.41	4.91	13.14	9.51	within
e101705	PGPPGPPGPPSFPGP*	3xOxidation [P4; P6; P7]	Collagen alpha-1(XVIII) chain	10.14	5.86	13.1	12.67	within
e009714	QTLQASEEQLQQ	none	Golgin subfamily A member 1	6.43	3.18	10.03	10.51	up
e211680	QPSHQPPGAMGIGQ	none	Chromodomain-helicase-DNA-binding protein 7	7.16	3.58	16.63	6.04	within
e201643	GPPGPAGPTGEKGEPPG	none	Collagen alpha-2(V) chain	7.73	3.75	16.76	6.04	within
e009768	DGPPGRDQQPGHKG*	2xOxidation [P4; P10]	Collagen alpha-2(I) chain	10.58	6.22	12.58	11.07	within
e094425	DGVPGKDGPGRGPTGP	none	Collagen alpha-1(III) chain	10.61	6.41	12.71	10.05	within
e094428	QGAPGSVGPAGPRGPA*	2xOxidation [P4; P9]	Collagen alpha-2(I) chain	9.5	6.21	11.68	5.74	down
e009788	PGPSGNDGSAGPPGPP*	3xOxidation [P12; P13; P15]	Collagen alpha-1(VII) chain	13.64	10.63	15.06	14.41	within
e009791	GPPGEAGKPGEQGVP*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	11.08	7.5	13.17	9.58	within
e009792	TGSPGSPGPDGKTGPP	none	Collagen alpha-1(I) chain	10.92	6.66	13.34	12.07	within
e009793	TTHARTTGPPDPGT	none	Maltase-glucoamylase	10.91	6.67	13.33	12.07	within
e009804	GPPGPPGPPGPPGPPS*	3xOxidation [P5; P6; P8]	Collagen alpha-1(I) chain	12.09	7.95	14.55	13.75	within
e009808	DWSNSSSATSGSGAP	none	Neuropilin-2	16.57	14.6	17.77	16.64	within
e103054	TDTEPAKFKMK	none	Retinol-binding protein 4	5.97	2.01	10.04	6.55	within
e009816	SEAGGAGHEEGRASP	none	(E3-independent) E2 ubiquitin-conjugating enzyme	10.0	5.92	12.19	10.9	within
e009819	DSYVGDEAQSKRG	none	Actin, cytoplasmic 1	12.18	7.52	16.16	11.02	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211696	PSTFSEEMTPTSV	none	Phosphatase and actin regulator 4	10.51	4.18	13.26	12.28	within
e207934	EDSDEEEDDDSE	none	Nucleolin	14.28	10.12	17.08	14.44	within
e009843	TALQPMVSALNIR	none	Uromodulin	10.32	6.83	12.39	11.54	within
e009851	PPGPMGPPGDRGFT*	2xOxidation [P2; P4]	Collagen alpha-1(XII) chain	10.67	5.94	12.5	11.44	within
e009872	GPPGPAGNPGPSPNSP*	1xOxidation [P3]	Collagen alpha-1(XXVI) chain	7.84	5.49	10.76	8.26	within
e097326	TLELKEEEDVLV	none	Neurogenin-2	7.96	2.67	12.93	7.31	within
e009898	WVKEATEGKIQE	none	Alpha-2-antiplasmin	8.11	5.05	12.78	9.41	within
e300031	AEILNVAKGIRSF	none	Collagen alpha-1(XVIII) chain	8.06	4.89	13.9	9.41	within
e009911	TAAAASGATSAPEGDAA	none	CaM kinase-like vesicle-associated protein	12.67	9.47	14.47	13.87	within
e101932	PGGLAASQNHSHQ	none	Multicilin	7.46	4.11	10.45	8.88	within
e009916	FSDSPITVTVPE	none	Clusterin	10.32	5.28	13.71	12.95	within
e009923	GNSGEPGAPGSKGDTG*	2xOxidation [P6; P9]	Collagen alpha-1(I) chain	10.26	7.21	12.74	9.79	within
e201689	HPGSPPHSQMSGDS	none	CUB and sushi domain-containing protein 2	7.79	5.0	10.81	11.13	up
e009933	GPPGRDGQPGHKGE*	2xOxidation [P3; P9]	Collagen alpha-2(I) chain	10.31	6.63	11.96	11.39	within
e104729	IGLEGPPGPPGFPGP*	2xOxidation [P7; P]	Collagen alpha-5(IV) chain	7.68	3.08	13.13	8.52	within
e009950	VTSMPTSTAGEGSTP	none	Mucin-17	6.3	2.96	9.05	5.85	within
e103679	PPGPAGAPGDKGESGP*	2xOxidation [P4; P8]	Collagen alpha-1(I) chain	8.81	5.44	11.87	7.29	within
e099824	EQGDSEDDQAGSGE	none	G patch domain-containing protein 1	12.39	8.4	14.77	15.25	up
e009963	DSVVQNNNTSQMS	none	Sickle tail protein homolog	13.62	11.54	14.98	13.66	within
e097330	GDAGAKGDAGPPGPAGP*	2xOxidation [P14; P]	Collagen alpha-1(I) chain	13.0	9.99	14.84	14.26	within
e201696	QASNYAESPWALS	none	HERV-H_2q24.1 provirus ancestral Env polyprotein	8.79	5.55	11.23	9.51	within
e211718	GLPGTGGPPGENGKPG*	2xOxidation [P3; P8]	Collagen alpha-1(III) chain	13.08	10.29	14.81	14.26	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e009969	FGAVHAQMHAAVGQ	none	Protein PML	8.86	5.0	11.11	10.06	within
e009980	VIDQSRVLNLGPI	none	Uromodulin	12.95	9.05	15.81	14.83	within
e009985	NNMYAWGQESGAP	none	Protein transport protein Sec23A	14.97	12.86	16.38	15.43	within
e009990	PSAPSAGGGPDGEQPT	none	SKI family transcriptional corepressor 1	14.92	12.82	16.34	15.39	within
e211723	TGPPGPAGQDGRPGP*	4xOxidation [P4; P6; P13; P15]	Collagen alpha-1(I) chain	14.88	12.31	16.34	15.39	within
e009997	GPPGEAGKPGEQGV*	3xOxidation [P3; P9; P15]	Collagen alpha-1(I) chain	13.22	10.47	14.68	14.74	up
e211725	TGSPGSPGPDGKTGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	11.31	7.67	13.96	13.85	within
e211726	PGERGAAGSGGPIGPP*	3xOxidation [P1; P12; P15]	Collagen alpha-2(XI) chain	13.22	10.44	14.66	14.74	up
e010000	KGNGKDPASHFGPP*	1xOxidation [P7]	Collagen alpha-4(IV) chain	9.81	5.64	11.75	4.15	down
e010002	DAHKSEVAHRFK	none	Albumin	8.01	4.62	11.91	10.68	within
e211731	GPPGPPGPPGPPGPPS*	4xOxidation [P5; P6; P8; P9]	Collagen alpha-1(I) chain	13.96	9.56	16.29	14.86	within
e211732	PGPPGPYGSPPGAPGIG*	3xOxidation [P4; P6; P10]	Collagen alpha-1(XXVIII) chain	13.97	9.55	16.29	15.03	within
e211735	DKKREEAPSLRP	none	Fibrinogen beta chain	7.49	0.65	11.73	9.23	within
e010019	SESPVFMDSPPDE	none	DNA polymerase zeta catalytic subunit	14.95	12.42	16.24	15.1	within
e010025	PGEKGEAGDEGNPGP*	1xOxidation [P]	Collagen alpha-1(VI) chain	14.99	12.14	16.29	15.16	within
e211736	ELGGQGNWGPEDAP	none	Aspartate beta-hydroxylase domain-containing protein 1	14.53	9.32	16.15	15.16	within
e211737	ERGAPGEKGEKGPPG*	2xOxidation [P5; P13]	Collagen alpha-1(III) chain	9.32	5.81	12.49	10.14	within
e100394	GPPGKPGPPGPPGPPG*	4xOxidation [P2; P9; P12; P15]	Collagen alpha-1(XIX) chain	10.81	5.93	14.04	10.69	within
e010027	LENEDRRSASLH	none	Alpha-1-antitrypsin	7.68	4.54	10.29	10.03	within
e102199	GYGGGFNERENVE	none	Zinc finger Ran-binding domain-containing protein 2	7.62	3.74	10.55	8.32	within
e211738	PPGKNGDDGEAGKPG*	2xOxidation [P2; P14]	Collagen alpha-1(I) chain	13.23	9.59	14.75	14.27	within
e106634	SVPGPPGPPGPPGPPG*	4xOxidation [P6; P9; P12; P15]	Collagen alpha-1(XVIII) chain	12.54	8.75	14.66	13.97	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e010045	PGEGGKPGDQGVPE*	3xOxidation [P1; P7; P13]	Collagen alpha-1(II) chain	7.59	3.98	10.64	8.28	within
e102175	LPGEPPVGGGGHPGQ*	1xOxidation [P]	Collagen alpha-5(IV) chain	11.4	7.12	14.42	12.54	within
e010063	SPGRDGSPGAKGDRG*	1xOxidation [P2]	Collagen alpha-1(I) chain	7.07	4.2	9.69	6.07	within
e211743	TDMETFHTTDSF	none	Cation channel sperm-associated auxiliary subunit epsilon	12.84	8.3	15.35	7.83	down
e010088	LSMDGGGSPKGDVDP	none	Sodium/potassium-transporting ATPase subunit gamma	9.51	6.41	11.87	10.23	within
e010102	GSSSGSSSGSSSGSSGSS	none	Dermokine	12.88	8.25	15.28	10.32	within
e010108	DGHPGKPRPGERG*	1xOxidation [P10]	Collagen alpha-2(I) chain	8.88	4.48	11.81	10.22	within
e010130	SNYQTNKAKHDE	none	Cystatin-B	10.33	6.23	12.04	11.64	within
e010132	SASDLTWDNLKGK	none	Serotransferrin	4.88	0.34	10.14	7.1	within
e207951	DPVLGPDGKTHGNK	none	Serine protease inhibitor Kazal-type 5	8.05	3.23	13.09	5.74	within
e010133	GPPGPAGKEGGKPRG*	1xOxidation [P3]	Collagen alpha-1(I) chain	7.93	2.22	13.46	4.31	within
e211752	EGPPGKQGFYGGPPG*	3xOxidation [P3; P4; P12]	Collagen alpha-1(XVI) chain	10.78	7.19	12.98	8.81	within
e010139	TDETNLPADIPSY	none	Leucine-rich repeats and immunoglobulin-like domains protein 3	7.33	4.38	10.57	5.29	within
e010142	RGPPGPSGRGVGTQ*	1xOxidation [P]	Collagen alpha-1(XXVIII) chain	8.69	6.0	11.73	9.08	within
e101421	DDDDEFGEFGGFS	none	Aftiphilin	8.79	5.07	12.05	12.57	up
e010153	SPGSPGPDGKTGPPGP*	2xOxidation [P2; P5]	Collagen alpha-1(I) chain	14.88	13.28	15.89	14.43	within
e010156	TPSAAGAPASAPGEPR	none	Ankyrin repeat domain-containing protein 9	10.72	5.75	12.86	9.44	within
e211756	PAGKDGEAGAQQPPGP*	2xOxidation [P1; P13]	Collagen alpha-1(I) chain	13.72	10.82	15.02	13.38	within
e010167	GAKGPEGPPGPTGRQ*	2xOxidation [P9; P11]	Collagen alpha-1(VII) chain	10.17	5.31	14.81	13.85	within
e201745	KGANGDPGRPGEPGL*	1xOxidation [P13]	Collagen alpha-1(II) chain	9.33	5.18	12.12	7.01	within
e010168	ELQEGARQKLHE	none	Apolipoprotein A-I	10.17	5.62	14.5	13.29	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e010169	ALEEYTKKLNTQ	none	Apolipoprotein A-I	8.66	3.07	12.39	6.94	within
e211757	PPEEDQGEEPR	none	Proline-rich acidic protein 1	7.68	4.07	10.99	9.32	within
e102227	IGPPGPAGAPGDKGES*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	12.77	10.47	14.16	11.95	within
e010178	PGTPGFPGNAGVPGTP*	1xOxidation [P]	Collagen alpha-1(XIV) chain	8.48	4.79	11.31	10.49	within
e010179	MIEQNTKSPLFM	none	Alpha-1-antitrypsin	12.77	10.38	14.09	12.01	within
e010180	EALISGNLATEAHL	none	Dedicator of cytokinesis protein 8	8.35	4.71	11.54	9.35	within
e211759	DDEEDEEEGEED	none	Nucleolar complex protein 2 homolog	15.97	13.69	17.64	17.62	within
e010194	GLPGTGPPGENGKPG*	3xOxidation [P3; P8; P9]	Collagen alpha-1(III) chain	15.33	13.01	16.18	15.89	within
e010212	DEAGSEADHEGTHS	none	Fibrinogen alpha chain	11.08	7.35	12.77	12.09	within
e100312	GPPGPPGPPGPPGPS*	5xOxidation [P5; P6; P8; P9; P11]	Collagen alpha-1(I) chain	11.62	8.03	14.01	14.03	up
e010218	YSLSENSEEDNR	none	Receptor-type tyrosine-protein phosphatase zeta	7.74	3.63	10.91	9.04	within
e010227	GPPGPPGPPGPPGEKG*	3xOxidation [P5; P6; P8]	Collagen alpha-1(IV) chain	11.92	6.71	14.51	12.63	within
e010245	GPTGSPGTSGPPGSAGP*	4xOxidation [P6; P11; P12; P17]	Collagen alpha-2(V) chain	9.01	5.41	11.65	10.07	within
e010250	AAWGVGAHAGEYGA	none	Hemoglobin subunit alpha	7.66	4.59	13.19	7.02	within
e010263	SPGRDGSPGAKGDRG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	10.06	5.95	12.13	11.41	within
e010275	PGPAGHPGEQQPGP*	4xOxidation [P3; P7; P13; P15]	Collagen alpha-1(XXVII) chain	9.56	5.29	12.69	5.84	within
e010280	GPMGPPGPPGPRGPQ*	3xOxidation [P6; P8; P9]	Collagen alpha-1(XI) chain	10.19	6.4	12.69	5.38	down
e211776	EEDSEEDGMVNHG	none	28S rRNA (cytosine(4447)-C(5))-methyltransferase	8.93	5.58	11.41	10.06	within
e010286	NHMDWSTNSDSGP	none	SET-binding protein	10.85	7.22	13.04	8.8	within
e010292	EEKAVADTRDQAD	none	Polymeric immunoglobulin receptor	6.97	4.7	9.9	7.7	within
e010295	PGPEGPAGLPGPPGTM*	1xOxidation [P12]	Collagen alpha-1(V) chain	8.06	4.73	10.82	10.92	up
e010308	DGHPGKPRPGERG*	2xOxidation [P4; P7]	Collagen alpha-2(I) chain	11.92	7.33	13.93	13.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e201794	GLPGADGPPGHPGKE*	4xOxidation [P3; P8; P9; P12]	Collagen alpha-1(XI) chain	8.7	2.7	11.66	10.36	within
e201795	SGQKGKQQTESKGS	none	Semenogelin-1	9.24	4.31	13.42	12.4	within
e010314	ITHRIHWESASL	none	Complement C3	10.16	4.18	14.82	10.15	within
e010317	VVAGVANALAHKYH	none	Hemoglobin subunit delta	9.86	4.05	14.57	11.03	within
e105768	PSLANGAAQDGDTHP	none	E3 ubiquitin-protein ligase HECW1	15.62	13.51	16.91	15.5	within
e010331	GQPPAQTGVSQGGVP	none	CREB-binding protein	8.77	5.06	11.33	9.53	within
e010333	RRLVNEKAAHEK	none	Ecto-NOX disulfide-thiol exchanger 2	9.65	4.96	13.6	8.36	within
e106230	EGSGDGGSSADSGSGAGP	none	Adenylate cyclase type 5	9.88	6.19	13.63	12.4	within
e105294	SGLPGESYGSEKGAP*	1xOxidation [P4]	Collagen alpha-3(IV) chain	14.66	11.85	16.05	14.76	within
e211782	VVVDVSHEDPEVQ	none	Immunoglobulin heavy constant gamma 2	10.67	6.71	14.03	11.58	within
e106047	KDDASQVSSTSNDV	none	Protein Jumonji	8.56	4.6	13.95	8.66	within
e211785	RGPQGPNGADGPQGP*	3xOxidation [P3; P6; P12]	Collagen alpha-1(XI) chain	17.39	16.13	18.13	17.2	within
e010346	SPGSPGPDGKTGPPGP*	3xOxidation [P2; P5; P7]	Collagen alpha-1(I) chain	17.42	16.14	18.16	17.23	within
e211788	APGKNGERGGPGGPGP*	3xOxidation [P2; P11; P14]	Collagen alpha-1(III) chain	14.27	12.59	15.29	14.18	within
e010365	TDGDLGDNGTVRFS	none	Protocadherin Fat 4	9.98	6.23	12.98	8.4	within
e207966	GPKGANGDPGRPGEP*	3xOxidation [P2; P9; P12]	Collagen alpha-1(II) chain	11.12	6.05	13.01	11.37	within
e010370	EPPQSPWDRVKD	none	Apolipoprotein A-I	11.79	6.95	13.81	8.88	within
e010378	DGQPGAKGEPGDAGAK	none	Collagen alpha-1(I) chain	11.28	6.1	12.9	10.95	within
e101371	PGADGEAGRPGSSGSPG	none	Collagen alpha-1(VI) chain	9.93	7.16	13.53	10.47	within
e010394	TPGVVGQPGTPGSSGP*	2xOxidation [P8; P11]	Collagen alpha-6(IV) chain	9.85	7.18	13.59	10.47	within
e010396	LGHPDTLNQGEFK	none	Protein S100-A9	9.99	3.82	15.59	13.01	within
e010404	PGNDGAKGDAGAPGAPG*	3xOxidation [P1; P13; P16]	Collagen alpha-1(I) chain	11.4	7.77	12.86	12.49	within
e010408	TIDEKGTEAAGAMF*	1xOxidation [M13]	Alpha-1-antitrypsin	11.6	8.57	13.03	12.49	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e102008	DPGFPGGRGALGPGGP*	3xOxidation [P5; P13; P16]	Collagen alpha-4(IV) chain	8.24	4.87	13.7	12.37	within
e010414	LSTPDAMGNPKVK	none	Hemoglobin subunit beta	9.01	5.17	14.18	9.24	within
e010418	NGAPGNDGAKGDAGAPG*	2xOxidation [P4; P16]	Collagen alpha-1(I) chain	11.16	7.42	12.74	10.37	within
e010420	PGGKGERGAPGEKGE*	2xOxidation [P1; P10]	Collagen alpha-1(III) chain	7.76	2.8	12.24	7.18	within
e211807	GDQGEPSGPPGFSG*	1xOxidation [P11]	Collagen alpha-4(IV) chain	11.49	7.91	13.03	11.69	within
e099065	SPGSPGPDGKTGPPGP*	1xCation:Na [D8]; 2xOxidation [P2; P5]	Collagen alpha-1(I) chain	12.04	8.23	13.94	11.93	within
e211808	AMGLPGQEGLPGKDG*	2xOxidation [P5; P11]	Collagen alpha-1(XXII) chain	11.81	7.47	13.78	10.64	within
e010434	GLPGADGPPGHPGKEG*	1xOxidation [P]	Collagen alpha-1(XI) chain	11.42	8.2	13.54	11.18	within
e010442	SPGENGAPQMGRG*	3xOxidation [P2; P8; M11]	Collagen alpha-1(I) chain	11.87	8.55	13.47	8.41	down
e010451	EPGPVGGGGHPGQPGP*	4xOxidation [P2; P4; P11; P14]	Collagen alpha-5(IV) chain	10.65	7.34	12.82	6.49	down
e102433	DSDSDSDSETSDS	none	H/ACA ribonucleoprotein complex non-core subunit NAF1	11.92	7.13	15.02	11.89	within
e010469	IDDILEDEEHYA	none	Sorting nexin-4	10.86	6.99	13.5	11.52	within
e010492	GVGASSSGGGPGSGGGSGG	none	Glycogen synthase kinase-3 alpha	9.73	4.46	13.58	5.91	within
e211825	GKAPGAEEYAQQDV	none	2',3'-cyclic-nucleotide 3'-phosphodiesterase	9.66	4.6	12.59	7.91	within
e211826	AHRFKDLGEENF	none	Albumin	7.71	4.0	11.67	5.69	within
e104154	DGRPGPPGPPGARGQ*	3xOxidation [P4; P7; P10]	Collagen alpha-1(I) chain	9.33	5.02	11.82	11.69	within
e211834	QGEPPGPPQQGNP*	3xOxidation [P6; P7; P13]	Collagen alpha-1(XI) chain	11.03	6.76	13.07	12.07	within
e100254	YVSGFHPSDIEVD	none	Beta-2-microglobulin	8.67	5.2	12.53	8.85	within
e010520	DGHPGKPRPGERG*	3xOxidation [P4; P7; P10]	Collagen alpha-2(I) chain	11.21	6.7	12.96	12.85	within
e211836	LMSRTPDTISDQT	none	Basic helix-loop-helix domain-containing protein USF3	8.86	5.41	13.29	8.85	within
e105688	DTQESSTTATEAAGP	none	E3 ubiquitin-protein ligase ZNRF3	11.11	7.21	12.94	11.82	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e103263	LEGSTGTMGGGSSAGTP	none	Testis-specific serine kinase substrate	10.03	5.29	11.74	10.51	within
e010548	GPPGSPGEQGPSGASGP*	2xOxidation [P3; P6]	Collagen alpha-1(I) chain	11.08	7.69	12.8	12.13	within
e207977	KGEPSAGPQGPGPS*	3xOxidation [P9; P12; P13]	Collagen alpha-2(I) chain	14.56	12.0	15.99	15.08	within
e099968	AQSGAWDPNNPNT	none	Transcription elongation factor SPT5	8.23	4.36	10.25	9.29	within
e010574	SPGSPGPDGKTGPPGP*	4xOxidation [P5; P7; P13; P]	Collagen alpha-1(I) chain	12.13	9.28	13.5	12.67	within
e010575	GPPGKNGDDGEAGKPG*	1xOxidation [P3]	Collagen alpha-1(I) chain	14.14	9.92	15.43	14.44	within
e010579	KQEGIATSDNFMQ	none	Eukaryotic translation initiation factor 4 gamma 2	14.08	11.55	15.41	14.89	within
e104247	DDQSAETHSHKQS	none	Osteopontin	9.32	5.37	11.39	6.01	within
e010586	TSGSASSDAGSGSRRS	none	Ubiquilin-4	12.48	6.36	13.86	13.17	within
e010587	TGPAGAAGARGNDGQPG*	1xOxidation [P16]	Collagen alpha-1(II) chain	12.12	4.7	13.76	7.92	within
e097357	DGAPGKNGERGGPGGP*	3xOxidation [P4; P13; P16]	Collagen alpha-1(III) chain	14.53	12.62	15.61	15.03	within
e099067	DGHPGKPRPGERG*	1xCation:Na [D1]; 2xOxidation [P7; P10]	Collagen alpha-2(I) chain	8.79	4.1	11.42	4.52	within
e010603	DGQPGAKGEPGDAGAK*	1xOxidation [P10]	Collagen alpha-1(I) chain	14.53	12.69	15.6	15.03	within
e211854	DQLGKNEEGAPQEG	none	Alpha-synuclein	12.9	8.63	14.54	13.4	within
e010617	PNPSPASSVGSQGSLS	none	AF4/FMR2 family member 3	10.34	6.65	12.48	10.06	within
e010628	HAGHGQQQKVIVVA	none	Pro-epidermal growth factor	9.07	5.96	11.62	11.54	within
e010640	EKGENGVDVGPMPGP*	2xOxidation [P13; P14]	Collagen alpha-1(XI) chain	8.76	5.12	11.91	12.46	up
e101391	ASVNSEHFNQNEP	none	Protein dispatched homolog 1	13.96	11.81	15.35	14.52	within
e097360	ERIAGEASRLAHY	none	Histone H2B type 2-E	8.02	4.02	12.41	7.37	within
e010661	SQDASDGLQRLHM*	1xOxidation [M13]	Endothelial protein C receptor	11.63	7.35	13.72	12.38	within
e211862	EHSGDWLDQDSVS	none	E3 ubiquitin-protein ligase Mdm2	12.38	7.74	14.25	12.72	within
e211863	FPGPSGNDGSAGPPGP*	4xOxidation [P2; P4; P13; P14]	Collagen alpha-1(VII) chain	13.5	10.0	15.72	10.79	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211864	DTGYSSDGISSSLGE	none	Protein piccolo	12.44	8.07	14.23	12.69	within
e099068	SPGSPGPDGKTGPPGP*	1xCation:Na [D8]; 3xOxidation [P2; P5; P7]	Collagen alpha-1(I) chain	13.54	10.53	15.74	10.79	within
e211865	ELSSSEGLEPGSADP	none	PH and SEC7 domain-containing protein 2	12.37	7.13	14.25	11.88	within
e211866	KSSSPSGSPGDPSSPT	none	Ral guanine nucleotide dissociation stimulator-like 3	11.63	6.93	14.17	11.1	within
e211867	GPPGPAGERGHGAPG*	4xOxidation [P3; P5; P12; P15]	Collagen alpha-1(XVI) chain	13.49	10.23	15.75	10.79	within
e211868	GPSGTSSSGSKASGPPN	none	Transcriptional activator MN1	13.38	9.68	15.76	10.79	within
e010682	RQGPPGPPGPPGPS*	5xOxidation [P5; P7; P8; P10; P11]	Collagen alpha-1(XVIII) chain	12.99	8.0	15.7	10.8	within
e207986	PPGSNGNPGPPGPPGP*	5xOxidation [P2; P8; P10; P11; P13]	Collagen alpha-1(II) chain	13.63	10.38	15.33	12.7	within
e010696	SAWNGPQLSSNNN	none	S100P-binding protein	13.65	9.25	15.39	12.69	within
e211871	DSVPSALFATEDSH	none	Midasin	9.84	6.27	12.26	11.26	within
e010699	DPGEVGRGHPGMPGP*	1xOxidation [P10]	Collagen alpha-2(IX) chain	13.62	10.21	15.31	12.7	within
e211873	GPPGPPGPPGPSFPG*	4xOxidation [P6; P8; P9; P11]	Collagen alpha-1(XVIII) chain	12.59	9.89	14.4	13.17	within
e010702	GRDGSPGAKGDRGET*	1xOxidation [P6]	Collagen alpha-1(I) chain	9.89	6.47	12.21	11.26	within
e211875	QATKNSGSSQGLGGSP	none	SH3 domain-binding protein 1	12.18	9.41	14.02	13.17	within
e010706	GPAAHTLREPQDPS	none	Small G protein signaling modulator 2	8.31	3.57	11.72	8.98	within
e010723	DSNNPTLHFGNNF	none	Zinc finger protein 215	9.62	5.73	11.78	11.18	within
e211881	AGSRGDGGPPGMTGFP*	1xOxidation [P16]	Collagen alpha-2(I) chain	13.22	10.33	14.65	12.41	within
e010729	KSSSADFGTFNTSQ	none	Arf-GAP domain and FG repeat-containing protein 1	11.97	9.27	13.63	12.36	within
e010730	LSDQVPDTESETR	none	Complement C3	13.03	9.13	14.57	12.41	within
e010736	GPPGPPGPPGTSGHPG*	7xOxidation [P2; P3; P5; P6; P8; P9; P15]	Collagen alpha-1(III) chain	13.38	9.2	15.41	12.67	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e010737	YEGQVSGMPNDPSP	none	ALK tyrosine kinase receptor	8.69	4.91	11.01	9.62	within
e211886	GEPGPQGHAGAQQPPG*	4xOxidation [P3; P5; P14; P15]	Collagen alpha-1(III) chain	13.39	9.61	15.47	12.67	within
e010745	VTEEDDDEETAP	none	Serine/threonine-protein kinase PAK 2	8.02	4.45	10.48	8.61	within
e211890	KSEAEKGESDQTQGP	none	Probable ATP-dependent RNA helicase DDX4	12.97	9.69	14.73	11.57	within
e010757	WSGVMGGSSGASRGPS	none	Immunoglobulin-like domain-containing receptor 2	8.9	5.7	11.15	9.62	within
e010762	YADKPETTKEQLG	none	Alpha-1-acid glycoprotein 1	7.76	4.42	11.69	8.31	within
e010775	EPDEEEFQEESL	none	RNA-binding protein 26	7.91	4.07	10.84	5.71	within
e010780	GPPGPPGPPGPPGPPSA*	3xOxidation [P5; P6; P]	Collagen alpha-1(I) chain	8.73	5.18	12.05	6.48	within
e010781	MGVPGRTMGVMFTP	none	Eukaryotic translation initiation factor 3 subunit F	7.35	3.83	10.18	3.81	down
e201847	ARGAPGPDGNGAQQP*	3xOxidation [P5; P7; P16]	Collagen alpha-2(I) chain	10.95	7.95	13.01	12.24	within
e010813	GPPGKPGDDGEAGKPG*	3xOxidation [P3; P6; P15]	Collagen alpha-1(II) chain	10.86	7.78	12.94	12.15	within
e010818	GPPGKNGDDGEAGKPG*	2xOxidation [P3; P15]	Collagen alpha-1(I) chain	12.13	8.2	14.07	13.38	within
e104545	DKGEPGPPGQPGYPG*	2xOxidation [P5; P14]	Collagen alpha-1(XVI) chain	8.04	4.79	11.68	5.44	within
e010835	KARDEGHAENFP	none	Sine oculis-binding protein homolog	10.56	6.94	12.9	12.71	within
e211906	TPSFTSSITTSEMP	none	Mucin-3A	10.96	6.9	13.03	12.71	within
e010849	DGQPGAKGEPGDAGAK*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	12.76	10.15	14.27	14.11	within
e010851	EHSDVIDSQELSK	none	Osteopontin	12.76	9.88	14.28	14.09	within
e010853	VAVEERKAAGSRDV	none	Polymeric immunoglobulin receptor	9.33	5.52	13.37	9.45	within
e010859	DGSPGAKGDRGETGPA*	1xOxidation [P4]	Collagen alpha-1(I) chain	13.24	10.75	14.55	13.57	within
e010860	PPGDPGSPGSPGAPAG*	1xOxidation [P1]	Collagen alpha-3(IV) chain	11.45	6.75	13.27	12.41	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e010872	SEEDGMVNHGDLW	none	28S rRNA (cytosine(4447)-C(5))-methyltransferase	12.55	6.24	15.47	4.07	down
e093729	GLSMDGGGSPKGDVDP	none	Sodium/potassium-transporting ATPase subunit gamma	11.36	7.58	13.65	12.89	within
e010883	HGNNQDSSSDNEA	none	Testis-specific Y-encoded-like protein 2	9.4	6.02	12.09	13.16	up
e010888	RSNISSYDGEYAQ	none	Protein HEG homolog 1	11.8	8.12	13.65	11.07	within
e099764	ANLYDVETSELVH	none	WD repeat-containing protein 37	6.97	4.31	9.89	10.09	up
e211921	PSSPDNDLPAPEST*	4xOxidation [P1; P4; P9; P11]	Collagen alpha-1(XXVI) chain	14.54	11.16	16.79	12.51	within
e105704	HEGDEGPGHHKPG	none	Protein S100-A9	9.05	4.98	11.67	10.11	within
e211923	DIFGAENGAPGEQGL*	1xOxidation [P10]	Collagen alpha-6(IV) chain	13.21	8.49	16.25	12.51	within
e211926	DGEDGPTGPPGPPGPP*	3xOxidation [P12; P13; P15]	Collagen alpha-2(I) chain	13.01	8.37	15.62	11.6	within
e010918	GDQGPDPGSPGSPGP*	1xOxidation [P15]	Collagen alpha-3(IV) chain	13.0	8.21	15.63	11.99	within
e211928	GAEGPPGPTGQAGEPGP*	1xOxidation [P15]	Collagen alpha-3(V) chain	12.45	7.94	15.24	11.91	within
e211931	SGRDGLPGPPGSPGPP*	3xOxidation [P10; P13; P15]	Collagen alpha-1(IV) chain	11.69	6.89	13.76	12.82	within
e211933	VGPPGPPGPPGPPGPPS*	2xOxidation [P]	Collagen alpha-1(I) chain	12.02	7.51	13.84	12.82	within
e010937	PEPAKSAPAPKKGSK	none	Histone H2B type 2-E	7.64	4.76	11.62	11.04	within
e211938	SAGDLSDSASSLAEP	none	Zinc finger homeobox protein 2	12.18	8.82	13.97	11.49	within
e010940	GPPGMPGPRGSPGPQG*	3xOxidation [P3; P6; P8]	Collagen alpha-1(III) chain	12.01	8.46	13.96	11.11	within
e102650	KEGRDGKPGPPGEPG*	1xOxidation [P14]	Collagen alpha-1(XXII) chain	8.13	2.64	13.26	3.94	within
e010945	PENNGNNSWPHND	none	Inner centromere protein	6.88	3.28	10.64	3.05	down
e010948	DGPPGPPGERGPQGP*	5xOxidation [P4; P6; P7; P12; P15]	Collagen alpha-1(XI) chain	11.49	7.4	13.46	11.07	within
e010951	GPPGKNGETGPQGPPG*	3xOxidation [P3; P11; P14]	Collagen alpha-1(III) chain	11.61	7.49	13.2	11.76	within
e010954	FGDTEEAKKQIND	none	Alpha-1-antitrypsin	7.78	2.12	12.18	5.62	within
e211942	PAGSPGERGAAGSGGPIG	none	Collagen alpha-2(XI) chain	7.62	3.51	12.41	11.0	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e010956	AHHFGKEFTPPVQ	none	Hemoglobin subunit beta	8.17	3.85	13.59	11.46	within
e010962	EPGDAGAKGDAGPPGPA*	2xOxidation [P2; P13]	Collagen alpha-1(I) chain	11.17	7.7	13.19	10.64	within
e300043	KKENKNEKVIEH	none	Protein S100-A9	10.21	5.25	14.19	13.7	within
e010979	DDEEEDEEEEDN	none	Midasin	11.59	7.57	13.54	13.37	within
e010982	DDLEGFAEGGMIDQ	none	SR-related and CTD-associated factor 8	11.45	6.88	14.31	10.06	within
e101732	GPPGPPGPPGPPGPPSA*	4xOxidation [P6; P8; P9; P]	Collagen alpha-1(I) chain	8.94	5.07	12.3	11.62	within
e211947	GPPGPPGPPGSIGHPGA*	3xOxidation [P5; P6; P8]	Collagen alpha-3(IX) chain	8.93	5.16	12.34	11.62	within
e103724	QDGATGSQSGPGDSAY	none	Semaphorin-6C	10.43	6.36	12.73	11.59	within
e104055	APGDKGESGPSGPAGPT*	1xOxidation [P2]	Collagen alpha-1(I) chain	11.27	7.73	13.2	12.23	within
e102198	PGPPGPPGPAGNPGPSP*	3xOxidation [P4; P6; P7]	Collagen alpha-1(XXVI) chain	9.34	6.11	12.06	10.41	within
e100005	PAGEPGREGSPGADGP*	3xOxidation [P1; P5; P11]	Collagen alpha-1(II) chain	10.11	5.75	12.57	9.44	within
e211953	GGTAPGAPGPGPGSGTSSS	none	Transcriptional activator MN1	11.02	6.84	12.82	11.5	within
e211955	TEIPEAQIHEGFQ	none	Alpha-1-antitrypsin	10.44	6.18	12.56	12.29	within
e011013	GPPGKDGPNGPPGPPGT	none	Collagen alpha-1(XXII) chain	8.96	4.62	11.65	9.87	within
e211958	PENVTNGTVGGTAEPG	none	Large neutral amino acids transporter small subunit 4	9.19	5.95	12.44	9.87	within
e011036	RQKLGPAGDVEGH	none	Apolipoprotein A-IV	7.36	2.2	13.14	7.17	within
e011043	SGPDVFPATPGSQNK	none	Microtubule-associated serine/threonine-protein kinase 4	7.06	4.71	11.71	8.82	within
e211963	SKGEPGIQGMPGASGL*	1xOxidation [P5]	Collagen alpha-1(XXI) chain	7.06	4.78	11.75	8.91	within
e211964	AAPSSPDDSSGMGPLN	none	Zinc finger protein 750	8.59	4.06	11.03	6.45	within
e011054	GSPGRDGSPGAKGDRG*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	6.68	2.19	10.04	8.49	within
e011063	PGLPAGFDDMEGSGGP	none	Collagen alpha-1(XVIII) chain	8.56	6.18	11.85	12.17	up
e211967	AHAGEYGAEALERM	none	Hemoglobin subunit alpha	7.06	4.69	10.88	8.37	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e211968	HTTAFPGSTTMPGLS	none	Mucin-12	8.93	5.09	11.6	10.27	within
e011081	AFTAELTAPFPPVGA*	1xOxidation [P11]	Collagen alpha-1(VIII) chain	8.89	4.34	12.37	8.48	within
e011099	EAEASGEEEEGDGTP	none	Helicase SRCAP	10.75	6.57	13.95	9.16	within
e011100	SESDQDERGDSGQP	none	RNA polymerase-associated protein LEO1	7.13	3.1	9.7	2.79	down
e011102	DEMAAVMGFSGFGST	none	Zinc finger matrin-type protein 2	6.48	3.61	11.08	7.53	within
e106218	ETEGEDEPESEGAE	none	Retinitis pigmentosa 1-like 1 protein	8.21	5.37	10.88	11.33	up
e011112	EFQIMDPTGNSATP	none	FRAS1-related extracellular matrix protein 1	13.97	11.45	15.83	15.27	within
e211975	VVSLGSPSGEVSHPR	none	Alpha-2-HS-glycoprotein	9.4	6.4	12.59	12.55	within
e211977	VGPPGPPGPPGPPGPS*	3xOxidation [P6; P7; P]	Collagen alpha-1(I) chain	14.7	11.92	16.14	15.09	within
e011152	GSPGSPGPDGKTGPPGP*	3xOxidation [P3; P6; P8]	Collagen alpha-1(I) chain	14.28	10.88	15.82	14.89	within
e099684	GPAGPRGERGPPGESG*	2xOxidation [P2; P5]	Collagen alpha-2(I) chain	11.11	7.04	13.19	9.19	within
e011169	TGPGGDKDGTGPPGPQG*	1xOxidation [P13]	Collagen alpha-1(III) chain	13.95	10.4	15.36	14.83	within
e011172	AGEKGEPGPPGSEGLP*	2xOxidation [P7; P9]	Collagen alpha-1(XVI) chain	7.84	3.82	11.58	8.92	within
e101286	DGATGAAGPPGPTGPAGP*	4xOxidation [P10; P12; P15; P18]	Collagen alpha-1(I) chain	12.28	7.96	14.42	12.58	within
e094535	GGAGEPGKNGAKGEPGP*	2xOxidation [P6; P15]	Collagen alpha-1(III) chain	12.09	8.23	14.15	14.65	up
e011194	SPGSNGAPGQRGEPGP*	3xOxidation [P2; P8; P14]	Collagen alpha-1(III) chain	11.8	7.93	13.61	12.26	within
e103875	AASGPNQMSFTFASP	none	ATP synthase F(1) complex subunit delta, mitochondrial	7.41	4.05	10.82	6.14	within
e211987	ESVRQMLQDEMF	none	Ciliogenesis and planar polarity effector 1	10.89	7.14	12.49	10.15	within
e011198	DGAKGDAGPAGPKGEPG*	2xOxidation [P9; P12]	Collagen alpha-1(I) chain	10.6	6.43	13.05	12.57	within
e011199	GLDGAKGDAGPAGPKGE*	1xOxidation [P14]	Collagen alpha-1(I) chain	10.75	6.98	12.97	12.0	within
e103039	PTQGYAQTQAYGQ	none	RNA-binding protein EWS	9.69	6.81	11.99	10.9	within
e011208	KNIHSAAPMGDEM	none	Engulfment and cell motility protein 3	8.54	5.27	11.48	10.66	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e011209	DITDGNSEHLKRE	none	Vesicular integral-membrane protein VIP36	8.45	5.29	11.53	10.72	within
e011216	DEEDEDEDESDDS	none	Bromodomain adjacent to zinc finger domain protein 2B	11.24	5.96	14.62	12.91	within
e211999	GPPGKDGPNGPPGPPGT*	1xOxidation [P]	Collagen alpha-1(XXII) chain	8.69	3.91	12.17	6.39	within
e011223	GLPGRDGSPGGKGDRG*	2xOxidation [P3; P9]	Collagen alpha-1(III) chain	7.61	3.64	11.44	10.75	within
e300138	FSDSPITVTVPVEV	none	Clusterin	12.72	7.35	15.01	14.79	within
e011273	PEETSSSSQTQDHS	none	Serine/threonine-protein kinase 17B	10.84	5.83	13.71	14.44	up
e104165	GPPDVPDHAAYHPF	none	Inter-alpha-trypsin inhibitor heavy chain H4	10.22	6.8	13.16	9.49	within
e011280	PPGRDGQPGHKGER*	2xOxidation [P2; P8]	Collagen alpha-2(I) chain	7.16	4.92	10.03	8.92	within
e201925	PEGPKGRTGPTGDPGP	none	Collagen alpha-2(XI) chain	9.17	5.36	14.22	10.08	within
e011284	NDGPPGRDGQPGHKG*	2xOxidation [P5; P11]	Collagen alpha-2(I) chain	7.71	3.94	10.68	10.73	up
e011285	GQDGRPGPPGPPGARG*	3xOxidation [P8; P9; P11]	Collagen alpha-1(I) chain	9.72	5.74	12.67	10.44	within
e011291	SEGARGAPGPAGPPGDP*	2xOxidation [P10; P13]	Collagen alpha-1(VI) chain	7.09	4.35	9.78	7.16	within
e201930	GDSDDDEPPPLPRL	none	Membrane-associated progesterone receptor component 1	9.97	6.48	14.21	11.5	within
e212019	PEPTKSAPAPKKGSK	none	Histone H2B type 1-D	8.8	5.19	12.5	11.31	within
e212021	SGGRGDPGDVGGPAGNPG	none	Choline O-acetyltransferase	12.28	8.93	14.23	13.39	within
e212022	KPGEQGVPGDLGAPGP*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	12.22	8.78	14.18	12.87	within
e011307	HKSEVAHRFKDLG	none	Albumin	8.08	5.12	12.81	9.8	within
e212025	AGAKGDAGPPGPAGPAGP*	5xOxidation [P9; P10; P12; P15; P18]	Collagen alpha-1(I) chain	15.62	13.31	16.88	15.88	within
e011313	KGTPGEPGPPGDDGFP	none	Collagen alpha-4(IV) chain	15.61	13.42	16.9	15.89	within
e212027	MGPPGIPGQPGEPGYA	none	Collagen alpha-1(XXII) chain	6.51	0.86	11.42	3.25	within
e212032	VGPPGPPGPPGPPGPS*	4xOxidation [P7; P9; P]	Collagen alpha-1(I) chain	16.54	14.32	17.98	16.89	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e011326	VIDQSRVLNLGPIT	none	Uromodulin	12.86	9.22	16.14	14.8	within
e212038	TESQDSSMEQIDR	none	Protein CFAP20DC	14.65	8.48	16.19	14.95	within
e011332	HSSPDASGTPSSAHS	none	Mucin-12	12.57	8.15	14.25	13.02	within
e106413	GSPGSPGPDGKTGPPGP*	4xOxidation [P3; P6; P14; P17]	Collagen alpha-1(I) chain	11.2	7.8	13.24	10.47	within
e011333	QGPPGSEGFTGPPGPQ*	1xOxidation [P]	Collagen alpha-2(IV) chain	12.35	7.44	14.26	11.58	within
e011334	TSPSHGSIAAYQGYS	none	Pleckstrin homology domain-containing family A member 5	15.14	8.75	16.37	15.16	within
e212040	GPPGPPGVPGPPGPGSP*	3xOxidation [P5; P6; P9]	Collagen alpha-1(XXII) chain	15.88	13.01	17.28	16.23	within
e100690	DDEDDDDTDDLDE	none	DDB1- and CUL4-associated factor 1	15.07	12.88	16.53	16.19	within
e011347	AGSGEESSEEDADAM	none	Scm-like with four MBT domains protein 2	11.74	7.33	14.44	13.47	within
e104619	EPEPSGDPTGAGSSAAP	none	C-Jun-amino-terminal kinase-interacting protein 3	14.41	11.64	15.7	13.78	within
e011350	RSPAPGSPDEEGGAEA	none	Synemin	11.89	7.31	13.52	12.22	within
e011351	EGLPGDRGDPGDTGAP*	1xOxidation [P10]	Collagen alpha-2(IV) chain	11.77	7.38	13.5	10.3	within
e105840	APGNDGAKGDAGAPGAP*	3xOxidation [P2; P14; P17]	Collagen alpha-1(I) chain	10.42	7.26	12.34	9.37	within
e097387	MIEQNTKSPLFMG*	2xOxidation [M1; M12]	Alpha-1-antitrypsin	9.42	6.58	12.13	9.19	within
e011367	EPFSQDGTLEDFGS	none	Rho guanine nucleotide exchange factor TIAM1	9.87	5.78	12.92	7.88	within
e011403	PGGGGFFGSSLPGPPGP*	3xOxidation [P1; P12; P14]	Collagen alpha-1(XVIII) chain	11.99	7.09	13.96	12.75	within
e102887	GPSGAPGEDGRPGPPGP*	2xOxidation [P12; P14]	Collagen alpha-1(II) chain	11.26	7.73	13.59	12.8	within
e208011	RDGEPGTPGNPGPPGP*	2xOxidation [P13; P]	Collagen alpha-1(II) chain	11.37	7.75	13.73	12.8	within
e106584	QGPQGEKGEAGPPGPP*	2xOxidation [P12; P13]	Collagen alpha-1(IV) chain	10.96	6.08	13.49	11.89	within
e101081	GDAGPVGPPGPPGPPGP*	7xOxidation [P5; P8; P9; P11; P12; P14; P15]	Collagen alpha-1(I) chain	10.79	5.8	13.46	11.89	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e212062	AGPPGVMGPPGPPGPPG*	6xOxidation [P4; P9; P10; P12; P13; P15]	Collagen alpha-1(XV) chain	7.56	4.1	10.69	10.84	up
e212063	AGPNGADGPQGPPGGVGN*	1xOxidation [P3]	Collagen alpha-2(XI) chain	9.3	5.14	11.7	11.54	within
e011425	PGPQGAPGLSGSDGHKG*	1xOxidation [P3]	Collagen alpha-4(IV) chain	7.38	4.6	10.91	8.92	within
e011430	SYGYGSGFGGYGYGSG	none	Keratin-associated protein 19-1	9.31	5.04	12.12	7.7	within
e011438	ARGAPGDRGEPGPPGP*	3xOxidation [P5; P11; P13]	Collagen alpha-1(I) chain	8.5	3.25	12.35	8.05	within
e011449	ADSGEGDFLAEGGGVR	none	Fibrinogen alpha chain	10.41	5.66	14.92	7.72	within
e094558	GNPGGPGADGIAGAAGPP*	4xOxidation [P3; P5; P6; P17]	Collagen alpha-1(XXII) chain	9.94	3.46	12.61	11.3	within
e011443	VEHSDLSFSKDWS	none	Beta-2-microglobulin	10.78	7.26	12.57	11.55	within
e212072	GPGAAAGPEAGPGSGAGTV	none	Voltage-dependent calcium channel beta subunit-associated regulatory protein	10.29	6.16	12.45	11.19	within
e212075	SKAASDDGSLKSSSPT	none	Unconventional myosin-XVIIIa	10.27	6.66	12.43	11.14	within
e212076	IPGEKGPA GERGAPGP*	3xOxidation [P2; P7; P14]	Collagen alpha-1(III) chain	8.09	4.79	11.56	6.87	within
e094562	SLGSPSGEVSHPRKT	none	Alpha-2-HS-glycoprotein	9.04	3.76	13.58	10.38	within
e011474	GAEEASGGTGYGGEGSGP	none	Ral guanine nucleotide dissociation stimulator-like 2	12.36	5.33	14.0	9.8	within
e212083	STGTSAGGSSSSQQNSP	none	Cytosolic carboxypeptidase-like protein 5	12.47	6.52	14.19	12.02	within
e201964	DGGGPGAGAPAGTGGAAGAGG	none	Doublesex- and mab-3-related transcription factor A2	9.57	6.39	12.1	11.13	within
e094563	PPGEAGKPGEQGVPGD*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	9.83	6.8	12.42	11.13	within
e011488	KDGDGTGPTGPQGPPGP*	2xOxidation [P13; P16]	Collagen alpha-1(XXII) chain	11.81	7.94	13.66	11.99	within
e103482	VGPPGEPGPPGQQGNH*	1xOxidation [P9]	Collagen alpha-3(V) chain	10.76	7.55	13.29	10.69	within
e208023	VGPPGPPGPPGPPGPPS*	5xOxidation [P6; P7; P9; P10; P12]	Collagen alpha-1(I) chain	14.1	7.75	16.03	15.68	within
e011497	HVDGPPPRPQLRAT	none	Alpha-1B-glycoprotein	9.33	4.32	13.51	6.45	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e011504	KGDRGPAGPPGHPGPP*	3xOxidation [P9; P10; P13]	Collagen alpha-1(XVII) chain	7.62	4.45	12.06	8.12	within
e212089	GPPGVPGPPGPGGSPGLP*	3xOxidation [P6; P8; P]	Collagen alpha-1(XXII) chain	15.22	11.95	16.76	14.96	within
e212090	PGPPGVPGPPGPGGSPGL*	3xOxidation [P4; P7; P9]	Collagen alpha-1(XXII) chain	15.22	12.3	16.77	14.96	within
e011510	SGSVIDQSRVLNLGP	none	Uromodulin	11.52	8.23	13.58	11.81	within
e011515	GLPGPPDVPDHAAYH	none	Inter-alpha-trypsin inhibitor heavy chain H4	5.81	0.0	11.06	3.87	within
e212095	RDGLPGPPGPPGPPSP*	3xOxidation [P10; P11; P]	Collagen alpha-6(IV) chain	13.95	10.86	15.68	13.83	within
e011522	DGQPGAKGEPGDAGAKG*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	10.6	6.8	12.54	11.46	within
e097395	RISHELDASSEVN	none	Osteopontin	10.57	6.98	12.51	11.44	within
e011537	SPDQDMREAGAQLK	none	Uteroglobin	7.0	2.35	11.62	4.99	within
e212104	SHEKMHEGDEGPGH	none	Protein S100-A9	6.66	2.93	9.67	8.37	within
e011543	GSLGSLGSGSGSGSHEGG	none	Period circadian protein homolog 1	11.31	6.58	13.69	6.22	down
e212108	PPGPPGAMGPPGPPGAP*	6xOxidation [P2; P4; P5; P10; P11; P]	Collagen alpha-1(XVII) chain	14.17	10.1	16.5	12.71	within
e212111	GEPGPPGSEGLPGPPGP*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XVI) chain	14.23	10.16	16.56	12.7	within
e106070	GETGPAGPPGAPGAPGAPG*	2xOxidation [P12; P]	Collagen alpha-1(I) chain	10.36	6.89	12.37	10.74	within
e104473	MRGMPGPPGPPGPPGP*	3xOxidation [P7; P8; P]	Collagen alpha-1(XVIII) chain	14.23	9.96	16.56	12.71	within
e011569	LNAPSDWDSRGKDS	none	Osteopontin	8.02	2.24	11.25	9.57	within
e212118	REGFPGPFIGPR*	4xOxidation [P5; P7; P8; P13]	Collagen alpha-2(IV) chain	6.83	2.72	11.02	8.85	within
e212120	GQHGASSGQSSSHGQH	none	Hornerin	11.61	7.23	13.79	8.71	within
e212122	RHGTTGQTGDTSGH	none	Filaggrin-2	12.24	7.05	14.48	8.04	within
e097401	FGDLSTPDV/MGNPK	none	Hemoglobin subunit beta	9.66	5.5	13.45	9.52	within
e011580	QKGDAGAPGPQGPPSGAPG	none	Collagen alpha-1(II) chain	6.69	2.83	10.19	9.1	within
e212123	NSTTTNNSKPSSLPT	none	Methylcytosine dioxygenase TET1	7.66	3.6	11.77	5.5	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e011591	GDAGAPGPQGPPSGAPGPQ*	2xOxidation [P11; P15]	Collagen alpha-1(II) chain	7.97	5.24	12.28	8.0	within
e099674	LDGPPGPDGLQGPPGP*	5xOxidation [P5; P7; P13; P14; P16]	Collagen alpha-5(IV) chain	12.32	7.99	14.25	13.14	within
e212125	QGPQGEKGEAGPPGPP*	3xOxidation [P3; P12; P13]	Collagen alpha-1(IV) chain	12.31	7.96	14.25	13.13	within
e011618	GGDKGEDGDPGQPGPPG*	1xOxidation [P16]	Collagen alpha-1(XI) chain	11.21	7.75	12.77	11.78	within
e011619	DTGAEDSSGSSPATSAI	none	Receptor-type tyrosine-protein phosphatase zeta	10.5	5.95	12.23	11.83	within
e212130	GTGGPPGENGKPGEPGP*	3xOxidation [P6; P12; P15]	Collagen alpha-1(III) chain	10.11	6.02	12.97	8.1	within
e212131	AGPPGEAGKPGEQGVPG*	3xOxidation [P4; P10; P16]	Collagen alpha-1(I) chain	10.1	6.04	13.16	8.1	within
e094575	TISEKTSDQIHFF	none	Antithrombin-III	8.17	5.1	11.19	8.76	within
e212133	DDDEGEEGEEDEGE	none	Protein SET	14.99	12.23	16.52	16.44	within
e011634	DFEKFLQQTGGRQ	none	Coiled-coil domain-containing protein 112	6.9	2.75	10.06	2.93	within
e100610	DGEDEDEDEEDE	none	Serine/threonine-protein kinase LMTK3	11.6	6.04	13.74	14.38	up
e201998	GADEDEDEGSGDDED	none	Dentin sialophosphoprotein	14.03	10.66	15.55	15.46	within
e011640	EKGSPGADGPAGAPGTPG*	2xOxidation [P5; P10]	Collagen alpha-1(I) chain	9.33	5.19	12.48	10.39	within
e104132	VGPPGEPGPPGQQGNH*	2xOxidation [P7; P10]	Collagen alpha-3(V) chain	9.1	5.27	12.36	6.81	within
e102764	GDIGPPGPQGPPGPQGP*	2xOxidation [P]	Collagen alpha-1(XII) chain	9.4	5.17	13.42	8.14	within
e011656	DPDADGDGVPNEKDN	none	Cartilage oligomeric matrix protein	9.79	6.57	11.78	14.26	up
e011660	PGVPGPPGPGGSPGLPGE*	2xOxidation [P]	Collagen alpha-1(XXII) chain	12.88	8.63	14.89	11.57	within
e202010	GYEAPVLFRTEDY	none	Biogenesis of lysosome-related organelles complex 1 subunit 4	5.98	1.59	10.15	1.38	down
e202016	FEKSKEQLTPLIK	none	Apolipoprotein A-II	7.12	2.83	11.49	5.72	within
e208041	GGSMGDYMAQEDDW	none	Alpha-actinin-4	11.39	7.63	13.86	12.81	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e011685	KDAAAMDPMGDTLEP	none	Transient receptor potential cation channel subfamily M member 2	7.6	5.36	11.16	10.18	within
e011689	EDGHPGKPGRPGERG*	1xOxidation [P11]	Collagen alpha-2(I) chain	9.62	5.8	12.2	11.07	within
e011690	GYLGEHSSVFQQPL	none	ETS translocation variant 4	9.58	5.88	12.31	10.99	within
e212154	GPVGFPGDPGPPGEPGP*	2xOxidation [P2; P6]	Collagen alpha-1(V) chain	10.47	6.64	12.48	11.13	within
e212155	GPPGFTGPPGPPGPPGP*	5xOxidation [P3; P8; P9; P11; P]	Collagen alpha-1(IV) chain	14.73	9.56	17.19	10.84	within
e101390	GEQGLPGSPGPDGPPGP*	3xOxidation [P6; P9; P11]	Collagen alpha-1(V) chain	14.32	10.05	16.63	11.93	within
e011721	PGSPGPPGSPGPRGPPG*	6xOxidation [P6; P7; P10; P12; P15; P16]	Collagen alpha-1(XIV) chain	14.23	11.91	15.62	14.46	within
e011719	GAPGADGPQGPPGGIGNP*	3xOxidation [P3; P8; P11]	Collagen alpha-1(V) chain	14.21	11.89	15.57	14.46	within
e101105	RGPSGAPGADGPQGPPGG*	2xOxidation [P3; P7]	Collagen alpha-1(V) chain	10.05	6.8	12.1	9.0	within
e011724	SSSDSDSGDEGDEYD	none	NF-kappa-B inhibitor beta	9.78	5.88	14.21	6.82	within
e102710	NSSSSLQPNMNSSDP	none	Rho GTPase-activating protein 26	13.34	9.45	14.92	13.22	within
e011727	SPGSPGPDGKTGPPGPAG*	2xOxidation [P2; P5]	Collagen alpha-1(I) chain	11.48	7.79	13.43	11.56	within
e202026	GETGAVGAPGAPGPPGSPG*	2xOxidation [P9; P12]	Collagen alpha-1(II) chain	13.31	8.43	15.03	13.65	within
e011728	EKETEGLRQEMSK	none	Apolipoprotein A-I	7.39	3.47	12.45	6.07	within
e212162	RVIVNVEDANDHSP	none	Protocadherin Fat 3	10.55	7.37	12.79	10.33	within
e101599	KGDAGAPGPQGSPGAPGP*	3xOxidation [P9; P12; P16]	Collagen alpha-1(II) chain	10.79	7.53	12.99	8.31	within
e011748	PGQGAPGPPGHPSHP*	5xOxidation [P1; P4; P7; P9; P10]	Collagen alpha-2(V) chain	11.38	7.41	12.83	12.19	within
e208048	GITGPPGPPGPPGPPGAP*	3xOxidation [P14; P]	Collagen alpha-2(VIII) chain	7.61	4.35	12.5	7.77	within
e212175	KGPQGPAGRDGVQGPV*	3xOxidation [P3; P6; P15]	Collagen alpha-1(XI) chain	6.82	3.51	10.22	3.26	down
e011765	GSQPQEEGGSVNENH	none	Tetra-peptide repeat homeobox protein 1	9.05	5.5	11.85	9.4	within
e094595	GSEADHEGTHSTKRG	none	Fibrinogen alpha chain	12.7	8.94	14.16	11.09	within
e011778	APGPVGPAGKSGDRGET*	1xOxidation [P2]	Collagen alpha-1(I) chain	7.76	3.32	11.38	6.88	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e100340	EGSPGHPGQPGPPGPPG*	3xOxidation [P10; P12; P13]	Collagen alpha-1(III) chain	10.23	6.76	12.63	8.56	within
e011790	FPHFDLSHGSAQVK	none	Hemoglobin subunit alpha	9.39	4.69	12.41	10.21	within
e011797	IDDESSDTPGATPEH	none	Archaemetzincin-2	8.46	4.92	11.64	8.97	within
e011800	EGFPGDIGPPGDNGPE*	1xOxidation [P15]	Collagen alpha-1(XXVII) chain	9.2	4.4	11.99	8.77	within
e212188	SPAPDPPDPPDSAGPGP	none	Serine/threonine-protein kinase WNK4	7.52	4.18	11.24	9.34	within
e102609	GAKGDAGAPGAPGSQGAPG*	3xOxidation [P9; P12; P18]	Collagen alpha-1(I) chain	9.95	5.58	13.03	10.61	within
e011802	SAGDPHGPGELEPPN	none	Ras association domain-containing protein 10	7.31	4.12	11.24	9.34	within
e212189	QGSSRHAAAYTTHPS	none	Homeodomain-interacting protein kinase 1	10.9	7.11	12.83	12.27	within
e011805	SRHPAENGKSNFLN	none	Beta-2-microglobulin	10.17	5.69	12.76	12.02	within
e212191	GPPGPSGVPGQPGSPGLP*	1xOxidation [P15]	Collagen alpha-5(IV) chain	8.83	5.2	12.64	11.84	within
e101086	AELGGHLDQQVEEF	none	Apolipoprotein A-IV	9.24	6.17	13.37	9.73	within
e212199	QGLPGENGVPVGPVPPG*	3xOxidation [P9; P12; P13]	Collagen alpha-1(XXII) chain	10.77	6.64	12.36	11.52	within
e100682	SPGTSGPPGSAGPPGSPGP*	1xOxidation [P]	Collagen alpha-2(V) chain	11.05	6.73	12.62	11.64	within
e011850	GPPGRDGQPGHKGGER*	2xOxidation [P3; P9]	Collagen alpha-2(I) chain	7.8	5.16	10.26	11.05	up
e011852	IFPPSDEQLKSGTAS	none	Immunoglobulin kappa constant	9.04	5.13	14.98	10.36	within
e011859	TKAPADLRGVAHNNL	none	Complement C4-B	7.79	4.81	12.85	10.67	within
e212208	PGMGNADDEQQEEGT	none	General transcription factor 3C polypeptide 4	14.13	11.31	15.8	14.27	within
e106359	SWPKQETWENGES	none	Zinc finger and BTB domain-containing protein 10	15.05	10.46	16.71	16.8	up
e212217	GTDTDIDGYPDQALP	none	Thrombospondin-3	10.27	6.61	12.49	11.0	within
e212218	SEESLSTTLQAAPD	none	Protein sidekick-2	12.05	8.16	13.94	13.64	within
e011873	EDGHPGKPRPGERG*	2xOxidation [P5; P8]	Collagen alpha-2(I) chain	12.17	8.51	13.95	13.64	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e212221	KGEEGSDDDETENGP	none	RNA polymerase-associated protein CTR9 homolog	13.62	10.82	15.3	13.65	within
e212223	VAESMYGDFQEAMT	none	Terminal nucleotidyltransferase 5D	13.23	8.25	15.79	9.71	within
e212225	GGGSGSRGGSGGSHGGGSGF	none	Keratin, type I cytoskeletal 9	13.68	9.42	15.97	9.7	within
e212228	PGPPGPPGPPGPPGTMG*	7xOxidation [P4; P6; P7; P9; P10; P12; P13]	Collagen alpha-1(XVIII) chain	13.8	9.52	15.96	11.1	within
e212231	PQTPQSTSSSMAEGGD	none	AT-rich interactive domain-containing protein 1A	11.79	7.64	14.94	8.9	within
e212233	GLPGEEDSGPDEPPSP	none	U5 small nuclear ribonucleoprotein TSSC4	12.6	8.2	14.96	8.9	within
e011900	DHGSDHHYRGKRD	none	RNA-binding protein 7	10.41	5.79	12.15	11.24	within
e106641	APGGKGDAGAPGERGPPG*	2xOxidation [P2; P11]	Collagen alpha-1(III) chain	9.1	5.97	11.47	10.56	within
e011903	VGPPGPPGPPGPPGPSA*	3xOxidation [P6; P7; P]	Collagen alpha-1(I) chain	12.27	7.98	14.16	12.74	within
e212238	AVAGMPGGSAGAMNSMTA	none	Hepatocyte nuclear factor 3-alpha	16.09	13.76	17.28	16.61	within
e011909	GGYSDGLGGNSLYSPH	none	Pre-B-cell leukemia transcription factor 3	16.09	13.73	17.27	16.61	within
e011910	SPGSPGPDGKTGPPGPAG*	3xOxidation [P5; P7; P]	Collagen alpha-1(I) chain	14.38	12.83	15.37	14.49	within
e202079	IDQSRVLNLGPITR	none	Uromodulin	14.42	9.86	16.53	13.75	within
e011925	NYKNVGEEDEEEK	none	Protein CLEC16A	11.82	9.23	13.63	10.93	within
e011937	SEDSNSQDSGEFAPD	none	Arginine/serine-rich protein PNISR	9.44	5.29	12.21	11.78	within
e011939	GSSSGGGAGSSNSGGGSGSGN	none	Cbp/p300-interacting transactivator 2	10.82	6.27	13.44	11.87	within
e011945	GAPGNDGAKGDAGAPGAPG*	3xOxidation [P3; P15; P18]	Collagen alpha-1(I) chain	9.56	6.06	11.74	9.23	within
e011946	NDGAPGKNGERGGPGGP*	3xOxidation [P5; P14; P17]	Collagen alpha-1(III) chain	12.35	8.43	13.76	13.5	within
e208068	EDSDSDSDLDEDED	none	Transcription factor HIVEP3	12.17	7.41	14.71	14.57	within
e011958	QTFTDLAAEASSEE	none	Uncharacterized protein UNQ6126/PRO20091	10.62	6.5	13.15	12.56	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e202084	EGSPGHPGQPGPPGPPG*	4xOxidation [P4; P7; P13; P16]	Collagen alpha-1(III) chain	11.12	7.74	13.24	12.24	within
e011959	SPGSMGPRGDTGPAGPP*	3xOxidation [P2; P7; P13]	Collagen alpha-3(V) chain	11.0	7.44	13.21	12.23	within
e011960	SLGSSESSSLEETSVS	none	Kinesin-like protein KIF17	10.7	6.6	13.17	12.81	within
e011973	GAAGPSGEEGDKGDVGAP*	1xOxidation [P5]	Collagen alpha-3(V) chain	11.3	6.67	12.7	8.09	within
e099072	SPGSPGPDGKTGPPGPAG*	1xCation:Na [D8]; 2xOxidation [P2; P5]	Collagen alpha-1(I) chain	11.77	6.78	13.33	11.91	within
e011986	SFPTTKTYFPHFD	none	Hemoglobin subunit alpha	7.97	1.15	12.47	10.51	within
e011987	GPPGPPGSAGARGEPPGG*	1xOxidation [P]	Collagen alpha-1(XII) chain	10.98	7.16	12.99	9.11	within
e212270	GGFPGPSGNDGSAGPPGP*	4xOxidation [P6; P15; P16; P18]	Collagen alpha-1(VII) chain	11.32	5.32	13.9	7.66	within
e011995	EDSPLGGSSGEDDPLG	none	Carbonic anhydrase 9	11.33	5.44	13.88	7.66	within
e011998	AFEISTEGHSGPSNR	none	Protein patched homolog 1	8.23	5.1	10.73	6.17	within
e012000	VEGPPGPSGVPGQPGSPG*	1xOxidation [P11]	Collagen alpha-5(IV) chain	10.62	6.89	12.41	10.0	within
e099829	QDTPTSAESPDAPEE*	1xOxidation [P10]	Collagen alpha-1(XVIII) chain	9.29	5.86	12.77	6.82	within
e012006	TGLSMDGGGSPKGDVDP	none	Sodium/potassium-transporting ATPase subunit gamma	11.97	7.49	13.95	11.62	within
e208072	PKGDGPDGPGSGPPGPP*	4xOxidation [P7; P10; P13; P14]	Collagen alpha-2(IX) chain	11.92	7.62	13.95	11.62	within
e012011	GPAGHPGEQQPGPEGS*	2xOxidation [P6; P]	Collagen alpha-1(XXVII) chain	11.17	5.22	13.91	10.99	within
e012012	PGPAGAAGPAGNPGADGQP*	2xOxidation [P1; P3]	Collagen alpha-1(I) chain	12.11	9.71	13.71	11.75	within
e012031	PGPPGPAGEKGSFGADGP*	3xOxidation [P3; P4; P6]	Collagen alpha-1(I) chain	10.37	5.41	12.37	9.97	within
e212277	DDFLSPSGMIEGTPQ	none	Otogelin-like protein	11.88	8.46	13.54	11.96	within
e012041	PGGPGSDGKPGPPGSQGE*	1xOxidation [P10]	Collagen alpha-1(III) chain	11.87	8.56	13.53	11.97	within
e012042	EDGHPGKPRPGERG*	3xOxidation [P5; P8; P11]	Collagen alpha-2(I) chain	11.48	7.55	13.24	13.12	within
e012043	AGEPGKPGAPGKPGTPGA*	3xOxidation [P4; P7; P10]	Collagen alpha-1(IX) chain	8.65	3.16	12.23	12.2	within
e012052	TTTAVTAAAASDDSPSE	none	Formin-binding protein 4	12.57	9.22	14.25	12.86	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e102616	PGTPGNPGPPGPPGPPGP*	3xOxidation [P4; P9; P12]	Collagen alpha-1(II) chain	9.63	6.02	12.02	10.08	within
e106211	PQGPNGADGPQGPPGSV*	4xOxidation [P1; P4; P10; P13]	Collagen alpha-1(XI) chain	10.47	7.34	12.48	10.37	within
e012061	APGGKGDAGAPGERGPPG*	3xOxidation [P2; P11; P16]	Collagen alpha-1(III) chain	10.78	5.18	13.18	10.46	within
e012064	DGPPGLPGTPGPPGPPGP*	2xOxidation [P]	Collagen alpha-1(VII) chain	13.76	10.6	15.17	14.46	within
e212284	KGGQGPPGPQGPIGYPG*	2xOxidation [P7; P9]	Collagen alpha-1(V) chain	13.74	10.65	15.11	14.45	within
e012074	MESMETAAAGSAGLAAE	none	Kelch-like protein 11	12.25	8.65	13.55	13.27	within
e012076	GPPGEAGKPGEQGVPGD*	3xOxidation [P3; P9; P15]	Collagen alpha-1(I) chain	12.35	9.91	13.5	12.85	within
e012077	FFGSSLPGPPGPPGPPG*	2xOxidation [P9; P10]	Collagen alpha-1(XVIII) chain	13.16	9.09	14.58	13.73	within
e012078	VETTTPSKQSNKY	none	Immunoglobulin lambda constant 2	9.77	4.12	12.25	11.44	within
e012079	PGLDQGPGAPGLPGPPGP*	1xOxidation [P]	Collagen alpha-5(IV) chain	13.13	9.38	14.48	13.74	within
e012083	DQTPHHMHSHPH	none	Cyclic AMP-responsive element-binding protein 5	11.03	7.23	12.65	11.49	within
e012085	GPPGHVGPPGPPGQPGP*	6xOxidation [P3; P8; P9; P11; P12; P15]	Collagen alpha-1(XVI) chain	10.55	7.35	12.54	11.87	within
e102413	GEKGPSGEAGTAGPPGTP*	2xOxidation [P15; P18]	Collagen alpha-2(I) chain	10.82	6.84	12.18	11.14	within
e300056	GSPGPPGTPGEPGMQGE*	3xOxidation [P6; P9; P12]	Collagen alpha-3(IV) chain	10.51	5.58	14.39	7.2	within
e012118	DDAMGDEEDEEESD*	1xOxidation [M4]	Charged multivesicular body protein 2a	12.45	8.73	14.3	14.31	up
e012123	DPGPPGQSGRDGYPGP*	3xOxidation [P4; P5; P14]	Collagen alpha-1(XXIII) chain	10.35	7.08	12.47	11.07	within
e012132	DQPDLYEYYPH	none	Trafficking protein particle complex subunit 12	11.61	6.45	14.25	10.08	within
e099074	SPGSPGPDGKTGPPGPAG*	1xCation:Na [C-Term]; 3xOxidation [P2; P5; P7]; 1xCation:Na [D8]	Collagen alpha-1(I) chain	10.86	6.69	13.08	11.26	within
e212297	GPMDASVEEEGVRRRA	none	Cystatin-C	7.55	4.03	11.85	8.75	within
e012136	IPVKQADSGSSEEKQ	none	Osteopontin	7.54	3.99	12.33	8.73	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e212299	GPPGPDGLPGSMGPPGTP*	1xOxidation [P]	Collagen alpha-1(IV) chain	11.11	7.84	12.85	9.92	within
e012142	SGPPGFPLGTTGEKGE*	1xOxidation [P]	Collagen alpha-6(IV) chain	10.86	7.36	12.64	9.88	within
e012143	LPSVGSEDLAVDSPAF	none	RNA-binding E3 ubiquitin-protein ligase MEX3C	7.42	1.39	12.52	7.97	within
e012153	AGLEQEAAAGGDEEEEE	none	Heterogeneous nuclear ribonucleoprotein U	11.61	7.48	13.49	13.0	within
e012154	SGRESGDEREEAPG	none	Coiled-coil domain-containing protein 195	9.34	5.33	12.05	8.9	within
e099668	PGPPGPPGPSISSGQ*	2xOxidation [P1; P3]	Collagen alpha-1(XVII) chain	10.18	5.97	12.09	8.92	within
e104491	FHDDGFLAFPGHVF	none	Basement membrane-specific heparan sulfate proteoglycan core protein	13.35	10.24	15.11	12.2	within
e103279	KTKVPS*	1xO-Glycan [T2] (HexNAc(1)Hex(1) NeuAc(2))	Ubiquitin-conjugating enzyme E2 R2	9.33	6.24	13.24	11.59	within
e012186	DGPAGPPGERGPNGPQG*	3xOxidation [P3; P6; P7]	Collagen alpha-1(V) chain	8.07	5.23	10.69	8.94	within
e106258	IENEEQEYVQTVK	none	Annexin A1	9.88	4.73	14.17	6.18	within
e012202	GPPGSNGNPGPSGSP*	5xOxidation [P3; P9; P11; P12; P14]	Collagen alpha-1(III) chain	11.42	7.95	12.88	10.97	within
e208086	SGDSDDDEPPPLPRL	none	Membrane-associated progesterone receptor component 1	11.98	8.19	13.72	12.56	within
e012215	TGSPGSPGDGKTGPPGP*	3xOxidation [P7; P9; P]	Collagen alpha-1(I) chain	13.49	10.25	15.15	14.75	within
e012221	NGSPGSPGEPGSGTPGQ*	2xOxidation [P12; P16]	Collagen alpha-1(XXII) chain	11.17	7.24	14.18	14.05	within
e212318	PGISPPGPRGKKGPPGP*	1xOxidation [P15]	Collagen alpha-4(IV) chain	13.42	9.03	15.9	14.42	within
e012233	MPGSPGGPGSDGKPGPPG*	4xOxidation [P2; P5; P8; P14]	Collagen alpha-1(III) chain	11.05	7.17	13.26	13.08	within
e012235	PGLDGQPGAPLPGPPGP*	2xOxidation [P10; P13]	Collagen alpha-5(IV) chain	11.88	6.99	13.85	10.81	within
e212321	LTDEEKRLMVELH	none	Peptidase inhibitor 16	8.59	2.32	13.09	8.17	within
e012238	GKVNVDVGEALGRL	none	Hemoglobin subunit beta	10.67	5.23	15.37	12.4	within
e212322	DPVAAFKRGVLEPLT	none	Protein TANC1	12.21	8.78	14.81	13.01	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e012252	ENVIENGSPNNSLNN	none	Zinc finger protein 654	10.07	6.25	12.43	11.55	within
e103707	GADGQPGAKGEPGDAGAK*	2xOxidation [P6; P12]	Collagen alpha-1(I) chain	10.76	6.31	12.94	11.94	within
e012251	IFPDPSGDSYTMIA	none	ATP-binding cassette sub-family A member 6	10.23	5.76	12.5	11.51	within
e012254	GDLSSPDAVMGNPKVK	none	Hemoglobin subunit delta	11.89	8.39	13.35	12.79	within
e212327	GGEDEEEATDYGGTSV	none	Tigger transposable element-derived protein 5	12.58	7.13	15.39	9.35	within
e012268	GAAGEAGAAGEAGGAGEAGGAG	none	Paraneoplastic antigen Ma6F	10.07	5.44	12.37	8.19	within
e102631	VGPPGSNGNPGPPGPPGP*	4xOxidation [P3; P10; P13; P16]	Collagen alpha-1(II) chain	8.56	5.02	11.89	5.72	within
e212328	GPRGDKGETGEQGDRG	none	Collagen alpha-1(I) chain	6.76	0.89	10.94	6.06	within
e012271	EPALPSGAGPLPDRA	none	Tigger transposable element-derived protein 5	9.97	6.34	12.11	8.93	within
e105310	NELRVAPEEHPVLL	none	Actin, cytoplasmic 1	9.91	6.41	14.18	8.94	within
e208088	PGEPPGPPQQGNHGSQG*	1xOxidation [P7]	Collagen alpha-3(V) chain	8.63	4.1	12.18	5.33	within
e012280	ETWLAEAQVPDNDE	none	ETS translocation variant 1	8.53	3.5	11.04	6.2	within
e012287	TPGEPGMQGEPPGPP*	1xOxidation [P]	Collagen alpha-3(IV) chain	10.73	6.03	14.16	6.24	within
e099028	APGGKGDAGAPGERGPPG*	1xCation:Na [D7]; 3xOxidation [P2; P11; P16]	Collagen alpha-1(III) chain	9.96	6.65	12.26	11.38	within
e212335	GPPGNPGLPGEPPVGGGG*	3xOxidation [P9; P12; P14]	Collagen alpha-5(IV) chain	10.83	6.31	13.93	6.24	down
e012293	WDNLEKETEGLRQ	none	Apolipoprotein A-I	7.76	2.52	11.61	11.39	within
e212340	NEGGEQAPTQNEEES	none	Protein BEX4	13.55	9.16	15.83	11.08	within
e012307	GPQGEPPGPPQQGNP*	3xOxidation [P6; P8; P9]	Collagen alpha-1(XI) chain	11.29	8.33	12.72	11.57	within
e012309	GNSGEPGAPGSKGDTGAK*	2xOxidation [P6; P9]	Collagen alpha-1(I) chain	11.32	8.25	12.69	11.55	within
e212342	PPPGTGEEAGPGGGDRAP	none	PAX3- and PAX7-binding protein 1	11.16	7.79	12.67	11.6	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e012323	HQSSYGQHSGSSQSS	none	Filaggrin-2	12.57	5.54	13.89	13.34	within
e012325	DHTGKPGPEDYPLF*	3xOxidation [P6; P8; P12]	Collagen alpha-1(V) chain	11.18	7.04	12.97	9.89	within
e101512	SGGEDASEGGAEEGAGGAGG	none	Lon protease homolog, mitochondrial	10.85	7.59	13.4	12.54	within
e208090	EEKSDGAASKEDSGP	none	Zinc finger protein castor homolog 1	11.5	7.77	13.3	11.67	within
e012336	GPSGQTGDPGLQGPPSGPP*	1xOxidation [P]	Collagen alpha-1(XXIV) chain	10.49	5.95	12.91	11.71	within
e012337	GSPGSPGPDGKTGPPGPAG*	2xOxidation [P3; P6]	Collagen alpha-1(I) chain	10.46	7.3	12.79	9.55	within
e212352	NPSASSGNETTFSGGGGP	none	Lysine-specific demethylase 3B	11.13	4.52	13.58	9.13	within
e097451	GLDGPPGPDGLQGPPGP*	6xOxidation [P5; P6; P8; P14; P15; P17]	Collagen alpha-5(IV) chain	11.47	7.56	13.41	11.49	within
e208092	PTGPGGDKGDTGPPGPQG*	2xOxidation [P4; P13]	Collagen alpha-1(III) chain	11.58	6.04	13.42	10.48	within
e212354	PAGSPGERGAAGSGGPIGP*	2xOxidation [P5; P16]	Collagen alpha-2(XI) chain	10.34	5.5	13.03	9.15	within
e100089	KGTSOSSSGNVSEGESP	none	PHD finger protein 10	10.11	5.6	12.93	10.8	within
e012369	DGAPGKNGERGGPGGPGP*	3xOxidation [P13; P16; P]	Collagen alpha-1(III) chain	15.61	14.04	16.66	16.14	within
e212362	GATGQPGPKGDVGQDGAP*	1xOxidation [P6]	Collagen alpha-3(V) chain	15.6	14.03	16.67	16.15	within
e094656	NDGAPGKNGERGGPGGPG*	2xOxidation [P14; P]	Collagen alpha-1(III) chain	14.64	12.04	15.97	15.32	within
e212369	KGEPGDAGAKGDAGPPGP*	3xOxidation [P4; P15; P16]	Collagen alpha-1(I) chain	14.66	11.48	15.97	15.3	within
e012392	GGSGAGGARGAFGYGNNGGV	none	V-set and immunoglobulin domain-containing protein 8	10.68	7.23	12.93	10.69	within
e099857	QDGVGGDKGEDGDPGQP	none	Collagen alpha-1(XI) chain	10.8	6.84	13.05	10.98	within
e212376	SVDEPGPGLSGEQGPPG*	3xOxidation [P5; P7; P15]	Collagen alpha-1(VII) chain	9.96	6.85	13.75	12.49	within
e102320	GPSEGGSSSTMYVSGPP*	2xOxidation [P2; P16]	Collagen alpha-1(XVII) chain	12.09	9.01	13.52	12.61	within
e212379	SQAGFSPYSIDSEPGS	none	Sterol regulatory element-binding protein 2	12.17	8.65	13.61	12.92	within
e212381	PGPPGPPGPSAGFDFS*	3xOxidation [P4; P6; P7]	Collagen alpha-1(I) chain	10.76	5.93	12.6	10.31	within
e012418	GRDGSPGAKGDRGETGP*	1xOxidation [P6]	Collagen alpha-1(I) chain	7.35	2.75	10.6	5.14	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e208103	DGAPASDSKPGSSEAAPS	none	Brain acid soluble protein 1	12.25	9.14	13.63	13.65	up
e012421	EDGAADASKGLGGSGGAGGP	none	Proline-rich protein 12	10.82	6.58	12.54	11.09	within
e012422	EGRASPAPGSGHPEGPGA	none	Mitochondrial import receptor subunit TOM70	8.07	4.88	10.62	10.8	up
e012424	GHHQAGPGQGGDEGEAAG	none	Putative golgin subfamily A member 8D	8.61	4.58	11.62	8.71	within
e012429	EGSPGRDGSPGAKGDRG*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	10.41	5.66	12.99	11.61	within
e012431	EEAPSLRPAPPPISGGG	none	Fibrinogen beta chain	10.01	6.77	12.55	7.56	within
e212395	GEDGHPGKPRPGERG*	2xOxidation [P6; P9]	Collagen alpha-2(I) chain	9.94	5.64	12.52	12.05	within
e012478	SFGDLSTPDVAMGNPK	none	Hemoglobin subunit beta	12.56	8.99	14.42	11.49	within
e012481	LPGSPGNIGPAGKEGPVG*	2xOxidation [P2; P5]	Collagen alpha-2(I) chain	12.47	9.23	14.12	11.56	within
e105515	EGPPGEPGPPGPPGPPG*	9xOxidation [P3; P4; P7; P9; P10; P12; P13; P15; P16]	Collagen alpha-2(V) chain	13.0	7.72	14.44	13.98	within
e012490	HVDANDHDQSRKSQ	none	Semenogelin-1	9.22	5.82	11.79	11.15	within
e012491	LDGEPGPQGLPGAPGDQ*	2xOxidation [P5; P7]	Collagen alpha-1(IX) chain	10.81	7.14	13.64	8.87	within
e012493	QPGEKGSPGAQGPPGAPG*	3xOxidation [P2; P8; P13]	Collagen alpha-1(III) chain	12.73	6.69	15.95	8.76	within
e012495	GSPGPAGPRGPVGPSPGP*	6xOxidation [P3; P5; P8; P11; P14; P17]	Collagen alpha-1(III) chain	12.79	7.85	15.99	8.67	within
e012497	VGPPGPPGPPGPPGPPSAG*	3xOxidation [P6; P7; P]	Collagen alpha-1(I) chain	13.1	9.22	14.73	13.4	within
e012507	IEGVDAEDGHGPGEQQ	none	Complement factor B	14.43	10.3	15.62	14.74	within
e012508	PPEPTDKSPEAEDP	none	Zinc finger protein 512B	13.15	9.88	15.11	14.47	within
e212402	GYISGPLVSDMDTDAP	none	Roundabout homolog 1	16.56	14.68	17.8	16.68	within
e012512	GSPGSPGPDGKTGPPGPAG*	3xOxidation [P6; P8; P]	Collagen alpha-1(I) chain	14.77	13.16	15.78	14.74	within
e212403	GPTGSPGTSGPPGSAGPPGS*	1xOxidation [P6]	Collagen alpha-2(V) chain	16.56	14.58	17.78	16.68	within
e093736	QGEAGQKGDAGAPGPQGP*	1xOxidation [P15]	Collagen alpha-1(II) chain	14.8	13.2	15.83	14.74	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e104906	SPASQPFMPIGPPSEP	none	Myosin-binding protein C, cardiac-type	11.37	6.68	13.49	11.53	within
e012538	LSLEVAGGTAQAPSLGPA	none	Zinc finger protein 628	8.82	3.96	13.18	5.04	within
e208115	GSLYDDDVAQWNIGS	none	Lysine-specific demethylase 4B	13.62	7.18	14.84	13.93	within
e012542	AGSEADHEGTHSTKRG	none	Fibrinogen alpha chain	13.84	11.16	14.86	13.93	within
e012569	AGSGEESSEEDADAMD	none	Scm-like with four MBT domains protein 2	15.18	11.42	17.09	15.69	within
e099997	NKNGDNNSNHNGEGNG	none	Transcription factor 20	10.11	7.08	12.48	10.11	within
e012576	PPGIAGPQGSQGERGAD*	3xOxidation [P1; P2; P7]	Collagen alpha-1(XXII) chain	8.51	4.88	11.18	11.17	within
e012584	DGQPQAKGEPGDAGAKGD*	1xOxidation [P10]	Collagen alpha-1(I) chain	10.1	6.27	12.45	7.33	within
e106633	GDPGQPGPPGPSGEAGPPG*	1xOxidation [P]	Collagen alpha-1(XI) chain	8.51	5.43	11.35	9.27	within
e094674	DGENDDRPPNPPKP	none	CD99 antigen	9.79	5.43	11.59	8.7	within
e012602	PGFPGMKGPSVPGSAGP*	3xOxidation [P4; P9; P13]	Collagen alpha-5(IV) chain	12.53	9.6	14.02	12.35	within
e012601	AAWGK/GAHAGEYGAEA	none	Hemoglobin subunit alpha	8.31	6.31	12.94	6.58	within
e012611	KPGLPGMPGADGPPGHP*	4xOxidation [P2; P5; P8; P13]	Collagen alpha-1(V) chain	9.16	5.44	11.38	11.71	up
e012612	TGPAGPPGAPGAPGAPVPG*	4xOxidation [P10; P13; P16; P18]	Collagen alpha-1(I) chain	9.1	5.35	11.45	11.64	up
e212419	RGETGPAGPPGAPGAPGAP*	2xOxidation [P10; P13]	Collagen alpha-1(I) chain	9.68	6.22	12.73	11.12	within
e012614	GAPGERGPPGLAGAPGLR*	1xOxidation [P]	Collagen alpha-1(III) chain	8.94	5.66	12.45	8.36	within
e300058	GPAGSRGDGGPPGMTGFP*	2xOxidation [P2; P11]	Collagen alpha-2(I) chain	11.05	2.63	12.96	10.07	within
e202229	PGEPGASGPMGPRGPPGP*	2xOxidation [P]	Collagen alpha-1(I) chain	10.62	5.99	12.48	8.65	within
e012641	KGEVGDVGSMGPHGAPGP	none	Collagen alpha-3(V) chain	9.86	5.89	12.5	5.77	down
e012650	EPPEQQEPGERQEP	none	Integrin alpha-7	10.29	7.17	12.77	8.3	within
e097470	KGEPGDPGRPGPVGEQG*	1xOxidation [P7]	Collagen alpha-1(XXVII) chain	9.36	6.56	13.83	8.33	within
e012653	IGTLDGFRHRHPDE	none	Fibrinogen alpha chain	6.45	3.4	10.41	4.93	within
e212431	GSDHETGSSGSSDEQGN	none	YTH domain-containing protein 1	8.56	4.42	12.47	10.21	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e212432	SPGGSGSDSNNTGEQGAE	none	SH2B adapter protein 2	9.77	5.57	12.22	13.08	up
e212433	NQSSDADSEALFGVPN	none	Sodium-dependent glucose transporter 1	13.21	11.14	14.49	13.1	within
e012659	GPPGPAGQPGDKGEGGAPG*	3xOxidation [P3; P5; P9]	Collagen alpha-1(III) chain	13.22	11.17	14.5	12.93	within
e208124	PGPPGQQGNPQPGLPG*	6xOxidation [P1; P3; P4; P10; P12; P16]	Collagen alpha-1(XI) chain	11.5	7.71	13.53	11.5	within
e012661	GEDGHPGKPRPGERG*	3xOxidation [P6; P9; P12]	Collagen alpha-2(I) chain	9.99	5.43	11.94	11.58	within
e012662	DITDGNSEHLKREH	none	Vesicular integral-membrane protein VIP36	9.55	5.06	11.89	11.26	within
e212435	VMSDFANGLGWRIAGG	none	Natural resistance-associated macrophage protein 2	8.45	3.43	13.69	7.22	within
e012670	REQPPASTPGHGPSH	none	Cell adhesion molecule CEACAM4	9.45	5.64	13.85	7.05	within
e012671	GPQGQPLPGPPGPPGPP*	3xOxidation [P11; P12; P14]	Collagen alpha-1(VIII) chain	8.76	5.86	12.93	10.13	within
e097471	ENEDRRSASLHLPK	none	Alpha-1-antitrypsin	7.54	4.23	11.82	6.38	within
e012674	VVDPKSKEEDKHLK	none	Osteopontin	7.2	4.4	13.99	6.89	within
e012681	ESLTMDADANLNDED	none	Transcriptional activator GLI3	12.15	6.45	13.73	13.34	within
e012682	FHSHEFHSHEDML	none	Osteopontin	8.78	4.57	11.4	11.68	up
e012684	GAPGGKGDAGAPGERGPPG*	3xOxidation [P3; P12; P17]	Collagen alpha-1(III) chain	11.28	4.51	13.31	13.11	within
e012688	TGDAGVPVGPPGPPGPPGPP*	2xOxidation [P]	Collagen alpha-1(I) chain	14.77	12.32	16.22	15.11	within
e012694	QAAYEDEEDEEPAAS	none	Histone-lysine N-methyltransferase PRDM16	8.66	4.35	11.96	11.16	within
e012695	DFLQNTHEFESAES	none	Coiled-coil domain-containing protein 141	10.71	6.07	12.35	12.86	up
e012697	GYISGPLVSDMDTDAP*	1xOxidation [M11]	Roundabout homolog 1	11.47	8.31	13.29	11.0	within
e012698	PGSPGPAGASGNPGTDGIP*	3xOxidation [P1; P4; P6]	Collagen alpha-1(II) chain	9.48	6.5	12.46	11.3	within
e012701	QGPPGPPGVPGPPGPGGSP*	3xOxidation [P12; P13; P15]	Collagen alpha-1(XXII) chain	7.36	2.92	11.21	7.77	within
e212445	GFFGSSLPGPPGPPGPPG*	2xOxidation [P10; P11]	Collagen alpha-1(XVIII) chain	14.36	11.42	15.69	14.49	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e012703	RGGPGSAGGAGFPREPSP	none	Transcription factor MafA	14.34	11.41	15.67	14.27	within
e212449	PGPPGPPGPPGPPGTPVY*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	14.35	11.48	15.66	14.47	within
e100381	KNGERIEKVEHSDL	none	Beta-2-microglobulin	8.04	2.29	12.59	7.82	within
e012717	SGSVIDQSRVLNLGPI	none	Uromodulin	14.22	9.27	17.04	14.56	within
e094686	GPAGPPGIAGMSGKPGAPG*	5xOxidation [P2; P5; P6; P15; P18]	Collagen alpha-1(XIX) chain	7.29	3.57	10.45	7.52	within
e012721	SPGEAGRPEAGLPGAKG*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	9.48	5.75	12.61	6.63	within
e212455	TKSQIKEGKPSWGLP	none	tRNA (guanine(6)-N(2))-methyltransferase THUMP3	13.3	8.85	16.3	13.97	within
e212456	AQYQKDAPDHQELN	none	Complement C3	9.63	4.73	12.3	8.6	within
e094688	YHAFSAMKKVETNM	none	Plasma protease C1 inhibitor	7.5	3.19	10.87	7.82	within
e212458	GPPGDQGPDPGPRGAP*	2xOxidation [P9; P11]	Collagen alpha-4(IV) chain	7.59	4.65	10.54	9.89	within
e012743	KVGAHAGEYGAEALER	none	Hemoglobin subunit alpha	7.39	4.8	11.81	9.5	within
e102312	ENGWTTFYEYDSF	none	Teneurin-4	10.94	4.52	12.85	12.39	within
e012747	QKGDAGNPGDPGTPGTTG*	2xOxidation [P8; P11]	Collagen alpha-1(XVI) chain	11.67	4.85	13.43	12.87	within
e212461	PGSPGFPGPQGDRGFPG*	2xOxidation [P7; P9]	Collagen alpha-1(IV) chain	10.83	5.89	12.53	9.11	within
e012758	DSMEANLNESERQH	none	Nesprin-1	12.37	8.36	14.87	7.51	down
e106302	GEPGAPGSKGDTGAKGEP*	3xOxidation [P3; P6; P18]	Collagen alpha-1(I) chain	9.08	4.37	12.3	11.63	within
e212466	GPPGPPGPPGSAGARGEPPG*	3xOxidation [P3; P5; P6]	Collagen alpha-1(XII) chain	10.78	7.01	13.5	6.46	down
e212469	GSVGEAGPEGPPGEPGPPG*	1xOxidation [P]	Collagen alpha-2(V) chain	12.31	8.83	14.4	11.15	within
e012766	GPPGFGRPGDPGPPGPPG*	3xOxidation [P3; P8; P11]	Collagen alpha-1(XV) chain	12.67	9.68	14.15	12.77	within
e212471	QPGPKGNVGPQGEPGPP*	3xOxidation [P2; P4; P10]	Collagen alpha-1(V) chain	12.47	9.0	14.07	12.72	within
e012776	PPGPPGPPGPRGPPGDT*	7xOxidation [P4; P5; P7; P8; P10; P13; P]	Collagen alpha-1(XXV) chain	13.93	10.57	15.86	14.68	within
e106482	EEGAHVSEEPSFIPEA	none	ADAMTS-like protein 1	10.36	5.58	12.63	11.84	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e202269	GDPGPPGEPGPAGQDGPP*	4xOxidation [P6; P9; P11; P17]	Collagen alpha-1(V) chain	13.17	8.9	15.6	11.68	within
e012786	GPPGPSGDQGASGPAGPSGP*	1xOxidation [P17]	Collagen alpha-1(II) chain	11.29	8.12	12.81	10.34	within
e012791	RRSLAPYAQDTQEK	none	Apolipoprotein A-IV	9.96	4.34	14.36	12.35	within
e104750	GEAGKPRPGERGPPGP*	3xOxidation [P9; P14; P]	Collagen alpha-1(I) chain	8.53	2.48	12.79	11.74	within
e012806	DDDDEFGEFGGFSEV	none	Aftiphilin	9.19	5.42	11.68	11.99	up
e012810	LSTPDAMGNPKVKAH	none	Hemoglobin subunit beta	9.59	5.17	13.16	11.87	within
e208132	EVGEKGDEGPPGDPGLP*	1xOxidation [P10]	Collagen alpha-1(VII) chain	12.95	10.35	14.96	12.49	within
e012818	GLPGTGGPPGENGKPGEP*	3xOxidation [P3; P8; P9]	Collagen alpha-1(III) chain	12.83	10.13	14.65	12.01	within
e212477	QGSPGPPGVPGSPGSSRP*	3xOxidation [P6; P7; P10]	Collagen alpha-3(IV) chain	7.25	2.78	10.11	4.69	within
e012820	GDPTSVTLFGESAGAASV	none	Acetylcholinesterase	7.28	2.75	10.59	4.71	within
e093741	ASPAGTAGGPGAGAAAGGTGPL	none	Transcription initiation factor TFIID subunit 10	12.32	8.76	13.88	12.01	within
e012832	TDGPKGASGPAGPPGAQGP*	3xOxidation [P10; P13; P14]	Collagen alpha-1(II) chain	12.41	10.18	14.13	11.68	within
e012834	GEVGMRGPPQPPGLPGP*	4xOxidation [P11; P12; P15; P17]	Collagen alpha-1(XXII) chain	12.51	9.26	14.27	11.68	within
e012837	TKGKRAPFTNFPDST	none	Carbonic anhydrase 1	6.9	4.35	12.08	7.08	within
e212480	GWSSSRGPYESGSSHS	none	Hornerin	8.53	4.52	11.05	11.37	up
e012841	SGKQSTSSQEASSASEP	none	Protein cordon-bleu	8.74	4.8	11.39	11.17	within
e212481	KPGEQGVPGDLGAPGPSG*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	11.37	7.56	13.28	12.02	within
e012856	AHVDDMPNALSALSDL	none	Hemoglobin subunit alpha	11.76	7.09	13.5	11.63	within
e212483	EPLEPGGAGRAEQGSTL	none	Multiple C2 and transmembrane domain-containing protein 1	8.67	4.91	12.84	10.55	within
e012865	GMPGSPGGPGSDGKPGPPG*	4xOxidation [P3; P6; P9; P15]	Collagen alpha-1(III) chain	9.13	5.81	12.21	7.78	within
e212487	PGEKGPIGPTGRDGVQG*	3xOxidation [P1; P6; P9]	Collagen alpha-2(XI) chain	13.87	10.1	15.49	13.82	within
e212489	PGPPGPPGPPGPGTPVY*	2xOxidation [P]	Collagen alpha-1(XVIII) chain	13.87	9.89	15.47	13.82	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e104308	FSNGADL*	1xO-Glycan [S2] (HexNAc(1)Hex(1) NeuAc(2))	Alpha-1-antitrypsin	14.55	9.97	16.79	11.05	within
e012880	DEAGSEADHEGTHSTK	none	Fibrinogen alpha chain	11.98	7.15	13.79	9.24	within
e102350	YWASTRESGVPDRF	none	Immunoglobulin kappa variable 4-1	12.38	9.45	14.17	13.49	within
e212496	PPGPEGGKGAAGPPGPPGAA*	2xOxidation [P16; P]	Collagen alpha-1(III) chain	12.8	8.52	14.58	12.25	within
e212498	YSPGAEDSDSLNNGEGS	none	Lymphocyte transmembrane adapter 1	13.53	7.27	16.0	7.09	down
e202295	SEGSPGHPGQPGPPGPPG*	4xOxidation [P8; P11; P14; P17]	Collagen alpha-1(III) chain	11.36	8.43	13.42	11.63	within
e012894	PGGVGFPGSRGDTGPPGP*	4xOxidation [P7; P15; P16; P18]	Collagen alpha-1(IV) chain	8.41	5.19	11.93	10.54	within
e012915	PGTPGEPGMQGEPPGPPG*	1xOxidation [P/M]	Collagen alpha-3(IV) chain	12.77	8.82	15.15	10.89	within
e212508	SGEPGLPGPPGPPGPPGQ*	5xOxidation [P10; P12; P13; P]	Collagen alpha-1(X) chain	12.77	8.93	15.18	10.77	within
e012919	KGDQGPDPGSPGSPGPA	none	Collagen alpha-3(IV) chain	6.03	0.65	11.21	1.07	within
e212509	GPPGSAGPPGSPGPQGSGTGP*	1xOxidation [P]	Collagen alpha-2(V) chain	7.23	2.17	10.06	8.39	within
e202303	GLDYGAGDGPGLAFGGPGP	none	SH3 and multiple ankyrin repeat domains protein 3	11.61	6.21	13.76	10.01	within
e212510	QSSRNQPGPPGPPGPPG*	3xOxidation [P7; P9; P10]	Collagen alpha-1(XII) chain	12.7	8.56	15.16	10.79	within
e012920	GAKGQEGAHGAPGAAGNPGA	none	Collagen alpha-1(XXII) chain	11.34	7.83	13.05	9.95	within
e012928	EGGENAGAEDVAAGGEDAG	none	Golgin subfamily A member 6-like protein 2	10.83	6.18	13.4	10.93	within
e212511	EEDLALMEEMEAH	none	DNA polymerase delta catalytic subunit	13.56	8.99	16.23	8.18	down
e212513	QSDINHSTSGSHYEN	none	Trinucleotide repeat-containing gene 6A protein	13.58	9.0	16.22	8.17	down
e212514	KGDPGNRGPDGYPGGEAG*	2xOxidation [P4; P9]	Collagen alpha-2(VI) chain	13.56	8.58	16.2	7.42	down
e212516	GNSGEPGAPGSKGDTGAKG*	2xOxidation [P6; P9]	Collagen alpha-1(I) chain	9.46	5.13	12.28	8.47	within
e012936	SPGRDGSPGAKGDRGET*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	10.54	6.52	12.45	12.63	up
e212517	AAASANGAAGGLAGTTNGPF	none	Pumilio homolog 1	10.49	6.71	12.59	12.38	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e012939	LSQGDASASFPGSEPLL	none	Histone-lysine N-methyltransferase 2D	8.94	5.22	12.34	7.69	within
e212519	KGSDGPPGKPGPPGPGI*	4xOxidation [P10; P12; P13; P15]	Collagen alpha-1(XIX) chain	8.8	6.23	13.09	7.69	within
e097486	PEGQVGVPGDPGLRGQP*	1xOxidation [P8]	Collagen alpha-3(IV) chain	10.09	6.3	13.03	11.34	within
e212523	PGEDGPAGEPGPPGPEGQ*	2xOxidation [P13; P15]	Collagen alpha-1(XV) chain	12.0	6.27	13.63	11.33	within
e103475	GPPGPPGTSGHPGSPGSPG*	5xOxidation [P5; P6; P12; P15; P18]	Collagen alpha-1(III) chain	12.46	8.84	13.8	10.89	within
e012952	TDERGPPGEQPPGPPG*	2xOxidation [P13; P15]	Collagen alpha-1(IX) chain	10.19	4.22	12.29	10.31	within
e212524	VGAHAGEYGAEALERM*	1xOxidation [M16]	Hemoglobin subunit alpha	9.67	6.12	12.01	10.72	within
e104986	LNSSSLQPNMNSSDP	none	Rho GTPase-activating protein 26	11.06	6.98	13.09	9.18	within
e202314	ENDPVLGPDGKTHGNK	none	Serine protease inhibitor Kazal-type 5	8.2	4.87	12.17	9.46	within
e012962	PPGPPKNGDDGEAGKPG*	2xOxidation [P]	Collagen alpha-1(I) chain	9.96	6.75	12.32	10.38	within
e012972	DSNTGIRSSPNMEQGS	none	Pleckstrin-2	10.29	7.28	12.52	9.42	within
e012973	GLPGFPGPQGAPGRDGAP*	2xOxidation [P8; P11]	Collagen alpha-1(XXII) chain	8.13	4.51	12.18	6.59	within
e012983	PGPPGHPGPPGPGTDGAA*	1xOxidation [P7]	Collagen alpha-1(XVI) chain	8.13	4.82	12.2	4.92	within
e012988	VIDQSRVLNLGPITR	none	Uromodulin	15.7	11.12	19.47	18.9	within
e103251	GSSDWVTSYSLMFSD	none	Contactin-associated protein-like 5	10.72	6.59	12.99	9.35	within
e212534	PGSPGYQGPPGEPGQAGP*	2xOxidation [P10; P13]	Collagen alpha-1(III) chain	14.67	12.44	15.64	14.96	within
e212537	LGDSLGGDHFAGGGDLPP	none	Non-homologous end joining factor IFFO1	14.63	12.43	15.64	14.93	within
e012994	DEPPQSPWDRVKDL	none	Apolipoprotein A-I	9.59	6.8	12.93	8.9	within
e012998	KGEEGGAGEPGKYDSMA	none	Collagen alpha-1(XIX) chain	10.77	6.99	12.85	10.92	within
e099661	STPGSGSGPAHGPDPAHGP	none	Transcription factor MafF	14.28	12.31	15.27	14.34	within
e212539	GEPGKQGAPGASGDRGPP*	3xOxidation [P3; P9; P17]	Collagen alpha-1(II) chain	14.29	12.05	15.21	14.42	within
e012999	GERGETGPPGPAGFPAGP*	2xOxidation [P11; P15]	Collagen alpha-1(III) chain	10.2	3.93	12.56	10.91	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e106185	APGQNGEPGGKGERGAPG*	3xOxidation [P2; P8; P17]	Collagen alpha-1(III) chain	9.11	5.16	11.16	7.22	within
e013006	SGQKGKQQTESKGSFS	none	Semenogelin-1	7.95	2.13	13.21	6.49	within
e013029	GEDAGPGGEDAGAGGEDAGP	none	Golgin subfamily A member 6-like protein 2	15.15	13.13	16.44	16.08	within
e212548	MGPPGSPGEDGPAGEPGP*	5xOxidation [P4; P7; P12; P16; P18]	Collagen alpha-1(XV) chain	15.13	8.81	16.5	16.08	within
e013032	GMPGSPGGPGSDGKPGPPG*	5xOxidation [P3; P6; P9; P15; P17]	Collagen alpha-1(III) chain	15.33	11.69	16.51	16.08	within
e013037	PQPSLPPEAAQEGDLH	none	Obscurin	7.07	3.87	12.4	7.72	within
e013047	EGAETESPEPGDEGEPPG	none	Rho guanine nucleotide exchange factor 1	14.82	12.93	16.0	15.5	within
e013060	ESGDSDEEDDEMSE	none	Ribosome biogenesis protein BMS1 homolog	12.24	8.4	13.87	13.95	up
e013064	DESMTEDEIEEQSF	none	Centrosome-associated protein 350	12.66	8.7	14.23	12.05	within
e094721	TVASHTSDSDVPSGVTE	none	Clusterin	11.9	8.22	13.85	11.7	within
e013076	PPGPTGPGGDKDGTGPPGP*	2xOxidation [P7; P16]	Collagen alpha-1(III) chain	10.5	7.02	13.52	11.9	within
e101462	VADNSLYDPESPVTPS	none	RELT-like protein 1	11.49	8.22	13.99	11.8	within
e013095	AGAEDVAAGGEDAGEEED	none	Golgin subfamily A member 6-like protein 2	9.67	5.98	11.79	9.96	within
e013099	DGPPGRDGGQPGHKGER*	2xOxidation [P4; P10]	Collagen alpha-2(I) chain	7.85	4.14	12.15	5.55	within
e013115	PGGYAAAGSGGAGGVSGGGSSL	none	Transcription factor GATA-6	9.33	5.16	12.01	10.69	within
e212574	GQASSPTPEPGVGAGDLPG	none	Mediator of DNA damage checkpoint protein 1	13.31	9.98	15.06	14.01	within
e212575	PPGEAGKPGEQGVPGDLG*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	13.32	9.68	15.11	13.8	within
e212577	GYRGHQGPSPGLPGP*	2xOxidation [P11; P15]	Collagen alpha-1(XXIV) chain	12.29	8.15	13.69	11.71	within
e212578	SVGPVGPRGPQGLQGQQ*	2xOxidation [P7; P10]	Collagen alpha-2(V) chain	13.04	9.21	15.03	13.83	within
e013126	PPGPPGKNGDDGEAGKPG*	3xOxidation [P4; P5; P17]	Collagen alpha-1(I) chain	10.83	6.0	12.61	7.29	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013129	ISPNSGNVTSASGSQMAS	none	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	11.26	6.74	13.11	10.82	within
e013132	GQQGNPGAQGLPGPQGA1*	3xOxidation [P6; P12; P14]	Collagen alpha-1(V) chain	10.28	5.9	12.64	7.29	within
e208145	QGPPGSEGFTGPPGPQGP*	2xOxidation [P3; P4]	Collagen alpha-2(IV) chain	10.39	6.5	12.19	10.65	within
e103247	GPAGARGNDGATGAAGPPGP*	3xOxidation [P17; P18; P20]	Collagen alpha-1(I) chain	10.27	5.97	12.18	11.88	within
e102934	EKGPSGEAGTAGPPGTPGP*	2xOxidation [P14; P17]	Collagen alpha-2(I) chain	9.54	6.38	12.71	7.9	within
e013137	ARNFGKEFTPQMCAA	none	Hemoglobin subunit delta	8.8	4.53	11.65	12.28	up
e013138	MGVVSLGSPSGEVSHPR	none	Alpha-2-HS-glycoprotein	7.83	3.64	11.96	11.71	within
e013144	PSGESRPGSPGPPGSPGP*	5xOxidation [P7; P10; P12; P13; P16]	Collagen alpha-1(XIV) chain	11.77	7.49	13.48	9.47	within
e212580	APGPQGFQGPAGEPGEPP*	3xOxidation [P2; P4; P10]	Collagen alpha-2(I) chain	11.22	7.2	13.64	12.07	within
e013150	SPGSNGAPGQRGEPPGQG*	3xOxidation [P2; P8; P14]	Collagen alpha-1(III) chain	10.94	7.56	12.48	7.31	down
e099655	GSPGVNGAPGEAGRDGNPG*	2xOxidation [P3; P9]	Collagen alpha-2(I) chain	10.41	5.25	13.46	11.99	within
e013152	LGHPDTLNQGEFKEL	none	Protein S100-A9	10.46	5.81	14.67	8.98	within
e013157	NGAPGNDGAKGDAGAPGAP*	3xOxidation [P4; P16; P19]	Collagen alpha-1(I) chain	13.78	11.96	14.66	14.37	within
e013159	GAGGGPPPPGPPGAGDRGGGGPG	none	Far upstream element-binding protein 2	10.43	5.03	12.86	10.66	within
e097496	SLGTKADTHDEILEGL	none	Alpha-1-antitrypsin	9.15	4.75	14.08	8.24	within
e013165	DEDSDSGSDEEEGEAE	none	Protein phosphatase 1 regulatory subunit 15A	12.46	6.6	15.49	11.73	within
e212583	EPGAPGENGTPGQTGARG*	3xOxidation [P2; P5; P11]	Collagen alpha-2(I) chain	12.76	9.94	13.88	13.01	within
e013188	GRDGSPGAKGDRGETGPA*	1xOxidation [P6]	Collagen alpha-1(I) chain	8.23	4.01	10.89	6.38	within
e013193	GSSNSGGGSGSQSGSSGSGSN	none	Dermokine	12.29	7.94	13.88	12.46	within
e099826	GFPGPSGNDGSAGPPGPPG*	5xOxidation [P3; P5; P14; P15; P17]	Collagen alpha-1(VII) chain	12.91	10.1	14.06	13.03	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013204	KGDTGEDGYPGGPGPPGP*	3xOxidation [P13; P15; P16]	Collagen alpha-4(IV) chain	13.04	9.52	13.98	12.36	within
e013205	ASSEVPAASPADSSNSPE	none	Histone acetyltransferase KAT6A	9.92	5.63	11.99	11.68	within
e212588	GVAGGAVSTPAPAPASAPAG	none	E3 ubiquitin-protein ligase TRIM33	11.41	7.15	13.82	12.71	within
e212589	DGLGELKKLLETHIH	none	Cullin-1	11.35	6.78	15.15	8.44	within
e013216	QGDSGPQGPPGSEGFTGP*	2xOxidation [P10; P18]	Collagen alpha-2(IV) chain	11.54	7.58	13.49	8.44	within
e013226	DHDVGSELPPEGVLGAL	none	ProSAAS	12.39	6.76	16.07	10.57	within
e013233	VPQQYMSALLQATGAQ	none	Gastricsin	10.35	6.24	14.26	10.5	within
e300034	GPPGTPGEPGMQGEPPGP*	3xOxidation [P6; P9; P15]	Collagen alpha-3(IV) chain	13.76	8.77	15.45	15.55	up
e212597	TPGEPGMQGEPPGPPGP*	3xOxidation [P2; P5; P11]	Collagen alpha-3(IV) chain	11.85	7.54	13.65	9.92	within
e013244	SDGESDNSDRVPVPSF	none	E3 ubiquitin-protein ligase RNF10	12.92	9.53	14.68	13.14	within
e212601	GSDIHGDPGFPGPPGER*	1xOxidation [P]	Collagen alpha-2(IV) chain	12.98	10.01	14.72	13.23	within
e013245	SAQNTPRGNYNESRGG	none	Protein virilizer homolog	8.3	4.36	11.2	10.38	within
e212603	QGPVGLPGPAGPAGSPGED*	3xOxidation [P9; P12; P16]	Collagen alpha-1(XI) chain	12.99	10.16	14.73	13.23	within
e212605	ATASVSEGGGLQGISMKD	none	Calcium-dependent secretion activator 1	12.67	7.86	14.69	12.68	within
e013250	KTSLVASSSGAVSGVMNI	none	Apolipoprotein L5	9.41	5.24	13.52	6.35	within
e013256	AAAAGAGAGAAAAGAEGPSGPV	none	Homeobox protein SIX5	11.47	7.51	14.15	12.9	within
e100756	KELVEVMVDMASNLM	none	Adhesion G protein-coupled receptor A2	12.41	8.77	14.06	13.14	within
e094749	PPGEAGKPGEQGVPGDLG*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	13.65	10.86	15.2	14.17	within
e013269	QTPVQNTGGKNPDPWA	none	Serotransferrin	13.53	10.62	15.2	14.16	within
e212613	GERGSPGTPGQVGQPGTP*	2xOxidation [P6; P9]	Collagen alpha-6(IV) chain	13.3	10.68	14.64	13.27	within
e100462	EKGPSGEAGTAGPPGTPGP*	3xOxidation [P4; P14; P17]	Collagen alpha-2(I) chain	9.43	6.42	12.6	9.12	within
e013284	SVGISAEVDMSSVTTTQ	none	UPF0606 protein KIAA1549	11.29	7.91	12.96	13.1	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099021	DGPPGRDQPGHKGER*	1xCation:Na [D7]; 2xOxidation [P4; P10]	Collagen alpha-2(I) chain	5.85	2.72	8.84	10.16	up
e013314	GLGDSGSEGHSSLSSHSN	none	Disabled homolog 2-interacting protein	10.96	7.14	12.92	10.77	within
e212620	APGFPGVAGMRGEPGLPG*	3xOxidation [P2; P5; P14]	Collagen alpha-6(IV) chain	10.82	6.83	13.07	8.35	within
e013321	KGEMGVMGTPGQPGSPGP*	2xOxidation [P13; P]	Collagen alpha-1(IV) chain	7.02	2.21	11.02	4.55	within
e212621	PGGGGPGGGSAGGPSQPPGGGGP	none	Far upstream element-binding protein 2	9.75	6.53	12.35	9.02	within
e212622	PPGEAGKPGEQGVPGDLG*	1xCation:Na [E10]; 2xOxidation [P2; P8]	Collagen alpha-1(I) chain	9.76	6.51	12.32	8.99	within
e013328	SLEGGAGDGPLPPGGAGPGPG	none	Protein bassoon	11.19	6.24	13.03	11.07	within
e013340	RDGDGDEEEYYGSEP	none	E3 ubiquitin-protein ligase MARCHF9	12.09	8.17	13.97	14.2	up
e013345	KGDPGDPGPPGTHGNPGI*	3xOxidation [P4; P7; P9]	Collagen alpha-1(XXVIII) chain	11.96	8.65	13.76	12.36	within
e212637	GPPGPPGPPGPPGEKGQM*	4xOxidation [P6; P8; P9; P11]	Collagen alpha-1(IV) chain	11.96	8.72	13.66	12.36	within
e013356	GPIGFRGPPGIPGAPGKAG*	1xOxidation [P12]	Collagen alpha-3(IX) chain	11.99	6.14	15.65	11.23	within
e099005	NGAPGNDGAKGDAGAPGAPG*	1xCation:Na [D12]; 3xOxidation [P4; P16; P19]	Collagen alpha-1(I) chain	12.25	7.21	14.01	7.51	within
e106051	GPPGPPGPKGDPGPVGEP*	7xOxidation [P2; P3; P5; P6; P8; P12; P14]	Collagen alpha-1(XIX) chain	8.6	5.56	11.09	11.03	within
e013378	GSPGEKGDGPDVGGPGPPGA*	1xOxidation [P17]	Collagen alpha-3(V) chain	12.18	8.57	13.89	7.51	down
e013382	DEEETIEEEEANEGV	none	E1A-binding protein p400	10.21	5.65	12.53	12.65	up
e102957	GGDGPA GPPGERGPNGPQG*	3xOxidation [P5; P8; P9]	Collagen alpha-1(V) chain	7.04	3.48	10.04	6.02	within
e101958	PGSAGPPGSPGPQGSGTPQG*	2xOxidation [P12; P18]	Collagen alpha-2(V) chain	12.33	9.39	13.91	12.42	within
e212653	GKEGPPGEKGGQGGPPGPQ*	3xOxidation [P5; P6; P14]	Collagen alpha-1(V) chain	11.91	8.59	13.85	12.38	within
e013387	TGSPGSPGPDGKTGPPGPAG*	2xOxidation [P4; P7]	Collagen alpha-1(I) chain	12.73	9.36	14.38	13.54	within
e101120	APGPVGPAGKSGDRGETGP*	1xOxidation [P2]	Collagen alpha-1(I) chain	6.89	3.96	10.6	7.06	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099652	PGPSGPRGQPGVMGFPGP*	2xOxidation [P6; P10]	Collagen alpha-1(III) chain	10.47	7.41	14.44	9.5	within
e212655	FIFPPSDEQLKSGTAS	none	Immunoglobulin kappa constant	10.4	7.43	15.33	7.65	within
e013421	AVAHVDDMPNALSALSD	none	Hemoglobin subunit alpha	8.6	5.69	12.22	9.66	within
e300032	GKVNVDVGGGALGRLL	none	Hemoglobin subunit beta	9.83	5.04	14.83	9.87	within
e208159	EPGSPGENGAPQMGPGR*	2xOxidation [P2; P11]	Collagen alpha-1(I) chain	10.82	7.19	12.8	8.71	within
e013436	APGEMGPQGPPGEPGR*	3xOxidation [P7; P10; P11]	Collagen alpha-2(IV) chain	5.78	1.39	13.39	3.86	within
e013441	ASVGSHSSTESSEHGSSSP	none	Dynamin-binding protein	8.43	4.83	11.53	9.45	within
e106536	ASTEGSETTVTTAGSET	none	Mucin-22	11.32	7.11	13.55	12.23	within
e212664	LQPQPPPKMGDFYDP	none	Histone-lysine N-methyltransferase SETD2	6.6	4.03	10.79	9.25	within
e212665	EGPPGPEGPAGLPGPPGTM*	1xOxidation [P16]	Collagen alpha-1(V) chain	12.72	9.49	14.66	12.89	within
e013456	TSPTVAPPLSSDTSTNR	none	Pyrin and HIN domain-containing protein 1	7.05	2.46	9.81	7.59	within
e099081	PPGEAGKPGEQGVPGDLG*	1xCation:Na [D16]; 3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	11.56	7.67	13.68	9.86	within
e013475	KSEEEKDSESLAED	none	Ankyrin-2	11.88	8.83	13.4	12.32	within
e105227	GGPGGGGPGGGSAGGPSQPPGGGG	none	Far upstream element-binding protein 2	12.01	7.17	13.9	12.28	within
e013479	PGPPGPDGLPGSMGPPGTP*	3xOxidation [P3; P4; P6]	Collagen alpha-1(IV) chain	12.04	8.59	14.06	12.13	within
e102467	DHGGRGGGRGNKHQGGW	none	Protein FAM98A	11.24	6.84	12.62	10.98	within
e013482	KGNPGVGTQGRGPPGPAG*	2xOxidation [P11; P14]	Collagen alpha-1(XIV) chain	11.74	6.74	15.54	13.97	within
e013485	HLPAEFTPAVHASLDK	none	Hemoglobin subunit alpha	11.71	7.29	15.59	13.97	within
e104824	EVPTSKSSNSEDDLPE	none	RING finger protein 39	10.51	6.2	12.44	7.81	within
e212672	KGDPGDPGPPGTHGNPGI*	4xOxidation [P7; P9; P10; P]	Collagen alpha-1(XXVIII) chain	14.68	11.97	15.94	14.99	within
e013492	EAVPGGPGREPEGLLQAG	none	Paraneoplastic antigen-like protein 6A	10.59	5.39	14.74	12.99	within
e013493	HIPESPYLVPVIAPSD	none	Filamin-B	10.56	5.85	14.76	12.8	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013499	ESTDSEEETSATSGHPA	none	Transcription factor HIVP3	10.67	6.33	12.63	9.97	within
e102603	SKADHNDGYFPDGPGGT	none	Matrix metalloproteinase-17	8.28	3.85	11.42	11.66	up
e013507	GPASATPALSSSPPPSTL	none	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2	9.39	3.56	13.12	12.11	within
e103672	LGEAGVATGSEAQSSPQF	none	E3 ubiquitin-protein ligase RNF213	9.92	6.38	12.36	11.83	within
e013518	ALQLANSFAVDLFKQ	none	Serpin B5	9.74	5.75	12.18	12.06	within
e013528	VVSLGSPSGEVSHPRKT	none	Alpha-2-HS-glycoprotein	9.86	5.21	14.72	12.81	within
e013533	GSHSRQSSTDSSGGHPGP	none	WW domain-containing transcription regulator protein 1	11.5	7.23	13.22	9.99	within
e101857	AAGAGLDGPEGDQGPQGPQ*	1xOxidation [P15]	Collagen alpha-3(IX) chain	11.91	9.44	13.69	11.24	within
e013534	GPAGPIGSAGPPGFPGAPGP*	5xOxidation [P5; P11; P12; P15; P18]	Collagen alpha-2(I) chain	10.88	6.36	13.64	9.94	within
e097524	TIEGVDAEDGHGPGEQQ	none	Complement factor B	14.75	12.17	15.99	14.96	within
e013548	NDGAPGKNGERGGPGGPGP*	3xOxidation [P5; P14; P17]	Collagen alpha-1(III) chain	15.69	14.1	16.59	16.34	within
e097525	TGSPGSPGPDGKTGPPGPAG*	3xOxidation [P4; P7; P16]	Collagen alpha-1(I) chain	14.93	12.95	16.06	14.96	within
e099082	VRYTKKVPQVSTPTL*	1xCation:Na [C-Term]	Albumin	9.6	5.84	14.68	6.75	within
e202522	KNGSPGSPGEPGSGTPGQ*	2xOxidation [P5; P8]	Collagen alpha-1(XXII) chain	13.98	10.51	15.49	14.46	within
e202523	GEKGSPGADGPAGAPGTPGP*	4xOxidation [P11; P15; P18; P20]	Collagen alpha-1(I) chain	13.79	10.32	15.02	11.25	within
e013576	TSAPKPSDLYEPSGE	none	Versican core protein	10.77	5.87	14.05	13.05	within
e097528	GTGPGSLGDLTALDDTPPG	none	Zinc finger protein GLI2	7.87	2.59	12.42	5.94	within
e013578	TEIPEAQIHEGFQEL	none	Alpha-1-antitrypsin	13.15	9.96	14.85	13.43	within
e013587	RTHLAPYSDELRQR	none	Apolipoprotein A-I	6.58	3.95	11.48	6.88	within
e013594	EPGSPGENGAPQMGPGRG*	3xOxidation [P2; P5; P11]	Collagen alpha-1(I) chain	11.53	7.74	13.41	11.73	within
e013595	PGDVGGPGPPGASGEPGAPGP*	1xOxidation [P21]	Collagen alpha-3(V) chain	9.39	3.92	13.42	10.42	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013603	NFPSPVDAAFRQGHNS	none	Hemopexin	7.77	3.19	11.59	9.29	within
e013614	ANDSDQGANAIEYTF	none	Protocadherin-1	10.82	6.29	12.32	10.51	within
e099646	DHIAQEIHSAESRDH	none	Zinc finger protein 831	7.69	4.17	10.17	9.5	within
e013624	EEMKEEMKEDVDPH	none	MRG/MORF4L-binding protein	9.36	5.47	12.59	4.89	down
e212708	TSAESPDAPREENIAGVGA*	2xOxidation [P6; P9]	Collagen alpha-1(XVIII) chain	9.19	4.45	13.36	8.25	within
e103671	GPPGPTGPGDKGDTGPPGP*	2xOxidation [P3; P18]	Collagen alpha-1(III) chain	10.15	4.55	13.59	10.77	within
e097532	WDNLEKETEGLRQE	none	Apolipoprotein A-I	9.32	4.41	13.01	8.24	within
e013644	DGPPGRDQGPGHKGERG*	2xOxidation [P4; P10]	Collagen alpha-2(I) chain	8.36	3.97	11.43	9.05	within
e013649	GPVGQPGAAGADGEPGARGP*	2xOxidation [P2; P6]	Collagen alpha-2(XI) chain	7.89	3.95	11.41	9.2	within
e104842	PSGASGPAGPRPPGSAGAPG*	3xOxidation [P7; P10; P13]	Collagen alpha-1(I) chain	11.84	7.99	14.5	11.97	within
e212713	KGPMGPPGPKGDQGEKGP*	1xOxidation [P7]	Collagen alpha-1(XVII) chain	7.32	3.77	11.37	9.25	within
e208176	RGDEGPPGSEGARGAPGPA*	1xOxidation [P18]	Collagen alpha-1(VI) chain	9.9	5.88	12.32	9.25	within
e013655	QEMEMLNAFSTTIHV	none	Vesicle-fusing ATPase	10.17	6.83	12.31	10.85	within
e013657	GPPGEAGKPGEQGVPGDLG*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	12.42	9.21	14.18	12.06	within
e212715	ASSPPDYTMAWAEYY	none	Far upstream element-binding protein 3	12.34	7.21	14.52	13.28	within
e013664	GPPGPPGKNGDDGEAGKPG*	3xOxidation [P5; P6; P18]	Collagen alpha-1(I) chain	13.18	9.44	15.05	14.38	within
e212718	KGPSGEAGTAGPPGTGPQG*	2xOxidation [P13; P16]	Collagen alpha-2(I) chain	11.78	7.65	13.72	12.02	within
e013669	LDETEQWEKFGLEK	none	Complement C3	12.15	7.39	14.55	13.54	within
e212720	GQPGTKGGPGDQGEPPQG*	2xOxidation [P3; P9]	Collagen alpha-2(IX) chain	12.98	10.16	14.68	14.24	within
e212721	PGEPGPVGGGGHPGQPPPG*	3xOxidation [P16; P18; P]	Collagen alpha-5(IV) chain	12.98	9.89	14.69	14.22	within
e013680	VADALTNAVAHVDDMPN	none	Hemoglobin subunit alpha	12.04	7.51	13.64	11.8	within
e212722	ASGISAKSASDNSKAEET	none	Actin remodeling regulator NHS	8.28	3.23	12.16	6.72	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013682	QHTPDQANS DRASIGR	none	Pleckstrin homology domain-containing family N member 1	8.47	3.58	12.16	9.44	within
e101558	TGDIVGQMGP PPGPPGRGP*	5xOxidation [P10; P12; P13; P15; P18]	Collagen alpha-1(V) chain	8.72	5.22	11.53	10.58	within
e212724	GEKGDHGFPGSSGPRGDP	none	Collagen alpha-1(IV) chain	10.74	5.33	12.68	12.33	within
e102679	PPGKNGDDGEAGKPRGP*	3xOxidation [P2; P14; P17]	Collagen alpha-1(I) chain	8.86	5.19	11.51	12.81	up
e100635	TGSPGSPGPDGKTGPPGPAG*	4xOxidation [P7; P9; P15; P16]	Collagen alpha-1(I) chain	9.7	5.67	15.13	8.66	within
e013711	TNRGASQAGMTGYGMPR	none	Transgelin-2	9.87	5.78	12.08	10.94	within
e212729	KPEQETTPRHKQEF	none	Band 4.1-like protein 1	8.42	4.69	14.56	4.53	down
e013742	SGSVIDQSRVLNLGPIT	none	Uromodulin	15.66	11.61	17.81	15.34	within
e212741	KMRNLLVTIENDTPL	none	Zinc finger protein 200	14.62	10.47	17.09	14.5	within
e103648	GEPGAPGENGTPGQTGARG*	3xOxidation [P3; P6; P12]	Collagen alpha-2(I) chain	9.34	5.53	12.74	12.94	up
e105043	EPGSPGENGAPGQMGRGP*	4xOxidation [P2; P5; P11; M14]	Collagen alpha-1(I) chain	10.59	6.32	13.19	11.08	within
e099084	NDGAPGKNGERGGPGGPGP*	1xCation:Na [C-Term]; 3xOxidation [P5; P14; P17]; 1xCation:Na [E10]	Collagen alpha-1(III) chain	11.54	6.86	13.83	9.88	within
e212750	GEGKGSTDDEAEDGRAAP	none	Voltage-dependent T-type calcium channel subunit alpha-1H	9.84	4.8	13.23	9.34	within
e103908	SPGTSGPPGSAGPPGSPGPQG*	1xOxidation [P19]	Collagen alpha-2(V) chain	11.54	7.88	13.4	12.46	within
e101399	NSQNSNPEGTSEGTPE	none	Putative ankyrin repeat domain-containing protein 30B-like	10.07	5.5	12.6	12.89	up
e013804	GPPGPPGPAGNPGSPNSP*	7xOxidation [P3; P5; P6; P8; P12; P14; P16]	Collagen alpha-1(XXVI) chain	11.46	8.15	13.1	8.88	within
e013807	GDPGKDGVGQPLGPPGP*	4xOxidation [P11; P14; P16; P17]	Collagen alpha-1(XVIII) chain	11.63	8.03	13.57	12.68	within
e101807	SPGEGPATEGGGLGPGEAP	none	Retina and anterior neural fold homeobox protein 2	11.09	7.84	12.92	7.73	down

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e212760	GPPGEAGKPGEQGVPGDLG*	3xOxidation [P3; P9; P15]	Collagen alpha-1(I) chain	13.88	11.41	15.32	14.96	within
e093744	GSPGAKGEVGPAGSPGSNGAP*	1xOxidation [P11]	Collagen alpha-1(III) chain	13.87	11.41	15.32	14.98	within
e212763	VAHVDDMPNALSALSDL	none	Hemoglobin subunit alpha	13.42	10.05	15.0	13.86	within
e094819	SVIDQSRVLNLGPITR	none	Uromodulin	15.39	10.4	18.08	17.13	within
e013856	EAGSEADHEGTHSTKRG	none	Fibrinogen alpha chain	11.7	7.71	12.95	12.58	within
e101258	GEKGPSGEAGTAGPPGTPGP*	3xOxidation [P5; P15; P18]	Collagen alpha-2(I) chain	13.11	10.27	14.84	12.33	within
e212766	KRELHTISFLGGLALN	none	Dolichyldiphosphatase 1	11.78	6.9	14.69	7.7	within
e013860	SRVAELLQRGASAAAR	none	Ankyrin repeat domain-containing protein 65	13.77	9.43	16.06	14.27	within
e212767	VNIVEEELGIISRAVK	none	Kinesin-like protein KIF21A	11.67	6.4	14.13	7.7	within
e013865	KPGQMGN SGKPGQQGPPG*	3xOxidation [P2; P11; P16]	Collagen alpha-1(IX) chain	10.35	5.98	12.54	9.45	within
e013867	SVKLGH PDTLNQGEFK	none	Protein S100-A9	11.59	6.63	15.12	7.69	within
e013869	EDAGAGGEDAGPGGEDVGP GG	none	Golgin subfamily A member 6-like protein 2	12.29	9.24	14.18	12.22	within
e013873	KSSTPPGESYFGVSSLQ	none	Serine/arginine repetitive matrix protein 2	10.69	6.36	13.88	9.02	within
e013876	PGAPGPKGEIGAVGNAGPAGP	none	Collagen alpha-2(I) chain	11.26	5.76	14.64	10.13	within
e013879	DPGGSEEENGLEDTEPP	none	Coiled-coil and C2 domain-containing protein 1B	12.16	8.41	14.87	11.77	within
e013878	QEMLSDGTD TGSEISSD	none	UPF0606 protein KIAA1549L	9.16	5.59	12.62	12.25	within
e212771	DGEPGQTGSPGPTGEPGPS*	3xOxidation [P10; P12; P16]	Collagen alpha-1(V) chain	12.18	8.35	14.9	11.47	within
e212774	PSAAEHPSHGEGPARSEG	none	3'-5' RNA nuclease TATDN2	11.75	6.2	14.07	10.09	within
e212775	GAVGEAGAAGEAGAVGEAGGTN	none	Paraneoplastic antigen Ma6E	11.71	6.24	14.07	10.08	within
e013896	ATGIPDRFSGSGSGTDFT	none	Immunoglobulin kappa variable 3-20	11.37	7.78	13.49	10.79	within
e212781	TGDPGLPGDMGKKGEMGQ	none	Collagen alpha-3(IV) chain	11.04	7.43	12.56	10.02	within
e212783	PGPPGPTGDPGLPGDMGKK	none	Collagen alpha-3(IV) chain	8.02	3.56	13.33	9.92	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e013913	GLPGMPGADGPPGHPGKEG*	3xOxidation [P11; P12; P15]	Collagen alpha-1(V) chain	7.85	4.57	10.6	8.43	within
e212790	FGASAGTGDLSDNHDIIS	none	Vesicular integral-membrane protein VIP36	12.48	9.09	14.68	11.92	within
e212791	GPPGPPGAAGTPGLQGMPGE*	2xOxidation [P2; P3]	Collagen alpha-1(III) chain	10.98	5.62	14.85	11.91	within
e100870	PGPTGPGDGKGDTPPGPQG*	2xOxidation [P3; P]	Collagen alpha-1(III) chain	11.5	7.74	13.8	11.62	within
e013941	LPGTGGPPGENGKPGEGPG*	4xOxidation [P7; P8; P14; P17]	Collagen alpha-1(III) chain	11.31	7.64	13.57	10.81	within
e100718	MAAAGAPDGMEEPGMDTE	none	Ubiquitin domain-containing protein UBF1	9.8	6.36	12.45	3.94	down
e212796	GEVFTWGHNAYSQNG	none	RCC1 and BTB domain-containing protein 2	11.81	7.77	14.04	13.11	within
e212797	GAALYTFRASDADGPGPN	none	Protocadherin-16	11.83	7.58	14.12	13.13	within
e102028	PSGVPGQPGSPGLPGQKGD*	3xOxidation [P1; P5; P8]	Collagen alpha-5(IV) chain	9.01	5.98	11.92	6.89	within
e013948	GAAGEPGKAGERGVPGPPGA*	3xOxidation [P6; P15; P17]	Collagen alpha-1(I) chain	11.44	6.98	13.82	13.16	within
e105427	EAGKPGEQGVPGDLGAPGP*	3xOxidation [P5; P11; P17]	Collagen alpha-1(I) chain	10.51	6.12	12.67	8.86	within
e013959	EVHSGGSHTHSGHHSQ	none	Filaggrin-2	7.2	2.85	11.39	4.66	within
e094832	APGPQGPRGDKGETGERG*	1xOxidation [P2]	Collagen alpha-1(III) chain	7.53	3.78	10.67	5.79	within
e106226	DLDPEVRPTS*	1xO-Glycan [T9] (HexNAc(1)Hex(1) NeuAc(1))	Apolipoprotein C-III	10.18	5.77	12.82	10.02	within
e104807	GQGDGTTSGHTSLWSFF	none	Transmembrane protein 229A	12.14	8.02	13.71	13.13	within
e212804	KGDGSSRPVGGTDPEGAEA	none	Peripheral-type benzodiazepine receptor-associated protein 1	8.95	5.27	11.26	8.46	within
e013991	PGPVGPPGSNGPVGEPGPEG*	2xOxidation [P3; P6]	Collagen alpha-2(V) chain	11.8	5.98	14.47	11.44	within
e212806	VSDALPAAEGGSRDQEEG	none	Chromodomain-helicase-DNA-binding protein 1-like	9.13	5.8	11.63	7.68	within
e014011	PGDKGDPGEDGQPGPDGPP	none	Collagen alpha-2(V) chain	11.57	8.5	13.61	11.49	within
e014012	PGPPGPTGPPGKDGPNGPP*	6xOxidation [P3; P4; P6; P9; P10; P15]	Collagen alpha-1(XXII) chain	11.55	8.1	13.59	11.52	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014023	ETGPAGRPGEVGGPPGPPGP*	4xOxidation [P8; P13; P14; P16]	Collagen alpha-1(I) chain	12.6	7.75	14.48	12.39	within
e014026	FPGSAGRVGPPGPAGAPGPAG*	1xOxidation [P2]	Collagen alpha-2(V) chain	8.93	5.11	12.66	6.85	within
e212813	KTSKAKKDQEGGEEKK	none	Protein diaphanous homolog 1	7.82	3.97	13.11	9.96	within
e014041	RGGSGGSYGGGSGGGYGGGSGS	none	Keratin, type I cytoskeletal 9	8.27	3.85	11.69	8.88	within
e100206	QRNSQTDALFNPSAN	none	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 5	7.24	4.01	10.68	6.93	within
e014046	GESGRPGPPGSPGRGQPG*	3xOxidation [P8; P9; P11]	Collagen alpha-1(III) chain	10.29	5.66	12.42	11.18	within
e014054	SGGDGPAGPPGERGPNGPQG*	2xOxidation [P9; P10]	Collagen alpha-1(V) chain	11.01	7.2	12.83	10.14	within
e014073	SVGTGGGGTGGVGGGAGSEDSGD	none	E3 ubiquitin-protein ligase RING1	10.67	7.29	12.44	11.35	within
e014074	EEAPSLRPAPPPISGGGY	none	Fibrinogen beta chain	11.86	7.89	14.56	11.08	within
e014078	EPAADDSSDDSDNEDVD	none	E3 ubiquitin-protein ligase HERC2	9.63	6.31	12.01	12.04	up
e014079	RSTNETDASNIEDQSE	none	Fibrillin-1	10.35	6.12	12.13	9.42	within
e014080	GNDGAPGKNGERGGPGGPGP*	3xOxidation [P6; P15; P18]	Collagen alpha-1(III) chain	14.6	12.5	15.57	15.26	within
e212829	RPGSSGSPGDEGQPGEPGP*	2xOxidation [P14; P17]	Collagen alpha-1(VI) chain	12.64	6.4	14.67	13.03	within
e103217	EPGSMGPRGENGVGDGAPGP*	1xOxidation [P]	Collagen alpha-1(XXIII) chain	14.04	10.92	15.2	15.03	within
e014095	GPPGSNGGWTWTSPGEGGP	none	Zinc finger protein 831	10.56	6.63	12.98	12.66	within
e014098	APGPQGRGDKGETGERG*	2xOxidation [P4; P]	Collagen alpha-1(III) chain	8.5	4.46	11.31	7.95	within
e014112	SFSSEQEASDDAVQGQD	none	Phosphofurin acidic cluster sorting protein 2	10.71	6.46	13.24	12.27	within
e104211	GEPGSPGENGAPGQMGRG*	3xOxidation [P3; P6; P12]	Collagen alpha-1(I) chain	12.85	8.87	14.14	13.16	within
e014113	NDGAKGDAGAPGAGSQGAPG*	3xOxidation [P11; P14; P20]	Collagen alpha-1(I) chain	12.91	10.54	14.03	13.17	within
e014114	FQAEIVPVTTTVHDDK	none	3-ketoacyl-CoA thiolase, peroxisomal	9.23	6.02	12.16	10.95	within
e106020	QGDSPGQGGPPGSEGFTGPP*	2xOxidation [P6; P9]	Collagen alpha-2(IV) chain	12.79	6.78	13.98	13.04	within
e212837	VSETESRGSESGIFTNT	none	Fibrinogen alpha chain	12.6	10.16	13.82	13.02	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014147	GPVGPPGSNGPVGEPGPEGP*	3xOxidation [P2; P5; P6]	Collagen alpha-2(V) chain	10.81	7.28	12.26	10.6	within
e103706	GLPGTGGPPGENGKPGEGP*	2xOxidation [P3; P9]	Collagen alpha-1(III) chain	8.1	4.94	11.86	9.93	within
e014175	GDPGQPGPPGPSGEAGPPGP*	5xOxidation [P9; P11; P17; P18; P20]	Collagen alpha-1(XI) chain	11.91	8.46	14.13	8.57	within
e212840	MGVAAHKKSHEESHKE	none	Protein S100-A8	7.52	4.15	12.06	10.95	within
e212841	KGSPGADGPAGAPGTPGPQGI*	1xOxidation [P18]	Collagen alpha-1(I) chain	6.91	3.83	11.94	10.56	within
e014187	NDGPPGRDQGPGHKGER*	2xOxidation [P5; P11]	Collagen alpha-2(I) chain	7.33	3.57	10.87	8.75	within
e014189	PGP HGLPGIGKPGGPGLPGQ*	1xOxidation [P18]	Collagen alpha-1(VIII) chain	11.48	5.83	15.46	5.85	within
e014197	YGRAPQLRETLQDF	none	Protein AMBP	11.3	6.13	14.6	7.84	within
e014207	STYPPPSWGSSSDQQPS	none	Serine/threonine-protein kinase PAK 5	7.81	3.78	10.43	9.69	within
e103560	GP GSGPGHSGSGSHPGPASGPGP	none	Sperm-associated antigen 8	11.19	7.36	13.5	9.25	within
e014214	PPGPAGSAGARGAPGERGET*	1xOxidation [P4]	Collagen alpha-1(II) chain	11.29	7.12	13.47	10.18	within
e212846	KAASYTEEDENHTAKD	none	Desmoglein-2	14.33	11.36	15.92	13.99	within
e014217	WERPFVKDTEED	none	Alpha-1-antitrypsin	10.87	4.83	12.66	11.79	within
e014216	EIGGTEIVTESEYTS GH	none	Zinc finger protein 711	14.32	11.32	15.94	13.98	within
e014221	TVNFGDTEEAKKQIND	none	Alpha-1-antitrypsin	10.68	4.72	12.83	11.92	within
e014222	TAITATATGYQESHLSSA	none	Nuclear pore membrane glycoprotein 210	13.88	8.74	15.82	12.21	within
e014225	VIDQSRVLNLGPITRK	none	Uromodulin	11.31	6.92	14.85	14.51	within
e212848	PQGPTGETGPMGERGHPG*	3xOxidation [P4; P10; P17]	Collagen alpha-1(V) chain	11.49	7.48	13.38	12.69	within
e014230	RQGSLESPSSGTGSMGSAGG	none	Neuron navigator 3	12.79	10.01	14.4	13.16	within
e212849	GESGDPGPQGPRGVQGGPG*	4xOxidation [P8; P11; P17; P18]	Collagen alpha-1(XI) chain	11.52	7.95	13.39	12.69	within
e212852	ALELRTKVVEEVLTPL	none	Metal transporter CNNM1	10.81	7.13	14.26	13.99	within
e212853	GTPGRDGE PGDPGEDGKPG*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	11.57	7.82	12.97	11.56	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014240	SSNVTSTSGHSSGSSSGAIT	none	Homeodomain-interacting protein kinase 2	7.95	4.55	12.94	11.63	within
e014241	GPPGKNGDDGEAGKPGRPG*	3xOxidation [P3; P15; P18]	Collagen alpha-1(I) chain	12.0	8.72	13.53	12.52	within
e103484	PGPQGPLGKPGAPGEPGPQG*	1xOxidation [P1]	Collagen alpha-1(VIII) chain	9.26	4.88	11.89	11.02	within
e014259	AVTVGQAKSVGKGLQVKAA	none	Treacle protein	7.95	4.33	14.34	5.36	within
e014267	VGPPGEPGPPGQQGNHGSQ*	1xOxidation [P]	Collagen alpha-3(V) chain	9.84	5.53	11.84	11.09	within
e014274	GEPGAPGSKGDTGAKGEPGP*	3xOxidation [P3; P6; P18]	Collagen alpha-1(I) chain	8.6	5.53	11.87	7.96	within
e014281	LRQKLGPAGDVEGHLS	none	Apolipoprotein A-IV	6.43	1.79	11.31	2.72	within
e014287	SGGYGGGYGGQSSMSGYDQ	none	Heterogeneous nuclear ribonucleoprotein H	14.72	8.78	16.52	15.75	within
e014303	GGSSNSGGGSGSQSGSSGSGSNG	none	Dermokine	14.34	10.93	16.08	15.18	within
e212863	GSSSGSGSSSAGEPGGAESSSS	none	Transcription factor Ovo-like 2	10.0	6.14	12.82	10.73	within
e014305	PGLMGESSESFSASEDEG	none	Phosphatase and actin regulator 2	14.17	8.7	16.02	15.2	within
e014306	SQSYSGYGQTTDSSYGQ	none	TATA-binding protein-associated factor 2N	10.12	6.57	12.87	10.72	within
e014310	GPPGPPGPPGVPIDGIDGD*	3xOxidation [P5; P6; P]	Collagen alpha-1(IX) chain	9.87	6.13	12.84	8.37	within
e014321	VNADYTISGTLPHSNGGN	none	Multiple epidermal growth factor-like domains protein 10	8.23	5.2	11.95	10.64	within
e208222	PPGARGPPGAVGSPGVNGAPG*	3xOxidation [P2; P7; P8]	Collagen alpha-2(I) chain	8.11	4.59	12.09	10.52	within
e014328	ESKSGLDVMPNISDVLL	none	Inositol 1,4,5-triphosphate receptor associated 1	6.94	3.84	12.63	10.52	within
e106064	GPPGKDGPVGKGENGHPG*	4xOxidation [P2; P3; P9; P18]	Collagen alpha-1(XIII) chain	7.57	4.7	11.07	9.28	within
e014334	SGNAGPPGPPGAGKEGGKGP*	2xOxidation [P7; P9]	Collagen alpha-1(I) chain	7.58	2.16	12.38	4.43	within
e014338	DHDVGSELPPEGLGALL	none	ProSAAS	10.18	6.05	13.59	9.15	within
e212868	EVQDSYEAYGQDDWN	none	KH domain-containing, RNA-binding, signal transduction-associated protein 1	14.84	11.9	16.73	16.35	within
e212872	PGYQGPPGEPGQAGPSGPPG*	1xOxidation [P]	Collagen alpha-1(III) chain	11.12	7.31	15.17	11.3	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014350	GLPGTGGPPGENGKPGEGPG*	3xOxidation [P8; P9; P]	Collagen alpha-1(III) chain	11.14	7.47	15.16	11.26	within
e014354	DGGQHWTYEGPHGQDH	none	Carbonic anhydrase 14	11.09	6.66	13.41	12.78	within
e212875	EAFTFADHEMGSNEVH	none	Fibrous sheath-interacting protein 2	10.76	5.94	13.38	12.8	within
e212876	SGPPGPPGPPGPKGDQGGP*	8xOxidation [P3; P4; P6; P7; P9; P10; P12; P18]	Collagen alpha-1(XVII) chain	15.48	13.62	16.76	15.42	within
e212878	TDGPKGASGPAGPPGAQGPPG*	3xOxidation [P13; P14; P19]	Collagen alpha-1(II) chain	11.53	8.1	14.3	11.12	within
e212880	GSPGQRGLPGKDGSSGPPGP*	1xOxidation [P18]	Collagen alpha-1(XIV) chain	9.93	5.73	13.61	10.46	within
e014363	NDGPPGRDGQPGHKGER*	3xOxidation [P4; P5; P11]	Collagen alpha-2(I) chain	8.17	4.2	11.32	10.52	within
e208225	GPPGEGRAGEPGTAGPTGPP*	4xOxidation [P2; P11; P16; P19]	Collagen alpha-2(VIII) chain	11.67	9.01	13.48	11.17	within
e014372	PGPSGEKGETGDVGPMGPPG	none	Collagen alpha-2(XI) chain	11.68	6.68	13.38	10.42	within
e212885	GAAAPPGEGISAAPTVEPSSG	none	Set1/Ash2 histone methyltransferase complex subunit ASH2	10.09	5.74	13.42	11.16	within
e014373	ESSSHHPGIAEFPSRGK	none	Fibrinogen alpha chain	7.01	4.26	12.15	8.62	within
e014382	EEDGEAYEEDPASQPGT	none	Protein Wiz	11.8	7.97	13.92	12.81	within
e212890	AGEKGPSGEAGTAGPPGTPGP*	2xOxidation [P16; P19]	Collagen alpha-2(I) chain	10.31	7.06	13.02	11.17	within
e101676	GAVEGGEGSGDGGSSADSGSGAG	none	Adenylate cyclase type 5	11.89	8.06	14.04	12.2	within
e014388	EGGDPQEAEPPQEGGAPQ	none	Sarcalumenin	11.24	7.96	13.04	11.76	within
e094881	GSVIDQSRVLNLGPITR	none	Uromodulin	13.03	7.9	16.34	12.19	within
e014402	DEAGSEADHEGTHSTKR	none	Fibrinogen alpha chain	14.36	11.0	15.23	14.97	within
e101889	GANGAPGNDGAKGDAGAPGAPG*	3xOxidation [P6; P18; P21]	Collagen alpha-1(I) chain	12.28	8.34	13.81	12.95	within
e212894	GLDQQQMAYEGQHWWHA	none	Prickle planar cell polarity protein 3	10.6	6.8	13.33	10.84	within
e212895	GEKGEPGADGEAGRPGSSGP*	1xOxidation [P20]	Collagen alpha-1(VI) chain	10.51	6.72	13.55	10.85	within
e202764	GNDDHWIVDTDYDTY	none	Retinol-binding protein 4	11.43	7.54	13.22	11.09	within
e014427	SPGRDGSPGAKGDRGETGP*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	9.32	4.59	11.91	7.51	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e105665	TGPPGPAGQDGRPGPPGPPG*	4xOxidation [P4; P13; P16; P19]	Collagen alpha-1(I) chain	8.34	5.75	11.71	9.64	within
e212905	GSLAGRSDDGLSAASSPEPG	none	B-cell lymphoma/leukemia 11B	10.53	6.04	12.78	10.9	within
e202771	GPPGPPGPPGPPGGLPAGF*	7xOxidation [P5; P6; P8; P9; P11; P12; P14]	Collagen alpha-1(XVIII) chain	8.24	5.14	14.14	9.26	within
e014445	VNDNEEGFFSARGHRP	none	Fibrinogen beta chain	9.88	6.21	12.18	10.1	within
e014460	GPPGPPGPPGPPGLGGNFAP*	6xOxidation [P5; P6; P8; P9; P11; P12]	Collagen alpha-1(I) chain	9.64	4.87	11.93	8.37	within
e014467	TYFPHFDLSHGSAQVK	none	Hemoglobin subunit alpha	8.39	5.38	11.82	10.82	within
e208230	VGGPGPPGASGEPGAPGPPGK*	6xOxidation [P6; P7; P13; P16; P18; P19]	Collagen alpha-3(V) chain	13.37	10.21	16.9	12.35	within
e014481	GLPGTGGPPGENGKPGEGP*	4xOxidation [P3; P9; P15; P18]	Collagen alpha-1(III) chain	13.27	10.11	16.72	12.56	within
e212918	GLPGTGGPPGENGKPGEGP*	4xOxidation [P3; P8; P9; P15]	Collagen alpha-1(III) chain	13.26	10.21	16.72	12.56	within
e014502	TDGPKGASGPAGPPGAQGGPPG*	4xOxidation [P10; P13; P14; P19]	Collagen alpha-1(II) chain	13.18	10.02	16.49	13.19	within
e014504	APGAPGGKGDAGAPGERGPPG*	4xOxidation [P2; P5; P14; P19]	Collagen alpha-1(III) chain	12.36	9.91	14.03	13.59	within
e212923	GSDGKPGPPGSQGESGRPG*	1xOxidation [P]	Collagen alpha-1(III) chain	13.17	10.15	16.47	13.18	within
e212924	APGGKGDAGAPGERGPPGLAG*	3xOxidation [P2; P11; P16]	Collagen alpha-1(III) chain	12.19	9.12	13.9	13.1	within
e212928	GGGGAAGAGAGSAGGGGFMFPVAG	none	Synergina gamma	13.21	9.64	14.95	12.66	within
e212929	GLGDSGAAGAAALSSASSETGT	none	Scaffold attachment factor B1	13.13	9.3	14.84	12.66	within
e212930	GEAGKPGEQGVPGDLGAPGP*	3xOxidation [P6; P12; P18]	Collagen alpha-1(I) chain	13.11	9.33	14.92	12.66	within
e014525	TESATPAAYSGSPKISSSP	none	Mucin-16	12.8	8.82	14.73	12.67	within
e014534	PGPPGKPGQDGIDGEGAPP*	6xOxidation [P1; P3; P4; P7; P18; P19]	Collagen alpha-3(IX) chain	13.29	9.66	14.48	12.77	within
e014536	AAGSQGNTASQGKEGPYSE	none	PALM2-AKAP2 fusion protein	13.3	9.67	14.59	12.88	within
e014537	GEGGPPGVAGPPGGSGPAGPPGP*	1xOxidation [P]	Collagen alpha-1(III) chain	13.08	9.87	14.87	12.88	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014549	LTDEEKRLMVELHNL	none	Peptidase inhibitor 16	10.3	5.38	14.56	5.97	within
e014552	EHDGSSGMTMDTESEID	none	Zinc finger X-chromosomal protein	10.45	5.8	13.12	9.55	within
e300092	SGETGPAGPPGNPGPPGPPGP*	3xOxidation [P9; P10; P19]	Collagen alpha-1(II) chain	9.89	5.55	12.76	9.21	within
e100697	DTTDSNGTVNQIMMAN	none	Dual specificity protein kinase TTK	11.19	7.18	13.12	12.46	within
e014580	GSKYDVAAEGEDEESVSA	none	Melanoma-associated antigen B6	11.46	7.88	13.63	10.79	within
e212937	NFPSPVDAAFRQGHNSV	none	Hemopexin	8.89	3.45	12.1	10.04	within
e014590	KDEDEPPGHLQGEPPAQ	none	Coiled-coil and C2 domain-containing protein 1B	10.74	7.05	14.62	11.33	within
e014591	YSQSGSKPGEDFRMATL	none	Prostaglandin-H2 D-isomerase	10.64	6.74	14.7	10.85	within
e104572	NSGEPGAPGSKGDTGAKGEP*	2xOxidation [P8; P20]	Collagen alpha-1(I) chain	11.43	6.51	13.92	11.66	within
e014596	GPPGVAGPPGGSGPAGPPGPQG*	5xOxidation [P3; P8; P9; P14; P17]	Collagen alpha-1(III) chain	11.22	6.33	12.88	9.96	within
e014597	PGDPGPMGPIGSRGPEGPPG*	1xOxidation [P19]	Collagen alpha-2(V) chain	11.08	5.79	13.15	7.89	within
e014603	RAHGQESAI FNEVAPGY	none	Secreted and transmembrane protein 1	8.49	4.38	13.18	9.85	within
e014606	DSAAGDPDSAAGQMAEEPQ	none	Nucleosome assembly protein 1-like 5	9.1	5.78	12.11	9.08	within
e014609	HEGDEGP GHHHKPGLGEG	none	Protein S100-A9	6.99	3.59	11.74	7.39	within
e099089	DEAGSEADHEGTHSTKR*	1xCation:Na [D8]	Fibrinogen alpha chain	10.94	6.41	12.98	10.88	within
e014636	SPGPKGDKGEPGGPGADGVPG*	1xOxidation [P]	Collagen alpha-1(III) chain	11.09	7.13	13.46	10.11	within
e212948	GPPGPPGFPGDPGPPGPAGL*	7xOxidation [P3; P5; P6; P9; P12; P14; P15]	Collagen alpha-3(V) chain	10.81	7.77	13.06	11.72	within
e212949	SGPQGP GPPGPKGNSGEPGA*	3xOxidation [P3; P6; P9]	Collagen alpha-1(I) chain	10.82	7.68	13.09	11.72	within
e014643	LEPPEQQEPGERQEPS	none	Integrin alpha-7	10.78	7.33	13.09	11.72	within
e014644	QLVMTMGVADSQLFFY	none	Protein transport protein Sec24D	7.98	5.05	12.13	10.86	within
e212952	GPPGSISSSGQEIQQYIS*	1xOxidation [P]	Collagen alpha-1(XVII) chain	11.27	6.83	12.93	11.81	within
e014660	PSELSFQDFEYPDYD	none	NEDD4-binding protein 2	9.18	5.43	11.59	10.28	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014661	GSPGPVGFPGDPGPPGEGPGP*	5xOxidation [P12; P14; P15; P18; P20]	Collagen alpha-1(V) chain	8.37	4.51	11.21	5.0	within
e104201	GEVGPAGPNGFAGPAGAAGQPG*	1xOxidation [P8]	Collagen alpha-2(I) chain	9.44	5.94	11.93	8.85	within
e212955	KDGPRGAQGPAGPKGEPGQ*	3xOxidation [P4; P10; P13]	Collagen alpha-1(XXIII) chain	8.7	5.65	12.02	8.97	within
e014666	GSAQVKGHGKKVADALTNA	none	Hemoglobin subunit alpha	9.08	5.24	13.01	8.86	within
e106077	TASPEDSDMPDHDLEPP	none	E3 ubiquitin-protein ligase UBR5	10.11	6.2	11.94	11.32	within
e014680	SAASSGSNSSASSEQGLLGR	none	Protein sprouty homolog 1	9.6	4.92	12.59	10.75	within
e208243	EPGPQGLPGFSGPPGKEGE*	1xOxidation [P13]	Collagen alpha-2(IX) chain	9.97	5.64	12.22	10.66	within
e097591	PAQGLAGRGNGVGESESPL	none	Putative uncharacterized protein FLJ46641	7.98	4.44	10.73	9.2	within
e014685	LKKENKNEKVEIHIM	none	Protein S100-A9	8.03	4.07	12.14	9.52	within
e094916	NGAPGEAGRDGNPGNDGPPG*	3xOxidation [P4; P13; P18]	Collagen alpha-2(I) chain	10.74	7.23	12.64	11.26	within
e212966	GSSGITGFPGMPGESGSQGI*	2xOxidation [P9; P12]	Collagen alpha-6(IV) chain	11.19	8.17	12.66	10.34	within
e014700	PGGSGAGEERMPPSLQER	none	Interleukin-2 receptor subunit beta	10.06	3.49	13.03	12.11	within
e014705	NNSRSSSSASGSYGHLAS	none	Transcriptional activator GLI3	16.18	13.4	17.65	17.39	within
e014732	SLGEGEESESNSVESLGF	none	Angio-associated migratory cell protein	10.29	5.93	12.24	9.9	within
e014738	QGSPGGNRYPPQGGGGWGQ	none	Major prion protein	8.99	5.06	12.13	8.73	within
e014746	GVGEAGAAGEAGAAGEAGAAGEAG	none	Paraneoplastic antigen Ma6F	8.89	4.65	11.77	11.67	within
e212971	IGSSPNSGHYISDVYDF	none	Ubiquitin carboxyl-terminal hydrolase 29	10.88	5.67	14.67	9.27	within
e300093	SGETGPAGPPGNPGPPGPPGP*	4xOxidation [P6; P9; P13; P19]	Collagen alpha-1(II) chain	12.1	6.25	13.71	11.36	within
e014753	EEMENEDEMSEEDGG	none	Chromodomain-helicase-DNA-binding protein 5	9.43	5.29	13.07	2.29	down
e014757	RKGDGTGEDGYPGGPGPPGP*	3xOxidation [P14; P16; P17]	Collagen alpha-4(IV) chain	10.4	6.29	14.19	9.75	within
e212974	PPGPTGPGGDKDGTGPPGPQG*	1xOxidation [P17]	Collagen alpha-1(III) chain	9.94	6.24	14.08	9.72	within
e014768	AEGEREEEGRAEAPDKS	none	Microtubule-associated protein 1A	10.01	6.16	12.34	6.55	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e208246	GDQGPDPGSPGSPGPAGPAG*	2xOxidation [P6; P9]	Collagen alpha-3(IV) chain	12.3	9.53	13.76	12.31	within
e014783	NSGEPGAPGSKGDTGAKGEP*	3xOxidation [P5; P8; P20]	Collagen alpha-1(I) chain	12.02	8.28	14.34	13.23	within
e212980	PGSRGENGPTGAVGFAGPQG*	3xOxidation [P1; P9; P18]	Collagen alpha-2(V) chain	11.82	8.33	14.22	13.19	within
e212982	HGTMAAPRVHTDYHPGGG	none	Putative uncharacterized protein encoded by AGPAT4-IT1	12.32	9.7	13.78	12.53	within
e014795	TANDIYAEFWAEGDEM	none	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A	11.82	7.04	14.17	13.87	within
e014796	QGGAGPTGPPGEPGDPGPMGP*	2xOxidation [P6; P9]	Collagen alpha-2(V) chain	10.37	7.11	12.75	10.25	within
e014797	EGSPGRDGSPGAKGDRGET*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	13.42	9.41	14.81	13.95	within
e097600	GKVGAHAGEYGAELERM*	1xOxidation [M18]	Hemoglobin subunit alpha	13.06	9.21	14.64	13.92	within
e014808	GSGAPEPTPSHTGSPDPEQ*	1xOxidation [P17]	Collagen alpha-1(XX) chain	8.6	6.01	11.08	8.48	within
e106058	GPAGSRGAPGPQGPRGDKGE*	1xOxidation [P2]	Collagen alpha-1(III) chain	9.16	5.74	12.02	8.65	within
e014817	EMVEVGADDDEGAERGE	none	Caveolae-associated protein 1	12.23	8.64	14.09	12.8	within
e212992	DAGPVGPPGPPGPPGPPGPS*	4xOxidation [P10; P11; P13; P14]	Collagen alpha-1(I) chain	14.14	10.23	16.2	14.77	within
e106546	EGAHGAPGAAGNPGAPGHVGAP*	1xOxidation [P]	Collagen alpha-1(XXII) chain	8.48	5.06	11.33	8.03	within
e014826	SGAAAGMALRYEAFQQGH	none	Seizure protein 6 homolog	7.38	4.17	11.76	6.22	within
e102022	RPSGVPRFSGSIDSSN	none	Immunoglobulin lambda variable 6-57	9.84	6.03	12.03	10.26	within
e014833	EAVEEETGDGLDESDR	none	Prothrombin	11.26	6.9	13.31	12.2	within
e212996	EDTSRTDVSEPATSGGAAD	none	Uncharacterized protein C11orf24	11.15	6.81	13.24	12.23	within
e212997	SESDKEDNGSEGQLTNR	none	Kinesin-like protein KIF26B	11.0	6.86	13.09	12.18	within
e212999	GQTGPPGAPGPPGSKGDRGQ*	3xOxidation [P8; P11; P12]	Collagen alpha-1(XXVI) chain	13.76	8.92	15.64	14.02	within
e213001	PGEKGHRGDPGSPGPPGPS*	1xOxidation [P]	Collagen alpha-1(V) chain	13.77	8.9	15.68	13.93	within
e100795	AGAAGPAGPAGPRGSPGERGE*	3xOxidation [P9; P12; P16]	Collagen alpha-2(I) chain	7.26	2.1	12.54	7.96	within
e014844	GGSFGGGFGGGGFGGGFGGGFGG	none	Keratin, type I cytoskeletal 10	9.65	6.15	11.74	11.48	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e105324	PPLING*	1xN-Glycan [N5] (HexNAc(3)Hex(4))	Protocadherin-19	8.07	5.07	10.8	10.1	within
e014851	GPAGAPGPQGFGNPGEPGE*	3xOxidation [P2; P6; P8]	Collagen alpha-1(II) chain	9.54	6.27	12.29	9.66	within
e014852	PWLTDGSYLDGTGFARI	none	Laminin subunit alpha-5	8.87	2.94	12.59	10.41	within
e014853	HTSDSDVPSGVTEVVVKL	none	Clusterin	10.45	5.56	13.66	10.41	within
e014866	NFLKKENKNEKVEIH	none	Protein S100-A9	9.16	4.75	12.67	12.08	within
e014869	DEAPGQEQRGPEDQDIS	none	Defensin alpha 4	10.33	6.06	11.99	11.7	within
e014873	GPPGERGAPGNRGFPGQDG*	3xOxidation [P3; P9; P15]	Collagen alpha-1(II) chain	10.57	6.51	12.62	12.95	up
e014874	GYPAPGGYPAPGGYPGAPQP	none	Annexin A7	9.46	5.93	11.96	11.87	within
e100847	PGANGMKGEKGDGMPGPQG	none	Collagen alpha-1(XXV) chain	9.08	6.24	11.64	9.92	within
e014881	LVGGPMDASVEEEGVRRRA	none	Cystatin-C	8.79	5.12	12.33	10.16	within
e213011	GSAAATGAGGAGAYGTGGPGGPGGP	none	T-cell leukemia homeobox protein 1	6.3	0.0	12.11	10.72	within
e202873	GPPGEQGPppppppgvpGI*	7xOxidation [P8; P9; P11; P12; P14; P15; P18]	Collagen alpha-1(IX) chain	7.41	1.54	12.39	10.74	within
e014887	VKGERGSPGGPGAAGFPGAR*	3xOxidation [P8; P11; P17]	Collagen alpha-1(III) chain	6.74	3.3	12.34	7.14	within
e014889	GFGYPGEQGPppppgpeGP*	5xOxidation [P5; P10; P11; P13; P14]	Collagen alpha-1(XXI) chain	10.56	7.57	15.24	8.73	within
e014901	ESEAESEEEYNDEGE	none	Transcription elongation factor SPT6	9.95	4.91	13.21	5.76	within
e014904	TDNEEGEEENPLEIKE	none	Midasin	7.13	2.89	10.75	12.62	up
e208260	PGAWTSSES LASDDGGAPGI	none	KN motif and ankyrin repeat domain-containing protein 3	11.72	6.42	14.19	11.57	within
e213013	GDSGPPGEKGDPRGPPGP*	3xOxidation [P17; P18; P20]	Collagen alpha-1(VII) chain	11.17	7.69	13.23	11.22	within
e014914	GPPGSGEKGERGAAGEPGPH*	2xOxidation [P17; P19]	Collagen alpha-1(XVII) chain	11.13	7.85	13.09	11.2	within
e014916	PQLVATMPVSPAGSHKQQ	none	Dynein axonemal intermediate chain 4	10.37	5.34	14.76	9.85	within
e014927	PGEKGEGGPPGVAGPPGGSGPA*	3xOxidation [P9; P10; P15]	Collagen alpha-1(III) chain	11.66	8.21	13.43	11.62	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e202887	DITFRSDYSNEKPFTG	none	Mannan-binding lectin serine protease 2	8.24	5.47	12.92	10.63	within
e213014	HGDPGFPGPPGERGDPGEA*	2xOxidation [P7; P9]	Collagen alpha-2(IV) chain	11.42	6.81	14.79	9.91	within
e014937	LEAGEVELSEGEDDTDGL	none	Tonsoku-like protein	11.65	6.72	13.31	13.2	within
e097606	SNGNPGPPGPSGSPGKDGPPG*	3xOxidation [P14; P19; P20]	Collagen alpha-1(III) chain	13.33	9.25	14.87	13.63	within
e014940	DDGEAGKPRPGERGPPGP*	2xOxidation [P11; P16]	Collagen alpha-1(I) chain	13.5	9.89	14.97	13.62	within
e100890	GPSGASGERGPPGPMGPGLA*	2xOxidation [P17; P18]	Collagen alpha-1(I) chain	8.89	5.79	11.95	6.1	within
e213015	PGFPGSKGDPGSPGPPGPAGI*	2xOxidation [P16; P]	Collagen alpha-1(X) chain	11.4	6.19	13.4	12.64	within
e202893	LENEDRRSASLHLPKL	none	Alpha-1-antitrypsin	8.5	4.37	11.89	8.06	within
e104054	GPELAGDWGGAGDAPLSPDP	none	Sphingosine kinase 2	10.2	6.68	13.25	10.46	within
e213019	GEPGDRGQEGPRGPKGDPG*	1xOxidation [P11]	Collagen alpha-1(VII) chain	12.96	10.04	14.46	13.14	within
e213020	PGADGQPGAKGANGAPGIAGAP*	3xOxidation [P7; P16; P22]	Collagen alpha-1(I) chain	11.57	7.38	13.17	8.65	within
e014961	MGGPPMGQMPPGMMSSVMPG	none	Pre-mRNA-processing factor 40 homolog A	9.53	4.1	12.31	13.49	up
e103386	PGFPGTPGLPGMPGHGAPG*	4xOxidation [P1; P7; P10; M12]	Collagen alpha-5(IV) chain	10.85	7.5	12.81	9.95	within
e213025	RDTDRFSSHVGTLGQF	none	Inter-alpha-trypsin inhibitor heavy chain H4	10.63	6.08	14.36	11.26	within
e213026	GPSGAAGPPGKKGPPGEDGAK*	3xOxidation [P2; P8; P9]	Collagen alpha-3(V) chain	8.95	3.65	10.89	9.37	within
e213028	PPGSQGPKGQRGSRGPDGL*	2xOxidation [P1; P2]	Collagen alpha-1(XXIV) chain	11.26	5.88	15.0	11.25	within
e014972	HLPAEFTPAVHASLDKF	none	Hemoglobin subunit alpha	11.27	6.09	15.08	11.34	within
e014978	GSYSFDDHITDSEALSH	none	Transcription factor HIVEP3	12.03	8.1	13.42	12.73	within
e014979	GEKGPSGEAGTAGPPGTPGPQ*	2xOxidation [P15; P18]	Collagen alpha-2(I) chain	10.91	6.8	12.74	10.46	within
e014980	GPQGPPGPVGSPPGERGSAGTA*	3xOxidation [P6; P8; P12]	Collagen alpha-1(XI) chain	6.75	3.42	9.91	6.77	within
e213030	GSPGAKGDRGETGPAGPPGAP*	3xOxidation [P3; P14; P17]	Collagen alpha-1(I) chain	9.37	4.39	11.73	9.82	within
e014982	ALQEEPDSKEGKAWR	none	Kinetochore-associated protein 1	6.79	3.36	11.06	8.88	within
e213033	GPPGPPGTAGFPGSPGAKGEV*	3xOxidation [P5; P6; P12]	Collagen alpha-1(III) chain	14.31	9.59	16.07	13.93	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e014989	YEKGRNHYTESISVAK	none	Sialidase-1	7.12	4.06	12.1	9.33	within
e213037	PGEAGRDGNPGNDGPPGRD*	3xOxidation [P10; P15; P16]	Collagen alpha-2(I) chain	10.02	5.22	13.26	12.95	within
e015001	DAGPAGPKGEPGSPGENGAPG*	4xOxidation [P7; P11; P14; P20]	Collagen alpha-1(I) chain	10.13	5.61	11.83	9.17	within
e213039	ESPPNELAAGEGVRGGAQSG	none	Adenomatous polyposis coli protein	9.88	5.89	12.96	11.58	within
e015011	DEAGSEADHEGTHSTKRG	none	Fibrinogen alpha chain	17.79	15.2	18.37	17.91	within
e015028	PGMGGDPRGVGAGDMASAGPE	none	Proline-rich protein 35	11.23	8.13	12.86	11.78	within
e015032	FDMGFYQVRSIASHV	none	ATP-dependent RNA helicase DDX42	7.4	4.32	11.37	9.24	within
e101325	KGSMGHPGMPGGMGTPGEPG*	3xOxidation [P10; P16; P19]	Collagen alpha-1(XXVII) chain	11.63	7.61	13.26	8.48	within
e202915	GGEGKGGSDGGGSHRKEGEE	none	CD99 antigen	11.25	5.97	13.36	10.65	within
e106269	GAPGPMGPKGPPGHKGEFGL	none	Collagen alpha-1(XV) chain	9.0	5.01	11.3	9.72	within
e202918	VIKMGVAAHKKSHEESH	none	Protein S100-A8	8.26	3.72	11.93	12.89	up
e015083	APGGSVFPAGGGPLLTGGAHVH	none	Band 4.1-like protein 4B	5.77	3.25	11.36	9.83	within
e015093	GKAGEDGHPGKPRPGERG*	2xOxidation [P9; P12]	Collagen alpha-2(I) chain	7.85	3.77	11.29	10.41	within
e213052	GSSGIPGKEGPGGKPGKPGVK	none	Collagen alpha-1(XVI) chain	6.22	1.61	11.66	9.34	within
e213055	AGVAGGTGGSGGGSTAQSFLRP	none	Forkhead box protein D3	6.89	3.74	9.86	6.03	within
e103170	PGEKGEGGPPGVAGPPGGSGPA*	4xOxidation [P1; P9; P10; P16]	Collagen alpha-1(III) chain	10.0	5.15	13.36	9.74	within
e015118	GSQASSNSDPFGEPSPGEPG	none	Disabled homolog 1	13.3	7.33	16.11	9.07	within
e213060	PTGDDGPKGNPGPVGFPGDP*	1xOxidation [P]	Collagen alpha-2(XI) chain	11.75	7.67	13.68	13.19	within
e015120	DDGEAGKPRPGERGPPGP*	3xOxidation [P8; P11; P16]	Collagen alpha-1(I) chain	11.81	8.24	13.66	12.03	within
e015121	GAPGAPGGKGDAGAPGERGPPG*	4xOxidation [P3; P6; P15; P20]	Collagen alpha-1(III) chain	10.1	5.52	12.92	12.13	within
e101169	RGANGAPGNDGAKGDAGAPGAP*	1xOxidation [P7]	Collagen alpha-1(I) chain	9.37	5.93	12.14	8.01	within
e213062	GKPGANGLSGERGPPGPQGL*	3xOxidation [P3; P14; P15]	Collagen alpha-1(III) chain	9.33	5.34	12.45	12.19	within
e015123	PGISVLMTFPQLGPVQPI	none	Kinesin-like protein KIF18A	10.81	7.13	13.12	11.71	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213064	SSEAKAEETGGGKEKGGG	none	Homeobox protein cut-like 1	10.92	6.92	12.69	10.26	within
e015132	QAGSTEDGLPPSHSSPSLQ	none	PH and SEC7 domain-containing protein 1	10.12	5.96	13.57	9.9	within
e104964	MEVDRRVEESGDEE	none	Protein phosphatase 1 regulatory subunit 7	8.19	4.44	10.48	8.12	within
e300095	QGPVGPPGFTGPPGPPGPPG*	2xOxidation [P12; P13]	Collagen alpha-1(IV) chain	8.02	5.19	12.1	10.78	within
e015145	SVIDQSRVLNLGPITRK	none	Uromodulin	9.97	5.49	13.09	12.24	within
e097614	KVADALTNAVAHVDDMPN*	1xOxidation [M16]	Hemoglobin subunit alpha	9.17	5.35	12.03	10.27	within
e015170	KDSAHGFLKVPPRMDAK	none	Serotransferrin	7.64	3.27	12.04	3.36	within
e015192	SSSGSGGSSKSQSSTSPEGQA	none	SH3 domain-binding protein 5	6.95	2.14	10.7	10.82	up
e213072	VDTAETSYLEMAAGSEPE	none	Inactive histone-lysine N-methyltransferase 2E	10.22	5.43	12.56	8.75	within
e099032	DDGEAGKPGRPGERGPPGP*	1xCation:Na [D/E]; 2xOxidation [P11; P16]	Collagen alpha-1(I) chain	8.6	3.77	12.12	8.84	within
e015199	EADVAIEEDLEEDDGDH	none	Zinc finger protein 711	10.54	6.39	12.72	13.36	up
e015201	ADGAGPEDDTEASRAAAPAE	none	Ankyrin repeat domain-containing protein 11	7.47	4.22	11.79	11.34	within
e015202	PGGEGASERIEETMSVHD	none	Ankyrin-3	9.94	5.65	12.19	11.77	within
e015203	SGEPGAPGSKGDTGAKGEPGP*	3xOxidation [P4; P7; P19]	Collagen alpha-1(I) chain	10.75	6.59	13.04	10.66	within
e015206	SPGRDGSPGAKGDRGETGPA*	2xOxidation [P2; P8]	Collagen alpha-1(I) chain	11.5	7.73	13.41	12.19	within
e213074	WGKVGAHAGEYGAEALER	none	Hemoglobin subunit alpha	10.07	6.27	12.75	11.75	within
e100960	DHEGTHSTKRGHAKSRP	none	Fibrinogen alpha chain	7.12	2.35	11.06	7.84	within
e099628	DSDEEEDDDSEDEED	none	Nucleolin	10.25	6.96	12.8	7.2	within
e015215	TTSSGANTATNSGSSVTSAGSG	none	Mucin-21	9.58	5.09	12.19	8.31	within
e015232	RAGGYLEEDTLSEGSV	none	Rho GTPase-activating protein 30	9.38	4.79	11.29	10.2	within
e015242	DAAQKTDTSHTDQDHPT	none	Alpha-1-antitrypsin	7.65	4.57	10.65	11.8	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e106090	PGDVGGPGPPGASGEPGAPGPP*	5xOxidation [P7; P9; P10; P16; P19]	Collagen alpha-3(V) chain	10.45	6.9	12.16	11.34	within
e208280	GDQGHGPGVPGFMGPPGNPGP*	2xOxidation [P15; P18]	Collagen alpha-1(XXII) chain	10.56	6.86	12.29	11.34	within
e015251	VAHVDDMPNALSALSDLH	none	Hemoglobin subunit alpha	7.22	3.05	9.48	10.83	up
e100209	DEAGSEADHEGTHSTKRG*	1xCation:Na [E/D]	Fibrinogen alpha chain	12.96	8.03	15.35	11.76	within
e015259	SEVAHRFKDLGEENFK	none	Albumin	6.98	3.94	12.17	5.57	within
e015262	GMGAGGGHRPHEGPGGSMGGSG	none	Serine/threonine-protein phosphatase 1 regulatory subunit 10	12.64	9.15	14.64	11.13	within
e015263	GKAGEDGHPGKPRPGERG*	3xOxidation [P9; P12; P15]	Collagen alpha-2(I) chain	7.77	4.21	11.41	9.48	within
e102044	IEKVEHSDLSFSKDWS	none	Beta-2-microglobulin	7.39	4.44	12.97	4.5	within
e105836	SDEMDAHANEEIPEQPP	none	Dynein axonemal heavy chain 11	9.66	5.41	12.12	6.06	within
e015279	KLNASDADEGPNSEIVYS	none	Protocadherin alpha-2	6.11	2.41	10.38	5.23	within
e105073	RGKMGMPGFPGVFGERGP*	2xOxidation [P10; P18]	Collagen alpha-1(XXVII) chain	8.46	5.12	11.83	8.59	within
e015280	AAAAAGMAGVAAPPNGNTRGTGG	none	Carbohydrate sulfotransferase 2	7.88	5.37	12.28	10.82	within
e093758	GQPGIRGPAGHPGPPGADGAQ*	1xOxidation [P3]	Collagen alpha-3(V) chain	9.7	5.88	12.58	11.86	within
e097621	WGKVVNDEVGGEALGRLL	none	Hemoglobin subunit beta	18.78	14.59	20.59	18.75	within
e213093	SGSVIDQSRVLNLGPITR	none	Uromodulin	18.83	14.94	20.64	18.77	within
e213095	RAVPHPDSPDTIDHDL	none	Complement factor D	7.62	4.5	14.57	5.1	within
e015313	VLVQSPSTQPAEKDTVTI	none	Matrix-remodeling-associated protein 5	17.89	9.29	19.9	18.14	within
e213098	RTMAPEKLLKSMPILQG	none	Clathrin coat assembly protein AP180	18.12	12.94	19.95	18.14	within
e102846	YTQTEPEGSQPSTMDATA	none	Zinc finger protein 653	10.04	5.45	12.31	11.93	within
e102718	NGAPGNDGAKGDAGAPGAPGSQ*	3xOxidation [P4; P16; P19]	Collagen alpha-1(I) chain	11.38	6.97	14.35	11.62	within
e015323	AIPMSIPPEVKFNKPFV	none	Alpha-1-antitrypsin	8.24	5.64	12.67	6.0	within
e015328	LTPSEGMTHSSVLSQML	none	Sushi domain-containing protein 5	7.58	3.03	12.13	11.47	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015337	FRTQTAPGGQGAPWAEEL	none	Roundabout homolog 4	9.85	5.63	13.37	7.47	within
e015339	GPRGPPGPVGPSPGKDGANGIP*	2xOxidation [P11; P21]	Collagen alpha-1(II) chain	7.48	3.82	13.4	10.37	within
e015349	QGPGGNLGLSPGGNGAAGGGGPPA	none	Striatin-3	10.92	6.66	13.18	11.23	within
e015355	GSGGGHSGGSGGGHSGGSGGNYGGG	none	Keratin, type I cytoskeletal 9	13.41	8.96	15.59	12.77	within
e015356	DENWYEGMIHGESGFF	none	Endophilin-A3	13.82	10.4	15.63	15.41	within
e015359	GNSGEPGAPGSKGDTGAKGEP*	3xOxidation [P6; P9; P21]	Collagen alpha-1(I) chain	8.52	4.82	11.52	10.41	within
e213110	TDQETTGVGPKGDTGPRG*	1xOxidation [P]	Collagen alpha-1(I) chain	7.92	4.68	12.37	5.08	within
e015360	GPPGIGLPGTPGDPGGPPGPK*	6xOxidation [P8; P11; P14; P17; P18; P20]	Collagen alpha-1(XVI) chain	7.08	4.29	11.05	8.51	within
e015362	DELPKDDPDAPLQPVTP	none	Complement C4-A	10.41	6.29	12.16	11.18	within
e015385	NQAQEHFGKDKSKEFQ	none	Serotransferrin	9.91	5.22	12.88	11.84	within
e015395	GPAGSPGSNGAPGQRGEPGPQ*	3xOxidation [P12; P18; P20]	Collagen alpha-1(III) chain	8.24	4.09	11.37	9.79	within
e015402	GDAGPAGPKGEPGSPGENGAPG*	3xOxidation [P12; P15; P21]	Collagen alpha-1(I) chain	12.21	6.83	14.03	10.22	within
e213119	GPAGAPGDKGESGPSGPAGPTGA*	2xOxidation [P6; P14]	Collagen alpha-1(I) chain	9.96	4.04	12.72	9.19	within
e015411	GGGSFGGGFGGGFGGGFGGGFGG	none	Keratin, type I cytoskeletal 10	10.45	6.24	12.55	10.79	within
e103462	EPSLTESDSVSAASSDQQ	none	Transmembrane channel-like protein 3	10.82	6.35	12.76	10.68	within
e106167	EAGKPGEQGVPGDLGAPGPSG*	3xOxidation [P5; P11; P17]	Collagen alpha-1(I) chain	10.24	5.88	12.36	10.48	within
e015414	GPKGSSGDPGKPEAGNAGVPG*	2xOxidation [P9; P12]	Collagen alpha-2(V) chain	10.01	5.43	12.47	10.19	within
e015416	AARGSGSNPARPGGFPGANSP	none	RNA-binding protein Musashi homolog 2	7.69	4.78	12.16	10.67	within
e015417	MGVVSLGSPSGEVSHPRKT	none	Alpha-2-HS-glycoprotein	9.26	4.73	15.59	13.9	within
e097627	AGGSLGAGGSRGPLPGGFSGGNP	none	Zinc finger and BTB domain-containing protein 12	6.77	4.45	9.61	8.72	within
e015434	NTGLPGFPGFPGAQGDPLK	none	Collagen alpha-3(IV) chain	8.17	4.26	13.48	12.32	within
e015442	GPPGSPGEDGPAGEPGPPGPEG*	1xOxidation [P3]	Collagen alpha-1(XV) chain	9.55	5.52	12.23	8.98	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015453	VSETESRGSESGIFTNTK	none	Fibrinogen alpha chain	8.6	4.54	13.52	5.5	within
e015463	REGPMGPRGEAGPPGSGEK*	4xOxidation [P4; P7; P13; P14]	Collagen alpha-1(XVII) chain	8.18	4.48	11.34	9.21	within
e015465	GPQGEPLQGTQGVPGAPGPP*	2xOxidation [P15; P18]	Collagen alpha-3(IV) chain	7.7	4.51	11.04	9.11	within
e015471	GISVPGKPGQQGPTGAPGPRG*	1xOxidation [P19]	Collagen alpha-1(X) chain	11.67	6.83	13.48	8.56	within
e015479	SPVVSTYDSEMSMDASPE	none	MAP7 domain-containing protein 3	8.73	4.59	11.77	11.98	up
e213126	EGSPGPGEEPAVPEGAPDVAA	none	Sarcalumenin	8.24	4.66	11.56	10.04	within
e208300	GPKGNDGAPGKNGERGGPGGPG	none	Collagen alpha-1(III) chain	10.64	6.82	12.57	11.13	within
e100680	KMGVAHKKSHKE	none	Protein S100-A8	7.8	3.48	13.12	12.79	within
e213128	DVFQYEVAVLVGAGIVTP	none	NADPH oxidase 1	13.56	9.3	16.66	12.12	within
e103872	PDWGTFEVSGNVSPGTR	none	Fibrinogen alpha chain	10.63	6.1	14.5	8.39	within
e015528	GDDGEAGKPRPGERGPPGP*	2xOxidation [P17; P]	Collagen alpha-1(I) chain	12.42	8.6	14.3	13.02	within
e015530	RQSRSRSRKGGSRRS	none	Serine/arginine-rich splicing factor 4	13.1	7.7	16.22	11.38	within
e213138	DGAEAQAPSPPALEDTAAG	none	General transcription factor 3C polypeptide 1	11.42	7.91	13.4	12.3	within
e213139	PPRMGSRAGPTTPLSPTR	none	Lamin-B1	11.13	6.95	13.94	10.13	within
e015548	GPALAGEPAGSLRELGVWR	none	Phospholipid transfer protein C2CD2L	10.92	7.38	13.8	10.11	within
e099620	PDGLKGDRGDPGPDGEHGE*	2xOxidation [P11; P13]	Collagen alpha-1(XXVII) chain	9.58	5.82	12.74	6.48	within
e015558	VADALTNVAHVDDMPNAL	none	Hemoglobin subunit alpha	8.78	6.15	14.31	11.04	within
e015560	EKQKPDGVFQEDAPVIH	none	Complement C3	6.61	3.38	11.03	5.19	within
e015563	DEQEEHGEENAEAGQH	none	E3 ubiquitin-protein ligase UBR5	10.82	6.53	13.94	13.64	within
e015564	GEKGPSGEAGTAGPPGTPGPQG*	2xOxidation [P15; P18]	Collagen alpha-2(I) chain	11.79	8.0	13.47	12.3	within
e213141	PAGKSGDRGESGPAGPAGAPGP*	3xOxidation [P16; P20; P22]	Collagen alpha-1(III) chain	11.76	7.99	13.49	12.26	within
e213142	NFGAPSGTSGTAAATAAPAGGFG	none	Nucleoporin p54	8.55	5.57	10.86	8.15	within
e015570	SPAAPSPGSSGGGGFFSSLSNA	none	Synapsin-1	11.92	8.16	13.4	12.19	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015580	EGSPGHPGQPGPPGPPGAPGP*	6xOxidation [P7; P10; P12; P13; P15; P16]	Collagen alpha-1(III) chain	9.72	6.5	12.12	7.81	within
e213149	ERGEAGPPGRGERGEPGAP*	4xOxidation [P7; P8; P16; P19]	Collagen alpha-1(XXV) chain	10.96	6.33	12.86	12.72	within
e015582	GLDGAKGDAGPAGPKGEPGSPG*	3xOxidation [P11; P14; P18]	Collagen alpha-1(I) chain	11.2	7.4	12.94	13.15	up
e097633	FSVDETGQMSATAKGRVR	none	Retinol-binding protein 4	9.42	5.57	12.31	12.27	within
e015597	GGGAGGAGGGPPPGAGDRGGGGP	none	Far upstream element-binding protein 2	10.04	4.9	12.13	10.78	within
e100131	TNAVAHVDDMPNALSALSD	none	Hemoglobin subunit alpha	10.28	5.6	12.84	8.48	within
e106391	AAKNLQEAEEWYKSKF	none	Vimentin	8.96	5.1	14.78	9.21	within
e015619	GLPGPPDVPDHAAYHPFR	none	Inter-alpha-trypsin inhibitor heavy chain H4	8.51	4.79	11.83	7.64	within
e100275	GPPGSPGEDGPAGEGPPGPEG*	2xOxidation [P3; P6]	Collagen alpha-1(XV) chain	11.01	7.18	12.55	12.19	within
e208305	GPPGRPLPGADGLGPPPGTM*	3xOxidation [P3; P6; P9]	Collagen alpha-1(V) chain	9.52	4.95	12.78	11.72	within
e015649	TVAAPSVFIFPPSDEQLK	none	Immunoglobulin kappa constant	10.39	7.2	12.4	11.42	within
e015654	AAAEPGFDDEAAEGGGPGAE	none	E3 ubiquitin-protein ligase RNF19B	9.85	4.32	12.09	9.45	within
e203073	APAGSSHPAASARIPPKFGGA	none	Protein transport protein Sec24B	9.5	5.86	11.81	10.25	within
e015665	ASAAGAAGSAGGSSGAAGAAGGGAGAGT	none	Protein CDV3 homolog	10.02	6.81	12.16	9.84	within
e208306	EPGLPGPPGEGRAGEPGTAGP*	3xOxidation [P5; P7; P]	Collagen alpha-2(VIII) chain	9.86	6.37	12.24	9.54	within
e015668	NVWGKVEADIPGHGQEV L	none	Myoglobin	7.35	3.32	13.15	9.14	within
e213163	KGDPGVGERGPPGPQGPPGP*	6xOxidation [P4; P11; P12; P14; P17; P18]	Collagen alpha-1(XVIII) chain	12.32	9.27	13.59	12.21	within
e213165	GPVGFPDGPDPGEPGPAGQD*	3xOxidation [P]	Collagen alpha-1(V) chain	7.91	4.62	11.3	11.5	up
e015689	EEGKRGPNGEAGSAGPPGPPG*	2xOxidation [P17; P19]	Collagen alpha-2(I) chain	11.03	7.72	12.97	11.24	within
e015690	GLKGEPGDVGPQGPRGVQGP*	3xOxidation [P11; P14; P20]	Collagen alpha-1(V) chain	14.95	9.21	17.97	11.92	within
e213166	PGVPGSVVQQEGLKGEQGAP*	1xOxidation [P]	Collagen alpha-1(XXII) chain	15.03	9.56	17.98	11.53	within
e015705	SFSLESDVDYSSDDNLTG	none	Homeobox protein GBX-2	10.01	5.22	12.44	12.34	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015707	GIDGSPGEKGDVGGPPPG*	2xOxidation [P6; P12]	Collagen alpha-3(V) chain	11.4	8.41	13.1	13.11	up
e208310	GDDGEAGKPRPGERGPPGP*	3xOxidation [P12; P17; P]	Collagen alpha-1(I) chain	11.39	8.62	13.11	13.11	within
e213170	GIPGFPGPRGDPGSYGSPGF*	2xOxidation [P12; P18]	Collagen alpha-4(IV) chain	10.59	6.79	12.75	11.37	within
e104451	VSGIDGSPGEKGDVGGPPG	none	Collagen alpha-3(V) chain	11.11	7.17	12.85	10.94	within
e213172	EEAPSLRPAPPPISGGGYR	none	Fibrinogen beta chain	14.53	9.7	17.32	10.74	within
e015719	GTDGPMPHGPAGPKGERGE*	3xOxidation [P8; P11; P]	Collagen alpha-1(XXV) chain	12.47	8.54	14.27	12.17	within
e105523	GLLYWEDPDDMGHHLGP	none	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5	10.33	7.05	12.04	10.99	within
e015723	KVADALTNAVAHVDDMPNA	none	Hemoglobin subunit alpha	9.13	5.86	12.64	7.28	within
e300060	DYQSSRNQPGPPGPPGPPG*	3xOxidation [P14; P15; P17]	Collagen alpha-1(XII) chain	12.56	7.41	14.78	13.77	within
e015732	GPLGPPGAAGPSGEEGDKGDVG*	2xOxidation [P6; P11]	Collagen alpha-3(V) chain	7.89	3.8	10.45	10.92	up
e015735	PGSPGPPGPPGIQGPAGLDGLD	none	Collagen alpha-1(XVI) chain	10.7	5.96	13.18	11.8	within
e095027	GEKGPSGEAGTAGPPGTPGPQG*	3xOxidation [P14; P15; P]	Collagen alpha-2(I) chain	9.67	6.34	11.9	11.01	within
e015743	LESSPSRSSTATSMDPLST	none	Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D	6.79	3.84	10.11	11.33	up
e099619	GEPGAPGSKGDTGAKGEPGPVG*	2xOxidation [P6; P18]	Collagen alpha-1(I) chain	8.68	4.8	11.24	9.65	within
e015744	DGAPAPSGPPPPGSGRASGKHG	none	Receptor expression-enhancing protein 1	8.67	4.8	12.23	8.94	within
e015750	GPRGDQQDGAAGPPGPPGPPG*	1xOxidation [P21]	Collagen alpha-1(XXIII) chain	10.49	5.98	12.25	9.18	within
e015751	PGRRGDGPPGQSGRDGYG*	2xOxidation [P10; P19]	Collagen alpha-1(XXIII) chain	7.1	3.18	10.36	10.8	up
e101742	LSEDFVKQGLASYLHTF	none	Aminopeptidase N	9.85	5.29	12.98	8.21	within
e015762	FPNQSNQGSMPPTTGMPVY	none	R3H domain-containing protein 1	6.62	3.52	9.56	8.23	within
e213181	PSGTEGQLSEEEKPDQQP	none	Seipin	8.82	4.77	12.64	6.03	within
e015768	SHTSDSDVPSGVTEVVVKL	none	Clusterin	10.94	6.01	13.86	12.25	within
e213183	APGKDGLNLPGPIGPPGPRG*	2xOxidation [P13; P16]	Collagen alpha-1(I) chain	10.81	5.48	14.12	12.24	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015783	AAGEAGAVGEAGAAGEAGAVGEAGG	none	Paraneoplastic antigen Ma6E	11.2	7.4	12.8	11.37	within
e015784	LYSQGSKGPGEDFRMATL	none	Prostaglandin-H2 D-isomerase	9.37	5.41	14.22	11.97	within
e015791	GSPGRDGSPGAKGDRGETGPA*	2xOxidation [P3; P9]	Collagen alpha-1(I) chain	9.49	5.81	12.26	10.44	within
e095030	LDTYPNDETTERTVFPY	none	Vesicular integral-membrane protein VIP36	9.71	5.59	13.37	8.57	within
e015806	GFPGSAGRVGPPGPAGAPGPAGP*	2xOxidation [P18; P20]	Collagen alpha-2(V) chain	9.73	6.32	13.15	9.86	within
e015812	HLQEEQSKALSTSDWTT	none	Unhealthy ribosome biogenesis protein 2 homolog	10.15	5.66	13.26	9.91	within
e015822	SEGSPGHPGQPGPPGPPGAPGP*	2xOxidation [P17; P20]	Collagen alpha-1(III) chain	8.6	5.39	12.83	6.93	within
e213192	SGTASSMSHVEDSDSDAPPS	none	Transcription factor SOX-8	11.19	6.95	13.51	12.82	within
e015833	GPAGSPGSNGAPGQRGEPGPQG*	2xOxidation [P2; P6]	Collagen alpha-1(III) chain	10.59	7.19	12.34	10.67	within
e015844	SGIDGSPGEKGDPGDVGGPGPP*	1xOxidation [P21]	Collagen alpha-3(V) chain	11.99	7.99	13.28	12.48	within
e208318	IDGSPGEKGDPGDVGGPGPPGA*	2xOxidation [P17; P19]	Collagen alpha-3(V) chain	11.99	7.99	13.28	12.47	within
e015851	VTQEGEDGDGLADEEEGT	none	Transcription initiation factor TFIID subunit 1	9.37	4.46	12.94	6.26	within
e101113	FAEEKAVADTRDQADGSR	none	Polymeric immunoglobulin receptor	8.11	4.78	11.4	7.79	within
e015856	RGESGLAGAPGPAGPPGPPGPPG*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	11.03	5.66	15.14	12.21	within
e208322	GPSGSPGKDGPPGPAGNTGAPGS*	3xOxidation [P6; P11; P12]	Collagen alpha-1(III) chain	9.67	5.88	11.35	13.09	up
e102480	GPRGANGAPGNDGAKGDAGAPGA*	2xOxidation [P2; P9]	Collagen alpha-1(I) chain	10.8	6.75	12.66	10.36	within
e015868	AHKSEVAHRFKDLGEEN	none	Albumin	6.85	3.77	11.02	5.01	within
e203115	RATASTASPATTSTAQSTTR	none	Mucin-6	11.46	6.38	14.59	11.39	within
e213209	LLKNGERIEKVEHSDLS	none	Beta-2-microglobulin	9.01	3.09	13.27	8.62	within
e104761	QGTPYNPDGQPMGGFVMDG	none	Homeobox protein Meis1	9.29	5.44	11.43	6.45	within
e015893	GEPGAPGSKGDTGAKGEPGPVG*	3xOxidation [P3; P6; P18]	Collagen alpha-1(I) chain	11.26	7.41	13.09	9.31	within
e213211	DPNMEANSHYGHND DVR	none	Platelet endothelial cell adhesion molecule	12.87	8.48	14.98	13.97	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e015903	SGETGPAGPPGNPGPPGPPGPP*	5xOxidation [P15; P16; P18; P19; P21]	Collagen alpha-1(II) chain	10.69	6.0	12.57	9.93	within
e100079	FAGEKGPSGEAGTAGPPGTPGP*	2xOxidation [P17; P20]	Collagen alpha-2(I) chain	10.47	5.66	12.59	9.33	within
e213213	QGYSDEERESMPRDGE	none	Zinc finger E-box-binding homeobox 2	12.29	8.98	14.37	13.14	within
e015925	SYGGIFGGGSFGGGSFGGGSFGG	none	Keratin, type I cytoskeletal 10	10.21	5.93	12.46	8.0	within
e015943	SGGEGKGGSDGGGSHRKEGEE	none	CD99 antigen	8.27	4.06	11.03	10.68	within
e106541	SGNAGPPGPPGAGKEGGKGP*	2xOxidation [P7; P10]	Collagen alpha-1(I) chain	8.55	5.42	11.59	9.1	within
e015951	ARGNDGATGAAGPPGPTGPAGPP*	2xOxidation [P13; P14]	Collagen alpha-1(I) chain	10.98	7.73	12.82	11.35	within
e015955	DNEEGFFSARGHRPLDK	none	Fibrinogen beta chain	7.7	5.11	10.92	9.28	within
e100171	GPQGLPGLAGTAGEPGRDGNPG	none	Collagen alpha-1(III) chain	10.96	6.48	14.53	8.35	within
e015966	PGSPGLKGESDGLGPQGPRGP*	1xOxidation [P18]	Collagen alpha-2(XI) chain	10.06	5.05	12.52	10.29	within
e015988	SEGSPGHPGQPGPPGPPGAPGP*	3xOxidation [P16; P17; P]	Collagen alpha-1(III) chain	12.04	8.62	13.51	12.57	within
e097666	QPGTKGGPGDQGEPPQGLPG*	3xOxidation [P14; P16; P20]	Collagen alpha-2(IX) chain	12.03	8.79	13.47	12.49	within
e015989	GPPSEGALGEGAGAGGAAGGGPER	none	Protein strawberry notch homolog 2	8.14	4.88	12.96	5.9	within
e015992	FVEAVEQNTLQEFLKLA	none	SH3 domain-binding glutamic acid-rich-like protein 3	9.83	5.15	14.16	12.18	within
e016005	KGTWTQPFDLASTREEN	none	Corticosteroid-binding globulin	9.44	5.82	12.17	11.45	within
e213227	AGSPGPQGLAGSPGPHGPNGVPG*	1xOxidation [P22]	Collagen alpha-2(V) chain	10.43	6.47	13.29	10.46	within
e213229	AASSSSLEKSYELPDGQVI	none	Actin, gamma-enteric smooth muscle	9.7	5.81	13.59	9.21	within
e016021	GPLSSSNPSYPGFVSNTPS	none	Proline and serine-rich protein 1	7.82	3.9	11.3	11.68	up
e101534	GAPGVKGEPPGAPGENTPGQTG*	3xOxidation [P3; P9; P12]	Collagen alpha-2(I) chain	9.8	5.74	12.58	8.48	within
e016045	SQSATSPSPAASAVPASGVGSPA	none	Homeobox protein Hox-B2	8.0	4.85	10.74	9.16	within
e106705	DGVSGGEGKGGSDGGGSHRKEG	none	CD99 antigen	7.66	5.0	11.02	8.9	within
e102318	GPRGDQGDGAAGPPGPPGPPG*	3xOxidation [P17; P18; P20]	Collagen alpha-1(XXIII) chain	8.12	4.76	13.46	9.77	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e105966	HNDAASRVAADAVPGSEAPGP	none	Cyclic AMP-responsive element-binding protein 3-like protein 3	9.4	5.87	12.35	9.34	within
e016093	GPAGPRGSPGERGEVGPAGPNG*	1xOxidation [P]	Collagen alpha-2(I) chain	10.6	5.6	14.02	8.73	within
e213245	DGPAGEPGPPGPEGQPGVDGAT*	2xOxidation [P7; P9]	Collagen alpha-1(XV) chain	11.48	7.87	12.97	12.18	within
e016113	SNGNPGPPGPSGSPGKDGPPGP*	4xOxidation [P8; P10; P14; P]	Collagen alpha-1(III) chain	11.46	7.89	12.95	12.09	within
e103149	SVGGGSSTIKYTTTSSSSRK	none	Keratin, type II cytoskeletal 6B	9.15	3.9	14.9	11.08	within
e105143	IKGHRGFPNGPAGSPGPAG*	4xOxidation [P8; P11; P14; P17]	Collagen alpha-1(III) chain	9.57	3.42	12.46	11.69	within
e213253	KGASGPAGPPGAQGPGLQGMP*	4xOxidation [P9; P10; P15; P16]	Collagen alpha-1(II) chain	12.87	9.8	14.45	13.27	within
e213254	GPPGPSGKDGPKGARGDSGPPG*	3xOxidation [P3; P5; P11]	Collagen alpha-1(II) chain	11.09	6.51	12.85	10.9	within
e016124	DGESGRPGRPGERGLPGPPG*	3xOxidation [P10; P16; P18]	Collagen alpha-1(III) chain	12.89	9.6	14.44	13.23	within
e093773	GKVGAHAGEYGAEALERMF	none	Hemoglobin subunit alpha	12.9	9.89	14.44	12.96	within
e213256	LRDTDRFSSHVGGTLGQF	none	Inter-alpha-trypsin inhibitor heavy chain H4	12.89	9.61	14.38	12.99	within
e016129	LVSSKPQAHGAPAPPSGSAPH	none	Pro-adrenomedullin	11.49	7.22	13.69	10.89	within
e016130	HLPAEFTPAVHASLDKFL	none	Hemoglobin subunit alpha	9.5	6.13	13.28	11.41	within
e213258	RGENGSPGAPGAPGHPGPPGPV*	2xOxidation [P19; P21]	Collagen alpha-1(III) chain	9.68	5.91	11.48	9.82	within
e016136	DDPRPPNPPKMPNPNPN	none	CD99 antigen	9.46	5.22	11.52	11.57	up
e016142	PGPTGPAGPPGFGAVGAKGEAG*	3xOxidation [P3; P6; P9]	Collagen alpha-1(I) chain	9.5	6.07	12.15	10.19	within
e016149	SEGSPGHPGQPGPPGPPGAPGP*	4xOxidation [P14; P16; P17; P]	Collagen alpha-1(III) chain	11.84	7.57	13.55	11.94	within
e213261	QGSPGQKGEMGIPGASGPIGPG*	1xOxidation [P]	Collagen alpha-2(XI) chain	10.82	6.98	13.4	8.34	within
e103915	GPAGSPGSNGAPGQRGEPGPQG*	4xOxidation [P2; P6; P12; P18]	Collagen alpha-1(III) chain	10.62	6.25	12.43	9.93	within
e016159	SGSGFGSGSGSGSGSGSGLTEM	none	Serglycin	9.97	5.34	11.82	10.46	within
e016172	EETEDANEEAPLRDRSH	none	Sarcalumenin	7.75	3.98	10.61	11.04	up
e213266	ATEPSTPSGPESGPTPASAEQ	none	MARCKS-related protein	7.77	4.12	10.68	11.02	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213268	RAGAEKGAGGADGQGAGPGAESGA	none	Alpha-2C adrenergic receptor	10.4	6.53	12.5	11.08	within
e016184	DGGPPGMTGFPGAAGRTGPPGP*	3xOxidation [P11; P19; P20]	Collagen alpha-2(I) chain	10.07	5.05	12.57	10.04	within
e016183	NSGEPGAPGSKGDTGAKGEGGP*	2xOxidation [P8; P20]	Collagen alpha-1(I) chain	10.34	5.69	12.51	10.97	within
e097679	AAAAEAGAASGEQAAAPGEEAAAG	none	Myristoylated alanine-rich C-kinase substrate	8.15	5.1	10.78	10.78	within
e213269	KGEGGPPGVAGPPGGSGPAGPPGP*	3xOxidation [P18; P21; P22]	Collagen alpha-1(III) chain	10.2	5.57	12.72	10.97	within
e016209	PPGPPGPPGVPSDGDIDNGP*	3xOxidation [P2; P4; P5]	Collagen alpha-2(IX) chain	9.01	4.38	12.4	10.43	within
e016216	GSPGSPGYQGPPGEPGQAGPSG*	4xOxidation [P6; P11; P12; P15]	Collagen alpha-1(III) chain	8.05	4.92	10.91	6.66	within
e213273	VQEKEASGIQEETTVEPQ	none	Cilia- and flagella-associated protein 251	6.71	2.52	10.51	10.29	within
e016217	GRPGEVGP GPPGPAGEKGSPG*	3xOxidation [P8; P9; P11]	Collagen alpha-1(I) chain	7.86	4.69	11.53	9.88	within
e095075	DKTNVKA AWGKVGAHAGEY	none	Hemoglobin subunit alpha	7.58	4.34	11.22	10.39	within
e213275	GQPGAKGEPGDAGAKGDAGPPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	8.84	4.47	12.11	5.47	within
e016232	GIPPTETEAYFGAKEPEPA	none	Potassium voltage-gated channel subfamily KQT member 2	8.33	4.13	12.38	5.52	within
e208350	GIPGASGPIGPGPPGLPGPAGP*	8xOxidation [P3; P8; P11; P14; P15; P18; P20; P23]	Collagen alpha-2(XI) chain	10.21	6.37	12.71	11.35	within
e105071	GLPGTGPPGENGKPGEPGPKG*	3xOxidation [P8; P9; P15]	Collagen alpha-1(III) chain	10.12	6.34	12.68	11.44	within
e103876	EPGDPGPMGPIGSRGPEGPPG*	3xOxidation [P7; M8; P20]	Collagen alpha-2(V) chain	8.13	5.53	13.11	10.69	within
e016247	TTVSTSGSGTTTASTAGSETTT	none	Mucin-22	5.87	2.43	9.07	2.94	within
e213282	EALGAVGMMGPPGPPGPPGYPG	none	Collagen alpha-2(IX) chain	9.96	5.93	12.78	10.48	within
e203210	QGEAGQKGDAGAPGPQGSPGAPG*	1xOxidation [P15]	Collagen alpha-1(II) chain	5.36	1.07	10.41	2.38	within
e016258	GEEGKRGPNGEAGSAGPPGPPG*	2xOxidation [P18; P20]	Collagen alpha-2(I) chain	8.69	3.65	11.2	10.31	within
e213286	GEKGSPGADGPAGAPGTPGPQGI*	2xOxidation [P18; P20]	Collagen alpha-1(I) chain	8.7	4.7	11.57	10.25	within
e016267	GEAGQKGDAGAPGPQGSPGAPGP*	3xOxidation [P12; P14; P17]	Collagen alpha-1(II) chain	10.82	5.54	12.98	11.13	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e097684	ESFGDLSTPDVAMGNPKVK*	1xOxidation [M13]	Hemoglobin subunit beta	9.97	3.62	13.42	9.53	within
e016270	GDLGRPGKGTGPGVAGPSGEPG*	3xOxidation [P6; P8; P12]	Collagen alpha-3(IX) chain	9.86	5.33	12.22	8.65	within
e213289	GPRGSPGPTGRPGVTGIDGAPG*	3xOxidation [P2; P6; P8]	Collagen alpha-3(V) chain	9.3	4.34	12.2	9.51	within
e213293	DGESGRPGRPGERGLPGPPG*	4xOxidation [P7; P10; P16; P18]	Collagen alpha-1(III) chain	14.16	12.08	15.41	14.2	within
e016285	ALQSGNSQESVTEQDSKDS	none	Immunoglobulin kappa constant	10.48	7.27	12.4	10.34	within
e016287	VPGSAFQSSAYHTQTQSLT	none	Lysine-specific demethylase 4E	5.94	3.16	10.2	9.72	within
e213297	GPTGRQGEKGEPGRPGDPAV*	3xOxidation [P2; P12; P15]	Collagen alpha-1(VII) chain	12.57	9.57	13.98	12.3	within
e016292	TSPSGVSSSTSGGVSSSTNMHG	none	Nuclear receptor coactivator 3	12.35	9.16	13.89	13.09	within
e016315	GPPGPPGRDGEDGPTGPPGPPG*	3xOxidation [P5; P6; P14]	Collagen alpha-2(I) chain	11.68	7.24	13.23	12.73	within
e016324	LGSAPNNDSGVEMPGTGPGSLG	none	Zinc finger protein GLI2	7.6	4.18	11.04	9.2	within
e016328	AGPPGPPGPPGTSGHPGSPGSPG*	6xOxidation [P7; P9; P10; P16; P19; P]	Collagen alpha-1(III) chain	11.5	7.71	13.14	12.06	within
e213306	PSTQASTASSAPEENAPSEG	none	Fractalkine	11.48	7.7	13.14	12.34	within
e016331	NSGEPGAPGSKGDTGAKGEPGP*	3xOxidation [P5; P8; P20]	Collagen alpha-1(I) chain	13.74	11.68	14.93	14.52	within
e016332	GTSAGFGGGPGTSTGFGGGLGTSAG	none	Trophinin	10.96	6.72	13.23	6.58	down
e016344	EGSPGRDGSPGAKGDRGETGP*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	14.76	12.75	16.08	15.15	within
e213309	GSPGNTGLPGFPGFPGAQGDGP*	2xOxidation [P12; P]	Collagen alpha-3(IV) chain	14.65	9.65	16.12	15.15	within
e208355	GPHGAPGPRGPQGPTGSEGTGP*	3xOxidation [P6; P8; P]	Collagen alpha-3(V) chain	10.0	6.5	12.45	8.91	within
e016346	EPGQAGPSGPPGPPGAIGPSGPA*	4xOxidation [P13; P14; P19; P22]	Collagen alpha-1(III) chain	12.2	8.41	14.19	13.23	within
e016362	GARDTQGDGEQSAGGGPGAEEA	none	Forkhead box protein Q1	10.82	6.78	12.9	11.29	within
e016363	PPGDPGFPGRYGETGDVGPP*	3xOxidation [P1; P2; P5]	Collagen alpha-4(IV) chain	12.06	8.98	14.21	10.87	within
e016364	EPGPQGLPGAPGDQGGRGPPG*	3xOxidation [P8; P11; P19]	Collagen alpha-1(IX) chain	11.95	8.74	13.67	12.34	within
e016376	GRPGEVGPPGPPGPAGEKGSPG*	4xOxidation [P8; P9; P11; P12]	Collagen alpha-1(I) chain	9.14	6.06	11.66	10.05	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e016408	DEAGSEADHEGTHSTKRGH	none	Fibrinogen alpha chain	8.88	4.73	11.35	11.57	up
e213316	GQPGAVGEKGERGDAGDPGPPG*	1xOxidation [P]	Collagen alpha-3(V) chain	12.27	8.76	13.75	9.91	within
e016411	EIGNPGRDGARGAPGAVGAPGP*	3xOxidation [P5; P14; P20]	Collagen alpha-2(I) chain	12.59	9.55	13.95	13.63	within
e016418	GPAGEPGREGSPGADGPPGRDG*	2xOxidation [P17; P]	Collagen alpha-1(II) chain	6.99	3.41	10.9	9.74	within
e016420	GGGGSAGGAAPSEGPVGGVPGGAGGGG	none	Alpha-1D adrenergic receptor	11.24	7.76	12.9	13.14	up
e213320	PGEKGQRGDFGHVQPGPPG*	3xOxidation [P1; P16; P18]	Collagen alpha-3(V) chain	11.32	8.41	12.94	13.19	up
e095096	AAHLPAEFTPAVHASLDKF	none	Hemoglobin subunit alpha	10.33	3.97	16.12	10.62	within
e016427	TGKSGAKGTSGGDGPHGPPGER*	1xOxidation [P]	Collagen alpha-2(XI) chain	11.19	7.39	12.64	10.52	within
e016428	GIDGEKGPQGKGDPGEPGPA*	2xOxidation [P8; P15]	Collagen alpha-1(XXIII) chain	11.24	7.39	12.9	10.86	within
e016429	SDKPDMAEIEKFDKSKL*	1xAcetylation [N-Term]	Thymosin beta-4	10.16	4.91	14.1	11.55	within
e016434	EELVSDSELHQDQPDILG	none	Reticulon-3	12.33	7.76	14.15	13.37	within
e105019	AGEKGPSGEAGTAGPPGTPGQG*	3xOxidation [P6; P16; P19]	Collagen alpha-2(I) chain	7.56	4.14	10.93	7.27	within
e213324	GADGGPGPRGLPGDAGREGFPG*	2xOxidation [P12; P21]	Collagen alpha-2(IV) chain	10.76	2.58	13.26	13.36	up
e213325	AVGEYNKASNDMYHSRAL	none	Cystatin-C	10.26	4.24	12.91	10.2	within
e213326	RAVPHPDSPDPTIDHDLL	none	Complement factor D	9.49	3.59	12.52	9.45	within
e213327	EPGDPGEDGKPGDTGPQGFPG*	1xOxidation [P16]	Collagen alpha-1(XVIII) chain	13.01	9.5	14.55	13.81	within
e101369	SEGSPGHGPGPPGPPGAPGP*	6xOxidation [P5; P8; P11; P13; P14; P16]	Collagen alpha-1(III) chain	13.01	9.88	14.52	13.81	within
e016460	GSPGSEGRQGGKGAKGDPGAIGA*	1xOxidation [P18]	Collagen alpha-2(XI) chain	8.69	5.37	12.44	7.62	within
e016461	ASHTSDSDVPSGVTEVVVKL	none	Clusterin	12.33	6.95	15.14	14.95	within
e016466	PNGQGPGQPKGDPGPPGIPGR*	3xOxidation [P15; P16; P]	Collagen alpha-1(III) chain	7.37	3.61	12.34	5.44	within
e016469	ATGLPEGPAVPVPSRGNLAQP	none	Zinc transporter ZIP11	10.32	5.45	12.76	11.19	within
e016473	PGPPGPPGVSGGGYDFGYDGD*	4xOxidation [P3; P4; P6; P7]	Collagen alpha-2(I) chain	10.63	6.51	12.75	11.84	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099607	GGNNPFSEFFDAEGSEVDL	none	DnaJ homolog subfamily B member 13	10.12	4.91	12.8	13.27	up
e016487	DNASLSTNGLGSSPGSAGHMNG	none	CUGBP Elav-like family member 4	7.85	3.55	11.46	9.31	within
e213332	GEPGVPGQPGAPGPPGHPSPGP*	3xOxidation [P3; P6; P9]	Collagen alpha-2(V) chain	10.05	6.14	12.38	6.27	within
e213334	GPPGKDGPNGPPGPPGPTKGEPG*	4xOxidation [P2; P3; P8; P11]	Collagen alpha-1(XXII) chain	10.04	6.11	12.3	6.27	within
e016502	EGSPGRDGSPGAKGDRGETGP*	3xOxidation [P4; P10; P21]	Collagen alpha-1(I) chain	11.52	8.09	13.33	10.53	within
e213335	VGSPNGGSETPKSNGGSGGGGSQ	none	Homeobox even-skipped homolog protein 1	12.49	8.64	14.22	11.29	within
e213338	RPGPPGPPGAGNPGSPNSP*	8xOxidation [P4; P5; P7; P8; P10; P14; P16; P18]	Collagen alpha-1(XXVI) chain	11.49	7.96	13.32	11.15	within
e016504	PPGEAGKPGEQGVPGDLGAPGP*	3xOxidation [P2; P8; P14]	Collagen alpha-1(I) chain	12.61	10.03	14.36	12.16	within
e213339	WGKVGAHAGEYGAEALERM	none	Hemoglobin subunit alpha	11.12	7.28	13.16	9.51	within
e016516	GPMGPPGNKGMGSPGHQGP*	2xOxidation [P5; P6]	Collagen alpha-1(XIX) chain	10.12	5.61	12.12	10.85	within
e213343	TTSASGSLGSLHGGSGGSGSAAL	none	Homeobox even-skipped homolog protein 2	10.1	5.72	12.07	9.04	within
e213344	GPRGFPGPPGPDGLPGSMGPPG*	2xOxidation [P2; P6]	Collagen alpha-1(IV) chain	12.61	9.36	14.15	12.86	within
e016522	GLMPGYQGHVPTVAFSFGAP	none	Ciliary microtubule inner protein 2C	8.2	5.6	12.83	6.49	within
e213346	GIPGEKPAGERGAPGAGPRG*	3xOxidation [P3; P8; P15]	Collagen alpha-1(III) chain	8.51	5.13	11.51	6.63	within
e016534	FPGPPGPDGLPGSMGPPGTPSV*	1xOxidation [P17]	Collagen alpha-1(IV) chain	6.6	2.64	13.05	4.4	within
e016542	GYPGSPGAPGGKGQPGDVGP*	2xOxidation [P20; P]	Collagen alpha-4(IV) chain	7.6	5.16	12.16	7.83	within
e103760	TQSHSAQVMEDFEERQN	none	Extracellular matrix organizing protein FRAS1	10.63	5.58	13.34	13.28	within
e213350	AGPNGADGPQGPPGGVGNLGP*	6xOxidation [P3; P9; P12; P13; P21; P22]	Collagen alpha-2(XI) chain	10.15	5.96	13.61	11.61	within
e016549	SERTEHSHSPGDSSAPIQN	none	Zinc finger protein Rlf	8.83	3.57	12.47	6.58	within
e016551	SGGASGTLQPSSGGGSSNSRER	none	Cyclin-dependent kinase 12	6.3	2.6	10.6	8.58	within
e016552	FGASAGTGDLSDNHDIISMK	none	Vesicular integral-membrane protein VIP36	10.1	6.23	13.75	11.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099097	NSGEPGAPGSKGDTGAKGEPGP*	1xCation:Na [E/D]; 3xOxidation [P5; P8; P20]	Collagen alpha-1(I) chain	10.41	5.14	12.57	10.13	within
e016564	GLPGTGGPPGENGKPGEPGPKG*	5xOxidation [P8; P9; P15; P18; P20]	Collagen alpha-1(III) chain	10.61	5.32	12.79	11.73	within
e016562	PMGERGHPPGPPGPEQGLPG*	1xOxidation [P20]	Collagen alpha-1(V) chain	10.52	5.22	12.74	11.8	within
e213351	TGGSTGDADGPGGPGIPDGPGGNAG	none	Cancer/testis antigen 1	9.93	5.18	12.66	12.69	up
e099098	EGSPGRDGSPGAKGDRGETGP*	1xCation:Na [C-Term]; 2xOxidation [P4; P10]	Collagen alpha-1(I) chain	10.33	5.41	13.67	10.26	within
e213352	QDLKNEGEAAASGGGPPSGGAPA	none	Cyclin-dependent kinase 5 activator 2	9.29	5.51	12.27	10.49	within
e213353	IGEQGISGPRGSGGAAGAPGERG	none	Collagen alpha-3(VI) chain	8.15	5.25	11.44	9.46	within
e213354	GAGEPKGPGPTGSGGGGAGTGGGAGGPG	none	SKI family transcriptional corepressor 1	9.97	6.15	11.71	10.07	within
e016588	SEKNFQAVSQGSPSSVMSA	none	Probable JmjC domain-containing histone demethylation protein 2C	5.91	2.29	10.3	8.36	within
e016589	SGSVIDQSRVNLGPITRK	none	Uromodulin	13.49	9.17	15.85	14.61	within
e106465	DAGPVGPPGPPGPPGPPGPPSAG*	7xOxidation [P10; P11; P13; P14; P16; P17; P19]	Collagen alpha-1(I) chain	8.73	5.09	10.94	11.02	up
e095104	TTPPNKELPP*	1xO-Glycan [T2] (HexNAc(1)Hex(1)NeuAc(2))	Microtubule-associated protein 4	8.57	4.81	11.44	12.42	up
e016600	PRGGPGGELPRGPAGLGPRRS	none	Eukaryotic translation initiation factor 4 gamma 1	10.51	6.74	13.6	9.97	within
e106722	WDLDEVRPTSA*	1xO-Glycan [T10] (HexNAc(1)Hex(1)NeuAc(1))	Apolipoprotein C-III	9.33	5.22	11.77	11.14	within
e213357	EKGDQGFQGQPGFPGPPGPP*	3xOxidation [P14; P16; P17]	Collagen alpha-1(XVI) chain	7.12	3.37	11.44	9.97	within
e104236	GGVMEPHAVYSGSAAAWPPSA	none	Forkhead box protein F1	10.82	6.29	13.63	11.99	within
e093777	VLTGYQVDKNKDELTF	none	Cystatin-A	10.37	5.74	14.88	8.43	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213360	GFPGFPGANGEKGGRGTPGKPG	none	Collagen alpha-1(V) chain	10.2	5.76	14.91	12.11	within
e016612	GQQGVRGEPGYPGPSGDAGAPG*	2xOxidation [P12; P14]	Collagen alpha-2(IX) chain	11.02	6.27	13.18	12.25	within
e095107	EAIPMSIPPEVKFNKPFV	none	Alpha-1-antitrypsin	9.34	5.16	14.54	12.24	within
e213363	ELIGILMAVWLKEMLLNG	none	N-formyl peptide receptor 3	10.14	5.91	15.08	12.27	within
e097700	VHSLNKFYKGISSKHNG	none	Protein strawberry notch homolog 1	9.43	5.18	13.32	10.9	within
e016654	SAGSRIEDGVLQFLVLLVAG	none	Collagen alpha-3(VI) chain	9.22	3.84	13.42	10.94	within
e016659	GEPGDAGAKGDAGPPGPAGPAGPP*	3xOxidation [P17; P20; P23]	Collagen alpha-1(I) chain	8.86	5.47	12.4	9.97	within
e016666	EDYQKMRDMGEMVTQGQ	none	Spectrin beta chain, non-erythrocytic 1	6.58	1.65	11.72	10.05	within
e213372	GATGPPGEEGPRGPPGRAGEKG*	1xOxidation [P6]	Collagen alpha-2(IX) chain	8.84	5.37	11.42	9.77	within
e213375	GGAGEAGGAGEEGGTGEEGGAGEAGG	none	Paraneoplastic antigen Ma6F	9.55	5.25	11.93	8.07	within
e213376	GSNGNPGPPGSPGSKDGPPGP*	4xOxidation [P9; P11; P15; P20]	Collagen alpha-1(III) chain	14.37	12.24	15.58	14.93	within
e016682	PGPAGPPGVAGEDGDKGEVGDGP*	1xOxidation [P1]	Collagen alpha-2(XI) chain	10.65	6.65	12.82	9.42	within
e097701	GPSGSPGKDGPPGPAGNTGAPGSP*	2xOxidation [P6; P11]	Collagen alpha-1(III) chain	10.55	6.51	12.77	9.43	within
e213378	GEVGPAGSPGSNGAPQGRGEPGP*	1xOxidation [P]	Collagen alpha-1(III) chain	14.27	12.02	15.61	14.92	within
e016684	PPGEAGKPGEQGVPGDLGAPGP*	4xOxidation [P2; P8; P14; P20]	Collagen alpha-1(I) chain	14.2	12.07	15.55	14.92	within
e213379	WGKVGAHAGEYGAEALERM*	1xOxidation [M19]	Hemoglobin subunit alpha	9.81	4.51	12.7	9.2	within
e213380	GGEKGSSPVGPPGPPGSPGVNGQ*	2xOxidation [P11; P12]	Collagen alpha-4(IV) chain	14.15	11.8	15.5	14.92	within
e213384	PRGDQQQDGAAGPPGPPGPPGA*	6xOxidation [P1; P13; P14; P16; P17; P19]	Collagen alpha-1(XXIII) chain	13.64	10.36	14.94	12.53	within
e213386	NDGATGAAGPPGPTGPAGPPGFPG*	2xOxidation [P]	Collagen alpha-1(I) chain	16.37	14.71	17.56	16.81	within
e213387	NGDDGEAGKPGRPGERGPPGP*	2xOxidation [P]	Collagen alpha-1(I) chain	16.37	14.71	17.56	16.81	within
e213388	DGFPLPGPPGDGIKPPGDPG*	3xOxidation [P4; P7; P9]	Collagen alpha-2(IV) chain	16.36	14.67	17.55	16.81	within
e213389	KGDAGQPGEKGSPGAQGPPGAPG*	2xOxidation [P18; P19]	Collagen alpha-1(III) chain	13.42	10.3	14.84	12.43	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213392	SPGSRGAPGQYGEKGFPGDPG*	2xOxidation [P2; P8]	Collagen alpha-5(VI) chain	13.7	10.94	15.2	14.25	within
e097703	GQEGLPGKGDGTGPTGPQGPQG	none	Collagen alpha-1(XXII) chain	12.42	9.3	14.86	11.31	within
e105179	GSPGSPGYQGPPGEPGQAGPSGP*	1xOxidation [P20]	Collagen alpha-1(III) chain	11.92	8.44	13.97	12.5	within
e016712	VGEAGPEGPPGEPGPPGPPGPPG*	3xOxidation [P16; P18; P19]	Collagen alpha-2(V) chain	11.89	8.36	13.99	12.52	within
e106160	FGASAGTGDLSDNHDIISMK*	1xOxidation [M19]	Vesicular integral-membrane protein VIP36	9.81	5.09	11.83	10.24	within
e016728	PGRDQGAGQQGEQDDGDGP*	1xOxidation [P]	Collagen alpha-1(XXVII) chain	11.61	6.58	14.11	10.79	within
e016730	QSEEELDWSQEEASHLH	none	Multiple C2 and transmembrane domain-containing protein 2	8.61	4.44	11.19	11.16	within
e016750	PGPAGSKGESGNGKEPGSAGPQG*	2xOxidation [P3; P16]	Collagen alpha-2(I) chain	9.5	5.67	12.66	8.53	within
e213402	AHHFGKEFTPPVQAAYQK	none	Hemoglobin subunit beta	7.28	3.69	12.08	7.25	within
e016765	SGEPGAPGSKGDTGAKGEPGPVG*	3xOxidation [P4; P7; P19]	Collagen alpha-1(I) chain	13.08	10.78	14.14	13.62	within
e097705	SFGDLSPDAVMGNPKVKAH	none	Hemoglobin subunit delta	6.33	3.06	9.86	3.95	within
e016778	GAAGEAGAAGEAGGAGEAGGAGEAGGAG	none	Paraneoplastic antigen Ma6F	11.44	6.5	13.06	12.35	within
e208381	GSNRASGVPDRFSGSGSGTDF	none	Immunoglobulin kappa variable 2-28	12.05	9.25	13.28	12.28	within
e016782	GGSAQAGQAGGSVQAGQAGGSVQAG	none	Coiled-coil domain-containing protein 57	5.03	2.66	9.85	4.29	within
e016794	AGSAGGSSGAAGAAGGGAGAGTRPGDGG	none	Protein CDV3 homolog	11.98	8.18	13.55	10.99	within
e016802	QGPPGPTGPGGDKGDTGPPGPQG*	2xOxidation [P6; P9]	Collagen alpha-1(III) chain	10.81	6.59	12.99	11.53	within
e213411	ARGNDGQPGPAGPPGPVGPAGGP*	5xOxidation [P8; P10; P13; P14; P16]	Collagen alpha-1(II) chain	10.84	6.49	13.06	11.65	within
e016804	PGAPGPQGVVGPSPPGPPGPFPG*	5xOxidation [P4; P6; P12; P15; P16]	Collagen alpha-3(V) chain	10.34	6.23	12.59	10.14	within
e016811	ELTETGVEAAAASAI SVARTL	none	Plasma protease C1 inhibitor	9.04	5.56	12.7	13.21	up
e016817	GGNGGPPNFGTNTQGAVAQPGY	none	Dermokine	10.46	6.03	12.34	12.08	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e016833	GERGSEGSPGHPGQPGPPGPP*	7xOxidation [P9; P12; P15; P17; P18; P20; P21]	Collagen alpha-1(III) chain	9.37	5.19	11.23	8.52	within
e016849	DAGAPGAPGGKGDAGAPGERGPPG*	3xOxidation [P8; P17; P22]	Collagen alpha-1(III) chain	11.83	8.22	13.54	12.05	within
e016850	LSDPEQGVEVTGQYEREK	none	Inter-alpha-trypsin inhibitor heavy chain H4	10.04	4.96	13.66	12.04	within
e213418	ANFQSSQDSDLGETSSVAHA	none	G patch domain-containing protein 1	10.2	6.2	12.38	11.35	within
e213419	NGDDGEAGKPRPGERGPPGPP*	3xOxidation [P10; P13; P18]	Collagen alpha-1(I) chain	15.43	13.79	16.59	16.33	within
e097715	GPRGTPGTRGPRGDPGEAGPQ*	3xOxidation [P11; P15; P20]	Collagen alpha-1(VI) chain	11.83	7.95	13.81	11.94	within
e016881	GSPGSRGAPGQYGEKGFPGDP*	3xOxidation [P3; P9; P18]	Collagen alpha-5(VI) chain	12.12	9.15	14.09	12.82	within
e213425	GEPGQKGDAGSPGPQGLAGSPGP*	3xOxidation [P12; P14; P21]	Collagen alpha-2(V) chain	11.74	9.21	13.67	10.84	within
e103152	KGPAGERGSPGPAGPKGSPGEAG*	3xOxidation [P3; P10; P12]	Collagen alpha-1(I) chain	11.21	7.26	13.57	8.06	within
e016911	ARGGSGGGGDSHHGGASYVPER	none	SH3 and multiple ankyrin repeat domains protein 1	10.45	6.14	12.23	10.77	within
e016915	PQVKTATIATERNKGK PENN	none	DNA-binding protein SATB1	7.32	3.74	13.78	7.47	within
e213436	GSGQSAGFGQHSGSGSQSSGFGQ	none	Filaggrin-2	10.43	6.23	13.98	12.29	within
e016930	EPATAPGSPEPPSELLEDGQ*	3xOxidation [P2; P6; P9]	Collagen alpha-1(XVIII) chain	9.28	5.89	12.22	10.77	within
e213437	PAGFAGPPGADGQPGAKGEPGDA*	3xOxidation [P7; P8; P14]	Collagen alpha-1(I) chain	10.25	6.83	12.35	12.17	within
e016940	PGPPGDQGPDPGPRGAPGPP*	6xOxidation [P9; P10; P12; P15; P19; P]	Collagen alpha-4(IV) chain	11.06	7.55	13.29	10.46	within
e016943	TNAVAHVDDMPNALSALSDL*	1xOxidation [M10]	Hemoglobin subunit alpha	10.07	5.95	13.02	10.3	within
e099101	NGDDGEAGKPRPGERGPPGPP*	1xCation:Na [D3]; 2xOxidation [P]	Collagen alpha-1(I) chain	12.22	7.98	14.44	9.24	within
e016951	AGSKGESGNKGEPGSAGPQGPPG*	3xOxidation [P13; P18; P21]	Collagen alpha-2(I) chain	8.6	4.76	12.86	8.26	within
e016952	DRSLFIMLDSLNSLDGSTS	none	Protein DOP1A	9.4	6.11	13.0	7.01	within
e213442	DKSKLKKTTETQEKNLPS	none	Thymosin beta-4	7.5	4.08	11.15	7.59	within
e016959	GNSGEPGAPGSKGDTGAKGEPGP*	3xOxidation [P6; P9; P21]	Collagen alpha-1(I) chain	12.89	10.52	14.33	13.89	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213443	RGGPGGPGPQGPCKNGETGPQG*	1xOxidation [P]	Collagen alpha-1(III) chain	11.86	7.52	13.97	13.28	within
e016967	GNVGPPGEPGPPGQQGNHGSQG*	3xOxidation [P6; P9; P11]	Collagen alpha-3(V) chain	10.1	5.7	12.36	11.8	within
e016968	VSGGEGKGGSDGGGSHRKEGEE	none	CD99 antigen	9.82	5.87	12.28	11.19	within
e101489	AAGSAGSSGAAGAAGGGAGAGTRPGDG	none	Protein CDV3 homolog	12.6	9.83	13.96	13.69	within
e104371	LDTYPNDETTERVFPYI	none	Vesicular integral-membrane protein VIP36	9.67	6.11	12.82	11.02	within
e016982	EDVDGGGAPTTGGNNAPSGGSQE	none	Pecanex-like protein 2	9.79	6.01	12.41	10.39	within
e213449	EGGGAGEAGGVGEVGAAGEAGGTGEA	none	Paraneoplastic antigen Ma6E	10.61	7.67	12.61	11.33	within
e213451	APAPAKDALRALTQRGHDSV	none	Phospholipid phosphatase-related protein type 3	9.25	5.7	12.04	10.49	within
e016996	PGGQEDVAEAESTGEMPGEEG	none	Sodium/potassium/calcium exchanger 1	6.96	3.03	10.4	8.99	within
e100194	PGSSGTGGTATWKPSSGPGSTGS	none	Fibrinogen alpha chain	10.18	5.51	12.71	10.66	within
e213457	GPPGPPGKNGDDGEAGKPGRPG*	4xOxidation [P5; P6; P18; P21]	Collagen alpha-1(I) chain	13.46	10.46	15.12	14.72	within
e213459	RGAPGDRGEPGPPGAGFAGPP*	4xOxidation [P10; P12; P13; P15]	Collagen alpha-1(I) chain	13.43	10.56	15.13	14.71	within
e099102	SGEPGAPGSKGDTGAKGEPGPVG*	1xCation:Na [E18]; 3xOxidation [P4; P7; P19]; 1xCation:Na [C-Term]	Collagen alpha-1(I) chain	6.37	2.88	11.74	4.75	within
e100959	TSQQSSASLAAATAATEAGPSAT	none	Zinc finger protein castor homolog 1	9.87	5.83	12.37	11.35	within
e017019	LAQAGSTEDGLPPSHSSPSLQ	none	PH and SEC7 domain-containing protein 1	9.53	5.8	12.43	11.36	within
e017020	LFAEEKAVADTRDQADGSR	none	Polymeric immunoglobulin receptor	11.21	7.15	13.87	13.9	up
e213465	DAGAPGAPGGKGDAGAPGERGPPG*	4xOxidation [P5; P8; P17; P22]	Collagen alpha-1(III) chain	15.8	14.21	16.67	16.33	within
e213463	GSPGEQGPSGASGPAGPRGPPGSA*	3xOxidation [P8; P14; P17]	Collagen alpha-1(I) chain	15.76	13.79	16.68	16.33	within
e213469	TAGPSGPSGLPGERGAAGIPGGKG*	2xOxidation [P4; P7]	Collagen alpha-2(I) chain	10.78	6.44	13.18	9.28	within
e213471	GGAGGGPPPGPPGAGDRGGGGPGGGP G	none	Far upstream element-binding protein 2	12.88	8.65	14.68	12.06	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213473	PKGDTGPSGPPGPPGVPGPAGRE	none	Pulmonary surfactant-associated protein D	10.75	5.8	13.11	10.12	within
e017043	DGPPGRDQGPGHKGERGYPG*	3xOxidation [P4; P10; P19]	Collagen alpha-2(I) chain	12.45	8.91	14.46	13.25	within
e017045	DAHKSEVAHRFKDLGEEN	none	Albumin	11.39	6.23	14.24	12.76	within
e213476	VDRNLQVSL LAVDEMHQD	none	Bestrophin-1	12.46	6.4	14.56	12.98	within
e017048	TLNQDTGMRKPAQSGFALF	none	Pleckstrin homology domain-containing family H member 2	12.53	8.58	14.74	12.97	within
e017053	SIGDDSTGWSNLSFEDEH	none	A-kinase anchor protein 11	10.24	5.28	12.85	10.23	within
e017054	SENLSYGEDDHIPAHSQSP	none	Synaptotagmin-16	11.01	6.67	12.99	11.64	within
e213478	DGQGP GPPGPGTAGFP GSPGAKG*	5xOxidation [P7; P9; P10; P16; P19]	Collagen alpha-1(III) chain	11.43	7.93	13.03	11.96	within
e105919	PGPKGAQGERGPVGS SGP KGSQ*	3xOxidation [P3; P12; P18]	Collagen alpha-2(V) chain	10.47	6.23	13.08	12.65	within
e017069	PPGKAGEDGHPGKPRPGERG*	2xOxidation [P2; P11]	Collagen alpha-2(I) chain	6.72	3.01	11.98	7.52	within
e097728	MADEAGSEADHEGTHSTKRG	none	Fibrinogen alpha chain	7.41	3.67	9.99	9.84	within
e203391	PGPPGDQGP GPDGPRGAPGPP*	7xOxidation [P3; P4; P9; P10; P12; P15; P19]	Collagen alpha-4(IV) chain	11.53	7.78	14.02	9.55	within
e017079	YVSQGGPMGMSMAQPSYTPP	none	Homeobox protein Meis2	9.18	6.11	11.63	10.01	within
e099018	DAGAPGAPGGKGDAGAPGERGPPG*	1xCation:Na [D13]; 3xOxidation [P8; P17; P22]	Collagen alpha-1(III) chain	7.72	4.13	10.68	6.6	within
e017081	ETTSHSTPGFTSSITTETT	none	Mucin-3A	9.09	5.94	11.54	10.13	within
e101884	GPPGPPGSIGHPGARGPPGYRG*	3xOxidation [P3; P12; P18]	Collagen alpha-3(IX) chain	8.29	5.03	11.17	10.58	within
e213482	GMPGSPGGPGSDGKPGPPGSQGE*	5xOxidation [P6; P9; P15; P17; P18]	Collagen alpha-1(III) chain	15.7	12.76	17.22	14.74	within
e017094	GEDGKDGSPGEPGANGLPGAAGE*	3xOxidation [P9; P12; P18]	Collagen alpha-1(III) chain	16.03	13.8	17.48	16.43	within
e213483	SEGSSISQLSFAEDISADED	none	Ribosomal RNA processing protein 1 homolog B	7.78	4.12	10.37	11.66	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e017096	EGSPGRDGSPGAKGDRGETGPA*	2xOxidation [P4; P10]	Collagen alpha-1(I) chain	16.24	14.39	17.56	16.15	within
e101744	PRDPDANWDSPSRVPFSSG	none	AF4/FMR2 family member 4	11.39	7.58	13.27	12.86	within
e017109	GPPGPPGSAALPGSKGDTGNPGAP*	2xOxidation [P5; P6]	Collagen alpha-2(IV) chain	7.28	4.35	13.85	5.98	within
e017111	RHGPPGFDGPPGPKGFPGPQG*	2xOxidation [P17; P19]	Collagen alpha-4(IV) chain	10.25	5.76	12.69	11.71	within
e213485	PGPAGSPGERGAAGSGGPIGPPGR*	2xOxidation [P3; P7]	Collagen alpha-2(XI) chain	9.86	6.5	12.56	11.71	within
e102204	DGEPGTPGNPGPPGPPGPPGPP*	9xOxidation [P10; P12; P13; P15; P16; P18; P19; P21; P22]	Collagen alpha-1(II) chain	10.3	5.82	13.14	12.87	within
e017116	GETGPAGPPGAPGAPGAPGVGPAG*	6xOxidation [P5; P8; P9; P12; P15; P18]	Collagen alpha-1(I) chain	11.02	7.32	13.81	7.81	within
e017122	GPPGEAGKPGEQGVPGDLGAPGP*	3xOxidation [P3; P9; P15]	Collagen alpha-1(I) chain	13.62	10.86	14.99	13.97	within
e017121	NDNEEGFFSARGHRPLDK	none	Fibrinogen beta chain	6.07	3.3	10.4	6.22	within
e213491	PGESGAAGPTGPIGSRGSPGPPGP*	2xOxidation [P21; P]	Collagen alpha-2(I) chain	13.62	10.32	14.91	14.03	within
e017129	HGSGSSSYSRGRHYESGSGQ	none	Hornerin	10.26	6.19	12.88	11.22	within
e213493	PTGSSPFSSTGPMTATSFQTT	none	Mucin-6	11.93	9.37	13.44	11.75	within
e017130	GPPGPSGSPGKDGPPGPAGNTGAP*	4xOxidation [P5; P9; P14; P15]	Collagen alpha-1(III) chain	9.18	4.64	12.73	5.77	within
e097731	ARGLDGEPGPQGLPGAPGDQGG*	1xOxidation [P]	Collagen alpha-1(IX) chain	12.13	8.58	13.61	13.03	within
e213495	STETRSSSESSHSSSSSHSH	none	Ribosomal protein S6 kinase alpha-5	10.15	5.66	12.48	11.04	within
e017135	TIQEEEDSDEDRPQGSQQ	none	Protein FAM13C	8.49	3.22	11.61	11.8	up
e213496	GPRGERGEKGESGQPGEPGPP*	1xOxidation [P]	Collagen alpha-2(XI) chain	11.49	7.21	13.09	11.75	within
e017138	GPQGETGPAGHPGLPGPPGPPGQ*	2xOxidation [P20; P]	Collagen alpha-1(XXII) chain	11.16	6.81	13.21	11.97	within
e213497	GTPGAPGLPGPKGSVGMGLPGTP*	2xOxidation [P11; P21]	Collagen alpha-1(IV) chain	8.86	4.71	13.26	11.23	within
e017145	DEAGSEADHEGTHSTKRGHA	none	Fibrinogen alpha chain	8.37	4.41	11.19	11.1	within
e213499	GTVGPPQRRRGPPGAPGEMGPQG*	2xOxidation [P12; P15]	Collagen alpha-2(IV) chain	9.02	4.58	11.81	10.9	within
e213500	PGKPGEAGLPGLPGVDGLTGRD*	2xOxidation [P10; P13]	Collagen alpha-3(IX) chain	9.21	4.89	12.94	10.34	within

a: Distribution in healthy female

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e017150	GSPGYQGPPGEPGQAGPSGPPGP*	3xOxidation [P12; P17; P20]	Collagen alpha-1(III) chain	9.85	6.11	13.06	10.47	within
e017151	WDNLEKETEGLRQEMSK	none	Apolipoprotein A-I	7.7	4.91	11.31	6.38	within
e099105	GNSGEPGAPGSKGDTGAKGEPGP*	1xCation:Na [E20]; 3xOxidation [P6; P9; P21]	Collagen alpha-1(I) chain	9.45	5.17	11.81	8.25	within
e017161	PGPVGGPGSSGAKGESGDPPGPQGP*	3xOxidation [P3; P7; P19]	Collagen alpha-1(XI) chain	9.93	5.8	12.02	9.08	within
e017165	GEKGDQGPDPGSPGSPGPAGP*	5xOxidation [P8; P9; P12; P15; P18]	Collagen alpha-3(IV) chain	11.18	6.85	13.21	11.75	within
e017193	GSPGPSGTGDTGPPGLQGMPE*	3xOxidation [P5; P9; P14]	Collagen alpha-2(V) chain	8.72	4.86	11.52	7.66	within
e213516	SPSPSPSLDFSAPGTPASHSAT	none	Cysteine-rich protein 2-binding protein	6.23	3.77	9.92	9.95	up
e017206	GANGAPGNDGAKGDAGAPGAPGSQG*	3xOxidation [P6; P18; P21]	Collagen alpha-1(I) chain	11.63	7.71	13.27	14.24	up
e017213	GTDGTPGAKGPTGSPGTSGPPGSAG*	2xOxidation [P20; P21]	Collagen alpha-2(V) chain	8.06	4.13	11.79	8.79	within
e103464	GGPGPQGPPEGKNGETGPQGPPEG*	4xOxidation [P5; P9; P17; P21]	Collagen alpha-1(III) chain	9.79	5.65	12.25	11.49	within
e213520	PPGKAGEDGHPGKPRPGERG*	3xOxidation [P2; P11; P14]	Collagen alpha-2(I) chain	8.49	4.4	11.37	9.0	within
e017230	FGGGSFGGGSFGGGGFGGGGFGGGGF	none	Keratin, type I cytoskeletal 10	11.94	8.35	14.09	9.55	within
e017238	GEDGEPGQPGSPGPTGENGPPGP*	1xOxidation [P]	Collagen alpha-2(XI) chain	12.44	8.13	14.91	11.97	within
e017240	DAGAAREDAGAGDDVGAGREDA	none	Golgin subfamily A member 6-like protein 2	11.05	6.47	13.52	6.54	within
e213523	AEGSPGRDGSPGAKGDRGETGP*	3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	12.28	7.69	14.88	11.95	within
e213524	EAGGNATAGGGPPGSSDSESSPGA	none	Proline-rich protein 12	9.65	6.12	11.81	9.15	within
e097739	TSQPEGEAGVGVESNSDGASPE	none	POU domain, class 5, transcription factor 1	9.65	5.98	11.76	9.04	within
e017267	EDNPVENEEASTHEAASFE	none	E3 ubiquitin-protein ligase HECW2	9.08	4.66	11.88	3.71	down
e213526	AQGPREGPTGSPGPAGASGNPG*	2xOxidation [P4; P8]	Collagen alpha-1(II) chain	13.93	11.55	15.2	14.66	within
e017269	GPPGEAGKPGEQGVPGDLGAPGP*	4xOxidation [P3; P9; P15; P21]	Collagen alpha-1(I) chain	13.92	11.52	15.19	14.66	within
e017287	QGPTGSEGTPGLPGGVGQPGAVGE	none	Collagen alpha-3(V) chain	12.74	8.7	14.24	14.29	up
e102236	PATPGGGTAQTPEAGTSQPMPPG	none	Cadherin-related family member 5	11.41	7.57	13.33	12.52	within

a: Distribution in healthy female

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e213529	KGEMGPAGIPGAPGLMGARGPPG*	2xOxidation [P13; P21]	Collagen alpha-1(III) chain	10.86	7.09	12.88	11.63	within
e213531	VGEPPKGDTPSGPPGPPGVPGP	none	Pulmonary surfactant-associated protein D	10.67	6.98	12.78	11.31	within
e099106	EGSPGRDGSPPGAKGDRGETGPA*	1xCation:Na [C-Term]; 2xOxidation [P4; P10]	Collagen alpha-1(I) chain	11.03	6.08	13.86	9.46	within
e203440	PGPSGEEGKRGPNGEAGSAGPPG*	3xOxidation [P1; P3; P12]	Collagen alpha-2(I) chain	11.68	7.09	14.44	11.09	within
e017319	ATGFYTGSYYFDGSLYNKG	none	Sialate:O-sulfotransferase 2	11.31	5.21	13.41	10.58	within
e208406	GDPGLPGDMGKKGEMGQPGPPG*	2xOxidation [P18; P20]	Collagen alpha-3(IV) chain	10.46	5.94	12.83	11.67	within
e101761	KPEYLEELPTMMQH*	1xO-Glycan [T10] (HexNAc(1)Hex(1))	Glutathione S-transferase Mu 4	10.73	6.89	13.5	11.8	within
e017321	TVSPGSSNSEATTSVGESGKTGA	none	Mucin-19	10.23	6.83	12.65	11.23	within
e017336	NPGAPGTPGKGWAGDSGPQGR*	3xOxidation [P2; P5; P8]	Collagen alpha-2(IV) chain	9.24	5.74	12.26	11.39	within
e213546	GPPGLPGIPGPFDDGLPGPPGP*	3xOxidation [P9; P11; P18]	Collagen alpha-4(IV) chain	8.4	5.48	12.8	11.37	within
e203451	SEAEDASLLSFMQGYMKHA	none	Apolipoprotein C-III	10.0	5.52	12.52	10.1	within
e017354	GAAGEEGSPGPVGRGDPGAPGLP*	1xOxidation [P11]	Collagen alpha-1(XXII) chain	9.43	5.62	12.78	9.85	within
e017357	RDGKPGPPGEPGKAGEPGLPGP*	3xOxidation [P7; P8; P11]	Collagen alpha-1(XXII) chain	9.26	5.87	12.11	9.68	within
e103202	STPSSGANTATNSESSTTSSGAN	none	Mucin-21	10.04	4.83	12.78	4.22	down
e017363	QGPMGPMGPRGPPGPAGAPGPQG*	3xOxidation [P12; P13; P15]	Collagen alpha-1(II) chain	9.57	5.98	12.11	10.96	within
e017379	GFGGGFGGGSGGGFGGGYGSGFGGFG	none	Keratin, type I cytoskeletal 9	13.07	8.55	15.33	5.54	down
e017381	DGIDGDNPPGKAGPPGPKGEPPG*	2xOxidation [P16; P18]	Collagen alpha-2(IX) chain	10.27	6.16	14.07	9.65	within
e017384	LDNAYSNEGFYDDMEAAGH	none	Leucine-rich repeat-containing protein 66	12.0	7.88	13.87	9.41	within
e017385	REDAGAGGEDVGAGGEDAGAGGED	none	Golgin subfamily A member 6-like protein 2	9.32	5.13	12.08	8.97	within
e203458	SHEKMHEGDEGPGHHKPG*	1xOxidation [M5]	Protein S100-A9	7.73	3.1	12.76	11.31	within
e208413	SNGNPGGPPSGSPGKDGPPGPAG*	4xOxidation [P8; P10; P14; P19]	Collagen alpha-1(III) chain	10.75	6.61	12.64	10.88	within
e017391	DGQPGAKGEPGDAGAKGDAGPPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	12.72	9.37	14.14	11.49	within

a: Distribution in healthy female

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e017392	EVGPAGSPGSNGAPGQRGEPGPQ*	1xOxidation [P]	Collagen alpha-1(III) chain	8.74	4.85	11.25	7.56	within
e213556	SPGAKGDGGIPGPAGPLGPPGPPG*	7xOxidation [P2; P11; P13; P16; P19; P20; P22]	Collagen alpha-1(XI) chain	12.0	5.49	14.77	11.79	within
e017394	EAGPPGKSLPGEPGLDGNPGAPG*	3xOxidation [P5; P10; P13]	Collagen alpha-1(XIX) chain	11.05	4.96	14.4	11.78	within
e017397	GERGSESGSPGHPGQPGPPGPPG*	7xOxidation [P9; P12; P15; P17; P18; P20; P21]	Collagen alpha-1(III) chain	9.78	5.16	12.14	9.5	within
e017399	GEPGTPGSPGPAGASGNPGTDGIPG*	1xOxidation [P24]	Collagen alpha-1(II) chain	9.14	4.37	12.09	8.29	within
e017404	FSTSGSSSFLNLQGPPGPPGP*	2xOxidation [P17; P19]	Collagen alpha-1(XVII) chain	9.94	5.7	11.79	11.27	within
e213559	RSGETGPAGPPGNPGPPGPPGPPG*	1xOxidation [P23]	Collagen alpha-1(II) chain	10.34	5.32	13.12	11.0	within
e017411	GDAGAPGAPGGKGDAGAPGERGPPG*	3xOxidation [P9; P18; P23]	Collagen alpha-1(III) chain	11.18	6.48	12.87	12.16	within
e017413	STYRGTYEQDGRFEKRQ	none	Zinc finger protein 396	10.16	5.73	12.59	11.55	within
e017424	PGPDGNKGEPGVVGAVGTAGPSGP*	3xOxidation [P3; P10; P21]	Collagen alpha-2(I) chain	7.54	4.44	11.61	7.87	within
e017430	ATPPDEQQGDAPPQLEDEE	none	Ubiquitin carboxyl-terminal hydrolase 9X	8.94	5.36	11.38	10.19	within
e017443	DAASEASSEPDYNYEFAQM	none	Kinesin-like protein KIF13A	13.09	8.67	16.0	7.5	down
e095177	AAPADPDSGATPEDPDSTAPAD	none	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	13.16	8.78	16.04	7.19	down
e093796	FESFGDLSSPDVVMGNPKVK	none	Hemoglobin subunit delta	7.97	3.95	13.18	5.6	within
e017450	EGNLEGTSGSDGNVEDSDQSE	none	Rhox homeobox family member 2B	10.05	5.27	12.37	12.22	within
e017452	PGYQGPPEGPGQAGPSGPPGPP*	8xOxidation [P1; P6; P7; P10; P15; P18; P19; P21]	Collagen alpha-1(III) chain	11.25	6.83	13.59	8.3	within
e100356	VHTEGNYGESGMDAFKELAA	none	Metabotropic glutamate receptor 1	9.78	5.85	12.33	9.87	within
e017461	EGASPTSSSNEDSAANGSAETSA	none	Pro-interleukin-16	9.5	5.05	11.51	9.68	within
e017464	GPQGAAGETGPMGERGHGPPGPP*	1xOxidation [P21]	Collagen alpha-2(XI) chain	11.41	5.98	13.63	10.76	within
e300082	VGQDGAPGIPGEKGLPGLQGPPG*	2xOxidation [P16; P21]	Collagen alpha-3(V) chain	7.44	5.2	9.72	5.73	within

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e017491	GKKGAPGMPGLMSGSPGQPGT*	3xOxidation [P6; P9; P18]	Collagen alpha-1(XI) chain	10.16	6.36	11.92	11.17	within
e017494	RPSSRGASPNRSTSVSSQAAQ	none	Dystonin	6.23	2.07	10.7	6.35	within
e095182	NGIPGEKGPA GERGAPGPAGPRG*	2xOxidation [P4; P9]	Collagen alpha-1(III) chain	10.51	5.96	12.36	11.08	within
e105516	SPFGQPFSQAGGQPMGATGVNP	none	CREB-binding protein	9.36	5.56	11.93	8.88	within
e213575	GQPGPPGHLGPAGPEGAPGSPGSPG	none	Collagen alpha-3(IV) chain	9.07	5.11	12.08	8.87	within
e017501	GPPGKTGPVGPQGAPGKPGPEGL*	5xOxidation [P3; P8; P11; P14; P18]	Collagen alpha-1(XI) chain	8.04	4.45	12.79	8.06	within
e017507	GRDGNPGNDGPPRGDQPGHK*	3xOxidation [P11; P12; P18]	Collagen alpha-2(I) chain	6.67	2.69	10.32	7.48	within
e213577	KSDADGSSFEEALDELSPVH	none	Teashirt homolog 1	8.01	3.74	12.53	6.78	within
e208421	SPGSPGPAGPAGPPGYGPQGEPL*	2xOxidation [P7; P10]	Collagen alpha-3(IV) chain	9.75	5.95	12.19	8.43	within
e017518	YSISSDNSDTTDSHATSTSAS	none	E3 ubiquitin-protein ligase Jade-2	12.78	8.41	14.88	14.01	within
e105762	QGNPGEPEGVSGPMGPRGPP*	4xOxidation [P7; P10; P15; P21]	Collagen alpha-1(II) chain	9.84	5.82	12.57	10.64	within
e017525	DGQPGA KGE PDAGAKGDAGPPGP*	2xOxidation [P10; P21]	Collagen alpha-1(I) chain	14.89	13.24	15.88	15.31	within
e017537	GGGFGAAGGFGGRGGGFGGGSSFGGGS	none	Keratin, type II cytoskeletal 2 epidermal	5.85	1.81	9.36	4.97	within
e213581	GETGAAGPPGPAGPAGERGEQGAP*	3xOxidation [P8; P9; P11]	Collagen alpha-1(II) chain	9.49	5.17	12.18	10.16	within
e017538	GPGMRGMPGSPGGPGSDGKPGPPG*	2xOxidation [P20; P]	Collagen alpha-1(III) chain	12.58	8.79	14.39	13.81	within
e017540	GEPGKQGPSGASGERGPPGPMGP*	2xOxidation [P17; P18]	Collagen alpha-1(I) chain	12.86	8.86	14.44	13.79	within
e017548	GYQGGGYQQDNRYQDGGHH	none	Protein FAM98A	11.94	8.2	13.86	8.6	within
e106390	GEQGSPGASGPAGPRGPPGSAGAPG*	4xOxidation [P11; P14; P17; P24]	Collagen alpha-1(I) chain	9.89	5.67	12.53	9.81	within
e017550	ARGNDGARGSDGQPGPPGPGTA*	3xOxidation [P16; P17; P]	Collagen alpha-1(III) chain	12.62	9.74	14.15	12.95	within
e102018	GAGGGPPPGPPGAGDRGGGGPGGGGPGGG	none	Far upstream element-binding protein 2	11.78	8.71	13.87	12.14	within
e017562	NGEPGKGGERGAPGEKGE GPPG*	3xOxidation [P13; P21; P]	Collagen alpha-1(III) chain	12.84	8.44	14.45	14.74	up
e017565	NSGEPGAPGSKGDTGAKGEPGPVG*	1xOxidation [P8]	Collagen alpha-1(I) chain	11.43	7.39	13.19	11.97	within

a: Distribution in healthy female

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e100584	TPGRDGEPPGDPGEDGKPGDTGP*	2xOxidation [P17; P22]	Collagen alpha-1(XVIII) chain	10.65	5.86	13.5	9.6	within
e103453	PPGHPGPPGEPGTDGAAGKEGPP*	4xOxidation [P7; P8; P11; P22]	Collagen alpha-1(XVI) chain	9.39	5.12	12.06	11.67	within
e213588	EKGDSGPSGAAGPPGKKGPPGED*	3xOxidation [P13; P14; P19]	Collagen alpha-3(V) chain	11.57	7.87	13.84	10.11	within
e017603	PGGPGSDGKPGPPGSQGESGRPGP*	1xOxidation [P22]	Collagen alpha-1(III) chain	10.1	5.64	12.36	9.28	within
e095196	APGPAGPPGPPGPPGPPGGLPAGF*	2xOxidation [P]	Collagen alpha-1(XVIII) chain	8.86	5.29	11.98	8.09	within
e017609	VIKMGVAAHKKSHEESHKE	none	Protein S100-A8	10.6	4.27	14.92	14.83	within
e097757	DNENVVNEYSSELEKHQL	none	Fibrinogen beta chain	8.1	4.52	11.46	9.91	within
e213598	RGEQGLPGSPGPPGLPGKPGED*	3xOxidation [P12; P13; P16]	Collagen alpha-1(VII) chain	7.72	4.6	10.83	9.91	within
e203496	LNQAQEHFGKDKSKEFQL	none	Serotransferrin	7.75	3.08	13.24	4.66	within
e017635	NSEGSHTGDGRFSHESND	none	Protogenin	9.9	5.1	13.21	7.82	within
e104206	FGASAGTGLSDNHDIIISMKL	none	Vesicular integral-membrane protein VIP36	10.97	7.12	13.83	13.81	within
e017641	PAATPVMPKPSSLSADTAALSH	none	Microtubule-associated serine/threonine-protein kinase 3	9.59	6.65	12.65	7.96	within
e213602	GAPGVPGPKGDPGFQGMPIGGSP*	1xOxidation [P3]	Collagen alpha-1(IV) chain	9.63	3.93	13.13	12.38	within
e017645	GIEEAFTSKADLSGITGARNL	none	Alpha-1-antichymotrypsin	8.82	5.86	12.77	9.26	within
e101074	STEGSSDFSWGYGELDQDAT	none	Primary cilium assembly protein FAM149B1	8.77	4.53	11.45	9.65	within
e017650	DGQPGAAGGEPGDAGAKGDAGPPGP*	3xOxidation [P4; P10; P21]	Collagen alpha-1(I) chain	13.75	11.2	14.86	14.73	within
e095204	HLPAEFTPAVHASLDKFLAS	none	Hemoglobin subunit alpha	7.87	3.25	14.01	6.08	within
e213605	PGGPGMRGMPGSPGGPGSDGKPGP*	3xOxidation [P4; P10; P13]	Collagen alpha-1(III) chain	11.41	7.76	13.43	9.32	within
e017656	GPKGEPGSMGPRGENGVGAPGP*	2xOxidation [P6; P11]	Collagen alpha-1(XXIII) chain	11.4	7.91	13.35	9.32	within
e017661	PQQAEDHPQNPPEDPNQDP	none	Lethal(3)malignant brain tumor-like protein 1	10.02	6.18	12.28	11.21	within
e017671	GERGTPGIGGFPGPSGNDGSAGPP*	1xOxidation [P6]	Collagen alpha-1(VII) chain	9.18	4.32	11.92	10.45	within
e099597	AVGEYNKASNDMYHSRALQ	none	Cystatin-C	7.81	4.74	11.41	6.37	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e017675	PGEDGKPGDTGPQGFPGTGPDVG*	1xOxidation [P12]	Collagen alpha-1(XVIII) chain	10.79	6.85	12.5	12.21	within
e213608	NGEPGGKGERGAPGEKGEPPG*	4xOxidation [P4; P13; P21; P22]	Collagen alpha-1(III) chain	10.74	6.89	12.51	11.9	within
e106183	NSGEKGDQGFQGPFGPPGP	none	Collagen alpha-1(XVI) chain	10.79	5.59	13.18	12.69	within
e017677	NSGEPGAPGSKGDTGAKGEPGPVG*	2xOxidation [P8; P20]	Collagen alpha-1(I) chain	14.79	13.17	15.68	14.8	within
e017679	PGPPGPSGSPGKDGPPGPAGNTGAP*	2xOxidation [P]	Collagen alpha-1(III) chain	9.83	3.84	12.07	11.81	within
e213610	QLTGQNSGDVNVEINVAPGKD	none	Keratin, type I cytoskeletal 9	14.2	11.19	15.5	14.8	within
e203520	DGGPGPRGLPGDAGREGFPGPP*	6xOxidation [P4; P6; P10; P19; P21; P22]	Collagen alpha-2(IV) chain	10.33	7.18	12.61	9.76	within
e213612	GTKGSPGSDGPKGEKGDGPEGP*	3xOxidation [P18; P20; P23]	Collagen alpha-2(VI) chain	8.46	4.67	10.79	7.9	within
e017689	FAGEKGPSGEAGTAGPPGTPGPQG*	2xOxidation [P17; P20]	Collagen alpha-2(I) chain	9.23	4.54	11.91	7.52	within
e105587	GLAGTAGEPGRDGNPGSDGLPGR*	3xOxidation [P9; P15; P21]	Collagen alpha-1(III) chain	10.21	6.6	12.99	9.86	within
e213613	DGQPGPAGPPGPVGPAGGPGFPGAP*	3xOxidation [P12; P15; P19]	Collagen alpha-1(II) chain	12.37	9.98	14.08	12.11	within
e017699	PGAPGPQGFQGPPEGPEPGASG*	7xOxidation [P1; P4; P6; P12; P13; P16; P19]	Collagen alpha-1(I) chain	11.77	6.93	13.9	9.0	within
e213615	ASNRATGIPARFSGSGSGTDF	none	Immunoglobulin kappa variable 3-11	11.27	7.21	13.43	9.38	within
e017713	AEGSPGRDGSFGAKGDRGETGPA*	2xOxidation [P5; P11]	Collagen alpha-1(I) chain	13.36	10.39	15.12	14.2	within
e017714	GSPGSMGPRGDTGPAGPPGPPGAPA*	1xOxidation [P14]	Collagen alpha-3(V) chain	10.66	5.78	12.7	10.79	within
e017715	GPPGKAGEDGHPGKPRPGERG*	3xOxidation [P3; P12; P15]	Collagen alpha-2(I) chain	8.35	4.4	11.66	12.21	up
e017721	PPGYRGPTGELGDPGPRGNQG*	5xOxidation [P1; P2; P7; P14; P16]	Collagen alpha-3(IX) chain	11.66	9.02	13.19	12.59	within
e213619	GGEGRGSASSGGAAGAGVGGLSGPES	none	Protein transport protein Sec16B	9.8	6.28	11.71	10.02	within
e213620	TNPAASSSASGSSVPPVSSSASAPG	none	Mediator of RNA polymerase II transcription subunit 13-like	9.73	6.29	11.72	10.45	within
e203527	SGPAGPTGARGAPGDRGEPGPPGP*	3xOxidation [P6; P13; P22]	Collagen alpha-1(I) chain	7.08	3.58	10.69	6.43	within
e095212	AGPPGEAGKPGEQGVPGDLGAPGP*	3xOxidation [P3; P10; P22]	Collagen alpha-1(I) chain	13.71	11.45	15.21	14.4	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099110	NGEPGGKGERGAPGEKGEPPG*	1xCation:Na [E]; 3xOxidation [P4; P13; P21]	Collagen alpha-1(III) chain	10.69	6.91	12.48	9.85	within
e017739	FPLGPGPEGMAAMSAMEPHH	none	Single-stranded DNA-binding protein 4	12.32	7.82	14.41	13.09	within
e099595	PGAVGEKGEPGEAGEPGLPGEPPG*	1xOxidation [P16]	Collagen alpha-1(V) chain	9.38	5.79	11.69	9.92	within
e213621	EAGEKGNPGAIEVPLPGEPPG*	3xOxidation [P16; P18; P21]	Collagen alpha-1(XIII) chain	12.86	9.98	14.48	13.31	within
e102669	PSGEPGKQGAPGASGDRGPPGPVG*	2xOxidation [P11; P19]	Collagen alpha-1(II) chain	12.53	9.34	14.14	10.45	within
e017746	VIKMGVAHKKSHKE*	1xOxidation [M4]	Protein S100-A8	10.76	3.63	14.82	11.03	within
e017751	GPQGESRTGPPGSTGSRGPPGP*	2xOxidation [P20; P22]	Collagen alpha-1(XII) chain	10.15	6.65	13.36	9.76	within
e100735	GPPGATGFPGAAGRVGPPGSNGNPG*	1xOxidation [P]	Collagen alpha-1(II) chain	9.97	5.7	12.07	9.67	within
e213623	GGSGGGGNRYGGFNRSGGGYSQ	none	Heterogeneous nuclear ribonucleoprotein U-like protein 1	9.68	4.96	12.47	9.73	within
e017762	RDFSAGQEPDWDNENEVVG	none	Plasma membrane calcium-transporting ATPase 3	7.7	3.69	10.96	10.86	within
e104802	FGASAGTGLSDNHDIIISMKL*	1xOxidation [M19]	Vesicular integral-membrane protein VIP36	9.39	4.45	13.6	8.2	within
e101287	PGRDGSPGQRGLPGKDGSSGPPG*	2xOxidation [P13; P22]	Collagen alpha-1(XIV) chain	7.99	4.47	12.23	5.39	within
e213628	DGDQHSPGRNQSSAFSPDPA	none	[F-actin]-monooxygenase MICAL2	7.55	3.43	10.88	9.02	within
e213629	APGRDGASGKDGRGSPGVPSPG*	1xOxidation [P20]	Collagen alpha-1(VII) chain	8.72	4.94	11.33	10.24	within
e213630	NLGPVGGGTSGSSLPGQAGGSLVPT	none	Homeobox protein CDX-4	7.02	3.74	11.9	9.72	within
e017775	RFIHGHRGGSGSGSGSGKASDP	none	Adenylate cyclase type 8	6.09	3.19	13.0	9.23	within
e017779	GNRSGGHGYWDGGAAGAEPPAPA	none	Opsin-3	7.36	3.3	10.57	10.88	up
e213633	GGGADPAWTSALSGNSSGPGGSSP	none	Zinc finger protein 503	17.53	16.3	18.16	17.85	within
e105786	PGPPGPPGTSGHPGSPGPGYQGP*	2xOxidation [P3; P]	Collagen alpha-1(III) chain	12.71	9.8	14.85	13.85	within
e017799	NSGEPGAPGSKGDTGAKGEPGPVG*	3xOxidation [P5; P8; P20]	Collagen alpha-1(I) chain	17.54	16.3	18.16	17.85	within
e017802	PGPVGFPGDPGPPGEPGAGQDGV*	1xOxidation [P]	Collagen alpha-1(XI) chain	6.33	2.99	11.01	8.15	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e017808	GGGSAAATGAGGAGAYGTGGPGGPGGPA GG	none	T-cell leukemia homeobox protein 1	13.93	10.06	15.55	14.45	within
e213637	LGRDSPDTMLASPQEEGEGPS	none	Pleckstrin homology domain-containing family M member 2	10.2	4.82	13.45	10.62	within
e017824	PGPVGPAGGPGFPGAPGAKGEAGPTG*	1xOxidation [P16]	Collagen alpha-1(II) chain	7.83	4.61	12.89	8.84	within
e213638	PGPPGPPAEKGAKGAMGRDGATGP	none	Macrophage receptor MARCO	7.91	4.62	13.02	8.34	within
e097772	PGRDGEDGPTGPPGPPGPPGPPG*	7xOxidation [P13; P15; P16; P18; P19; P21; P22]	Collagen alpha-2(I) chain	11.18	6.55	12.99	9.39	within
e213643	AGPPGEAGKPGEQGVPGDLGAPGP*	4xOxidation [P4; P10; P16; P22]	Collagen alpha-1(I) chain	15.44	13.75	16.63	16.11	within
e017847	GPPGTPGEPMQGEPPGPPGPPGN*	6xOxidation [P9; P15; P17; P18; P20; P21]	Collagen alpha-3(IV) chain	10.5	6.08	12.71	10.79	within
e203568	NGDDGEAGKPGRPGERGPPGPQ*	2xOxidation [P18; P]	Collagen alpha-1(I) chain	10.24	5.6	12.54	11.77	within
e213647	GIDGIDGDRGPKGPPGPPGPAGE*	4xOxidation [P11; P14; P15; P17]	Collagen alpha-1(IX) chain	12.89	10.46	14.28	12.92	within
e017857	DGKPGLRGDPGPAGPPGLMGPPG*	5xOxidation [P4; P10; P12; P15; P16]	Collagen alpha-1(XVI) chain	13.13	10.28	14.86	12.92	within
e017859	RDGSPGAKGDRGETGPAGPPGAPG*	1xOxidation [P20]	Collagen alpha-1(I) chain	13.05	10.18	14.5	12.92	within
e017860	FPGPKNDGAPGKNGERGPGGGPG	none	Collagen alpha-1(III) chain	13.11	10.26	14.75	12.92	within
e213648	GGSPGAGPPGPQGKGERGSPGGPG*	4xOxidation [P5; P8; P9; P11]	Collagen alpha-1(III) chain	10.81	5.77	12.99	8.11	within
e103401	GPPGATGFPGAAGRVGPPGSNGNPG*	2xOxidation [P3; P9]	Collagen alpha-1(II) chain	10.64	6.81	12.55	9.21	within
e017869	EALAGGDKSDPNLNNPADEDH	none	Sine oculis-binding protein homolog	9.6	6.11	12.62	11.77	within
e017877	GDFSSSDFQSRDSSQLDFR	none	RNA-binding protein 6	8.35	3.99	11.13	10.28	within
e213651	GRTGDAGVPVGPVPPGPPGPPGPPG*	6xOxidation [P11; P12; P14; P15; P17; P18]	Collagen alpha-1(I) chain	7.29	3.99	11.69	8.74	within
e017880	AGGLQDTAANSFSSGSSVTSPSG	none	Neuron navigator 2	7.77	3.69	10.91	8.77	within
e208446	NSGEKGDQGFQGGPFGPPGPGP*	2xOxidation [P14; P20]	Collagen alpha-1(XVI) chain	11.02	7.4	12.76	12.16	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e017922	PSGPVGP TAGAEAE GSG LGWGSDV*	2xOxidation [P1; P4]	Collagen alpha-1(XV) chain	11.03	7.4	12.78	12.39	within
e106393	AVTEDDEDEDDKEDVGY	none	Testican-1	9.81	5.46	11.71	11.84	up
e017935	GKDGTPGTPGMKSAGQAGQPGSP*	3xOxidation [P6; P9; P21]	Collagen alpha-2(IX) chain	12.47	9.89	14.05	12.58	within
e105140	KGDPGDVGGPGPPGASGEPGAPGPP*	4xOxidation [P4; P13; P19; P24]	Collagen alpha-3(V) chain	10.39	6.1	12.54	11.8	within
e213659	EDINGEIYDEYDEEEDDP	none	Transcription factor SOX-5	9.75	5.93	11.61	10.61	within
e213660	FGGASGGGYSSSGFGGGFGGGSGGGF	none	Keratin, type I cytoskeletal 9	12.15	8.35	14.17	10.82	within
e213661	EGNIDDSLIGNASAE GPEGEGT	none	Translationally-controlled tumor protein	14.21	11.01	15.75	15.35	within
e105348	AWEEESPGLSGGPGGSGAGSTVAE	none	Heparan sulfate glucosamine 3-O-sulfotransferase 3A1	14.21	10.82	15.74	15.35	within
e102300	DLTNAGYSAANSNSIFANSSNA	none	BRD4-interacting chromatin-remodeling complex-associated protein-like	10.5	6.51	12.42	11.27	within
e213663	PGPRGEDGPEGPKGRGGPNGDPG*	2xOxidation [P1; P3]	Collagen alpha-1(V) chain	11.59	7.51	13.93	11.69	within
e017952	FQGPPGEPGEPGASGPMGPRGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	10.4	6.65	12.42	11.34	within
e213666	EMHEMAQKTAELQEELSGE	none	Centromere protein F	12.19	9.79	13.77	13.84	up
e017966	ADGQPGAKGEPGDAGAKGDAGPPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	12.79	10.42	14.12	13.24	within
e017968	EAIPMSIPPEVKFNKPFVF	none	Alpha-1-antitrypsin	10.51	2.96	14.05	11.27	within
e017971	SPGQAPENVKVAQLLVNIQGQ	none	Krueppel-like factor 15	10.62	1.98	14.75	11.17	within
e017978	APGDFGPRGDQGDGAAGPPGPPG*	1xOxidation [P23]	Collagen alpha-1(XXIII) chain	12.03	7.47	13.9	12.4	within
e213669	PGPSGEEGRGPNGEAGSAGPPGP*	2xOxidation [P12; P21]	Collagen alpha-2(I) chain	12.3	9.9	13.85	12.13	within
e017981	DVPGPPGERGSPGIPGAPGPIGPP*	1xOxidation [P20]	Collagen alpha-5(IV) chain	6.11	1.94	10.1	8.96	within
e097780	TQSLPTRPPTFPPTIPPAKE*	1xOxidation [P5]	Collagen alpha-1(XIV) chain	10.11	4.88	14.57	11.51	within
e017986	LSDPEQGVEVTGQYEREKAG	none	Inter-alpha-trypsin inhibitor heavy chain H4	11.29	6.76	13.46	10.64	within
e017997	GPPGEKGENDVGPMGPPGPPGP*	6xOxidation [P3; P14; P17; P18; P20; P]	Collagen alpha-1(XI) chain	12.69	8.1	15.48	11.48	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213673	NSGEPGAPGSKGDTGAKGEPGPVG*	1xCation:Na [E/D]; 3xOxidation [P5; P8; P20]	Collagen alpha-1(I) chain	12.79	8.61	15.52	11.58	within
e018001	NGDDGEAGKPRPGERGPPGPQ*	3xOxidation [P13; P18; P]	Collagen alpha-1(I) chain	11.36	6.51	13.92	13.58	within
e213674	APAGAPTTTQTNGQGDDQNPAPA	none	Far upstream element-binding protein 1	11.29	6.3	13.89	13.54	within
e018003	KNGDDGEAGKPRPGERGPPGP*	3xOxidation [P14; P19; P]	Collagen alpha-1(I) chain	7.64	3.94	10.92	9.78	within
e203602	GAPGIDGEGKPGKQKGDPEGP*	3xOxidation [P3; P11; P18]	Collagen alpha-1(XXIII) chain	8.85	5.52	12.01	10.88	within
e213676	FPGPKGNDGAPGKNGERGGPGGPG*	1xOxidation [P]	Collagen alpha-1(III) chain	9.25	5.78	12.1	10.81	within
e018010	STQLGEEPFSYGYGGTGKKST	none	Heterogeneous nuclear ribonucleoprotein U-like protein 1	11.88	7.58	13.74	13.0	within
e018012	AAGAAGSAAPAAAAGAPSGGAPSGSQGV	none	Cyclin-L2	9.83	5.55	12.42	10.58	within
e102826	DGETEGSGLDESNPJHLKEP	none	Immunoglobulin superfamily member 10	10.15	5.82	12.46	9.55	within
e018017	PDGPDGKPGIDGLTGAKGEPGPM*	2xOxidation [P1; P4]	Collagen alpha-2(IX) chain	9.76	6.39	11.46	10.89	within
e018023	NGAPGNDGAKGDAGAPGAPGSQGAPG*	3xOxidation [P16; P19; P25]	Collagen alpha-1(I) chain	10.5	6.01	12.8	11.63	within
e101899	NDGPPGRDQPGHKGGERGYPG*	3xOxidation [P5; P11; P20]	Collagen alpha-2(I) chain	10.34	5.39	13.01	12.34	within
e213678	GPRGDQGPVGRTEVGAVGPPPGF*	2xOxidation [P20; P21]	Collagen alpha-2(I) chain	7.87	4.24	12.11	6.41	within
e100825	GLYPESHGIVGNSMYDPVFD	none	Autotaxin	11.35	6.73	13.36	12.19	within
e213679	SASPEPGPGSTGSSESPGSQGGPGSP	none	von Willebrand factor A domain-containing protein 5B2	12.78	9.44	15.12	9.54	within
e300048	PAGPNGADGPQGPPGGVGNLPPGE*	2xOxidation [P22; P23]	Collagen alpha-2(XI) chain	10.42	6.25	13.46	9.27	within
e213680	GPPGPAGPSGESRPGSPGPPGSPGP*	3xOxidation [P14; P17; P19]	Collagen alpha-1(XIV) chain	12.77	9.25	15.08	9.57	within
e018043	PGPPGAVGPAGKDGEAGAQQPPGPAG*	2xOxidation [P9; P21]	Collagen alpha-1(I) chain	7.97	4.11	11.65	7.94	within
e100765	STGSSESPGSQGPSPEGSAPLEP	none	von Willebrand factor A domain-containing protein 5B2	12.02	7.95	14.22	10.7	within
e018053	VGEAGAAGEAGGAGEAGGVGEAGAAGEA	none	Paraneoplastic antigen Ma6E	11.15	7.19	13.29	10.01	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e095246	KGNSGEPGAPGSKGDTGAKGEPGP*	3xOxidation [P7; P10; P22]	Collagen alpha-1(I) chain	9.52	5.22	12.44	10.48	within
e018066	GPMGPPGNKGSMSGSPGHQGPSP*	1xOxidation [P21]	Collagen alpha-1(XIX) chain	9.57	5.24	11.4	6.47	within
e103593	LTGPIGPPGPAGAPGDKGESGPSGP*	2xOxidation [P8; P10]	Collagen alpha-1(I) chain	6.92	4.31	12.29	6.32	within
e018079	LSDNGSSGIEWSNVTSSQYD	none	DmX-like protein 2	10.05	6.36	11.93	11.92	within
e018081	VGEVGAAGEAGGTGEAGATGEAGAAGE	none	Paraneoplastic antigen Ma6E	10.03	6.47	11.99	12.02	up
e300107	NSGEKGDQGFQGPFGPPGP*	3xOxidation [P14; P19; P20]	Collagen alpha-1(XVI) chain	9.05	5.45	12.55	8.83	within
e203621	QGVPGPPGFQGEPPQGEPGPPG*	4xOxidation [P6; P7; P13; P15]	Collagen alpha-2(VIII) chain	8.71	5.0	11.6	9.88	within
e018084	PGASAAPGSPTTTGGPGAPAEVPQE	none	Transmembrane protein PMIS2	6.3	2.6	9.27	5.98	within
e097788	KGEPGDAGAKGDAGPPGPAGPAGPP*	5xOxidation [P4; P15; P16; P18; P21]	Collagen alpha-1(I) chain	9.01	4.78	12.18	11.15	within
e018101	RYDDYSSSRDGYGGSRDY	none	RNA-binding motif protein, X chromosome	7.13	3.89	10.66	9.65	within
e018103	ADGQPGAKGEPGDAGAKGDAGPPGP*	2xOxidation [P11; P22]	Collagen alpha-1(I) chain	16.21	14.77	17.13	16.82	within
e018117	GEKGDKGAMGEPGPPGPSGLPGES	none	Collagen alpha-3(IV) chain	6.23	3.97	12.47	5.95	within
e300147	EAEDLQVGQVELGGGPGAGSLQP	none	Insulin	10.38	5.59	13.66	12.42	within
e018123	GTGSGGGGPGGSGGVGGGSGGYTYFTT	none	Leucine-rich repeat-containing protein 4B	15.05	11.59	17.07	12.8	within
e018133	LKKENKNEKVEIHIMEDL	none	Protein S100-A9	7.47	4.21	12.09	9.33	within
e018135	ESGNKGEPGSAGPQGPPGPSGEEG*	2xOxidation [P13; P16]	Collagen alpha-2(I) chain	11.51	7.96	13.14	11.66	within
e018137	PKGETGPHGYKGMVGAIGATGPP*	2xOxidation [P1; P7]	Collagen alpha-2(IX) chain	7.71	4.82	11.58	10.8	within
e213699	NGAPGNDGAKGDAGAPGAGSQGAPG*	4xOxidation [P4; P16; P19; P25]	Collagen alpha-1(I) chain	15.18	13.1	16.48	16.43	within
e018143	PEPPSELLEDGQDTPTSASP*	1xOxidation [P4]	Collagen alpha-1(XVIII) chain	8.98	4.87	12.07	9.54	within
e018145	GNSGEPGAPGSKGDTGAKGEPGPVG*	2xOxidation [P9; P21]	Collagen alpha-1(I) chain	12.03	9.08	13.79	12.15	within
e213703	PGSKGQPGDSGEMGFPGMAGLFG*	2xOxidation [P1; P7]	Collagen alpha-1(XXVII) chain	14.58	11.35	15.85	14.15	within
e213704	TSATFSGGASSGFGGTLSTTAGFSG	none	Trophinin	7.99	4.78	11.5	11.16	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213705	SNGAPGQRGEPGPQGHAGAQQPPG*	2xOxidation [P13; P22]	Collagen alpha-1(III) chain	10.78	6.54	12.69	10.18	within
e213707	QTTHGQTGDTTEHGHPSHGQT	none	Filaggrin-2	13.17	9.35	15.4	10.98	within
e208459	NPGLPGEPGPVGGGGHPGQPGPPG*	8xOxidation [P2; P5; P8; P10; P17; P20; P22; P23]	Collagen alpha-5(IV) chain	13.09	8.33	15.33	11.08	within
e018165	KMADEAGSEADHEGTHSTKRG	none	Fibrinogen alpha chain	5.84	2.73	9.49	5.68	within
e018173	NSSTDSAASASAASDVSVESTAEA	none	Pro-interleukin-16	10.5	5.8	13.72	10.27	within
e018175	ERGSESPGHPGQPGPPGPPGAP*	6xOxidation [P11; P14; P16; P17; P19; P]	Collagen alpha-1(III) chain	12.62	8.99	14.63	10.39	within
e213711	HGSGSGRSSSSGQHGPGLGESSGF	none	Hornerin	11.57	7.19	13.14	11.03	within
e097794	EGLDGPGRDGPQPGPPGEQGPPG*	3xOxidation [P15; P16; P21]	Collagen alpha-3(IV) chain	11.56	7.76	13.13	11.03	within
e101376	AAGARGNDGARGSDGQPGPPGPPGT	none	Collagen alpha-1(III) chain	12.21	7.25	13.99	10.5	within
e018190	IGPPGPAGAPGDKGESGPSGAPGPTG*	2xOxidation [P6; P]	Collagen alpha-1(I) chain	12.31	8.34	14.11	10.55	within
e102607	KGEKGDGSGASGREGFPGVPGGTGP*	1xOxidation [P19]	Collagen alpha-1(VII) chain	8.01	4.03	10.9	6.1	within
e213714	KNGERIEKVEHSDLFSKDK	none	Beta-2-microglobulin	6.97	3.93	11.1	7.29	within
e018195	KSEVAHRFKDLGEENFKAL	none	Albumin	7.44	3.94	11.57	7.15	within
e018204	DEAGSEADHEGTHSTKRGHAK	none	Fibrinogen alpha chain	8.57	4.38	11.75	8.97	within
e213717	AGYPGPAGPPGPPGPPGTSGHPGSPG	none	Collagen alpha-1(III) chain	8.44	3.96	11.58	9.11	within
e102777	GRTGDAGPVGPPGPPGPPGPPGPPS*	3xOxidation [P14; P15; P17]	Collagen alpha-1(I) chain	9.44	5.43	12.09	9.98	within
e104814	PGRNGEKGSQGFYGPGEQGPPG*	3xOxidation [P15; P20; P21]	Collagen alpha-1(XXI) chain	7.71	4.08	10.6	10.92	up
e103690	GVGEKGEPGEAGNPGPPGEAGVGGP*	3xOxidation [P16; P17; P25]	Collagen alpha-1(XI) chain	10.49	5.84	13.01	12.92	within
e104992	PPGSVGSVGGVGEKGEPGEAGNPGP*	2xOxidation [P1; P2]	Collagen alpha-1(XI) chain	8.08	4.98	11.29	9.46	within
e018215	GEPGPKGDAGAPGAPGGKGDAGAPGE*	3xOxidation [P3; P5; P12]	Collagen alpha-1(III) chain	9.69	5.11	13.08	12.92	within
e018216	ADGQPGAKGEPGDAGAKGDAGPPGP*	3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	15.84	14.29	16.69	16.72	up
e018220	LPGEMGRPGPPGPPGAGNPGPSP*	2xOxidation [P]	Collagen alpha-1(XXVI) chain	8.55	4.54	12.27	8.91	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018225	PGPSGEEGKRGPNGEAGSAGPPGP*	4xOxidation [P3; P12; P21; P22]	Collagen alpha-2(I) chain	13.31	10.2	14.82	13.95	within
e213723	ERGETGPPGPAGFAGPPGADGQPG*	3xOxidation [P7; P8; P10]	Collagen alpha-1(II) chain	10.2	6.2	12.77	6.94	within
e213724	GHPGHEGPTGEKGAQGGPPGSAGPP*	3xOxidation [P17; P18; P23]	Collagen alpha-3(V) chain	10.65	7.02	13.87	10.18	within
e018244	GGGIGGGGFGGFGSGGGGFGGGGFGGG GY	none	Keratin, type II cytoskeletal 1	7.39	3.59	10.66	7.34	within
e018245	PGEPGPPGDDGFPGERGDKGTPG*	2xOxidation [P13; P22]	Collagen alpha-4(IV) chain	9.51	4.32	12.87	7.99	within
e018252	LNPTTGELVFDPLSASDTGEY	none	Junctional adhesion molecule A	8.38	3.51	12.43	11.82	within
e018258	YGQHGSGSSQSSGYGQHGSSSGQ	none	Filaggrin-2	11.07	6.1	13.84	12.28	within
e106260	NGTQGDSPQGPPGSEGFTGPPGP*	2xOxidation [P9; P12]	Collagen alpha-2(IV) chain	8.72	5.04	11.69	7.87	within
e103773	EPGVPGQPGAPGPPGHPSHPGPDG*	2xOxidation [P5; P8]	Collagen alpha-2(V) chain	8.42	4.58	12.29	9.79	within
e203690	VNDTLNGWYKNGKHPEHAF	none	Serine/threonine-protein kinase LATS1	6.48	2.93	10.62	9.84	within
e018266	SKAVHKAVLTIDEKGTEAAGAM	none	Alpha-1-antitrypsin	7.4	2.89	12.74	8.75	within
e097801	PGSPGSPGYQGPPGEPGQAGPSGP*	6xOxidation [P7; P12; P13; P16; P21; P24]	Collagen alpha-1(III) chain	10.52	7.22	13.22	12.61	within
e018271	GNSGEPGAPGSKGDTGAKGEPGPVG*	3xOxidation [P6; P9; P21]	Collagen alpha-1(I) chain	16.33	14.31	17.53	16.89	within
e102689	DDPRPPNPPKMPNPNPNHP	none	CD99 antigen	7.76	3.38	12.83	6.34	within
e213740	MRGMPGSPGGPGSDGKPGPPGSQG*	4xOxidation [P8; P11; P17; P19]	Collagen alpha-1(III) chain	14.31	10.06	16.04	14.33	within
e093815	PGYPGPSGDAGAPGVQGYPPGP*	5xOxidation [P13; P19; P21; P22; P24]	Collagen alpha-2(IX) chain	10.93	6.91	13.28	12.31	within
e100725	KEAGEGGEAEAPAAEGGKDEAAGGA	none	Myristoylated alanine-rich C-kinase substrate	10.96	4.98	13.58	6.79	within
e213741	GTPGAKGPTGSPGTSGPPGSAGPPGS*	6xOxidation [P8; P12; P17; P18; P23; P24]	Collagen alpha-2(V) chain	14.27	10.79	16.05	14.34	within
e018289	GEKGDPGDVGGPGPPGASGEPGAPGP*	1xOxidation [P6]	Collagen alpha-3(V) chain	14.91	12.19	16.58	14.31	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018298	DRGENSPGAPGAPGHPGPPGPVG*	6xOxidation [P8; P11; P14; P17; P19; P20]	Collagen alpha-1(III) chain	9.96	5.77	13.13	11.23	within
e018299	SASTAPRSTEESESDVFTES	none	Oxidation resistance protein 1	12.7	8.95	15.11	7.3	down
e099592	ESGREGAPGAEGSPGRDGSPGAKG*	3xOxidation [P8; P14; P20]	Collagen alpha-1(I) chain	9.63	5.14	12.11	6.29	within
e018315	NQPGPPGPPGPPGSAGARGEPPGP*	8xOxidation [P3; P5; P6; P8; P9; P11; P12; P21]	Collagen alpha-1(XII) chain	12.05	7.87	14.17	11.1	within
e018316	IGPPGPAGAPGDKGESGSPGAGPTG*	3xOxidation [P4; P6; P10]	Collagen alpha-1(I) chain	10.65	6.62	12.62	10.69	within
e018321	TSGEHAESEHASGEPAATEHAE	none	Acrosomal protein SP-10	9.51	5.18	12.55	8.22	within
e106316	GPTGDDGPKGNPGVGFPGDPGPP*	3xOxidation [P12; P14; P18]	Collagen alpha-2(XI) chain	11.15	6.58	13.68	9.53	within
e018322	NGDDGEAGKPGRPGERGPPGPQG*	2xOxidation [P]	Collagen alpha-1(I) chain	11.87	9.21	13.61	13.54	within
e018324	GKNGDDGEAGKPGRPGERGPPGP*	2xOxidation [P]	Collagen alpha-1(I) chain	12.21	8.74	14.0	13.15	within
e213747	HSGGSSTPGSGGSSTPGSGSSSGGGA G	none	Cbp/p300-interacting transactivator 2	11.47	7.12	13.7	7.16	within
e213749	AGPSGPPGPPGAIGPSGPAGKDGESG*	4xOxidation [P7; P9; P10; P15]	Collagen alpha-1(III) chain	10.12	5.77	12.4	10.34	within
e099944	NDGATGAAGPPGPTGPAGPPGFPGAV*	3xOxidation [P19; P20; P23]	Collagen alpha-1(I) chain	10.43	6.37	12.68	11.89	within
e018341	GPPGEDGVIGMMGFPGAIGPPGPP*	2xOxidation [P23; P24]	Collagen alpha-3(IV) chain	9.41	4.62	11.86	10.99	within
e213753	GRTGDAGVGP GPPGPPGPPGPPS*	4xOxidation [P12; P14; P15; P17]	Collagen alpha-1(I) chain	12.49	8.14	14.59	12.72	within
e018343	SAGPPGATGFPGAAGRVP GPPGSGNA*	2xOxidation [P11; P19]	Collagen alpha-1(I) chain	12.45	7.78	14.6	12.71	within
e203715	GPQGPPGKDGPPGVKGENGHPGSP*	1xOxidation [P11]	Collagen alpha-1(XIII) chain	12.2	8.35	14.48	12.71	within
e018353	GAMRPLNALGGPGMPGMNMGPGG	none	Single-stranded DNA-binding protein 2	8.15	4.89	11.32	9.75	within
e018352	KGESGVDGLMPAGPKGQPGDPGP*	2xOxidation [P22; P24]	Collagen alpha-1(XXI) chain	7.71	4.2	10.42	10.53	up
e213756	PSAGRARDGGDGREAAVAGEGPSP	none	Zygote arrest protein 1	11.13	6.57	12.96	10.58	within
e213757	SHIANVERVPFDAATLHTSTA	none	Gelsolin	6.83	4.21	12.17	4.37	within
e018356	ADGQPGAKGEPGDAGAKGDAGPPGP*	4xOxidation [P5; P11; P22; P23]	Collagen alpha-1(I) chain	11.6	8.34	13.34	13.44	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213758	GPGMRGMPPGSPGGPGSDGKPGPPGS*	3xOxidation [P11; P14; P20]	Collagen alpha-1(III) chain	11.77	8.56	13.21	11.89	within
e018366	PGRDGEPPGDPGEDGKPGDTGPQG*	3xOxidation [P10; P16; P21]	Collagen alpha-1(XVIII) chain	6.7	2.04	9.53	6.7	within
e105938	LSSLTETIEGVDAEDGHGPGEQ	none	Complement factor B	8.72	4.8	12.09	11.04	within
e018392	HKSEVAHRFKDLGEENFKA	none	Albumin	7.27	2.87	12.1	8.38	within
e213766	ADGQPGAKGEPGDAGAKGDAGPPGP*	1xCation:Na [D19]; 3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	14.42	11.23	16.13	13.76	within
e018412	TWPFGASPSHAAQGHSAAGRH	none	Zinc finger protein 469	5.1	1.48	9.89	4.69	within
e213767	HTPDEESIDWTKIEPSVNF	none	Vesicular integral-membrane protein VIP36	13.4	9.06	15.37	13.74	within
e213768	GEPGPGRPGFPGTPGMQGPGE*	7xOxidation [P3; P5; P9; P12; P15; P20; P21]	Collagen alpha-1(XII) chain	14.23	10.59	15.57	11.0	within
e095286	DGVSGGEGKGGSDGGGSHRKEGEE	none	CD99 antigen	10.38	6.35	12.38	11.86	within
e213769	GNRSGAASGEASEGAEASDAPPTR	none	Protein shisa-9	14.25	11.31	15.56	12.93	within
e018420	KANDESNEHSDVIDSQELSK	none	Osteopontin	7.64	3.61	12.94	11.13	within
e099588	SGPPGPPGPPGPKGDQGPGRGH*	3xOxidation [P12; P18; P]	Collagen alpha-1(XVII) chain	7.74	3.34	11.35	4.81	within
e018426	EGAGGAATPEDGAGGRGSEGSQSPGS	none	Zinc finger protein ZFPM1	12.55	9.0	14.39	12.35	within
e018431	AAGQVGKEADKLIHGVVHHGAN	none	Suprabasin	7.45	2.81	11.22	9.48	within
e018434	GADGQPGAKGEPGDAGAKGDAGPPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	12.12	7.97	13.7	10.89	within
e203741	PGKQGSRGDPGDAGPRGDSGQPGP	none	Collagen alpha-2(VI) chain	9.79	5.52	15.62	11.68	within
e213775	VGPAGPNGFAGPAGAAGQPGAKGERG	none	Collagen alpha-2(I) chain	5.93	2.61	10.32	6.66	within
e018452	KGDAGAPGAPGGKGDAGAPGERGPPG*	3xOxidation [P10; P19; P24]	Collagen alpha-1(III) chain	9.61	5.86	11.52	4.67	down
e018453	GDLSTPDVAMGNPKVKAHGKKV	none	Hemoglobin subunit beta	5.7	1.24	11.99	10.6	within
e203754	PGFPGAQGEPSQGEPPGDPGLPGP*	3xOxidation [P16; P19; P22]	Collagen alpha-2(IV) chain	17.16	15.78	18.06	17.42	within
e213779	FPGAQGEPSQGEPPGDPGLPGPPG*	3xOxidation [P17; P20; P22]	Collagen alpha-2(IV) chain	10.33	5.92	12.71	12.33	within
e213780	PENVSWADLEGPADGYGYPRG	none	Ceramide synthase 5	17.16	15.72	18.07	17.43	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018460	NGDDGEAGKPRPGERGPPGPQG*	3xOxidation [P13; P18; P]	Collagen alpha-1(I) chain	10.42	5.93	12.72	12.36	within
e213782	PGFPGQGPMPGRAGSPGRDGHGP*	4xOxidation [P7; P10; P16; P22]	Collagen alpha-1(IV) chain	17.16	15.8	18.06	17.43	within
e018464	GKNGDDGEAGKPRPGERGPPGP*	3xOxidation [P12; P15; P20]	Collagen alpha-1(I) chain	11.57	7.94	13.66	14.41	up
e018465	PGERGEVGPAGPNGFAGPAGAAGQP*	2xOxidation [P1; P9]	Collagen alpha-2(I) chain	10.21	5.76	12.74	10.83	within
e213784	AGKEGLRGPRGDQGPVGRTGEVG	none	Collagen alpha-2(I) chain	9.01	4.75	12.86	8.25	within
e099583	GGYGGGSGSRGGSGGSYGGGSGSGGS GGG	none	Keratin, type I cytoskeletal 9	12.75	8.15	15.01	10.8	within
e213785	PGPSGEKGETGDVGMPGPPGPPGP*	5xOxidation [P15; P18; P19; P21; P22]	Collagen alpha-2(XI) chain	14.56	12.0	15.97	14.78	within
e018475	AVGSPGVNGAPGEAGRDGNPGNDGP*	2xOxidation [P5; P11]	Collagen alpha-2(I) chain	14.59	12.0	15.95	14.81	within
e213787	VGEKGEPGEAGEPGLPEGGPPGP*	5xOxidation [P13; P16; P21; P22; P24]	Collagen alpha-1(V) chain	14.95	12.73	16.26	14.79	within
e213789	GQPGLYGPPGLHGFPGAPGQEGP*	4xOxidation [P3; P8; P9; P15]	Collagen alpha-2(IV) chain	11.15	7.17	12.9	11.4	within
e097809	VPGSPGSSRPGLRGAPGWPLKG*	4xOxidation [P5; P10; P16; P19]	Collagen alpha-3(IV) chain	8.5	4.31	13.65	7.28	within
e018479	PVEHQQQKQEVQWPPKHK	none	Involucrin	7.78	3.15	12.79	11.59	within
e018484	NLSQAGGGSGNSIPGSMGPGGGGQAH	none	Polyhomeotic-like protein 1	11.75	7.42	13.8	11.37	within
e018490	LTVKTISHESGEHSAQGKTKN	none	Endomucin	7.68	3.7	12.31	11.35	within
e018496	GESGVDGLMGPAKPGKQPGDGPQ*	3xOxidation [P14; P18; P21]	Collagen alpha-1(XXI) chain	10.82	5.8	12.98	11.62	within
e018497	FPGDPGPPGEGGPRGQDGAKGDR*	2xOxidation [P8; P13]	Collagen alpha-2(XI) chain	7.07	2.67	10.54	10.18	within
e018499	ERGEAGIPGVPAGKGEDGKDGP*	1xOxidation [P11]	Collagen alpha-1(III) chain	7.4	3.61	10.79	10.22	within
e213798	TGPIGPPGPAGANGEKGEVGPAG*	1xOxidation [P]	Collagen alpha-1(II) chain	7.29	3.82	11.91	9.49	within
e213801	PGSPGSPGAPAGPPGYGPQGEPL	none	Collagen alpha-3(IV) chain	9.37	4.18	12.55	10.25	within
e018527	SPADKTNVKAAGKVGAHAGEY	none	Hemoglobin subunit alpha	7.77	3.11	12.43	4.33	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213803	PPGSNGNPGPPGSPGKDGPPGP*	5xOxidation [P2; P8; P10; P11; P13]	Collagen alpha-1(III) chain	12.63	9.15	14.81	13.85	within
e213804	GP GSDGKPGPPGSQGESRPGPPGP*	2xOxidation [P10; P]	Collagen alpha-1(III) chain	12.48	8.76	14.53	13.5	within
e018539	RGGAAGEDEAGGPEGDPEEEDSQ	none	Transforming acidic coiled-coil-containing protein 1	13.14	7.21	15.56	14.81	within
e018540	GPPGEKGEPDDGPSGAEGPPGPQG*	1xOxidation [P]	Collagen alpha-1(II) chain	12.67	7.99	14.78	12.29	within
e018545	TPGGGSGMGSGMGGYGRDGMNQG	none	Heterogeneous nuclear ribonucleoprotein H3	11.68	6.8	14.36	12.95	within
e018550	DRGPRGERGPPGPPGRDGEDGP*	2xOxidation [P11; P13]	Collagen alpha-2(I) chain	6.79	3.49	10.25	5.05	within
e018560	GMPGGMGTPGEPGPQGPPGSRGPPG*	2xOxidation [P23; P24]	Collagen alpha-1(XXVII) chain	10.2	5.85	12.6	8.41	within
e018561	APGPQGLPGPPGFPVGPVPPGPPG*	10xOxidation [P2; P4; P8; P10; P11; P14; P16; P19; P20; P22]	Collagen alpha-3(IV) chain	9.59	5.75	11.89	11.21	within
e095302	DGNPNDGPPGRDQPGHKGER*	3xOxidation [P4; P9; P10]	Collagen alpha-2(I) chain	5.77	1.8	10.97	5.28	within
e018570	PGSKGDTGAKGEPGPVGVQGP GP A*	3xOxidation [P13; P15; P21]	Collagen alpha-1(I) chain	9.05	5.42	11.96	11.01	within
e213812	MIEQNTKSPLFMGKVVNPTQ	none	Alpha-1-antitrypsin	8.65	4.87	11.25	10.06	within
e018578	GADGQPGAKGEPGDAGAKGDAGPPGP*	2xOxidation [P12; P23]	Collagen alpha-1(I) chain	14.67	12.82	15.58	15.08	within
e213813	ESGPSGPAGPTGARGAPGDRGEPGP*	2xOxidation [P10; P17]	Collagen alpha-1(I) chain	14.58	12.19	15.59	15.09	within
e018583	GDPGFVGPEGLAGEGPPGLPGPP*	6xOxidation [P15; P17; P18; P21; P23; P24]	Collagen alpha-1(XVI) chain	12.63	9.66	13.89	13.2	within
e213817	GARGSAGPPGATGFPGAAGRVGP GP *	3xOxidation [P9; P15; P23]	Collagen alpha-1(I) chain	10.88	5.51	13.18	12.73	within
e104839	PGDFGPRGDQGDGAAGPPGP GP *	4xOxidation [P19; P21; P22; P24]	Collagen alpha-1(XXIII) chain	8.39	4.79	12.03	6.88	within
e018590	SGPGSGPGHSGSHPGPASGPGPDTGP	none	Sperm-associated antigen 8	12.55	9.2	13.98	13.44	within
e099802	GEVGPAGSPGSNGAPQGRGEPGPQG*	3xOxidation [P15; P21; P23]	Collagen alpha-1(III) chain	12.51	8.52	13.88	13.43	within
e213820	KGDAGAPGAPGGKGDAGAPGERGPPG*	4xOxidation [P7; P10; P19; P24]	Collagen alpha-1(III) chain	11.41	7.48	13.65	10.53	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e100236	EAGLEGPPGKTGPIGPQGAPGKPG*	6xOxidation [P7; P8; P13; P16; P20; P23]	Collagen alpha-1(V) chain	6.85	2.48	11.35	6.72	within
e018593	SPGAKGDGGIPGPAGPLGPPGPPGLP*	3xOxidation [P20; P22; P]	Collagen alpha-1(XI) chain	6.32	2.47	11.53	6.69	within
e213823	GGGSFGGGYGGGSSGGGSSGGGHGGGH GGS	none	Keratin, type I cytoskeletal 10	10.2	6.59	12.52	8.78	within
e018600	RGEDGPAGNGTEGFPFGYPGN*	1xOxidation [P18]	Collagen alpha-1(VI) chain	15.28	13.03	16.74	15.34	within
e213828	DAVPGQEGSDIEAGELNHQNGE	none	Zinc finger and SCAN domain-containing protein 32	10.22	6.49	12.37	8.68	within
e097818	GESGPAGPAGAPGPAGSRGAPGPQGP*	7xOxidation [P5; P8; P12; P14; P21; P23; P26]	Collagen alpha-1(III) chain	15.27	13.05	16.72	15.35	within
e018604	MPGSPGGPGSDGKPGPPGSQGESGR*	1xOxidation [P8]	Collagen alpha-1(III) chain	11.17	7.13	13.22	6.94	down
e213830	GMKGPSGVPGSAGPEGEPLGPPG*	4xOxidation [P5; P9; P14; P18]	Collagen alpha-5(IV) chain	14.5	10.89	16.06	15.35	within
e213832	DRGPAGPPGGPGDKGDPGEDGQPG*	5xOxidation [P4; P7; P8; P11; P17]	Collagen alpha-2(V) chain	13.8	10.57	15.65	12.79	within
e213833	GETGPQGPPGPTGPGGDKGDTGPPG*	5xOxidation [P8; P9; P11; P14; P23]	Collagen alpha-1(III) chain	13.23	9.97	15.43	11.29	within
e018610	ANGAPGNDGAKGDAGAPGAGSQGAPG*	3xOxidation [P17; P20; P26]	Collagen alpha-1(I) chain	12.04	7.94	13.76	11.78	within
e018612	GNPGAVGEKGEPGEAGEPLPGEgg*	3xOxidation [P3; P12; P18]	Collagen alpha-1(V) chain	13.71	10.46	15.54	11.32	within
e213835	QNGEPGGKGERGAPGEKGEggPPG*	3xOxidation [P14; P22; P]	Collagen alpha-1(III) chain	15.56	13.49	16.66	16.41	within
e213838	DGPPGHPGKEGPPGEKGGQGPpPG*	4xOxidation [P13; P21; P22; P24]	Collagen alpha-1(V) chain	15.56	13.36	16.65	16.41	within
e018623	GGGRGSGFGGGYGGGFGGGGFGGGGF GG	none	Keratin, type II cytoskeletal 1	11.5	7.69	13.51	10.65	within
e203796	GESGNKGEPGSAGPQGPPGPSGEEG*	2xOxidation [P9; P14]	Collagen alpha-2(I) chain	10.96	6.59	12.67	11.04	within
e018624	PGEGRAGEPGTAGPTGPPGVPGSPG*	7xOxidation [P1; P9; P14; P17; P18; P21; P24]	Collagen alpha-2(VIII) chain	10.91	6.64	12.64	11.17	within
e213839	PGQPGFEQEgQTRGAQGPAGPAGP*	3xOxidation [P18; P21; P24]	Collagen alpha-3(VI) chain	12.52	7.4	14.6	12.62	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213840	PGDPGTPGTTGRPGLSGEPGVQGP*	5xOxidation [P4; P7; P13; P19; P24]	Collagen alpha-1(XVI) chain	13.62	10.68	14.94	12.62	within
e018626	SAGPPGATGFPGAAGRVGPPGPSGNA*	4xOxidation [P5; P11; P19; P20]	Collagen alpha-1(I) chain	10.65	6.68	12.84	10.62	within
e213841	RDGAAGVKGDRGETGAVGAPGAPGP*	3xOxidation [P20; P23; P25]	Collagen alpha-1(II) chain	9.58	6.36	12.5	10.47	within
e018633	KGKWERPFVEKDTTEEDF	none	Alpha-1-antitrypsin	6.88	2.94	12.97	10.57	within
e018638	NSSNSWEEGSSGSSSDEEHGGG	none	REST corepressor 1	11.94	6.02	14.0	9.01	within
e102355	PSGPPGAGSPGERGAAGSGGPIGPPG*	2xOxidation [P5; P25]	Collagen alpha-2(XI) chain	8.41	4.75	11.45	7.34	within
e095311	TPPTVLDPNFP RYP*	1xO-Glycan [T1] (Hex(1)HexNAc(1) NeuAc(1))	Insulin-like growth factor 2	10.52	5.72	12.91	8.08	within
e097819	NAGPPGPPGAGKEGGKGPRGETGP*	2xOxidation [P7; P]	Collagen alpha-1(I) chain	7.76	2.73	11.31	7.03	within
e102059	GGAGEAGAAGEGGAAGEAGGAGEAGGVG EA	none	Paraneoplastic antigen Ma6E	12.2	8.09	15.06	11.25	within
e018652	QGAAGETGPMGERGHPGPPGPPGE*	2xOxidation [P19; P21]	Collagen alpha-2(XI) chain	9.47	4.3	11.9	7.24	within
e018654	SPGMAQKGYSESAWARSTTTR	none	Microtubule cross-linking factor 1	7.64	3.14	11.1	5.64	within
e208486	EGVEAQDAEGEAQPESEGIEAQ	none	Retinitis pigmentosa 1-like 1 protein	9.08	5.03	13.99	8.83	within
e018658	HGSGSGRSSSGQHGPGLGESSGFG	none	Hornerin	11.15	6.86	14.83	9.12	within
e203805	SHEKMHEGDEGPGHHHKPGLG	none	Protein S100-A9	6.75	2.45	10.8	12.12	up
e213845	PGAAALEGGTRRRVPVAAAEVPGA	none	Cystin-1	10.61	6.73	12.58	12.47	within
e018667	DQGDPEGEDGRNGSPGSSGPKGDR*	2xOxidation [P5; P14]	Collagen alpha-1(VII) chain	8.97	5.35	12.52	9.47	within
e213847	EGQPGEPPGPEKGEAGDEGNPGP*	1xOxidation [P24]	Collagen alpha-1(VI) chain	10.18	6.44	12.74	7.16	within
e213848	DPGPGPPGPRGPLGDPGPRGPP*	9xOxidation [P4; P7; P8; P10; P13; P17; P19; P22; P23]	Collagen alpha-1(VII) chain	11.68	7.29	13.89	12.28	within
e103938	QGLPGAPGDQGQRGPPGEAGPKGD*	2xOxidation [P4; P7]	Collagen alpha-1(IX) chain	11.69	7.12	13.92	12.48	within
e203812	AGEPKGGPGTGSGGGGAGTGGGAGGPGA SH	none	SKI family transcriptional corepressor 1	12.91	6.79	15.36	9.55	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018689	ADGQPGAKGEPGDAGAKGDAGPPGPA*	2xOxidation [P11; P22]	Collagen alpha-1(I) chain	13.67	11.08	15.49	14.15	within
e018691	PAGKSGDRGESGPAGPAGAPGPAGSR*	1xOxidation [P1]	Collagen alpha-1(III) chain	5.74	2.55	10.32	6.63	within
e018693	GPAGIMGPPGLQGPTGPPGDPGDR*	5xOxidation [P2; P8; P9; P14; P17]	Collagen alpha-1(XI) chain	14.2	10.57	15.62	15.29	within
e100365	SMEVDSGAAYELKSYTESPTN	none	Atos homolog protein A	9.24	5.03	11.21	7.02	within
e213854	GADGQPGAKGEPGDAGAKGDAGPPGP*	3xOxidation [P6; P12; P23]	Collagen alpha-1(I) chain	14.0	11.72	14.98	15.23	up
e018703	PRGQDGAKGDRGEDGEPGQPGSP*	1xOxidation [P1]	Collagen alpha-2(XI) chain	11.24	6.84	13.43	11.17	within
e213855	ETKEDKSTATESTKEEPQLE	none	Zinc finger homeobox protein 4	11.03	6.81	12.91	11.06	within
e300156	AAGAPGPQGFQGPAGEPGEPGQTGP*	3xOxidation [P7; P17; P25]	Collagen alpha-2(I) chain	9.8	4.71	12.57	12.71	up
e018705	QMLVPHGLLGPGPIANGFPPGGPG	none	Serine/threonine-protein phosphatase 1 regulatory subunit 10	8.85	5.8	11.45	12.03	up
e100195	EPGPAGSKGESGNKGEPGSAGPQGP*	2xOxidation [P22; P25]	Collagen alpha-2(I) chain	11.98	8.3	13.59	11.7	within
e213858	GLPGRDGSPGGKGDRGENGSPGAPG*	2xOxidation [P3; P9]	Collagen alpha-1(III) chain	8.86	4.74	11.54	9.02	within
e018712	GGSGGGGAVAAASGAAPGSLQALSVL	none	Integral membrane protein GPR137C	8.69	5.85	11.28	11.37	up
e018716	GQDGVGGDKGEDGDPGQPGPPGPGSG*	3xOxidation [P20; P]	Collagen alpha-1(XI) chain	12.86	8.11	15.31	10.89	within
e208491	DQGEPPGQGLPGFSGPPGKEGEP*	3xOxidation [P11; P16; P17]	Collagen alpha-2(IX) chain	10.68	7.22	12.86	12.62	within
e018721	FFLPDEGLQLHLENELTHD	none	Alpha-1-antitrypsin	9.82	6.3	12.59	11.43	within
e213862	ANGAPGNDGAKGDAGAPGAPGSQGAPG*	4xOxidation [P5; P17; P20; P26]	Collagen alpha-1(I) chain	16.1	14.22	17.21	16.62	within
e018726	GPPGESGREGAPGAEGSPGRDGSPG*	3xOxidation [P2; P3; P12]	Collagen alpha-1(I) chain	16.1	14.23	17.21	16.62	within
e018727	ASSGSSSTRSRSSSTSSSGSSTSTG	none	RNA-binding protein with serine-rich domain 1	5.76	3.27	9.42	7.46	within
e104598	QNGEPGKGGERGAPGEKGEGLPPG*	4xOxidation [P5; P14; P22; P23]	Collagen alpha-1(III) chain	12.79	8.97	14.43	14.3	within
e203837	GPAGFPGAPGQNGEPGGKGERGAPG*	4xOxidation [P6; P9; P15; P24]	Collagen alpha-1(III) chain	10.71	6.42	13.22	11.12	within
e213863	PGPQGGPPGKNGETGPQGPPGPTGPG*	3xOxidation [P7; P15; P18]	Collagen alpha-1(III) chain	12.74	9.16	14.37	14.46	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018737	GSQGEPPGLPGPPGLSIGDGDQ*	5xOxidation [P6; P9; P12; P14; P15]	Collagen alpha-2(IV) chain	13.41	9.62	14.96	9.96	within
e203839	HSGYHSHHTTPQGRSDASHGQ	none	Filaggrin	13.26	9.02	15.0	7.66	down
e018738	GFQGPAGEPEPGQTGPAGARGPAG*	4xOxidation [P9; P12; P17; P23]	Collagen alpha-2(I) chain	11.57	8.38	13.51	12.13	within
e018739	REAFSELDMTSEVLQITMSP	none	Cell cycle checkpoint protein RAD1	5.98	3.08	11.16	8.34	within
e099118	GADGQPGAKGEPGDAGAKGDAGPPGP*	1xCation:Na [D20]; 2xOxidation [P12; P23]; 1xCation:Na [C-Term]	Collagen alpha-1(I) chain	11.52	7.17	13.39	10.97	within
e213868	HPGSPSPGYQGPPGEPGQAGPSGP*	1xOxidation [P]	Collagen alpha-1(III) chain	11.34	7.2	13.31	10.96	within
e102408	QSKHPGDFGADAQGAMNKALEL	none	Myoglobin	8.91	5.36	11.63	9.68	within
e208493	EAGGNATAGGGPPGSSDSESSPGAPS	none	Proline-rich protein 12	14.52	10.43	16.9	10.8	within
e018759	PMGPPGPPGPRGPQGPNGADGPQG*	6xOxidation [P7; P8; P10; P13; P16; P22]	Collagen alpha-1(XI) chain	8.75	4.1	11.67	7.79	within
e018764	PGEPGPPGDDGFPGERGDKGTPG*	6xOxidation [P1; P4; P6; P7; P13; P22]	Collagen alpha-4(IV) chain	13.32	9.29	15.35	11.16	within
e018767	DPGSPGSPGAPAGPPGYGPQGEPPG*	2xOxidation [P10; P13]	Collagen alpha-3(IV) chain	7.62	3.51	11.55	6.11	within
e099006	QNGEPGKGGERGAPGEKGEPPG*	1xCation:Na [C-Term]; 3xOxidation [P5; P14; P22]	Collagen alpha-1(III) chain	10.74	5.51	13.1	6.47	within
e100097	EPGDSPGFLSGAAEGEDGDGPDVD	none	Zinc finger and BTB domain-containing protein 7A	11.84	7.93	14.24	9.49	within
e018774	GSNGNPGPPGSPGKDGPPGPAGN*	4xOxidation [P15; P20; P21; P23]	Collagen alpha-1(III) chain	10.23	5.68	13.81	8.79	within
e208496	PSGPPGKGLPGEPGPQGPQGPIG*	7xOxidation [P1; P4; P5; P11; P14; P16; P19]	Collagen alpha-1(XXVII) chain	10.91	5.71	13.1	11.42	within
e018783	RTGDAGVPVPPGPPGPPGPPSAG*	3xOxidation [P13; P14; P]	Collagen alpha-1(I) chain	10.79	6.19	13.06	11.81	within
e018787	AADDTWEPFASGKTSESSELHG	none	Transthyretin	9.42	5.21	11.84	8.33	within
e018793	DAAQKTDTSHHDQDHPTFNK	none	Alpha-1-antitrypsin	8.01	3.94	11.83	10.02	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e018794	ADGQPGAKGEPGDAGAKGDAGPPGPA*	3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	15.03	12.69	16.4	15.92	within
e018796	SAGPQGPPGPSGEEGKRGNGEAGS*	1xOxidation [P]	Collagen alpha-2(I) chain	9.61	4.9	12.57	12.06	within
e018798	AAHLPAEFTPAVHASLDKFLAS	none	Hemoglobin subunit alpha	9.96	4.12	15.11	10.86	within
e203866	MADEAGSEADHEGTHSTKRGA	none	Fibrinogen alpha chain	5.84	3.05	10.44	7.22	within
e104069	DGSPGAKGDRGETGPAGPPGAPGAPG*	4xOxidation [P18; P19; P22; P25]	Collagen alpha-1(I) chain	13.16	10.43	14.48	14.31	within
e018802	AVPTPEESASAAVAVPTPEESASP	none	Microtubule-actin cross-linking factor 1, isoforms 6/7	8.21	4.71	11.16	10.97	within
e018805	SRQSSYGQHGSGSSQSSGYGQY	none	Filaggrin-2	8.2	3.83	11.21	3.19	down
e018806	DGAKGDAGPAGPKGEPGSPGENGAPG*	3xOxidation [P16; P19; P25]	Collagen alpha-1(I) chain	10.99	5.92	12.6	12.15	within
e213878	VSGIDGSPGEKGDGPDVGGPGPPGAS*	2xOxidation [P14; P]	Collagen alpha-3(V) chain	11.17	6.47	12.75	12.17	within
e018807	ATGFSHVLQFMYGTIELSM	none	Kelch-like protein 15	7.67	3.52	11.03	10.84	within
e018825	SPGPDGKTGPPGPAGQDGRPGPPGP*	3xOxidation [P22; P23; P]	Collagen alpha-1(I) chain	9.64	5.88	12.22	11.14	within
e102775	GPDGPKGSPGSPGTPGDTGPPGLQG*	7xOxidation [P2; P5; P9; P11; P15; P20; P21]	Collagen alpha-2(V) chain	10.87	6.1	13.46	11.46	within
e099025	ADGQPGAKGEPGDAGAKGDAGPPGPA*	1xCation:Na [D19]; 2xOxidation [P11; P22]	Collagen alpha-1(I) chain	10.38	6.16	13.26	9.53	within
e101322	PPGPPGPPGVPGSDGIDGNGPPGK*	4xOxidation [P2; P4; P5; P8]	Collagen alpha-2(IX) chain	11.97	7.61	13.67	12.85	within
e018834	PGQPGFEGEQGTRGAQGPAGPAGP*	5xOxidation [P1; P4; P18; P21; P24]	Collagen alpha-3(VI) chain	10.59	6.15	12.46	11.57	within
e203880	FRGETGPQGPRGQPGPPGPPGAPG*	2xOxidation [P14; P16]	Collagen alpha-1(XXIV) chain	8.34	4.09	14.34	8.6	within
e018839	QGAAGLKGSPGSPGNTGLPGFPGFP*	2xOxidation [P10; P13]	Collagen alpha-3(IV) chain	5.95	3.09	10.9	12.31	up
e208504	QGDSGPQGPPGSEGFTGPPGPQGP*	6xOxidation [P9; P10; P18; P19; P21; P24]	Collagen alpha-2(IV) chain	12.3	7.81	14.25	10.86	within
e018843	GPSEGGSSSTMYVSGPPGPPGPPGP*	3xOxidation [P19; P20; P]	Collagen alpha-1(XVII) chain	12.31	7.97	14.27	11.23	within
e018847	GSPGSPGYQGPPGEPGQAGPSGPPGP*	1xOxidation [P26]	Collagen alpha-1(III) chain	11.73	8.15	13.69	10.82	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e097831	PGEMGRPGPPGPPGAGNPGSPN*	7xOxidation [P7; P9; P10; P12; P13; P15; P19]	Collagen alpha-1(XXVI) chain	10.1	5.53	12.62	6.45	within
e208508	DDAGAGGEDAGAGREDAGAGGEDVGAG	none	Golgin subfamily A member 6-like protein 2	12.3	6.28	15.63	11.08	within
e018869	STDPAGADEGSGPDRPTEDMGQD	none	FYVE, RhoGEF and PH domain-containing protein 5	12.86	7.47	15.39	8.13	within
e213892	PAGPPGGPGDKGDPGEDGQPGPDGP*	5xOxidation [P1; P4; P5; P8; P14]	Collagen alpha-2(V) chain	12.63	8.53	15.2	10.64	within
e208509	GPPGESGREGAPGAEGSPGRDGSPPG*	1xCation:Na [D21]; 3xOxidation [P2; P3; P12]	Collagen alpha-1(I) chain	12.68	8.81	15.19	10.67	within
e018886	AQGVPGPPGFQGEPPQGEPGPPG*	6xOxidation [P8; P14; P16; P20; P22; P23]	Collagen alpha-2(VIII) chain	6.84	3.06	10.56	10.0	within
e018887	DEAGSEADHEGTHSTKRGHAKS	none	Fibrinogen alpha chain	9.48	5.63	12.27	12.85	up
e102324	GGILPTSQAGANPDVQDGLPAGGAG	none	Amelotin	10.82	6.13	13.47	9.02	within
e018891	GANGAPGNDGAKGDAGAPGAPGSQGAPG*	2xOxidation [P6; P18]	Collagen alpha-1(I) chain	8.57	5.08	11.94	7.12	within
e018895	PGQDGIDGEAGPPGLPGPPGPKGAPG*	1xOxidation [P25]	Collagen alpha-3(IX) chain	10.79	6.48	12.94	11.55	within
e018902	ADGQPGAKGEPGDAGAKGDAGPPGPA*	4xOxidation [P5; P11; P22; P23]	Collagen alpha-1(I) chain	11.85	8.72	13.29	12.78	within
e213899	KGRAGMPGGPGKSGSMGPVGPAG*	3xOxidation [P21; P22; P24]	Collagen alpha-1(XVI) chain	8.08	4.99	10.94	7.99	within
e203909	IQRTPKIQVYSRHPAENGKS	none	Beta-2-microglobulin	6.87	1.91	11.36	6.0	within
e018906	GDPTSSEPSSSDAASGDATSGDAPSG	none	Activating transcription factor 7-interacting protein 1	7.93	3.62	11.45	5.73	within
e213900	PAGPAGSPGEDGDKGEIGEPGQKGS*	1xOxidation [P]	Collagen alpha-1(XI) chain	10.53	6.35	12.7	12.16	within
e203914	QIDPTIQRVRAEEREQIKT	none	Keratin, type II cytoskeletal 6A	8.15	4.45	13.88	11.18	within
e018917	GEAEAEAEADSGVPVGGERPAGE	none	Calmodulin-regulated spectrin-associated protein 3	10.7	6.14	12.47	11.17	within
e104518	DGAKGDAGPAGPKGEPGSPGENGAPG*	4xOxidation [P12; P16; P19; P25]	Collagen alpha-1(I) chain	10.73	6.51	12.61	9.3	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e203915	TPSSQALTETPTSSDWQSTDAT	none	Glycogen synthase kinase-3 alpha	10.11	6.08	12.14	10.89	within
e018919	DHDRGPLLGPSSLQQSPIHGV	none	Uncharacterized protein KIAA1614	9.12	5.39	12.14	9.9	within
e208511	PVQKVEIGQKRASEDTTSGSPP	none	Apoptosis inhibitor 5	9.11	5.56	12.1	9.66	within
e018920	GPAGPAGPPGPIGNVGAPGAKGARGSAG*	1xOxidation [P]	Collagen alpha-1(I) chain	6.5	1.65	11.67	9.2	within
e018921	LREGETKAVKTVRTPGAAANLE	none	Alpha-1B-glycoprotein	8.37	2.53	14.6	10.22	within
e203916	ALKDAKNKLEGLDALQKAKQ	none	Keratin, type II cytoskeletal 6C	7.49	2.41	12.8	9.64	within
e213902	LTVGGAQASGTLIGVGQSVTAVGRI	none	Major facilitator superfamily domain-containing protein 9	7.47	3.58	12.33	10.27	within
e102560	EAGIPGVPGAKGEDGKDGSPGEPGA*	4xOxidation [P5; P8; P20; P23]	Collagen alpha-1(III) chain	8.08	3.46	11.7	9.01	within
e018932	SPGPDGKTGPPGPAGQDGRPGPPGP*	4xOxidation [P10; P20; P22; P23]	Collagen alpha-1(I) chain	10.18	5.97	12.95	9.74	within
e018934	QLNSLSGDITILGGLDYEDSGF	none	Protocadherin gamma-A4	7.3	4.35	11.32	5.83	within
e213905	PNDYQSSRNQPPGPPGPPPGS*	7xOxidation [P1; P11; P13; P14; P16; P17; P19]	Collagen alpha-1(XII) chain	13.09	10.19	14.98	11.28	within
e018937	GPPGSNGNPGPSGSPGKDGPPGP*	5xOxidation [P11; P12; P14; P]	Collagen alpha-1(III) chain	12.89	9.84	14.51	13.52	within
e099120	ADGQPGAKGEPGDAGAKGDAGPPGPA*	1xCation:Na [D19]; 3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	13.06	10.03	15.02	11.28	within
e106494	EGVGEFSSPGQEQLSGQAQPPEG	none	General transcription factor 3C polypeptide 1	12.76	8.43	14.33	13.52	within
e102381	DGEPGTPGNPGPPGPPGPPGLG*	9xOxidation [P7; P10; P12; P13; P15; P16; P18; P19; P21]	Collagen alpha-1(II) chain	12.53	7.4	14.64	10.2	within
e102880	PPGPPGPPGTSGHPGSPGSPGYQGP*	5xOxidation [P2; P4; P5; P7; P8]	Collagen alpha-1(III) chain	11.52	5.06	14.81	10.2	within
e103396	RGPDGYPGGEAGSPGERGDQGGKGD	none	Collagen alpha-2(VI) chain	11.31	7.12	13.39	12.16	within
e018942	VNDNEEGFFSARGHRPLDKK	none	Fibrinogen beta chain	7.42	2.96	11.53	8.55	within
e018947	APGPQGFQGNPGEPEGVSGPMG*	6xOxidation [P2; P4; P11; P14; P17; P22]	Collagen alpha-1(II) chain	12.85	9.26	14.58	10.72	within
e018948	DGSPGGKGDRENGSPGAPGAPGHPG*	2xOxidation [P22; P25]	Collagen alpha-1(III) chain	11.11	7.2	12.82	12.62	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213906	PTSPPNEEFGPGVPAETDITET*	2xOxidation [P5; P11]	Collagen alpha-1(XI) chain	10.62	6.08	12.83	7.95	within
e018953	YGGIFGGGSFGGGSFGGGSFGGGFGGG	none	Keratin, type I cytoskeletal 10	10.64	5.58	13.01	8.91	within
e203948	GQQGMFGQKGDEGARGFPGP*	3xOxidation [P18; P20; P21]	Collagen alpha-1(XI) chain	7.4	3.4	10.47	7.71	within
e097838	AGPPGEAGKPGEQGVPGDLGAPGPG*	4xOxidation [P4; P10; P16; P22]	Collagen alpha-1(I) chain	11.74	7.2	13.74	12.33	within
e213910	GKGEGQPPGPPGFQGLPGSPGAGE*	3xOxidation [P10; P11; P17]	Collagen alpha-2(I) chain	11.55	7.36	13.69	12.25	within
e018977	SWSTGSGPESSQTLPPDSTATDI	none	Collagen alpha-1(VII) chain	9.11	4.79	11.73	10.33	within
e018980	ERGSESPGHPGQPGPPGPPGAPG*	3xOxidation [P17; P]	Collagen alpha-1(III) chain	8.69	4.77	11.87	9.76	within
e018981	KNGDDGEAGKPRPGERGPPGPQ*	3xOxidation [P11; P14; P19]	Collagen alpha-1(I) chain	10.78	6.88	12.95	12.71	within
e018988	EEKESEDEESEEPDSTTGTPP	none	Lysine-specific demethylase 6B	10.86	6.4	13.4	8.1	within
e018989	SMGHPGMPGGMGTGEPGPQGP*	3xOxidation [P17; P19; P22]	Collagen alpha-1(XXVII) chain	11.1	6.36	13.55	9.09	within
e018990	PAGPGAPEAAAGTEASSEEVGIAEAGP	none	Eukaryotic translation initiation factor 3 subunit B	8.01	4.01	10.32	10.68	up
e018991	PGDPGIPGHKHTGLMGPQGLPGE*	1xOxidation [P22]	Collagen alpha-1(XXII) chain	9.83	5.93	12.07	11.54	within
e018992	DKKREEAPSLRPAPPPISGGGY	none	Fibrinogen beta chain	9.59	5.13	12.89	10.88	within
e101077	PGDFGDRGPAGLDGSPGLVGGTGPPG*	1xOxidation [P25]	Collagen alpha-1(XXIV) chain	10.21	6.27	12.43	11.0	within
e018995	PSLLLLDYDGSVLPFLGGLGGGY	none	Solute carrier family 22 member 23	9.25	5.97	12.47	10.09	within
e019000	GQNGEPGKGGERGAPGEKGEKGPPG*	3xOxidation [P6; P15; P23]	Collagen alpha-1(III) chain	11.78	8.38	13.44	13.14	within
e019003	QGPPGSVGSVGGVGEKGEPEAGNPG*	3xOxidation [P3; P4; P19]	Collagen alpha-1(XI) chain	11.07	6.38	12.81	12.62	within
e019008	SLTAEYDEDSPGGDFDFFSNL	none	Epimerase family protein SDR39U1	9.17	5.14	12.58	6.67	within
e019009	GAVAGMPGGSAGAMNSMTAAGVTAMGT	none	Hepatocyte nuclear factor 3-alpha	11.05	6.95	12.77	9.69	within
e019025	GRYGSGGSKGGSISGGGYGSGGGKHS	none	Keratin, type II cytoskeletal 2 epidermal	9.08	4.66	12.0	8.29	within
e203967	DRGETGPAGPPGAPGAPGAPGVPAG*	4xOxidation [P11; P14; P17; P20]	Collagen alpha-1(I) chain	8.69	4.62	11.94	8.2	within
e019036	IDTKSYWKALGISPFHEHAE	none	Transthyretin	7.11	4.18	11.95	11.15	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019043	GGEAAGAGEADVGAGGEDAGSGAEDVGP	none	Golgin subfamily A member 6-like protein 2	8.25	4.08	11.61	3.34	down
e213922	QLPSINPSASSGNETTFSGGGGPAP	none	Lysine-specific demethylase 3B	10.08	6.37	11.89	10.39	within
e213923	GEKGIPGFPGPRGDPGSYGSPGFP	none	Collagen alpha-4(IV) chain	9.33	6.22	11.62	9.77	within
e105789	PDEGKLQHLENELTHDIITK	none	Alpha-1-antitrypsin	7.57	3.31	14.95	9.52	within
e208529	PESLSPEDVGNASTENSMDMPAPS	none	Apoptosis-stimulating of p53 protein 2	12.65	8.01	15.0	9.16	within
e019053	PKGNMGPPQGEPGPPGQQGNPGPQG*	3xOxidation [P11; P13; P14]	Collagen alpha-1(XI) chain	9.13	5.2	11.9	10.46	within
e100496	LKNGERIEKVEHSDLSFSKD	none	Beta-2-microglobulin	5.34	2.31	14.37	8.0	within
e213926	ALSALSDLHAHKLRVDPVNFK	none	Hemoglobin subunit alpha	5.07	1.27	14.61	7.8	within
e019058	PGEDGKPGDTGPQGFGTPGDVGP*	6xOxidation [P1; P7; P12; P16; P19; P24]	Collagen alpha-1(XVIII) chain	12.39	8.69	14.39	10.11	within
e019060	YVNGFTHQSSMTTTRTPDTST	none	Mucin-16	7.13	3.61	11.46	4.07	within
e019062	KGAAGEEGSPGPVGPGRGDPGAPGLPG*	3xOxidation [P12; P15; P19]	Collagen alpha-1(XXII) chain	6.11	3.49	11.75	10.1	within
e100495	EHMMESVLISDSPNSEGDAGDL	none	Trafficking protein particle complex subunit 12	15.77	10.81	17.34	17.58	up
e019077	TGGPPGENGKPGEPGPKGDPAGAPGAP*	4xOxidation [P4; P14; P16; P23]	Collagen alpha-1(III) chain	11.12	6.91	12.93	11.5	within
e213929	PVSSKSSLDVLP SQVYSLVGSSP	none	Homeodomain-interacting protein kinase 1	7.57	2.59	12.67	9.05	within
e019084	GADGQPGAKGEPGDAGAKGDAGPPGPA*	2xOxidation [P12; P23]	Collagen alpha-1(I) chain	10.24	5.95	11.98	11.36	within
e101365	PGPPGHPGPPGEPGTDGAAGKEGPPG*	3xOxidation [P3; P10; P25]	Collagen alpha-1(XVI) chain	10.8	6.9	12.6	11.74	within
e019088	VTAAHLPAEFTPAVHASLDKF	none	Hemoglobin subunit alpha	7.71	1.62	14.37	5.2	within
e103890	GPPGDPGSPGSPGAPGAGPPGYGPQ*	7xOxidation [P3; P6; P9; P12; P14; P17; P20]	Collagen alpha-3(IV) chain	10.94	6.43	13.23	10.15	within
e019099	ERGSESPGHPGQPGPPGPPGAPGP*	4xOxidation [P16; P17; P]	Collagen alpha-1(III) chain	10.71	4.85	12.9	11.62	within
e106427	ERGSESPGHPGQPGPPGPPGAPGP*	4xOxidation [P11; P16; P20; P23]	Collagen alpha-1(III) chain	10.85	5.7	12.7	11.54	within
e019101	LAAPPGHQLHRAHYDLRHTF	none	Alpha-2-HS-glycoprotein	6.2	0.36	10.83	9.57	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099567	GDPGPPGEPGAGQDGPBGDKGDDG*	6xOxidation [P5; P6; P9; P11; P17; P18]	Collagen alpha-1(V) chain	11.05	5.66	13.52	8.51	within
e103193	LSDPEQGVETGQYEREKAGF	none	Inter-alpha-trypsin inhibitor heavy chain H4	8.54	4.74	13.49	5.89	within
e019115	VGMGQKDSYVGDEAQSKRGILT	none	Actin, cytoplasmic 1	9.45	4.85	13.8	10.39	within
e019117	IADLTEQIAENGKTIHELEKS	none	Myosin-3	8.39	4.47	12.5	11.01	within
e019118	GSMGHPGMPGGMGTPGEPGPQGPPG*	6xOxidation [P9; P15; P18; P20; P23; P24]	Collagen alpha-1(XXVII) chain	9.57	4.8	12.32	6.92	within
e213937	GANGAPGNDGAKGDAGAPGAGSQGAPG*	4xOxidation [P6; P18; P21; P27]	Collagen alpha-1(I) chain	12.74	9.08	14.51	13.7	within
e103562	PGDPGVSGIDGSPGEKGDGPDVGGPG*	4xOxidation [P1; P4; P13; P19]	Collagen alpha-3(V) chain	12.3	8.63	14.05	13.16	within
e106073	EGPMGQRGREGPMGRGEAGPPG*	4xOxidation [P3; M4; P15; P22]	Collagen alpha-1(XVII) chain	10.13	5.45	12.37	11.83	within
e019131	PSGDPGKPLTGPGQPQLPGTPGR*	1xOxidation [P1]	Collagen alpha-1(XVII) chain	8.55	4.94	12.18	7.68	within
e019134	EAIKAMSSKGPSASAALSPPLGSSP	none	F-box only protein 42	8.79	3.34	13.02	11.19	within
e019148	WDDDQELDEEEDPIWFDF	none	Protein ARM CX6	10.16	4.65	13.88	3.93	down
e099564	TAPGSPEPPSELLEDGQDTPTSA*	3xOxidation [P3; P6; P8]	Collagen alpha-1(XVIII) chain	10.55	6.35	13.16	7.86	within
e019169	QQQDGAAGPPGPPGPPGARGPPGDTG*	5xOxidation [P13; P15; P16; P21; P]	Collagen alpha-1(XXIII) chain	10.38	5.48	12.86	9.02	within
e019170	EKGEGGPPGVAGPPGGSGPAGPPGPQG*	5xOxidation [P13; P14; P19; P22; P23]	Collagen alpha-1(III) chain	10.36	6.24	12.59	9.14	within
e204016	GLPGSPGEPGKQGAPGASGDRGPPGP*	3xOxidation [P5; P9; P15]	Collagen alpha-1(II) chain	9.44	5.79	12.01	8.4	within
e019179	FESFGDLSTPDVAMGNPKVKAH	none	Hemoglobin subunit beta	7.64	2.97	12.71	6.93	within
e019181	QPGLYGPPGLHGFPAGPGQEGLG*	3xOxidation [P7; P8; P14]	Collagen alpha-2(IV) chain	7.75	3.36	11.04	8.73	within
e213956	PGEMGPKGPPGAVGEPGLGEAGMK*	2xOxidation [P1; P6]	Collagen alpha-1(XXVII) chain	8.52	4.12	11.47	9.21	within
e213957	KGELGPPGLGKEGPAGLRGFGP*	4xOxidation [P7; P9; P15; P22]	Collagen alpha-3(V) chain	8.82	5.13	13.05	8.22	within
e019195	GADGQPGAKGEPGDAGAKGDAGPPGPA*	3xOxidation [P6; P12; P23]	Collagen alpha-1(I) chain	10.78	6.79	12.64	12.3	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019198	LGPKPALPAGTEDTAKEDAANRK	none	Gelsolin	7.77	3.4	12.18	9.48	within
e019204	EGPQGEPGPQGSKGDKGEMGSPGAP	none	Complement C1q tumor necrosis factor-related protein 6	10.42	6.39	12.3	11.37	within
e019205	AGTSPGSSAASSVTSASSSLSSSPSP	none	E3 ubiquitin-protein ligase COP1	7.57	3.96	11.5	6.98	within
e106164	VSGIDGSPGEKGDVGGPGPPGASG*	2xOxidation [P22; P]	Collagen alpha-3(V) chain	9.96	5.87	11.93	11.34	within
e099562	ERGSESPGHPGQPGPPGPPGAPG*	5xOxidation [P11; P14; P16; P17; P19]	Collagen alpha-1(III) chain	12.2	9.01	13.84	12.63	within
e019221	KDLQNFLKKENKNEKVIEWH	none	Protein S100-A9	8.59	3.86	12.35	11.48	within
e019227	HKSEVAHRFKDLGEENFKAL	none	Albumin	7.06	3.05	11.91	8.45	within
e213964	KGNSGEPGAPGSKGDTGAKGEPGPVG*	3xOxidation [P7; P10; P22]	Collagen alpha-1(I) chain	12.99	9.86	14.78	13.96	within
e019231	PGQDGIDGEGPPGLPGPPGPKGAPG*	4xOxidation [P13; P16; P18; P19]	Collagen alpha-3(IX) chain	6.97	3.65	10.85	8.91	within
e213965	GPDVGAAGDAPAPAPNKDGDAGVGS GH	none	Diacylglycerol O-acyltransferase 1	10.8	6.76	12.61	11.55	within
e213966	AGEKGRAGMPGGPGKSGSMGPVGP PG*	4xOxidation [P10; P13; P21; P24]	Collagen alpha-1(XVI) chain	10.74	6.94	12.58	11.55	within
e019249	APGPRGPQGPTGSEGTPLPGGVGQP*	2xOxidation [P2; P4]	Collagen alpha-3(V) chain	10.52	6.64	12.48	11.36	within
e019250	DAHKSEVAHRFKDLGEENFK	none	Albumin	9.97	3.35	14.98	10.63	within
e099750	SPGFKGEAGSPGAPGQDGTGRGEPGI*	2xOxidation [P11; P14]	Collagen alpha-1(XXI) chain	8.08	4.89	11.15	7.7	within
e019262	GEDVGAGGEDAGAGGEDAGAGGEDAGPG G	none	Golgin subfamily A member 6-like protein 2	9.27	4.47	12.66	6.39	within
e101043	PPGFPGQPGSHGRDGHAGEKGDPG*	3xOxidation [P5; P8; P23]	Collagen alpha-4(IV) chain	10.07	5.94	12.76	10.38	within
e208550	QQQDGAAGPPGPPGPPGARGPPGDTG*	6xOxidation [P12; P13; P15; P16; P21; P22]	Collagen alpha-1(XXIII) chain	10.38	6.05	12.52	11.04	within
e019278	GGGTGAVGGGTSQASAGAATGATGASG GGGP	none	Biorientation of chromosomes in cell division protein 1	9.91	5.03	12.52	11.05	within
e213976	MPGERGEAGHRGSAGALGPQGPPGA*	3xOxidation [P2; P19; P22]	Collagen alpha-3(IX) chain	10.81	6.68	12.9	11.62	within
e019291	KNGDDGEAGKPGRPGERGPPGPQG*	2xOxidation [P19; P]	Collagen alpha-1(I) chain	10.82	6.77	12.87	11.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e213977	KGDRGFPGEMGPIGPPGPQGPPGE*	2xOxidation [P18; P21]	Collagen alpha-1(X) chain	9.77	5.77	11.76	11.6	within
e019304	ENGLPGPPGPQGPPGYGKMATGPM	none	Collagen alpha-1(XVI) chain	7.17	2.36	11.35	4.69	within
e204087	DIGPGGGYGAAAEAGMYAGNGGLLGAD	none	Collagen alpha-1(XVII) chain	9.38	5.45	11.57	9.87	within
e101059	EPGPPGPSGLPGESYGSEKGAPGDP*	2xOxidation [P11; P22]	Collagen alpha-3(IV) chain	11.22	4.47	13.86	8.44	within
e019330	ERGSESPGHPGQPGPPGPPGAGP*	6xOxidation [P8; P11; P14; P16; P17; P19]	Collagen alpha-1(III) chain	11.6	7.0	13.51	12.78	within
e019331	LSSLTETIEGVDAEDGHGPGEQQ	none	Complement factor B	9.75	4.92	12.93	10.61	within
e213985	PAGPPGPVGPAGGPGFPGAPGAKGEAGP*	3xOxidation [P17; P20; P28]	Collagen alpha-1(II) chain	6.32	3.53	11.44	7.07	within
e019334	GEPGPAGSKGESGNKGEPGSAGPQGP*	4xOxidation [P5; P18; P23; P26]	Collagen alpha-2(I) chain	10.34	6.29	12.92	12.11	within
e101015	PPGSNGNPGPPGPSGSPGKDGPPEGAG*	4xOxidation [P2; P8; P10; P17]	Collagen alpha-1(III) chain	8.43	4.03	11.86	8.88	within
e103455	NSETQSGQDSVGTDSQEDSGQ	none	Target of Myb1 membrane trafficking protein	13.34	7.39	16.09	12.81	within
e019351	GQAGEKGRAGMPGGPGKSGSMGPVGP*	3xOxidation [P12; P15; P23]	Collagen alpha-1(XVI) chain	10.25	6.33	12.52	12.31	within
e204094	QGLPGPSGEKGETGDVGPMPGPPGPPG	none	Collagen alpha-2(XI) chain	7.19	4.75	10.31	9.37	within
e100237	PGYPGRQGLAGPEGNPGPKGAQGF*	4xOxidation [P1; P4; P12; P16]	Collagen alpha-1(XXIV) chain	9.73	5.29	12.41	11.41	within
e019361	VQGPEGKLGPLGAPGEDGRPGPPGS*	3xOxidation [P14; P20; P22]	Collagen alpha-2(V) chain	8.32	5.08	11.94	7.71	within
e019367	PTGPKGEAGHPGPPGPPGPPGEVIQ*	3xOxidation [P13; P14; P16]	Collagen alpha-1(V) chain	7.02	1.49	12.01	9.69	within
e019381	PGGKGFPGLGPPGKAGPVGPPGLGF*	4xOxidation [P1; P7; P9; P12]	Collagen alpha-4(IV) chain	10.84	4.95	14.6	13.31	within
e019396	IIGPRGPPGQPGTRGFGFPGPIG*	3xOxidation [P7; P8; P]	Collagen alpha-1(XIII) chain	9.67	5.01	14.57	13.16	within
e019398	PTLEMFLSRILASWTNSAIQV	none	tRNA (32-2'-O)-methyltransferase regulator THADA	9.91	5.23	14.21	13.15	within
e099855	SWEEGSSGSSSDEEHGGGGMRVGP	none	REST corepressor 1	10.99	5.6	13.7	6.79	within
e019403	KNGDDGEAGKPGRPGERPPGPQG*	3xOxidation [P14; P19; P]	Collagen alpha-1(I) chain	13.94	11.21	15.48	15.25	within
e019405	ADRSRPTSAPAITQGQVAEGGV	none	Protein 4.1	6.88	4.25	12.07	8.97	within
e213998	KGDRGFPGEMGPIGPPGPQGPPGE*	3xOxidation [P16; P18; P21]	Collagen alpha-1(X) chain	12.45	9.53	13.91	13.33	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019421	NGSPGQPGTPGSKGSKGEPGIQGMPPG	none	Collagen alpha-1(XI) chain	6.99	4.12	11.18	7.6	within
e019420	PGVKGATGPVGPPGASVSGPPGRDQG*	5xOxidation [P1; P9; P12; P13; P20]	Collagen alpha-1(XVI) chain	7.1	3.88	12.69	10.43	within
e019422	DPGSYLVTVTASNISAANDSALV	none	Polycystin-1	12.04	8.45	13.7	13.37	within
e019426	SGPLSHSASFSSPMGSTEDLNSKG	none	Signal-induced proliferation-associated 1-like protein 1	9.21	4.79	12.1	10.63	within
e019429	AGPKGETGPHGYKGMVGAIGATGPPG*	1xOxidation [P]	Collagen alpha-2(IX) chain	7.24	4.12	11.83	9.33	within
e019430	AGVTGSTVLSAGVTATTGQSVGTGTT	none	Mucin-19	8.16	3.75	12.33	7.92	within
e097868	LSNNAKEAVEHLQKSELTQQL	none	Apolipoprotein A-IV	8.32	3.96	11.78	8.01	within
e095415	SVGSVGGVGEKGEPGEAGNPGPPGEAG*	2xOxidation [P14; P20]	Collagen alpha-1(XI) chain	10.36	6.01	12.7	12.48	within
e019433	LSTATDGLAATPFMSLESTRPSQ	none	Otogelin	7.65	4.02	13.71	8.43	within
e019435	RDFVSAGAAAGVSAAFGAPVGGVLFS	none	H(+)/Cl(-) exchange transporter 7	7.37	3.77	12.23	4.6	within
e214001	ENVSDVAPTQPWWPNTPGDSVS	none	Gamma-tubulin complex component 6	8.52	5.13	11.55	10.37	within
e204107	GPAGPRGERGPQNSGEKGDQGFQ	none	Collagen alpha-1(XVI) chain	7.67	3.42	12.15	7.94	within
e102901	GPAGPPKGAGEDGHPGKPRPGERG*	3xOxidation [P5; P18; P21]	Collagen alpha-2(I) chain	5.89	3.05	10.81	9.02	within
e095419	GAPGAEGSPGRDGSPGAKGDRGETGP*	3xOxidation [P3; P9; P15]	Collagen alpha-1(I) chain	8.2	3.89	11.0	9.27	within
e214004	PPGSNGNPGPPGSPGSPGKDGPMPAG*	5xOxidation [P10; P11; P13; P17; P22]	Collagen alpha-1(III) chain	12.72	8.83	14.57	12.54	within
e106469	PGSNGNPGPPGSPGSPGKDGPMPAGN*	4xOxidation [P7; P9; P10; P12]	Collagen alpha-1(III) chain	11.83	7.34	13.35	10.72	within
e019461	IFFKGTWTQPFDLASTREEN	none	Corticosteroid-binding globulin	6.82	3.93	11.55	8.7	within
e019464	NDESNEHSDVIDSQELSKVSR	none	Osteopontin	7.7	3.46	10.5	7.33	within
e204119	QGLPGPSGEKGETGDVGPMPGPPGPPG*	1xOxidation [P25]	Collagen alpha-2(XI) chain	6.21	3.36	10.49	7.66	within
e019465	ASSPGSGSSSGSNSGGGAGSGSVHPAGT AG	none	Syntaxin-binding protein 5-like	8.6	4.76	10.79	11.29	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019466	PGTPGSPGPAGASGNPGTDGIPGAKGSAG	none	Collagen alpha-1(II) chain	6.56	2.76	11.4	5.28	within
e019467	GQPLPGPSGQPGLYGPPGLHGFP*	3xOxidation [P12; P17; P18]	Collagen alpha-2(IV) chain	7.41	4.58	12.56	5.88	within
e214006	TKGLPGAPGIAGPPGPPGFGKPLPG*	6xOxidation [P13; P14; P16; P17; P22; P25]	Collagen alpha-1(X) chain	8.94	5.67	12.0	9.31	within
e019476	MIEQNTKSPLFMGKVVNPTQK	none	Alpha-1-antitrypsin	10.17	3.97	15.21	13.02	within
e019481	LGDSNSHSLKKDPVVPQGTAPLM	none	Testis-expressed protein 13C	7.04	3.41	9.94	8.9	within
e100155	TGVPGPAGLPGPKEGKGYPGIGAP*	3xOxidation [P6; P10; P]	Collagen alpha-6(IV) chain	9.73	5.53	14.02	8.85	within
e019501	PMPPSMGTSTSHQPATPGGGTAQTP	none	Cadherin-related family member 5	9.75	4.07	13.25	8.04	within
e099967	PPGRDGEDGPTGPPGPPGPPGLG*	4xOxidation [P17; P19; P20; P22]	Collagen alpha-2(I) chain	6.89	3.66	11.41	9.35	within
e105339	KGEAGDEGNPGPDGAPGERGGPGER*	2xOxidation [P16; P22]	Collagen alpha-1(VI) chain	10.45	5.94	12.92	11.7	within
e214010	GVMVGSHADMAPASTAEGAGEKPGPA	none	Zinc finger protein 628	6.92	2.97	12.6	5.53	within
e214011	GAKGQEGAHGAPGAAGNPGAPGHVGAPG*	3xOxidation [P12; P18; P21]	Collagen alpha-1(XXII) chain	7.43	2.57	12.3	1.85	down
e100706	FFLPDEGKLQHLENELTHDI	none	Alpha-1-antitrypsin	8.44	0.65	12.46	6.49	within
e019515	QHPGKAPKLMIEVSNRPSGVS	none	Immunoglobulin lambda variable 2-14	5.98	1.96	11.86	5.01	within
e204134	GENGPTGAVGFAGPQGPDPGVKGE*	1xOxidation [P17]	Collagen alpha-2(V) chain	9.32	4.94	11.48	10.95	within
e019517	GPGFPGAPGAKGEAGPTGARGPEGAQG*	3xOxidation [P2; P5; P8]	Collagen alpha-1(II) chain	9.35	4.93	11.5	10.96	within
e100258	GPAGQKGEPGSDGIPGSAGEKGEPEGL*	3xOxidation [P2; P9; P15]	Collagen alpha-1(IV) chain	5.89	1.07	11.8	10.28	within
e019526	SSGAAGAAGGGAGAGTRPGDGGTASAGAAGPG	none	Protein CDV3 homolog	8.45	5.26	11.58	7.79	within
e214014	YSFFDASEDILTTFQINPFSG	none	Protocadherin beta-9	8.3	4.55	11.46	7.79	within
e019528	GPAGPPGKAGEDGHPGKPRPGERG*	4xOxidation [P5; P6; P15; P18]	Collagen alpha-2(I) chain	7.67	3.28	11.03	10.73	within
e214015	RWFQPVANAADAEAVRGAQDVAG	none	Insulin receptor substrate 4	6.7	2.14	12.45	8.05	within
e204139	YAMAKKDPEGLFLQDNIVAEF	none	Retinol-binding protein 4	7.6	4.25	13.29	6.85	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214016	VSGIDGSPGEKGDPGDVGGPGPPGASG*	5xOxidation [P8; P14; P20; P22; P23]	Collagen alpha-3(V) chain	9.03	4.62	11.92	4.79	within
e099123	WMGPNYGVQPPQGQNGSMLPNQ	none	Cytotoxic granule associated RNA binding protein TIA1	9.07	3.14	11.96	5.16	within
e019541	DDPRPPNPPKMPNPNPNHPSS	none	CD99 antigen	7.98	5.77	13.36	6.59	within
e019546	PPGDSGPPGEKGDPRGPPGPVGP*	8xOxidation [P2; P7; P8; P14; P17; P19; P20; P22]	Collagen alpha-1(VII) chain	8.46	4.73	11.51	10.06	within
e019551	DDILASPPRLPEPQYPYGAPHH	none	Collagen alpha-1(XVIII) chain	9.08	5.53	11.48	11.16	within
e019554	SYGGIFGGGSFGGGSFGGGSFGGGFGG G	none	Keratin, type I cytoskeletal 10	12.5	9.03	14.16	13.8	within
e095436	MIEQNTKSPLFMGKVVNPTQK*	1xOxidation [M12]	Alpha-1-antitrypsin	8.99	2.88	14.22	11.82	within
e019563	GSRGGSYGSGGSGGGYGGGSGSRG GSGG	none	Keratin, type I cytoskeletal 9	9.27	5.36	12.77	7.35	within
e214024	ADRLRAVLLDLALQGAGDAEAAVV	none	SAC3 domain-containing protein 1	7.85	3.27	13.18	3.79	within
e019588	PGTDVFMGPPGSPGEDGPAGEPPPG*	2xOxidation [P22; P24]	Collagen alpha-1(XV) chain	10.12	5.01	13.05	13.76	up
e019590	LDGAKGDAGPAGPKGEPGSPGENGAPG*	3xOxidation [P17; P20; P26]	Collagen alpha-1(I) chain	12.25	9.22	13.78	13.34	within
e019607	ERGPQGPPGPPGDDGMRGEDGEIG*	2xOxidation [P8; P10]	Collagen alpha-1(XI) chain	8.17	3.8	11.34	9.22	within
e214034	ENGKPGEPGPKGDAGAPGAPGGKGDAG*	4xOxidation [P5; P8; P10; P17]	Collagen alpha-1(III) chain	10.96	6.7	12.81	11.51	within
e214035	MPGERGGLGSPGPKGDKGEPGGPGAD*	2xOxidation [P20; P23]	Collagen alpha-1(III) chain	11.39	8.12	13.08	12.75	within
e214037	GGISGGGYGSGGGKHSSGGGSRGSSS GG	none	Keratin, type II cytoskeletal 2 epidermal	8.9	4.88	11.06	9.45	within
e019620	MTDGLHNMGGDPITVIDEIRDL	none	Complement factor B	8.04	4.13	10.46	9.37	within
e019628	RGGAGPPGPEGGKGAAGPPGPPGAAGTP G*	4xOxidation [P9; P18; P19; P21]	Collagen alpha-1(III) chain	10.57	6.59	12.61	9.8	within
e106124	DGSPGGKGDRENGSPGAPGAPGHPGP*	2xOxidation [P16; P19]	Collagen alpha-1(III) chain	8.96	4.78	11.65	10.82	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019638	NSQFGFSDQPSLNHVAEEHQG	none	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	9.53	4.97	11.85	11.65	within
e208565	GPAGPPGKAGEDGHPGKGRPGERG*	5xOxidation [P5; P6; P15; P18; P21]	Collagen alpha-2(I) chain	9.28	4.41	12.65	12.11	within
e019640	APGLRGTPGKDGERGEKGAAGEEGS*	2xOxidation [P2; P8]	Collagen alpha-1(XXII) chain	9.23	4.51	12.58	11.87	within
e214042	AMGPQGRPGPPGHVGP GPPGPGQPGPA*	3xOxidation [P16; P17; P19]	Collagen alpha-1(XVI) chain	7.05	3.31	11.45	8.53	within
e019646	ALHPEEDPEGRQGRLLGRWKA	none	Brevican core protein	8.46	3.89	12.22	8.44	within
e019647	YHSYDPYYSYSPYMHPGQVGAP	none	Zinc finger protein 608	8.88	2.5	11.78	11.23	within
e214045	GLPGTGGPPGENGKPGEPGPKGDAGAP*	3xOxidation [P9; P15; P18]	Collagen alpha-1(III) chain	8.01	2.71	11.32	11.16	within
e019657	GEKGESGQPGEPGPPGPKGTGDDGP*	1xOxidation [P]	Collagen alpha-2(XI) chain	9.23	5.23	11.86	11.49	within
e019665	TPGIGGFPGPSGNDGSAGPPGPPGSGVGP*	2xOxidation [P8; P10]	Collagen alpha-1(VII) chain	7.59	4.74	12.23	9.24	within
e097894	GQLQDELEKGERDNAELQEFA	none	ELKS/Rab6-interacting/CAST family member 1	7.33	3.15	11.63	7.15	within
e101531	TQQPQQDEMPSPTFLTQVKES	none	Apolipoprotein C-II	8.34	4.11	11.31	11.5	up
e019669	VGGGSSTIKYTTTSSSRKSYKH	none	Keratin, type II cytoskeletal 6B	7.4	3.67	13.21	11.65	within
e214048	AASGAGPGTQQGSPGWSQAGADGAAYT	none	Transcription factor GATA-4	8.46	4.46	11.46	10.59	within
e103168	MADEAGSEADHEGTHSTKRGHAK	none	Fibrinogen alpha chain	6.85	1.94	10.68	9.59	within
e019684	INGSPGGKGEMGPAGIPGAPGLMGARG*	1xOxidation [P17]	Collagen alpha-1(III) chain	5.26	0.14	10.2	7.03	within
e214052	IQRTPKIQVYSRHPAENGKSN	none	Beta-2-microglobulin	5.84	1.15	11.69	9.53	within
e214055	LDGAKGDAGPAGPKGEPGSPGENGAPG*	4xOxidation [P13; P17; P20; P26]	Collagen alpha-1(I) chain	11.23	7.79	13.08	12.65	within
e019696	LREGETKAVKTVRTPGAAANLEL	none	Alpha-1B-glycoprotein	9.07	2.04	15.87	7.18	within
e106805	GQDGGPPGDKGDDGEPGQTGSPGPTGE*	1xOxidation [P5]	Collagen alpha-1(V) chain	10.8	6.14	13.02	8.86	within
e214056	DPGDRGPIGLTGRAGPPGDSGPPGE*	6xOxidation [P2; P7; P16; P17; P22; P23]	Collagen alpha-1(VII) chain	11.2	8.04	13.4	12.09	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e097897	MPGERGGLGSPGPKGDKGEPGGPGAD*	3xOxidation [P13; P20; P23]	Collagen alpha-1(III) chain	11.81	7.46	13.49	13.56	up
e208568	GASEEPGHFSLTNAASTHTTNEGI	none	Basement membrane-specific heparan sulfate proteoglycan core protein	9.64	6.17	12.08	11.35	within
e019707	GEPGEPGVSGPMGPRGPPGPPGKPGD*	3xOxidation [P20; P21; P24]	Collagen alpha-1(II) chain	7.41	3.45	11.36	7.09	within
e019709	DAHKSEVAHRFKDLGEENFKA	none	Albumin	7.54	1.13	15.77	8.03	within
e101939	SGHPGSPGSPGYQGPPGEPGQAGPSGP*	1xOxidation [P16]	Collagen alpha-1(III) chain	7.64	3.88	11.54	8.09	within
e102817	QDGIPGPAQKGEPGQPGFGNPGPPG*	1xOxidation [P]	Collagen alpha-5(IV) chain	9.95	5.58	12.02	10.09	within
e214062	DGGARWSAGPAPGLEGGPRDPGSAP	none	Rab11 family-interacting protein 3	8.23	3.09	13.05	8.52	within
e099124	LDGAKGDAGPAGPKGEPGSPGENGAPG*	1xCation:Na [E22]; 3xOxidation [P17; P20; P26]	Collagen alpha-1(I) chain	9.6	5.21	11.59	9.09	within
e019718	PPGEDGAKGSVGPTGLPGDLGPPGDPG*	2xOxidation [P2; P13]	Collagen alpha-3(V) chain	8.9	4.99	11.39	8.35	within
e019720	AGPPGAPGAPGAPGVGPAGKSGDRGET*	3xOxidation [P7; P10; P]	Collagen alpha-1(I) chain	8.2	3.54	11.79	8.79	within
e019731	ADGQPGAKGEPGDAGAKGDAGPPGPAGP*	2xOxidation [P11; P22]	Collagen alpha-1(I) chain	12.11	9.25	13.74	13.08	within
e214068	GPAGIMGPPGLQGPTGPPGDPGDRGP*	5xOxidation [P2; P8; P9; P14; P17]	Collagen alpha-1(XI) chain	9.57	6.16	11.68	10.87	within
e099758	LPGPPGPSGDQGASGPAGPSGPRGPPG*	7xOxidation [P4; P5; P7; P16; P19; P22; P25]	Collagen alpha-1(II) chain	11.17	6.71	13.22	12.61	within
e214070	VEPPPMSLPGAGLSSQELSGGPGDGP	none	Transcription intermediary factor 1-beta	5.95	2.8	10.01	7.92	within
e019744	GMAALASLMGALLQAALSVFGMVGGP	none	Sodium-coupled monocarboxylate transporter 1	7.75	2.45	13.13	5.68	within
e101991	GSTGSWNSGSSGTGSTGNQNPGRPRP	none	Fibrinogen alpha chain	8.34	4.64	11.11	9.56	within
e019748	GEAGPQGDQGREGPVGPVPGDPGEAGP*	3xOxidation [P14; P18; P21]	Collagen alpha-1(VI) chain	8.93	3.64	12.77	9.14	within
e019765	GVVEITGKHEERQDEHGYISR	none	Heat shock protein beta-1	5.87	0.74	11.49	5.0	within
e019766	LRFDPVRGVPPRYPRDVRD	none	Hemopexin	6.18	2.69	12.15	7.43	within
e019769	LDGAKGDAGPAGPKGEPGSPGENGAPG*	5xOxidation [P10; P13; P17; P20; P26]	Collagen alpha-1(I) chain	9.32	4.98	11.55	11.51	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e095462	HQYSVKLGHPDTLNQGEFKEL	none	Protein S100-A9	6.81	0.28	11.6	8.24	within
e105334	MGPAGPTGPRGFPGPPGPDGLPGSMG*	5xOxidation [P3; P6; P9; P13; P15]	Collagen alpha-1(IV) chain	9.46	4.65	11.95	10.33	within
e019771	MPGGPGKSGSMGPPVGPPGPAGERGHPG*	1xOxidation [P26]	Collagen alpha-1(XVI) chain	7.12	3.98	10.6	7.12	within
e105210	TGFPGAAGRVPGPSGNAGPPGPPGPA*	3xOxidation [P13; P]	Collagen alpha-1(I) chain	6.42	2.54	9.43	10.14	up
e019773	GSSTPGGSGSSSGGAGSSNSGGGSGSG NMP	none	Cbp/p300-interacting transactivator 2	9.99	5.08	12.7	7.09	within
e204213	FQGEPPGQGEPPGDRGLKGDNG*	5xOxidation [P5; P7; P11; P13; P14]	Collagen alpha-2(VIII) chain	7.21	3.45	11.64	9.25	within
e214081	GPPGSNGNPGPSGSPGKDGPPGPAG*	5xOxidation [P11; P12; P14; P18; P23]	Collagen alpha-1(III) chain	12.92	9.49	14.68	13.65	within
e019777	MDSGDGVTHTVPIYEGYALPHAI	none	Actin, cytoplasmic 1	8.72	4.81	12.0	11.54	within
e019778	GRAGEPGTAGPTGPPGVGSPGITGPPG*	3xOxidation [P15; P18; P21]	Collagen alpha-2(VIII) chain	8.81	4.84	12.17	10.63	within
e101996	PKGSMGHPGMPGGMGTPGEPGPQGGP*	2xOxidation [P22; P]	Collagen alpha-1(XXVII) chain	11.49	7.05	13.13	11.95	within
e019782	PGIPGQPGLPGYPGSPGAPGGKGQPGD*	2xOxidation [P1; P4]	Collagen alpha-4(IV) chain	6.39	3.03	12.43	5.22	within
e214084	EDDEDGGEEAPAPGGAGKSEGSTPAD	none	SURP and G-patch domain-containing protein 2	9.66	5.93	12.2	9.84	within
e101833	SPGGPGAAGFPGARGLPGPPGSNGNPGP*	3xOxidation [P19; P20; P26]	Collagen alpha-1(III) chain	9.12	4.28	11.51	11.8	up
e214086	QKGEIGPMGIPGPQGPPGPHGLPGIG	none	Collagen alpha-1(VIII) chain	4.84	0.0	14.47	8.21	within
e099549	GPPGDPGFPGRYGETGDVGPPGPPG*	7xOxidation [P3; P6; P9; P20; P21; P23; P24]	Collagen alpha-4(IV) chain	10.47	5.6	12.32	10.42	within
e208576	ALSGEKGDQGGPDGSPGSPGAPAG*	2xOxidation [P21; P23]	Collagen alpha-3(IV) chain	10.24	5.89	12.36	10.57	within
e019796	AGMNPRTQNKDSLEDSVSTSPDP	none	GATOR1 complex protein DEPDC5	8.29	2.25	11.04	12.58	up
e104777	GLPGPPGEKGETGDVGQMGP GPPGPPG*	4xOxidation [P3; P6; P20; P24]	Collagen alpha-1(V) chain	9.78	5.9	12.37	8.07	within
e019807	ADGQPGAKGEPGDAGAKGDAGPPGPAGP*	3xOxidation [P5; P11; P22]	Collagen alpha-1(I) chain	11.81	8.99	13.3	12.46	within
e105896	RPSSMYFQTHDQIGMISAGPSH	none	Regulator of nonsense transcripts 1	10.69	5.9	13.03	11.9	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019816	EKGAPGDFGPRGDQGDGAAGPPGPP*	1xOxidation [P]	Collagen alpha-1(XXIII) chain	9.76	6.0	11.68	12.11	up
e019840	PGPPGPAGAAGPAGNPGADGQPGAKGANGA*	1xOxidation [P]	Collagen alpha-1(I) chain	5.6	0.0	11.77	9.64	within
e214095	VGMGQKDSYVGDEAQSKRGILT	none	Actin, gamma-enteric smooth muscle	9.2	4.18	12.5	11.14	within
e019843	GREIDLGLAGDHQQLILYRLG	none	Adhesion G-protein coupled receptor G4	8.97	5.47	11.49	10.39	within
e099126	ADGQPGAKGEPGDAGAKGDAGPPGPAGP*	1xCation:Na [D19]; 2xOxidation [P11; P22]	Collagen alpha-1(I) chain	9.53	5.37	12.33	6.78	within
e019847	VAMGASNTSMAMQAAALGSSIGTAVVG	none	Ammonium transporter Rh type A	7.88	4.13	11.41	8.22	within
e019851	HKSEVAHRFKDLGEENFKALV	none	Albumin	6.88	1.02	12.86	6.69	within
e019853	GDPGPAGLPGSQGAPGTPGPVGAPGDAGQ*	1xOxidation [P18]	Collagen alpha-2(V) chain	7.58	4.15	11.46	7.98	within
e106755	PGADGGRGMPGEPGAKGDRGFDGLPG*	2xOxidation [P13; P25]	Collagen alpha-1(XI) chain	8.11	2.55	11.7	9.23	within
e019868	GERGYPGNIGPVGAAGAPGHPVGPA*	3xOxidation [P20; P23; P]	Collagen alpha-2(I) chain	7.83	2.4	11.86	9.16	within
e214099	GPPGPPGRDGEDGPTGPPGPPGPPGPP*	3xOxidation [P21; P23; P24]	Collagen alpha-2(I) chain	8.24	4.54	11.41	8.64	within
e100172	PAGERGEQGPAGSPGFQGLPGPAGPPG*	1xOxidation [P14]	Collagen alpha-1(I) chain	8.59	4.88	11.57	7.03	within
e102061	GPAGPPGEKGEPGDDGPSGAEGPPGPQ*	3xOxidation [P2; P5; P23]	Collagen alpha-1(II) chain	10.06	6.1	12.31	8.25	within
e019874	SHEKMHEGDEGPGHHHKPGLGEG	none	Protein S100-A9	7.58	2.71	12.72	12.6	within
e019875	ANDESNEHSDVIDSQELSKVSR	none	Osteopontin	6.86	3.04	11.1	8.42	within
e019876	MVFQALAQYQKDAPDHQELNL	none	Complement C3	6.46	4.1	10.86	8.39	within
e214102	TSGRITEEFLGKYLSTTPFPSQ	none	Versican core protein	9.21	4.7	11.43	11.17	within
e097904	LPGPPGFGRPGDPGPPGPPGPPGPP*	12xOxidation [P4; P5; P10; P13; P15; P16; P18; P19; P21; P22; P24; P25]	Collagen alpha-1(XV) chain	9.33	4.95	11.79	7.35	within
e100775	PPGKNGDDGEAGKPRPGERGPPGP*	4xOxidation [P2; P14; P17; P22]	Collagen alpha-1(I) chain	8.3	3.7	11.27	10.33	within
e204254	TWASHEKMHEGDEGPGHHHKPG	none	Protein S100-A9	6.88	2.69	11.27	11.27	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214107	DPGVSGIDGSPGEKGDPGDVGGPGPPGA*	1xOxidation [P]	Collagen alpha-3(V) chain	10.07	6.21	12.28	8.71	within
e214108	GQEGAHGAPGAAGNPGAPGHVGAPGPSG P*	2xOxidation [P15; P18]	Collagen alpha-1(XXII) chain	9.21	5.36	11.71	10.9	within
e019891	SSDLARPNAGRSGRDTSSTEVGSGP	none	Uncharacterized protein C4orf54	9.41	5.27	11.9	11.39	within
e214110	EGLKLVDKFLEDVKKLYHSEA	none	Alpha-1-antitrypsin	6.75	3.42	9.45	9.8	up
e019895	GTDPPEGPYDYTYGYGDDYRE*	2xOxidation [P5; P8]	Collagen alpha-2(XI) chain	7.87	4.01	11.85	8.8	within
e019897	VGEPGAKGAMGPAGPDGHQGPRGEQG*	3xOxidation [P12; P15; P21]	Collagen alpha-1(XVII) chain	7.61	4.47	12.77	9.69	within
e104409	QSETSSSPAFTQSSSESVGSDNIM	none	A-kinase anchor protein 6	9.13	4.27	11.98	5.34	within
e019914	TQISSNMPSSPDSSSDSSTGSPGNH	none	Ubiquitin carboxyl-terminal hydrolase 9X	7.99	3.11	10.91	10.61	within
e019919	PPGEAGVGGPKGERGEKGEAGPPGAAG*	5xOxidation [P1; P2; P10; P22; P23]	Collagen alpha-1(XI) chain	5.49	2.22	12.37	6.73	within
e019922	RDGPPGPKGAPGERGSLGPPGPGLGG*	2xOxidation [P20; P22]	Collagen alpha-3(IX) chain	6.37	0.53	11.64	2.43	within
e019945	PGTGGPPGENGKPGEPGPKG DAGAPGAP*	3xOxidation [P18; P25; P28]	Collagen alpha-1(III) chain	9.85	5.69	12.2	10.84	within
e019950	GADGQPGAKGEPGDAGAKGDAGPPGPAG P*	1xOxidation [P]	Collagen alpha-1(I) chain	6.91	3.05	10.14	5.66	within
e019951	VQGEPPPPGRGVQGPQGEPGAPGLPG*	5xOxidation [P7; P8; P15; P19; P22]	Collagen alpha-1(XVI) chain	11.27	7.12	13.56	9.66	within
e019955	VRKDLQNFLKKENKNEKVIE	none	Protein S100-A9	8.01	1.95	12.21	10.69	within
e019957	PPGADGQPGAKGEPGDAGAKGDAGPPGP*	3xOxidation [P8; P14; P25]	Collagen alpha-1(I) chain	10.12	6.49	12.33	10.83	within
e019958	DGLPGAPGDKGESPPGVPGPRGEPGA*	3xOxidation [P7; P15; P16]	Collagen alpha-2(VIII) chain	11.19	7.55	12.98	10.64	within
e019961	EDDDDEDDDEAEDNDEDEDD	none	Transcription termination factor 4, mitochondrial	9.49	5.29	12.72	9.61	within
e019967	GRDGNPGNDGPPGRDGQPGHKGER*	3xOxidation [P11; P12; P]	Collagen alpha-2(I) chain	8.39	4.43	11.23	10.29	within
e214126	DVAGGSNPGAHNPSANLARGDNQAGGA	none	Insulin receptor substrate 4	8.52	4.4	11.07	9.47	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e019972	LAATTEKTEPNSQEDKNDGGKSR	none	LIM and calponin homology domains-containing protein 1	6.6	1.34	12.21	9.95	within
e100548	TWASHEKMHEGDEGPGHHHKPG*	1xOxidation [M8]	Protein S100-A9	8.78	4.27	11.63	10.68	within
e105732	LPDTGSKDGYKLPTWDTPSGR	none	Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D	9.02	4.73	11.68	12.92	up
e019981	PDEGKLQHLENELTHDIITKF	none	Alpha-1-antitrypsin	8.2	3.46	14.35	7.08	within
e019987	PGAPGPKGKGESGTRGPKSGKDRG*	1xOxidation [P1]	Collagen alpha-1(XV) chain	5.64	2.0	10.51	7.13	within
e300108	NKTPIR*	1xN-Glycan [N1] (HexNAc(4)Hex(4) NeuAc(1))	Titin	13.39	7.96	15.34	15.48	up
e214130	SPGPVGFPDGPDPGPPGPGAGQDGP*	9xOxidation [P2; P4; P8; P11; P13; P14; P17; P19; P25]	Collagen alpha-1(V) chain	10.37	5.27	12.89	9.45	within
e214132	PTPHNADGAPVQPSQVEYTADSTV	none	Splicing factor, suppressor of white-apricot homolog	7.76	4.28	12.53	11.47	within
e100028	SLGSGPGGRGGTRAGAGTEARAGPGAAG AG	none	Transcriptional repressor scratch 1	8.67	5.37	11.58	9.31	within
e020002	GAQGPPGATGFPGAAGRVGPPGSNGNPG*	5xOxidation [P6; P12; P20; P21; P27]	Collagen alpha-1(II) chain	9.61	5.08	12.67	9.45	within
e214133	PKGETGDLGPMGVPGRDGVPGGPGET*	3xOxidation [P10; P14; P20]	Collagen alpha-3(VI) chain	9.28	4.03	12.57	11.69	within
e214134	QANGSAPAADKEEPAAGSGAASPSAAE	none	Myristoylated alanine-rich C-kinase substrate	7.68	3.11	11.94	10.58	within
e020007	MPGEKGEKGTGLPGPQGIPGGVGSP*	4xOxidation [P2; P14; P16; P20]	Collagen alpha-1(XIV) chain	7.61	3.48	12.14	10.61	within
e020008	PGLMGPPGPPGLPGPKGNMGLNFQG*	6xOxidation [P6; P7; P9; P10; P13; P15]	Collagen alpha-5(IV) chain	10.34	6.71	12.44	11.4	within
e214135	PGAPGQEGPLGLPGIPGREGLPGDRG*	2xOxidation [P16; P22]	Collagen alpha-2(IV) chain	6.56	1.96	11.66	11.27	within
e101946	VSGGEGKGGSDGGGSHRKEGEEADAPG	none	CD99 antigen	6.3	2.83	12.35	9.0	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020014	QGVRGEPGPPGAGAAGPAGNPGADGQP*	3xOxidation [P7; P9; P10]	Collagen alpha-1(I) chain	11.72	7.58	13.39	12.94	within
e214139	GERGAPGEKGEggPPGVAGPPGGSGPAGP*	2xOxidation [P]	Collagen alpha-1(III) chain	12.23	8.99	13.66	11.78	within
e103972	NEGLDGRGDPGQPGPPGEQGPGR*	3xOxidation [P17; P22; P]	Collagen alpha-3(IV) chain	9.36	5.22	13.94	9.76	within
e020037	GADGQPGAKGEPGDAGAKGDAGPPGPAGP*	2xOxidation [P12; P23]	Collagen alpha-1(I) chain	10.54	6.66	12.43	11.88	within
e020038	APGERGETGPPGPAGFAGPPGADGQPGA*	1xOxidation [P]	Collagen alpha-1(II) chain	10.35	6.65	12.31	11.64	within
e020047	PPGADGQPGAKGEPGDAGAKGDAGPPGP*	4xOxidation [P2; P8; P14; P25]	Collagen alpha-1(I) chain	11.27	7.47	13.06	12.44	within
e214144	RGNDGATGAAGPPGPTGPAGPPGFPGAVG*	2xOxidation [P12; P13]	Collagen alpha-1(I) chain	8.93	5.19	12.02	5.39	within
e214146	PGVKGDLGLPLPGAPGVVGFPQTGP*	3xOxidation [P1; P10; P13]	Collagen alpha-1(VII) chain	9.14	1.84	15.01	12.65	within
e214148	IPGPPGIPGFDGAPGQKGEMGPAGPTG*	2xOxidation [P2; P4]	Collagen alpha-1(IV) chain	9.23	5.09	12.5	7.87	within
e102691	KNGERIEKVEHSDLFSKDW	none	Beta-2-microglobulin	7.17	2.87	11.31	8.22	within
e020065	DDILASPPRLPEPQYPGAPHHS	none	Collagen alpha-1(XVIII) chain	9.7	5.47	12.32	11.64	within
e020073	GVPPSAPLQGAVPPTSSVPPVAGAPSVG	none	Clathrin coat assembly protein AP180	6.28	0.16	9.69	5.16	within
e214151	VREDRGRRVHRFQSPAGTEAL	none	Alpha-1B-glycoprotein	5.36	0.0	13.22	9.46	within
e097920	LSSLTETIEGVDAEDGHGPGEQK	none	Complement factor B	7.73	4.4	11.73	10.16	within
e100558	PPGESGREGAPGAEGSPGRDGSPPGAKG*	4xOxidation [P2; P11; P17; P23]	Collagen alpha-1(I) chain	8.04	3.33	10.8	8.85	within
e020088	NTGAPGSPGVSGPKGDAGQPGEKGSPGA*	4xOxidation [P8; P13; P20; P26]	Collagen alpha-1(III) chain	7.29	4.03	11.28	9.1	within
e214152	ISSKSGSLGGGFSSGGFSGGSFSRGSSG	none	Keratin, type I cytoskeletal 10	8.03	3.31	10.77	8.77	within
e020103	GPPGKNGDDGEAGKPGRPGERPPGP*	3xOxidation [P3; P15; P18]	Collagen alpha-1(I) chain	9.47	5.25	11.87	11.65	within
e102865	PVGDDLFWQATIMGPPDSAYQG	none	Ubiquitin-conjugating enzyme E2 D1	9.45	5.47	12.72	10.73	within
e214155	SRHGEGGHYHYDTTPDIVEYLG	none	Ester hydrolase C11orf54	10.03	5.37	12.57	10.42	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e095494	LMIEQNTKSPLFMGKVVNPTQK	none	Alpha-1-antitrypsin	10.15	3.02	15.3	13.14	within
e020118	GADGQPGAKGEPGDAGAKGDAGPPGPAGP*	3xOxidation [P12; P23; P]	Collagen alpha-1(I) chain	9.84	5.82	12.27	10.93	within
e101891	GPQGPPGPSGEEGKRGPNGEAGSAGPP*	4xOxidation [P5; P6; P8; P17]	Collagen alpha-2(I) chain	9.29	5.16	11.62	11.69	up
e020128	PSITGVPGPAGLPKPKGEKGYPGIGIG*	2xOxidation [P7; P]	Collagen alpha-6(IV) chain	8.17	2.7	13.34	11.3	within
e020132	ERGSPGPAGPKGSPGEAGRPGEAGLPG*	4xOxidation [P10; P14; P20; P26]	Collagen alpha-1(I) chain	7.0	1.3	10.47	5.85	within
e204313	GEPGPRGERGEAGIPGVPAKGEDGK*	2xOxidation [P3; P18]	Collagen alpha-1(III) chain	5.14	0.22	11.65	9.52	within
e020133	SVGGGSSTIKYTTTTSSSRKSYKH	none	Keratin, type II cytoskeletal 6A	6.13	0.44	11.54	9.88	within
e020136	LMPPMPGPGPGPGPGPGPGPGPGH S	none	RNA-binding protein 27	8.22	4.02	11.56	10.22	within
e020140	SQAVSRSTEVKV/VSPAPTAQPRDP	none	Papilin	6.88	4.24	11.89	7.03	within
e214163	TPGSPGPAGASGNPGTDGIPGAKGSAGAPG*	3xOxidation [P7; P14; P20]	Collagen alpha-1(II) chain	10.01	5.18	12.37	11.88	within
e106350	TSHVDSOSSSHSRQETPPSAAAAP	none	Sprouty-related, EVH1 domain-containing protein 3	10.6	6.73	12.52	11.82	within
e214170	QDGLPGLPGPKGEPGGITFKGERGP*	3xOxidation [P10; P14; P25]	Collagen alpha-5(IV) chain	7.0	4.68	12.25	7.16	within
e020161	SDKPDMAEIEKFDKSKLKKTE*	1xAcetylation [N-Term]	Thymosin beta-4	6.7	3.51	12.14	8.05	within
e204317	RKDLQNFLKKENKNEKVIEH	none	Protein S100-A9	7.81	3.28	11.96	11.54	within
e102660	GPPGADGQPGAKGEPGDAGAKGDAGPPGP P*	2xOxidation [P3; P27]	Collagen alpha-1(I) chain	7.14	3.43	10.25	9.04	within
e020185	TSGFGQHRPGSGQSSGFGQYGS GSGQ	none	Filaggrin-2	6.63	4.61	9.72	5.97	within
e204327	GPPGPPGRDGEDGPTGPPGPPGPPGPPG*	3xOxidation [P3; P23; P27]	Collagen alpha-2(I) chain	7.34	3.49	10.52	7.87	within
e020191	GERGRTGPAGAAGARGNDGQPGPAGPPG *	2xOxidation [P8; P21]	Collagen alpha-1(II) chain	8.96	4.67	11.45	11.75	up
e208580	DISDSVQQFRVYMTAQGDPE*	1xOxidation [P21]	Collagen alpha-1(XIV) chain	10.36	5.91	12.2	11.84	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020197	TDTSHHDQDHPTFNKITPNLAE	none	Alpha-1-antitrypsin	9.88	4.87	12.12	11.75	within
e020198	FESFDLSSPDVAMGNPKVKAHGK	none	Hemoglobin subunit delta	8.16	2.4	11.63	8.85	within
e020199	GAKGEPGVRGPPGPSGRGVGTQGPKG*	4xOxidation [P12; P14; P17; P25]	Collagen alpha-1(XXVIII) chain	5.39	0.58	10.05	8.22	within
e020204	EAGRDGNPGNDGPPGRDGGPGHKGE*	3xOxidation [P13; P14; P]	Collagen alpha-2(I) chain	9.6	5.42	11.8	9.63	within
e020206	QNATPSPAAFINNNTAANGSSAGSAW	none	Cytoplasmic polyadenylation element-binding protein 4	7.07	4.37	11.85	11.14	within
e020208	WRNKFDPSLTQRDSFHLDEQ	none	Alpha-2-antiplasmin	8.91	4.96	11.89	9.72	within
e020209	GPPGKPGQDGIDGEGPPGLPGPPGPKG*	1xOxidation [P]	Collagen alpha-3(IX) chain	6.75	3.23	12.2	11.06	within
e020211	DRRPSRQTPRETPEAAEGRRPG	none	Putative transmembrane protein INAFM1	6.43	2.39	10.3	10.69	up
e020225	LEALKENGGARLAEYHAKATEHL	none	Apolipoprotein A-I	6.09	2.88	10.86	7.59	within
e214185	AGLHGPPGKPGALGPQQGPGLPGPPGPP*	1xOxidation [P]	Collagen alpha-1(VIII) chain	6.24	3.54	11.04	9.54	within
e020243	DQAESEGLVLRLVRDTPPPVTS	none	B-cell acute lymphoblastic leukemia-expressed protein	5.91	0.78	14.46	8.72	within
e101149	QGFQGNPGEPEGVSGPMGRGPPG*	4xOxidation [P10; P13; P18; P25]	Collagen alpha-1(II) chain	8.42	4.48	13.04	9.14	within
e105591	ERGTPGIGGFPGPSGNDGSAGPPGPPGS*	3xOxidation [P22; P23; P25]	Collagen alpha-1(VII) chain	7.51	3.52	10.32	10.45	up
e020252	HGSSSGLSSSYGQHSGSHQSSGHGR	none	Hornerin	6.82	2.69	9.95	10.13	up
e106471	GPPGPSGDQGASGPAGPSGPRGPPGPVG P*	4xOxidation [P3; P17; P20; P23]	Collagen alpha-1(II) chain	7.82	3.99	11.11	8.61	within
e020254	MTDGLHNMGGDPITVIDEIRDLL	none	Complement factor B	9.42	5.88	12.76	11.42	within
e020258	AHKSEVAHRFKDLGEENFKALV	none	Albumin	7.3	1.81	12.05	9.41	within
e214187	LRGGAGPPGPEGGKAAGPPGPPGAAGT PG*	4xOxidation [P10; P19; P20; P22]	Collagen alpha-1(III) chain	12.24	8.5	14.14	11.52	within
e020271	GFRGSQGMPPGMPGLKGQPLPGPSGQ*	2xOxidation [P21; P23]	Collagen alpha-2(IV) chain	7.39	3.5	10.59	9.91	within
e214191	STEATTSIGGSASTRGGIATEATGSTR	none	Mucin-19	11.47	6.47	13.35	9.84	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e100088	IDTKSYWKALGISPFHEHAEVV	none	Transthyretin	7.97	3.22	14.72	10.27	within
e204361	GPPGAPGAPGAPGPGVGPAGKSGDRGETG P*	4xOxidation [P2; P6; P9; P12]	Collagen alpha-1(I) chain	9.54	5.24	12.45	9.84	within
e214194	GAPGERGETGPPGPAGFAGPPGADGQPG A	none	Collagen alpha-1(II) chain	5.92	0.44	11.45	5.42	within
e020287	IFFKGKWERPFVKDTEED	none	Alpha-1-antitrypsin	7.83	3.28	12.79	10.01	within
e020293	ASHEKMHEGDEGPGHHHKPLGEG	none	Protein S100-A9	6.99	1.89	12.16	11.88	within
e214195	GPPGADGQPGAKGEPGDAGAKGDAGPPG P*	3xOxidation [P9; P15; P26]	Collagen alpha-1(I) chain	11.11	5.68	12.81	12.04	within
e208586	QGPPGEPGRPGSPGAPGEQGPPTPGF*	3xOxidation [P10; P13; P]	Collagen alpha-1(XIV) chain	11.05	5.2	12.68	12.08	within
e020297	APGAVGAPGPAGATGDRGEAGAAGPAGP AGP*	3xOxidation [P2; P8; P10]	Collagen alpha-2(I) chain	11.13	5.73	12.83	12.15	within
e020300	EQGEAGQKGDAGAPGPQGSPGAPGPQGP *	2xOxidation [P25; P28]	Collagen alpha-1(II) chain	9.47	4.92	11.63	9.2	within
e020302	PGEAGPRGELSVSTPVPGLPPGPPGPP*	8xOxidation [P1; P6; P15; P17; P19; P20; P22; P23]	Collagen alpha-3(IV) chain	9.22	5.28	11.45	9.24	within
e020304	GRDGNPGNDGPPGRDQPGHKGERG*	3xOxidation [P11; P12; P]	Collagen alpha-2(I) chain	6.93	2.69	10.0	10.1	up
e020311	GRAGSDGARGMPGQTGPKGDRGFDGL*	1xOxidation [P17]	Collagen alpha-1(V) chain	7.7	3.79	10.48	10.65	up
e097939	SVPSPGQPGSPSVSKKKHGSSKPTDG	none	Protein piccolo	7.79	3.62	13.53	12.55	within
e020318	EPGEPGQKGDAGSPGPQGLAGSPGPHGP	none	Collagen alpha-2(V) chain	6.08	0.07	13.01	7.41	within
e099841	LQSTEFSETPSPDSVNSVEGHS	none	1-phosphatidylinositol 3-phosphate 5-kinase	8.77	3.87	10.98	11.18	up
e020335	QGIDGEPGVPQGPGAPPPGHPSHPGP*	3xOxidation [P7; P10; P13]	Collagen alpha-2(V) chain	9.64	5.64	12.28	11.09	within
e020336	VQGPMPAGEEGKRGARGEPTGLPG*	1xOxidation [P]	Collagen alpha-1(I) chain	8.66	3.08	14.42	10.02	within
e020343	PTGDDGPKGNPGVPFGDPGPPGEGGP*	1xOxidation [P]	Collagen alpha-2(XI) chain	8.08	4.19	11.53	8.26	within
e020342	KNGETGPQGPPTGPGDKGDTGPPGP*	1xOxidation [P28]	Collagen alpha-1(III) chain	10.53	6.72	12.39	11.3	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214204	ENGVVGPTGPVGAAGPAGPNGPPGPAGS R*	3xOxidation [P10; P16; P]	Collagen alpha-2(I) chain	10.48	6.18	12.32	11.14	within
e020345	ITSDMVKEGAAVIDVGINYVHDPV	none	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase 2, mitochondrial	7.17	0.0	12.4	5.35	within
e105020	STKSMMSVQNSGTQQQGNLFFQQG	none	Nuclear factor of activated T-cells 5	6.48	3.41	10.24	7.99	within
e020359	GPTGPAGPPGPGAVGAKGEAGPQGPRG S*	1xOxidation [P12]	Collagen alpha-1(I) chain	5.87	3.32	14.11	4.42	within
e020361	DASPNEEKGDVPKDTLDDLPNE	none	Kinesin light chain 2	7.18	3.7	11.57	11.51	within
e100961	GPPGVTGMDGQPGPKGNVGPQGEPGPP*	4xOxidation [P3; P12; P14; P26]	Collagen alpha-1(V) chain	7.88	4.4	11.39	10.79	within
e020366	GSLANTAPHGSSPTPGVGSLLGGPGGTQA	none	Zinc finger protein 469	7.46	3.65	12.8	6.34	within
e020369	ASHEKMHEGDEGPGHHHKPGLGEG*	1xOxidation [M6]	Protein S100-A9	6.57	2.17	11.87	9.93	within
e214208	GPPGADGQPGAKGEPGDAGAKGDAGPPG P*	4xOxidation [P3; P9; P15; P26]	Collagen alpha-1(I) chain	10.88	7.13	12.69	12.59	within
e214209	ATEAQTQTPTATEAQTTPLAAMEAL	none	P-selectin glycoprotein ligand 1	6.05	1.07	11.49	8.81	within
e020380	HPESMLFEMNGYLDSAIYNDS	none	Putative C->U-editing enzyme APOBEC-4	10.33	5.89	12.53	11.57	within
e105632	SETPGPSPAGPTRDEPAESPSETPGP	none	Opioid growth factor receptor	7.75	4.13	11.31	8.39	within
e204402	GPGGSASGPGGTGGGKASVGAMGGGVGA SSSGGG	none	Glycogen synthase kinase-3 alpha	10.5	6.32	12.45	11.62	within
e214210	WSPSLPASSDHSTPASQSPHSSNPS	none	Nonsense-mediated mRNA decay factor SMG7	8.49	4.69	11.89	10.29	within
e105005	DGLPGRDGSPGGKGDRGENGSPGAPGAP *	1xOxidation [P22]	Collagen alpha-1(III) chain	7.3	3.66	10.96	7.11	within
e020386	NAIPMNKANSGEASLEEDLFLTSP	none	Capping protein-inhibiting regulator of actin dynamics	7.0	1.46	12.09	8.88	within
e020389	SEGLKLVDKFLEDVKKLYHSEA	none	Alpha-1-antitrypsin	8.03	1.7	12.18	10.77	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020390	YGNYSAYGGDQNYSGYGGYDYT	none	Heterogeneous nuclear ribonucleoprotein D-like	11.21	6.79	13.82	13.34	within
e020391	GAPGQNGEPGGKGERGAPGEKGEPPG*	3xOxidation [P9; P18; P26]	Collagen alpha-1(III) chain	9.01	4.74	11.79	11.05	within
e020392	AATSTPVSSSQSAPPMSPFSSASKPAA	none	Nuclear pore complex protein Nup214	6.69	2.06	10.65	9.62	within
e214211	DKKREEAPSLRPAPPPISGGGYRA	none	Fibrinogen beta chain	7.95	3.95	12.12	8.66	within
e020396	PGAESSENADDPNKDTSENADGQSD	none	Matrin-3	10.45	6.12	13.23	13.01	within
e020401	GQEQRGPEDQDISISFAWDKSSA	none	Defensin alpha 4	8.44	4.47	11.29	11.55	up
e020405	SDGQPGPPGPPGTAGFPGSPGAKGEVGP*	5xOxidation [P8; P10; P11; P17; P20]	Collagen alpha-1(III) chain	10.8	6.63	12.94	11.1	within
e020406	LSMLNGTKVLSDSAVGIDLSTGDTT	none	Coiled-coil domain-containing protein R3HCC1L	5.89	4.29	11.79	7.86	within
e020408	IASEFSSEMSTSEVSSEVGSTASDE	none	PH domain leucine-rich repeat-containing protein phosphatase 2	10.13	4.11	13.33	11.49	within
e020410	TPGNEGLDGRGDPGQPGPPGEQPPG*	1xOxidation [P26]	Collagen alpha-3(IV) chain	10.34	5.68	12.47	10.32	within
e020419	GGSSSGGGYGSGGGGSSSVKGSSGEAFGSSV	none	Keratin, type II cytoskeletal 2 epidermal	10.8	6.03	15.56	13.35	within
e020430	QAGQPQQPGPKGDPGISGTPGAPGLPGP*	4xOxidation [P20; P23; P26; P28]	Collagen alpha-1(IV) chain	4.45	0.86	8.46	5.85	within
e020432	GPEGAPGKDGGRGTLTGPIPPGPAGANGE*	1xOxidation [P]	Collagen alpha-1(II) chain	11.28	4.68	13.8	11.47	within
e020435	GPAGERGEQGAPGPSGFQGLPGPPGPPG*	2xOxidation [P24; P26]	Collagen alpha-1(II) chain	11.26	5.69	13.41	12.65	within
e020436	FPGLPGPSGEPGKQGAPGASGDRGPPGP*	1xOxidation [P28]	Collagen alpha-1(II) chain	11.35	5.49	13.41	12.6	within
e214218	GLPGIAGHHGDQGAPGSVGPAGPRGPAGP*	1xOxidation [P29]	Collagen alpha-2(I) chain	7.5	3.71	12.61	8.38	within
e020441	VQQMEQLRQKLGPAGDVEGHLS	none	Apolipoprotein A-IV	6.87	3.29	12.32	4.41	within
e020444	KNGETGPQGPPTGPGDKGDTGPPGP*	2xOxidation [P]	Collagen alpha-1(III) chain	11.01	7.9	12.54	11.72	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214220	GLDGEPGPQGLPGAPGDQGGQRPPGEA*	3xOxidation [P8; P12; P15]	Collagen alpha-1(IX) chain	6.41	2.69	10.85	8.33	within
e020450	PDSGATGLPGRPGPPGPPGPPGENGFP*	5xOxidation [P9; P12; P14; P15; P17]	Collagen alpha-1(IX) chain	10.49	6.68	12.42	11.9	within
e097952	SHEKMHEGDEGPGHHHKPGLGEGT	none	Protein S100-A9	12.44	6.43	15.09	15.24	up
e020455	PPGADGQPGAKGEPGDAGAKGDAGPPGP A*	4xOxidation [P2; P8; P14; P25]	Collagen alpha-1(I) chain	10.75	6.83	12.48	11.79	within
e020457	DEAGSEADHEGTHSTKRGHAKSRP	none	Fibrinogen alpha chain	12.53	6.07	15.25	15.18	within
e020460	AGNPGSDYFPGGTAPGAPGPGPSGTSSS G	none	Transcriptional activator MN1	9.99	5.65	12.58	10.09	within
e100867	GFRGDMGDPGFGGKEGSSPVGPPGPPG*	3xOxidation [M6; P23; P26]	Collagen alpha-4(IV) chain	9.41	5.02	12.18	10.45	within
e020461	QGPNGADGPQGPPGSGVGGVGEKGEP G*	1xOxidation [P12]	Collagen alpha-1(XI) chain	10.29	5.92	12.9	11.83	within
e104241	PGARGPSGPQGPGPPGPKGNSGEPGAP *	8xOxidation [P1; P6; P9; P12; P15; P16; P18; P25]	Collagen alpha-1(I) chain	6.88	3.8	10.3	10.55	up
e099127	DAHKSEVAHRFKDLGEENFKAL*	1xCation:Na [C-Term]; 1xCation:Na [E17]	Albumin	6.16	2.91	11.36	8.31	within
e020471	GEHGPPGPPGPIGPVGQPGAAGADGEPGA *	4xOxidation [P5; P6; P8; P9]	Collagen alpha-2(XI) chain	12.73	8.9	14.62	14.23	within
e204439	GEPAIIPEGMLIEGPPGPEGPAGLPG*	7xOxidation [P3; P8; P15; P16; P18; P21; P25]	Collagen alpha-1(V) chain	6.07	3.79	11.84	6.34	within
e214225	APEPPGPQPGSAESEGLAPQGAAPASPP	none	Rho GTPase-activating protein SYDE1	12.43	7.91	14.41	14.22	within
e214226	GAPGQNGEPGGKGERGAPGEKGEGLPPG *	4xOxidation [P3; P9; P18; P26]	Collagen alpha-1(III) chain	14.31	10.92	16.26	15.87	within
e105129	ANGAPGNDGAKGDAGAPGAPGSQGAPGL QG*	3xOxidation [P17; P20; P]	Collagen alpha-1(I) chain	14.33	10.81	16.26	15.86	within
e214227	FPGAPGPKGEIGAVGNAGPAGPAGPRGE*	5xOxidation [P5; P7; P19; P22; P25]	Collagen alpha-2(I) chain	13.93	9.98	16.05	15.86	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020486	ESLIATVTDMFGAGTETTSTTLRY	none	Cytochrome P450 2C18	5.19	0.0	9.62	8.17	within
e020487	HGPVGPAGKHGNRGETGPSGPVGPAGAV*	3xOxidation [P6; P18; P21]	Collagen alpha-2(I) chain	10.95	6.37	15.02	6.8	within
e204447	PGADGQPGAKGEQGEAGQKGDAGAPGPQ*	2xOxidation [P1; P25], 2xDeamidation [Q13; Q18]	Collagen alpha-1(II) chain	8.73	2.94	12.1	3.6	within
e020491	GFPGNPGAPGSPGPAGQQGAIGSPGPAGP*	7xOxidation [P3; P6; P9; P12; P14; P24; P26]	Collagen alpha-1(III) chain	12.7	9.79	14.42	13.31	within
e214231	DKGEIGEPGQKGSKGDKEQGPPGPT*	1xOxidation [P25]	Collagen alpha-1(V) chain	12.18	7.17	14.21	13.08	within
e020498	WLYTAPASGLGPEKSVSVPGARSHV	none	Collagen alpha-1(XX) chain	5.37	0.0	11.31	3.79	within
e104562	GKSGPSGQTGDPGLQGSPGPPGPEGFPG*	3xOxidation [P12; P17; P20]	Collagen alpha-1(XXIV) chain	10.59	6.28	13.43	11.2	within
e101694	TQGSPPGAKGDGGIPGPAGPLGPPGPPGLP*	4xOxidation [P14; P16; P19; P22]	Collagen alpha-1(XI) chain	10.14	5.68	12.96	9.99	within
e214234	GNSGGDGPAGPPGERGPNGPQGPTGFPG*	5xOxidation [P11; P12; P17; P20; P23]	Collagen alpha-1(V) chain	8.2	3.42	10.93	9.75	within
e104049	DGSPGGKGDRENGSPGAPGAPGHGPPG*	2xOxidation [P27; P28]	Collagen alpha-1(III) chain	10.08	6.07	12.28	10.19	within
e214235	GDVGPMGPPGPPGPRGPQGPNADGPQG*	3xOxidation [P14; P17; P20]	Collagen alpha-1(XI) chain	7.82	4.04	11.35	10.04	within
e020513	AGPPGAPGAPGAPGPVGPAGKSGDRGETGP*	2xOxidation [P7; P]	Collagen alpha-1(I) chain	10.57	6.83	12.45	11.26	within
e097960	GQPKAAPSVTLFPPSSEELQANKAT	none	Immunoglobulin lambda constant 2	9.69	5.92	11.83	10.75	within
e020521	PPGMRGKSGPSGQTGDPGLQGSPGPPG*	6xOxidation [P2; P10; P17; P22; P25; P]	Collagen alpha-1(XXIV) chain	10.56	6.32	12.8	11.26	within
e208594	PGEQGPppppppgvpGIDGIDGRGP*	5xOxidation [P10; P12; P13; P16; P27]	Collagen alpha-1(IX) chain	10.35	6.11	12.81	11.25	within
e106788	LMVEHTPDEESIDWTKIEPSVN	none	Vesicular integral-membrane protein VIP36	11.04	7.41	12.77	12.03	within
e020523	PKGNDGAPGKNGERGGPGGPGPQGPPGK*	2xOxidation [P22; P25]	Collagen alpha-1(III) chain	7.09	4.16	12.49	8.83	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020527	APPNEMGSDAENEAPVEASELSDNP	none	Glutamate-rich protein 3	5.99	1.75	11.03	9.7	within
e020529	AGPRGSPGERGETGPPGPAGFPAGPGQ*	7xOxidation [P3; P7; P15; P16; P18; P22; P25]	Collagen alpha-1(III) chain	7.59	4.5	12.03	7.68	within
e208595	GFPGLPGSPGEPGKQGPSGASGERGPP*	6xOxidation [P3; P6; P8; P12; P17; P26]	Collagen alpha-1(I) chain	7.24	4.47	11.58	7.69	within
e214237	SPGGPGSDGKPGPPGSQGESGRPGPPGPS*	1xOxidation [P]	Collagen alpha-1(III) chain	7.12	2.96	11.87	5.46	within
e020533	ESGPPGQPGPQGPBGKDKGEQGDQG*	1xOxidation [P]	Collagen alpha-1(XXV) chain	16.05	11.78	17.63	17.09	within
e214238	GDYQLGNSSHPAVNMHLGMSLLET	none	Integrin alpha-10	16.14	12.88	17.67	17.07	within
e097962	PPGPSGEEGKRGPNGEAGSAGPPGPPGL*	3xOxidation [P22; P23; P25]	Collagen alpha-2(I) chain	8.32	4.49	11.35	10.22	within
e100963	EGRAGEPGTAGPTGPPGVPGPSGITGPPG*	3xOxidation [P15; P16; P28]	Collagen alpha-2(VIII) chain	7.4	3.74	11.64	5.72	within
e020537	PPGAPGPQGQVVGPSGPPGPPGFPGDGP P*	2xOxidation [P2; P]	Collagen alpha-3(V) chain	8.4	4.81	11.32	9.74	within
e020538	DKTNVKAAWGKVGAHAGEYGAEALE	none	Hemoglobin subunit alpha	7.63	2.86	11.26	8.96	within
e020540	TVPTPPQGSSVGGGFAGLEFARPQES	none	SLC2A4 regulator	7.46	3.72	10.82	11.26	up
e020543	HQTVPQNTGGKNPDPWAKNLNEK	none	Serotransferrin	8.18	4.05	11.4	9.76	within
e020548	KGSAGQAGQPGSPGHQGLAGVPGQPGTK*	3xOxidation [P13; P22; P25]	Collagen alpha-2(IX) chain	8.57	4.44	11.16	10.96	within
e020555	PQGDAAQKTDTSHHQDHPFTFNK	none	Alpha-1-antitrypsin	10.12	5.75	11.95	11.33	within
e020556	KGQQGSAGSMGPRGPPGDVGLPGEHGI*	2xOxidation [P16; P22]	Collagen alpha-1(XIX) chain	5.53	1.78	9.54	11.34	up
e020557	STEERRLHYGENGVQKDVSQRS	none	Semenogelin-1	9.11	5.35	11.68	7.8	within
e020561	RKAADDTWEPFASGKTSESGELHG	none	Transthyretin	5.87	1.61	10.44	6.53	within
e020563	KGDRGFPGEMGPIGPPGPQGPGERG*	2xOxidation [P18; P21]	Collagen alpha-1(X) chain	5.9	0.56	10.44	2.79	within
e020569	LPHENKPLTLSNYQTNKAKHDE	none	Cystatin-B	7.02	3.84	11.88	9.94	within
e214242	AFEPDYNESDSESNVSVKEEESS	none	E3 ubiquitin-protein ligase RBBP6	10.33	6.03	12.98	9.5	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020573	WSAADVGSSPEPTSSEYEPLDAVS	none	Matrix-remodeling-associated protein 5	10.4	5.86	12.82	9.81	within
e214243	DGPQGPPGSGVGGVGEKGEPGEAGNP G*	2xOxidation [P22; P]	Collagen alpha-1(XI) chain	10.32	5.63	12.82	8.87	within
e020576	DDILASPPRLPEPQYPYGAPHHSS	none	Collagen alpha-1(XVIII) chain	11.44	7.17	13.11	12.65	within
e105617	VNGAPGEAGRDGNPGNDGPPGRDGGPG*	4xOxidation [P5; P14; P19; P20]	Collagen alpha-2(I) chain	10.01	5.89	12.78	10.41	within
e214247	GPPGPVGPAGKSGDRGESGPAGPAGAPG PAG	none	Collagen alpha-1(III) chain	9.13	5.24	12.03	8.81	within
e020587	DKSPSEESAPTTSPESVSGSVSSGSS	none	UV excision repair protein RAD23 homolog A	6.56	3.88	10.12	8.31	within
e214249	EAGPKGEPGPHGIQGPIGPPGEEGKR*	2xOxidation [P8; P10]	Collagen alpha-2(V) chain	7.93	5.37	11.5	7.32	within
e208599	GAPGQNGEPGGKGERGAPGEKGEGLPPG *	5xOxidation [P3; P9; P18; P26; P27]	Collagen alpha-1(III) chain	13.01	10.41	14.64	14.57	within
e214250	KGGPGDQGEPPGQGLPGFSGPPGKEGE*	3xOxidation [P4; P10; P12]	Collagen alpha-2(IX) chain	13.02	10.18	14.66	14.6	within
e104526	QGFGYPGEQPPGPPGEGPPGISKE*	3xOxidation [P12; P15; P21]	Collagen alpha-1(XXI) chain	7.96	4.88	11.19	9.21	within
e214251	GDPGVGGPPGLPGVGPAGAKGMPGHNG E*	3xOxidation [P9; P12; P]	Collagen alpha-1(X) chain	12.78	9.36	14.48	14.55	up
e214252	LRSEETKENEGFTVTAEGKGQGT	none	Complement C3	10.06	5.4	13.54	10.24	within
e020602	LNGQEVEGGENGIDGLNGEQGDNGLP	none	Collagen alpha-6(VI) chain	11.55	7.69	13.41	12.88	within
e208600	DEAGSEADHEGTHSTKRGHAKSRP*	1xCation:Na [E/D]	Fibrinogen alpha chain	8.24	2.98	11.64	9.47	within
e020604	FQTYGAIQGPPGQKGEMGTPGPKGD*	4xOxidation [P10; P11; P20; P22]	Collagen alpha-1(XVII) chain	7.99	3.88	10.83	10.34	within
e020609	LEQESGRSSGFYEDPSSTGGPDSP	none	Dapper homolog 3	8.42	4.34	12.96	7.84	within
e204474	YTYHVDANDHDQSRKSQQYDL	none	Semenogelin-1	6.98	3.16	11.05	7.9	within
e101051	GSPGEKGDGPDVGGPGPPGASGEPGAPG PP*	2xOxidation [P9; P15]	Collagen alpha-3(V) chain	10.06	6.32	12.19	12.36	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099540	GIDGSPGEKGDPGDVGGPGPPGASGEPGA*	6xOxidation [P6; P12; P18; P20; P21; P27]	Collagen alpha-3(V) chain	8.76	4.96	11.3	10.41	within
e105848	ERGEAGIPGVPAKGEDGKDGSPGEPG*	4xOxidation [P8; P11; P23; P26]	Collagen alpha-1(III) chain	11.47	8.04	13.07	12.92	within
e020622	AGPPGAPGAPGAPGPVGPAGKSGDRGETGP*	3xOxidation [P4; P7; P10]	Collagen alpha-1(I) chain	12.13	9.11	13.69	12.38	within
e214256	GYPGPAGPPGPPGPPGTSGHPGSPGSPGY*	2xOxidation [P15; P21]	Collagen alpha-1(III) chain	9.74	5.41	11.77	9.94	within
e020628	EVGPPGPAGSAGARGAPGERGETGPPGPA*	2xOxidation [P17; P25]	Collagen alpha-1(II) chain	10.54	6.37	12.58	10.09	within
e106175	AGPPGADGQPGAKGEPGDAGAKGDAGPPGP*	2xOxidation [P16; P28]	Collagen alpha-1(I) chain	10.58	6.55	12.56	10.09	within
e020629	LTGPIGPPGPAGAPGDKGESGPSGPAGPTG*	2xOxidation [P10; P]	Collagen alpha-1(I) chain	12.58	8.89	14.49	12.77	within
e105360	MGTPGPKGDRGPAGPPGHPGPPGPRGH*	3xOxidation [P21; P22; P24]	Collagen alpha-1(XVII) chain	9.71	6.47	12.18	8.12	within
e106229	PEQTPVLKPEEEAPAPEVGASKPEG	none	Vitronectin	8.25	5.03	10.77	10.28	within
e020634	KANDESNEHSDVIDSQELSKVSR	none	Osteopontin	8.41	4.48	12.31	10.01	within
e020636	SGPAGPPGPQGKGERGSPGGPGAAGFPGA*	1xOxidation [P28]	Collagen alpha-1(III) chain	9.16	5.58	11.58	10.92	within
e214261	QGPPGPTGKPGKRGRPGADGGRGMPGE*	1xOxidation [P]	Collagen alpha-1(XI) chain	9.4	5.88	11.4	9.99	within
e105403	SESGSFRPDSPGSGNARPNPDWGT	none	Fibrinogen alpha chain	8.0	3.98	11.51	9.39	within
e020641	GSPGEQGPSGASGPAGPRGPPGSAGAPGKD*	2xOxidation [P20; P]	Collagen alpha-1(I) chain	10.37	6.38	12.32	11.82	within
e214266	PQQQRGETGPPGPVGSPLPGAIGTDGT*	2xOxidation [P17; P20]	Collagen alpha-2(V) chain	7.99	4.37	11.51	7.5	within
e020646	WGQQPSSGYQEENQGNWSEQNH	none	Protein prune homolog 2	10.87	5.6	12.79	8.44	within
e020647	ERSSSSESTGTSPNPDLDAGVSEHSG	none	E3 ubiquitin-protein ligase Mdm2	11.03	6.74	12.72	10.37	within
e020653	FLPDEGKLQHLENELTHDIITK	none	Alpha-1-antitrypsin	7.65	4.02	12.71	6.46	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020655	PSHPLDLGTSSPNTSQIHWTPYR	none	Vinexin	6.85	3.25	10.22	10.48	up
e020656	LDGQKGEAGRNGAPGEKGPNGLPGLPG*	3xOxidation [P19; P23; P26]	Collagen alpha-3(IX) chain	8.58	5.1	11.76	8.59	within
e106787	PGDKGDDGEPGQTGSPGPTGEPGSPGPP*	3xOxidation [P16; P18; P22]	Collagen alpha-1(V) chain	8.51	4.35	11.25	10.72	within
e020667	SQTTDERGPPGEQGPPGPPGPPGVPG*	8xOxidation [P10; P15; P16; P18; P19; P21; P22; P25]	Collagen alpha-1(IX) chain	10.12	5.58	12.23	10.41	within
e100414	GKPGTDVFMGPPGSPGEDGPAGEPGPPG*	2xOxidation [P3; P27]	Collagen alpha-1(XV) chain	10.13	5.17	13.15	9.65	within
e099982	FSPEKSKLPGIVAEGRDDLYVSDA	none	Antithrombin-III	6.94	4.16	11.6	9.3	within
e101146	ARGPAGPPGKAGEDGHPGKPRPGERG*	2xOxidation [P8; P23]	Collagen alpha-2(I) chain	6.76	3.31	11.49	7.54	within
e214273	GAPGEKGEPPGVPAGPPGGSGPAGPPG PQG*	3xOxidation [P18; P23; P26]	Collagen alpha-1(III) chain	7.88	4.41	11.12	7.2	within
e020681	PGPAGAAGPAGNPGADGQPGAKGANGAP GIAG*	1xOxidation [P28]	Collagen alpha-1(I) chain	7.39	3.55	12.51	9.95	within
e020686	GEPGPKGDAGAPGAPGGKGDAGAPGERG PP*	1xOxidation [P]	Collagen alpha-1(III) chain	7.81	4.51	11.72	9.01	within
e020689	TGPTGPQGPQGPRGPPGKNGSPGSPGEP*	2xOxidation [P12; P15]	Collagen alpha-1(XXII) chain	8.97	4.79	11.68	10.26	within
e106580	GNPGAVGEKGEPGEAGEPGLPGEGGPPG P*	2xOxidation [P12; P27]	Collagen alpha-1(V) chain	9.87	5.2	12.9	11.71	within
e020702	QGPPGPPGPPGSPGLGHPGLPGMPGPP*	6xOxidation [P7; P9; P10; P12; P15; P19]	Collagen alpha-1(XIII) chain	6.5	3.12	10.9	8.63	within
e020707	AGPPGAPGAPGAPGPVGPAGKSGDRGET GP*	4xOxidation [P4; P7; P10; P13]	Collagen alpha-1(I) chain	10.58	5.84	13.24	9.32	within
e102947	SETPGPPGPQGPPGLPGRNGTPGEQGF*	1xOxidation [P]	Collagen alpha-1(XX) chain	10.91	6.44	13.2	11.19	within
e100388	LTGPIGPPGPAGAPGDKGESGSPGAPGPT G*	3xOxidation [P10; P14; P22]	Collagen alpha-1(I) chain	9.03	4.91	11.86	6.39	within
e020712	AGGEDAGAAREDAAGGDDVGAGREDAG AG	none	Golgin subfamily A member 6-like protein 2	9.05	2.45	12.03	6.82	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e100805	SNKSGGDSNKNRRTSSTLDSEGTf	none	TBC1 domain family member 5	4.28	0.54	9.6	7.12	within
e214282	GGSRGFGGASGGGYSSSGFGGGFGGGS GGGF	none	Keratin, type I cytoskeletal 9	12.41	7.82	14.8	11.31	within
e100344	QGPAGPPGEKGEPGDDGPSGAEGPPGPQ *	4xOxidation [P3; P6; P7; P24]	Collagen alpha-1(II) chain	8.47	4.58	11.41	8.64	within
e103458	PGSWGAGGPAGPTGYPGEPGLVGPPGQP G*	2xOxidation [P19; P24]	Collagen alpha-4(IV) chain	9.92	4.34	13.02	12.57	within
e106432	GSPGPPGTPGEPGMQGEPPGPPGNLG*	7xOxidation [P9; P12; P18; P20; P21; P23; P24]	Collagen alpha-3(IV) chain	11.85	6.41	14.08	10.33	within
e020728	GDQGPDPGSPGSPGAPGAPPGYGP Q*	5xOxidation [P12; P15; P17; P20; P23]	Collagen alpha-3(IV) chain	10.86	6.81	13.23	10.37	within
e105633	NASQEEEEAADEGGEEDELAELR	none	Zinc fingers and homeoboxes protein 3	8.41	4.89	11.38	11.48	up
e204537	PPGAPGAPGAPGVGPAGKSGDRGETGP A*	8xOxidation [P1; P2; P5; P8; P11; P13; P16; P28]	Collagen alpha-1(I) chain	7.32	3.75	11.5	5.55	within
e020741	GKRSDGEQDGAAGSMDASTQGLLEGIG	none	E3 ubiquitin-protein ligase HUWE1	8.05	3.04	11.69	11.4	within
e105058	APGNDGAKGDAGAPGAPGSQGAPGLQGM PG*	3xOxidation [P2; P14; P17]	Collagen alpha-1(I) chain	10.15	5.19	12.95	12.13	within
e214286	QQSPYAQQGTYYTQPLYAAPPV	none	Myelin-associated neurite-outgrowth inhibitor	7.06	2.04	13.75	7.54	within
e020754	NDKESEAQISWFAPEDHGYGTEV	none	ATP-dependent DNA/RNA helicase DHX36	13.82	8.15	16.75	11.26	within
e020751	GARGDPGFPGAQGEPSQGEPGDPGLPG *	3xOxidation [P6; P21; P27]	Collagen alpha-2(IV) chain	8.86	4.94	11.6	9.52	within
e214287	GQPGAKGEQGEAGQKGDAGAPGPQGSPG A*	3xOxidation [P3; P21; P23]	Collagen alpha-1(II) chain	8.87	5.24	12.83	8.96	within
e020760	VRKDLQNFLKKENKNEKVIEH	none	Protein S100-A9	9.7	3.3	14.35	14.2	within
e214290	SEGQLAEQSLASSEDETEITEDLE	none	Protein fantom	12.93	7.21	15.31	9.77	within
e020761	SAGSPANQSPTSPVSNQGFSPGSSPQH	none	CREB-regulated transcription coactivator 1	6.52	3.21	12.11	6.97	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099882	PGEPGPKGDAGAPGAPGGKGDAGAPGER GP*	2xOxidation [P4; P6]	Collagen alpha-1(III) chain	12.23	8.57	13.99	13.51	within
e095605	GEAGAAGPAGPAGPRGSPGERGEVGPAG PN*	1xOxidation [P]	Collagen alpha-2(I) chain	12.16	8.03	13.98	13.49	within
e020776	GLDGPPGPDGLQGPPGPPGTSSVAHGFL*	2xOxidation [P6; P8]	Collagen alpha-5(IV) chain	5.89	2.6	10.1	5.81	within
e214291	TSHDASTNGLINFIKQQREARVQ	none	Glucose-6-phosphate isomerase	7.1	1.81	13.41	9.45	within
e214292	GNLGLSPGGNGAAGGGGPPASEGAGPAA GPEL	none	Striatin-3	11.27	7.49	13.14	12.15	within
e020783	KDLQNFLKKENKNEKVIEHIM*	1xOxidation [M21]	Protein S100-A9	4.98	0.11	10.27	8.39	within
e020784	APGPAGARGESGLAGAPGAPGPPGPPGPP G*	9xOxidation [P2; P4; P17; P19; P22; P23; P25; P26; P28]	Collagen alpha-1(XVIII) chain	7.21	3.91	10.33	9.43	within
e214295	TGKPGPKGTSGGDGPPGPPGERGPQGPQ *	3xOxidation [P19; P24; P27]	Collagen alpha-1(XI) chain	6.82	3.9	10.4	6.48	within
e100605	GKNGETGPQGPPGPTGPGGDKGDTGPPG P*	2xOxidation [P17; P27], 1xDeamidation [N3]	Collagen alpha-1(III) chain	8.74	4.67	11.22	11.2	within
e020787	IDGDNGPPGKAGPPGPKGEPGKAGPDGP*	5xOxidation [P14; P16; P20; P25; P28]	Collagen alpha-2(IX) chain	7.58	4.06	12.08	10.17	within
e214296	TDGTPGAKGPTGSPGTSGPPGSAGPPGSP GP*	1xOxidation [P10]	Collagen alpha-2(V) chain	4.58	0.17	8.29	6.91	within
e020788	GPPGADGQPGAKGEPGDAGAKGDAGPPG PA*	4xOxidation [P3; P9; P15; P26]	Collagen alpha-1(I) chain	10.69	6.28	12.75	11.99	within
e020789	EASSPPPTAEGTSMPTSTPSEGSTPLT	none	Mucin-17	6.15	2.0	10.65	9.39	within
e214298	GDAGQKGERGEPGGGGFFGSSLPGPPGP*	3xOxidation [P23; P25; P26]	Collagen alpha-1(XVIII) chain	10.63	6.59	12.62	9.02	within
e101071	GPAGPRGANGAPGNDGAKGDAGAPGAPG SQG*	2xOxidation [P5; P]	Collagen alpha-1(I) chain	7.14	3.76	11.44	7.38	within
e020798	DGPPGDKGDDGEPGQTGSPGPTGEPGPS G	none	Collagen alpha-1(V) chain	10.76	5.35	13.25	6.11	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e101159	MVEHTPDEESIDWTKIEPSVNF*	1xOxidation [M1]	Vesicular integral-membrane protein VIP36	7.5	3.8	11.33	10.15	within
e106514	GLDYGGYEPMDSGGGPSPGPGGGPRGDG G	none	Ubiquitin carboxyl-terminal hydrolase 24	10.74	6.52	13.0	10.56	within
e102581	AGPRGDSGQPGPKGDPGRPGFSYPGP*	7xOxidation [P3; P10; P12; P16; P19; P24; P26]	Collagen alpha-2(VI) chain	8.39	3.78	11.76	9.06	within
e020808	PSGNDGSAGPPGPPGSGVPRGPEGLQGQ*	6xOxidation [P10; P11; P13; P14; P19; P22]	Collagen alpha-1(VII) chain	9.11	4.87	11.88	10.8	within
e099896	PTDPGAGAEIPTSTADTSNSSNPAPPPG*	1xOxidation [P27]	Collagen alpha-1(V) chain	8.61	4.87	11.34	9.75	within
e097979	PGPAGATGDRGEAGAAGPAGPAGPRGSP GE*	5xOxidation [P3; P18; P21; P24; P28]	Collagen alpha-2(I) chain	9.32	4.45	11.89	10.8	within
e020817	VGEAGPEGPPGEPGPPGPPGPPGHLTAA*	8xOxidation [P6; P9; P10; P13; P15; P16; P18; P19]	Collagen alpha-2(V) chain	7.57	4.36	10.61	7.43	within
e020823	ELDMALSDLEAADFAELSEDYYD	none	Protein inturned	8.26	4.37	11.46	9.62	within
e020829	PPGDDGPKGNPGPVGFPGDPGPPGEGGP*	4xOxidation [P20; P22; P23; P26]	Collagen alpha-1(XI) chain	8.12	4.19	11.3	7.75	within
e020834	PMGIPIGISQGEQGIQGPPIPGPQGPA*	2xOxidation [P18; P21]	Collagen alpha-1(XXVIII) chain	6.08	1.3	10.84	8.9	within
e020836	DPGPPGPVGPGEKGEPGKPGPPGLPGA GG	none	C1q-related factor	5.77	2.25	9.3	5.63	within
e020840	GPNGADGPQGPPGGVGNLGPGEKGEPG E*	2xOxidation [P20; P21]	Collagen alpha-2(XI) chain	9.33	5.55	12.07	10.46	within
e204568	VGPQGPTGETGPIGERGHPGPPGPPGE*	6xOxidation [P3; P6; P12; P19; P21; P22]	Collagen alpha-1(XI) chain	9.57	4.92	12.08	5.64	within
e214306	GAPGLWMGSSWQPGPQGPPGIPGPPGP*	3xOxidation [P24; P]	Collagen alpha-1(XVI) chain	9.27	5.41	11.94	10.35	within
e020843	GPQGERTGPPGSTGSRGPPGPPGRPGN*	1xOxidation [P]	Collagen alpha-1(XII) chain	7.2	1.96	11.24	5.17	within
e020844	GPSGPPGKPGYGSPGLQGEPLGPPGPS *	2xOxidation [P20; P23]	Collagen alpha-1(X) chain	5.86	0.63	9.67	8.72	within
e020847	GDSEAPGGGGSASDSTYAHNGYQET	none	E3 ubiquitin-protein ligase ZNRF1	6.97	2.17	10.48	7.26	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020848	PGQPGMAGVDGPPGPKGNMGPQGEGPP*	3xOxidation [P15; P21; P]	Collagen alpha-1(XI) chain	9.61	6.15	12.4	10.56	within
e214308	VRGEPGPPGPAGAAGPAGNPGADGQPGA KG*	4xOxidation [P10; P16; P20; P]	Collagen alpha-1(I) chain	9.2	4.95	11.35	10.51	within
e300080	VKQADSGSSEKQLYNKYPDAVAT	none	Osteopontin	10.19	4.52	14.54	4.18	down
e020855	GEPGPAGQDGP PGDKGDDGEPGQTGSPG*	6xOxidation [P3; P5; P11; P12; P21; P27]	Collagen alpha-1(V) chain	7.12	3.55	11.4	5.6	within
e020856	GGEDVGP GGEDVGAGGEDVGAGGDAREG GE	none	Golgin subfamily A member 6-like protein 2	7.74	3.54	10.82	8.26	within
e020864	EGPPGISIPGPPGLDGQPGAPGLPGPPG*	9xOxidation [P3; P4; P9; P11; P12; P18; P21; P24; P26]	Collagen alpha-5(IV) chain	12.76	8.77	14.49	14.3	within
e020860	PAGERGEQGAPGPSGFQGLPGPPGPPGE*	2xOxidation [P]	Collagen alpha-1(II) chain	12.77	8.78	14.44	14.3	within
e020858	EAGAAGPAGPAGPRGSPGERGEVGPAGP NG*	2xOxidation [P17; P25]	Collagen alpha-2(I) chain	9.84	5.74	12.13	11.0	within
e214310	PGAVGEKGEPGEAGEPGLPGEGGPPGPK G*	3xOxidation [P16; P19; P24]	Collagen alpha-1(V) chain	12.77	8.78	14.48	14.3	within
e020870	LPGKDGETGAAGPPGPAGPAGERGEQGA P*	2xOxidation [P19; P29]	Collagen alpha-1(II) chain	6.73	4.11	10.95	9.28	within
e214311	SPGVSGPKGDAGQPGEKGSPGAQGP PGA PG*	2xOxidation [P26; P]	Collagen alpha-1(III) chain	11.21	7.05	13.35	12.32	within
e020872	PGPPGPRGPAGPNGADGPQGPPGGVGNL GP*	2xOxidation [P22; P30]	Collagen alpha-2(XI) chain	11.19	6.68	13.35	12.3	within
e020875	LLKNGERIEKVEHSDLSFSKDW	none	Beta-2-microglobulin	6.24	2.26	11.63	6.1	within
e020877	TWASHEKMHEGDEGPGHHHKPGLG	none	Protein S100-A9	7.23	3.03	11.65	11.68	up
e020878	PAGAAGQPGAKGERGAKGPKGENGVVGP T*	1xOxidation [P1]	Collagen alpha-2(I) chain	5.8	0.0	12.22	7.39	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e020882	NRGERGSEGSPGHGPGPPGPPGAPGP*	2xOxidation [P]	Collagen alpha-1(III) chain	8.05	3.19	11.07	8.84	within
e020883	EVGPPGPPGPAGEKGSPGADGPAGPGTGP	none	Collagen alpha-1(I) chain	9.58	4.97	12.06	11.08	within
e214313	GEKGGEVDVGSMGPHGAPGPRGPQGPTG*	3xOxidation [P14; P18; P20]	Collagen alpha-3(V) chain	10.25	5.45	12.6	12.51	within
e020887	PGEPGANGLPGAAGERGAPGFRGPAGPN G*	3xOxidation [P10; P19; P24]	Collagen alpha-1(III) chain	6.33	3.43	10.48	5.45	within
e214315	ISSTMNGTNSNSPSGNHQSSFANRPR	none	Polycomb complex protein BMI-1	8.63	4.49	11.47	11.63	up
e106280	AAGAPGPQGFQGPAGEPGEPGQTGPAGAR*	3xOxidation [P5; P7; P13]	Collagen alpha-2(I) chain	10.51	5.48	13.03	11.07	within
e020911	SDPTPPSGPSLDGTGWNSFQSSDATE	none	ADP-ribosylation factor-binding protein GGA1	7.16	1.79	10.44	5.38	within
e020913	TLSPVSTFSLNSRDEDFMVEFSE	none	5'-3' DNA helicase ZGRF1	7.15	4.11	10.53	8.34	within
e105034	KGQEGAHGAPGAAGNPGAPGHVGA PGSP*	5xOxidation [P16; P19; P25; P27; P]	Collagen alpha-1(XXII) chain	9.26	5.29	11.68	7.78	within
e020918	PAGSPGSNGAPGQRGEPGPQGHAGA QGP P*	3xOxidation [P5; P11; P17]	Collagen alpha-1(III) chain	9.96	6.55	12.42	9.56	within
e020922	SAGARGEPPGGRPGFPGTPGMQGP PGE*	4xOxidation [P14; P17; P20; P25]	Collagen alpha-1(XII) chain	6.62	3.14	10.55	8.82	within
e020923	PTGPVGAAGPAGPNGPPGPAGSRGDGGP PGM*	2xOxidation [P1; P4]	Collagen alpha-2(I) chain	7.54	3.36	10.3	7.89	within
e300143	EAQVSVQPNFQQDKFLGRWFSAG	none	Prostaglandin-H2 D-isomerase	8.51	4.07	10.89	9.38	within
e103165	APGEKGPPQGPAGRDGVQGPVGLPGPAGP A*	3xOxidation [P19; P23; P25]	Collagen alpha-1(XI) chain	7.24	2.83	11.13	5.44	within
e020925	GHGARGAEREWEWWGGAQEEERE	none	C-type lectin domain family 11 member A	6.35	1.87	11.1	9.83	within
e020926	ERVTDSESGDSSGEDPEGNKGFRK	none	Protein capicua homolog	5.67	1.74	10.82	6.91	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214320	PGLPGPPGPPGPPGPPGLGGNFAPQLSY*	3xOxidation [P4; P6; P7]	Collagen alpha-1(I) chain	11.04	6.69	13.09	11.58	within
e020935	SNQSNSYPSMSDPYLSSYYPPSIG	none	YTH domain-containing family protein 1	7.61	3.69	11.01	9.7	within
e020936	YIAIILENFSVATEESADPLSEDD	none	Sodium channel protein type 8 subunit alpha	9.79	5.77	11.36	10.42	within
e020939	GAPGPAGARGESGLAGAPGAPGPPGPPGPPGP*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	10.52	5.71	12.5	11.69	within
e020942	KGSKGDPVLAPGSFKGMKGDPGLPGLD*	1xOxidation [P21]	Collagen alpha-6(IV) chain	7.92	4.22	13.47	10.64	within
e020943	WVAKNTNNKISRLLDSLPSDTRL	none	Plasma protease C1 inhibitor	9.3	5.24	12.01	12.41	up
e020951	GAKGSSGPTGPKGEAGHPGPPGPPGPPGE*	7xOxidation [P8; P11; P18; P20; P21; P23; P24]	Collagen alpha-1(V) chain	6.15	3.34	10.5	6.84	within
e020952	DQGPQGPQGVPGTSKDGQDGAPGEPGPP*	1xOxidation [P]	Collagen alpha-3(IX) chain	11.85	8.66	13.33	13.02	within
e214326	DGTPGAKGPTGSPGTSGPPGSAGPPGSPGPQ*	1xOxidation [P]	Collagen alpha-2(V) chain	11.93	9.11	13.3	13.01	within
e020955	PGGAGGGSGQRGSGVAQSPQQPPPPQQQ	none	Phosphofurin acidic cluster sorting protein 1	5.39	2.28	10.49	7.97	within
e214328	KGNDGAPGKNGERGGPGGPGPQGPQGNKG*	2xOxidation [P7; P16]	Collagen alpha-1(III) chain	11.93	9.18	13.31	12.99	within
e020961	GPPGEKGEPGDDGPSGAEGPPGPQGLAGQ*	2xOxidation [P3; P9]	Collagen alpha-1(II) chain	7.58	3.61	11.42	4.4	within
e214332	VRGEPGPPGPAGAAGPAGNPGADGQPGA KG*	5xOxidation [P8; P10; P16; P20; P26]	Collagen alpha-1(I) chain	11.46	8.76	12.82	11.87	within
e020964	ISAPTTSTTSTPQTSTISSPTTSTTST	none	Mucin-5AC	11.42	8.59	12.79	11.84	within
e104102	SEAEDASLLSFMQGYMKHATKTAK	none	Apolipoprotein C-III	7.03	2.75	10.65	9.1	within
e020970	GKDGETGAAGPPGPAGPAGERGEQGAPGPS*	1xOxidation [P]	Collagen alpha-1(II) chain	7.15	3.77	11.02	6.32	within
e020971	GPPGKNGDDGEAGKPGRPGERGPPGPQ*	4xOxidation [P3; P15; P18; P23]	Collagen alpha-1(I) chain	11.33	6.69	13.81	13.07	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214334	RSEAPGGTSGEFPGTRITSGGSYTATT	none	Mucin-19	8.81	2.01	12.84	11.82	within
e020976	ESEQYKKEMLVDGQTHLVLIRE	none	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	5.77	1.22	10.24	5.52	within
e214335	GSPGEGQPSGASGPAGPRGPPGSAGAPG KDG*	2xOxidation [P20; P21]	Collagen alpha-1(I) chain	8.63	4.85	11.59	11.61	up
e204601	APGSPGVSGPKGDAGQPGEKGSPGAQGP PG*	3xOxidation [P2; P5; P10]	Collagen alpha-1(III) chain	8.87	5.14	11.64	11.64	up
e214336	PGPIGLDGKPGHPPKGDMLTGPPGQ*	7xOxidation [P1; P3; P10; P13; P15; P24; P25]	Collagen alpha-1(XIII) chain	6.47	2.12	11.52	6.1	within
e020979	LGPHAGDVEGHLSFLEKDLRDKVN	none	Apolipoprotein A-IV	5.82	0.88	10.68	9.52	within
e105487	MAASGESGTSGGGSTEEAFMTFYSEV	none	DnaJ homolog subfamily C member 8	7.92	3.45	13.87	7.47	within
e020985	RGETGPPGPAGFPAGPQNGEPGGKGER*	1xOxidation [P]	Collagen alpha-1(III) chain	8.8	4.75	11.72	9.0	within
e020991	NRGERGSEGSPGHPPGPPGPPGAPGP *	3xOxidation [P22; P23; P]	Collagen alpha-1(III) chain	9.93	5.46	12.37	8.75	within
e214339	PGDPGPKGFQGNKGEPGPPGYPGSPGAP*	2xOxidation [P4; P]	Collagen alpha-1(XXVIII) chain	9.94	5.39	12.41	8.74	within
e214341	DNNSNMDIEERLSNNMEQRPSR	none	YEATS domain-containing protein 2	9.82	5.93	12.14	10.99	within
e214342	ISGPPGNPLPGEPGPVGGGGHPGQPGPP *	7xOxidation [P5; P8; P11; P14; P16; P23; P26]	Collagen alpha-5(IV) chain	9.8	5.7	12.01	10.96	within
e020996	PPGDDGPKGNPGPVGFPGDPGPPGEPGP A*	1xOxidation [P22]	Collagen alpha-1(XI) chain	9.82	5.7	12.01	10.9	within
e214343	GADGQPGAKGANGAPGIAGAPGFPGARGP SG*	2xOxidation [P21; P24]	Collagen alpha-1(I) chain	9.67	6.12	12.11	10.92	within
e214345	PGSVGSVGGVGEKGEPGEAGNPGPPGEA GV*	3xOxidation [P1; P16; P22]	Collagen alpha-1(XI) chain	8.57	4.48	12.09	11.02	within
e102401	AVGPPPGFAGEKGPSGEAGTAGPPGTPGPQ G*	3xOxidation [P5; P23; P26]	Collagen alpha-2(I) chain	8.23	4.43	12.76	6.36	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214346	GPQGHAGAQQPPGPPGINGSPPGKGEMGPA*	1xOxidation [P]	Collagen alpha-1(III) chain	8.71	5.02	12.44	10.87	within
e021010	PPGPAGPAGERGEQAGPSPGFGQLPGP*	7xOxidation [P1; P2; P4; P7; P17; P19; P26]	Collagen alpha-1(II) chain	11.46	7.23	13.66	7.64	within
e097994	LPGPPGSNGNPGPPGSPGKDGPPGPAAG*	5xOxidation [P5; P11; P13; P14; P]	Collagen alpha-1(III) chain	9.75	5.75	12.3	8.99	within
e021028	ERGEAGIPGVPGAEGDKDGPGEPGA*	4xOxidation [P8; P11; P23; P26]	Collagen alpha-1(III) chain	12.03	9.11	13.73	13.37	within
e021032	DGVSGGEGKGGSDGGGSHRKEGEEADAPG	none	CD99 antigen	9.2	2.73	11.54	11.9	up
e021035	GMRGDRGPPGAAGDKDGKPTGVPGFPG*	3xOxidation [P20; P24; P27]	Collagen alpha-4(IV) chain	11.31	8.45	13.0	12.07	within
e021040	SHEKMHEGDEGPGHHKPLGEGTP	none	Protein S100-A9	7.47	1.87	12.01	9.55	within
e021041	ISLPGSPGPPGTPGEPGMQGEPPGPP*	6xOxidation [P4; P7; P9; P10; P13; P16]	Collagen alpha-3(IV) chain	9.26	5.0	12.06	10.86	within
e214355	EGPKGEVGA PGSKGEAGPTGPMGAMGPLG*	4xOxidation [P3; P10; P18; P21]	Collagen alpha-2(V) chain	9.61	6.03	11.8	10.81	within
e208632	ADGLVGEDGAADASKGLGGSGGAGGPPGTPY	none	Proline-rich protein 12	7.75	3.39	11.32	9.18	within
e021046	DEAGSEADHEGTHSTKRGHAKSRPV	none	Fibrinogen alpha chain	13.94	7.67	16.66	16.08	within
e214359	GGGWGSGSSFRGTPGGGGPRPPSPRDGY	none	M-phase-specific PLK1-interacting protein	11.76	6.98	14.33	13.82	within
e214361	QENSELSLQAGEVVDVIEKNESGW	none	SH3 and PX domain-containing protein 2A	11.7	7.01	14.28	13.84	within
e214363	PPGQQGNPQPQLPGPQGPPIGPPGEKGP*	3xOxidation [P19; P]	Collagen alpha-1(XI) chain	9.2	3.61	12.75	9.52	within
e021056	EPGEPGASGPMGPRGPPGPPGKNGDDGE*	3xOxidation [P5; P10; P13]	Collagen alpha-1(I) chain	7.26	3.8	10.74	7.24	within
e021059	KGDGPPGLDVPGPGERGSPGIPGAPGP*	2xOxidation [P27; P29]	Collagen alpha-5(IV) chain	9.08	3.43	12.06	10.19	within

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e021060	LSEGLKLVDFLEDVKKLYHSEA	none	Alpha-1-antitrypsin	7.11	2.46	11.59	9.36	within
e021061	QGPPGKNGETGPQGPPGPTGPGGDKGDTG*	3xOxidation [P16; P18; P21]	Collagen alpha-1(III) chain	7.1	3.22	11.41	9.59	within
e021062	SPEFETETLHNKESGFPLRGEQG*	1xOxidation [P17]	Collagen alpha-6(IV) chain	10.11	4.07	12.66	5.07	within
e021066	GRAGEPGTAGPTGPPGVGSPGITGPPGPG*	1xOxidation [P21]	Collagen alpha-2(VIII) chain	7.62	3.73	11.85	10.89	within
e104248	PGPAGPPGPPGPPGTSGHPGSPGSPGYQGP*	3xOxidation [P1; P3; P6]	Collagen alpha-1(III) chain	7.1	3.28	10.87	7.62	within
e100379	GEPGNIGFPGPKGPTGDPKNGDKGHAG*	3xOxidation [P3; P9; P18]	Collagen alpha-2(I) chain	8.9	5.53	11.24	11.44	up
e021069	GAAGPAGPAGPRGSPGERGEVGPAGPNGFA*	3xOxidation [P5; P8; P11]	Collagen alpha-2(I) chain	9.44	5.49	12.17	8.04	within
e204628	TDGTPGAKGPTGSPGTSGPPGSAGPPGSPGP*	4xOxidation [P5; P10; P14; P29]	Collagen alpha-2(V) chain	5.44	2.15	8.67	7.17	within
e106798	NRGERGSEGSPGHGQPGPPGPPGAPGP*	4xOxidation [P20; P22; P23; P]	Collagen alpha-1(III) chain	11.96	7.79	13.99	12.65	within
e214367	EAGVDGQVGPPGQPGDKGERGAAGEQGP*	3xOxidation [P11; P14; P28]	Collagen alpha-1(XIII) chain	12.15	9.0	14.14	12.08	within
e214369	RGETGPPGPAGFAGPPGADGQPGAKGEQG*	3xOxidation [P7; P9; P]	Collagen alpha-1(II) chain	7.69	3.77	11.9	10.3	within
e214371	GPPGPRGKPGMSGHNSRGDPGFPGGR*	5xOxidation [P3; P5; P9; P21; P24]	Collagen alpha-4(IV) chain	10.1	4.93	13.86	9.86	within
e021097	TAASSMTAASSTPMTLALPAPTSTSTGR	none	Uncharacterized protein C11orf24	7.39	2.6	11.58	5.74	within
e021098	ELELEVEPEDVTELLQSHDKTLT	none	Tigger transposable element-derived protein 1	7.42	3.23	12.1	5.79	within
e021100	GVGGDKGEDGDPGQPPGPPGSPGEAGPPGPP*	2xOxidation [P26; P27]	Collagen alpha-1(XI) chain	10.82	5.7	13.37	11.32	within
e214374	LPGPPGSNGNPGPPGSPGSPGDKGPPGPPAG*	6xOxidation [P4; P5; P11; P13; P14; P16]	Collagen alpha-1(III) chain	8.49	4.32	11.49	8.15	within

a: Distribution in healthy female

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e214375	TDETSVSSPPPYTAYAAPAEQAYG	none	Pleckstrin homology domain-containing family B member 2	8.47	4.25	11.54	8.13	within
e214377	AGPTGPPGVPGSPGITGPPGPPGPPGPPG A*	11xOxidation [P6; P7; P10; P13; P18; P19; P21; P22; P24; P25; P27]	Collagen alpha-2(VIII) chain	7.31	3.2	11.44	7.69	within
e021108	DGKTGPPGPAGQDGRPGPPGPPGARGQA G*	4xOxidation [P9; P16; P18; P19]	Collagen alpha-1(I) chain	6.97	3.84	10.47	10.44	within
e021110	VSDTVALGVPGPREHPQPEDSPEAE	none	Phosphofurin acidic cluster sorting protein 2	11.89	6.32	15.32	13.7	within
e098002	MPGADGPPGHPGKEGPPGEGKGQGGPPGP *	7xOxidation [P2; P7; P8; P11; P16; P17; P25]	Collagen alpha-1(V) chain	10.5	6.49	12.92	8.89	within
e102026	AAGPTGPIGSRGSPGPPGPDGNKGEPGVV G*	2xOxidation [P17; P26]	Collagen alpha-2(I) chain	8.28	4.96	11.65	9.79	within
e204647	PSGGPFSEPQFHNGESEESHEQFL	none	Hepatocyte growth factor-regulated tyrosine kinase substrate	7.82	4.83	11.01	7.3	within
e021123	EAGRDGNPGNDGPPGRDQPGHKGER*	3xOxidation [P13; P14; P]	Collagen alpha-2(I) chain	9.2	4.65	11.6	10.61	within
e021134	DEDISLLPESEEQEREEDGSEIE	none	U3 small nucleolar ribonucleoprotein protein MPP10	6.32	1.85	10.82	8.88	within
e021135	GVQGGKGEGQPPGPPGFQGLPGPSGPAG E*	4xOxidation [P12; P14; P15; P21]	Collagen alpha-2(I) chain	9.64	5.06	12.0	11.95	within
e021156	SGPPPRVEFDDNNPFSESFQERE	none	Histone-lysine N-methyltransferase 2C	6.61	2.29	12.1	9.22	within
e102123	NRGERGSESGPHGPGQPPGPPGAPGP *	5xOxidation [P19; P20; P22; P]	Collagen alpha-1(III) chain	14.18	11.38	15.74	15.0	within
e101976	GQRGSGSGQSPSYGRHSGSGRSSSSGR	none	Hornerin	6.18	1.17	11.69	7.97	within
e103333	SSSTEERRLHYGENGVQKDVSQSS	none	Semenogelin-1	8.16	2.26	12.9	10.02	within
e021163	GGPGGPGPQGPPGKNGETGPQGPPGPTG PGG*	4xOxidation [P8; P11; P12; P20]	Collagen alpha-1(III) chain	12.87	8.51	14.55	13.78	within
e099128	DEAGSEADHEGTHSTKRGHAKSRPV*	1xCation:Na [E6]	Fibrinogen alpha chain	9.3	4.29	13.34	8.86	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214395	GGYGGGYGGGMGGGLGGGFSAGGGSGS GFGRGGG	none	Keratin, type II cytoskeletal 3	13.2	10.87	14.73	13.58	within
e021174	WEPPANDTREEAGPPAAGEDEASWT	none	Chondroitin sulfate proteoglycan 5	9.7	5.11	12.6	9.54	within
e021173	SPEGPMPLGGGEDEDAEEAVELPEASA	none	Condensin-2 complex subunit H2	13.23	10.43	14.77	13.62	within
e214396	EQVDSQPDASSSQTVPVAEPPSTEP	none	Protein Aster-A	7.43	3.05	11.32	7.68	within
e099527	PGEPGEPGASGPMGPRGPPGPPGKNGDD G*	3xOxidation [P7; P12; P15]	Collagen alpha-1(I) chain	10.02	5.2	12.73	9.3	within
e021185	AGFPGARGLPGPSNGNPGPPGPSGSP GK*	3xOxidation [P4; P10; P12]	Collagen alpha-1(III) chain	7.1	2.78	11.28	10.8	within
e021188	GEVPGGSAHYGGPSPEKKAKSSSGGSSLA	none	ATP-dependent DNA helicase Q5	9.2	3.94	12.32	8.41	within
e214400	AGAGGEDVGAGREDAGAGGEDVGAGGED VGAG	none	Golgin subfamily A member 6-like protein 2	6.92	4.23	10.88	8.22	within
e214403	KGSMGHGMPGGMGTPGEPGPQGPPGS RG*	1xOxidation [P]	Collagen alpha-1(XXVII) chain	6.17	2.33	10.13	5.17	within
e021193	KDGEAGAQQPPGPAGPAGERGEQGPAGS PG*	2xOxidation [P13; P16]	Collagen alpha-1(I) chain	10.27	6.61	12.36	11.36	within
e021196	LPGTGGPPGENGKPGEPGPKGDAGAPGA PG*	6xOxidation [P8; P14; P17; P19; P26; P29]	Collagen alpha-1(III) chain	10.78	6.82	12.44	11.83	within
e300150	DLQVGQVELGGGPGAGSLQPLALEGSLQ	none	Insulin	11.37	3.67	15.56	15.28	within
e021208	PSPSSGSEPGQVDSGRGSDTEASEGAEG	none	von Willebrand factor A domain-containing protein 5B2	7.48	3.51	10.89	8.22	within
e021212	YKRKANDESNEHSDVIDSQELSK	none	Osteopontin	5.73	1.31	10.7	8.32	within
e021213	GPPGSAALPGSKGDTGNPGAPGTPGTKG WA*	2xOxidation [P21; P]	Collagen alpha-2(IV) chain	6.5	2.36	11.12	9.13	within
e204687	IGSPGPAGPRGPVGPSPGPPGKDGTSGHPG P*	3xOxidation [P4; P15; P28]	Collagen alpha-1(III) chain	7.21	3.64	12.06	3.51	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214412	GPQGNSGEKGDQGFQQPGFPGPPGPPG*	3xOxidation [P23; P24; P26]	Collagen alpha-1(XVI) chain	14.61	11.2	16.22	15.97	within
e214414	NRGERGSEGSPGHGPGQPGPPGPPGAPGP*	6xOxidation [P14; P17; P19; P20; P22; P]	Collagen alpha-1(III) chain	14.62	11.32	16.22	15.97	within
e214418	SDVPGPAGLPGVPGREGPPGFPLGPPG*	4xOxidation [P19; P22; P25; P27]	Collagen alpha-1(XVIII) chain	13.47	8.27	15.81	14.71	within
e021233	PGSNGNPGGPSGSPGKDGPPGPAGNT GAP*	3xOxidation [P]	Collagen alpha-1(III) chain	13.16	9.89	14.86	14.4	within
e098013	TYFPHFDLSHGSAQVKGHGKKVADA	none	Hemoglobin subunit alpha	8.85	3.12	13.49	9.8	within
e101762	GPPGDKGDDGEPGQTGSPGPTGEPGSPG PP	none	Collagen alpha-1(V) chain	9.45	4.41	13.23	7.37	within
e021238	IDGSPGEKGDPGDVGGPGPPGASGEPGAP GP*	1xOxidation [P]	Collagen alpha-3(V) chain	11.26	6.45	13.37	13.07	within
e021239	PPGADGQPGAKGEPGDAGAKGDAGPPGP AGP*	3xOxidation [P8; P14; P]	Collagen alpha-1(I) chain	10.77	6.66	12.46	10.75	within
e021241	KMFHLNSLTGEISTLEGLDYEETA	none	Protocadherin gamma-A7	8.55	2.93	12.39	9.12	within
e021244	QGVETPSQNRVVG YFAQVKHLYN	none	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2	10.04	6.24	12.33	10.86	within
e021247	APGSPTTTGGPGAPAEVPQEPQEPTQTP	none	Transmembrane protein PMIS2	6.31	3.06	10.78	9.03	within
e204704	GNPEQTPVLKPEEEAPAEV GASKPE	none	Vitronectin	7.12	3.72	11.1	8.94	within
e021256	QGPDGQPGVKGEPEGQKGDAGSPGPQG*	1xOxidation [P16]	Collagen alpha-2(V) chain	9.21	4.74	13.03	8.39	within
e103558	PPGPPGPPGQAVMPEGFIKAGQRPSLS*	2xOxidation [P]	Collagen alpha-1(X) chain	7.16	4.17	12.07	8.36	within
e021259	PGEPGEPGASGPMGPRGPPGPPGKNGDD G*	4xOxidation [P7; P12; P15; P18]	Collagen alpha-1(I) chain	10.93	5.6	13.75	6.32	within
e021260	PVGPPGSNGPVGEPGPEGPAGNDGTPGR D*	4xOxidation [P4; P5; P10; P14]	Collagen alpha-2(V) chain	10.87	5.47	13.63	6.35	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214422	AYATSSYLHDSTPSWTLSPFQDAAS	none	Pro-neuregulin-3, membrane-bound isoform	10.54	5.63	14.2	12.34	within
e214421	AMAGMPSPHLPSEHSSVSSSPEPGMPV	none	Transcription factor SOX-5	10.53	5.85	14.06	12.33	within
e214423	EEKQVTEPEEKQMVEDPLTTENA	none	Doublecortin domain-containing protein 1	10.51	5.61	14.03	12.32	within
e021275	AATQVSPLGFYQFSEEEGDEEEEGG	none	Radial spoke head protein 6 homolog A	8.92	4.86	11.78	5.29	within
e102787	GKKGDDGTPSQPGPPGPKGEPGSMGPRG*	4xOxidation [P12; P14; P15; P21]	Collagen alpha-1(XXIII) chain	8.05	2.23	11.19	6.56	within
e021295	AGPGSAPSSAASGASSPAPASGPAPSAVS SSSP	none	Armadillo repeat-containing protein 5	8.25	4.3	12.22	10.09	within
e100504	TRDQADGSRASVDSGSSEEQGGSSRAL	none	Polymeric immunoglobulin receptor	9.7	5.18	12.33	10.65	within
e214443	LDQPQPMEQGSSGVLGGKEEGKPER	none	Sal-like protein 2	5.69	2.1	9.84	7.14	within
e105539	RGGAGPPGPEGGKGAAGPPGPPGAAGTP GLQG*	4xOxidation [P6; P19; P22; P28]	Collagen alpha-1(III) chain	6.73	4.34	14.46	4.27	down
e021308	EGEGSGESERGSQS SVPSVDQFTGVG	none	Structural maintenance of chromosomes protein 3	7.66	3.15	11.43	9.75	within
e104139	GSVGEAGPEGPPGEPGPPGPPGPHLTA*	9xOxidation [P8; P11; P12; P15; P17; P18; P20; P21; P23]	Collagen alpha-2(V) chain	9.02	4.8	12.05	8.52	within
e021309	GPAGKDGEGAAGQPPGPAGPAGERGEQG PAG*	1xOxidation [P15]	Collagen alpha-1(I) chain	6.93	4.08	11.34	10.37	within
e214449	PPGADGQPGAAGGEPGDAGAKGDAGPPGP AGP*	4xOxidation [P2; P8; P14; P25]	Collagen alpha-1(I) chain	9.96	5.71	11.85	11.63	within
e093864	EWGSHVYFFFREIAMEFNYLE	none	Semaphorin-6B	6.55	2.4	9.23	8.11	within
e021355	WASHEKMHEGDEGPGHHHKPLGEG	none	Protein S100-A9	6.66	3.24	11.75	10.47	within
e021362	GFGGGSRGFGGASGGGYSSSGFGGGFG GGSGGG	none	Keratin, type I cytoskeletal 9	10.7	5.64	12.94	8.81	within
e106499	GAKGQEGAHGAPGAAGNPGAPGHVGAPG PSGP*	2xOxidation [P27; P29]	Collagen alpha-1(XXII) chain	8.3	4.59	11.69	7.22	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214454	GEPGKPGAPGKPGTPGADGLTGPDGSPGSIG*	2xOxidation [P]	Collagen alpha-1(IX) chain	7.14	3.23	14.06	12.6	within
e021366	LLKNGERIEKVEHSDLSFSKDWS	none	Beta-2-microglobulin	7.35	3.85	13.99	12.49	within
e021373	GPPGPPGTSGHPGSPGSPGYQGPPGEPGQ*	7xOxidation [P5; P6; P12; P15; P18; P23; P24]	Collagen alpha-1(III) chain	10.95	7.32	13.22	8.34	within
e021380	SYGVNFYQSHGPSGQYTHEFDGDE	none	HLA class II histocompatibility antigen, DQ alpha 2 chain	9.95	4.07	13.1	3.49	down
e204732	TGSGTQTQAGATQTVEQDSSHQTGRTS	none	Cornulin	6.46	2.5	11.98	5.1	within
e021382	VYKGGREERTEEQMEEYRGRITF	none	Butyrophilin subfamily 2 member A1	7.19	1.31	11.81	9.84	within
e021385	PTSGGGPMSPQDDEAEEESDNLSSGT	none	Rab GTPase-activating protein 1-like	8.81	5.25	11.14	10.99	within
e021386	SGAFAADPDGAAPADPDGAAPDAPAD	none	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	8.83	5.18	11.24	10.36	within
e021390	AHGETEAEEGAPEGAIEVPQGGEETSGAQ	none	Chloride intracellular channel protein 6	6.43	3.13	10.9	8.11	within
e101773	PDGPPGFPQGPGSHGRDGHAGEKGDPPG*	3xOxidation [P11; P26; P28]	Collagen alpha-4(IV) chain	9.7	5.65	11.93	10.15	within
e214462	PAGERGHGAPGSPGSPGLPGVPGSMGDMV	none	Collagen alpha-1(XVI) chain	10.01	6.07	12.84	10.72	within
e021398	VDVLKDSGRDYVSQFEGSALGKQLN	none	Apolipoprotein A-I	8.81	5.17	12.55	9.6	within
e204737	GSPGPVGFPGDPGPPGEPGPAGQDGGPPGDK*	2xOxidation [P5; P18]	Collagen alpha-1(V) chain	6.0	2.82	10.05	7.32	within
e021410	GREGAPGAEGSPGRDGSFGAKGDRGETGP*	3xOxidation [P6; P18; P29]	Collagen alpha-1(I) chain	7.24	3.5	11.61	10.07	within
e021408	KNGETGPQGPPGPTGPGDKGDTGPPGPQG*	1xOxidation [P]	Collagen alpha-1(III) chain	10.5	6.53	12.33	10.95	within
e021409	GSEKGAPGDPGLQGKPGKDGVPGFPGSEG*	3xOxidation [P10; P16; P22]	Collagen alpha-3(IV) chain	15.19	10.54	17.09	17.18	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214465	PPGPPGPRGHSGEPLGPPGPPGPPGQ A*	7xOxidation [P5; P7; P14; P17; P19; P20; P22]	Collagen alpha-1(X) chain	15.18	11.84	17.06	17.18	up
e021412	VDDMPNALSALSDLHAHKLRVDPVN	none	Hemoglobin subunit alpha	6.87	0.87	12.73	9.14	within
e021414	ASHEKMHEGDEGPGHHHKPLGEGTP	none	Protein S100-A9	6.51	0.51	12.31	10.09	within
e214467	TPGAPGQPGMAGVDGPPGPKGNMGPPQGE PG*	1xOxidation [P]	Collagen alpha-1(XI) chain	10.93	6.84	12.7	11.35	within
e214468	DRILPDSSGGVAKTMMESSLADFMQE	none	CCR4-NOT transcription complex subunit 1	13.16	9.24	14.92	13.85	within
e021415	PDSGATGLPGRPGPPGPPGPPGENGFPQ Q*	4xOxidation [P9; P12; P14; P15]	Collagen alpha-1(IX) chain	10.92	6.62	12.6	11.23	within
e021419	LENEDRRSASLHLPKLSITGTIDL	none	Alpha-1-antitrypsin	6.8	1.22	12.56	4.76	within
e214471	EVGPAGSPGSNGAPGQRGEPGPQGHAGA QG*	3xOxidation [P8; P14; P20]	Collagen alpha-1(III) chain	8.87	5.36	12.15	10.31	within
e021420	SGRGGNFGFGDSRGGGGNFGPGPSNFR G	none	Heterogeneous nuclear ribonucleoproteins A2/B1	7.7	3.67	12.22	9.75	within
e021421	DRGEPGPPGAGFAGPPGADGQPGAKGE PG*	2xOxidation [P]	Collagen alpha-1(I) chain	8.82	5.15	12.24	10.42	within
e021422	DPGKNKGDKGHAGLAGARGAPGPDGNNGA QG*	1xOxidation [P20]	Collagen alpha-2(I) chain	8.71	5.16	11.91	10.41	within
e021424	EAAKPAPAPAPAPAPAPAPEAPKEPAF	none	Myosin light chain 4	6.73	2.85	12.28	8.51	within
e021427	HAKATEHLSTLSEKAKPALEDLRQG	none	Apolipoprotein A-I	5.58	3.22	11.12	8.22	within
e021433	SIASSMSFVSKPEGGSEGGGPGGRQDHD	none	Tetratricopeptide repeat protein 28	7.92	3.86	11.09	10.19	within
e021435	PGEPGEPGASGPMGPRGPPGPPGKNGDD G*	6xOxidation [P1; P4; P7; P12; P15; P18]	Collagen alpha-1(I) chain	12.16	6.67	15.75	8.72	within
e101649	TSGWSSSGTSTGASNTPGATGSSTGQTDTS	none	Mucin-19	8.99	3.03	13.43	1.58	down

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098025	RGSPGPQGVKGESGKPGANGLSGERGPPG*	3xOxidation [P6; P16; P27]	Collagen alpha-1(III) chain	9.08	4.65	12.65	9.27	within
e214476	MAAATLRTPTQGTVTEDVAVHFSW	none	Zinc finger protein 154	8.45	4.55	11.97	8.23	within
e021445	GYSGSQASDNEGHSESDTQSVSAHGQ	none	Filaggrin	7.61	3.68	10.81	6.27	within
e021448	GAAGAGLDGPEGDQGPQGPQGVPGTSKD GQ*	2xOxidation [P10; P16]	Collagen alpha-3(IX) chain	9.44	4.67	13.04	10.04	within
e095676	IPVKQADSGSSEEKQLYNKYPDAVA	none	Osteopontin	9.43	5.64	14.62	11.02	within
e214477	FFLPDEGKLQHLENELTHDIITK	none	Alpha-1-antitrypsin	8.43	4.29	14.5	9.22	within
e021460	KVILGAHQEVNLEPHVQEIEVSRL	none	Plasminogen	7.88	3.8	14.69	8.44	within
e021469	TGGGGAGSLGAGGAFGEAAGDRGPYGTDI GPG*	2xOxidation [P24; P31]	Collagen alpha-1(XVII) chain	9.09	4.8	11.62	11.65	up
e106367	GPPGADGQPGAKGEPGDAGAKGDAGPPG PAGP*	2xOxidation [P3; P27]	Collagen alpha-1(I) chain	8.29	5.08	11.09	8.66	within
e105672	NDGARGSDGQPPGPPPGTAGFPGSPGAKG*	5xOxidation [P14; P16; P17; P23; P26]	Collagen alpha-1(III) chain	11.05	7.3	12.52	11.22	within
e214484	PQGHQGPAGPPGPPGPPGPGVSGGGYD FG*	3xOxidation [P11; P13; P14]	Collagen alpha-2(I) chain	8.58	3.32	11.41	11.05	within
e105449	GPQGLQGQGGAGPTGPPGEPGDPGPM GPI*	2xOxidation [P]	Collagen alpha-2(V) chain	10.3	4.83	13.15	11.78	within
e021477	PGPPGEQGLPGTAGKEGTKGDPPPGAP GK*	2xOxidation [P22; P24]	Collagen alpha-2(XI) chain	7.84	2.49	10.73	10.2	within
e021481	RRGEKELLVPRSSTSPDRIFHL	none	Alpha-1B-glycoprotein	5.79	1.19	10.62	8.63	within
e021482	GSPGALEDEGEQPAPEEDELEEEDELG	none	BAH and coiled-coil domain-containing protein 1	8.91	4.19	12.54	4.99	within
e204760	GPAGPPGPPGPSSNQGDTGDPGFPGIPGPK*	2xOxidation [P2; P9]	Collagen alpha-6(IV) chain	7.77	3.81	12.11	6.87	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021484	SEGPQGVVRGEPGPPGPAGAAGPAGNPGA DGQ*	2xOxidation [P16; P22]	Collagen alpha-1(I) chain	9.65	6.25	11.61	10.7	within
e099524	PAGERGHGAPGPSGSPGLPGVPGSMGD MV*	1xOxidation [P]	Collagen alpha-1(XVI) chain	9.31	5.02	12.69	11.41	within
e021485	PGPVGPAGKSGDRGESGPAGPAGAPGPA GSRG*	1xOxidation [P]	Collagen alpha-1(III) chain	7.4	3.25	12.2	10.78	within
e021488	SPGPVGFPGDPGPPGEPGAGQDGPDPD KG*	3xOxidation [P2; P4; P8]	Collagen alpha-1(V) chain	8.55	5.33	10.7	9.32	within
e104664	GGGGTGAVGGGGTSQASAGAATGATGAS GGGGPINP	none	Biorientation of chromosomes in cell division protein 1	8.02	4.16	11.86	10.38	within
e021494	DPAPMASGQSQQSSHSADYSPADDF	none	Protein prune homolog 2	9.85	5.44	12.16	10.38	within
e021497	KNGETGPQGPPGPTGPGGDKGDTGPPGP QG*	2xOxidation [P]	Collagen alpha-1(III) chain	14.03	11.89	15.28	14.17	within
e021499	TLYPLMNVDDLGTLYVPHDGTMD	none	Sarcosine dehydrogenase, mitochondrial	13.08	7.59	15.48	15.4	within
e021506	ASHEKMHEGDEGPGHHHKPLGEGTP*	1xOxidation [M6]	Protein S100-A9	7.47	2.26	11.98	10.34	within
e214487	RQPGLNTPEFFLGGGPGDAQQNDGNT	none	Taste receptor type 1 member 3	12.11	6.84	14.64	13.7	within
e021508	GPPGADGIAGAAGPPGIQGSPGKEGPPGP QG*	6xOxidation [P2; P3; P14; P15; P21; P26]	Collagen alpha-1(XXII) chain	12.06	7.62	13.92	13.18	within
e021509	MMSEFPGHTGPVNVVEFHPNEYLL	none	Katanin p80 WD40 repeat-containing subunit B1	12.11	6.82	14.68	13.96	within
e021514	NNYSGGYGTPDGLGGYGRGGGGSGGYYG Q	none	Heterogeneous nuclear ribonucleoprotein H3	9.17	4.58	13.17	8.96	within
e100836	GPPGGIGNPGAVGEKGEPEAGEPGLPGE GG*	3xOxidation [P2; P3; P9]	Collagen alpha-1(V) chain	9.86	6.21	12.44	10.46	within
e021517	EVRPHHGKEAVDPRQGRARGGDPSH	none	Integral membrane protein DGCR2/IDD	9.08	5.3	12.67	10.81	within
e100273	PGEKGEVGDVGSMPHGAPGRGPQGPT G*	4xOxidation [P1; M13; P15; P19]	Collagen alpha-3(V) chain	8.33	3.59	11.98	8.29	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021520	PKFHSGWEPPVDVLQEAPWEVEGL	none	Epidermal growth factor receptor kinase substrate 8-like protein 2	6.1	2.16	10.18	8.53	within
e021527	EMRNALGNQSTPAPPTGEVADTPLEPG	none	Transforming acidic coiled-coil-containing protein 2	7.61	3.87	11.32	6.42	within
e101297	SSSTEERRLHYGENGVQKDVSQRS	none	Semenogelin-1	7.2	3.59	13.26	9.54	within
e106039	TTLEIVLSVLLLVLFIISIVLIVLL	none	Maltase-glucoamylase	9.56	4.51	12.34	10.37	within
e214498	GAPPPGYGAPPAGYGAQPVGNEGPPVGYR	none	Postacrosomal sheath WW domain-binding protein	6.83	2.65	15.34	9.61	within
e021530	LKNGERIEKVEHSDLSFSKDWSF	none	Beta-2-microglobulin	7.14	3.1	12.69	10.12	within
e021534	RGRRVYYDEGVASSDDSSGDESDD	none	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	6.11	2.48	10.21	7.89	within
e214500	GDAGREGFPGPFGIGPRGSKGAVGLPGP*	3xOxidation [P17; P27; P29]	Collagen alpha-2(IV) chain	11.53	7.63	13.17	11.71	within
e101985	GHPGSPGEKGEKGETGQAGSPGEKGEAGE*	2xOxidation [P3; P6]	Collagen alpha-1(XIII) chain	8.54	4.61	11.45	4.88	within
e021544	WKVDNALQSGNSQESVTEQDSKDST	none	Immunoglobulin kappa constant	9.78	5.26	12.19	10.94	within
e021545	LPTTTTVTTFSQLPTAVPTATSSAAD	none	Nuclear envelope pore membrane protein POM 121C	10.07	6.04	12.21	10.93	within
e204774	GAPGLPGPPGKGKDGEPLRGSPGLPGPLG*	4xOxidation [P6; P8; P9; P17]	Collagen alpha-1(XXII) chain	9.81	5.52	12.23	11.1	within
e021551	DAHKSEVAHRFKDLGEENFKALVL	none	Albumin	9.81	4.05	17.52	9.47	within
e021588	GGMVSSQELAEDLTGIEILLERHQE	none	Spectrin alpha chain, erythrocytic 1	9.17	5.13	11.38	9.27	within
e214516	TWGAGQAKGSSLAHGAHGNKGGSGKSA GK	none	Lysine-specific demethylase PHF2	8.91	2.94	16.28	10.18	within
e021612	GPPGADGQPGAKGEPGDAGAKGDAGPPGPAGP*	3xOxidation [P9; P15; P26]	Collagen alpha-1(I) chain	12.0	8.26	13.37	12.39	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e103756	PGSPGGPGSDGKPGPPGSQGESGRPGPPGPS*	3xOxidation [P7; P13; P15]	Collagen alpha-1(III) chain	10.3	5.71	12.06	12.12	up
e021622	TPGTDGPKGASGPAGPPGAQGPPGLQGM PGE*	1xOxidation [P]	Collagen alpha-1(II) chain	10.47	6.31	12.35	12.11	within
e021623	PTGARGPEGAQQPRGEPGTPGSPGPAGASGN*	1xOxidation [P17]	Collagen alpha-1(II) chain	9.86	5.99	12.76	13.6	up
e021624	PAGPTGPRGFPGPPGPDGLPGSMGPPGTPS*	3xOxidation [P1; P4; P7]	Collagen alpha-1(IV) chain	10.01	5.49	13.01	11.44	within
e100238	RGDAGQKGERGEPGGGGFFGSSLPGPPGP*	2xOxidation [P27; P]	Collagen alpha-1(XVIII) chain	9.47	5.3	11.43	12.93	up
e021626	STPGSGGSSTPGSGSSSGGAGSSNSGGGSGSGN	none	Cbp/p300-interacting transactivator 2	9.19	2.48	12.47	6.29	within
e021627	DGLPGRDGSPGGKGDRENGSPGAPGAPGH*	2xOxidation [P10; P22]	Collagen alpha-1(III) chain	10.63	5.84	12.45	11.4	within
e214526	GDPGPPGIPGRNGDPGIPGQPGSPGSPGPPG*	1xOxidation [P30]	Collagen alpha-1(III) chain	10.46	5.8	12.79	11.32	within
e021632	KNGETGPQGPPGPTGPGGDKGDTGPPGPQG*	3xOxidation [P]	Collagen alpha-1(III) chain	10.01	6.07	11.87	10.86	within
e021633	TNAETAKEWFLQAAKDPSAVAKHFV	none	Glucose-6-phosphate isomerase	6.67	1.1	13.47	8.59	within
e021634	TWASHEKMHEGDEGPGHHHKPGLGE	none	Protein S100-A9	6.5	2.43	10.97	7.75	within
e214528	PGPKGTPGVAGPSGEPGMPGKDGQNGVPL*	3xOxidation [P/M]	Collagen alpha-3(IX) chain	6.75	2.16	11.07	3.91	within
e204787	ERGETGPPGPAGFAGPPGADGQPGAKGEQG*	1xOxidation [P]	Collagen alpha-1(II) chain	5.79	3.02	12.1	8.87	within
e021641	ERGSPGPAGPKGSPGEAGRPGEAGLPGAKG*	4xOxidation [P10; P14; P20; P26]	Collagen alpha-1(I) chain	11.62	5.79	14.94	13.98	within
e214538	ERGLPGEFGPGPKGEKGSEGPTGPQGLQ	none	Collagen alpha-1(XXVIII) chain	9.73	4.69	12.73	11.87	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214543	GPAGSKGESGNKGEPGSAGPQGPPGPSG EEG*	2xOxidation [P2; P15]	Collagen alpha-2(I) chain	12.96	7.01	16.16	11.97	within
e099129	KNGETGPQGPPGPTGPGGDKGDTGPPGP QG*	1xCation:Na [D]; 2xOxidation [P16; P25]	Collagen alpha-1(III) chain	10.19	6.06	12.73	7.99	within
e214546	GLDGAKG DAGPAGPKGEPGSPGENGAPG QMG*	2xOxidation [P11; P14]	Collagen alpha-1(I) chain	12.94	6.67	16.16	11.98	within
e103879	PGASGPIGPGGPPGLPGPAGPKGAKGATG PGGP*	5xOxidation [P16; P18; P21; P]	Collagen alpha-2(XI) chain	7.01	4.72	13.57	9.28	within
e204790	PKRKAEGDAKGDKAKVKDEPQRRSA	none	Non-histone chromosomal protein HMG-17	6.97	1.38	12.8	8.2	within
e204792	FGHGAEDSLADQAANEWGRSGKDPNH	none	Serum amyloid A-1 protein	7.73	3.2	11.29	6.52	within
e214547	WSEVSSLSDSTRRLTSESDYSSEG	none	Ankyrin repeat domain-containing protein 11	12.14	6.29	14.5	11.41	within
e021663	DQGGPDGSPGSPGAGPAGPPGYGPQ GEP*	1xOxidation [P]	Collagen alpha-3(IV) chain	10.32	5.88	12.29	10.78	within
e021665	SPGGPGAAGFPGARGLPGPSNGNPGP PGPS*	2xOxidation [P20; P26]	Collagen alpha-1(III) chain	8.85	4.13	12.13	6.95	within
e214551	LSFQGPKGDKGDQGVSGPPGVPGQAQVQ*	2xOxidation [P6; P18]	Collagen alpha-1(IV) chain	6.66	1.68	13.61	8.03	within
e021666	QPGFPGPPGPPGFPKGVGSPGPPGPQAEK *	2xOxidation [P23; P25]	Collagen alpha-1(XVI) chain	9.07	4.63	12.2	5.46	within
e021672	PPGPTGPGGDKGDTGPPGPQLQLPGT GGP*	3xOxidation [P19; P26; P31]	Collagen alpha-1(III) chain	11.28	7.13	12.94	11.41	within
e214553	GPVGALGLKGNEGPPGPPGAGSPGERGP AG*	4xOxidation [P2; P14; P15; P17]	Collagen alpha-1(V) chain	6.74	0.64	19.93	3.39	within
e093867	QPGLPGPPGPPGPPGGLGGNFAPQLSY *	3xOxidation [P5; P7; P8]	Collagen alpha-1(I) chain	11.28	7.27	12.96	11.4	within
e021673	KEGGKGPRGETGPAGRPGEVPPGPPGP AG*	3xOxidation [P22; P23; P]	Collagen alpha-1(I) chain	11.25	7.17	12.94	11.4	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e100302	ERGEAGIPGVPGA [*] KGEDGKDGSPGEPGAN [*]	4xOxidation [P8; P11; P23; P26]	Collagen alpha-1(III) chain	8.14	4.1	11.23	8.96	within
e204804	PPGADGQPGA [*] KGE [*] PGDAGAKGDAGPPGPAGPA [*]	3xOxidation [P1; P14; P26]	Collagen alpha-1(I) chain	6.79	3.05	10.42	8.15	within
e214554	GPPGRDGAAGVKGDRGETGAVGAPGAPGPPGS	none	Collagen alpha-1(II) chain	10.32	5.84	12.35	10.97	within
e021682	TGISGPPGQPLPGLPGPPGSLGFPGQKG ^E	1xOxidation [P6]	Collagen alpha-5(IV) chain	6.43	2.43	14.14	3.9	within
e021686	GDVGEKGPEGAPGKDGGRGLTGPIGPPGPAG [*]	1xOxidation [P27]	Collagen alpha-1(II) chain	7.9	4.49	11.38	8.47	within
e021687	IMYKVPLIRKKSLRRTLSE ^R GLL	none	Pepsin A-4	5.96	0.38	11.76	4.28	within
e214555	GPPGADGQPGA [*] KGE [*] PGDAGAKGDAGPPGPAGP [*]	4xOxidation [P9; P15; P26; P]	Collagen alpha-1(I) chain	9.59	6.03	11.83	11.56	within
e106703	PGPPGPAGFAGPPGADGQPGA [*] KGE [*] PGDAGAKG [*]	2xOxidation [P]	Collagen alpha-1(I) chain	6.14	2.43	13.74	4.93	within
e214558	APGPQGFQGNPGE [*] PGEPGVSGPMGRGP ^P	3xOxidation [P4; P11; P]	Collagen alpha-1(II) chain	10.0	5.9	12.09	9.3	within
e021698	PTGARGPEGAQGP ^R GE [*] PGTPGSPGPAGASGN [*]	2xOxidation [P1; P7]	Collagen alpha-1(II) chain	10.69	6.08	13.01	11.2	within
e214559	ASSTSPSPEPADAAGSGTG ^F QPVAVPPPH ^G	none	Mitogen-activated protein kinase kinase kinase 1	9.64	5.17	12.27	10.36	within
e021704	PPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPG [*]	1xOxidation [P19]	Collagen alpha-1(I) chain	6.15	1.83	10.65	10.32	within
e099522	FPGPRGPPGPQGATG ^L PLGPKQTGE ^P GIA [*]	5xOxidation [P4; P7; P8; P10; P16]	Collagen alpha-1(II) chain	9.71	3.56	14.41	11.61	within
e095715	TPAPLDSVFSSSERAHQ [*]	1xO-Glycan [T1] (Hex(1)HexNAc(1)NeuAc(2))	Vitamin K-dependent protein C	10.62	4.71	12.63	12.62	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021712	PQGQQQPGPGQQLGGQGAAPGAGGGPGGGPGPG	none	Ubiquitin-conjugating enzyme E2 Q1	8.81	3.9	12.1	3.36	down
e214563	PGGPGKSGSMGPVGP PG PAGERGHPGAPGPSG*	1xOxidation [P28]	Collagen alpha-1(XVI) chain	9.45	3.75	12.38	9.95	within
e102866	GPPGPRGAKGDMGERGPRGLDGDKGPRG*	2xOxidation [P5; P17]	Collagen alpha-1(VII) chain	8.58	4.36	13.5	11.4	within
e103625	GPPGPKGNSGEPGAPGSKGDTGAKGEPGPVG*	4xOxidation [P3; P12; P15; P27]	Collagen alpha-1(I) chain	7.45	4.09	11.36	9.65	within
e021724	SPGPGASASAGAGAGASAGSNGSNYLEEVRE	none	E3 ubiquitin-protein ligase Praja-1	7.6	2.94	11.18	6.58	within
e021725	GPSGESRPGSPGPPGSPGPRGPPGHLGVPG*	5xOxidation [P14; P17; P19; P22; P23]	Collagen alpha-1(XIV) chain	10.15	5.09	12.61	11.65	within
e300145	EAEDLQVGQVELGGGPGAGSLQPLALEGS	none	Insulin	10.18	4.09	13.23	13.47	up
e021728	QEKLSPLGEEMRDRARAHVDALRT	none	Apolipoprotein A-I	7.21	2.26	13.92	12.32	within
e021734	EISLSEIKDAPKVNAVDTLNVKDIAP	none	Rho GTPase-activating protein 7	7.75	2.51	14.02	12.54	within
e021736	DGAAGVKGDRGETGAVGAPGAPPPGSPGPAG*	6xOxidation [P19; P22; P24; P25; P28; P30]	Collagen alpha-1(II) chain	9.33	4.45	12.06	11.15	within
e214572	PPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGA*	2xOxidation [P2; P4]	Collagen alpha-1(I) chain	7.52	4.07	13.06	5.95	within
e021742	TGPAGPPGNPGPPGPPGPPGIDMSAFAG*	10xOxidation [P6; P7; P10; P12; P13; P15; P16; P18; P19; P]	Collagen alpha-1(II) chain	11.13	6.9	13.71	6.88	down
e021747	AGPPGGPGDKGDPGEDGQPGPDGPPGPA GTTG*	1xOxidation [P]	Collagen alpha-2(V) chain	11.18	6.91	13.54	9.78	within
e021749	GPLGPPGLPGFAGNPGPPGLPMKGDPGEI*	2xOxidation [P2; P5]	Collagen alpha-1(IV) chain	6.14	2.1	11.79	10.93	within
e021751	DQGPPGDPGSPGSPGAPGAPPPGYGPQGE*	2xOxidation [P11; P14]	Collagen alpha-3(IV) chain	9.0	4.86	12.16	10.36	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214577	HVTDHIHAGMETTYTVLQNETKSG	none	Ceruloplasmin	7.28	3.56	11.36	8.45	within
e214578	GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPG*	1xOxidation [P18]	Collagen alpha-1(I) chain	7.34	3.7	11.36	8.65	within
e099807	GPPGAPGPQGFGPPGEPGEPGASGPMGPR*	3xOxidation [P3; P15; P29]	Collagen alpha-1(I) chain	10.07	5.6	12.98	10.82	within
e021758	SKEEDKHLKFRISHELDSASSEVN	none	Osteopontin	6.87	3.38	13.08	7.84	within
e021759	SPGLKGESGDLGPQGPRGPQGLTGPPGKAG*	1xOxidation [P19]	Collagen alpha-2(XI) chain	6.75	2.9	12.59	8.61	within
e105748	GIDGSPGEKGDVGGPDPGASGEPGAPGP*	3xOxidation [P6; P12; P27]	Collagen alpha-3(V) chain	7.64	4.35	10.84	6.88	within
e300036	ATIPRQDEVPPQTVAPQQQ*	1xO-Glycan [T13] (Hex(1)HexNAc(1)NeuAc(1))	Tumor necrosis factor receptor superfamily member 10D	9.21	4.46	12.39	8.87	within
e214586	RGFPGIQGPPGLPGPPGAAMGPPGPPGF*	7xOxidation [P4; P9; P10; P13; P15; P16; P23]	Collagen alpha-5(IV) chain	8.49	4.13	15.05	9.1	within
e214587	PGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG	none	Collagen alpha-1(I) chain	8.06	3.84	12.87	9.6	within
e214588	GPPGIQGLPGPTGIPGIGPPGPPGLMGPP*	7xOxidation [P3; P9; P11; P15; P17; P20; P21]	Collagen alpha-5(IV) chain	8.38	4.34	14.94	10.4	within
e021790	VVDYSQFQESDDADEDYGRDSGPPT	none	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	4.51	1.96	11.91	2.81	within
e021791	QSLPHENKPLTSLSNYQTNKAKHDE	none	Cystatin-B	10.96	5.21	15.04	12.94	within
e021797	GPAGKDGEAGAQQPPGPAGPAGERGEQGPAG*	6xOxidation [P2; P14; P15; P17; P20; P29]	Collagen alpha-1(I) chain	8.77	4.21	11.5	5.95	within
e214590	PQGPDPGPPGRDGTGPRDGEPPGDPGEDGKP	none	Collagen alpha-1(XVIII) chain	8.52	3.47	12.93	7.99	within
e021798	HKSVQANLDQSQRGSSPQNTTTPKPS	none	Inverted formin-2	8.92	4.38	13.01	10.45	within
e021806	HPEDVQSSNGSVYTWREAFNETNQ	none	Phospholipid-transporting ATPase ABCA1	9.82	5.32	12.15	8.22	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021815	TGTTGLSAGETGKIGSSAGVTGKTGSSARVT	none	Mucin-19	6.38	2.77	11.53	10.61	within
e021814	TGGIKEAAAAGAAAGAATGTVAGALSVAAA NSAP	none	Golgi-associated RAB2 interactor protein 4	6.19	2.29	12.89	10.69	within
e021816	GEKGEPGADGEAGRPSSGPGSGDEGQPG EP*	2xOxidation [P20; P27]	Collagen alpha-1(VI) chain	11.11	5.98	12.88	11.17	within
e105226	AKGEAGPTGARGPEGAQGPGEPTPGSPGP	none	Collagen alpha-1(II) chain	8.18	5.26	11.43	7.54	within
e103426	PPGPPGSPGEQGPSGASGPAGPRGPPGS AGAP*	6xOxidation [P8; P13; P19; P22; P25; P26]	Collagen alpha-1(I) chain	8.57	4.34	12.13	10.86	within
e021822	EPGDPGPMGPISRGPEGPPGKPGEDGE P*	2xOxidation [P7; P10]	Collagen alpha-2(V) chain	8.48	4.69	11.03	10.47	within
e214594	ADKTNVKAAWGKVGHAHAGEYGAEALER	none	Hemoglobin subunit alpha	5.72	2.09	12.36	8.19	within
e021825	SGGGYGGGSSGGGSSGGGYGGGSSSGG HGGSSSGGY	none	Keratin, type I cytoskeletal 10	14.83	12.56	16.24	16.5	up
e021831	RGPRGDPGEAGPQGDQGREGPVGVPGDP G*	2xOxidation [P3; P7]	Collagen alpha-1(VI) chain	9.34	4.0	12.4	2.35	down
e098050	FKDSAHGFLKVPPRMDAKMYLGYE	none	Serotransferrin	6.9	2.17	11.62	9.22	within
e021836	SSGGGSSGGGHGGGHGGSSGGGYGGGS SGGGSSGGGY	none	Keratin, type I cytoskeletal 10	14.42	12.25	15.93	16.43	up
e021838	GPQGFQGPAGEPGEPGQTGPAGARGPAG PPG*	3xOxidation [P26; P29; P]	Collagen alpha-2(I) chain	8.55	4.3	11.51	3.85	down
e021839	KNGERIEKVEHSDLSFSKDWSFY	none	Beta-2-microglobulin	7.4	3.74	11.35	5.87	within
e021840	EDAGAGGEDVGAGGEDAGAGGEDAGAGG EDAGPG	none	Golgin subfamily A member 6-like protein 2	11.69	8.81	13.32	15.37	up
e021842	DKKREEAPSLRPAPPPISGGGYRARP	none	Fibrinogen beta chain	6.47	2.26	11.32	9.59	within
e021847	PVPFGGPLVGGTFPRPGTPFIPEPLSGL	none	Myozenin-3	5.93	2.06	11.09	7.27	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021856	PGDKGSPGSRGLPGFPGPQGPAGRDGAPGN*	3xOxidation [P7; P13; P16]	Collagen alpha-1(XXII) chain	8.89	4.45	11.75	11.0	within
e021861	AGPQQPRGSEGPQGVRGEPGPPGPAGAA GPAG*	1xOxidation [P]	Collagen alpha-1(I) chain	8.89	5.65	12.35	9.21	within
e214610	KDGETGAAGPPGPAGPAGERGEQGAPGPSGF*	2xOxidation [P16; P26]	Collagen alpha-1(II) chain	7.99	3.89	11.72	9.51	within
e021878	MGLMGRGPPGAAGAPGPQGFQGPAGEPGE*	4xOxidation [P6; P9; P10; P16]	Collagen alpha-2(I) chain	12.13	9.24	14.0	12.17	within
e204889	GFPGAPGQNGEPGGKGERGAPGEKGEGGPP*	4xOxidation [P3; P6; P12; P21]	Collagen alpha-1(III) chain	11.62	7.69	13.72	12.26	within
e204894	KDGENGQPGIPLPGDPGYPGEPGRDGE*	3xOxidation [P8; P11; P14]	Collagen alpha-5(IV) chain	12.17	8.09	14.06	11.07	within
e214611	VMGFPGPKGNDGAPGKNGERGGPGGPGPQG*	4xOxidation [P14; P23; P26; P28]	Collagen alpha-1(III) chain	12.74	10.16	14.23	12.07	within
e204895	RGPSGAPGADGPQGGPGGIGNPGAVGEKGEPP*	1xOxidation [P7]	Collagen alpha-1(V) chain	12.53	9.43	14.15	12.06	within
e021884	SWGLPGSKGEKGDQGAQGGPPGPLDLAY*	2xOxidation [P20; P22]	Collagen alpha-1(XV) chain	8.96	3.32	11.76	11.63	within
e101294	SPGPKGDKGEPGGPGADGVPGKDGPRGPTGP*	1xOxidation [P]	Collagen alpha-1(III) chain	11.34	6.76	13.0	11.19	within
e021887	RGGPGGGPGPQGGPKNGETGPQGGPPGPTGPG*	6xOxidation [P7; P9; P12; P13; P21; P24]	Collagen alpha-1(III) chain	9.08	4.79	12.3	9.13	within
e021891	EDLEETLFEEFENYSYDLDYYS	none	Chemerin-like receptor 2	6.66	3.47	11.7	5.55	within
e021914	TWASHEKMHEGDEGPGHHHKPGLGEG	none	Protein S100-A9	6.98	1.76	12.69	11.14	within
e021922	GVPGKDGQAGQPGQPQPGKDPGISGTPGAPG*	5xOxidation [P3; P12; P15; P17; P21]	Collagen alpha-1(IV) chain	10.6	6.13	12.53	10.65	within
e021923	GGKPGDQGVPGGEAGAPGLVGPRGERGFGE*	1xOxidation [P10]	Collagen alpha-1(II) chain	6.62	0.79	11.07	9.16	within

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e021928	FGGGSFGGGSFGGGGFGGGGFGGGFGG GFGGDGGL	none	Keratin, type I cytoskeletal 10	9.58	5.2	12.69	10.0	within
e101997	FAGPPGADGQPGAKGEPGDAGAKGDAGP PGPA*	3xOxidation [P11; P17; P28]	Collagen alpha-1(I) chain	9.6	5.11	12.71	9.93	within
e021933	DGKSESSYSGGGGHSSSEPWEYKSSGNG	none	NHS-like protein 1	8.11	4.1	11.54	9.89	within
e098057	GDPGDVGGPGPPGASGEPGAPGPPGKRG PSGH*	3xOxidation [P18; P21; P23]	Collagen alpha-3(V) chain	6.36	2.87	13.2	12.28	within
e106331	VTGSGTQTQAGATQTVEQDSSHQTGRTS	none	Cornulin	7.99	3.48	11.36	10.01	within
e021937	SRGKDSYETSQLDDQSAETHSHKQS	none	Osteopontin	7.93	4.02	11.83	9.4	within
e100292	GFAGPPGADGQPGAKGEPGDAGAKGDAG PPGP*	4xOxidation [P6; P12; P18; P30]	Collagen alpha-1(I) chain	9.94	4.8	12.13	10.93	within
e021938	REGLPGDRGDPGDTGAPGPVGMKGLSGD R	none	Collagen alpha-2(IV) chain	9.41	4.81	11.9	11.43	within
e021939	PPGATGFPGAAGRVGPPGPSGNAGPPGPP GPAG*	3xOxidation [P19; P25; P26]	Collagen alpha-1(I) chain	6.75	2.78	10.2	6.68	within
e021946	PLHSLRYFISMVGLFSKPGLLPWY	none	tRNA (uracil-5-)-methyltransferase homolog B	5.8	0.98	9.94	10.39	up
e021951	TGARGLVGEPGPAGSKGESGNKGEPGSA GPQ*	1xOxidation [P10]	Collagen alpha-2(I) chain	8.19	3.36	12.25	9.48	within
e021958	ARGNDGARGSDGQPGPPGPPGTAGFPGS PGA*	4xOxidation [P16; P17; P19; P20]	Collagen alpha-1(III) chain	7.99	5.02	10.75	7.21	within
e208664	PGPAGPPGPPGPPGTSGHPGSPGSPGYQ GPP*	7xOxidation [P7; P9; P10; P12; P13; P19; P22]	Collagen alpha-1(III) chain	8.33	4.89	11.75	10.29	within
e214627	GSQGGNDTSPTGNSTPGLNTGNNPPAQN GI	none	Enamelin	12.44	9.44	13.98	12.23	within
e021963	LRGGAGPPGPEGGKAAGPPGPPGAAGT PGLQG*	4xOxidation [P10; P19; P20; P22]	Collagen alpha-1(III) chain	12.36	8.03	13.94	12.1	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e021964	NSSDVPGPAGLPGVPGREGPPGFPGLPGP P*	3xOxidation [P24; P27; P29]	Collagen alpha-1(XVIII) chain	8.0	5.05	11.23	10.25	within
e105614	DIPDPGPPGDQPPGPDGPRGAPGPPGLP *	9xOxidation [P8; P13; P14; P16; P19; P23; P25; P26; P29]	Collagen alpha-4(IV) chain	11.08	6.19	13.7	8.86	within
e021969	FPGAPGQNGEPGGKGERGAPGEKGE ^{GGP} PG*	5xOxidation [P2; P5; P11; P20; P28]	Collagen alpha-1(III) chain	9.14	6.1	12.4	9.99	within
e021970	GPPGFPGAPGPKGEIGAVGNAGPAGPAGP RGE*	2xOxidation [P3; P6]	Collagen alpha-2(I) chain	10.79	6.4	13.7	11.0	within
e214630	ERGEAGIPGVPGA ^{KGEDGKDGSPGE} PGAN G*	4xOxidation [P8; P11; P23; P26]	Collagen alpha-1(III) chain	17.05	15.53	18.07	17.6	within
e214631	ERGEAGIPGVPGA ^{KGEDGKDGSPGE} PGAN G*	4xOxidation [P8; P11; P23; P26]	Collagen alpha-1(III) chain	17.06	15.54	18.11	17.61	within
e021977	RKGPAGDRGPRGERGPPGPPGRDGEDGP *	2xOxidation [P19; P20]	Collagen alpha-2(I) chain	5.72	1.87	9.51	9.62	up
e102287	GKNGSPGSPGEPGSGTPGQKGS ^{KGENG} SPG*	4xOxidation [P9; P12; P14; P18]	Collagen alpha-1(XXII) chain	13.0	8.64	15.12	14.53	within
e100517	KTETQEKNPLPSKETIEQEKQAGES	none	Thymosin beta-4	6.9	3.73	12.13	7.27	within
e204942	PSGFPGTPGFPGPKGS ^{RGLPGTPGQPGSS} G*	6xOxidation [P1; P5; P8; P11; P13; P20]	Collagen alpha-6(IV) chain	7.44	3.18	12.13	5.0	within
e021998	DAAQKTDTSHHDQDHPTFNKITPNL	none	Alpha-1-antitrypsin	7.4	3.49	11.38	4.94	within
e021999	GPPGKAGPPGPKGE ^{PGKAGPDGPDGKPGI} D*	8xOxidation [P3; P8; P9; P11; P15; P20; P23; P27]	Collagen alpha-2(IX) chain	7.34	1.78	14.51	7.17	within
e101860	DLLKNGERIEKVEHSDLSFSK ^{DWS}	none	Beta-2-microglobulin	6.12	1.6	14.14	2.81	within
e022001	ERSDSTGSSSVYFTASSGATFTDAESEG	none	Regulator of microtubule dynamics protein 3	10.07	4.46	13.87	5.81	within
e214637	GPPGAPGLGPPGFG ^{RPGDPGPPGPPGP} PGPP*	2xOxidation [P9; P11]	Collagen alpha-1(XV) chain	7.85	5.13	12.37	4.18	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022005	RQEREGFLPSRGPAPGSKPVQFMDF	none	Sodium-coupled neutral amino acid transporter 5	7.0	3.45	11.8	7.03	within
e103323	DTEEGPENSQGAQELSLAPHPEVSQSV	none	Microtubule-associated serine/threonine-protein kinase 2	6.38	2.13	11.08	7.91	within
e101642	PGAPGQPGMAGVDGPPGPKGNMGPGGEPGP*	8xOxidation [P1; P4; P7; P15; P16; P18; P24; P28]	Collagen alpha-1(XI) chain	10.89	4.49	12.59	8.64	within
e022012	HAQPSYQQPQSQPPQLQSSQPPYS	none	AT-rich interactive domain-containing protein 1A	7.77	3.61	12.74	10.52	within
e214644	AQGPPGATGFPGAAGRVGPPGSNGNPGPGPP*	3xOxidation [P11; P19; P]	Collagen alpha-1(II) chain	13.23	6.8	17.24	10.77	within
e214645	GAKGQEGAHGAPGAAGNPGAPGHVGAPGPSGPPG	none	Collagen alpha-1(XXII) chain	12.72	8.18	15.89	11.4	within
e103888	TQGPPGATGFPGSAGRVGPPGPAGAPGPA GPLG*	2xOxidation [P]	Collagen alpha-2(V) chain	12.66	7.83	15.9	11.88	within
e214650	PAGPRGPPGSAGAPGKDGLNGLPGPIGPPGP*	8xOxidation [P4; P7; P8; P14; P23; P25; P28; P29]	Collagen alpha-1(I) chain	13.07	9.64	14.76	12.62	within
e022038	RGAKGDPGAPGVGLRGEMGPPGIPGQPGEP*	2xOxidation [P10; P20]	Collagen alpha-1(XXII) chain	13.06	9.67	14.76	12.54	within
e103600	FPGAPQNGEPGGKGERGAPGEKGEGGPPG*	6xOxidation [P2; P5; P11; P20; P28; P29]	Collagen alpha-1(III) chain	12.38	8.53	14.24	11.44	within
e022041	PPGSRGASGPAGVRGPNGDAGRPGEPGLMGP*	1xOxidation [P]	Collagen alpha-2(I) chain	12.68	9.79	14.3	12.13	within
e022040	VPGKKGDDGTPSQPGPPGPKGEPGSMGPRG	none	Collagen alpha-1(XXIII) chain	7.02	4.28	12.26	3.86	down
e214656	ERGYTGSAKEGEPGPPGSEGLPGPPGPAG*	5xOxidation [P17; P23; P25; P26; P28]	Collagen alpha-1(XVI) chain	13.8	11.4	15.08	15.21	up
e022045	QPGAAGANGAPGIAGAPGFPGARGPSGPQGP*	2xOxidation [P20; P25]	Collagen alpha-1(I) chain	13.46	10.46	14.8	15.37	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022054	EALDAVSTLEEGHAQYLTSLADASALVA	none	Huntingtin-interacting protein 1-related protein	7.89	4.05	12.36	10.66	within
e022061	GPKGNMGPPQGEPGPPGQQGNPGPQGLP GP*	9xOxidation [P2; P8; P12; P14; P15; P21; P23; P27; P29]	Collagen alpha-1(XI) chain	12.64	8.85	15.14	10.83	within
e022064	SWYDNEFGYSNRVVDLMAHMASKE	none	Glyceraldehyde-3-phosphate dehydrogenase	11.92	7.38	14.33	10.2	within
e100855	GRDGNPGNDGPPGRDQPGHKGERGYP G*	3xOxidation [P12; P18; P27]	Collagen alpha-2(I) chain	7.85	3.34	11.21	9.89	within
e022072	DPSLAVSDVVGHFDDLADPSSSQDGSFS	none	TOX high mobility group box family member 4	9.74	4.62	12.71	8.59	within
e105220	SQTSQAVTGGHTQIQAGSHTETVEQDR	none	Cornulin	9.5	4.7	13.11	10.85	within
e022088	RGFDGLPGLPGDKGHRGERGPQGPPGPP*	3xOxidation [P21; P24; P25]	Collagen alpha-1(XI) chain	7.82	0.03	10.91	9.16	within
e022089	VRKDLQNFLKKENKNEKVEIHIM	none	Protein S100-A9	7.01	0.31	11.93	9.97	within
e214659	PTGARGPEGAQQPRGEPGTPGSPGPAGA SGNP*	1xOxidation [P23]	Collagen alpha-1(II) chain	10.47	5.86	13.23	12.44	within
e214660	LSDPEQGVVEVTGQYEREKAGFSWIE	none	Inter-alpha-trypsin inhibitor heavy chain H4	11.32	5.67	13.51	12.51	within
e022091	GFPGSDGLPGPKGAQGERGPVGSSGPKG SQG*	2xOxidation [P9; P]	Collagen alpha-2(V) chain	10.36	5.85	13.2	12.32	within
e214661	GPAGPNGIPGEKGPAGERGAPGPAGPRGA AGE*	3xOxidation [P2; P5; P9]	Collagen alpha-1(III) chain	11.32	5.98	13.46	12.66	within
e095780	GTAGPTGPPGVPGSPGITGPPGPPGPPGP PGAPG*	3xOxidation [P12; P15; P20]	Collagen alpha-2(VIII) chain	11.14	4.4	13.52	12.52	within
e022102	ISGGGYGSGGGSGGRYGSGGGSKGGSIS GGGYGSG	none	Keratin, type II cytoskeletal 2 epidermal	8.73	4.84	11.86	11.57	within
e022105	PPGPPGKNGDDGEAGKPRPGERGPPGP Q*	5xOxidation [P4; P5; P17; P20; P25]	Collagen alpha-1(I) chain	9.6	4.59	12.27	12.04	within

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e214663	LPGKDGETGAAGPPGPAGPAGERGEQGA PGPS*	1xOxidation [P19]	Collagen alpha-1(II) chain	8.88	5.02	11.98	11.75	within
e214664	GPPGAKGQEGAHGAPGAAGNPGAPGHVG APGPSG*	1xOxidation [P]	Collagen alpha-1(XXII) chain	9.53	4.29	12.25	10.79	within
e214667	AVGAPGAPGPPGSPGPAGPTGKQGDRGE AGAQQ*	2xOxidation [P5; P8]	Collagen alpha-1(II) chain	14.71	11.85	16.53	14.84	within
e022114	ARGAQPPGATGFPGAAGRVGPPGSNGN PGPP*	2xOxidation [P31; P32]	Collagen alpha-1(II) chain	9.54	4.52	12.12	10.2	within
e022116	FQTVTDYGKDLMEKVKSPQLQAEAK	none	Apolipoprotein A-II	8.98	4.31	12.01	11.31	within
e214669	AGARGAPGPDGNNGAQGPPGPQGVQGGK GEQG*	1xOxidation [P18]	Collagen alpha-2(I) chain	7.13	4.18	10.7	10.17	within
e214670	QEGAHGAPGAAGNPGAPGHVGAPGPSGP PGSVGA*	1xOxidation [P28]	Collagen alpha-1(XXII) chain	8.95	5.07	11.85	10.39	within
e098063	PEAGGWEDASVGRQLQWRRVSAQESQG	none	Apical endosomal glycoprotein	12.44	9.12	14.37	12.78	within
e214672	GFPGPPGPPGFPKGVGSPGPPGPQAEKGS EG*	1xOxidation [P]	Collagen alpha-1(XVI) chain	11.35	5.77	13.8	12.54	within
e022128	GPQGPPGSGVSGGVGEKGEPGEAGNPG PPGE*	3xOxidation [P27; P29; P30]	Collagen alpha-1(XI) chain	6.13	2.24	9.9	2.41	within
e022132	MADEAGSEADHEGTHSTKRGHAKSRPV	none	Fibrinogen alpha chain	6.89	2.48	11.16	8.31	within
e300068	DVSTPPTVLPDNFPRYP*	1xO-Glycan [T4] (Hex(1)HexNAc(1) NeuAc(2))	Insulin-like growth factor 2	14.11	8.75	15.91	16.08	up
e022143	GRPGSSGSPSGDEGQPGEPGPPGEKGEAG DEG*	1xOxidation [P8]	Collagen alpha-1(VI) chain	14.02	8.84	16.75	11.02	within
e022144	GNPGVGTQGPGRGPPGPAGPSGESRPGSP GPPG*	2xOxidation [P28; P30]	Collagen alpha-1(XIV) chain	13.73	8.0	16.49	11.08	within
e022146	GRTGPAGAAGARGNDGQGPAGPPGPVG PAGGPG*	2xOxidation [P24; P26]	Collagen alpha-1(II) chain	13.17	7.3	16.15	11.14	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022150	GRDGNPGNDGPPGRDGGPGHKGERGYPG*	4xOxidation [P6; P11; P12; P18]	Collagen alpha-2(I) chain	11.56	7.33	13.89	13.04	within
e022155	ENTMAENEAGKEEQEGMEESPQSVGR	none	RNA-binding protein 20	9.78	5.18	12.5	12.24	within
e022157	GEPGIQGMPGASGLKGEPGATGSPGEPGYM*	5xOxidation [P3; P9; P18; P24; P27]	Collagen alpha-1(XI) chain	11.15	6.48	13.12	13.46	up
e022159	DAHKSEVAHRFKDLGEENFKALVLI	none	Albumin	6.62	1.72	16.4	4.95	within
e214679	GPTGPRGFPGPPGPDGLPGSMGPPGTPSV D*	7xOxidation [P2; P5; P9; P11; P12; P14; P18]	Collagen alpha-1(IV) chain	8.88	3.3	11.72	10.94	within
e101876	GPPGESGREGAPGAEGSPGRDGSPGAKG DRG*	3xOxidation [P3; P12; P18]	Collagen alpha-1(I) chain	9.13	4.9	11.81	11.1	within
e022162	GENGDVGPMPGPPGPPGRGPQGPNGADG PQG*	3xOxidation [P12; P14; P15]	Collagen alpha-1(XI) chain	8.24	3.18	11.76	10.47	within
e214682	GPSGLSIQGMGMPGEKGEKGDGLPGPQG*	2xOxidation [P2; P11]	Collagen alpha-1(XIV) chain	6.62	2.16	12.66	7.95	within
e022167	GVGGDKGEDGDPGQPGPGPSGEAGPPG PPGK*	3xOxidation [P27; P29; P]	Collagen alpha-1(XI) chain	9.62	5.59	12.61	11.97	within
e214684	GLPGSWGAGGPAGPTGYPGEPGLVGPPG QPG*	8xOxidation [P3; P11; P14; P18; P21; P26; P27; P30]	Collagen alpha-4(IV) chain	8.25	3.94	11.72	11.19	within
e022168	FGYFSSEEDPIASQLDEENLVFFVS	none	WD repeat-containing protein 64	10.17	6.06	12.0	9.62	within
e106429	TQQPQQDEMPSPTFLTQVKESLSSY	none	Apolipoprotein C-II	7.71	3.82	11.29	7.47	within
e022169	RLDQGNLHTSVSSAQGQDAAQSEKRG	none	Cornulin	9.35	4.85	12.93	11.81	within
e022174	PGGGISGGSGHRPHEGPGGGMGAGGGHR PHEG	none	Serine/threonine-protein phosphatase 1 regulatory subunit 10	6.76	2.38	11.5	7.75	within
e103057	PGLPGSWGAGGPAGPTGYPGEPGLVGPP GQPG*	2xOxidation [P]	Collagen alpha-4(IV) chain	8.88	4.31	11.53	9.72	within
e022182	LTWASHEKMHEGDEGPGHHHKPGLGE	none	Protein S100-A9	6.17	2.34	10.32	9.59	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e205049	PGQSYAGVVQYSHSQMQEHVSLRSPS*	1xOxidation [P25]	Collagen alpha-1(VI) chain	6.2	2.18	12.46	11.41	within
e022189	DKTNVKAAWGKVGGAHAGEYGAEALERM*	1xOxidation [M27]	Hemoglobin subunit alpha	7.35	4.43	13.35	9.09	within
e205052	ENDDPRPPNPPKMPNPNPNHPSSSGS	none	CD99 antigen	7.66	1.22	11.66	8.89	within
e022206	RGLPGEMGRPGPPGPPGAGNPGPSPNS PQ*	3xOxidation [P13; P15; P]	Collagen alpha-1(XXVI) chain	10.42	5.83	13.86	8.46	within
e214687	PGPAGKPGRRGRAGSDGARGMPGQTGPK GD*	2xOxidation [P1; P3]	Collagen alpha-1(V) chain	6.75	3.51	12.8	7.18	within
e214690	EVGAVGPPGFAGEKGPSGEAGTAGPPGTP GPQ*	3xOxidation [P26; P29; P]	Collagen alpha-2(I) chain	10.81	5.8	14.02	9.99	within
e022223	VEQQHSVEFDSPDGLPSSRNYSVASG	none	Small G protein signaling modulator 2	11.46	7.08	13.77	10.74	within
e022224	RDFVHSVQETHSQLLSWDPWEEP	none	Baculoviral IAP repeat-containing protein 7	7.41	3.35	12.16	8.32	within
e022230	TSPAGSSPAVAGGTQRPAEDSSSSEESDS E	none	Treacle protein	11.53	5.69	14.24	9.72	within
e022231	GITGPPGDGPKGFQGNKGEPGPPGPGYGS P*	4xOxidation [P6; P9; P11; P21]	Collagen alpha-1(XXVIII) chain	11.23	5.4	13.98	7.94	within
e022234	GRDGNPGNDGPPGRDQPGHKGERGYG*	5xOxidation [P6; P11; P12; P18; P27]	Collagen alpha-2(I) chain	9.66	5.55	12.3	11.24	within
e022235	GFGDIVDALSDPKKFLSITEKRADQM	none	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4	6.81	3.22	11.84	4.85	within
e022240	DSGATGLPGRPGPPGPPGPPGENGFPGQ MG*	8xOxidation [P11; P13; P14; P16; P17; P19; P20; P26]	Collagen alpha-1(IX) chain	5.43	1.47	8.49	7.02	within
e214695	NEKIQNEQLEKLQEQVTDLRSQNT	none	Nucleoprotein TPR	6.13	3.72	12.56	7.43	within
e022250	GMMGPPGVPGPKGSMGHPGMPGGMGTP GE*	8xOxidation [P5; P6; P9; P11; P18; P21; P27; P30]	Collagen alpha-1(XXVII) chain	10.32	5.39	13.23	8.49	within
e022254	GLPGSDGPLGHPGHEGPTGEKGAQGPPG SAG*	1xOxidation [P]	Collagen alpha-3(V) chain	10.13	5.35	12.69	12.63	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022257	AGFPGAPGQNGEPGGKGERGAPGEKGE GPPG*	1xOxidation [P]	Collagen alpha-1(III) chain	9.42	5.25	11.88	11.84	within
e022259	VGPMGPPGPPGPRGPQGPNADGPQGPP GSVG*	3xOxidation [P3; P6; P7]	Collagen alpha-1(XI) chain	8.84	4.36	11.92	10.46	within
e214700	GEVGPPGPPGPAGEKGSPGADGPAGAPG TPGPQG*	1xOxidation [P]	Collagen alpha-1(I) chain	11.98	8.75	13.55	12.18	within
e022260	ARGEPNIGFPGPKGPTGDPGKNGDKGHA G*	3xOxidation [P5; P11; P13]	Collagen alpha-2(I) chain	7.61	3.03	11.07	11.85	up
e214701	MPEPTSSPTIGPRKDSAAGPHGRMAGPST	none	t-SNARE domain-containing protein 1	11.9	8.9	13.43	12.61	within
e098080	PQGFQGPPEGEPGASGPMGPRGPPGP PG*	8xOxidation [P7; P8; P11; P14; P19; P22; P25; P26]	Collagen alpha-1(I) chain	9.33	5.15	12.02	9.76	within
e208686	GFDGLPLPGEKGQRGDFGHVQPGPPG E*	2xOxidation [P26; P27]	Collagen alpha-3(V) chain	10.33	6.3	12.56	10.37	within
e300144	EAEDLQVGQVELGGGPGAGSLQPLALEGS L	none	Insulin	8.28	2.58	12.2	12.06	within
e214702	EAEARGTRGAHGETEAEEGAPEGAEVPQG	none	Chloride intracellular channel protein 6	9.06	4.97	11.95	10.74	within
e214703	PAGNTGAPGSPGVSGPKGDAGQPGEKGS PGAQQ*	3xOxidation [P11; P16; P23]	Collagen alpha-1(III) chain	9.09	4.86	11.95	10.59	within
e022271	GEPGPKGQQGVRGEPGYPGPSGDAGAPG VQG*	2xOxidation [P]	Collagen alpha-2(IX) chain	9.77	5.34	12.99	11.31	within
e214705	ARGGGRSGFGGGYGGGGFGGGGFGGG GFGGGGIGGG	none	Keratin, type II cytoskeletal 1	9.63	5.4	12.09	10.68	within
e214706	QSLSSLEEFSEFHGSESGGWPEEEKPL	none	Rho GTPase-activating protein 31	10.89	5.98	13.08	12.21	within
e214709	LPGSKGDTGNPGAPGTPGTKGWAGDSGP QGR*	1xOxidation [P2]	Collagen alpha-2(IV) chain	10.48	4.98	13.19	12.27	within
e205080	QQLPGPPGNGEQGSAGIPGPFGRGPPG PV*	3xOxidation [P24; P27; P28]	Collagen alpha-2(V) chain	8.73	4.73	11.95	10.81	within

a: Distribution in healthy female

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e022285	GEVGPPGPAGSAGARGAPGERGETGPPG PAGF*	5xOxidation [P6; P8; P18; P26; P27]	Collagen alpha-1(II) chain	9.25	4.31	12.66	5.25	within
e022295	PGGPGMRGMPSGPGSDGKPGPPGS QGESG*	6xOxidation [P4; P10; P13; P16; P22; P24]	Collagen alpha-1(III) chain	6.64	3.17	10.87	8.27	within
e022297	TGSPGSPGPDGKTGPPGPAGQDGRPGPP GPPG*	6xOxidation [P15; P16; P18; P25; P]	Collagen alpha-1(I) chain	11.24	6.91	12.91	12.44	within
e214713	SPSSQSAAASSLGPYGAQPSASALSSYG GQA	none	RNA-binding protein 14	11.26	6.82	12.87	12.17	within
e214715	GDPGPMGPIGSRGPEGPPGKPGEDGEPEG RN*	2xOxidation [P18; P21]	Collagen alpha-2(V) chain	8.63	5.51	11.77	10.87	within
e098084	SGPPGDKGSPGSRGLPGFPGQGPAGRD GAPG*	1xOxidation [P]	Collagen alpha-1(XXII) chain	8.14	5.11	11.59	10.88	within
e022322	GAPGPAGARGNDGATGAAGPPGPTGPAG PPGFPG*	6xOxidation [P3; P5; P20; P21; P23; P26]	Collagen alpha-1(I) chain	6.5	3.91	9.64	9.53	within
e022323	DRGSPGVPGSPGLPGVPKGEPTGAP GQ*	8xOxidation [P5; P8; P11; P14; P16; P19; P23; P25]	Collagen alpha-1(VII) chain	9.69	5.17	12.48	11.17	within
e214720	NTWSSDSGSGGGGVTSSEYSTGPLNTP E	none	Mucin-19	7.1	3.11	11.74	9.61	within
e104075	SGERGPPGPMGPPGLAGPPGESGREGAP GAE*	5xOxidation [P7; P9; P12; P13; P18]	Collagen alpha-1(I) chain	10.78	5.56	12.34	10.73	within
e022329	FEGPPGAPGPQGVPVGPSPGPPGPFPGD PGPP*	2xOxidation [P]	Collagen alpha-3(V) chain	9.72	4.44	12.05	11.34	within
e022331	QSLPHENKPLTLSNYQTNKAKHDEL	none	Cystatin-B	9.77	4.23	13.75	10.6	within
e300088	TGEVGAVGPPGFAGEKGPSGEAGTAGPPG TPGP*	3xOxidation [P18; P28; P31]	Collagen alpha-2(I) chain	11.73	6.71	13.58	12.7	within
e022338	GESGNKGEPGSAGPQGPSPGSEEGKRG PNG*	4xOxidation [P17; P18; P20; P29]	Collagen alpha-2(I) chain	9.03	4.71	12.16	10.01	within

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e104483	TSPSYSPSSPRYTPQSPTYTPSSPSYS	none	DNA-directed RNA polymerase II subunit RPB1	9.8	5.29	12.42	11.37	within
e208690	ETGPAGRPGEVGPPGPPGAGEKGSPGADGPAG*	2xOxidation [P8; P13]	Collagen alpha-1(I) chain	9.03	4.35	12.22	10.08	within
e214724	GPPGAVGPAGKDGEAGAQQGPPGPAGPAGERGEQ*	1xOxidation [P23]	Collagen alpha-1(I) chain	7.25	4.14	11.76	9.99	within
e022340	RGPSGLPGSPGPPGPPGIQGPAGLDGLDKDG*	2xOxidation [P3; P7]	Collagen alpha-1(XVI) chain	8.63	4.42	11.96	11.17	within
e205109	TGELGDPGPRGNQGDRGDKGAAGAGLDGPEG*	2xOxidation [P7; P9]	Collagen alpha-3(IX) chain	8.91	4.61	12.31	9.9	within
e103963	GFPSPGAKGEVGPAGSPGSNGAPGQRGEPGP*	5xOxidation [P6; P14; P18; P24; P30]	Collagen alpha-1(III) chain	7.34	4.08	10.75	8.85	within
e095819	ESGREGAPGAEGSPGRDGSFGAKGDRGETGP*	1xOxidation [P20]	Collagen alpha-1(I) chain	10.25	5.81	12.35	12.36	up
e214730	ASPSLSYSTGHSPALSGHGGGWGPSSLGGGGE	none	Proline-rich protein 12	10.11	4.74	12.25	10.91	within
e022354	GPPGPPGKNGDDGEAGKPRPGERGPPGPQ*	5xOxidation [P5; P6; P18; P21; P26]	Collagen alpha-1(I) chain	9.28	4.86	12.59	11.4	within
e022358	PGAKGPTGSPGTSGPPGSAGPPGSPGPQGSTGPQ*	2xOxidation [P6; P]	Collagen alpha-2(V) chain	8.14	4.15	11.5	9.16	within
e022360	AGQDGPPGDKGDDGEPGQTGSPGPTGEPGPS*	6xOxidation [P6; P7; P16; P22; P24; P28]	Collagen alpha-1(V) chain	11.32	7.87	13.7	12.82	within
e214735	GEQGSPGASGPAGPRGPPGSAGAPGKDLNLGP*	3xOxidation [P17; P18; P24]	Collagen alpha-1(I) chain	11.11	6.89	13.12	13.42	up
e022377	STGAPGKPGQMNSGKPGQQGPPGEVGP RGP*	2xOxidation [P8; P17]	Collagen alpha-1(IX) chain	10.15	5.5	12.62	11.45	within
e022382	KDYYPNPYPSPYEGGAGTPSGTAAVAAD	none	Retinoic acid-induced protein 1	5.58	1.74	9.85	6.76	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214739	PAGATGDRGEAGAAGPAGPAGPRGSPGERGEVG*	2xOxidation [P16; P19]	Collagen alpha-2(I) chain	12.58	6.06	16.49	6.83	within
e022396	EVFLKLEGGKSTIDESDIGIWGQLQTD	none	ATP-binding cassette sub-family A member 9	6.97	2.96	10.01	4.82	within
e104549	ADDTWEPFASGKTSESGELHGLTTEEE	none	Transthyretin	9.17	3.91	11.89	10.54	within
e205129	TGEVGAVGPPGFAGEKGPSGEAGTAGPPGTPGP*	4xOxidation [P9; P18; P28; P31]	Collagen alpha-2(I) chain	11.24	6.23	13.09	12.92	within
e214744	LQGPRGPPGPVGGHGDGPPGAPGLAGPAGPQG*	3xOxidation [P10; P17; P19]	Collagen alpha-1(VII) chain	11.3	6.63	13.0	13.05	up
e022405	GPPGTEGESGLQGEPAKGDVGTAGSVGTGEP*	1xOxidation [P33]	Collagen alpha-1(XXIV) chain	6.14	1.94	10.24	8.3	within
e102062	SGLPGLPGPPGPPGPPHGPVLPEGATDLQ*	10xOxidation [P4; P7; P9; P10; P12; P13; P15; P16; P19; P23]	Collagen alpha-3(IX) chain	6.65	3.23	11.8	8.34	within
e022406	GQPGPSGLPGPKGEKGYPGEDSTVLGPPGP*	6xOxidation [P5; P9; P11; P18; P27; P28]	Collagen alpha-1(XXIV) chain	10.81	4.91	13.02	10.45	within
e214748	QQGRPGPSGVAGPQGEKGDVGPAGPPGPVPGSV*	2xOxidation [P7; P]	Collagen alpha-1(XXII) chain	10.2	5.45	12.4	9.95	within
e022410	TPEEKSAVTALWGKVNVDDEVGGEALGRL	none	Hemoglobin subunit beta	9.2	3.9	15.18	9.4	within
e022420	GAAGEAGGAGEAGGVGEAGAAGEAGGAGEAGAAGEAGGA	none	Paraneoplastic antigen Ma6E	9.03	4.6	11.32	10.36	within
e214751	GPPGPAGPSGESRPGSPGPPGSPGPRGPPGH*	11xOxidation [P3; P5; P8; P14; P17; P19; P20; P23; P25; P28; P29]	Collagen alpha-1(XIV) chain	11.67	8.46	13.83	13.2	within
e022422	PGMAGVDGPPGPKGNMGPQGEPGPPGQQGNP*	3xOxidation [P9; P10; P12]	Collagen alpha-1(XI) chain	7.76	3.7	11.72	7.53	within
e022421	ESGREGAPGAEGSPGRDGSFGAKGDRGETGP*	2xOxidation [P14; P20]	Collagen alpha-1(I) chain	11.65	8.22	13.81	13.09	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022428	GAGGEDVGAGREDAGAGGEDVGAGGEDV GAGRR	none	Golgin subfamily A member 6-like protein 2	6.86	2.49	11.26	5.78	within
e022429	APGADGPQGPPGGIGNPGAVGEKGEPEA GEPG*	3xOxidation [P10; P11; P17]	Collagen alpha-1(V) chain	10.46	7.02	12.58	12.11	within
e022430	RMAETVDTSEMVNGATEQRTSSKESSP	none	Spectrin beta chain, non-erythrocytic 1	6.95	2.68	12.14	6.14	within
e022432	EGGAPGLPGIAGPRGSPGERGETGPPGPA GFP*	2xOxidation [P8; P13]	Collagen alpha-1(III) chain	6.14	1.31	12.65	7.03	within
e214753	QTGSPGPTGEPGSPGPPGKRGP GPAGP EGR*	6xOxidation [P13; P16; P17; P22; P23; P25]	Collagen alpha-1(V) chain	7.96	4.1	12.23	11.14	within
e022435	PGAKGEQGPAGLPKPGLTGPPGNMGPG GPK*	5xOxidation [P13; P16; P21; P22; P27]	Collagen alpha-1(X) chain	7.44	3.62	11.6	10.02	within
e022443	LTWASHEKMHEGDEGPGHHHKPGLGEG	none	Protein S100-A9	8.52	1.59	14.36	11.42	within
e022445	HLASDFAFSPPPGGGGDGP GGPEPGWVD PR	none	POU domain, class 5, transcription factor 1	6.22	0.01	11.56	3.87	within
e208695	ESGNKGEPGSAGPQGPPGPSGEEGKRGP NGE*	1xOxidation [P13]	Collagen alpha-2(I) chain	10.32	5.42	12.82	7.38	within
e208696	PPGLQGPVGAPGIAGGDGEPGRGQQGM FGQ*	3xOxidation [P1; P2; P7]	Collagen alpha-1(XI) chain	11.02	7.31	13.19	13.19	within
e102801	EVGAVGP PGFAGEKGPSGEAGTAGPPGTP GPQG*	3xOxidation [P16; P25; P26]	Collagen alpha-2(I) chain	10.28	5.38	12.28	11.53	within
e022462	GPSGPPGPAGSPGERGAAGSGGPIGPPGR PGPQG*	3xOxidation [P5; P6; P8]	Collagen alpha-2(XI) chain	10.14	5.07	12.27	11.67	within
e104253	GEAGAPGVKGESGSPGENGSPGPMGPRG LPGE*	3xOxidation [P15; P21; P23]	Collagen alpha-1(II) chain	6.85	3.44	10.46	7.5	within
e022483	PGPPGAPGPQGFGPPGEPGEPGASGPM GPRG*	3xOxidation [P15; P16; P19]	Collagen alpha-1(I) chain	6.93	3.62	10.3	7.12	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022491	GPRGTPGAPGQPGMAGVDGPPGPKGNMG PQGE*	1xOxidation [P2]	Collagen alpha-1(XI) chain	11.12	6.08	13.38	11.53	within
e022495	KDFLKHHNLNPARKYFPQWEAPTL	none	Pepsin A-4	6.4	3.14	11.51	10.09	within
e214762	FGQHVSGSDNFSSSGQHISDSGQSTGFGQ	none	Filaggrin-2	9.93	5.49	12.36	10.62	within
e022498	SGEKGDQGPDPGSPGSPGAPAGPP GYGPP*	1xOxidation [P]	Collagen alpha-3(IV) chain	7.46	3.41	11.02	6.86	within
e102800	PGDLGPPGDPGVSGIDGSPGEKGDGPDVG GPGP*	2xOxidation [P25; P31]	Collagen alpha-3(V) chain	9.9	5.26	12.64	10.62	within
e103313	GNPGPPGPPGPPGPGIDMSAFAGLGPREG GP*	4xOxidation [P5; P6; P8; M18]	Collagen alpha-1(II) chain	10.06	5.39	12.64	10.59	within
e022500	VEFGSVNTQNFQSLHNIGSVVQHSEK	none	26S proteasome non-ATPase regulatory subunit 9	9.07	5.37	12.38	7.86	within
e100204	QDGVGGDKGEDGDPGQPPGPSGEAGP PGPP*	4xOxidation [P22; P28; P29; P31]	Collagen alpha-1(XI) chain	8.95	4.9	11.71	10.11	within
e022504	ESGREGAPGAEGSPGRDGSFGAKGDRGE TGP*	3xOxidation [P8; P14; P20]	Collagen alpha-1(I) chain	15.13	13.25	16.36	15.85	within
e105228	DGHPYSTQSIQQGSAVSRDLTFDGTFE	none	Plexin-B1	9.03	4.74	11.73	10.12	within
e022505	GEAPAPAAELGESAPSPKGSSSAALNGPTP GAP	none	Myosin-binding protein C, cardiac-type	8.93	4.18	12.57	10.02	within
e214765	EQTAPTGGADIEADQGGEAADSQREEAI	none	Coiled-coil domain-containing protein 8	12.83	9.67	14.53	12.67	within
e022509	GDDGPKGNPGPVGFPGDPGPPGEGGPRG QDGA*	2xOxidation [P21; P26]	Collagen alpha-2(XI) chain	8.81	2.12	12.25	6.51	within
e214766	NNGVPGGAAAASSATVAASATTAASSSLA TPEL	none	WD repeat-containing protein 26	5.74	0.09	12.43	5.93	within
e022519	QPGAKGEQGEAGQKGDAGAPGPQGPPSGA PGPP*	4xOxidation [P20; P22; P25; P29]	Collagen alpha-1(II) chain	11.83	6.08	13.76	11.3	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e106273	NSGEPGAPGSKGDTGAKGEPGPVGVQGP PGPAG*	4xOxidation [P5; P8; P20; P29]	Collagen alpha-1(I) chain	10.41	5.76	12.16	10.97	within
e214770	EVGPAGSPGSNGAPGQRGEPGPQGHAGA QGPPG*	1xOxidation [P8]	Collagen alpha-1(III) chain	7.6	4.69	11.42	10.28	within
e205169	APGAKGEAGPTGARGPEGAQGPRGEPGT PGSP*	5xOxidation [P2; P10; P16; P22; P26]	Collagen alpha-1(II) chain	7.16	4.29	9.73	9.66	within
e102114	GGYHPHQHHPHSHPAQQPPPPQPAQAG	none	Forkhead box protein J2	7.13	4.07	10.09	10.46	up
e022525	PNSGGPSQNFTSNSSRVSVISGPQNTRSS	none	Zinc finger protein 292	6.74	3.22	13.18	11.51	within
e022529	YNNRNQDNYVSWDSEDDDEDEEI	none	Endoribonuclease Dicer	8.74	3.26	12.17	8.99	within
e205177	WKADSSPVKAGVETTTSPKQSNNKYAAS	none	Immunoglobulin lambda constant 2	8.4	3.97	15.02	10.26	within
e022535	AVADTRDQADGSRASVDSGSSEEQGGSSR A	none	Polymeric immunoglobulin receptor	10.04	5.21	13.51	13.67	up
e214771	NAGPPGPPGPAGKEGGKGRGETGPAGR PGEV*	3xOxidation [P19; P25; P29]	Collagen alpha-1(I) chain	7.43	3.77	12.01	4.48	within
e022544	TVKTKDGVVEITGKHEERQDEHGYIS	none	Heat shock protein beta-1	6.66	2.45	11.46	9.66	within
e214773	RGPEGSRLPGVEGPRGPPGPRGVQGEQ GA*	3xOxidation [P10; P15; P18]	Collagen alpha-1(IX) chain	6.27	1.39	11.55	9.64	within
e022548	HAKATEHLSTLSEKAKPALEDLRQGLL	none	Apolipoprotein A-I	6.31	2.0	11.07	9.56	within
e104150	ERGVLGPFPAGPRGANGAPGNDGAKGD AGAPG*	3xOxidation [P7; P8; P10]	Collagen alpha-1(I) chain	8.38	3.77	11.9	10.78	within
e214775	DVGLPGAPGFPVAGMRGEPGLPGSSGH QGAI*	1xOxidation [P20]	Collagen alpha-6(IV) chain	8.05	1.15	12.87	4.14	within
e105051	ESGREGAPGAEGSPGRDGSPGAKGDRGE TGP*	4xOxidation [P8; P14; P20; P31]	Collagen alpha-1(I) chain	9.97	5.92	12.1	12.16	up
e022561	QSQSPVGPQGSSSSASGPGASPGGSEAG SQSGE	none	Oxysterols receptor LXR-beta	12.37	4.28	14.71	5.29	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e205193	LVGEPGPAGSKGESGNKGEPGSAGPQGP PGPSG*	3xOxidation [P7; P20; P25]	Collagen alpha-2(I) chain	9.08	5.22	11.76	10.25	within
e022567	ASVGGTIPGPGPGGGQGPGE GEGQTAR GGSPGSD	none	Putative Polycomb group protein ASXL2	7.63	4.2	10.74	13.4	up
e022568	AGSPGSNGAPGQRGEPGPQGHAGAQQGP GPPGI*	3xOxidation [P27; P28; P30]	Collagen alpha-1(III) chain	10.68	5.77	12.5	11.27	within
e098106	PGAPGGKGDAGAPGERGPPGLAGAPGLR GGAGPPG*	2xOxidation [P1; P4]	Collagen alpha-1(III) chain	7.85	4.54	11.56	7.04	within
e022572	SEYKTETYDDYKDETTIDDSIMDAD	none	Microtubule-associated protein 2	7.77	3.94	11.31	8.62	within
e022573	KLIDDYGGEDDELAGGPGGGAGGPGGGLY GEL	none	Transcriptional regulator protein Pur-beta	6.53	3.67	11.32	10.4	within
e022596	PAPSSTSGSYGSSSQSSSYGQPQSGSYSQ Q	none	RNA-binding protein FUS	6.76	2.28	10.98	4.58	within
e022602	EEGAPGDPEAALEDNLARIRENHERAL	none	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	6.96	1.51	9.48	9.64	up
e022604	FAGPPGADGQPGAKGEPGDAGAKGDAGP PGPAGP*	3xOxidation [P17; P28; P]	Collagen alpha-1(I) chain	6.92	3.5	11.77	10.73	within
e022605	GGPGGGGPGGGSAGGPSQPPGGGGPGIR KDAFADAV	none	Far upstream element-binding protein 2	8.77	5.08	11.98	8.88	within
e208705	EKGDRGLPGTQGSPGAKGDGGIPGPAGPL GPP*	5xOxidation [P14; P23; P25; P28; P31]	Collagen alpha-1(XI) chain	11.48	5.56	13.92	13.39	within
e214785	NVGAPGAKGARGSAGPPGATGFPGAAGR VGPPGP*	4xOxidation [P16; P17; P23; P31]	Collagen alpha-1(I) chain	11.9	7.08	14.18	12.95	within
e022615	ASGPAGPRGPPGSAGAPGKDGLNGLPGPI GPPGP*	3xOxidation [P26; P28; P31]	Collagen alpha-1(I) chain	8.91	4.11	12.17	10.98	within
e214788	GPMGIPGVKGQPLPGPPGLPGPGFAGPP GPPG*	4xOxidation [P]	Collagen alpha-2(IX) chain	5.82	1.45	12.38	5.45	within

a: Distribution in healthy female

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e214789	GIQGPGLDGAKEKASGERGPSGLPGP VGP*	3xOxidation [P5; P23; P27]	Collagen alpha-1(XXIII) chain	6.88	2.04	11.88	4.26	within
e022621	GLDGITGPQGAPGFPGAVGPAGPPGLQGP PGPPG*	2xOxidation [P]	Collagen alpha-6(IV) chain	7.82	4.47	10.63	8.69	within
e022623	PAGPALQTVPGPQGPGRDGTGRDGE*	3xOxidation [P1; P4; P10]	Collagen alpha-1(XVIII) chain	7.32	3.74	12.78	7.32	within
e214791	SPNPAAVNTSVTLAELAGGSGVVYTWSLE	none	Polycystin-1	7.98	4.21	13.73	5.07	within
e101037	GPAGKSGDRGESGPAGPAGPAGSRG APGPQG*	6xOxidation [P2; P14; P17; P21; P23; P30]	Collagen alpha-1(III) chain	10.52	6.37	12.33	12.28	within
e022637	EVGPAGSPGSNGAPGQRGEPGPQGHAGA QGPPG*	3xOxidation [P20; P22; P]	Collagen alpha-1(III) chain	11.13	5.11	12.85	10.86	within
e022639	RGEPGPPGPAGAAGPAGNPGADGQPGAK GANGAPG*	3xOxidation [P6; P7; P]	Collagen alpha-1(I) chain	10.82	6.08	12.56	11.17	within
e103040	EGVQKEDIPPADLSDQVPDTESETRIL	none	Complement C3	8.7	4.56	11.42	11.55	up
e022649	EKGERGAAGEPGPHGPPGVPGSVGPKGS SGSPG*	2xOxidation [P13; P16]	Collagen alpha-1(XVII) chain	9.33	4.62	11.94	10.64	within
e214796	GMAGVDGPPGPKGNMGPQGEPGPPGQQ GNPGP*	3xOxidation [P23; P24; P30]	Collagen alpha-1(XI) chain	7.33	3.45	11.28	7.94	within
e022658	GESGREGAPGAEGSPGRDGSPGAKGDRG ETGP*	2xOxidation [P15; P21]	Collagen alpha-1(I) chain	11.05	7.61	13.28	12.01	within
e022678	NVGAPGAKGARGSAGPPGATGFPGAAGR VGPPGP*	5xOxidation [P5; P16; P17; P23; P31]	Collagen alpha-1(I) chain	11.1	5.82	13.43	12.42	within
e022679	QRRDDEFYKTPSLSSSGSSDGGTRPSSS	none	Ubiquitin carboxyl-terminal hydrolase 4	8.47	4.18	12.32	4.33	within
e208710	SQFPHGQKGQHYSGQKGKQTESKGSF	none	Semenogelin-1	6.35	1.98	12.5	6.32	within
e022684	SPGGPGAAGFPGARGLPGPPGSNGNPGP PGPSGSP*	1xOxidation [P35]	Collagen alpha-1(III) chain	10.25	6.3	12.67	10.89	within

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e101903	GPQGPPGKNGETGPQGPPGPTGPGGDKGDTGPP*	2xOxidation [P14; P17]	Collagen alpha-1(III) chain	9.32	5.59	11.95	8.35	within
e100508	SNGNPGPPGPSGSPGKDGPPGPAGNTGAPGSPGVS*	1xOxidation [P]	Collagen alpha-1(III) chain	11.28	6.78	13.13	10.86	within
e214808	LTGSPGSPGPDGKTGPPGPAGQDGRPGPGPPG*	5xOxidation [P16; P17; P19; P26; P]	Collagen alpha-1(I) chain	10.6	7.1	12.19	11.49	within
e022696	DKGDPGFPGQPGMPGRAGSPGRDGHPLPGP*	2xOxidation [P26; P29]	Collagen alpha-1(IV) chain	10.19	6.13	11.92	10.76	within
e022697	EGAPAPESSGEPAEDEGPTDTAEAGSDPQAE	none	A-kinase anchor protein 8	11.57	2.53	14.69	5.95	within
e101814	GTHSLYTTYKDYEIFHVMSTMLPYT	none	Signal-induced proliferation-associated 1-like protein 1	10.52	5.98	12.47	10.29	within
e022706	ANTASYSYGAYYAPGYTQTSYSTVEPSTY	none	BAG family molecular chaperone regulator 4	6.48	3.2	10.42	7.43	within
e022707	GESGREGAPGAEGSPGRDGSPGAKGDRGETGP*	3xOxidation [P9; P15; P21]	Collagen alpha-1(I) chain	13.8	11.25	15.34	14.97	within
e105763	ASVGAMGGGVGASSSGGGPGGSGGGSGGGPGGAGTSFPPP	none	Glycogen synthase kinase-3 alpha	11.66	8.11	14.0	11.27	within
e022715	GPKGEGGITGSPGPIGPPGPPGLPGPPGPKGA*	11xOxidation [P2; P11; P14; P17; P18; P20; P21; P24; P26; P27; P29]	Collagen alpha-1(V) chain	9.95	5.21	12.95	9.11	within
e022716	QGPPGQKGEMGTPGPKGDRGPAGPPGHPGPPG*	2xOxidation [P13; P15]	Collagen alpha-1(XVII) chain	9.47	5.98	12.77	11.62	within
e103973	GEVGAPGSKGEAGPTGPMGAMGPLGPRGMPGE*	6xOxidation [P6; P14; P17; P23; P26; P30]	Collagen alpha-2(V) chain	10.51	6.01	12.66	8.33	within
e104108	NGPTGPPGPPGPRGHSGEPLGPPGPPGPPGQ*	2xOxidation [P7; P9]	Collagen alpha-1(X) chain	16.6	14.23	18.14	17.02	within
e022724	GGDDVGAGREDAGAGGEDVGAGGEDAGAGGEDAGAG	none	Golgin subfamily A member 6-like protein 2	8.88	4.05	11.73	7.72	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022725	LESPGGSGSDSNNTGEQGAETDPEAEPEL E	none	SH2B adapter protein 2	10.62	5.97	12.87	12.55	within
e214816	YHLGDYDKALYYLKEARTQQPTDTN	none	Tetratricopeptide repeat protein 9A	14.01	10.57	16.23	15.59	within
e104479	KGNSEPGAPGSKGDTGAKGEPGPVG VQ GPPGP*	4xOxidation [P10; P22; P24; P31]	Collagen alpha-1(I) chain	9.71	3.88	12.69	9.3	within
e214818	EPGPKGDAGAPGAPGGKGDAGAPGERGP PGLAGAP*	1xOxidation [P14]	Collagen alpha-1(III) chain	9.57	4.2	14.44	6.32	within
e022733	QSLPHENKPLTLSNYQTNKAKHDELT	none	Cystatin-B	9.37	3.96	14.45	8.49	within
e022735	GRAGMPGGPGKSGSMGPVGP GPAGERG HPGAPG*	1xOxidation [P9]	Collagen alpha-1(XVI) chain	9.24	5.22	11.95	9.23	within
e022740	SPGGPGAAGFPGARGLPGPPGSNGNPGP PGPSGSP*	2xOxidation [P]	Collagen alpha-1(III) chain	11.26	7.05	13.29	12.99	within
e214825	LTGSPGSPGPDGKTGPPGAGQDGRPGP PGPPG*	6xOxidation [P16; P17; P19; P26; P]	Collagen alpha-1(I) chain	14.01	11.24	15.18	14.56	within
e214828	DLGPPGDPGVSGIDGSPGEKGDPGDVGGP GPPGA*	2xOxidation [P]	Collagen alpha-3(V) chain	11.23	6.05	13.58	13.13	within
e022751	GQPGAKGEQGEAGQKGDAGAPGPQG PSG APGPQG*	1xOxidation [P]	Collagen alpha-1(II) chain	11.23	6.44	13.67	13.41	within
e022750	PGPVGPPGLTG PAGEPGREGSPGADGPP GRDGA*	5xOxidation [P1; P3; P6; P7; P12]	Collagen alpha-1(II) chain	11.05	5.8	13.42	12.75	within
e022752	TSPPPVSSITPTNTMTSMRTTTYWPTA	none	Mucin-3A	10.07	4.45	12.95	11.37	within
e022761	ESGREGAPGAEGSPGRDGSPGAKGDRGE TGPA*	3xOxidation [P8; P14; P20]	Collagen alpha-1(I) chain	15.63	13.09	17.33	16.49	within
e214832	QGPMGPMGPRGPPGPAGAPGPQGFQGN PGEPG*	4xOxidation [P3; P6; P9; P12]	Collagen alpha-1(II) chain	12.06	9.19	13.98	13.64	within
e022768	TWASHEKMHEGDEGPGHHHKPGLGEGTP	none	Protein S100-A9	8.29	2.99	13.87	8.58	within
e022773	NEESSVVDYVEVTVGEEDAISDRSDSW	none	Zinc fingers and homeoboxes protein 2	10.87	5.1	13.04	11.53	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214835	GSPGLPGQVGETGKPGAPGRDGASGKDG DRGSP	none	Collagen alpha-1(VII) chain	7.63	3.61	11.98	6.13	within
e214836	RTIIGWSAQEESTIPSWQEDEEEAEV	none	TPR and ankyrin repeat-containing protein 1	13.83	6.08	16.39	16.68	up
e022789	GERGRPGAPGPAGARGNDGATGAAGPPG PTGPAGP*	1xOxidation [P27]	Collagen alpha-1(I) chain	8.32	4.31	12.59	6.14	within
e022791	PGSPGGPGSDGKPGPPGSQGSGRPGPP GPSGP*	10xOxidation [P4; P7; P13; P15; P16; P25; P27; P28; P30; P33]	Collagen alpha-1(III) chain	14.08	11.37	15.52	15.58	up
e208717	DGVSGGEGKGGSDGGGSHRKEGEEADAP GVIPG	none	CD99 antigen	14.0	11.2	15.42	15.56	up
e022797	SGREGAPGAEGSPGRDGSPGAKGDRGET GPAGP*	2xOxidation [P7; P13]	Collagen alpha-1(I) chain	11.48	7.28	13.45	12.34	within
e214845	ARGNDGARGSDGQPGPPPGTAGFPGS PGAKG*	5xOxidation [P17; P19; P20; P26; P29]	Collagen alpha-1(III) chain	11.85	8.48	13.75	11.28	within
e022803	GSSDSLSTSKSPPGKSSLGLDNSLSTSSD P	none	Protein AF-17	11.93	6.97	15.01	10.87	within
e022800	QGPPGSATAKGERGFPGADGRPGSPGRA GNPG*	4xOxidation [P4; P16; P22; P25]	Collagen alpha-1(VII) chain	11.25	7.5	13.19	11.35	within
e022805	WSLTASEGESTTAHFFLGAGDEGLGTRGIG	none	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	11.85	6.68	14.97	10.91	within
e022806	IPVKQADSGSSEEKQLYNKYPDAVATW	none	Osteopontin	11.68	7.66	13.74	12.3	within
e208720	MPGSPGGPGSDGKPGPPGSQGSGRPGP PGPSGP*	2xOxidation [P17; P26]	Collagen alpha-1(III) chain	11.29	6.42	12.92	11.36	within
e022808	GPTGAVGFAGPQGPDGQPGVKGEPEGEPG QKGD*	5xOxidation [P2; P11; P14; P18; P24]	Collagen alpha-2(V) chain	9.27	4.67	12.42	9.72	within
e214848	GLQGPTGPPGDPGDRGPPGRPLPGADG LPGP*	7xOxidation [P8; P9; P12; P17; P18; P21; P24]	Collagen alpha-1(XI) chain	10.15	5.58	12.89	10.88	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022812	GPPGEPGKAGEPGLPPEGARGPPGFKGHTGD*	3xOxidation [P3; P6; P12]	Collagen alpha-1(XXII) chain	9.55	3.15	12.75	11.23	within
e208721	GVSGQKDGQTESNEEGKENRDRDRDY	none	Ubiquitin-associated protein 2-like	9.45	5.49	11.69	10.4	within
e214850	GRAGEPGLQGPPAGPPGEKGEPGDDGPSGAEGPP*	2xOxidation [P6; P11]	Collagen alpha-1(II) chain	9.37	6.11	11.82	10.4	within
e214851	GSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRG*	3xOxidation [P24; P26; P]	Collagen alpha-1(III) chain	9.42	5.69	11.85	10.4	within
e214852	GAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAV*	3xOxidation [P5; P20; P21]	Collagen alpha-1(I) chain	7.22	4.17	11.74	11.82	up
e022828	GADGPQGPPEGGIGNPGAVGEKGEPGEAGEPGLPG*	3xOxidation [P8; P9; P]	Collagen alpha-1(V) chain	9.9	6.1	11.66	11.58	within
e103871	PNSETLASAYHANTRAHAYGDPNAGLNSQ	none	Transcription factor 20	6.16	2.87	10.28	4.77	within
e208722	ERGAPGEKGEPPGVAGPPGGSGPAGPPGQGV*	6xOxidation [P13; P14; P19; P20; P25; P28]	Collagen alpha-1(III) chain	9.89	6.26	11.66	11.58	within
e022831	DGPQGPPEGGIGNPGAVGEKGEPGEAGEPGLPGE*	3xOxidation [P6; P7; P]	Collagen alpha-1(V) chain	9.13	3.8	11.8	10.24	within
e022833	GEKGPPQGPAGRDGVQGPVGLPGPAGPAGSPGED*	4xOxidation [P8; P17; P21; P23]	Collagen alpha-1(XI) chain	7.34	3.46	12.79	9.36	within
e022837	AAGPAGPAGPRGSPGERGEVGPAGPNGFAGPAGAA*	3xOxidation [P10; P14; P22]	Collagen alpha-2(I) chain	5.62	3.14	11.32	8.37	within
e214854	GPPGSEGARGAPGPAGPPGDPGLMGERGEDGPA*	4xOxidation [P17; P18; P21; P32]	Collagen alpha-1(VI) chain	7.53	3.92	12.06	6.66	within
e022839	TWASHEKMHEGDEGPGHHHKPGLGEGTP*	1xOxidation [M8]	Protein S100-A9	8.17	3.46	13.52	9.43	within
e022845	NGERGGPGGPPGQGPKNGETGPQGPPGPTGPG*	1xOxidation [P]	Collagen alpha-1(III) chain	10.4	5.82	12.98	12.29	within
e104605	QFEGPPGAPGPQGVVGPSPGPPGPPGFPGDPGPP*	2xOxidation [P21; P23]	Collagen alpha-3(V) chain	9.99	5.73	12.21	11.71	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022851	APGDRGEPGPPGPAGFAGPPGADGQPGA KGEPG*	7xOxidation [P8; P10; P11; P13; P19; P20; P26]	Collagen alpha-1(I) chain	11.25	6.89	13.2	9.84	within
e214855	MPGERGGLGSPGPKGDKGEPGGPGADGV PGKDG*	3xOxidation [P20; P23; P29]	Collagen alpha-1(III) chain	6.1	2.67	9.46	5.28	within
e101109	SYGGGGSGGGYGGGSGSRGGSGGSYGG GSGSGGSGGGY	none	Keratin, type I cytoskeletal 9	13.45	7.56	15.37	15.21	within
e104339	MPGFKGPTGYKGEQGEVGKDGEKDPGP PG*	4xOxidation [M1; P7; P26; P28]	Collagen alpha-3(IX) chain	12.2	8.49	14.09	10.48	within
e022870	PGAVGPAGKDGEAGAQQPPGPAGPAGER GEQQPAG*	1xOxidation [P]	Collagen alpha-1(I) chain	6.76	3.28	10.47	5.35	within
e022872	QASDLSLIDKESDDVLERIMDEKTASE	none	Transcription initiation factor TFIID subunit 5	6.94	2.98	11.26	9.26	within
e022874	GADGEAGRPSSSGPSGDEGQPGEPGPPG EKGEA*	3xOxidation [P24; P26; P27]	Collagen alpha-1(VI) chain	11.57	7.16	13.86	11.9	within
e105489	LTPEEKSAVTALWGKVVNDEVGGEALGRL	none	Hemoglobin subunit beta	10.31	2.77	15.7	7.53	within
e022885	GPAGPPGQTGPPGPAGPPGSKGDRGQTG EKGPAG*	3xOxidation [P14; P17; P18]	Collagen alpha-1(XXVI) chain	6.94	2.96	11.06	7.9	within
e022890	KKAPSPSQLSMTELPGDAVQLAWVAAAPS G*	2xOxidation [P6; P]	Collagen alpha-1(XX) chain	9.31	4.62	13.54	12.4	within
e022897	ARGNDGARGSDGQPGPPGPPGTAGFPGS PGAKG*	6xOxidation [P16; P17; P19; P20; P26; P]	Collagen alpha-1(III) chain	10.09	6.27	12.17	10.04	within
e214860	GPSGAPGADGPQGPPGGIGNPGAVGEKG EPGEAGE*	1xOxidation [P2]	Collagen alpha-1(V) chain	13.73	9.66	16.36	11.69	within
e214862	DVGGPGGPGASGEPGAPGPPGKRGPSGH MGREG*	4xOxidation [P17; P19; P20; P]	Collagen alpha-3(V) chain	13.77	10.37	16.36	11.72	within
e214863	RGPAGPNGADGPQGPPGGVGNLPPGGEK GEPGE*	4xOxidation [P12; P15; P]	Collagen alpha-2(XI) chain	13.72	9.96	16.34	11.75	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e105492	AREPEEPSQDAPRDPAGEPAGGEEVPAPAD	none	APC membrane recruitment protein 2	10.3	6.86	13.75	8.65	within
e103539	GEPGTPGNPGPPGPPGPPGLGGNFAAQMAGG*	5xOxidation [P12; P14; P15; P17; P18]	Collagen alpha-1(II) chain	8.55	4.7	11.55	10.24	within
e022911	VRGPPPPYQMTNSEGWAPGGTEPFSDGIN	none	B-cell CLL/lymphoma 9 protein	11.98	6.89	14.7	5.41	down
e214868	FQGPPGEPGEPGASGPMGPRGPPGPPGKNGDD*	2xOxidation [P19; P22]	Collagen alpha-1(I) chain	14.06	12.23	15.23	14.81	within
e214870	PQGPRGSEGPQGVREGPPGPAGAAAGPAGNPG*	7xOxidation [P1; P4; P10; P17; P19; P20; P22]	Collagen alpha-1(I) chain	14.06	12.15	15.25	14.8	within
e214871	EGFRGPPGPQGDGVRGPAGEKGDRGPPGLD*	1xOxidation [P28]	Collagen alpha-1(VII) chain	6.78	3.79	9.83	8.69	within
e214874	GEKGETGDVGQMPPGPPGPRGPGSAGPADGPQ*	2xOxidation [M/P]	Collagen alpha-1(V) chain	11.11	5.81	12.72	4.31	down
e022917	GKPGEDGEPRNGNPGEVGFAGSPGARGFPGA*	3xOxidation [P15; P24; P30]	Collagen alpha-2(V) chain	11.28	6.55	13.12	14.1	up
e022921	ARGAPGPDGNNGAQGPPGPQGVQGGKGEQGPPG*	5xOxidation [P5; P7; P16; P17; P19]	Collagen alpha-2(I) chain	11.16	5.9	13.31	13.97	up
e022926	GEKGDPSQGSPPSRGAPGQYGEKGFPDGN	none	Collagen alpha-5(VI) chain	9.86	5.18	13.1	12.41	within
e022927	PAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGF*	1xOxidation [P]	Collagen alpha-1(I) chain	7.02	3.29	9.97	8.08	within
e022928	FPGERGNSEHGEIGLPGLPGTPGNEGL*	2xOxidation [P23; P26]	Collagen alpha-3(IV) chain	6.86	4.3	14.07	5.54	within
e022931	IDGEPGVPGQPGAPGPPGHPSHPGPDGLSRP*	7xOxidation [P5; P8; P11; P14; P16; P17; P20]	Collagen alpha-2(V) chain	9.74	5.68	12.07	11.25	within
e214878	DQGEPPGPQGLPGFSGPPGKEGEPGPRGEIGP*	3xOxidation [P17; P23; P25]	Collagen alpha-2(IX) chain	9.65	4.48	11.9	11.09	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022930	PEPLSAPPGSPPPSAAPTSATSNSSNGGGP SKSG	none	Homeobox protein Hox-B3	7.66	2.5	12.64	3.46	within
e214880	GNPGMKGEAGPTGARGPEGPQQGRGETG PPGP*	3xOxidation [P17; P20; P29]	Collagen alpha-2(V) chain	10.0	5.17	12.05	9.26	within
e022939	DNPRRYDSDDDLRLGSSREGSLPNSQ	none	Integral membrane protein GPR137C	12.01	6.11	14.12	11.3	within
e103970	EKGEVGDVGSMGPHGAPGPRGPQGPTGS EGTP*	3xOxidation [P13; P17; P19]	Collagen alpha-3(V) chain	9.56	5.14	11.96	10.93	within
e022944	DGENDDPRPPNPPKMPNPNHPSSSGS	none	CD99 antigen	8.46	3.98	11.81	11.97	up
e100632	PPGEPGKAGEPGLPGEARGPPGFKGHT GD*	8xOxidation [P1; P2; P5; P11; P14; P16; P22; P23]	Collagen alpha-1(XXII) chain	9.19	4.83	11.78	10.61	within
e098135	EAGRDGNPGNDGPPGRDQPGHKGERGY PG*	3xOxidation [P14; P20; P29]	Collagen alpha-2(I) chain	8.03	4.14	11.77	10.05	within
e022950	QFEGPPGAPGPQGVVGPSPGPPGPFPG DPGPP*	3xOxidation [P11; P17; P20]	Collagen alpha-3(V) chain	10.61	4.65	12.69	10.91	within
e208725	PEGVPGERGLPGEFGPGKGEKSEGPTG PQ*	3xOxidation [P5; P11; P16]	Collagen alpha-1(XXVIII) chain	8.41	4.21	12.34	11.38	within
e022951	KGKWERPFVKDTEEDFHVDQVTT	none	Alpha-1-antitrypsin	8.56	3.69	12.54	10.22	within
e022953	GEPGPPGDRGLKGDNGVGQPLPGAPGQ GGAPGP*	2xOxidation [P26; P32]	Collagen alpha-2(VIII) chain	11.24	7.01	13.06	10.96	within
e022958	GSERTITSTEGSETTTVSATGSETTVSTEGS	none	Mucin-22	5.91	1.71	10.42	7.96	within
e022959	KGNMGPPQGEPPGQQGNPQPGLPGP QGPIG*	3xOxidation [P13; P19; P21]	Collagen alpha-1(XI) chain	5.97	2.57	10.42	5.89	within
e022960	GYQVSKPDALSKLERGEEPWTMEDER	none	Zinc finger protein 432	6.67	2.93	11.34	5.48	within
e022962	GVMQGPMPGMPGRPPGPAGAPGPQGF QGNPG*	6xOxidation [P9; P12; P15; P16; P18; P22]	Collagen alpha-1(II) chain	10.31	5.88	12.23	7.82	within
e214883	LGSPGSASDLETSGLQEQRNHLQGLSEL	none	Natriuretic peptides B	6.26	3.28	11.53	8.57	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e022968	GGIFGGGSFGGGSFGGGSFGGGGFGGGG FGGGFGGGFG	none	Keratin, type I cytoskeletal 10	12.13	7.45	15.45	10.11	within
e022978	GEPGEPGASGPMGPRGPPGPPGKNGDDG EAGKP*	2xOxidation [P11; P14]	Collagen alpha-1(I) chain	8.01	4.5	11.14	11.67	up
e022986	EGPGGGISGGSGHRPHEGPGGGMGAGGG HRPHEG	none	Serine/threonine-protein phosphatase 1 regulatory subunit 10	9.26	2.98	14.11	9.38	within
e106192	APQGQQQPPSQPPQGGQPPSGPGQPAPA ATQAA	none	Transcriptional coactivator YAP1	8.31	4.64	11.54	5.2	within
e214888	PNGDAGRPGEPGLMGPRGLPGSPGNIGPA GKE*	3xOxidation [P20; P23; P28]	Collagen alpha-2(I) chain	13.71	7.73	16.63	12.1	within
e023004	AGGDGEPGPRGQQGMFGQKGDGARGF PGPP*	3xOxidation [P9; P28; P30]	Collagen alpha-1(XI) chain	9.61	4.9	11.78	10.83	within
e214890	ARGAPGPDGNGAQQPPGPQGVQGGKGE QGPPG*	6xOxidation [P5; P7; P16; P17; P19; P31]	Collagen alpha-2(I) chain	9.28	4.42	12.27	10.83	within
e023006	QNGEPGGKGERGAPGEKGEPPGVPAGP PGGSGP*	4xOxidation [P14; P22; P23; P28]	Collagen alpha-1(III) chain	12.02	9.02	13.6	13.67	up
e105108	ERGAPGEKGEPPGVPAGPPGSGPAGP PGPQGV*	8xOxidation [P5; P13; P14; P19; P20; P25; P28; P29]	Collagen alpha-1(III) chain	9.72	5.13	11.79	10.84	within
e214892	ERGEQGAPGSGFQGLPGPPGPPGEGGK PGDQ*	3xOxidation [P17; P]	Collagen alpha-1(II) chain	9.64	4.52	12.15	10.84	within
e214893	GLPGMPGADGPPGHPGKEGPPGEKGGQG PPGPQ*	3xOxidation [P21; P29; P30]	Collagen alpha-1(V) chain	12.01	8.9	13.54	13.65	up
e105535	PPGSNGNPGPPGSGSPGKDGP GPAGN TGAPGSPG*	1xOxidation [P]	Collagen alpha-1(III) chain	11.5	7.35	13.22	13.01	within
e214895	VGPPGEDGDKGEIGEPGQKGSKGDKEQ GPPG	none	Collagen alpha-1(V) chain	9.35	5.43	11.85	8.93	within
e023015	GPQGNSGEKGDQGFQGGPFPGP GPPG FPG*	7xOxidation [P2; P18; P21; P23; P24; P26; P27]	Collagen alpha-1(XVI) chain	11.58	7.25	13.75	12.2	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023017	RGMPGSPGGPGSDGKPGPPGSQGESGRP GPPGP*	6xOxidation [P4; P7; P10; P16; P18; P19]	Collagen alpha-1(III) chain	11.44	7.35	13.72	11.46	within
e214897	SAGVPPSAPLQGAVPPTSSVPPVAGAPSV GQPGAG	none	Clathrin coat assembly protein AP180	7.78	4.5	12.27	9.53	within
e300344	AGPPGADGQPGAKGEQGEAGQKGDAGAP GPQGPS*	4xOxidation [P4; P10; P28; P30]	Collagen alpha-1(II) chain	8.64	3.46	11.57	7.83	within
e023025	KGNVGPQGEPPGQGNPGAQGLPGPQ GAIGP*	3xOxidation [P12; P13; P19]	Collagen alpha-1(V) chain	8.93	4.98	12.19	9.67	within
e214900	GHRGFSLQGPPGPPGSPGEQGPSGASG PAGPRG	none	Collagen alpha-1(I) chain	13.31	10.56	14.71	14.14	within
e023033	EAGRDGNPGNDGPPGRDQPGHKGERGY PG*	4xOxidation [P13; P14; P20; P29]	Collagen alpha-2(I) chain	11.7	7.77	13.84	13.22	within
e023035	HGMGPAGGFPNAGGHYIYLEADEFQAGQ S	none	Zonadhesin	8.45	4.01	12.08	10.57	within
e023037	PGPKGDPGAFLKGEKGEADGEAGRP GSSGP*	2xOxidation [P1; P3]	Collagen alpha-1(VI) chain	11.75	7.83	13.49	11.58	within
e214901	GAPGASGDRGPPGVPGLTGPAEPG REGSPGA*	2xOxidation [P17; P18]	Collagen alpha-1(II) chain	11.5	7.09	13.73	13.15	within
e214902	QKGSKGSPGSMGPRGDTGPAGPPGPPGA PAELH*	1xOxidation [P29]	Collagen alpha-3(V) chain	11.63	5.26	13.36	11.76	within
e023045	PGPVGFPGDPGPPGEGGPRGQDGAKGDR GEDG*	5xOxidation [P1; P3; P7; P10; P12]	Collagen alpha-2(XI) chain	11.16	7.15	13.31	12.96	within
e023047	DSPLSSRLDDGFGMDPFPDDLTASWPD	none	Heat shock protein beta-8	8.53	3.6	12.02	9.09	within
e101264	QLGSAGSTSGGGGTGAGAAGGAGGGQGA ASDERKSAF	none	PR domain zinc finger protein 8	10.12	5.21	12.99	10.37	within
e023066	GESGREGAPGAEGSPGRDGSPGAKGDRG ETGPA*	3xOxidation [P9; P15; P21]	Collagen alpha-1(I) chain	9.29	5.67	12.86	12.21	within

a: Distribution in healthy female

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e023077	GPPGSNGNPGPPGPSKDGPPGPAGNTGAPGSP*	2xOxidation [P]	Collagen alpha-1(III) chain	10.81	4.53	13.24	10.89	within
e023082	INAEFMDDDVETEDFEENSEEIDVNE	none	Calmegin	12.16	7.53	13.96	14.4	up
e214907	GGRGGGFGGGSSFGGGSGFSGGGFGGGFGGGGRFGGF	none	Keratin, type II cytoskeletal 2 epidermal	10.19	5.24	12.55	12.29	within
e023086	ELGEAGPSGEPGVPGDAGMPGERGEAGHRGSAG*	2xOxidation [P11; P]	Collagen alpha-3(IX) chain	8.93	4.65	11.95	5.58	within
e023087	RGMPGSPGGPGSDGKPGPPGSQGESGRPGPPGP*	7xOxidation [P4; P7; P10; P16; P18; P19; P28]	Collagen alpha-1(III) chain	10.18	5.01	12.58	13.08	up
e023088	ADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIG*	2xOxidation [P11; P22]	Collagen alpha-1(I) chain	8.37	4.35	11.43	8.61	within
e214909	GGNYGGGSGSGGGSGGGYGGGSGSRGSGGSHGGGSGFGG	none	Keratin, type I cytoskeletal 9	10.87	6.93	13.0	12.58	within
e214912	ENGVVGTGPVGAAGPAGPNGPPGPAGSRGDGGPPG*	3xOxidation [P23; P25; P34]	Collagen alpha-2(I) chain	10.56	4.74	12.95	9.92	within
e023103	GPAGQDGVGGDKGEDGDPGQPPGPSGEAGPPGP*	1xOxidation [P]	Collagen alpha-1(XI) chain	11.94	7.42	14.46	11.55	within
e214913	RTGEVGAVGPPGFAGEKGPSGEAGTAGPPGTPGP*	4xOxidation [P11; P19; P28; P29]	Collagen alpha-2(I) chain	11.75	5.71	13.93	11.5	within
e023107	EAGRDGNPGNDGPPGRDQPGHKGERGYPG*	5xOxidation [P8; P13; P14; P20; P29]	Collagen alpha-2(I) chain	9.5	4.86	11.91	8.29	within
e023108	TGDPGKNGDKGHAGLAGARGAPGPDGNNGAQGPP*	1xOxidation [P]	Collagen alpha-2(I) chain	11.47	7.6	13.27	11.71	within
e214915	AGTAGEPGRDGNPGSDGLPGRDGSPGGKGDRGE*	2xOxidation [P13; P19]	Collagen alpha-1(III) chain	11.84	7.98	13.19	12.66	within
e214916	FPGLHGMPGSKGEMGAKGDKGSPGFYGKKA*	2xOxidation [P8; P23]	Collagen alpha-1(XXI) chain	11.67	8.51	13.11	12.9	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e095927	PGQTGSPGPTGEPGSPGPPGKRGPPGPA GPEGR*	6xOxidation [P18; P19; P24; P25; P27; P30]	Collagen alpha-1(V) chain	10.39	6.17	12.19	12.64	up
e023116	GNDGAPGKNGERGGPGGPGQGPKN GETGPQG*	2xOxidation [P23; P]	Collagen alpha-1(III) chain	9.86	5.47	11.72	11.01	within
e023117	FHGFPGVQGP GPPGSPGPALEGPKGNPG PQG*	6xOxidation [P13; P14; P17; P19; P24; P]	Collagen alpha-5(IV) chain	9.88	3.82	11.81	11.0	within
e023120	NSQNSNPEGTSEGTPDEAAPLAERTPD TAE	none	Putative ankyrin repeat domain-containing protein 30B-like	8.42	4.22	11.73	5.1	within
e023123	PPGPAGSAGARGAPGERGETGPPGPAGFA GPPGAD*	3xOxidation [P2; P4; P14]	Collagen alpha-1(II) chain	10.58	5.72	12.82	8.64	within
e023128	GEQGPAGSPGFQGLPGPAGPPGEAGKPG EQGVPG*	3xOxidation [P21; P27; P33]	Collagen alpha-1(I) chain	9.16	4.92	12.23	7.46	within
e023138	GHGAEDSLADQAANEWGRSGKDPNHFRP A	none	Serum amyloid A-1 protein	5.22	1.98	13.54	6.2	within
e023139	RPQELETFSLLSNGTAAGVADQGTSNGLGS I	none	Zinc finger CCCH domain-containing protein 7B	5.66	1.37	9.96	10.41	up
e023145	GPAGAAGARGNDGQGPAGPPGPVGPAG GPGFPGAPG*	3xOxidation [P26; P30; P33]	Collagen alpha-1(II) chain	12.38	8.57	13.97	13.87	within
e023147	ADGVSGGEGKGGSDGGGSHRKEGEEADA PGVIPG	none	CD99 antigen	9.02	5.18	11.86	12.56	up
e023148	TGEVGAVGPPGFAGEKGPSGEAGTAGPPG TPGPQG*	3xOxidation [P27; P28; P]	Collagen alpha-2(I) chain	10.43	6.11	13.34	12.39	within
e106129	ADGQPGAKEPGDAGAKGDAGPPGPAGP AGPPGPIG*	3xOxidation [P]	Collagen alpha-1(I) chain	12.31	9.52	13.86	13.5	within
e023154	AWAVSQSEEEEEQEEARAESQSEEQQA	none	Obscurin	10.18	4.08	13.04	10.33	within
e023155	GSPGSNGAPGQRGEPGPQGHAGAQQPPG PPGING*	5xOxidation [P9; P15; P17; P26; P27]	Collagen alpha-1(III) chain	8.65	3.4	11.4	10.16	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e104015	GPPGNPGPPGADGIAGAAGPPGIQGSPGK EGPPGP*	7xOxidation [P9; P20; P21; P27; P32; P33; P35]	Collagen alpha-1(XXII) chain	9.72	4.91	12.52	11.14	within
e023158	GQPGAKGEQGEAGQKGDAGAPGPQGPPSG APGPQGP	none	Collagen alpha-1(II) chain	10.63	6.45	12.75	12.12	within
e214928	AGPKGEKGDVGPAGPRGATGVQGERGPP GLVLP*	1xOxidation [P]	Collagen alpha-1(VII) chain	7.94	3.59	10.97	10.97	within
e023164	GGGFGGGFGGGRGMGGGFGGAGGFGGA GGFGGAGGFGGPG	none	Keratin, type II cytoskeletal 3	7.48	2.13	14.33	8.18	within
e214929	DPGPMGPIGSRGPEGPPGKPGEDGEPR NGNP*	1xOxidation [P20]	Collagen alpha-2(V) chain	6.68	3.79	9.97	7.95	within
e214930	EPGRPGSPGAPGEQPPGTPGFPGNAGV PGTPGE*	1xOxidation [P]	Collagen alpha-1(XIV) chain	8.68	5.14	11.9	8.25	within
e214931	ESGPSGPAGPTGARGAPGDRGEPGPPGP AGFAGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	6.64	3.76	9.82	8.08	within
e023169	GPGPGGPGPAGPMGPFNPGPFNQPPGA PPHAGGP	none	Far upstream element-binding protein 2	7.22	3.41	12.94	11.44	within
e023170	LSPADKTNVKAAWGKVGAHAGEYGAEALE R	none	Hemoglobin subunit alpha	6.67	1.85	11.43	9.34	within
e023171	WTSESSVSGSTGQWHSESGSFRPDSPGS GN	none	Fibrinogen alpha chain	10.68	5.53	12.79	7.94	within
e023172	AGPRGSPGERGETGPPGPAGFPGAPGQN GEPGG*	8xOxidation [P3; P7; P15; P16; P18; P22; P25; P31]	Collagen alpha-1(III) chain	10.67	5.27	13.73	8.28	within
e023178	TAGFPGSPGAKGEVGPAGSPGSNGAPGQ RGEPGP*	6xOxidation [P5; P8; P16; P20; P26; P32]	Collagen alpha-1(III) chain	11.46	8.07	12.72	11.26	within
e023180	PPGPSGSPGKDGPPGPAGNTGAPGSPGV SGPKGDAG*	4xOxidation [P14; P16; P23; P26]	Collagen alpha-1(III) chain	12.35	9.69	13.9	13.61	within
e214940	GPVSSSGPKGSQGDPRPGEPGLPGARG LTGNPG*	2xOxidation [P8; P15]	Collagen alpha-2(V) chain	12.22	7.09	13.85	13.12	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023186	GPNGPPGPAGSRGDGGPPGMTGFPGAAGRTGPPGP*	3xOxidation [P24; P32; P33]	Collagen alpha-2(I) chain	11.41	7.09	13.01	12.9	within
e104421	GPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPPGPA*	3xOxidation [P15; P21; P32]	Collagen alpha-1(I) chain	11.61	7.05	13.51	11.17	within
e214943	TSPGTPAPAAEETMTTSPGTPAPAAEETMTS	none	Tumor necrosis factor receptor superfamily member 10C	11.16	6.82	13.55	11.93	within
e205386	ANGEKGEVGPPEGAGSAGARGAPGERGETGPPGP*	4xOxidation [P10; P11; P23; P32]	Collagen alpha-1(II) chain	6.82	2.32	9.25	4.81	within
e023203	GADGQPGAKGEQGEAGQKGDAGAPGPQG PSGAPGP*	3xOxidation [P26; P29; P33]	Collagen alpha-1(II) chain	10.76	6.1	12.86	11.09	within
e101543	GTPGAKGPTGSPGTSGPPGSAGPPGSPGPGQSTGPQ*	4xOxidation [P8; P12; P17; P18]	Collagen alpha-2(V) chain	10.73	6.62	12.9	11.1	within
e214946	DEGQPGEPGPPGEKGEAGDEGNPGPDGAPGER*	3xOxidation [P11; P23; P25]	Collagen alpha-1(VI) chain	7.62	2.66	10.87	8.99	within
e023207	QQSSYPGYGQQPAPSSTSGSYGSSSQSSSYG	none	RNA-binding protein FUS	8.79	4.26	12.29	7.76	within
e023208	WDRAGSSGYLAEKGPQGPGGDGHQESLPPP	none	Interferon lambda receptor 1	9.35	4.46	12.83	7.76	within
e023212	LGDIMGHYDESMPLPEFTEDQAAPDD	none	Collagen alpha-2(V) chain	8.5	3.85	11.9	9.46	within
e023216	DSIPLEWDHTGDVGGSSSHEEDEEGPYY	none	Nesprin-2	8.98	3.73	11.66	9.57	within
e214947	EPGGKGERGAPGEKGEPPGVAGPPGGSGPAGPPG*	2xOxidation [P31; P]	Collagen alpha-1(III) chain	5.7	1.59	9.07	8.32	within
e023226	PGDPGPPGEPGPAGQDGVGGDKGEDGDPGQPGPP*	3xOxidation [P10; P12; P]	Collagen alpha-1(XI) chain	11.88	6.03	13.56	12.98	within
e214948	ADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIG*	4xOxidation [P5; P11; P22; P23]	Collagen alpha-1(I) chain	12.67	9.74	14.14	13.78	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023230	GFPGDPGPPGEPGPAGQDGVGGDKGEDG DPGQP*	6xOxidation [P8; P9; P12; P14; P30; P33]	Collagen alpha-1(XI) chain	9.43	5.03	12.01	11.01	within
e023231	GPPGPAGPRGANGAPGNDGAKGDAGAPG APGSQGAPG*	3xOxidation [P3; P5; P]	Collagen alpha-1(I) chain	10.42	5.24	12.72	12.98	up
e214951	AAGTPGLQGMPPGERGGLGSPGPKGDKGE PGGPGA*	6xOxidation [P5; P11; P20; P22; P29; P32]	Collagen alpha-1(III) chain	9.94	4.29	12.54	8.34	within
e023232	GQPGAKGEQGEAGQKGDAGAPGPQGPPSG APGPQGP*	1xOxidation [P3]	Collagen alpha-1(II) chain	10.71	6.6	12.72	12.98	up
e023235	RGAPGDRGEPGPPGPAGFAGPPGADGQP GAKGEP*	2xOxidation [P22; P]	Collagen alpha-1(I) chain	9.93	4.8	12.56	8.35	within
e214953	PGSGEKGERGAAGEPGPHGPPGVPGSVG PKGSSGS*	1xOxidation [P15]	Collagen alpha-1(XVII) chain	10.73	6.11	12.69	12.98	up
e023238	VVDPKSKEEDKHLKFRISHELDSASSE	none	Osteopontin	7.32	2.06	13.51	12.61	within
e023240	EGPPGTEGESGLQGEPGAKGDVGTAGSV GGTGEPG*	1xOxidation [P16]	Collagen alpha-1(XXIV) chain	10.16	5.46	11.99	12.55	up
e214954	GIDGDNGPPGKAGPPGPKGEPGKAGPDGP DGKPG*	4xOxidation [P14; P15; P]	Collagen alpha-2(IX) chain	9.05	4.78	12.08	7.57	within
e023242	GEPGKAGEPGLPGPEGARGPPGFKGHTG DSGAPG*	1xOxidation [P9]	Collagen alpha-1(XXII) chain	8.67	4.65	11.68	7.7	within
e023243	TVKTKDGVVEITGKHEERQDEHGYISR	none	Heat shock protein beta-1	7.53	2.39	12.38	12.56	up
e023248	GVQGPAGPRGANGAPGNDGAKGDAG APGAPGSQ*	3xOxidation [P6; P8; P]	Collagen alpha-1(I) chain	9.13	4.82	11.54	10.92	within
e214955	VQGPAGPRGANGAPGNDGAKGDAGA PGAPGSQG*	3xOxidation [P7; P10; P17]	Collagen alpha-1(I) chain	7.44	3.14	10.63	10.35	within
e023254	GETGDVGPMPGPPGPPGRGPAGPNGADG PQGPPG*	7xOxidation [P12; P14; P15; P17; P20; P23; P29]	Collagen alpha-2(XI) chain	9.5	4.94	12.34	11.81	within

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e101168	GPPGESGREGAPGAEGSPGRDGSPGAKGDRGET*	4xOxidation [P3; P12; P18; P24]	Collagen alpha-1(I) chain	9.17	4.74	12.37	9.91	within
e023256	AGPSGEEGDKGDVGAPGHKGSKGDKGDA GPPGQP	none	Collagen alpha-3(V) chain	6.79	2.91	10.28	10.77	up
e023260	STTSGPGSTPSPVPTTSTTSAPTSTTSASTAST	none	Mucin-5AC	9.75	5.41	11.83	11.69	within
e023261	GAPGERGPPGLAGAPGLRGAGPPGPEGKGAAGPPG*	1xOxidation [P]	Collagen alpha-1(III) chain	6.84	0.94	14.02	8.87	within
e023263	GGGYGGGSSGGGSSGGGYGGGSSSGHGGSSSGGYGGGSSG	none	Keratin, type I cytoskeletal 10	8.36	3.48	11.64	10.26	within
e023264	PEPPSELLEDGQDTP TSAESPD APEENIA*	5xOxidation [P1; P3; P4; P15; P21]	Collagen alpha-1(XVIII) chain	8.81	4.18	12.11	3.38	down
e214957	GSDGQPGPPPGTAGFPGSPGAKGEVGPAGSPGSN*	1xOxidation [P]	Collagen alpha-1(III) chain	11.56	8.56	13.18	12.46	within
e214962	RGYTSAGEKGEPPGSEGLPGPPGPAGPRGE*	3xOxidation [P24; P]	Collagen alpha-1(XVI) chain	9.48	3.79	13.41	12.5	within
e023278	GEPGRDGVPGGPGMRGMPGSPGGPGSDGKPGPPG*	6xOxidation [P9; P12; P18; P21; P24; P]	Collagen alpha-1(III) chain	9.91	5.24	12.92	11.6	within
e023279	PSGSPGKDGPPGPAGNTGAPGSPGVSGPKGDAGQP*	7xOxidation [P5; P10; P11; P13; P20; P23; P28]	Collagen alpha-1(III) chain	11.79	7.48	13.66	12.33	within
e100677	NGERGGPGGPGPQGPPGKNGETGPQGPPGPTGPGG*	3xOxidation [P16; P24; P27]	Collagen alpha-1(III) chain	10.91	5.99	13.06	12.26	within
e023281	NGIPGEKGPA GERGAPGPAGPRGAAGEPGRDGV*	1xOxidation [P]	Collagen alpha-1(III) chain	6.94	4.56	11.28	11.2	within
e205413	SPGERGETGPPGPAGFPAGPQNGEPGGKGERG*	4xOxidation [P2; P10; P11; P26]	Collagen alpha-1(III) chain	7.06	3.92	10.6	9.9	within
e023282	PGRDGSPGGKDRGENGSPGAPGAPGHPGPPGPV*	5xOxidation [P22; P25; P28; P30; P31]	Collagen alpha-1(III) chain	12.69	9.83	14.02	13.44	within

a: Distribution in healthy female

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e023284	PGARGPSGPQGPGPPGPKGNSGEPGAPGSKGDT*	9xOxidation [P1; P6; P9; P12; P15; P16; P18; P25; P28]	Collagen alpha-1(I) chain	10.62	6.8	12.67	12.77	up
e023286	GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGP*	3xOxidation [P12; P14; P]	Collagen alpha-1(I) chain	7.03	3.49	10.58	8.87	within
e023291	GLQGDKGEPGYSEGTRPGPPGPTGDPGLPDGM*	2xOxidation [P19; P20]	Collagen alpha-3(IV) chain	8.37	3.46	11.45	11.02	within
e023296	PQGPNGADGPQGPPGSGVSGGVGEKGE PGEAGNP*	1xOxidation [P]	Collagen alpha-1(XI) chain	9.14	4.14	11.42	9.83	within
e023300	TYIYTGLSKHVEDVPAFQALGSLNDLQF	none	Zinc-alpha-2-glycoprotein	8.62	0.69	13.0	11.15	within
e023307	LTWASHEKMHEGDEGPGHHHKPGLGEGTP	none	Protein S100-A9	7.99	1.06	13.36	10.87	within
e104337	RGEKGESGPSGAAGPPGPKGPPGDDGPKGSPGPV*	5xOxidation [P15; P16; P18; P21; P22]	Collagen alpha-1(V) chain	11.06	6.12	12.66	11.19	within
e023314	AGMPGGPGKSGSMGPVGP GPAGERGHPGAPGPSG*	7xOxidation [P7; P15; P18; P19; P21; P28; P31]	Collagen alpha-1(XVI) chain	8.99	4.76	12.19	4.04	down
e023315	PAGPAGPPGYGPQGEPGLQGTQGVPGAPGPPGEA*	7xOxidation [P8; P12; P16; P25; P28; P30; P]	Collagen alpha-3(IV) chain	10.09	4.69	12.42	7.26	within
e023321	TGGPPGENGKPGEPGPKGDAGAPGAPGGKGDAGAPG*	6xOxidation [P5; P11; P14; P16; P23; P26]	Collagen alpha-1(III) chain	10.38	5.67	12.18	10.21	within
e103992	TGLPGDLGPPGDPGVSGIDGSPGEKGDGPDVGGPG*	3xOxidation [P9; P10; P]	Collagen alpha-3(V) chain	10.34	5.29	12.2	10.22	within
e214970	GADGQPGAQGEKPGDAGAKGDAGPPGPAGPAGPPGPIG*	2xOxidation [P]	Collagen alpha-1(I) chain	9.98	5.94	12.22	11.42	within
e214973	SEGPQGVVRGEPGPPGPAGAAGPAGNPGADGQPGQPGAQK*	1xOxidation [P]	Collagen alpha-1(I) chain	9.12	4.28	11.44	9.19	within
e023333	PQGVVRGEPGPPGPAGAAGPAGNPGADGQPGAQKANG*	3xOxidation [P8; P10; P11]	Collagen alpha-1(I) chain	10.33	4.51	12.84	11.27	within

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e205428	STPRTEETMSPLTNTTT*	1xN-Glycan [N14] (HexNAc(4)Hex(3))	Mucin-5B	6.64	3.5	11.07	4.3	within
e100656	DPGLMGERGEDGPAGNGTEGFPGFPGYPGNR*	2xOxidation [P13; P22]	Collagen alpha-1(VI) chain	11.37	7.81	13.57	11.46	within
e101735	GEPGRDGVPGGPGMRGMPGSPGGPGSDGKPGPPG*	7xOxidation [P3; P9; P12; P18; P21; P24; P30]	Collagen alpha-1(III) chain	11.42	5.7	13.25	13.34	up
e214974	HPGPIGPPGPRGNRGERGSEGSPPGHGQPGPP*	3xOxidation [P7; P]	Collagen alpha-1(III) chain	7.34	4.27	10.93	8.52	within
e023339	GRDGEDGPTGPPGPPGPPGGLGNFAAQYDG*	5xOxidation [P8; P11; P12; P14; P15]	Collagen alpha-2(I) chain	11.64	7.47	13.23	13.11	within
e023337	SSSPPIADGTSMTSTYSEGSTPLTNMSFST	none	Mucin-17	10.43	5.24	12.27	8.48	within
e214975	NDGARGSDGQPPGPPGTAGFPGPSGAKGEVGP*	6xOxidation [P14; P16; P17; P23; P26; P]	Collagen alpha-1(III) chain	11.63	7.46	13.36	13.07	within
e214977	APGADGPQGPPGGIGNPGAVGEKGEPEGEGEGLP*	3xOxidation [P17; P26; P32]	Collagen alpha-1(V) chain	11.56	7.97	13.21	13.01	within
e023344	MGVPGRDGVPGGPGETGKNGGFGRRGPPGAKGN*	3xOxidation [P4; P10; P13]	Collagen alpha-3(VI) chain	9.9	5.41	11.87	11.2	within
e023346	QGPPGPPGRDGTGPRDGEPPGEDGKPGDTGP*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	11.69	7.6	13.68	11.92	within
e023348	NIGSPGYPRQGLAGPEGNPGPKGAQGFIGSPG*	3xOxidation [P20; P22; P32]	Collagen alpha-1(XXIV) chain	8.71	4.81	11.44	8.15	within
e023356	GPPGPPGTAGFPGPSGAKGEVGPAGSPGSNGAPGQR*	1xOxidation [P]	Collagen alpha-1(III) chain	7.06	3.81	10.19	9.86	within
e214978	GVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPG*	3xOxidation [P5; P6; P11]	Collagen alpha-1(III) chain	12.55	7.62	15.07	13.62	within
e214982	GPQGEPLPLPGTKGERGEAGPPGRGERGEP*	3xOxidation [P23; P24; P32]	Collagen alpha-1(XXV) chain	9.7	5.61	12.67	10.63	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214984	GEPGPAGSKGESGNKGEPGSAGPQGPPG PSGEEGK	none	Collagen alpha-2(I) chain	13.51	9.58	15.62	16.71	up
e104859	SPGGPGAAGFPGARGLPGPSNGNPGP PGPSGSPG*	7xOxidation [P11; P17; P19; P20; P26; P28; P29]	Collagen alpha-1(III) chain	10.23	5.64	12.47	11.31	within
e023374	GREGAPGAEGSPGRDGSPGAKGDRGETG PAGPPGA*	1xOxidation [P33]	Collagen alpha-1(I) chain	9.08	3.74	11.94	15.41	up
e023375	RQKLGPAGDVEGHLSFLEKDLRDKVNS	none	Apolipoprotein A-IV	5.99	0.49	10.43	3.73	within
e023378	SRHRWPTENYGPDSVPDGYQGSQTFHGA	none	RANBP2-like and GRIP domain-containing protein 1	6.88	4.62	10.76	6.61	within
e104893	MLDKARRDTTVESVPVSPSEVNDAGDNDE	none	Replication protein A 30 kDa subunit	13.36	8.23	15.31	14.75	within
e214992	PAGSKGESGNKGEPGSAGPQGPPGPSGE EGKRGP*	2xOxidation [P1; P14]	Collagen alpha-2(I) chain	13.3	6.86	15.27	14.76	within
e023385	LAGYPGPAGPPGPPPGTSGHPGSPGSP GYQGP*	8xOxidation [P5; P7; P10; P11; P13; P14; P16; P17]	Collagen alpha-1(III) chain	10.11	4.6	12.23	4.18	down
e023389	PQGPIGQPGPSGADGEPGPRGQQGLFGQ KGDE*	2xOxidation [P1; P4]	Collagen alpha-1(V) chain	4.85	2.02	9.78	9.49	within
e214993	PPGTAGFPGSPGAKGEVGPAGSPGSNGAP GQRGEP*	3xOxidation [P2; P8; P11]	Collagen alpha-1(III) chain	4.55	1.97	10.44	5.84	within
e214995	KRTIIGWSAQEESTIPSWQEDEEEAEV	none	TPR and ankyrin repeat-containing protein 1	9.57	5.08	12.23	11.84	within
e023391	ELGEAGPSGEPGVPGDAGMPGERGEAGH RGSAGA*	2xOxidation [P11; P14]	Collagen alpha-3(IX) chain	10.79	5.69	12.79	10.4	within
e023393	EPVTPTSGGGPMSPQDDEAEESDNELSS GT	none	Rab GTPase-activating protein 1-like	9.84	4.75	12.67	12.79	up
e023394	GPPGEKGETGDVGQMPPGPPGPRGPSG APGADG*	7xOxidation [P2; P3; P17; P18; P20; P21; P23]	Collagen alpha-1(V) chain	11.47	7.46	13.24	11.87	within
e095954	GADGQPGAKGEPGDAGAKGDAGPPGPAG PAGPPGPIG*	3xOxidation [P12; P23; P24]	Collagen alpha-1(I) chain	12.17	8.96	13.93	13.4	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e214997	GQKGDQGHGVPVGFPMGPPGNPGPPGADG IAGAAGP*	2xOxidation [P]	Collagen alpha-1(XXII) chain	10.72	5.65	12.9	11.35	within
e105513	PNGADGPQGPPGSGVSGVGGVGEKGEPGE AGNPGPPG*	1xOxidation [P]	Collagen alpha-1(XI) chain	9.66	4.92	11.58	10.12	within
e023405	AAGAPGPQGFGQPAGEPGEPGQTGPAGARGPAGPPG*	2xOxidation [P20; P25]	Collagen alpha-2(I) chain	9.65	5.2	12.15	9.0	within
e023414	GEPGRDGVPGGPGMRGMPGSPGGPGSD GKPGPPG*	8xOxidation [P3; P9; P12; P18; P21; P24; P30; P32]	Collagen alpha-1(III) chain	11.82	7.98	13.95	14.59	up
e023415	GSVGDPGMEGPMGQREGPMGPRGEA GPPGSG*	2xOxidation [P23; P29]	Collagen alpha-1(XVII) chain	11.77	7.85	13.85	14.59	up
e106440	GPRGENGVGDGAPGPKGEPGHRGTDGAAG PRGAPG*	3xOxidation [P14; P18; P29]	Collagen alpha-1(XXIII) chain	8.48	2.31	11.3	11.3	up
e214999	QTGDPGLQGSPGPPGPEGFPDIDIGPQN GPE*	8xOxidation [P5; P10; P13; P14; P16; P20; P26; P31]	Collagen alpha-1(XXIV) chain	10.21	5.18	12.83	11.91	within
e102270	DKGPPGPVGGANGSPGERGPLGPAGGIGLP GQSGSE*	2xOxidation [P22; P29]	Collagen alpha-3(V) chain	5.87	2.01	10.72	9.22	within
e023427	GADGQPGAKGEPGDAGAKGDAGPPGPAG PAGPPGPI*	7xOxidation [P23; P24; P26; P29; P32; P33; P35]	Collagen alpha-1(I) chain	10.07	5.02	12.44	10.52	within
e023428	GAPGAEGSPGRDGSFGAKGDRGETGPAG PPGAPGAP*	3xOxidation [P30; P33; P]	Collagen alpha-1(I) chain	10.14	5.26	12.53	5.47	within
e023429	ARLTWASHEKMHEGDEGPGHHHKPLGEG	none	Protein S100-A9	6.54	2.9	10.65	7.26	within
e023432	TGSPHTTLSPSSSTTHEGEPTTFQSWPSSK	none	Mucin-12	12.14	8.63	14.22	13.79	within
e023433	GMPGFKGPTGYKGEQGEVGKDGEKGDGP PPGP*	2xOxidation [P27; P29]	Collagen alpha-3(IX) chain	12.19	9.09	14.1	13.79	within
e215008	PPGPPGTSGHPGSPGSPGYQGPPGEPGQ AGPSGP*	9xOxidation [P1; P2; P4; P5; P11; P14; P17; P22; P23]	Collagen alpha-1(III) chain	11.58	7.34	13.59	12.01	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e099510	PAGPRGAAGEPRDGVPGGPGMRGMPGS PGGPGSD*	3xOxidation [P1; P4; P11]	Collagen alpha-1(III) chain	11.52	7.42	13.51	12.24	within
e101308	QGPPGPTGFQGLPGPPGPPGEGGKPGDQ GVPGDP*	4xOxidation [P4; P6; P18; P31]	Collagen alpha-2(V) chain	7.57	3.04	11.96	6.28	within
e102849	ERGQPGVPGVPGMKGDDGSPGRDGLDGF PGLP*	3xOxidation [P5; P8; M/P]	Collagen alpha-2(IV) chain	12.44	8.58	13.99	13.56	within
e103877	EPGPAGQDGVGGDKGEDGDPGQPGPPGP SGEAGP*	8xOxidation [P2; P4; P20; P23; P25; P26; P28; P34]	Collagen alpha-1(XI) chain	11.84	6.56	14.6	13.18	within
e215011	GPAGAPGDKGESGPSGPAGPTGARGAPG DRGEPP*	2xOxidation [P33; P35]	Collagen alpha-1(I) chain	10.28	6.24	12.56	11.3	within
e215013	PIGPPGPAGAPGDKGESGPSGPAGPTGAR GAPDRG*	3xOxidation [P5; P7; P11]	Collagen alpha-1(I) chain	10.23	6.04	12.47	11.3	within
e023453	SSSGFGGGFGGGSGGGFGGGYGSGFG GFGGFGGGAGGGD	none	Keratin, type I cytoskeletal 9	11.51	6.6	13.94	13.07	within
e205479	PGEPPGAGQDGPDPKGGDDGEPGQTGSP GPTGEPG	none	Collagen alpha-1(V) chain	6.86	2.85	10.58	6.98	within
e102020	ENGSPGAPGAPGHPGPPGPVGPAGKSGD RGESGPA*	6xOxidation [P11; P14; P16; P17; P19; P22]	Collagen alpha-1(III) chain	6.73	4.27	9.61	10.06	up
e023457	LPDGLGPPGDPGVSGIDGSPGEKGDPGDV GGPGPP*	3xOxidation [P7; P8; P11]	Collagen alpha-3(V) chain	9.63	4.92	11.77	11.9	up
e215015	PTTSTTSGPGTTSSPVTTSTTSAPTSTTS APT	none	Mucin-5AC	9.8	5.53	11.74	11.85	up
e023464	DPGLMGERGEDGPAGNGTEGFPFGYP GNR*	4xOxidation [P13; P22; P25; P28]	Collagen alpha-1(VI) chain	10.55	4.4	13.39	11.5	within
e023465	GEPGRDGVPGGPGMRGMPGSPGGPGSD GKPGPPG*	9xOxidation [P3; P9; P12; P18; P21; P24; P30; P32; P33]	Collagen alpha-1(III) chain	12.76	9.52	14.34	13.6	within
e105408	GEPGSPGENGAPGQMGRGLPGERGRPG APGPAG*	3xOxidation [P21; P27; P30]	Collagen alpha-1(I) chain	10.42	5.23	12.56	11.68	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023468	NPGPVGDPPERGGPPGRAGLPGSDGAPGP PGTSLM*	3xOxidation [P8; P13; P14]	Collagen alpha-2(XI) chain	7.41	3.34	12.61	8.62	within
e023469	RGAAGEPGPHGPPGVPGSVGPKGSSGSP GPQGPPGP*	2xOxidation [P34; P]	Collagen alpha-1(XVII) chain	11.6	7.25	13.87	11.68	within
e023473	VGEPPGAGSKGESGNKGEPGSAGPQGPP GPSGEE*	7xOxidation [P4; P6; P19; P24; P27; P28; P30]	Collagen alpha-2(I) chain	11.24	7.4	13.09	12.11	within
e102535	GAPGAVGAPGPAGATGDRGEAGAAGPAG PAGPRGSPGE*	3xOxidation [P11; P26; P29]	Collagen alpha-2(I) chain	6.13	2.47	11.59	3.68	within
e215018	ATGDRGEAGAAGPAGPAGPRGSPGERGE VGPA PNG*	1xOxidation [P]	Collagen alpha-2(I) chain	9.96	5.2	12.36	7.81	within
e023476	VERRAQLQSAKAAEYEHFHRGHDHVLQ	none	Periplakin	5.45	1.58	9.07	8.64	within
e215023	AGEPGPPGPEGQPGVDGATGLPMKGEK GARGPN*	2xOxidation [P13; P22]	Collagen alpha-1(XV) chain	8.69	4.18	11.36	7.94	within
e023479	AGFAGPPGADGQPGAKGEPGDAGAKGDA GPPGPAGPA*	3xOxidation [P30; P31; P33]	Collagen alpha-1(I) chain	11.23	6.63	12.97	10.31	within
e098153	GMPGERGGLGSPGPKGDKGEPGGPGADG VPGKDG*	2xOxidation [P12; P14]	Collagen alpha-1(III) chain	8.02	2.86	11.66	10.43	within
e023484	PGSEGARGAPGPAGPPGDPGLMGERGED GPAGNGT*	2xOxidation [P10; P12]	Collagen alpha-1(VI) chain	8.98	4.23	11.17	10.06	within
e104798	GPAGFPAGPGQNGEPGGKGERGAPGEKG EGGPPGV*	3xOxidation [P15; P24; P32]	Collagen alpha-1(III) chain	9.12	3.53	11.43	10.17	within
e023486	GRPEAQPPPLSSEHKEPVAGDAVPGPKDG SAP	none	Neurosecretory protein VGF	7.85	4.0	10.96	11.65	up
e103034	GERGSPGGPGAAGFPGARGLPGPPGSNG NPGPPGP*	8xOxidation [P9; P15; P21; P23; P24; P30; P32; P]	Collagen alpha-1(III) chain	10.47	5.12	12.83	10.8	within
e023491	QDGVGGDKGEDGDPGQPGPPGPSGEAGP PGPPGK*	7xOxidation [P19; P20; P22; P28; P29; P31; P32]	Collagen alpha-1(XI) chain	8.45	4.89	12.17	6.24	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215028	TGPQGFPGTGPDVGPKGDKGDPGVGERGPPGPQ*	4xOxidation [P10; P15; P22; P29]	Collagen alpha-1(XVIII) chain	7.59	4.77	12.53	6.25	within
e023499	PGQPGTRGLDGPPGPDGLQGPPGPPGTSVAHGF*	1xOxidation [P]	Collagen alpha-5(IV) chain	9.11	4.9	12.06	10.76	within
e102952	ISLPTTSTTSAPITSMTSGPGTTPSPVPTTST	none	Mucin-5AC	7.38	1.66	11.56	11.9	up
e023503	PPGESGREGAPGAEGSPGRDGSPGAKGDRGETGP*	2xOxidation [P11; P]	Collagen alpha-1(I) chain	10.29	5.62	12.88	10.36	within
e103473	PGLPGSDGPLGHPGHEGPTGEKGAQGPPGSAGPP*	7xOxidation [P4; P9; P13; P18; P27; P28; P33]	Collagen alpha-3(V) chain	11.6	5.7	13.61	11.5	within
e023506	DAAQKTDTSHTDQDHPTFNKITPNLAEF	none	Alpha-1-antitrypsin	10.01	5.19	12.39	9.79	within
e215029	GNDGARGSDGQPGPPGPGTAGFPGSPGAKGEVGP*	5xOxidation [P15; P17; P18; P24; P27]	Collagen alpha-1(III) chain	10.52	5.85	13.3	12.35	within
e023516	EGTRPGPPGPTGDPGLPGDMGKKGEMGQPGPP*	7xOxidation [P5; P7; P8; P10; P14; P17; P29]	Collagen alpha-3(IV) chain	9.87	5.68	12.7	11.72	within
e023520	AGSPGSNGAPGQRGEPGPQGHAGAQQPPGPPGING*	6xOxidation [P16; P18; P27; P28; P30; P31]	Collagen alpha-1(III) chain	10.57	4.91	13.0	12.2	within
e023522	GIGKPGQDGIPGQPGFPGGKGEQGLPGLPGPPGL*	3xOxidation [P29; P31; P32]	Collagen alpha-1(VIII) chain	6.45	0.53	12.76	5.82	within
e106285	GLQGDKGEPGYSEGTRPGPPGPTGDPGLPGDMG*	2xOxidation [P20; P22]	Collagen alpha-3(IV) chain	8.89	4.77	11.56	10.55	within
e102658	APGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAG*	3xOxidation [P29; P31; P32]	Collagen alpha-1(I) chain	9.02	3.65	11.49	10.51	within
e102948	NITILVVVLV*	1xN-Glycan [N1] (HexNAc(5)Hex(4)Fuc(1)NeuAc(1))	Disintegrin and metalloproteinase domain-containing protein 7	7.38	2.92	10.61	5.05	within
e102164	SPGLPGPPGLPGQRGEEGPPGMRGSPGPPGPIG*	8xOxidation [P7; P8; P11; P19; P20; P26; P28; P29]	Collagen alpha-1(XVI) chain	10.22	5.18	11.94	10.84	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e205492	GPAGATGDRGEAGAAGPAGPAGPRGSPG ERGEVGPAG*	1xOxidation [P17]	Collagen alpha-2(I) chain	10.41	5.55	12.25	10.83	within
e023537	GSGWSSSNGPHGSVSGQSSGFHKSGSG QSSGYS	none	Hornerin	11.43	7.24	13.47	10.61	within
e215035	PSGASGERGPPGPMGPPGLAGPPGESGR EGAPGAE*	3xOxidation [P]	Collagen alpha-1(I) chain	10.89	5.72	13.07	11.02	within
e023538	DGLNGEQGDNLPGRKGEKGDEGSQGS GKRG*	2xOxidation [P13; P28]	Collagen alpha-6(VI) chain	11.37	6.75	13.48	10.47	within
e023539	RHGSDFGHSSSYGQHSGSGWSSSNGPH GSVS	none	Hornerin	9.75	5.43	11.72	10.95	within
e102364	GPQGFQGPAGEPGEPGQTGPAGARGPAG PPKGAGE*	3xOxidation [P2; P26; P29]	Collagen alpha-2(I) chain	8.63	4.61	10.77	9.93	within
e023541	ATGDRGEAGAAGPAGPAGPRGSPGERGE VGPAGPNG*	2xOxidation [P19; P23]	Collagen alpha-2(I) chain	9.94	5.05	11.89	10.74	within
e023543	ARGNDGATGAAGPPGPTGPAGPPGFPGAV GAKGEAGP*	3xOxidation [P19; P22; P23]	Collagen alpha-1(I) chain	8.45	3.7	10.71	9.18	within
e023548	GSETTTASTAGSETTTTSTSMAGSEATTT TADS	none	Mucin-22	10.92	6.86	13.67	12.69	within
e023549	SSSFGGSYGGIFGGGSFGGGSFGGGSF GGFGGGGFG	none	Keratin, type I cytoskeletal 10	9.96	5.59	12.34	7.41	within
e023550	SSGFGQHESGSGKSSGFGQHESRSSQSN YGQ	none	Filaggrin-2	10.96	6.85	13.78	12.69	within
e023554	GELGEAGPSGEPGVPGDAGMPGERGEAG HRGSAGA*	1xOxidation [P12]	Collagen alpha-3(IX) chain	9.75	5.87	12.04	9.97	within
e023556	PGAPGPQGFQGGPPGEPGEPGASGPMGPR GPPGPPG*	3xOxidation [P30; P]	Collagen alpha-1(I) chain	10.63	3.7	12.39	11.87	within
e023564	PPGTSGHPGSPGSPGYQGPPGEPGQAGP SGPPGPP*	5xOxidation [P20; P23; P28; P31; P32]	Collagen alpha-1(III) chain	10.1	5.99	13.0	9.44	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023566	PGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAG*	1xOxidation [P]	Collagen alpha-1(I) chain	6.84	3.16	11.2	8.32	within
e023569	PPGESGREGAPGAEGSPGRDGSPGAKGDRGETGP*	3xOxidation [P2; P11; P17]	Collagen alpha-1(I) chain	12.95	9.96	14.92	13.84	within
e103856	QIPNDYQSSRNQPGPPGPPGPPGSAGARGEP*	7xOxidation [P3; P13; P15; P16; P18; P19; P21]	Collagen alpha-1(XII) chain	8.7	4.01	12.08	11.38	within
e023572	GNDGARGSDGQPGPPGPPGTAGFPGPSGAKGEVGP*	6xOxidation [P15; P17; P18; P24; P27; P]	Collagen alpha-1(III) chain	9.53	5.27	12.72	11.77	within
e093872	VLSPADKTNVKAAGWKVGAHAGEYGAEALER	none	Hemoglobin subunit alpha	10.03	2.63	16.67	12.53	within
e215041	PPGPVGPPGSNGPVGEPGPEGPAGNDGTPGRDGAV*	5xOxidation [P4; P7; P8; P13; P17]	Collagen alpha-2(V) chain	7.87	4.13	11.19	10.95	within
e101855	QGPRGEPGTPGSPGPAGASGNPGTDGIPGAKGSAGA*	7xOxidation [P3; P7; P10; P13; P15; P22; P28]	Collagen alpha-1(II) chain	10.44	4.9	12.69	10.95	within
e023577	FKGKWERPFEVKDTEEDFHVDQVTT	none	Alpha-1-antitrypsin	6.67	1.74	12.57	7.24	within
e023584	GATGPPGEEGPRGPPGRAGEKGDEGSPGIRGPQG*	1xOxidation [P]	Collagen alpha-2(IX) chain	6.0	1.89	12.17	6.7	within
e023586	VAHVDDMPNALSALSDLHAHKLRVDPVNF*	1xOxidation [M7]	Hemoglobin subunit alpha	6.14	0.12	11.14	8.4	within
e205514	LSNVEGDNAVPMQHNNRPTQPLKGRTVRA	none	Carbonic anhydrase 1	7.73	3.24	12.84	13.67	up
e023595	PPGTSMSSNSVSNLSYLFGTESHSYPYS	none	Zinc finger protein GLIS3	9.34	3.95	11.83	8.43	within
e208770	QGFQGNPGEPEGVSGPMGRGPPGPPGKPGD*	6xOxidation [P18; P21; P24; P25; P27; P28]	Collagen alpha-1(II) chain	10.19	5.84	12.41	11.7	within
e023603	DLGPPGDPGVSGIDGSPGEKGDPGDVGGPGPPGASG*	5xOxidation [P5; P8; P17; P23; P29]	Collagen alpha-3(V) chain	10.96	5.41	12.94	10.99	within
e205525	EDAMMPFPGATIISQLLKNNMNKNGGTEPS	none	Prospero homeobox protein 1	10.21	4.48	12.46	4.39	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e023606	EEVFASEDESEESSLSAEEDSENEEAI	none	Ribosome biogenesis protein BMS1 homolog	12.61	8.17	14.28	14.48	up
e023608	ADGVDHIDIYADVGEFNQEAIEYGGHDQI	none	Cleavage and polyadenylation specificity factor subunit 6	8.19	2.49	11.52	3.14	within
e023611	RPGEVGPFGPPGPGPAGEKGGSPGADGPAGA PGTPGPQG*	5xOxidation [P10; P11; P13; P20; P25]	Collagen alpha-1(I) chain	9.49	5.29	11.51	11.33	within
e215048	ADGQPGAKGEPGDAGAKGDAGPPGPAGP AGPPGPIGN*	3xOxidation [P25; P28; P31]	Collagen alpha-1(I) chain	9.37	5.02	11.45	11.34	within
e023614	MRGMPGSPGGPGSDGKPGPPGSQGESG RPGPPGP*	7xOxidation [P8; P11; P17; P19; P20; P29; P31]	Collagen alpha-1(III) chain	10.06	4.94	13.1	11.19	within
e023615	FPGDPGPPGEPGPAGQDGVGGDKGEDGD PGQPGPP	none	Collagen alpha-1(XI) chain	8.69	4.24	12.71	11.24	within
e023616	EPGRDGNPGSDGLPGRDGSPGGKGDGRGE NGSPGA*	2xOxidation [P2; P8]	Collagen alpha-1(III) chain	9.86	4.07	12.77	11.02	within
e023617	DKGEQGPPGPTGPQGPIGQPGPSGADGEP GPRGQ*	2xOxidation [P13; P]	Collagen alpha-1(V) chain	10.14	4.26	12.36	10.51	within
e106612	GPAGQDGVGGDKGEDGDPGQPGPPGPSG EAGPPGPP*	3xOxidation [P33; P]	Collagen alpha-1(XI) chain	10.78	4.31	13.16	7.85	within
e023619	GDKGAAGAGLDGPEGDQGPQGVPVGT SKDGQDG*	2xOxidation [P13; P19]	Collagen alpha-3(IX) chain	10.14	5.15	12.89	7.8	within
e023621	GESGREGAPGAEGSPGRDGSPGAKGDRG ETGPAGP*	2xOxidation [P21; P]	Collagen alpha-1(I) chain	10.33	6.2	14.11	12.91	within
e215050	PPGESGREGAPGAEGSPGRDGSPGAKGD RGETGP*	4xOxidation [P2; P11; P17; P23]	Collagen alpha-1(I) chain	15.78	14.07	17.05	16.62	within
e023629	PGEPPGPPGPKGPTGDDGPKGNPVGFP GDGPP*	7xOxidation [P7; P9; P12; P18; P22; P24; P28]	Collagen alpha-2(XI) chain	11.92	6.46	14.35	15.01	up
e205537	GPPGEPGDGPMGPIGSRGPEGPPGKPG DGEPPG*	5xOxidation [P14; P20; P23; P24; P27]	Collagen alpha-2(V) chain	6.01	2.05	10.15	6.49	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e095994	ETEEHYFEDKLIEDLAKPGAEPPEDEG	none	Ryanodine receptor 2	10.05	5.51	12.1	12.51	up
e102083	GPGMRGMPGSPGGPGSDGKPGPPGSQG ESGRPGPP*	4xOxidation [P23; P32; P34; P35]	Collagen alpha-1(III) chain	8.86	4.49	11.89	9.48	within
e205545	GAIGTDGTPGAKGPTGSPGTSGPPGSAGP PGSPGPQGS*	3xOxidation [P30; P33; P35]	Collagen alpha-2(V) chain	6.28	2.13	10.08	8.43	within
e023653	VGRTGEVGAVGPPGFAGEKGPSGEAGTAG PPGTGP*	3xOxidation [P13; P21; P30]	Collagen alpha-2(I) chain	10.48	5.98	12.14	11.57	within
e102977	EGVQKEDIPPADLSDQVPDTESETRILLQ	none	Complement C3	8.73	4.5	11.38	10.71	within
e215058	EKGERGAAGEPGPHGPPGVPGSVGPKGS SGSPGPQ*	3xOxidation [P11; P13; P16]	Collagen alpha-1(XVII) chain	9.71	5.19	11.95	11.12	within
e023668	FGGRGGGFGGGSSFGGGSGFSGGGFGG GGFGGGRFGGF	none	Keratin, type II cytoskeletal 2 epidermal	9.14	5.22	11.73	9.23	within
e205555	GPTGPRGFPGPPGPDGLPGSMGPPGTPSV DHGF*	8xOxidation [P2; P5; P9; P11; P12; P14; P18; P23]	Collagen alpha-1(IV) chain	8.87	3.88	11.71	9.22	within
e105991	SSSGGFGGGFGGGSGGGFGGGYGSGFG GFGGFGGGAGGGDG	none	Keratin, type I cytoskeletal 9	9.94	5.26	12.68	11.26	within
e215062	GDKGAAGAGLDGPEGDQGPQGPQGVPGT SKDGQDG*	3xOxidation [P19; P22; P26]	Collagen alpha-3(IX) chain	9.66	5.45	12.0	10.96	within
e023677	LSEDGIQTGDSPDEAPQNTPPATVEGREEE G	none	Rho guanine nucleotide exchange factor 15	10.64	5.12	13.03	14.64	up
e215064	SGEKGDQGPDPGSPGSPGAPAGPP GYGPQGEP*	1xOxidation [P]	Collagen alpha-3(IV) chain	9.65	5.45	12.15	10.98	within
e215065	SWGSADSDSGHDSGVNVGEERPPTGPALP SPY	none	Kinesin-like protein KIF26A	10.33	5.09	12.92	14.51	up
e023679	ERGPPGESGAAGPTGPIGSRGSPGPPGPD GNKGEP*	2xOxidation [P5; P13]	Collagen alpha-2(I) chain	8.27	3.75	12.01	10.41	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e205559	PPGDDGPKGNPGVPVFGDPGPPGEPGP AGQDGVG*	5xOxidation [P11; P13; P17; P20; P22]	Collagen alpha-1(XI) chain	8.11	3.56	11.17	9.81	within
e101141	PPGESGREGAPGAEGSPGRDGSPGAKGD RGETGP*	5xOxidation [P2; P11; P17; P23; P34]	Collagen alpha-1(I) chain	10.41	6.21	12.08	12.24	up
e096001	GQPGAKGEQGEAGQKGDAGAPGPQGPPSG APGPQGPT*	2xOxidation [P]	Collagen alpha-1(II) chain	7.22	3.14	10.23	7.08	within
e215068	GAPGQNGEPGGKGERGAPGEKGEPPGPPG VAGPPGGSG*	3xOxidation [P26; P27; P]	Collagen alpha-1(III) chain	6.38	0.73	8.97	9.89	up
e023695	PGDRGEPGPPGAGFAGPPGADGQPGAK GEPGDAGA*	4xOxidation [P18; P19; P25; P31]	Collagen alpha-1(I) chain	8.84	3.14	11.85	10.45	within
e023698	DEEGSGDEDESEGLGLEEYDEDDLGAEEQ E	none	Protein AATF	8.6	4.58	11.88	10.78	within
e105778	KGEKGNPGVGTQGPRGPPGAGPSGESR PGSPGPP*	1xOxidation [P7]	Collagen alpha-1(XIV) chain	9.1	4.26	13.19	11.79	within
e215072	GPPGESGREGAPGAEGSPGRDGSPGAKG DRGETGP*	2xOxidation [P]	Collagen alpha-1(I) chain	7.11	3.66	11.93	3.77	within
e023718	AGENFATPFHGHVGRGAFSDVYEPAEDTFL	none	Methyltransferase HEMK2	7.06	2.55	10.77	7.57	within
e104738	QAFGSGNNSYSGSNSGAAIGWGSASNAGS GSGFNNG	none	TAR DNA-binding protein 43	8.61	3.3	12.27	5.47	within
e215077	ESGPSGPAGPTGARGAPGDRGEPGPPGP AGFAGPPGA*	2xOxidation [P28; P34]	Collagen alpha-1(I) chain	8.87	4.96	11.43	11.93	up
e096009	NTGAPSPGVSGPKGDAGQPGEKGSPGA QGPPGAPGP*	3xOxidation [P26; P31; P32]	Collagen alpha-1(III) chain	9.55	5.29	11.28	10.07	within
e023735	PAGQDGVGGDKGEDGDPGPPGPPSGE AGPPGPPG*	5xOxidation [P23; P25; P31; P32; P]	Collagen alpha-1(XI) chain	10.63	6.16	12.87	13.27	up
e023736	GAGGGPPPGPPGAGDRGGGGPGGGGGPG GGSAGGPSQPPGGGGP	none	Far upstream element-binding protein 2	10.66	5.86	12.86	11.81	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e106668	ERGPQGPQGPVGFPGPKGPPGPPGKDGLPGHP*	11xOxidation [P4; P7; P10; P14; P16; P19; P20; P22; P23; P29; P32]	Collagen alpha-1(XI) chain	9.96	5.87	12.61	10.73	within
e215082	ENGKPGEPGPKGDAGAPGAPGGKGDAGAPGERGPPG*	5xOxidation [P10; P17; P20; P29; P34]	Collagen alpha-1(III) chain	10.02	5.87	12.47	11.25	within
e205582	GQPGAQGEQGEAGQKGDAGAPGPQGPSGAPGPQGPT*	3xOxidation [P21; P23; P30]	Collagen alpha-1(II) chain	8.35	4.09	11.03	11.04	up
e023741	GPAGFAGPPGADGQPGAQGEQGEAGQKGDAGAPGPQG	none	Collagen alpha-1(II) chain	10.04	5.52	12.5	11.19	within
e023744	EDPQGDAAQKTDTSHHQDHPNFKITPN	none	Alpha-1-antitrypsin	6.58	1.87	11.97	8.83	within
e023750	AGGAATPEDGAGGRGSEGSQSPGSSVDDAEDDPSR	none	Zinc finger protein ZFPM1	7.45	4.32	11.27	7.3	within
e100970	GGSFRRSYGSSSFSGSYGGIFGGGSFSGGGSF	none	Keratin, type I cytoskeletal 10	9.52	4.0	12.67	10.65	within
e023764	GAAGEPGPHGPPGVPGSVGPKGSSGSPGPQGPPGPVG*	7xOxidation [P8; P11; P12; P15; P20; P27; P]	Collagen alpha-1(XVII) chain	11.22	7.32	13.49	11.62	within
e205590	PAGAPGPQGFQGNPGEPEGPVSGPMGPRGPPGPP*	3xOxidation [P25; M26; P32]	Collagen alpha-1(II) chain	6.11	2.61	10.61	4.29	within
e023765	DAAQKTDTSHHQDHPNFKITPNLAEFA	none	Alpha-1-antitrypsin	10.32	4.05	13.09	11.3	within
e023767	RTGEVGA VGPPGFAGEKGPSGEAGTAGPPGTPGPQG*	3xOxidation [P19; P28; P]	Collagen alpha-2(I) chain	13.99	11.62	15.42	14.96	within
e208778	PGAQGEQDAGAKGDAGPPGAPGAPGGPIGNVGAPG*	5xOxidation [P21; P24; P27; P]	Collagen alpha-1(I) chain	9.22	4.17	13.39	11.28	within
e023768	PGIAGAPGFPGARGPSGPQGPGGPPGPKGNSGEPPGAP*	3xOxidation [P1; P7; P10]	Collagen alpha-1(I) chain	8.5	4.14	11.33	10.39	within
e023769	AAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQQPPGP*	2xOxidation [P5; P14]	Collagen alpha-1(I) chain	11.61	6.49	13.36	12.25	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e103330	GPPGYGPQGEPGLQGTQGVPGAPGPPGEAGPRGE*	8xOxidation [P3; P7; P11; P20; P23; P25; P26; P31]	Collagen alpha-3(IV) chain	11.58	7.37	13.74	12.59	within
e215088	TSATFSGGASSGFGGTLSTTAGFSGVLSTS TSFGSA	none	Trophinin	11.17	5.1	13.56	11.71	within
e023776	GPPGESGREGAPGAEGSPGRDGSPGAKG DRGETGP*	3xOxidation [P12; P18; P]	Collagen alpha-1(I) chain	10.87	6.35	13.78	12.58	within
e023777	EPGRPGSPGAPGEQPPGTPGFPGNAGV PGTPGER*	1xOxidation [P]	Collagen alpha-1(XIV) chain	6.84	2.12	10.25	5.18	within
e023785	GVSGPMGPRGPPGPPGKPGDDGEAGKPG KAGERGP*	2xOxidation [P27; P35]	Collagen alpha-1(II) chain	6.44	2.29	12.0	7.93	within
e106708	GGPGPQQPPGKNGETGPQGGPGTGPGG DKGDTGPP*	5xOxidation [P17; P20; P21; P23; P26]	Collagen alpha-1(III) chain	8.03	4.69	11.78	7.34	within
e023786	GSLGEAGAPGHKGSKGAPGPAGARGESGL AGAPGPAGP*	3xOxidation [P9; P18; P20]	Collagen alpha-1(XVIII) chain	6.69	2.11	10.08	5.38	within
e215095	NTGAPGSPGVSGPKGDAGQPGEKGSPPGA QGPPGAPGP*	4xOxidation [P26; P]	Collagen alpha-1(III) chain	11.54	6.35	13.06	11.97	within
e100673	AVEEEAQVETSPETSRSSDAFTTQHALHQA	none	Chromosome-associated kinesin KIF4B	9.44	2.56	12.73	10.59	within
e023796	VGERGDRGDPGPAGLPGSQGAPGTPGPV GAPGDAGQ*	3xOxidation [P]	Collagen alpha-2(V) chain	11.45	6.94	13.07	11.94	within
e215096	QRGERGFPLPGPSGEPGKQGAPGASGD RGPPGP*	2xOxidation [P]	Collagen alpha-1(II) chain	7.18	3.44	11.08	9.35	within
e105233	PQGEPPGPPQQGNPQPGLPGPQQPIGP PGEKGP*	5xOxidation [P7; P8; P14; P16; P20]	Collagen alpha-1(XI) chain	12.86	7.43	15.71	13.61	within
e023807	FPGNPGMKGEAGPTGARGPEGPQGQRGE TGPPGP*	1xOxidation [P32]	Collagen alpha-2(V) chain	9.82	3.47	12.48	8.78	within
e215099	PQGEPLQGTQGVPGAPGPPGEAGPRGE LSVSTP*	5xOxidation [P17; P19; P20; P25; P34]	Collagen alpha-3(IV) chain	8.32	2.59	11.41	8.79	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215100	ENGKPGEPGPKGDAGAPGAPGGKGDAGAPGERGPPG*	6xOxidation [P8; P10; P17; P20; P29; P34]	Collagen alpha-1(III) chain	13.71	11.47	15.21	15.35	up
e023814	GATGDRGEAGAAGPAGPAGPRGSPGERGEVGPAGPNG*	3xOxidation [P24; P32; P35]	Collagen alpha-2(I) chain	8.86	2.83	12.05	8.95	within
e023812	DAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRG*	3xOxidation [P8; P14; P20]	Collagen alpha-1(I) chain	5.69	1.59	8.53	4.83	within
e104529	GAPGQNGEPGGKGERGAPGEKGEggPPGVAGPPGGSG*	5xOxidation [P9; P18; P26; P27; P32]	Collagen alpha-1(III) chain	10.68	7.25	12.73	12.04	within
e023816	ELGDPGPRGNQGDRGDKGAAGAGLDGPEGDQGPQ*	1xOxidation [P]	Collagen alpha-3(IX) chain	11.37	7.29	13.36	12.57	within
e215108	EVKPEWGMPPGEGVQGPDPGTEEQLSQDPGD	none	Zinc finger and SCAN domain-containing protein 25	12.25	5.82	14.27	14.44	up
e215111	PPGSNGNPGPPGSPGSGPKDGPPGPAGNTGAPTGAPGSPGVs*	2xOxidation [P17; P22]	Collagen alpha-1(III) chain	11.13	6.68	13.31	8.68	within
e023825	NGNPGPPGSPGSGPKDGPPGPAGNTGAPGSPGVSGPKG*	2xOxidation [P13; P18]	Collagen alpha-1(III) chain	10.11	6.25	12.56	11.72	within
e100767	PGPVGPAGKSGDRGESGPAGPAGAPGPA GSRGAPGPQG*	2xOxidation [P1; P3]	Collagen alpha-1(III) chain	8.19	5.07	12.22	9.45	within
e208781	RTGEVGAvgPPGFAGEKGPSGEAGTAGPPGTPGPQG*	4xOxidation [P11; P19; P28; P29]	Collagen alpha-2(I) chain	12.19	8.52	13.6	13.48	within
e023831	AAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQQPPGP*	3xOxidation [P5; P14; P16]	Collagen alpha-1(I) chain	13.41	11.01	14.74	14.08	within
e096033	AGPPGPPGPPGTSGHPGSPGSPGYQGPPGEPGQAGP*	7xOxidation [P9; P10; P16; P19; P22; P27; P28]	Collagen alpha-1(III) chain	11.03	6.57	13.73	12.6	within
e023836	LEKPEGEDGFTSFPSDTSTHTFGAGKDDF	none	Protein SIX6OS1	10.95	6.2	13.71	12.61	within
e023837	PAGPPGPPGPSSNQGDTGDPGFGIPGPKGPKGdQ*	2xOxidation [P10; P20]	Collagen alpha-6(IV) chain	8.71	5.39	10.88	10.02	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215118	GAKGQEGAHGAPGAAGNPGAPGHVGAPG PSGPPGSVGAP*	1xOxidation [P12]	Collagen alpha-1(XXII) chain	11.43	6.78	13.49	12.38	within
e023839	GPAGSPGFQGLPGPAGPPGEAGKPGEQG VPGDLGAPG*	2xOxidation [P12; P14]	Collagen alpha-1(I) chain	8.58	4.59	10.69	9.96	within
e023840	PGHPGQRGEVGFQGKTGPPGPPGVVGPG GAAGETG*	2xOxidation [P19; P21]	Collagen alpha-2(XI) chain	11.42	6.35	13.48	12.41	within
e105555	GPPGESGREGAPGAEGSPGRDGSPGAKG DRGETGP*	4xOxidation [P3; P12; P18; P24]	Collagen alpha-1(I) chain	14.39	11.68	16.31	15.66	within
e102141	ATPGAAGGATAAAASGATSAPEGDAARAA KSDNVAPAD	none	CaM kinase-like vesicle-associated protein	9.57	6.34	11.22	11.43	up
e023848	GPAGQKGEPPGPGFGNPGPPGLPLSGQ KGDGGLPG*	2xOxidation [P20; P23]	Collagen alpha-5(IV) chain	8.69	5.4	11.12	10.83	within
e103429	PGPPGPPGVSGGGYDFGYDGFYRADQP RSAP*	1xOxidation [P3]	Collagen alpha-2(I) chain	10.86	5.79	13.08	12.1	within
e023850	QGSRGDPGDAGPRGDSGQPGKGDPRP GFSYP*	3xOxidation [P21; P25; P28]	Collagen alpha-2(VI) chain	11.72	7.56	13.55	12.24	within
e099136	EVGPPGPAGSAGARGAPGERGETGPPGP AGFAGPPGA*	4xOxidation [P5; P7; P17; P25]	Collagen alpha-1(II) chain	11.52	7.57	13.51	12.52	within
e023857	PPGPPGINGSPPGKGEMGPAGIPGAPGLM GARGPPG*	7xOxidation [P4; P5; P11; P19; P23; P26; P34]	Collagen alpha-1(III) chain	7.8	3.29	11.93	8.67	within
e300140	ETGAVGAPGAPGPPGSPGAPPTGKQGD RGEAGAQGP*	4xOxidation [P8; P11; P13; P14]	Collagen alpha-1(II) chain	10.65	5.11	13.58	12.2	within
e098162	GEVGPPGPAGSAGARGAPGERGETGPPG PAGFAGPPG*	5xOxidation [P5; P6; P8; P18; P26]	Collagen alpha-1(II) chain	10.5	6.14	12.98	13.05	up
e103296	GEPGPQGHAGAQQPPGPPGINGSPPGKG EMGPAGIPG*	2xOxidation [P32; P36]	Collagen alpha-1(III) chain	9.14	4.03	12.24	11.48	within
e023868	GGGGFGGGRFGGFGGPGGVGGLGGPGG FGPGGYPGGIHE	none	Keratin, type II cytoskeletal 2 epidermal	11.48	7.65	13.04	12.7	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215125	EPGREGSPGADGPPGRDGAAGVKGDRGETGAVGAPG*	1xOxidation [P35]	Collagen alpha-1(II) chain	8.26	4.1	11.68	11.59	within
e096040	VHLTPEEKSAVTALWGKVVNDEVGGEALGRL	none	Hemoglobin subunit beta	10.7	4.98	16.12	6.75	within
e023872	ENGKPGEPGPKGDAGAPGAPGGKGDAGAPGERGPPG*	7xOxidation [P5; P8; P10; P17; P20; P29; P34]	Collagen alpha-1(III) chain	8.89	5.2	10.9	11.35	up
e215127	APEPATEPAPEPATEPAPEPAPEPATESAPEPT	none	Diacylglycerol kinase kappa	6.41	2.74	10.01	9.33	within
e023874	DTGPQGFPPTPGDVGPDKGDPGVGERGPPGPQ*	3xOxidation [P16; P23; P30]	Collagen alpha-1(XVIII) chain	7.07	3.99	10.1	8.84	within
e215129	DGLPGRDGSPPGKGDRGENGSPGAPGAPGHPGPPGP*	3xOxidation [P10; P22; P25]	Collagen alpha-1(III) chain	6.63	2.35	9.96	10.01	up
e023885	GPAGSAGARGAPGERGETGPPGPAGFAGPPGADGQPG*	6xOxidation [P2; P12; P20; P21; P23; P29]	Collagen alpha-1(II) chain	6.19	0.95	10.19	8.38	within
e100822	GPPGPAGSAGARGAPGERGETGPPGPAGFAGPPGADG*	8xOxidation [P3; P5; P15; P23; P24; P26; P32; P33]	Collagen alpha-1(II) chain	7.54	2.74	10.5	9.52	within
e215137	ERGDRGDPGPAGLPGSQGAPGTGPVGPAGDAGQRG*	1xOxidation [P]	Collagen alpha-2(V) chain	12.76	10.22	14.17	13.32	within
e104775	AGPPGPPGPPGTSGHPGSPGSPGYQGPPGEPGQAGP*	8xOxidation [P9; P10; P16; P19; P22; P27; P28; P]	Collagen alpha-1(III) chain	12.86	8.97	15.06	14.81	within
e023903	PAGKSGDRGESGPAGPAGAPGPAGSRGAPGPQGPGRD*	2xOxidation [P31; P]	Collagen alpha-1(III) chain	10.8	5.92	12.97	11.89	within
e023905	VPGGPGMRGMPGSPGGPSDGKPGPPGSQGEGSRP*	8xOxidation [P2; P5; P11; P14; P17; P23; P25; P26]	Collagen alpha-1(III) chain	12.7	7.43	14.29	12.75	within
e106505	TAGFPGSPGAKGEVGPAGSPGSNGAPGQRGEPGPQG*	6xOxidation [P5; P8; P16; P20; P26; P32]	Collagen alpha-1(III) chain	10.59	5.77	12.17	12.4	up
e215142	GPPGERGGPGSRGFPAGDGVAGPKGPAGERGSPGPAG*	1xOxidation [P2]	Collagen alpha-1(I) chain	6.69	3.78	10.25	6.0	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215145	SSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSH	none	Mucin-21	7.27	3.33	10.67	9.27	within
e023909	APGDRGEPGPPGPAGFAGPPGADGQPGA KGEPGDAGA*	3xOxidation [P10; P11; P13]	Collagen alpha-1(I) chain	8.39	4.32	10.91	11.95	up
e023910	RLTWASHEKMHEGDEGPGHHHKPLGEG TP	none	Protein S100-A9	5.16	0.0	10.97	2.7	within
e023914	PQTSTTSAPTTSTTSAPTTSTTSAPTTSTTS TPQ	none	Mucin-5AC	10.55	5.91	13.57	10.75	within
e023917	SPLQGLTNQDLQEGEDWEQEDMDPRL	none	RNA polymerase II elongation factor ELL3	6.19	2.59	12.97	11.61	within
e023920	QAGSPGEKGEAGEKGNPGAIEVPLPGPE GPPGPPG*	7xOxidation [P17; P22; P25; P27; P30; P31; P33]	Collagen alpha-1(XIII) chain	12.21	8.42	14.26	12.26	within
e023924	TDGTPGAKGPTGSPGTSGPPGSAGPPGSP GPQGSTGPQ*	2xOxidation [P20; P25]	Collagen alpha-2(V) chain	6.15	1.82	13.18	11.69	within
e023925	EQGPRGRDGDKEKGAAPGRGRDGEPT PGNPG*	2xOxidation [P19; P]	Collagen alpha-1(II) chain	9.97	4.58	12.03	10.33	within
e215150	SFPTTKTYFPHFDLSHGSAQVKGHGKKVAD	none	Hemoglobin subunit alpha	5.72	0.38	9.4	7.45	within
e023932	NTGAPGSPGVSGPKGDAGQPGEKGSPGA QGPPGAPGP*	6xOxidation [P13; P20; P26; P31; P32; P]	Collagen alpha-1(III) chain	14.65	12.71	15.94	15.78	within
e215155	GFNGPPGPIGLQGLPGPSGEKGETGDVGP MGPPGP*	4xOxidation [P15; P17; P29; P32]	Collagen alpha-2(XI) chain	9.7	5.67	11.89	11.72	within
e023936	SGPSGAAGPPGPKGPPGDDGPKGSPGPV GFPGDPGPPG*	1xOxidation [P]	Collagen alpha-1(V) chain	9.77	5.05	12.37	11.75	within
e215156	PRGANGAPGNDGAKGDAGAPGAGPSQGA PGLQGMPGE*	3xOxidation [P1; P8; P20]	Collagen alpha-1(I) chain	9.45	4.99	13.77	14.56	up
e023939	FAGPPGADGQPGAKGEQGEAGQKGDAGA PGPQGPPSGA*	1xOxidation [P]	Collagen alpha-1(II) chain	11.27	6.38	13.99	14.58	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e105554	GPPGPPGRDGEDGPTGPPGPPGPPGPPG LGGNFAAQ*	4xOxidation [P3; P5; P6; P18]	Collagen alpha-2(I) chain	11.02	5.55	13.11	10.49	within
e023943	GVGLGPGPMGLMGPRGPPGAAGAPGPQG FQGPAEP*	6xOxidation [P6; P8; P14; P17; P18; P24]	Collagen alpha-2(I) chain	10.33	5.52	12.65	12.63	within
e023947	FSGLQGPPGPPGSPGEQGPSGASGPAGP RGPPGSAGA*	6xOxidation [P11; P14; P19; P25; P28; P31]	Collagen alpha-1(I) chain	10.82	5.39	13.18	13.93	up
e215157	GESGREGAPGAEGSPGRDGSPGAKGDRG ETGPAGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	11.08	6.17	13.46	13.92	up
e099963	GEPGRRGDPTGKSPGSDGPKGEKGDGP PEGPRG*	3xOxidation [P9; P15; P20]	Collagen alpha-2(VI) chain	8.96	4.67	11.58	9.22	within
e215159	YSPQYDSYDVKSGVAVGGLAGYPGPAGPP GPPGP*	1xOxidation [P]	Collagen alpha-1(III) chain	9.38	4.06	12.13	13.13	up
e205648	GPAGPPGQTGPPGPAGPPGSKGDRGQTG EKGPAGPPG*	3xOxidation [P2; P11; P14]	Collagen alpha-1(XXVI) chain	9.27	4.5	13.04	13.2	up
e023951	DGVSGGEGKGGSDGGGSHRKEGEEADAP GVIPGIVG	none	CD99 antigen	13.06	10.2	14.81	15.34	up
e023954	SSYGQQGSGSGQSPSRGRHGSGSGHSSS YGQHGS	none	Hornerin	9.14	4.28	12.35	9.29	within
e103207	GPPGPAGPAGERGEQGAPGSGFQGLPG PPGPPGEGG*	3xOxidation [P3; P5; P8]	Collagen alpha-1(II) chain	9.42	2.93	12.04	11.29	within
e023956	DGVIGMMGFPGAIGPPGPPGNPGTPGQRG SPGIPG*	6xOxidation [P10; P15; P16; P18; P19; P22]	Collagen alpha-3(IV) chain	10.85	6.8	12.8	11.6	within
e215165	DVSTPPTVLPDNFPRYPVGKF*	1xO-Glycan [T4] (Hex(1)HexNAc(1) NeuAc(2))	Insulin-like growth factor 2	16.1	11.5	17.64	17.08	within
e215166	MPGGPGKSGSMGPVGPAGPAGERGHPGA PGPSGSPGL*	3xOxidation [P26; P29; P31]	Collagen alpha-1(XVI) chain	6.54	1.22	10.48	8.55	within
e023962	FGHGAEDSLADQAANEWGRSGKDPNHFR PAG	none	Serum amyloid A-1 protein	5.4	0.87	10.41	7.8	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215168	SDAENGHDYGSSETPKMTRGVLSRTSSIQPS	none	Transmembrane channel-like protein 5	10.93	5.85	14.8	15.54	up
e215170	ESQNVDFESVSSVTALEALSKLLNPEEEDD	none	Dynein axonemal assembly factor 6	11.91	6.54	15.3	15.54	up
e104391	SEISSAAESRKKPGHYSEAAAADMSSDVEVG	none	Homeobox even-skipped homolog protein 2	11.16	5.19	13.82	10.0	within
e215171	SDWMLGYPDTWNPPPTSLDLPSHVAVDVW	none	Telomerase-binding protein EST1A	7.61	3.62	12.26	13.68	up
e215173	KGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP*	2xOxidation [P]	Collagen alpha-1(I) chain	10.82	6.62	12.65	10.95	within
e023973	GPPGRDGEDGPTGPPGPPGPPGPPGLGGNFAAQY*	10xOxidation [P3; P11; P14; P15; P17; P18; P20; P21; P23; P24]	Collagen alpha-2(I) chain	10.87	5.38	13.96	11.29	within
e215177	PGKKGEKGDSEDGAPGLPGQPGSPGEQGPRGPPGA*	2xOxidation [P29; P32]	Collagen alpha-1(VII) chain	10.73	6.56	12.33	11.65	within
e101451	ARGAPGPAGPPGDPGLMGERGEDGPAGNGTEGFPG*	6xOxidation [P7; P10; P11; P14; P25; P34]	Collagen alpha-1(VI) chain	9.32	5.53	12.34	3.6	down
e215179	ERGPPGESGAAGPTGPIGSRGPSGPPGPDGNKGEPG*	3xOxidation [P13; P16; P22]	Collagen alpha-2(I) chain	9.22	4.2	11.79	9.95	within
e023977	GPAGPAGPRGSPGERGEVGPAGPNGFAGPAGAAGQPGA*	3xOxidation [P5; P8; P]	Collagen alpha-2(I) chain	8.28	4.12	11.26	11.13	within
e023984	VGFPDGPDPGPEGPAGQDGVGGDKGEDGDPGQPGP*	2xOxidation [P]	Collagen alpha-1(XI) chain	12.08	6.07	14.65	11.63	within
e023992	AQQTNTAGSNVTTSSTPNSNSTSGSATSNPFG LGG	none	Ubiquilin-1	7.43	2.12	11.83	4.33	within
e023994	HSHEFHSHEDMLVDPKSKEEDKHLKF*	1xOxidation [M11]	Osteopontin	4.78	1.82	9.69	5.97	within
e215182	PGEVEASGVAPGELDLMSAQSLGEEATVGPSSE*	1xOxidation [P11]	Collagen alpha-1(XV) chain	11.28	7.22	13.05	11.09	within
e215184	EVGPPGPAGSAGARGAPGERGETGPPGPGAGFAGPPGA*	6xOxidation [P7; P17; P25; P26; P28; P34]	Collagen alpha-1(II) chain	10.34	5.04	12.78	6.52	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024008	PAGAPGDKGESGPSGAPGTGARGAPGDRGEPPGPA	none	Collagen alpha-1(I) chain	4.25	0.0	9.96	6.7	within
e024011	GRPEAQPPPLSSEHKEPVAGDAVPGPKDGSAPE	none	Neurosecretory protein VGF	10.63	6.17	12.82	13.51	up
e215186	RDGNPGSDGLPGRDGSPGGKGDRGENSGAPAGAPG*	2xOxidation [P11; P]	Collagen alpha-1(III) chain	12.31	8.52	13.89	13.67	within
e098166	MARLTWASHEKMHEGDEGPGHHHKPGLGEG*	1xOxidation [M12]	Protein S100-A9	5.11	0.84	9.6	10.31	up
e215188	GPQGIDGEPGVPGQPAGPPGHPGHPGDGLSRP*	2xOxidation [P27; P29]	Collagen alpha-2(V) chain	12.22	8.83	13.75	13.68	within
e024021	GPKGVDVGASGEQGIPGPPGPQGIRGYPGMAGPKGE*	2xOxidation [P15; P17]	Collagen alpha-2(IX) chain	5.9	0.84	9.64	4.43	within
e024022	GIPGQPGEPGYAKDGLPGIPGPQGETGPA GHPGLP*	2xOxidation [P32; P]	Collagen alpha-1(XXII) chain	8.91	4.82	11.69	11.61	within
e215190	AGAGLDGPEGDQGPQGPQGVPGTSKDGQDGAPGEPG*	3xOxidation [P8; P14; P17]	Collagen alpha-3(IX) chain	8.71	4.43	12.34	12.93	up
e024033	GPMGPRGEAGPPGSSEKGERGAAGEPGPHGPPGVP*	3xOxidation [P11; P12; P26]	Collagen alpha-1(XVII) chain	6.64	3.66	11.16	6.46	within
e215193	REGPMGPRGEAGPPGSSEKGERGAAGEPGPHGPPG*	1xOxidation [P4]	Collagen alpha-1(XVII) chain	8.66	4.8	12.36	12.92	up
e024035	SASTTGSETTTASTTSSETTMASIMGSETTMAST	none	Mucin-22	10.49	6.4	13.25	6.16	down
e102237	GESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPP*	2xOxidation [P32; P35]	Collagen alpha-1(I) chain	7.89	4.06	11.12	11.27	up
e215195	QASGSPDVSGEIPGLFGVSGQPSGFPDTSGETSGV	none	Aggrecan core protein	6.99	3.07	10.92	7.99	within
e024040	GPAGPNGPPGPAGSRGDGGPPGMTGFPGAAGRTGPPGP*	2xOxidation [P27; P35]	Collagen alpha-2(I) chain	8.94	4.16	11.99	12.16	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024044	QQLPGPPGEKGENGDVGMGPPGPPGPRGPQGP*	7xOxidation [P6; P7; P18; P21; P22; P24; P25]	Collagen alpha-1(XI) chain	11.8	7.64	13.8	10.72	within
e024050	EVGPAGSPGSNGAPGQRGEPGPQGHAGAQGPPGPPG*	8xOxidation [P4; P8; P14; P20; P22; P31; P32; P34]	Collagen alpha-1(III) chain	10.08	6.08	12.48	8.78	within
e024051	TQSSATTSTTTSTGSGSGNSSSNATGNTVA AANYVA	none	Ubiquilin-2	7.49	2.61	10.95	2.87	within
e024063	GPPGRDGEDGPTGPPGPPGPPGPPGLGGNFAAQY*	11xOxidation [P2; P3; P11; P14; P15; P17; P18; P20; P21; P23; P24]	Collagen alpha-2(I) chain	9.67	3.5	12.38	7.9	within
e106687	ERGDRGDPGPAGLPGSQGAPGTPGPVGA PGDAGQRG*	3xOxidation [P14; P20; P23]	Collagen alpha-2(V) chain	10.9	6.36	12.88	11.75	within
e024073	AGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGP*	5xOxidation [P4; P13; P16; P21; P25]	Collagen alpha-1(III) chain	10.57	6.36	12.48	12.26	within
e096071	GDEGEAGDPGDDNNDIAPRGVKGAKGYRGPEGP*	3xOxidation [P9; P18; P30]	Collagen alpha-1(VI) chain	12.2	7.49	14.33	14.09	within
e024082	YPVAQPSLGNASNMELSLDHFDISFNQFS	none	Calmodulin-binding transcription activator 1	11.86	6.87	14.63	12.75	within
e024088	GIDGAPGAKGNV/GPPGEPGPPGQQGNHGSQGLPGPQ*	2xOxidation [P21; P33]	Collagen alpha-3(V) chain	9.7	5.69	11.88	11.39	within
e104286	LDGNKPAESSLAFSNEETSTEKTAETETSR S	none	A-kinase anchor protein 13	11.68	6.56	14.49	12.42	within
e024092	PGTAGFPGSPGAKGEVGPAGSPGSNGAPGQRGEPGPQ*	2xOxidation [P28; P34]	Collagen alpha-1(III) chain	8.57	4.88	11.01	10.88	within
e024104	AGRPGEVGP GPPGPAGEKGSPGADGPA GAPGTPGPQG*	4xOxidation [P12; P]	Collagen alpha-1(I) chain	11.38	6.92	12.87	12.38	within
e024110	PGERGVQGP GPPGAPRGANGAPGNDGAKGDAGAPGAPG*	2xOxidation [P9; P10]	Collagen alpha-1(I) chain	9.02	5.33	11.48	11.11	within
e024112	GPAGQDGVGGDKGEDGDPGQPGPPGPSGEAGPPGPP*	10xOxidation [P2; P18; P21; P23; P24; P26; P32; P33; P35; P36]	Collagen alpha-1(XI) chain	9.25	3.63	12.84	2.94	down

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024114	LQQNQTSPPDSSNENSPATPPDEQQGGDA PPQ	none	Ubiquitin carboxyl-terminal hydrolase 9X	8.26	3.77	12.04	7.68	within
e024115	DLADGVSGGEGKGGSDGGGSHRKEGEEA DAPGVIPG	none	CD99 antigen	9.55	5.62	12.5	12.12	within
e024117	GPAGAPGDKGESGPSGPAGPTGARGAPG DRGEPPPGP*	2xOxidation [P36; P38]	Collagen alpha-1(I) chain	8.39	4.0	11.54	9.23	within
e215214	EKGSQGFYGPGEQPPGPPGPEGPPGISK EGPPG*	5xOxidation [P19; P21; P24; P25; P32]	Collagen alpha-1(XI) chain	8.5	4.39	10.67	12.17	up
e103086	GMAGPKGETGPHGYKGMVGAIGATGPPGE EGPRGP*	3xOxidation [P11; P26; P27]	Collagen alpha-2(IX) chain	8.52	4.08	11.21	10.97	within
e024119	VVDPKSKEEDKHLKFRISHELDSASSEVN	none	Osteopontin	10.65	5.43	15.62	12.46	within
e024124	LPYTAQTNATRFRLWQPYNNGKKEEIW	none	Reelin	10.46	3.22	14.36	12.38	within
e024127	SQGFYGPGEQPPGPPGPEGPPGISKEGP PGDPG*	8xOxidation [P12; P13; P15; P16; P18; P21; P22; P29]	Collagen alpha-1(XI) chain	10.15	5.21	13.97	9.43	within
e024126	GHPGSPGSPGYQGPPGEPGQAGPSGPPG PPGAIGPSG*	7xOxidation [P18; P23; P26; P27; P29; P30; P35]	Collagen alpha-1(III) chain	9.73	5.46	12.39	12.47	up
e024132	GDPGQHGLPGFPLKGVPGNIGAPGPKGA KGDSRT*	2xOxidation [P12; P18]	Collagen alpha-2(IV) chain	7.74	1.23	14.98	12.85	within
e215221	AGEAGAAGEGGAAGEAGGAGEAGGVGEA GAAGEAGGAGEAGGVG	none	Paraneoplastic antigen Ma6E	6.57	2.75	11.31	11.96	up
e024136	EEEKPRVSEEQRQSEEEQQUELEEPEPE	none	Histone acetyltransferase KAT6A	6.69	3.63	11.55	11.95	up
e024137	VLSPADKTNVKAAGWKVGAHAGEYGAEAL ERM	none	Hemoglobin subunit alpha	11.17	5.01	15.64	13.4	within
e024140	PGPAGPPGDPGLMGERGEDGPAGNGTEG FPGFPGY*	1xOxidation [P21]	Collagen alpha-1(VI) chain	7.67	4.35	10.64	11.54	up
e215222	PGEKGENGDVGPMPGPPGPRGPQGP GADGPQG*	6xOxidation [P15; P16; P18; P19; P21; P]	Collagen alpha-1(XI) chain	11.17	7.15	14.03	9.66	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215223	QPGVMGFPGPKGNDGAPGKNGERGGPGG PGPQGPPG*	3xOxidation [P17; P26; P29]	Collagen alpha-1(III) chain	10.74	5.75	13.58	9.24	within
e024141	QTGEKGPAAGPPGLGPPGPRGLPGEMGRP GPPGPP*	3xOxidation [P17; P]	Collagen alpha-1(XXVI) chain	10.56	4.5	15.33	13.22	within
e215224	VTSGPGDEEDLAAATTEEPLITAGGEESGS PPPD*	2xOxidation [P31; P32]	Collagen alpha-1(XV) chain	10.69	6.24	13.33	9.68	within
e104676	GGGPGGSASGPGGTGGGKASVGAMGGG VGASSGGGPGSGGGGSG	none	Glycogen synthase kinase-3 alpha	12.25	5.97	15.82	10.6	within
e100201	RQSPSYGRHGSGSGRSSSSGQHGSGLGE SSGFGH	none	Hornerin	12.46	7.1	15.86	10.8	within
e215229	TAAPVPSPTLNSGENGTGDWAPRLVFIEEP PGG	none	Metal transporter CNNM1	8.27	1.75	13.0	12.98	within
e104488	NKGEPGSAGPQGPSPGSGEKGKRGPNGE AGSAGPPG*	6xOxidation [P10; P13; P14; P16; P25; P34]	Collagen alpha-2(I) chain	8.4	3.53	11.47	8.29	within
e024179	DVGSYQEKVDVVLGPIQLQTPPRREEEP	none	Scavenger receptor cysteine-rich domain-containing protein DMBT1	9.52	4.35	12.9	11.86	within
e215232	AGRPGEVGPPGPPGPAGEKGSPGADGPA GAPGTPGPQG*	5xOxidation [P12; P13; P15; P22; P27]	Collagen alpha-1(I) chain	10.89	6.95	12.72	12.37	within
e024186	PPGPAGFAGPPGADGQPGAKGEPGDAGA KGDAGPPGPAG*	2xOxidation [P2; P4]	Collagen alpha-1(I) chain	9.56	5.39	11.56	11.19	within
e102370	LVETINENVIEDNKENILENTDSMETDE	none	Activating transcription factor 7-interacting protein 1	13.59	7.25	15.99	14.22	within
e024195	SGPMGPRGPPGPPGKNGDDGEAGKPRP GERGPPG*	3xOxidation [P12; P13; P25]	Collagen alpha-1(I) chain	8.28	4.47	11.2	8.9	within
e024197	PSSAGSGGSFNLGSGDMFLGMPGLNGDS YSASQV	none	Pre-B-cell leukemia transcription factor 2	11.5	6.48	13.92	7.79	within
e215236	GPPGESGREGAPGAEGSPGRDGSFGAKG DRGETGPA*	4xOxidation [P3; P12; P18; P24]	Collagen alpha-1(I) chain	12.36	9.25	14.49	14.04	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215238	GIVGEKGDRGMMGPPGVPGPKGSMGHPGMPGGMG* [*]	3xOxidation [P14; P15; P18]	Collagen alpha-1(XXVII) chain	11.59	6.25	14.56	11.03	within
e024202	EEKAVADTRDQADGSRASVDSGSSEEQGSSRA	none	Polymeric immunoglobulin receptor	13.51	10.64	15.46	14.56	within
e024204	DEEAPDYGSGIRQSGTAKISFDNEYFNQSD	none	Kinesin-like protein KIF1B	5.72	1.4	9.45	10.09	up
e215241	GPMGPRGPPGPAGAPGPGQGFQGNPGEPEPGVSGPM* [*]	3xOxidation [P17; P24; P27]	Collagen alpha-1(II) chain	11.19	7.31	13.11	11.57	within
e024209	GDVGQMGPPGPPGPRGSPGAPGADGPQGPPGGIGNP* [*]	8xOxidation [P9; P11; P12; P14; P17; P21; P26; P29]	Collagen alpha-1(V) chain	9.96	5.62	12.51	10.16	within
e024212	SPGGKGDRGENSPGAPGAPGHGPPGPVGPAGKSGD* [*]	7xOxidation [P14; P17; P20; P23; P25; P26; P28]	Collagen alpha-1(III) chain	11.01	5.56	13.67	11.2	within
e024215	WDRELISERWKNFSPVDAAFRQGHNSV	none	Hemopexin	7.74	4.72	12.37	5.5	within
e215246	AKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGA* [*]	2xOxidation [P]	Collagen alpha-1(I) chain	11.11	5.07	16.69	8.58	within
e024230	GYPGPAGPPGPPGPPGTSGHPGSPGSPGYQGPPGEP* [*]	8xOxidation [P8; P9; P11; P12; P14; P15; P21; P24]	Collagen alpha-1(III) chain	9.63	5.73	12.27	9.18	within
e215248	GEAGGVNEERSAGEDEAGGIGEAGGVGEAGAAGEAGAAG	none	Paraneoplastic antigen Ma6F	6.3	3.99	9.46	4.47	within
e024232	ALGPRGEKGPIGAPGIGPPGEPGLPGIPGPMGPPGA* [*]	4xOxidation [P20; P23; P26; P29]	Collagen alpha-1(VIII) chain	10.4	1.86	16.27	7.68	within
e024235	GEKGMAGGHGPDGPKGSPGSGTPGDTGPPGLQGMPG* [*]	3xOxidation [P14; P18; P20]	Collagen alpha-2(V) chain	10.92	6.56	13.3	11.81	within
e024236	PPGADGQPGAKGEPGDAGAKGDAGPPGPAAGPAGPPGPIG* [*]	3xOxidation [P14; P]	Collagen alpha-1(I) chain	10.85	6.31	13.26	11.87	within
e215250	PGADGQPGAKGEPGDAGAKGDAGPPGPA GPAGPPGPIGN* [*]	2xOxidation [P24; P25]	Collagen alpha-1(I) chain	9.04	4.94	11.45	9.59	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215253	RGSAGHWTSESSVSGSTGQWHSESGSFR PDSP	none	Fibrinogen alpha chain	6.28	2.53	12.21	6.39	within
e096083	ATISPGASRTTGAAPAAETTTSLGGGTTG AEIKSGA	none	Mucin-19	6.17	0.65	11.32	9.4	within
e215257	DGPPGFPGQPGSHGRDGHAGEKGDGPP GDHEDA*	3xOxidation [P4; P7; P10]	Collagen alpha-4(IV) chain	11.62	5.12	13.51	10.65	within
e024257	AGYPGAPGPPGPPPGTSGHPGSPGSP GYQGPPGE*	10xOxidation [P9; P10; P12; P13; P15; P16; P22; P25; P28; P33]	Collagen alpha-1(III) chain	8.02	3.66	12.85	3.55	down
e024270	AGRPGEVGPPGPPGPAGEKGSPGADGPA GAPGTPGPQG*	6xOxidation [P12; P13; P15; P22; P27; P31]	Collagen alpha-1(I) chain	10.25	6.73	12.34	12.02	within
e205717	SGPSGAAGPPGPKGPPGDDGPKGSPGPV GFPGDPGPPG*	5xOxidation [P12; P15; P16; P21; P25]	Collagen alpha-1(V) chain	7.78	4.53	12.02	12.56	up
e024272	PGEKGMAGGHGPDGPKGSPGSGTPGDT GPPGLQGMP*	1xOxidation [P]	Collagen alpha-2(V) chain	8.71	3.43	11.49	12.43	up
e024273	RGTPGAPGQPMAGVDGPPGPKGNMGPPQ GEPGPPGQ*	3xOxidation [P4; P7; M25]	Collagen alpha-1(XI) chain	10.37	5.7	12.15	11.49	within
e024276	AVADTRDQADGSRASVDSGSSEEQGGSSR ALVST	none	Polymeric immunoglobulin receptor	8.11	3.67	13.13	12.87	within
e024280	SRLDVLIVPANFPSLGMASPHIMFLSQSILT	none	Aminopeptidase O	10.08	4.77	14.98	5.98	within
e024281	AGSGAGTGGGTASGGTEGGSASESEGAkid ASKNEDEG	none	Heterogeneous nuclear ribonucleoprotein D0	6.37	2.9	10.47	4.04	within
e024288	GMPGLPGPKGDRGPAGVPGLLGDRGEPG EDGEPPGE*	2xOxidation [P8; P14]	Collagen alpha-2(VIII) chain	6.4	0.23	11.38	9.39	within
e024294	MGPSGPRGLPGPPGAPGPQGFGPPGEP GEPGASGP*	7xOxidation [P16; P18; P24; P25; P28; P31; P]	Collagen alpha-1(I) chain	8.65	4.13	12.08	7.85	within
e024296	GPPGPAGFAGPPGADGQPGAKGEQGEAG QKGDAGAPGP*	3xOxidation [P5; P11; P]	Collagen alpha-1(II) chain	11.48	7.94	13.45	13.07	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215264	ARGGGRGSGFGGGYGGGGFGGGGFGGG GFGGGGIGGGGFGGF	none	Keratin, type II cytoskeletal 1	9.32	5.43	12.45	3.05	down
e024303	GEAGPTGARGPEGAQQPRGEPGTPGSPG PAGASGNPGT*	3xOxidation [P11; P17; P21]	Collagen alpha-1(II) chain	9.53	4.77	12.44	2.77	down
e205723	GGKGERGAPGEKGEGLPPGVAGPPGGSG PAGPPGPQGV*	8xOxidation [P17; P18; P23; P24; P29; P32; P33; P35]	Collagen alpha-1(III) chain	9.29	4.94	11.6	10.99	within
e215268	PPGADGQPGAKEPGDAGAKGDAGPPGP AGPAGPPGPIG*	4xOxidation [P8; P14; P25; P26]	Collagen alpha-1(I) chain	13.46	10.23	15.13	14.05	within
e024321	PGADGQPGAKEPGDAGAKGDAGPPGPA GPAGPPGPIGN*	3xOxidation [P24; P25; P27]	Collagen alpha-1(I) chain	10.05	5.33	12.61	13.0	up
e024324	PPGPRHSGEPGLPGPPPPGPPGQAVM PEGFIK*	6xOxidation [P14; P16; P17; P19; P20; P22]	Collagen alpha-1(X) chain	7.31	3.25	12.0	11.1	within
e024325	GPMGPPGLPGIDGVKGDKNPGWPGAPG VPGPKGDP*	2xOxidation [P21; P24]	Collagen alpha-1(IV) chain	7.24	2.52	11.99	10.57	within
e215271	GPDGQPGVKGEPEPGQKGDAGSPGPQG LAGSPGPHG*	2xOxidation [P]	Collagen alpha-2(V) chain	9.31	5.72	12.75	10.52	within
e106656	DGVSGGEGKGGSDGGGSHRKEGEEADAP GVIPGIVGA	none	CD99 antigen	9.38	5.14	11.91	11.57	within
e024334	GEAGPQQPRGSEGPQGVRGEPGPPGPAG AAGPAGNPGA*	3xOxidation [P21; P23; P24]	Collagen alpha-1(I) chain	9.35	3.81	13.57	8.65	within
e215277	PGGPGMRGMPGSPGGPGSDGKPGPPGS QGESGRPGPPG	none	Collagen alpha-1(III) chain	11.26	6.57	13.76	12.75	within
e024347	VGERGDRGDPGPAGLPGSQGAPGTPGPV GAPGDAGQR	none	Collagen alpha-2(V) chain	7.98	3.22	11.41	10.59	within
e024349	GSGSSQSSGYGQHSSSGQTSGFGQHRS SSGQYSG	none	Filaggrin-2	9.48	5.18	12.09	12.03	within
e101650	GDPGAPGVGLRGEMGPPGIPGQPGEPGYA KDGLPG*	7xOxidation [P3; P6; P16; P17; P20; P23; P26]	Collagen alpha-1(XXII) chain	10.0	6.1	11.86	12.17	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024355	GESGPSGAAGPPGPKGPPGDDGPKGSPG PVGFPDGP*	10xOxidation [P5; P11; P12; P14; P17; P18; P23; P27; P29; P33]	Collagen alpha-1(V) chain	8.39	4.89	11.04	9.78	within
e102632	GDRGPPGPVGPGLTGPAEGREGSPG ADGPPGRD*	5xOxidation [P6; P8; P11; P12; P17]	Collagen alpha-1(II) chain	10.14	5.79	12.31	11.92	within
e103732	PQGFQPPGEPGEPGASGPMGPRGPPGP PGKNGDD*	5xOxidation [P14; P19; P22; P25; P26]	Collagen alpha-1(I) chain	5.29	2.25	9.75	8.67	within
e096094	VAWKADSSPVKAGVETTTSPKQSNKYAA SSY	none	Immunoglobulin lambda constant 2	10.94	3.67	16.57	2.58	down
e024392	MGPSGPRGLPGPPGAPGPQGFQGPGE GEPGASGP*	8xOxidation [P13; P16; P18; P24; P25; P28; P31; P36]	Collagen alpha-1(I) chain	8.38	4.55	11.06	7.1	within
e024393	SGNKGEPSAGPQGPGPSGEEGKRGN GEAGSAGPP*	3xOxidation [P15; P]	Collagen alpha-2(I) chain	8.45	4.36	11.53	10.86	within
e215296	AEVTGTTGPSGGVTGTSVLSVEVTGTTGPS AEVTGLP	none	Mucin-19	10.16	3.2	16.02	4.46	within
e215299	PPGADGQPGAKGEPGDAGAKGDAGPPGP AGPAGPPGPIG*	5xOxidation [P2; P8; P14; P25; P26]	Collagen alpha-1(I) chain	13.35	9.82	15.11	14.34	within
e024416	GPPGPAGFAGPPGADGQPGAKGEPGDAG AKGDAGPPGPAG*	1xOxidation [P]	Collagen alpha-1(I) chain	12.82	9.39	14.61	13.81	within
e024423	GVQGPPGPAGPRGANGAPGNDGAKGDAG APGAPGSQGAPG*	2xOxidation [P8; P]	Collagen alpha-1(I) chain	12.13	8.02	13.71	13.19	within
e106593	NAPTLDVDGASDSGSGDEGEGAGRGGGP YDAPGGDDS	none	Cadherin-related family member 5	10.95	5.68	13.92	13.27	within
e215308	PAGATGDRGEAGAAGPAGPAGPRGSPGE RGEVGPAGPNG	none	Collagen alpha-2(I) chain	9.62	5.12	12.25	11.93	within
e208803	AGPPGADGQPGAKGEPGDAGAKGDAGPP GPAGPAGPPGP*	8xOxidation [P10; P16; P27; P28; P30; P33; P36; P37]	Collagen alpha-1(I) chain	9.65	4.67	12.23	7.86	within
e024440	GPPGVTGMDGQPGPKGNVGPQGEPGPPG QQGNPGAQ*	4xOxidation [P14; P20; P24; P26]	Collagen alpha-1(V) chain	9.64	5.0	12.42	7.54	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024447	FFGHGAEDSLADQAANEWGRSGKDPNHF RPA	none	Serum amyloid A-1 protein	5.44	2.26	6.72	12.37	up
e215318	RGAPGDRGEPGPPGAGFAGPPGADGQP GAKGEPGDA*	4xOxidation [P10; P12; P13; P15]	Collagen alpha-1(I) chain	9.88	5.39	11.99	10.8	within
e215319	GEVGPAGSPGSNGAPGQRGEPGPQGHAG AQGPPGPPGI*	2xOxidation [P]	Collagen alpha-1(III) chain	9.83	5.3	11.94	10.72	within
e096098	PGADGRAGVMGPPGSRGASGPAGVRGPN GDAGRPGEP*	3xOxidation [P13; P21; P27]	Collagen alpha-2(I) chain	7.86	4.48	10.33	9.24	within
e024457	VKGERGSPGGPGAAGFPGARGLGPPGS NGNPGPPGP*	7xOxidation [P11; P17; P23; P25; P26; P32; P]	Collagen alpha-1(III) chain	14.09	10.15	15.93	15.52	within
e215324	PGLDGIPGHGPPGPRGKPGMSGHNGSR GDPGFPGG*	1xOxidation [P]	Collagen alpha-4(IV) chain	13.68	7.62	15.88	15.53	within
e215325	QGPTGSEGTPGLPGGVGQPGAVGEKGER GDAGDPGPP*	3xOxidation [P13; P19; P34]	Collagen alpha-3(V) chain	13.61	8.04	15.61	14.48	within
e215329	PGKNGERGGPGGPGQGGPPGKNGETGPQ GPPGPTGPGG*	2xOxidation [P]	Collagen alpha-1(III) chain	13.83	8.79	15.74	15.43	within
e024472	PGEVGPppppGPGAGEKGSFGADGPAGAP GTPGPQGIAGQ*	3xOxidation [P24; P28; P31]	Collagen alpha-1(I) chain	13.14	8.78	15.06	14.74	within
e103767	ERGEAGIPGVPGAAGEDGKDGSPGEPGAN GLPGAAGE*	2xOxidation [P8; P11]	Collagen alpha-1(III) chain	11.33	6.74	13.37	12.31	within
e024479	SDGKPGYPGKPGLDGPKGNPLGPKGDP GVGGPPG*	7xOxidation [P11; P16; P20; P23; P25; P29; P34]	Collagen alpha-1(X) chain	11.14	5.9	13.39	12.46	within
e024486	PGAAGEDGKDGSPGEPGANLPGAAGER GAPGFRGPA*	2xOxidation [P1; P13]	Collagen alpha-1(III) chain	10.56	5.3	13.09	11.73	within
e103309	WKVDNALQSGNSQESVTEQDSKDSTYSLS ST	none	Immunoglobulin kappa constant	6.8	2.72	11.2	11.04	within
e215335	DGPQGGPPGIGNPGAVGEKGEPGEAGEP GLPGEGGPPG*	3xOxidation [P7; P13; P22]	Collagen alpha-1(V) chain	9.86	5.16	11.96	11.17	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215336	GVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQGAPG*	3xOxidation [P8; P11; P18]	Collagen alpha-1(I) chain	8.74	4.39	11.37	9.67	within
e215340	GFGGRGGGFGGGSSFGGGSGFSGGGFGGGGFGGGRFGGFGG	none	Keratin, type II cytoskeletal 2 epidermal	7.48	3.16	10.9	3.99	within
e215345	RAGELGEAGPSGEPGVPGDAGMPGERGEAGHRGSAGA	none	Collagen alpha-3(IX) chain	11.57	7.86	13.58	12.64	within
e215346	APGNDGAKGDAGAPGAPGSQGAPGLQGM PGERGAAGLPG*	2xOxidation [P23; P29]	Collagen alpha-1(I) chain	11.04	6.16	13.11	12.66	within
e208806	GTDGTPGAKGPTGSPGTSGPPGSAGPPGSPGPQGSTGPQG*	2xOxidation [P21; P26]	Collagen alpha-2(V) chain	11.28	6.46	13.35	13.24	within
e024535	PGPSGEKGETGDVGPMPGPPGPPGPRGPA GPNGADGPQG	none	Collagen alpha-2(XI) chain	11.15	6.59	13.04	12.28	within
e024538	PGARGLPGPSNGNPGPPGPSGSPGKD GPPGPAGNTGA*	3xOxidation [P1; P7; P9]	Collagen alpha-1(III) chain	12.68	7.81	14.69	14.16	within
e024542	PRGQPGVMGFPGPKGNDGAPGKNGERGG PGGPGPQG*	4xOxidation [P11; P13; P20; P29]	Collagen alpha-1(III) chain	11.07	5.91	13.03	12.28	within
e215348	VKGERGSPGGPGAAGFPGARGLPGPS NGNPGPPGP*	8xOxidation [P8; P11; P17; P23; P25; P26; P32; P34]	Collagen alpha-1(III) chain	12.67	7.87	14.69	14.17	within
e096103	GRPEAQPPPLSSEHKEPVAGDAVGPCKDGSAPV	none	Neurosecretory protein VGF	12.78	8.47	14.64	15.05	up
e024548	ERGEQGPAGSPGFQGLPGAGPPGEAGK PGEQGVPG*	5xOxidation [P17; P19; P22; P23; P29]	Collagen alpha-1(I) chain	10.48	4.94	12.55	11.48	within
e024549	GPGGDKGDTGPPGPQGLQGLPGTGPPG ENGKPGEGP*	1xOxidation [P]	Collagen alpha-1(III) chain	12.11	7.09	14.26	14.02	within
e024554	GAPGPPGEAGPRGELSVSTPVPGP GPPGPPGPPGHPGPQ*	3xOxidation [P27; P28; P30]	Collagen alpha-3(IV) chain	11.92	7.4	14.13	14.91	up
e024556	RAGEPGTAGPTGPPGVP GSPGITGPPGPPGPPGPPGAPGA*	1xOxidation [P]	Collagen alpha-2(VIII) chain	11.9	7.32	14.11	14.69	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e104560	VEPGMLVEGPPGPAGPAGIMGPPGLQGPTGPPGDPGD*	2xOxidation [P16; P22]	Collagen alpha-1(XI) chain	11.7	8.17	13.35	12.29	within
e215353	EQGPRGPPGAIGPKGDRGFPGPLGEAGEKGERGP*	5xOxidation [P7; P8; P13; P20; P22]	Collagen alpha-1(VII) chain	10.49	4.33	15.59	13.17	within
e215356	GPPGPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAGP*	6xOxidation [P3; P5; P11; P12; P18; P36]	Collagen alpha-1(II) chain	12.32	8.64	14.36	14.06	within
e215357	NGERGGPGGPGPQGPPGKNGETGPQGPPGPTGPGGDKG*	2xOxidation [P24; P27]	Collagen alpha-1(III) chain	12.34	8.57	14.39	14.11	within
e024566	PAGPRGHGPGSGPPGKPGYGSPGLQGEPGLPGPPGP*	8xOxidation [P10; P13; P14; P17; P22; P28; P31; P33]	Collagen alpha-1(X) chain	12.59	9.86	14.77	14.07	within
e024570	ARGNDGARGSDGQPGPPGPGTAGFPGSPGAKGEVGP*	5xOxidation [P17; P19; P20; P26; P]	Collagen alpha-1(III) chain	14.38	11.73	15.87	15.14	within
e024573	GYGGGGFGGGGFGGGGFGGGGIGGGGGFGGFGSGGGGFGGGGFGGG	none	Keratin, type II cytoskeletal 1	6.26	2.03	10.56	2.07	within
e215358	SPGAPGAPGHGPPGPVGPAGKSGDRGESGPAGPAGAPG*	8xOxidation [P8; P11; P13; P14; P16; P19; P31; P34]	Collagen alpha-1(III) chain	12.62	6.2	14.3	13.34	within
e205783	DGLPGRDGSPGGKGDRENGSPGAPGAPGHPGPPGPV*	5xOxidation [P10; P22; P25; P28; P31]	Collagen alpha-1(III) chain	12.55	7.53	14.25	13.36	within
e215361	GDRGEVGVPGSRGEDGPEGPKGRTGPTGDPGPPGL*	6xOxidation [P9; P17; P20; P26; P30; P32]	Collagen alpha-2(XI) chain	12.55	6.03	14.31	13.38	within
e100862	LPGDLGPPGDPGVSGIDGSPGEKGDPGDVGGPGPPGASG*	1xOxidation [P7]	Collagen alpha-3(V) chain	8.75	3.27	11.54	10.72	within
e024588	FPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA*	1xOxidation [P]	Collagen alpha-1(II) chain	11.65	6.53	13.89	13.53	within
e104028	AGDPGPPGLPAYSPHPSLAKGARGDPGFGAQQGEPG*	2xOxidation [P10; P14]	Collagen alpha-2(IV) chain	11.55	7.35	13.6	13.88	up
e104639	GIPGSKGEQGFMGPPGPQGQPLPGSPGHATEGPKG*	3xOxidation [P21; P24; P27]	Collagen alpha-1(IV) chain	8.91	5.0	11.8	12.66	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024603	AGPPGADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGP*	10xOxidation [P4; P10; P16; P27; P28; P30; P33; P36; P37; P39]	Collagen alpha-1(I) chain	10.78	5.1	13.58	11.83	within
e024607	GAEDRMAGAPMAAAVQPAEVTVEVGEDLHMHQV	none	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 9	11.85	7.03	13.71	13.06	within
e215371	VGPAGKDGEAGAQQPPGPAGPAGERGEQGPAGSPGFQG*	3xOxidation [P3; P15; P16]	Collagen alpha-1(I) chain	13.3	9.76	15.02	14.53	within
e024615	GPPGADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIG*	4xOxidation [P9; P15; P26; P27]	Collagen alpha-1(I) chain	13.31	9.7	15.02	14.53	within
e103754	SSPAPSSENGGPASPLPAEASGSGPGSPHLHPPDKS	none	182 kDa tankyrase-1-binding protein	8.69	3.26	11.85	4.36	within
e105193	PAGNTGAPGSPGVSGPKGDAGQPGEKSGPGAQGPAGP	none	Collagen alpha-1(III) chain	8.66	3.93	11.33	10.49	within
e024620	FAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAP*	3xOxidation [P29; P31; P34]	Collagen alpha-1(II) chain	13.01	9.34	14.71	14.53	within
e300131	GHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGS*	1xOxidation [P11]	Collagen alpha-1(I) chain	8.31	3.67	11.84	11.34	within
e024623	PGAPGPQGVVGPSGPPGPPGFPGDPGPPGPAGLPGIPG*	10xOxidation [P6; P12; P15; P16; P18; P19; P22; P25; P27; P28]	Collagen alpha-3(V) chain	11.76	7.31	13.29	13.17	within
e024627	PGSNGPVGEPGPEGPAGNDGTPGRDGAVERGDRGD*	4xOxidation [P6; P10; P12; P]	Collagen alpha-2(V) chain	8.08	2.87	11.6	11.18	within
e215378	ARGNDGARGSDGQPGPPGPPGTAGFPGSPGAKGEVGP*	6xOxidation [P17; P19; P20; P26; P29; P37]	Collagen alpha-1(III) chain	12.95	10.24	14.71	14.83	up
e215381	DPGLPGNPGYPGQPGQDGKPGYQGIAGTPGVPGSPG*	5xOxidation [P14; P20; P29; P32; P35]	Collagen alpha-1(XXI) chain	12.85	9.96	14.53	14.66	up
e024636	HHHAAGHHHHTAGAPGAAGSAAASAGGAGGAGGGGPASAGG	none	Transcription factor Maf	12.59	8.9	14.98	13.29	within
e098177	GLPGDLGPPGDPGVSGIDGSPGEKGDPGDVGGPGPPGAS*	2xOxidation [P]	Collagen alpha-3(V) chain	10.29	6.23	12.87	12.46	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e205803	GIPGSSGFPGNPGMKGEAGPTGARGPEGP QQQRGET*	2xOxidation [P12; P20]	Collagen alpha-2(V) chain	12.55	8.93	14.87	13.3	within
e208811	RDGNPGSDGLPGRDGSPGGKGDRENGS PGAPGAPGH*	1xOxidation [P35]	Collagen alpha-1(III) chain	11.95	6.75	13.88	13.24	within
e024645	SEGPQGVVRGEPGPPGAGAGPAGNPGA DGQPGAKGANG*	4xOxidation [P14; P16; P]	Collagen alpha-1(I) chain	11.28	6.42	14.02	12.85	within
e100931	GELALSGEKGDQGGPDGSPGSPGAPG AGPPGYGPQ*	1xOxidation [P37]	Collagen alpha-3(IV) chain	11.95	7.36	13.84	13.52	within
e024655	NTGAPGSPGVSGPKGDAGQPGEKGSPGA QGPPGAPGLG*	4xOxidation [P8; P13; P20; P26]	Collagen alpha-1(III) chain	13.86	10.55	15.36	15.21	within
e215387	PAGATGDRGEAGAAGPAGPAGPRGSPGE RGEVGPAGPNG*	3xOxidation [P22; P]	Collagen alpha-2(I) chain	13.41	10.58	14.83	14.74	within
e024663	QPGAQGEQGEAGQKGDAGAPGPQGPSGA PGPQGPVT*	2xOxidation [P25; P29]	Collagen alpha-1(II) chain	13.39	10.64	14.81	14.74	within
e215389	RPGPPGSPGPRGQPGVMGFPGPKNDGA PGKNGER*	3xOxidation [P2; P4; P5]	Collagen alpha-1(III) chain	13.12	6.66	14.78	14.74	within
e215391	QSGSSGSGSNGDNNNGSSSGSSGSSGSS GGSSGGSSGGSSGN	none	Dermokine	9.35	5.37	11.83	11.5	within
e024671	NGIPGEKGPAGERGAPGAPGPRGAAGEPG RDGVPGGP*	7xOxidation [P4; P9; P16; P18; P21; P28; P34]	Collagen alpha-1(III) chain	12.03	7.85	13.7	13.8	up
e215394	GPAGSAGARGAPGERGETGPPGPAGFAG PPGADGQPGAQ*	3xOxidation [P2; P12; P20]	Collagen alpha-1(II) chain	10.17	5.83	12.2	12.25	up
e024680	YPGPAGPPGPPPGTSGHPGSPGSPGY QGPPGEPPQA*	1xOxidation [P]	Collagen alpha-1(III) chain	7.64	2.86	11.9	6.18	within
e103738	KGPPGEDGAKGSVGPTGLPGDLGPPGDPG VSGIDGSPG*	5xOxidation [P3; P4; P15; P19; P24]	Collagen alpha-3(V) chain	7.4	2.79	10.71	10.54	within
e024686	GPSGPPGKDGTSGHPIGPPGPRGNRGE RGSESPG*	1xOxidation [P36]	Collagen alpha-1(III) chain	11.08	6.06	13.17	13.65	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215398	PPGPAGNTGAPGSPGVSGPKGDAGQPGE KGSPGAQGPPGA*	1xOxidation [P]	Collagen alpha-1(III) chain	13.6	9.5	15.38	15.13	within
e215401	SGEKGETGDVGPMPGPPGPPGRGPAGPN GADGPQGPPG*	2xOxidation [P]	Collagen alpha-2(XI) chain	13.11	9.95	14.85	14.56	within
e099828	PGADGQPGAKGEQGEAGQKGDAGAPGPQ GPSGAPGPQGP	none	Collagen alpha-1(II) chain	8.0	3.97	10.69	6.64	within
e215402	GSEGPQGVRGEPGPPGPAGAAGPAGNPG ADGQPGAKGANG*	1xOxidation [P]	Collagen alpha-1(I) chain	13.08	9.89	14.87	14.57	within
e099783	PPGAAGAPGPQGFQGPAGEPGEPGQTGP AGARGPAGPPG*	4xOxidation [P10; P16; P20; P23]	Collagen alpha-2(I) chain	12.19	8.44	13.84	13.64	within
e024700	GSPGHATEGPKGDRGPQQPGLPGLPGP MGPPGLPG*	7xOxidation [P10; P16; P20; P23; P26; P28; P31]	Collagen alpha-1(IV) chain	10.06	3.42	12.53	10.84	within
e024707	VVGAGMAAAALAAEAGMVAAGAAVGATGA AVVGGGVGAGLAAT	none	RING finger protein 112	7.8	0.97	18.37	7.43	within
e215408	VAHVDDMPNALSALSDLHAHKLRVDPVNF L*	1xOxidation [M7]	Hemoglobin subunit alpha	8.15	2.46	14.12	4.43	within
e205824	SPHPSLAKGARGDPGFPGAQGEPSQGE GDGPLPG*	4xOxidation [P2; P4; P29; P32]	Collagen alpha-2(IV) chain	8.61	5.09	11.5	8.2	within
e215412	NTGAPGSPGVSGPKGDAGQPGEKGSPGA QGPPGAPGLG*	5xOxidation [P13; P20; P26; P31; P]	Collagen alpha-1(III) chain	16.16	13.75	17.39	17.0	within
e215415	AGAPGDKGESGPSGPAGPTGARGAPGDR GEPGPPGPAGF*	2xOxidation [P18; P25]	Collagen alpha-1(I) chain	15.98	10.08	17.21	17.0	within
e215417	GIAGHHGDQAGPSVGPAGPRGPAGPSG PAGKDGRTH*	3xOxidation [P23; P26; P]	Collagen alpha-2(I) chain	16.15	13.69	17.4	17.0	within
e215422	PGADGRAGVMGPPGSRGASGPAGVRGPN GDAGRPEPG*	3xOxidation [P12; P13; P21]	Collagen alpha-2(I) chain	15.66	12.95	16.92	16.7	within
e215425	GEPGPAGQDGVGGDKGEDGDPGQPGPPG PSGEAGPPGPP	none	Collagen alpha-1(XI) chain	10.95	6.16	14.15	8.08	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024744	GIAGPQGSQGERGADGEVQKGDQGHGP VPGFMGPP*	1xOxidation [P]	Collagen alpha-1(XXII) chain	14.73	12.02	16.15	16.01	within
e096133	NGPTGAVGFAGPQQPDGQPGVKGEPEGEP GQKGDAGSPG*	1xOxidation [P]	Collagen alpha-2(V) chain	14.72	11.89	16.07	15.94	within
e215427	EPGPAGSKGESGNKGEPGSAGPQGPPGP SGEEGKRGP*	3xOxidation [P25; P26; P28]	Collagen alpha-2(I) chain	12.13	7.5	14.15	13.31	within
e024751	GLVGEPGPAGSKGESGNKGEPGSAGPQG PPGSGEEGK*	2xOxidation [P8; P21]	Collagen alpha-2(I) chain	11.83	5.37	13.98	12.98	within
e024758	GPPGVVGPQGAAGETGPMGERGHGPPGP PPGEQGLPG*	6xOxidation [P2; P3; P8; P17; P24; P26]	Collagen alpha-2(XI) chain	10.66	5.16	12.97	12.29	within
e024769	GPPGADGQPGAKGEPGDAGAKGDAGPPG PAGPAGPPGPIG*	6xOxidation [P15; P26; P27; P29; P]	Collagen alpha-1(I) chain	10.7	6.21	12.94	12.42	within
e215431	PGPAGPRGANGAPGNDGAKGDAGAPGAP GSQGAPGLQGMP*	1xOxidation [P]	Collagen alpha-1(I) chain	10.83	5.93	12.71	12.58	within
e024776	ADGPQGPVSVGSVGGVGEKGEPEGAGN PGPPGEAGVGGP*	1xOxidation [P40]	Collagen alpha-1(XI) chain	9.71	4.73	12.05	11.86	within
e024781	SGEPGKQGPSGASGERGPPGPMGPPGLA GPPGESGREG	none	Collagen alpha-1(I) chain	8.56	3.98	14.54	10.07	within
e215436	PGPPGPPGTSGHPGSPGSPGYQGPPGEP GQAGPSGPPGP*	2xOxidation [P]	Collagen alpha-1(III) chain	8.65	4.04	13.86	6.76	within
e215437	GSPGERGSAGTAGPIGLPGRPGPQGPPGP AGEKGAPGE*	5xOxidation [P18; P21; P23; P26; P27]	Collagen alpha-1(XI) chain	7.22	2.97	10.78	9.45	within
e024788	GDSGPPGRAGEPGLQGPPAGPPGEKGEPEG DDGPSGAEGP*	3xOxidation [P6; P12; P17]	Collagen alpha-1(II) chain	7.28	3.65	10.29	3.05	down
e024800	GPPGPAGFAGPPGADGQPGAKGEPGDAG AKGDAGPPGPAG*	6xOxidation [P3; P5; P11; P12; P18; P24]	Collagen alpha-1(I) chain	12.91	7.16	15.86	17.27	up
e024801	DKLTFIDMEGSGFGDLEALRGPRGFPGPP GPPG*	1xOxidation [P]	Collagen alpha-1(XVIII) chain	6.19	1.1	9.94	9.22	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e024804	NGTSTNSTEAENGNGSSGGDNGEEGEEES VTGANAE	none	Integrin-binding sialoprotein	7.71	4.14	10.23	10.31	up
e215444	NTGAPGSPGVSGPKGDAGQPGEKGSPGA QGPPGAPGLG*	6xOxidation [P13; P20; P26; P31; P32; P]	Collagen alpha-1(III) chain	17.45	15.63	18.6	18.3	within
e215447	GTPGRDGAVERGERDGRDPGPAGLPGSQG APGTPGPVGA*	4xOxidation [P20; P24; P30; P]	Collagen alpha-2(V) chain	17.44	15.5	18.63	18.3	within
e024815	FAGPPGADGQPGAKGEQGEAGQKGDAGA PGPQGPSGAPG*	2xOxidation [P]	Collagen alpha-1(II) chain	16.67	11.4	18.01	18.02	up
e215451	AGGPGFPGAPGAKGEAGPTGARGPEGAQ GPRGEPGTPGS*	3xOxidation [P10; P18; P24]	Collagen alpha-1(II) chain	17.0	15.29	18.2	18.02	within
e215454	GDPGVSGIDGSPGEKGDGPDVGGPGPPG ASGEPGAPGPP*	7xOxidation [P24; P26; P27; P33; P36; P38; P39]	Collagen alpha-3(V) chain	10.88	6.46	13.83	6.69	within
e024818	NGERGGPGGPGPQGPPGKNGETGPQGPP GPTGPGGDK*	9xOxidation [P7; P10; P12; P15; P16; P24; P27; P28; P30]	Collagen alpha-1(III) chain	10.76	5.18	13.55	7.78	within
e024821	GPQGESRTGPPGSTGSRGPPGPPGRPGN SGIRGPPG*	8xOxidation [P11; P19; P20; P22; P23; P26; P34; P35]	Collagen alpha-1(XII) chain	15.94	13.58	17.09	17.2	up
e024820	VGAPGPAGATGDRGEAGAAGPAGPAGPR GSPGERGEVGP*	6xOxidation [P4; P6; P21; P24; P27; P31]	Collagen alpha-2(I) chain	15.97	13.62	17.11	17.21	up
e101770	GPMGPRGPPGPAGAPGPQGFGNPGEPG EPGVSGPMG*	7xOxidation [P5; P8; P9; P11; P15; P17; P24]	Collagen alpha-1(II) chain	10.2	5.63	13.63	7.38	within
e024825	QGPRGSEGPQGVRGEPGPPGPAGAAGPA GNPGADGQPGA*	2xOxidation [P27; P]	Collagen alpha-1(I) chain	12.66	6.4	14.65	9.12	within
e102809	DGQPGPKGDQGEKGERGTPGIGGFPGPS GNDGSAGPP*	2xOxidation [P4; P6]	Collagen alpha-1(VII) chain	12.37	7.66	14.22	13.19	within
e215457	GMDGQPGPKGNVGPQGEPGPPGQQGNP GAQGLPGPQG*	3xOxidation [P27; P33; P35]	Collagen alpha-1(V) chain	12.57	8.27	14.99	12.2	within
e215458	ERGFPLPGPSGEPGKQGPSGASGERGP PGPMGPPG*	7xOxidation [P5; P8; P10; P14; P19; P28; P29]	Collagen alpha-1(I) chain	12.48	8.22	14.4	12.2	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215459	GPPGLKGTIGDMGFPGPQGVGPPGPSGVPGQPGSPG*	8xOxidation [P2; P3; P15; P17; P23; P24; P26; P30]	Collagen alpha-5(IV) chain	12.56	8.32	14.99	12.46	within
e024843	RGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGA*	1xOxidation [P12]	Collagen alpha-1(I) chain	12.43	8.34	14.73	12.23	within
e215463	TGSSGPRGLPGPPGPQGESRTGPPGSTGSRGPPGPP*	11xOxidation [P6; P10; P12; P13; P15; P23; P24; P32; P33; P35; P36]	Collagen alpha-1(XII) chain	11.37	7.26	13.05	11.81	within
e103292	PSSSSGMASEISSELSTSEMSSEVGSTASDEPPPGA	none	PH domain leucine-rich repeat-containing protein phosphatase 1	9.38	4.97	12.14	8.66	within
e300042	VLSPADKTNVKAAGWKVGAHAGEYGAEALERMF	none	Hemoglobin subunit alpha	6.8	1.7	16.49	8.06	within
e215468	ESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAP*	2xOxidation [P]	Collagen alpha-1(I) chain	15.25	13.0	16.53	16.3	within
e215471	NTGAPGSPGVSGPKGDAGQPGEKGSPGAQGPPGAPGPLG*	7xOxidation [P8; P13; P20; P26; P31; P32; P]	Collagen alpha-1(III) chain	15.24	13.05	16.53	16.3	within
e024877	SAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPP*	5xOxidation [P14; P16; P19; P20; P22]	Collagen alpha-1(I) chain	5.92	0.53	11.6	6.46	within
e024881	GPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPS*	3xOxidation [P9; P15; P33]	Collagen alpha-1(II) chain	14.71	12.23	15.99	15.92	within
e024884	DPGIPGLDRSGFPGETGSPGIPGHQGEMLPLGQRG*	3xOxidation [P19; P22; P30]	Collagen alpha-3(IV) chain	14.69	12.2	15.99	15.92	within
e024886	LADGVSGGEGKGGSDGGGSHRKEGEEADAPGVIPGIVG	none	CD99 antigen	8.36	3.31	13.36	12.16	within
e024887	GAVGAKGEAGPQGPRGSEGPQGVRGEPGPPGPAGAAGPAG*	1xOxidation [P29]	Collagen alpha-1(I) chain	5.64	1.01	10.34	7.89	within
e215478	VPGDPGEAGPIGPKGYRGDEGPPGSEGARGAPGPAGP*	6xOxidation [P10; P13; P22; P23; P32; P34]	Collagen alpha-1(VI) chain	13.64	10.99	15.25	14.91	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215480	GPPGERGGPGSRGFPGADGVAGPKGPAG ERGSPGPAGP*	7xOxidation [P3; P9; P15; P23; P26; P33; P35]	Collagen alpha-1(I) chain	13.6	10.54	15.24	14.84	within
e215483	EDDEEEEDAEDSAGSPGGRGTGPSAPRDA SLVYD	none	C-Jun-amino-terminal kinase-interacting protein 2	12.67	9.26	14.69	14.12	within
e024908	GPAGFAGPPGADGQPGAKGEPGDAGAKG DAGPPGPAGPAGP*	3xOxidation [P]	Collagen alpha-1(I) chain	14.62	10.44	16.89	13.54	within
e215488	GDLGPPGDPGVSGIDGSPGEKGDPGDVGG PGPPGASGEPG*	1xOxidation [P]	Collagen alpha-3(V) chain	14.4	11.05	16.54	13.18	within
e215489	SRDLVDGINRLSFSSTGSTRSNMSTSSTSS KES	none	Enhancer of filamentation 1	14.19	10.12	16.27	13.2	within
e024920	GRDGNPGSDGLPGRDGSPGGKGDRGENG SPGAPGAPGH*	1xOxidation [P12]	Collagen alpha-1(III) chain	13.85	9.82	15.69	12.83	within
e215491	DYTRAQELDALDNSHPIEVSVGHPSEVDEIF	none	Puromycin-sensitive aminopeptidase-like protein	13.71	10.33	15.65	12.82	within
e215492	GRGGAGSGGAGSGAAGGTGGSGGGGFG AATFASTSATPPQSNGG	none	GATA zinc finger domain-containing protein 1	10.89	3.4	13.92	12.16	within
e024926	GGPGMRGMPGSPGGPGSDGKPGPPGSQ GESGRPGPPGPS*	2xOxidation [P24; P33]	Collagen alpha-1(III) chain	12.21	8.57	14.14	12.17	within
e300061	DAAQKTDTSHHDQDHPTFNKITPNLAFAF S	none	Alpha-1-antitrypsin	9.49	3.85	15.22	6.47	within
e024931	EEAGIASGGEAGTASGGEEAGTASGGDEA WTTSGKEEA	none	Apolipoprotein B receptor	6.96	3.25	11.79	2.35	down
e205886	GLDGERGRPGPAGPPGPPGSSNQGDG DPGFPGIPG*	4xOxidation [P14; P20; P30; P33]	Collagen alpha-6(IV) chain	9.95	3.9	12.98	9.14	within
e024949	ESGREGAPGAEGSPGRDGSPGAKGDRGE TGPAGPPGAP*	3xOxidation [P31; P34; P]	Collagen alpha-1(I) chain	12.4	7.46	14.22	14.09	within
e024954	MGPPGDRGFTGKDGAMGPRGPPGPPGSP GSPGVTGPSG*	3xOxidation [P18; P21; P22]	Collagen alpha-1(XII) chain	11.84	5.94	13.46	13.38	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215501	EEGKRGARGEPTGLPGPPGERGGPGS RGFPGADG*	5xOxidation [P13; P17; P19; P20; P26]	Collagen alpha-1(I) chain	8.76	3.9	11.48	11.96	up
e024969	GPPGVVGPQGAAGETGPMGERGHGPPG PPGEQGLPG*	9xOxidation [P2; P3; P8; P17; P24; P26; P27; P29; P30]	Collagen alpha-2(XI) chain	15.26	11.22	17.66	13.6	within
e215504	GDLGPPGDPGVSGIDGSPGEKGDPGDVGG PGPPGASGEPG*	2xOxidation [P6; P]	Collagen alpha-3(V) chain	14.82	10.82	17.3	13.18	within
e102647	ERGEQGPAGSPGFQGLPGAGPPGEAGK PGEQGVPGD*	4xOxidation [P11; P17; P23; P29]	Collagen alpha-1(I) chain	11.0	5.98	14.67	9.83	within
e104192	PTGPPGAKGQEGAHGAPGAAGNPGAPGH VGAPGPSGPPGS*	8xOxidation [P4; P5; P17; P23; P26; P32; P34; P37]	Collagen alpha-1(XXII) chain	10.42	5.09	14.54	8.87	within
e104120	RGFTGLQGLPGPPGPSGDQGASGPAGPS GPRGPPGPVGP*	1xOxidation [P]	Collagen alpha-1(II) chain	7.4	2.22	12.41	10.95	within
e100329	GEPGPPGSEGLPGPPGPAGPRGERGPQG NSGEKGDQ*	8xOxidation [P3; P5; P6; P12; P14; P15; P17; P20]	Collagen alpha-1(XVI) chain	10.61	5.01	14.07	9.63	within
e024995	DADLADGVSGGEGKGGSDGGGSHRKEGE EADAPGVIPG	none	CD99 antigen	6.85	3.92	9.41	8.1	within
e024998	NGQRDAPWNNQPDAAWNSQFEGPWNSQ HEQ	none	Calcium homeostasis endoplasmic reticulum protein	6.71	2.8	11.44	7.36	within
e104744	GRPGLDGERGRPGPAGPPGPPGPSSNQG DTGDPGFPG*	3xOxidation [P21; P23; P33]	Collagen alpha-6(IV) chain	10.48	5.86	13.27	11.77	within
e025018	KGENGDVGMGPPGPPGPRGPQGPNGAD GPQGPPGSV*	8xOxidation [P9; P12; P13; P15; P16; P18; P21; P24]	Collagen alpha-1(XI) chain	12.51	8.77	14.96	14.25	within
e208826	ESGPSGAAGPPGPKGPPGDDGPKGSPGP VGFPDGP GPPG*	7xOxidation [P17; P22; P26; P28; P32; P35; P37]	Collagen alpha-1(V) chain	12.46	8.64	14.87	14.61	within
e025021	GPPGPAGAPGDKGESGPSGAGPTGARG APGDRGEPGPP*	8xOxidation [P9; P17; P20; P23; P30; P36; P38; P39]	Collagen alpha-1(I) chain	11.61	7.34	13.91	11.81	within
e103134	PKG DAGAPGPGKG DAGAPGERGPPGL AGAPGLRGGAGPP*	3xOxidation [P32; P40; P41]	Collagen alpha-1(III) chain	10.25	2.95	15.17	6.27	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025046	MQAEGRGTGGSTGDADGPGGPGIPDGPG GNAGGPGEAGATGG	none	Cancer/testis antigen 1	10.98	6.52	13.77	12.35	within
e100550	EPGPPGPAGFAGPPGADGQPGAKGEPGD AGAKGDAGPPG*	10xOxidation [P2; P4; P5; P7; P13; P14; P20; P26; P37; P38]	Collagen alpha-1(I) chain	11.71	6.26	14.2	5.83	down
e025051	LALSGEKGDQGPDPGSPGSPGAPGAG PPGYGPQGEP*	1xOxidation [P]	Collagen alpha-3(IV) chain	12.24	7.81	14.39	14.28	within
e105807	PGMRGMPGSPGPGSDGKPGPPGSQGES GRPGPPGSPG*	2xOxidation [P22; P31]	Collagen alpha-1(III) chain	11.65	7.01	13.49	5.43	down
e025052	ERGPPGPMGPPGLAGPPGESGREGAPGA EGSPGRDGSP*	2xOxidation [P17; P26]	Collagen alpha-1(I) chain	11.76	7.27	13.79	13.84	up
e215516	TTSHSTPSYITSITTETPSSSTPSFSSSITTT E	none	Mucin-3A	11.16	5.9	13.49	13.04	within
e215520	GLPGPPGERGGPGSRGFPADGVAGPKG PAGERGSPGPA*	3xOxidation [P5; P6; P12]	Collagen alpha-1(I) chain	5.66	2.77	9.82	7.96	within
e025063	ASHTSDSDVPSGVTEVVVKLFSDPITVTVP VEV	none	Clusterin	12.21	6.96	15.56	14.19	within
e025071	TAPGSPEPPSELLEDGQDTPTSAESPDAP ENIA*	5xOxidation [P6; P8; P9; P20; P26]	Collagen alpha-1(XVIII) chain	10.28	5.01	13.21	10.14	within
e025073	GEQGTGPPGPAGPRGHPGSPGPPGKPG YGSPGLQGEP*	3xOxidation [P11; P14; P18]	Collagen alpha-1(X) chain	8.27	5.05	11.37	11.83	up
e208832	NGEAGSAGPPGPPGLRGSPGSRGLPGAD GRAGVMGPPGS*	5xOxidation [P12; P13; P19; P25; P36]	Collagen alpha-2(I) chain	12.15	6.72	14.54	14.53	within
e215526	GPSGPAGPTGARGAPGDRGEPGPPGAG FAGPPGADGQPGA*	1xOxidation [P]	Collagen alpha-1(I) chain	12.14	7.43	14.09	14.46	up
e025083	GQPGTPGSKGSKGEPGIQGMPGASGLKGE PGATGSPGEP*	1xOxidation [P3]	Collagen alpha-1(XXI) chain	12.03	7.31	14.13	13.03	within
e025084	GPPGEPGAGQDGVGGDKGEDGDPGQPG PPGPSGEAGPPG*	2xOxidation [P32; P38]	Collagen alpha-1(XI) chain	10.87	5.68	13.91	11.7	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025086	GLDRSGFPGETGSPGIPGHQGEMGPLGQR GYPGNPG	none	Collagen alpha-3(IV) chain	10.34	3.89	12.79	13.6	up
e215527	GSPGAKGEVGPAGSPGSNGAPGQRGEPG PQGHAGAQQPPG*	3xOxidation [P3; P11; P15]	Collagen alpha-1(III) chain	11.73	6.78	15.56	11.64	within
e025089	GEPGPPGPAGAAGPAGNPGADGQPGAAG ANGAPGIAGAPGFP*	3xOxidation [P33; P39; P42]	Collagen alpha-1(I) chain	9.07	4.48	11.97	11.75	within
e100757	PPGPAGFAGPPGADGQPGAAGQGEAGQ KGDAGAPGPQGP	none	Collagen alpha-1(II) chain	9.6	4.51	13.7	11.23	within
e025099	GTDVFMGPPGSPGEDGPAGEGPPGPEG QPGVDGATGL*	5xOxidation [P17; P21; P23; P24; P26]	Collagen alpha-1(XV) chain	9.15	4.04	12.85	8.31	within
e101834	PAGGPGFPGAPGAKGEAGPTGARGPEGA QGPRGEPGTPGS*	2xOxidation [P1; P5]	Collagen alpha-1(II) chain	6.89	3.45	10.02	7.2	within
e025115	AGEPGTAGPTGPPGVGSPGITGPPGPPG PPGPPGAPGAFD*	3xOxidation [P19; P24; P]	Collagen alpha-2(VIII) chain	9.09	3.77	12.24	13.45	up
e205964	AKVQWKVDNALQSGNSQESVTEQDSKST YSL	none	Immunoglobulin kappa constant	8.07	3.18	11.46	12.94	up
e101674	GIPGFDGAPGQKGEMGPAGPTGPRGFPGP PGPDGLPGS*	4xOxidation [P9; M15; P17; P30]	Collagen alpha-1(IV) chain	8.61	4.84	11.28	9.69	within
e025133	PGDKGESGSPGAGPTGARGAPGDRGEP GPPGPAGFAGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	11.21	6.51	13.67	10.82	within
e025137	DPGPPGEPGAGQDGPPGDKGDDGEPGQ TGSPGPTGEPG*	1xOxidation [P]	Collagen alpha-1(V) chain	10.87	5.06	14.93	7.34	within
e025144	GPPGPAGSAGARGAPGERGETGPPGPAG FAGPPGADGQPGA*	3xOxidation [P3; P5; P]	Collagen alpha-1(II) chain	8.75	4.2	11.77	11.93	up
e106368	SRGSGGSHGGSGFGGESGGSYGGGE EASGSGGGYGGSGKS	none	Keratin, type I cytoskeletal 9	7.37	3.66	10.8	9.93	within
e025149	DGQPPGPPPGTAGFPGSPGAKGEVGPA GSPGSNGAPGQR*	2xOxidation [P31; P37]	Collagen alpha-1(III) chain	9.64	5.06	12.48	12.0	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025150	GGEEAGTASGGEEAGIASGGEAGTASGGE EAGTASGGDEAW	none	Apolipoprotein B receptor	7.97	3.83	10.66	9.59	within
e215539	REPGGYAAAGSGGAGGVSGGGSSLAAMG GREPQYSSLSAA	none	Transcription factor GATA-6	10.02	5.89	12.04	11.91	within
e205988	RQAQAMLSSHGDLGPPDTGMGDPASSDLT RVSSTL	none	Transcriptional-regulating factor 1	5.52	0.38	10.56	5.7	within
e102402	PPGSRGNPGSRGENGPTGAVGFAGPQGP DGQPGVKGEP*	1xOxidation [P]	Collagen alpha-2(V) chain	9.44	4.68	11.95	11.95	up
e215541	QEIQQYISEYMQSDSIRSYSLSGVQPPGPP GP*	3xOxidation [P26; P27; P29]	Collagen alpha-1(XVII) chain	9.57	4.42	11.78	11.61	within
e025160	FAEEKAVADTRDQADGSRASVDSGSSEEQ GGSSRA	none	Polymeric immunoglobulin receptor	12.55	8.71	14.77	14.13	within
e215543	FPGARGLPGPPGSNGNPGPPGSPGSPGK DGPPGPAGNTG*	8xOxidation [P8; P10; P11; P17; P19; P20; P22; P26]	Collagen alpha-1(III) chain	12.33	9.55	14.31	13.96	within
e025168	AGYPGPAGPPGPPPGTSGHPGSPGSP GYQPPGEPGQA*	1xOxidation [P]	Collagen alpha-1(III) chain	12.33	9.49	14.34	13.99	within
e025169	GRPEAQPPPLSSEHKEPVAGDAVPGPKDG SAPEVR	none	Neurosecretory protein VGF	8.91	5.03	12.1	12.59	up
e025171	ESGNKGEPGSAGPQGPPGPSGEEGKRGP NGEAGSAGPPG*	3xOxidation [P28; P37; P38]	Collagen alpha-2(I) chain	10.46	5.89	13.22	13.43	up
e025172	GHKGSKGAPGPAGARGESGLAGAPGPAG PPGPPGPPGPPGPG*	2xOxidation [P35; P]	Collagen alpha-1(XVIII) chain	7.73	4.6	12.07	12.54	up
e025175	DGVSGGEGKGGSDGGGSHRKEGEEADAP GVIPGIVGAVV	none	CD99 antigen	12.83	9.16	14.54	15.12	up
e025177	MGTPGQPGSPGPVGAAGLPGEKGDHGFP GSSGPRGDPG*	6xOxidation [P4; P7; P10; P12; P16; P19]	Collagen alpha-1(IV) chain	9.39	4.67	12.07	9.12	within
e025180	PGPKGEPGHRGTDGAAGPRGAPGLKGEQ GDTVVIDY*	3xOxidation [P3; P7; P18]	Collagen alpha-1(XXIII) chain	12.49	7.68	14.12	14.95	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098185	QQLPGPSGEKGETGDVGPMGPPGPPGPRGPAGPNGADGP*	3xOxidation [P4; P25; P27]	Collagen alpha-2(XI) chain	9.13	3.77	13.57	5.22	within
e025187	AVADTRDQADGSRASVDSGSSEEQGGSSRALVSTLV	none	Polymeric immunoglobulin receptor	7.15	1.97	11.45	12.06	up
e106142	GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ*	3xOxidation [P24; P26; P29]	Collagen alpha-1(I) chain	7.45	2.37	11.05	6.4	within
e215552	LPGDLGPPGDPGVSGIDGSPGEKGDPGDVGGPGPPGASGE*	3xOxidation [P8; P11; P20]	Collagen alpha-3(V) chain	9.28	4.62	13.06	7.06	within
e025197	ADVGAGGEDAGSGAEDVGPGGEDVGAGREAAGEGGENAGAE	none	Golgin subfamily A member 6-like protein 2	8.69	4.64	12.67	9.34	within
e206014	GEKGENGDVGPMGPPGPPGPRGPQGPNGADGPQGPPEGSV	none	Collagen alpha-1(XI) chain	8.8	4.83	11.61	11.26	within
e102485	STTMVASSETSTLSTTPADTSTPVTYSQASSSTT	none	Mucin-17	10.74	6.69	13.25	11.94	within
e025207	VDGLMGPAKPKQPGDGPQGPGLDGKPGREFSEQ*	3xOxidation [P22; P23; P29]	Collagen alpha-1(XXI) chain	6.25	3.34	10.56	10.65	up
e025210	GSPGQKGHKGEPEGENLHGAPGFPGQKGEQGFEGSK*	2xOxidation [P3; P12]	Collagen alpha-1(XIX) chain	7.76	2.5	10.5	9.8	within
e025218	PAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEE	none	Tumor necrosis factor receptor superfamily member 10C	5.02	0.0	12.27	4.67	within
e025220	EVGKPGERGLHGEFGLPGPAGPRGERGPPGESGAAGP*	3xOxidation [P5; P17; P19]	Collagen alpha-2(I) chain	7.26	3.08	11.05	9.4	within
e025222	SHINSNSMTPNGTEVKTEPMSSETASTTADGSLN	none	Protein phosphatase EYA1	5.39	0.89	8.61	10.16	up
e025223	GQSPSRGRHSGSGHSSSYQHGSGSGWSSSSGRHGS	none	Hornerin	6.57	3.26	10.76	8.6	within
e215557	GPVGPPGLTGPAEPGREGSPGADGPPGRDGAAGVKGDR*	4xOxidation [P11; P15; P21; P26]	Collagen alpha-1(II) chain	11.39	5.24	14.73	15.48	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025226	GD LGPPGD PGVSGIDGSPGEKGD PGDVGG PGPPGASGEPGA*	3xOxidation [P18; P24; P30]	Collagen alpha-3(V) chain	10.03	6.19	11.93	12.1	up
e025228	GE PGPGQG PGPIGPPGEMGPKGPPGAVG EPGLPGEAGM*	8xOxidation [P8; P11; P14; P15; P20; P23; P24; P30]	Collagen alpha-1(XXVII) chain	10.69	5.95	12.6	12.15	within
e025237	GPPGIPGFPGSKGDPGSPGPPGAGIATKG LNGPTGPPG*	11xOxidation [P3; P6; P9; P15; P18; P20; P21; P23; P34; P37; P38]	Collagen alpha-1(X) chain	12.02	7.72	14.35	14.45	up
e025238	PPGPPGPPGSIGHPGARGPPGYRGPTGEL GDPGRGN*	7xOxidation [P4; P5; P7; P8; P14; P19; P20]	Collagen alpha-3(IX) chain	11.11	6.75	13.75	14.08	up
e025240	LPGRNGEKG SQGFGYPGEQGPPGPPGPE GPPGISKE*	4xOxidation [P24; P25; P27; P30]	Collagen alpha-1(XXI) chain	9.32	3.99	12.53	12.33	within
e025241	VVSPTVTGASGMAGTTGGVDAATTGAASE NTSERAGTPR	none	Mucin-19	9.24	4.41	12.38	11.03	within
e025243	SGPSGDEGQPGEPGPPGEKGEAGDEGNP GPDGAPGERG*	6xOxidation [P13; P15; P16; P28; P30; P34]	Collagen alpha-1(VI) chain	10.04	4.9	13.66	15.05	up
e215561	GPAGSPGFQGLPGPAGPPGEAGKPGEQG VPGDLGAPGPSGA*	3xOxidation [P14; P17; P]	Collagen alpha-1(I) chain	5.89	1.83	13.48	5.75	within
e215565	DNLQGEAAAGGDQDPGQSDGAEGIEAPEA EGEAQPES	none	Retinitis pigmentosa 1-like 1 protein	9.18	3.79	12.62	14.32	up
e025250	MGPAGPTGPRGFPGPPGPDGLPGSMGPP GTPSVDHGF*	9xOxidation [P6; P9; P13; P15; P16; P18; P22; P27; P28]	Collagen alpha-1(IV) chain	6.84	0.11	13.45	4.99	within
e206050	GPQGVKGERGSPGGPGAAGFPGARGLPG PPGSNGNPGPPG*	5xOxidation [P15; P21; P27; P29; P30]	Collagen alpha-1(III) chain	8.29	3.23	15.42	7.56	within
e215569	EVGKPGERGLHGEFGLPGAGPRGERGPP GESGAAGP*	4xOxidation [P5; P17; P19; P22]	Collagen alpha-2(I) chain	10.47	5.69	13.92	12.14	within
e215572	GQVGETGKPGAPGRDGASGKDGRGSPG VPGSPGLPGPVG*	1xOxidation [P]	Collagen alpha-1(VII) chain	10.3	5.24	13.23	12.12	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215574	RGEQGPAGSPGFQGLPGPAGPPGEAGKP GEQGVPGDLGA*	3xOxidation [P16; P18; P21]	Collagen alpha-1(I) chain	9.87	5.35	12.39	8.9	within
e025266	HPGQPGPPGEKKGKPGQDGIPGAGQKGE PGQPGFGNPG*	1xOxidation [P]	Collagen alpha-5(IV) chain	9.99	5.68	12.57	11.73	within
e099871	FAGPPGADGQPGAKGEPGDAGAKGDAGP PGPAGPAGPPGPIG*	2xOxidation [P4; P5]	Collagen alpha-1(I) chain	7.05	3.49	10.51	9.47	within
e099951	ADGQPGAKGEPGDAGAKGDAGPPGPAGP AGPPGPIGNVGAPG*	4xOxidation [P11; P28; P31; P41]	Collagen alpha-1(I) chain	10.07	5.6	12.09	12.55	up
e025278	GPIGPPGPAGAPGDKGESGSPGAGPTGA RGAPGDRGEPGP*	3xOxidation [P23; P26; P33]	Collagen alpha-1(I) chain	9.61	4.61	11.87	12.63	up
e025280	GAQGPPTSAGPPGYGPRGVKGTSGNRG LQGEKGEKGE*	1xOxidation [P]	Collagen alpha-3(V) chain	7.04	1.31	12.36	8.87	within
e025282	DDNFGEGNDGGILDDKLISNNDGGIFDDPP ALSEA	none	Double-strand-break repair protein rad21 homolog	10.97	6.57	13.1	13.42	up
e215577	PPGEKGEVGDVGSMPHGAPGPRGPQGP TGSEGTPLPG*	2xOxidation [P25; P28]	Collagen alpha-3(V) chain	8.54	4.39	11.32	11.25	within
e025285	PQPDRDMAVSTPASEPQSDRDMVSTPAS EPQPD	none	PGC-1 and ERR-induced regulator in muscle protein 1	6.04	1.75	9.75	7.02	within
e025290	PAEIEGAAEDGDPGDTGAELDDQHWSD SPSDAD	none	[F-actin]-monooxygenase MICAL3	7.66	3.68	11.18	10.8	within
e101097	DGEKGDKEAGPPGRPGLAGHKGEMGEP GVPGQSGAPG*	5xOxidation [P13; P16; P28; P31; P]	Collagen alpha-1(VII) chain	7.44	2.61	10.12	8.51	within
e025295	DQGPVGRTEVGAVGPPGFAGEKGPSGE AGTAGPPGTGPG*	3xOxidation [P]	Collagen alpha-2(I) chain	10.72	6.2	12.83	12.38	within
e102661	SEGPQGVRGEPGPPGPAGAAGPAGNPGA DGQPGAKGANGAPG*	2xOxidation [P]	Collagen alpha-1(I) chain	10.82	6.19	13.11	12.69	within
e025296	AAGEPGKAGERGVPGPPGAVGPAGKDGE AGAQQPPGPAGPAG*	3xOxidation [P5; P14; P16]	Collagen alpha-1(I) chain	9.26	4.89	11.76	10.27	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e102321	FAGPPGADGQPGAKGEPGDAGAKGDAGP PGPAGPAGPPGPIG*	3xOxidation [P]	Collagen alpha-1(I) chain	10.76	6.36	12.65	13.11	up
e025298	GEKGPPGNPGIPGLPGSDGPLGHPGHEGP TGEKGAQGPP*	1xOxidation [P]	Collagen alpha-3(V) chain	8.38	4.45	11.05	9.7	within
e106194	GPQGPNGADGPQGPPGSVGSVGGVGEKG EPGEAGNPGPPGE*	1xOxidation [P]	Collagen alpha-1(XI) chain	11.35	7.05	12.98	13.1	up
e025300	GEKGEKGETGQAGSPGEKGEAGEKGNPG AEVPLPGPE*	2xOxidation [P]	Collagen alpha-1(XIII) chain	7.05	2.8	12.82	9.7	within
e215578	GAAGPAGPNGPPGPAGSRGDGGPPGMTG FPGAAGRTGPPGPSG	none	Collagen alpha-2(I) chain	11.36	7.54	13.05	13.46	up
e025304	ERGEQGPPGPTGFQGLPGPPGPPGEGGK PGDQGVPGDP*	3xOxidation [P10; P17; P19]	Collagen alpha-2(V) chain	11.11	6.9	12.76	12.83	up
e025306	MKGSAGQAGQPGSPGHQGLAGVPGQPQT KGGPGDQGEPP*	1xOxidation [P]	Collagen alpha-2(IX) chain	7.12	2.85	10.39	10.0	within
e215580	IFVNEDGIPETDEPFYIILLNSTGDTVYQYG	none	Adhesion G-protein coupled receptor V1	8.2	1.85	12.84	8.14	within
e215581	EPGITGLPGEKGMAGGHGPDGPKGSPGPS GTPGDTGPPGL*	2xOxidation [P]	Collagen alpha-2(V) chain	7.62	4.51	11.32	11.6	up
e103235	DQGPVGRTEVGAVGPPGFAGEKGPSGE AGTAGPPGTPGP*	4xOxidation [P16; P17; P35; P38]	Collagen alpha-2(I) chain	8.67	4.59	11.47	11.69	up
e025325	RGPAGPNGADGPQGPPGGVGNLGPPEK GEPGESGSPGIQ*	2xOxidation [P6; P12]	Collagen alpha-2(XI) chain	9.94	5.03	12.38	12.2	within
e215586	AAGEPGKAGERVPGPPGAVGPAGKDGE AGAQQPPGPAGPAG*	4xOxidation [P5; P14; P16; P17]	Collagen alpha-1(I) chain	10.81	7.21	12.75	12.08	within
e025329	REGSPGADGPPGRDGAAGVKGDRGETGA VGAPGAPPPGSP	none	Collagen alpha-1(II) chain	10.22	5.64	12.42	11.22	within
e104646	GSTAVFFGAATSSGFGATTQTASSGSSSSV FGSTTPSPF	none	Nuclear envelope pore membrane protein POM 121	11.75	7.64	13.35	13.16	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215590	PGPMLMGPRGPPGAAGAPGPQGFQGPAGEPGEQGQTGPA*	2xOxidation [M/P]	Collagen alpha-2(I) chain	11.65	7.42	13.36	13.06	within
e025332	EVGPPGPAGSAGARGAPGERGETGPPGPAGFAGPPGADGQP*	2xOxidation [P25; P26]	Collagen alpha-1(II) chain	6.87	2.94	10.81	6.79	within
e105551	QGPTGSEGTPLPGGVGQPGAVGEKGERGDAGDPGPPGAPG*	1xOxidation [P]	Collagen alpha-3(V) chain	10.68	5.6	12.22	12.3	up
e105634	GSPGKEGPPGPQGPSGLPGIPGEEGKEGRDGKPGPPGE*	5xOxidation [P9; P11; P14; P18; P21]	Collagen alpha-1(XXII) chain	7.79	3.48	11.38	10.45	within
e105561	AKGDRGEDGEPGQPGSPGTGENGPPGPLGKRGPAGSPG*	3xOxidation [P17; P19; P25]	Collagen alpha-2(XI) chain	9.32	4.75	11.59	10.38	within
e025337	KDGETGAAGPPGPAGPAGERGEQGAPGPSGFQGLPGPPGP*	4xOxidation [P11; P13; P16; P26]	Collagen alpha-1(II) chain	9.04	3.8	11.28	11.97	up
e215594	GAGGEDAGAGREDAGAGGEDVGAGREDAGAGGEDVGAGGEDV	none	Golgin subfamily A member 6-like protein 2	7.09	2.5	10.29	2.72	within
e208846	GPAGERGEQGAPGPSGFQGLPGPPGPPGEGGKPGDQGVPG*	3xOxidation [P]	Collagen alpha-1(II) chain	8.58	4.34	11.24	9.84	within
e105580	GPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAP	none	Collagen alpha-1(II) chain	9.94	5.39	12.15	11.59	within
e025347	VGFPGSRGDTGPPGPPGYGPAGPIGDKQAGFPGGPGSPG*	5xOxidation [P12; P13; P15; P16; P20]	Collagen alpha-1(IV) chain	9.19	4.95	11.83	11.19	within
e025349	PGPPGPSGDQGASGPAGPSGPRGPPGPVGPSPGKDANGIPG*	9xOxidation [P1; P3; P4; P6; P15; P18; P21; P24; P25]	Collagen alpha-1(II) chain	9.18	2.81	12.46	10.73	within
e025354	PEGPPGKPGEDGEPEGRNGNPGEVGFAGSPGARGFPGAPG*	2xOxidation [P35; P38]	Collagen alpha-2(V) chain	13.75	8.77	15.91	15.11	within
e025355	GDQGPVGRGTGEVGA VGPPGFAGEKGPSGEAGTAGPPGTGP*	2xOxidation [P18; P]	Collagen alpha-2(I) chain	7.54	3.59	10.78	5.87	within
e101330	GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPG*	4xOxidation [P12; P26; P32; P42]	Collagen alpha-1(I) chain	8.72	4.61	10.93	11.59	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025361	AVADTRDQADGSRASVDSGSSEEQGGSSRALVSTLVP	none	Polymeric immunoglobulin receptor	9.96	4.91	13.98	14.49	up
e025362	TLRGSQTIDESLSELAEQMTIEENSSKDNEPIV	none	Cyclin-dependent kinase 17	8.67	2.66	13.04	14.12	up
e025366	DAVVDGENDDPRPPNPPKMPNPNPNHPSSSGSFS	none	CD99 antigen	8.59	2.52	11.42	12.15	up
e025369	GEPGPPGAGFAGPPGADGQPGAKGEPGDAGAKGDAGPPGPA*	5xOxidation [P21; P27; P38; P39; P]	Collagen alpha-1(I) chain	7.51	1.9	11.64	11.14	within
e025373	FAEEKAVADTRDQADGSRASVDSGSSEEQGGSSRAL	none	Polymeric immunoglobulin receptor	12.12	7.51	14.7	14.29	within
e206145	RGGGFGGGSSFGGGSGFSGGGFSGGGFGGGRFGGFGGPGGVGGLG	none	Keratin, type II cytoskeletal 2 epidermal	6.02	1.01	10.05	7.96	within
e025377	KGESGNKGEPGSAGPQGPPGPSGEEGKRGPNGEAGSAGPP*	2xOxidation [P19; P]	Collagen alpha-2(I) chain	11.31	6.08	14.33	13.82	within
e025378	GPKNNDGAPGKNGERGGPGGPGPQGPPGKNGETGPQGPP*	9xOxidation [P9; P18; P21; P23; P26; P27; P35; P38; P]	Collagen alpha-1(III) chain	7.32	3.42	11.0	9.39	within
e215600	RGNDGARGSDGQPPGPPGTAGFPGPSGAKGEVGPAGSPG*	3xOxidation [P28; P36; P40]	Collagen alpha-1(III) chain	10.05	4.78	12.77	12.93	up
e025382	GELGDPGPRGNQGDRGDKGAAGAGLDGPEGDQGPQGPQG*	2xOxidation [P6; P8]	Collagen alpha-3(IX) chain	8.62	3.45	11.38	9.0	within
e215602	GETGPMGERGHPGPPGPPGEQGLPGTAGKEGTKGDPGPP*	1xOxidation [P]	Collagen alpha-2(XI) chain	7.51	3.87	11.05	9.72	within
e215605	GDTGLPGVDGRDGIPGMPGPKGEPGKPGPPGDAGLQGLPG	none	Collagen alpha-1(IX) chain	11.36	6.16	13.89	10.04	within
e025390	PGTPGPPGLPGLQGPVGGFTGPPGPPGPPGPPGKEGQM*	3xOxidation [P7; P10; P15]	Collagen alpha-1(IV) chain	10.86	5.51	13.41	11.64	within
e105685	ARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPRG*	3xOxidation [P22; P23; P]	Collagen alpha-1(I) chain	8.84	3.94	12.05	9.96	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098189	AVGPAGKDGEAGAQQPPGPAGPAGERGE QQPAGSPGFQGLP*	2xOxidation [P]	Collagen alpha-1(I) chain	8.32	4.28	11.42	9.95	within
e025393	GPPGADGQPGAQGEQGEAGQKGDAGAPG PQGPAGAPGPQGP*	6xOxidation [P9; P27; P29; P32; P36; P38]	Collagen alpha-1(II) chain	9.62	4.85	11.93	11.36	within
e025394	PGPVGPAGGPGFPGAPGAKGEAGPTGAR GPEGAQQPRGEPG*	7xOxidation [P3; P6; P10; P13; P16; P24; P30]	Collagen alpha-1(II) chain	5.68	2.41	9.7	10.02	up
e025398	EPGPVGVQGPMPGPAGEEGKRGARGEPPG TGLPGPPGERG*	2xOxidation [P26; P28]	Collagen alpha-1(I) chain	12.26	7.62	15.05	14.48	within
e215609	PGKNGERGGPGGPQGPKNGETGPQ GPPGPTGPGGDKG*	2xOxidation [P10; P13]	Collagen alpha-1(III) chain	11.9	6.24	14.59	14.32	within
e025402	QNGEPGGKGERGAPGEKGEPPGPVAGP PGGSGPAGPPGPQG*	2xOxidation [P]	Collagen alpha-1(III) chain	11.55	7.05	13.44	12.98	within
e025403	GAPGQNGEPGGKGERGAPGEKGEPPGP VAGPPGGSGPAGPPG*	2xOxidation [P]	Collagen alpha-1(III) chain	8.54	3.47	11.19	8.58	within
e300134	GAPGQNGEPGGKGERGAPGEKGEPPGP VAGPPGGSGPAGPPG*	2xOxidation [P38; P41]	Collagen alpha-1(III) chain	5.8	1.77	10.47	10.66	up
e215611	TSGLQEADGVAEILEAVTYTQASPKEAKVE PINTP*	2xOxidation [P31; P35]	Collagen alpha-1(XV) chain	11.37	6.74	13.44	12.84	within
e025409	DQQHVASPGPGEHDQVYPDAAQHGHAFSL FDSHD	none	Glutamine-rich protein 2	10.65	5.31	14.19	7.69	within
e025412	DLGPPGDPGVSGIDGSPGEKGDGPDVGGP GPPGASGEPPGAPG*	4xOxidation [P8; P17; P23; P29]	Collagen alpha-3(V) chain	11.08	4.44	13.33	8.58	within
e215622	ARGNDGATGAAGPPGPPTGPAGPPGFPGAV GAKGEAGPQGPRG*	4xOxidation [P22; P]	Collagen alpha-1(I) chain	10.08	5.09	12.32	11.3	within
e215623	TGPMGAMGPLGPRGMPGERGRLGPQGAP GQRGAHGMPG*	3xOxidation [P24; P28; P37]	Collagen alpha-2(V) chain	9.96	5.43	12.24	11.23	within
e206185	GPRGETGPAGRPGEVGPMPGPAGEKG SPGADGPAGAPGTP*	2xOxidation [P18; P20]	Collagen alpha-1(I) chain	7.94	3.6	11.76	10.09	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e106056	GPPGLPGPPGIAGPQGSQGERGADGEVG QKGDQGHGPGVPG*	2xOxidation [P3; P6]	Collagen alpha-1(XXII) chain	9.06	4.39	11.11	10.51	within
e215624	PGSPGHQGLAGVPGQPGTKGGPGDQGEF GPQGLPGFSGPPG*	1xOxidation [P1]	Collagen alpha-2(IX) chain	6.99	3.86	11.83	9.91	within
e106207	ETGPAGRPGEVGPVPPGPPGAGEKGSPPG DGPAGAPGTPGPQG*	4xOxidation [P8; P13; P14; P16]	Collagen alpha-1(I) chain	10.4	5.17	12.81	11.88	within
e025429	GPSGAPGADGPQGPVGGIGNPGAVGEKG EPGEAGEPGLPGEKG*	1xOxidation [P]	Collagen alpha-1(V) chain	10.85	6.17	13.55	13.02	within
e100035	ASAAPEVSGESTTTSDVGTEAPGLPSATPT ASGDRTEIS	none	Aggrecan core protein	10.53	5.68	12.61	13.67	up
e215625	QNGEPGGKGERGAPGEKGEVGPVAGP PGGSGPAGPPGPQG*	3xOxidation [P]	Collagen alpha-1(III) chain	10.76	6.34	13.5	12.91	within
e215627	GPTGARGAPGDRGEPVPPGPAFAGPPG ADGQPGAKGEPPGDA	none	Collagen alpha-1(I) chain	10.74	5.38	13.49	12.75	within
e215628	DGEVGGKGDQGHGPGVPGFMGPPGNPGPP GADGIAGAAGPPG*	2xOxidation [P25; P27]	Collagen alpha-1(XXII) chain	10.97	6.07	13.21	12.92	within
e215629	RGNDGQPGPAGPPGPVGPAGGPGFPGAP GAKGEAGPTGARGP*	4xOxidation [P22; P25; P28; P]	Collagen alpha-1(II) chain	10.81	5.62	13.23	12.89	within
e215631	RGEQGAPGPSGFQGLPGPPGPPGEGGKP GDQGVPEAGAPG*	2xOxidation [P19; P21]	Collagen alpha-1(II) chain	10.57	5.16	12.82	12.52	within
e025445	ERGSPGGPGAAGFPGARGLPGGPSNGN PGPPGPSGSPGKDG*	2xOxidation [P]	Collagen alpha-1(III) chain	11.82	6.95	14.69	12.98	within
e025452	ANGLSGERGPPGPQGLPGLAGTAGEPGRD GNPGSDGLPGR*	1xOxidation [P32]	Collagen alpha-1(III) chain	11.41	5.71	14.08	12.53	within
e025454	TVNFGDTEEAKKQINDYVEKGTQGKIVDLV KEL	none	Alpha-1-antitrypsin	7.97	1.9	12.77	10.75	within
e025456	AGEVGKPGERGLHGEFGLPGPAGPRGER GPPGESGAAGP*	3xOxidation [P7; P19; P21]	Collagen alpha-2(I) chain	9.05	3.58	12.7	11.26	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025457	NEVEQMIRDLEASIARYKEEYAVLISEAQAIK	none	Cytoplasmic dynein 1 heavy chain 1	7.35	4.3	12.36	9.41	within
e215635	GERGKPLTGMKGAIGPMGPPGNKGSMG SPGHQGPSPG*	1xOxidation [P]	Collagen alpha-1(XIX) chain	7.82	4.14	11.42	8.33	within
e025461	HPGQPGPPEKGKPGQDGIPGAGQKGE PGQPFGNPGP*	2xOxidation [P14; P]	Collagen alpha-5(IV) chain	8.27	3.13	11.96	12.68	up
e215636	IAGPRGSPGERGETGPPGPAGFPAGPQN GEPGKGERGA*	2xOxidation [P19; P]	Collagen alpha-1(III) chain	8.62	3.67	11.74	12.96	up
e025462	GARGSDGQPGPPPGTAGFPGSPGAKG EVGPAGSPGSNGAPG*	3xOxidation [P14; P]	Collagen alpha-1(III) chain	6.75	3.43	9.67	8.94	within
e025463	GEPGAVGPKGPPGVDGVPGAAGLPGP QGSPGAKGEPGTR*	8xOxidation [P3; P8; P11; P12; P20; P26; P28; P31]	Collagen alpha-2(VIII) chain	6.1	1.05	10.3	11.81	up
e025471	ETGPAGRPGEVGP GPPGPAGEKGSPGA DGPAGAPGTPGPQG*	5xOxidation [P13; P14; P16; P17; P]	Collagen alpha-1(I) chain	11.98	7.99	14.03	12.87	within
e215637	QNGEPGKGERGAPGEKGE GPPGVAGP PGGSPAGPPGPQG*	4xOxidation [P22; P23; P28; P29]	Collagen alpha-1(III) chain	11.48	7.68	13.57	13.27	within
e215638	RGEPGPPGPAGFAGPPGADGQPGAKGEP GDAGAKGDAGPPGP*	3xOxidation [P4; P6; P7]	Collagen alpha-1(I) chain	12.24	8.71	14.05	13.47	within
e025474	GPTGARGAPGDRGEPGPPGPAGFAGPPG ADGQPGAKGEPGDA*	1xOxidation [P33]	Collagen alpha-1(I) chain	11.48	7.45	13.6	13.2	within
e025478	GLEDRPSSGSWGS GDQSSSFDPSRTFSE GTHFTE	none	Transcription factor E2-alpha	10.69	6.48	13.02	12.78	within
e025479	ESGNKGEPGSAGPQGPPGPSGEEGKRGP NGEAGSAGPPGPP*	1xOxidation [P]	Collagen alpha-2(I) chain	11.67	7.41	13.38	13.07	within
e215640	ERGPPGPPGRDGEDGPTGPPGPPGPPGP PGLGGNFAAQY*	3xOxidation [P4; P5; P7]	Collagen alpha-2(I) chain	11.16	6.84	13.35	13.09	within
e215641	GEPGAKGAMGPAGPDGHQGPRGEQGLTG MPGIRGPPGPSG*	2xOxidation [P11; P14]	Collagen alpha-1(XVII) chain	11.56	7.8	13.28	13.0	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025481	STTSSGTSTATNSESSTVSSGASTATTSES STTSSGASTAT	none	Mucin-21	7.7	5.04	11.58	10.7	within
e105909	GDRGEPGPPGAGFAGPPGADGQPGAAG EPGDAGAKGDAGPP*	2xOxidation [P]	Collagen alpha-1(I) chain	11.71	7.67	13.77	13.88	up
e025486	GNPGPDGAPGERGGPGERGPRGTPGTRG PRGDPGEAGPQ*	3xOxidation [P29; P]	Collagen alpha-1(VI) chain	9.34	5.43	11.96	11.89	within
e215642	GEAGAAGPAGPAGPRGSPGERGEVGPAG PNGFAGPAGAAGQPGA*	1xOxidation [P42]	Collagen alpha-2(I) chain	11.67	7.46	13.64	13.7	up
e215644	GVRGMDGPQGPKGSLGPQGEPGPPGQQ GTPGTQGLPGPQ*	3xOxidation [P30; P36; P38]	Collagen alpha-2(XI) chain	13.46	8.33	15.78	15.16	within
e215646	GDRGDKGEKGAPGPRGRDGEPTGNPG PPGPPGPPGPPG*	2xOxidation [P35; P36]	Collagen alpha-1(II) chain	13.28	9.53	15.48	14.93	within
e025499	GPPGPKGPTGDDGPKGNGPVGFGPDGP PPGEGGPRGQDG*	6xOxidation [P3; P5; P8; P14; P18; P]	Collagen alpha-2(XI) chain	6.26	2.26	10.25	7.73	within
e025500	AGEVGKPGERGLHGEFGLPGPAGPRGER GPPGESGAAGP*	4xOxidation [P7; P19; P21; P24]	Collagen alpha-2(I) chain	12.49	7.67	14.6	14.3	within
e025503	PPGPAGFAGPPGADGQPGAAGQEAGQ KGDAGAPGPQGSPG*	3xOxidation [P2; P4; P10]	Collagen alpha-1(II) chain	7.16	2.86	10.84	7.74	within
e025505	ERGAAGEPGPHGPPGVPGSVGPKGSSGS PGPQGPVGLQ*	4xOxidation [P31; P34; P35; P37]	Collagen alpha-1(XVII) chain	7.71	2.61	12.02	8.99	within
e025517	GPAGPPGPPGPGTSGHPGSPGSPGYQG PPGEPGQAGPSGPPG*	2xOxidation [P]	Collagen alpha-1(III) chain	11.43	7.56	13.52	12.78	within
e105165	PGADGEAGRPGSSGSPGDEGQPGEPGPP GEKGEAGDEGNP*	5xOxidation [P10; P15; P22; P25; P27]	Collagen alpha-1(VI) chain	8.55	3.98	11.68	5.33	within
e025520	VPGGPGMRGMPGSPGGPSDGKPGPPGS QGESGRPGPPGSPG*	2xOxidation [P26; P35]	Collagen alpha-1(III) chain	10.3	5.72	13.41	11.37	within
e215649	GERGVQGPAGPRGANGAPGNDGAKG DAGAPGAPGSQGAPG*	3xOxidation [P9; P11; P]	Collagen alpha-1(I) chain	11.7	7.85	13.52	12.94	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215651	PPGADGIAGAAGPPGIQGSPPGKEGPPGPQGPSGLPGIPGEE*	7xOxidation [P13; P14; P20; P25; P26; P28; P31]	Collagen alpha-1(XXII) chain	11.55	7.36	13.44	12.97	within
e025524	MMGPPGVPGPKGSMGHPGMPGGMGTPGEPGPQGPPGSRGP*	3xOxidation [P34; P35; P40]	Collagen alpha-1(XXVII) chain	10.47	6.34	12.56	11.81	within
e215654	GDLGPPGDPGVSGIDGSPGEKGDPGDVGGPGPPGASGEPGAPG*	3xOxidation [P30; P]	Collagen alpha-3(V) chain	9.81	5.28	11.82	11.4	within
e215655	GAPGAKGEAGPTGARGPEGAQGPGEPTGSPGPAGASGNPG*	3xOxidation [P11; P17; P23]	Collagen alpha-1(II) chain	9.87	4.59	11.95	11.4	within
e025529	EEKAVADTRDQADGSRASVDSGSSEEQGSSRALVST	none	Polymeric immunoglobulin receptor	11.0	6.42	13.46	12.78	within
e102740	PPGSSEKGERGAAGEPGPHGPPGVPGSVGPKGSSGSPGPQG*	7xOxidation [P2; P16; P18; P21; P22; P25; P30]	Collagen alpha-1(XVII) chain	8.76	4.19	11.1	10.37	within
e100772	GAPGAPGHPPGPPVGPAGKSGDRGESGPAGPAGAPGPAGSRGA*	3xOxidation [P12; P14; P17]	Collagen alpha-1(III) chain	7.45	4.1	10.85	6.66	within
e215656	GPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAK*	6xOxidation [P21; P23; P24; P26; P32; P33]	Collagen alpha-1(I) chain	11.04	6.81	13.36	12.72	within
e103189	LPGFSTSGSSSFGLNLQGPPGPPGPQGPKGDKGDPGVPG*	6xOxidation [P2; P19; P20; P22; P23; P25]	Collagen alpha-1(XVII) chain	8.75	3.69	11.14	11.28	up
e215657	GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQP*	5xOxidation [P8; P11; P18; P24; P26]	Collagen alpha-1(I) chain	9.36	4.43	11.98	8.74	within
e103388	GETGPPGPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQ*	1xOxidation [P14], 1xDeamidation [Q42]	Collagen alpha-1(II) chain	9.27	4.55	12.01	9.43	within
e025531	GPGPMGLMGPGRPPGAAGAPGPQGFQGPAGEPGEPGQTGPA*	5xOxidation [P13; P14; P20; P22; P]	Collagen alpha-2(I) chain	9.19	4.15	12.0	6.63	within
e099823	ESGRPGPPGPSGRGQPGVMGFPGPKGNDGAPGKNGERG*	2xOxidation [P23; P25]	Collagen alpha-1(III) chain	7.39	3.44	11.13	11.03	within
e025535	GEAGPPGAAGPPGAKGPPGDDGPKGNPGPVGFPDGPGE*	10xOxidation [P6; P11; P12; P17; P18; P23; P27; P29; P33; P36]	Collagen alpha-1(XI) chain	9.5	4.42	12.15	7.36	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215658	KGNEGPSGPPGPAGSPGERGAAGSGGPIG PPGRPGPQGPPG*	11xOxidation [P9; P10; P12; P16; P27; P30; P31; P34; P36; P39; P40]	Collagen alpha-2(XI) chain	9.23	4.18	11.88	11.2	within
e025543	GAPGEKGEKGPPGVAGPPGGSGPAGPPG PQGVKGERGSPGGP*	11xOxidation [P3; P11; P12; P17; P18; P23; P26; P27; P29; P39; P42]	Collagen alpha-1(III) chain	6.86	1.29	10.67	9.65	within
e025544	GYPGPAGPPGPPGPPGTSGHPGSPGSPG YQPPGEPGQAGPS*	2xOxidation [P24; P27]	Collagen alpha-1(III) chain	8.89	3.78	12.19	7.9	within
e025545	AGSPGSNGAPGQRGEPGPQGHAGAQQGP GPPGINGSPPGGKGE*	3xOxidation [P27; P28; P30]	Collagen alpha-1(III) chain	9.49	4.29	12.8	5.51	within
e025547	GGLAGYPGPAGPPGPPGPPGTSGHPGSP GSPGYQPPGEPGQ*	3xOxidation [P]	Collagen alpha-1(III) chain	10.58	6.7	12.25	13.17	up
e215663	DSGAPGRGESGAMGLPGQEGLPGKDGD TGPTGPQGPQGP*	4xOxidation [P7; P17; P23; P31]	Collagen alpha-1(XXII) chain	10.01	5.95	11.99	12.55	up
e025555	SPGKDGPPGPAGNTGAPGSPGVSGPKGD AGQPGEKGSPGAQG*	7xOxidation [P2; P7; P8; P10; P17; P20; P25]	Collagen alpha-1(III) chain	9.45	5.14	11.59	12.08	up
e215665	VGPAGKDGEAGAQQPPGPAGPAGERGEQ GPAGSPGFQGLPGP*	1xOxidation [P]	Collagen alpha-1(I) chain	4.66	0.0	13.85	4.34	within
e215666	GPTGARGAPGDRGEPGPPGPAGFAGPPG ADGQPGAKGEPGDA*	3xOxidation [P15; P17; P18]	Collagen alpha-1(I) chain	7.91	3.95	10.84	10.46	within
e102514	EVSAQVATVMWDYFSQLSNNAKEAVEHL QKSE	none	Apolipoprotein A-IV	7.37	3.2	10.91	9.66	within
e025558	GPPGEPGPAGQDGPPGDKGDDGEPGQTG SPGPTGEPGSPGPP	none	Collagen alpha-1(V) chain	9.85	5.31	12.64	9.61	within
e215668	GESGPSGPAGPTGARGAPGDRGEPGPPG PAGFAGPPGADGQP*	6xOxidation [P5; P8; P11; P18; P24; P26]	Collagen alpha-1(I) chain	9.91	5.12	12.62	9.88	within
e215669	GFAGPPGADGQPGAKGEQGEAGQKGDAG APGPQGPSGAPGPQ*	3xOxidation [P30; P32; P35]	Collagen alpha-1(II) chain	9.81	5.48	12.54	9.42	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215670	AKQQDGAAAMEMQPLKSAEGGDADDRKK ASMHKKE	none	Plasma membrane calcium-transporting ATPase 2	5.37	1.98	8.68	7.09	within
e206255	LPGTPGTDGPKGASGPAGPPGAQGPPGLQ GMPGERGAAGIAGP	none	Collagen alpha-1(II) chain	6.14	0.0	8.96	6.36	within
e025569	TGLPGDLGPPGDPGVSGIDGSPGEKGDGP DVGGPGPPGASGE*	5xOxidation [P4; P9; P10; P13; P22]	Collagen alpha-3(V) chain	8.68	4.04	11.82	6.55	within
e025571	YPGPAGPPGPPGPPGTSGHPGSPGSPGY QGPPGEPPQAGPSG*	3xOxidation [P2; P4; P7]	Collagen alpha-1(III) chain	8.71	3.38	11.78	3.04	down
e025575	GSPGIRGPQGITGPKGATGPPGINGKDGP GTPGMKGSAGQ*	3xOxidation [P3; P8; P14]	Collagen alpha-2(IX) chain	8.65	3.36	13.83	12.22	within
e025582	KEKESQDKTSLPELEQQQEQQQEQQEQ VQ	none	Apolipoprotein A-IV	8.35	4.63	11.72	12.14	up
e206270	PGPPGLPGPKGNMGLNFQGPKEKGEQG LQGPPGPPGQ*	6xOxidation [P3; P4; P7; P9; P20; P32]	Collagen alpha-5(IV) chain	7.92	3.36	13.56	6.89	within
e106370	IEGPPGPEGPAGLPGPPGTMGPTGQVGDP GERGPPRPG*	11xOxidation [P5; P7; P10; P14; P16; P17; P22; P29; P34; P35; P38]	Collagen alpha-1(V) chain	8.58	4.53	10.82	11.32	up
e025588	GPPGEPGAGQDGPBGDKGDDGEPGQTG SPGPTGEPGSPGPP*	1xOxidation [P]	Collagen alpha-1(V) chain	9.33	4.72	11.9	10.65	within
e215676	PGEPPAGQDGVGGDKGEDGDPGQPGPP GPSGEAGPPGPPGK*	3xOxidation [P30; P36; P37]	Collagen alpha-1(XI) chain	9.79	4.81	12.26	10.32	within
e025594	AVADTRDQADGSRASVDSGSSEEQGGSSR ALVSTLVPL	none	Polymeric immunoglobulin receptor	10.81	5.56	14.55	15.06	up
e025597	MGPDGLKGRDGPDPGEHGEKGQEGLM GEDGPPGPPG*	5xOxidation [P13; P15; P33; P34; P36]	Collagen alpha-1(XXVII) chain	9.5	4.99	11.91	7.44	within
e025600	DADLADGVSGGEGKGGSDGGGSHRKEGE EADAPGVIPGIVG	none	CD99 antigen	12.82	9.41	15.32	15.85	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215681	GEQGEKGDRLPGPQQSPGQKGEIMGIPG ASGPIGPGGPPG*	7xOxidation [P12; P14; P18; P27; P32; P35; P38]	Collagen alpha-2(XI) chain	12.75	8.16	15.29	15.51	up
e025605	GGRGSSSSGGYSSGSSSYSGGRQSGSR GGSGGGGSISGGGYGSG	none	Keratin, type II cytoskeletal 2 epidermal	8.98	4.1	11.57	8.75	within
e105061	PGSRGENGPTGAVGFAGPQQPDGQPGVK GEPGEPGQKGD*	4xOxidation [P9; P18; P21; P25]	Collagen alpha-2(V) chain	6.57	3.31	11.08	9.86	within
e025609	GPKNSEGEPAAGSKGDTGAKGEPGPVG VQPPGPAGEEGK*	7xOxidation [P2; P9; P12; P24; P26; P32; P33]	Collagen alpha-1(I) chain	12.13	9.09	14.21	15.16	up
e025610	GHGAEDSLADQAANEWGRSGKDPNHFRP AGLPEKY	none	Serum amyloid A-1 protein	4.08	1.32	9.35	5.54	within
e025611	ESGLQGEPAKGDVGTAGSVGGTGEPLR GEPGAPGEEGLQ*	1xOxidation [P]	Collagen alpha-1(XXIV) chain	12.19	9.02	14.42	15.17	up
e105994	SPGKDGPPGPAGNTGAPGSPGVSGPKGD AGQPGEKGSPGAQGP*	3xOxidation [P25; P32; P38]	Collagen alpha-1(III) chain	6.12	1.6	10.65	11.06	up
e103128	GARGLPGPPGSNGNPGPPGSPGSPKDG PPGPAGNTGAPGSPGV*	2xOxidation [P]	Collagen alpha-1(III) chain	3.63	0.22	10.34	8.41	within
e025625	GSGNGSSTLNPSTSSSTQGDPAFPEMNGN GAVAPMDFTT	none	Nucleolar protein 4-like	5.72	2.32	9.52	6.83	within
e025627	GPPGEPGPAGQDGPPGDKGDDGEPGQTG SPGPTGEPGSPGPP*	2xOxidation [P2; P3]	Collagen alpha-1(V) chain	8.26	3.98	10.75	7.84	within
e098193	GLDGITGPQGAPGFPAGVPAGPPGLQGP PGPPGPLGPDGNM*	4xOxidation [P20; P23; P24; P]	Collagen alpha-6(IV) chain	8.98	4.59	12.14	11.97	within
e025630	DGATGAAGPPGPTGPAGPPGFPGAVGAKG EAGPQGPRGSEGPQG	none	Collagen alpha-1(I) chain	10.52	4.51	12.63	14.07	up
e025631	AENEGKGVLDTGRHMPGAGKRREKGDGV YQKGMDF	none	Tafazzin	10.28	4.42	12.72	12.21	within
e025650	AGHWTSESSVSGSTGQWHSESGSFRPDS PGSGNARPN	none	Fibrinogen alpha chain	5.94	2.86	8.81	3.57	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025655	DQGPVGRTEVGAVGPPGFAGEKGPSGE AGTAGPPGTGPQG*	3xOxidation [P]	Collagen alpha-2(I) chain	11.26	7.22	13.45	12.85	within
e099925	ANGAPNDGAKGDAGAPGAPGSQQAPGL QGMPGERGAAGLPGP*	6xOxidation [P5; P17; P20; P26; P32; P41]	Collagen alpha-1(I) chain	10.97	5.63	14.08	13.28	within
e025656	GPAGFPGAPGQNGEPGGKGERGAPGEKG EGGPPGVAGPPGGSGP	none	Collagen alpha-1(III) chain	10.88	6.42	13.33	13.27	within
e215690	GTPGEQQLIGQRGEPGLEDSGPMGPDGL KGRDGPDP*	2xOxidation [P3; P15]	Collagen alpha-1(XXVII) chain	10.53	4.65	13.59	12.41	within
e215691	GEKGESGPSGAAGPPGPKGPPGDDGPKG SPGPVGFPDGPDPG*	2xOxidation [P14; P15]	Collagen alpha-1(V) chain	10.82	5.95	13.33	12.79	within
e025662	GEPGEAGEPGLPGEPPGPKGERGEKG ESGPSGAAGPPGPK*	1xOxidation [P]	Collagen alpha-1(V) chain	10.79	5.78	13.29	12.75	within
e102017	GPPGVPGPPGPGGSPGLPGEIGFPGKPGP PGPTGPPGKDGPNG*	3xOxidation [P3; P6; P8]	Collagen alpha-1(XXII) chain	9.44	4.59	11.55	10.08	within
e215694	QQGAIGSPGPAGPRGPVPSGPPGKDGTG GHPGPIGPPGPRG*	3xOxidation [P23; P32; P34]	Collagen alpha-1(III) chain	8.35	3.3	11.37	9.6	within
e025665	GAPGPTGPPGLMGRGTGHPGTGAKGEKG SDGPPGKPGPPGP*	2xOxidation [P]	Collagen alpha-1(XIX) chain	6.94	2.67	10.64	7.19	within
e300101	PGPPGPAGFAGPPGADGQPGAKGEPGDA GAKGDAGPPGPAGPAGP*	2xOxidation [P13; P19]	Collagen alpha-1(I) chain	6.64	2.08	10.24	8.58	within
e025671	GEPGRDGNPGSDGLPGRDGSPGGKGDRG ENGSPGAPGAPGH*	4xOxidation [P21; P33; P36; P39]	Collagen alpha-1(III) chain	5.7	1.23	12.97	4.6	within
e025677	GESGPSGPAGPTGARGAPGDRGEPGPPG PAGFAGPPGADGQPG*	6xOxidation [P18; P24; P26; P27; P]	Collagen alpha-1(I) chain	9.58	3.56	12.8	7.15	within
e103354	TSPNNEEFGPGVPAETDITETSINGHGAYG EKGQKGE*	1xOxidation [P10]	Collagen alpha-1(XI) chain	8.35	3.63	11.17	9.69	within
e215696	ERMQSRVGQRGSGLSMSAARSEHEVSEIID GLSEQ	none	Nuclear receptor corepressor 2	7.66	1.61	11.32	10.43	within

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e025682	AGFPGSPGAKGEVGPAGSPGSNGAPGQR GEPGPQGHAGAQQGP*	1xOxidation [P25]	Collagen alpha-1(III) chain	10.71	5.39	13.83	13.1	within
e106089	DQGPVGRTEVGAVGPPGFAGEKGPSGE AGTAGPPGTPGPQG*	4xOxidation [P17; P25; P35; P38]	Collagen alpha-2(I) chain	9.12	4.89	11.61	11.71	up
e215698	QPGPPGPPGTAGFPGSPGAKGEVGPAGSP GSNGAPGQRGEPGP*	2xOxidation [P]	Collagen alpha-1(III) chain	10.99	5.7	13.09	12.42	within
e215700	QGPPGPAGPAGERGEQGPAGSPGFQGLP GPAGPPGEAGKPGE*	3xOxidation [P33; P]	Collagen alpha-1(I) chain	9.57	4.74	12.56	11.96	within
e025692	RGETGPAGPPGAPGAPGAPGVGPAGKS GDRGETGPAGPAGPVG*	5xOxidation [P19; P21; P24; P36; P]	Collagen alpha-1(I) chain	7.3	2.87	11.82	11.57	within
e215701	PQGITGPKGATGPPPINGKDGTPGTPGMK GSAGQAGQPGSPG*	5xOxidation [P1; P7; P13; P14; P23]	Collagen alpha-2(IX) chain	9.31	4.33	12.5	11.98	within
e215704	REGREESEAEAPRGAEFAETLHTGS DAPSPWP	none	Nestin	9.03	4.54	12.34	10.96	within
e215705	QGPPGISKVFSAYSNVTADLMDFFQTYGAI QGPPGQ*	2xOxidation [P4; P33]	Collagen alpha-1(XVII) chain	8.52	3.93	12.12	10.88	within
e206339	RGDQGPVGRTEVGAVGPPGFAGEKGPS GEAGTAGPPGTPGP*	3xOxidation [P18; P37; P40]	Collagen alpha-2(I) chain	5.13	0.9	8.1	7.74	within
e206341	AVHVRKAADDTWEPFASGKTSESGELHG LTTEEE	none	Transthyretin	5.5	1.4	8.83	1.93	within
e025707	GPVGFPDGPDPGEPGPAGQDGVGGDKG EDGDPGQPGPPGPSG*	1xOxidation [P2]	Collagen alpha-1(XI) chain	9.8	5.55	13.35	11.0	within
e025709	AVADTRDQADGSRASVDSGSSEEQGGSSR ALVSTLVPLG	none	Polymeric immunoglobulin receptor	10.92	5.72	15.06	15.15	up
e025710	GAKGPTGSPGTSGPPGSAGPPGSPGPQG STGPQGIRGQPGDPGV*	1xOxidation [P24]	Collagen alpha-2(V) chain	10.46	4.71	14.45	14.83	up
e102266	GPVGVPDGPGEAGPIGPKGYRGDEPPGS EGARGAPGAPG*	9xOxidation [P2; P6; P9; P14; P17; P26; P27; P36; P38]	Collagen alpha-1(VI) chain	7.73	3.65	11.5	11.21	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025714	GAGLDGPEGDQGPQGPQGVPGTSKDGQD GAPGEPGPPGDPGL*	1xOxidation [P40]	Collagen alpha-3(IX) chain	6.14	2.33	9.47	8.22	within
e025715	DRGEPGPPGAGFAGPPGADGQPGAKGE PGDAGAKGDAGPPGP*	3xOxidation [P29; P40; P41]	Collagen alpha-1(I) chain	6.75	2.86	11.16	11.44	up
e215713	NGDVGPMGPPGPPGPRGPQGPNGADGPQ GPPGSVGSVGGVGE*	8xOxidation [P6; P9; P10; P12; P13; P15; P18; P21]	Collagen alpha-1(XI) chain	9.33	3.55	12.64	6.93	within
e025725	SGEKGDQGPDPGSPGSPGAPGAGPP GYGPQGEPLQGTQ*	3xOxidation [P16; P19; P21]	Collagen alpha-3(IV) chain	9.05	2.24	12.39	7.07	within
e215716	AKGEAGPTGARGPEGAQQGPRGEPGTPGS PGPAGASGNPGTDGI*	3xOxidation [P7; P13; P19]	Collagen alpha-1(II) chain	11.0	5.51	14.49	15.08	up
e215717	FTGPPGPPGPPGPPGEKGMGLSFQGP GDKGDQGVSGPP*	2xOxidation [P27; P39]	Collagen alpha-1(IV) chain	10.83	5.0	14.48	15.09	up
e025730	DADLADGVSGGEGKGGSDGGGSHRKEGE EADAPGVIPGIVGA	none	CD99 antigen	7.06	2.76	11.39	10.0	within
e025733	VDNVENVVSFNAKEHENFLETIQEQTTES AGQD	none	DNA excision repair protein ERCC-5	7.5	3.37	9.98	10.85	up
e215720	EAGRAGEPDGEDGQKGAPGPKGFKGD PGVGVPGSPGPPGP*	1xOxidation [P40]	Collagen alpha-1(VII) chain	5.82	1.51	10.64	10.19	within
e025737	EEKAVADTRDQADGSRASVDSGSSEEQGG SSRALVSTL	none	Polymeric immunoglobulin receptor	8.68	2.97	15.39	8.76	within
e215721	SETSTSLKDLFSQTLYTVSVSAVHDEGES PVTAQE*	1xOxidation [P30]	Collagen alpha-1(XII) chain	4.28	1.04	8.0	9.18	up
e106329	GEAGPQGPGRGSEGPQGVRGEPGPPGAG AAGPAGNPGADGQPGA*	1xOxidation [P]	Collagen alpha-1(I) chain	7.22	2.82	12.77	10.33	within
e104302	GQSSRSEQHGSSSGLSSSYGQHSGSHQ SSGHGRQGSGSG	none	Hornerin	6.28	2.18	10.34	4.17	within
e215727	GFPDGPDPGEGGPRGQDGAKGDRGEDG EPGQPGSPGPTGE*	2xOxidation [P9; P14]	Collagen alpha-2(XI) chain	7.27	1.85	10.96	7.74	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025745	DLADGVSGGEGKGGSDGGGSHRKEGEEA DAPGVIPGIVGAVV	none	CD99 antigen	12.77	8.34	14.62	14.88	up
e025746	EGYGYGYGYQDNTTNYGYGMATSHSWE MPSSDTN	none	A-kinase anchor protein 8-like	5.9	2.11	8.7	8.35	within
e025749	SSEATTPTPGASPPAPEMERPPAPESVGTE EMPEDGEPEP	none	E3 ubiquitin-protein ligase synoviolin	4.43	1.75	8.39	6.4	within
e105415	QGLPGPPGSPGDQASGPAGPSGPRGPP GPVGPSPGKDANGIP*	7xOxidation [P6; P7; P9; P18; P21; P24; P27]	Collagen alpha-1(II) chain	8.64	4.31	11.16	11.15	within
e215733	PGDKGESGPSGPAGPTGARGAPGDRGEP GPPGPAGFAGPPGADG*	2xOxidation [P1; P9]	Collagen alpha-1(I) chain	8.62	3.93	10.71	11.28	up
e025762	PPPGGGVVGPPGPTGETGPIGERGHPGPP GPPGEQGLPGAAG*	8xOxidation [P1; P2; P4; P10; P13; P19; P26; P28]	Collagen alpha-1(XI) chain	9.18	4.48	11.65	10.96	within
e215736	EPGPVGGGGHPGQPGPPGEKKGKPGQDGI PGPAGQKGEPGQP*	7xOxidation [P14; P16; P17; P23; P29; P31; P38]	Collagen alpha-5(IV) chain	11.42	7.41	13.27	13.2	within
e025766	DGLPGRDGSPPGGKDRGENGSPGAPGAP GHPGPPGPVGPAGKS*	3xOxidation [P34; P36; P39]	Collagen alpha-1(III) chain	11.32	7.55	13.23	13.15	within
e025770	QGPRGSEGPQGVRGEPGPPGPAGAAGPA GNPGADGQPGAKGANG*	1xOxidation [P]	Collagen alpha-1(I) chain	9.44	4.49	12.1	11.98	within
e025773	READPESEADRAAVEDINPADDPNNQGED EFEEAE	none	Golgi integral membrane protein 4	6.67	0.97	10.95	13.09	up
e025775	SRGENGPTGAVGFAGPQGPDGQPGVKGE PGEPGQKGDAGSPG*	1xOxidation [P]	Collagen alpha-2(V) chain	11.22	7.34	12.87	13.1	up
e025778	WERPFEVKDTEEDFHVDQVTTVKVPMMK RLG	none	Alpha-1-antitrypsin	6.14	0.78	11.01	2.23	within
e025780	GGYGGDRGGGSGYGGDRSGGYGGDRSG GGYGGDRGGGYGGDRG	none	TATA-binding protein-associated factor 2N	3.91	0.0	7.16	4.02	within
e215738	EKGDPGDVGGPGPPGASGEPGAPGPPGK RGPSGHMGREGRE*	2xOxidation [P]	Collagen alpha-3(V) chain	6.45	2.66	10.67	9.59	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025792	FGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDT	none	Alpha-1-antitrypsin	7.36	0.0	16.31	8.37	within
e025793	GKDGVPGLPGLPGLPGDGGQGFPGEKGLPLGPGKEGHPGPPG*	2xOxidation [P23; P29]	Collagen alpha-6(IV) chain	7.53	0.54	15.07	9.7	within
e100293	GESGNKGEPGSAGPQQPPGPSGEEGKRGPNGEAGSAGPPGPPG*	4xOxidation [P9; P20; P39; P42]	Collagen alpha-2(I) chain	6.15	1.27	11.09	10.94	within
e025795	GEKGEKGETGQAGSPGEKGEAGEKGNPGEVPLPGPEGPP*	3xOxidation [P35; P37; P40]	Collagen alpha-1(XIII) chain	9.37	5.57	11.92	11.23	within
e025796	QGGAGPTGPPGEPGDPGPMGPIGSRGPEGPPGKPGEDGEPEGR*	2xOxidation [P30; P31]	Collagen alpha-2(V) chain	9.08	4.73	11.14	11.03	within
e025797	MGPSGPRGLPGPPGAPGPQGFGPPGEPGEFGASGPMGPRGP*	3xOxidation [P]	Collagen alpha-1(I) chain	10.13	5.07	12.47	11.88	within
e215750	GSQGESGRPGPPGPSGPRGQPGVMGFPGPKGNDGAPGKNGE*	4xOxidation [P14; P17; P21; P27]	Collagen alpha-1(III) chain	7.79	4.09	10.38	10.94	up
e025803	SNGNPGGPPSGSPGKDGPPGPAGNTGAPGSPGVSGPKGDAGQPG*	3xOxidation [P22; P29; P32]	Collagen alpha-1(III) chain	8.58	4.36	12.35	11.91	within
e215751	AGMPGGPGKSGSMGPVGP GPAGERGHGAPGPSGSPGLPGVPG*	7xOxidation [P21; P28; P31; P33; P37; P]	Collagen alpha-1(XVI) chain	12.36	8.58	14.34	14.59	up
e025810	PGVPGAEGEDGKDGSPGEPGANGLPGAA GERGAPGFRGPAGP*	8xOxidation [P1; P4; P16; P19; P25; P34; P39; P42]	Collagen alpha-1(III) chain	11.63	7.99	13.41	13.73	up
e025811	GREGAPGAEGSPGRDGSFGAKGDRGETGPAGPPGAPGAPGAPGP*	4xOxidation [P33; P36; P39; P42]	Collagen alpha-1(I) chain	6.46	2.13	10.84	8.17	within
e300110	NAPPEPVPPPRAAPATHVRSPQPPPPAPAPARDELDPD	none	Neurosecretory protein VGF	9.71	4.59	12.8	13.13	up
e025820	KGNDGAPGKNGERGGPGGPGPQGPPGKNGETGPQGPPGPTGPG*	4xOxidation [P7; P16; P19; P21]	Collagen alpha-1(III) chain	8.22	3.28	11.46	9.6	within
e104554	GQAGPPGPPGPPGPRGPPGDTGKDGPRGMPGVPGEPGKPGE*	9xOxidation [P9; P11; P12; P14; P17; P18; P26; P30; P33]	Collagen alpha-1(XXV) chain	6.79	2.54	11.7	10.63	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e103080	AGMPGGPGKSGSMGPVGGPPGAGERGHP GAPGPSGSPGLPGVPG*	8xOxidation [P19; P21; P28; P31; P33; P37; P40; P43]	Collagen alpha-1(XVI) chain	8.82	3.91	12.65	12.25	within
e025830	GPQGLAGQRGIVGLPGQRGERGFPLPGP SGEPGKQGAPGA*	3xOxidation [P2; P15; P24]	Collagen alpha-1(II) chain	7.16	5.32	13.38	8.42	within
e025849	DFLGRQDTDYRSMEYRDVDHRLPGSQMF GYGQS	none	RNA-binding protein 6	6.25	1.36	11.63	10.77	within
e025850	GDKGAAGAGLDGPEGDQGPQGPQGVPGT SKDQDQDAPGEPGPP*	3xOxidation [P19; P22; P26]	Collagen alpha-3(IX) chain	9.25	4.54	12.07	10.44	within
e025851	GRDGVPGGPGMRGMPGSPGGPGSDGKP GPPGSQGESGRPGPPG*	5xOxidation [P18; P21; P27; P29; P30]	Collagen alpha-1(III) chain	10.54	5.58	12.71	12.64	within
e025853	VAVHVFRKAADDTWEPFASGKTSSEGLH GLTTEE	none	Transthyretin	6.9	2.65	10.87	10.94	up
e025854	AGQPGSPGHQGLAGVPGQPCTKGGPGDQ GEPGPQGLPGFSGPP*	3xOxidation [P16; P19; P25]	Collagen alpha-2(IX) chain	8.74	3.37	11.21	10.43	within
e025859	GEPGAKGAMGPAGPDGHQGPGEQGLTG MPGIRGPPGPSGDP*	2xOxidation [P36; P38]	Collagen alpha-1(XVII) chain	5.89	2.42	9.2	6.27	within
e103779	DVKSGVAVGGLAGYPGAPPPGPPPGT SGHPGSPGSPGYQGP*	3xOxidation [P26; P27; P33]	Collagen alpha-1(III) chain	9.62	4.19	12.56	11.77	within
e025867	FPGARGLPGPPSGNPNPGPPSGSPGK DGPPGPAGNTGAPGSPG*	3xOxidation [P11; P17; P19]	Collagen alpha-1(III) chain	10.73	5.67	12.93	12.79	within
e098197	GLAGYPGAPPPGPPPGTSGHPGSPGS PGYQGPPEPGQAG*	11xOxidation [P6; P8; P11; P12; P14; P15; P17; P18; P24; P27; P30]	Collagen alpha-1(III) chain	10.44	5.89	12.8	13.5	up
e025869	GPMGPSGPRGLPGPPGAPGPQGFGPPG EPGEPGASGPMGPRG*	3xOxidation [P8; P12; P14]	Collagen alpha-1(I) chain	10.57	4.86	12.57	12.41	within
e025870	GPAGPNGPPGPAGSRGDGGPPGMTGFPG AAGRTGPPGPSGISGPPG*	1xOxidation [P]	Collagen alpha-2(I) chain	8.88	3.99	12.52	11.71	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025871	APGPQGFQGNPGEPEPGVSGPMGPRGP PGPPGKPGDDGEA*	9xOxidation [P11; P14; P17; P22; P25; P28; P29; P31; P32]	Collagen alpha-1(II) chain	10.35	5.84	12.34	13.02	up
e025873	GAKGPTGSPGTSGPPGSAGPPGSPGPQG STGPQGIRGQPGDGPV*	2xOxidation [P24; P26]	Collagen alpha-2(V) chain	11.14	7.14	13.61	13.24	within
e101052	ERGDRGDPGPAGLPGSQGAPGTPGPVGA PGDAGQRGDPSRGP*	1xOxidation [P20]	Collagen alpha-2(V) chain	12.13	9.1	13.97	13.25	within
e025875	DIELDAKGDPLPGAPGPQGLPGPPGFP PVGPPGPPGFF*	11xOxidation [P16; P18; P22; P24; P25; P28; P30; P33; P34; P36; P37]	Collagen alpha-3(IV) chain	11.44	7.76	13.24	12.66	within
e025876	GSDGQPGPPGPPGTAGFPGSPGAKGEVG PAGSPGSNGAPQRGEP	none	Collagen alpha-1(III) chain	6.32	2.54	10.14	9.1	within
e025877	GTPGAKGPTGSPGTSGPPGSAGPPGSPGP QGSTGPQGIRGQPGDP*	2xOxidation [P3; P8]	Collagen alpha-2(V) chain	11.41	8.35	13.16	12.54	within
e025882	PGPAGFAGPPGADGQPGAKGEQGEAGQK GDAGAPGPQGSPGAPGP*	3xOxidation [P10; P16; P34]	Collagen alpha-1(II) chain	6.37	3.3	10.94	8.14	within
e025888	FAEEKAVADTRDQADGSRASVDSGSSEEQ GGSSRALVST	none	Polymeric immunoglobulin receptor	9.95	5.22	12.91	12.64	within
e025889	PGAGAEIPTSTADTSNSSNPAPPPGEGADD LEGEFTEETI*	2xOxidation [P1; P8]	Collagen alpha-1(V) chain	9.84	3.75	13.73	14.88	up
e025890	GANENLESQSALLENDKDEEDMSLDSDG EISHIEV	none	Protein TASOR	9.58	3.63	13.52	14.62	up
e025891	GPAGFAGPPGADGQPGAKGEQGEAGQKG DAGAPGPQGSPGAPGPQ*	2xOxidation [P]	Collagen alpha-1(II) chain	9.37	4.45	12.02	9.49	within
e025895	DGPPGPAGNTGAPGSPGVSGPKGDAGQP GEKGSPGAQGPPGAPGP*	8xOxidation [P13; P16; P21; P28; P34; P39; P40; P43]	Collagen alpha-1(III) chain	8.11	4.21	11.49	9.29	within
e025897	GDAYGDAGYQGPGGYGPQDSYGPQGG YQPDYGPAGSGGSG	none	Synaptophysin	13.56	9.22	15.78	15.61	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e206475	KGEPGADGEAGRPSSGSPSGDEGQPGEP GPPGEKGEAGDEGN*	6xOxidation [P13; P18; P25; P28; P30; P31]	Collagen alpha-1(VI) chain	13.53	8.39	15.74	15.87	up
e025899	AETASGGEEAETASGGEEAGTASGGEEAGI ASGGEAGTASGGEEAG	none	Apolipoprotein B receptor	13.48	9.51	15.42	15.45	up
e025907	RARGRGGGPSQNWQGYSNYWNQGYGN YGYNSQGY	none	Heterogeneous nuclear ribonucleoprotein D0	8.23	2.79	12.89	9.64	within
e025921	SGGEEAGTASGGEEAGIASGGEAGTASGG EEAGTASGGDEAWTTSG	none	Apolipoprotein B receptor	14.17	10.73	16.73	17.18	up
e025922	GFPDPGPPGEPGPAGQDGP PGDKGDDG EPGQTGSPGPTGEPG*	6xOxidation [P14; P]	Collagen alpha-1(V) chain	13.93	9.89	16.42	16.99	up
e025923	SSGSPSGDEGQPGEPGPPGEKGEAGDEGN PGPDGAPGERGGPGE*	4xOxidation [P]	Collagen alpha-1(VI) chain	11.39	6.83	13.97	13.53	within
e215792	PGPPGDDGERGDDGEVGPRGLPGEPGPR GLLGPKGPPGPPGP*	2xOxidation [P37; P39]	Collagen alpha-1(V) chain	5.86	2.94	8.76	3.66	within
e025935	AKMPAPEPGAAPSNEEDSDDDDLAPSG ATAAGAGDEGDGQ	none	Ran-binding protein 3	11.53	6.11	14.43	14.62	up
e025942	VQVESTEEEQESGAMEFEDGDFDEPMEVE EVDLEP	none	DNA polymerase alpha catalytic subunit	12.24	7.2	15.5	7.34	within
e025944	GFPDPGPPGEPGPAGQDGP PGDKGDDG EPGQTGSPGPTGEPG*	7xOxidation [P14; P20; P21; P30; P36; P38; P42]	Collagen alpha-1(V) chain	12.31	7.05	15.24	11.46	within
e025947	NDGARGSDGQPPGPPGTAGFP GSPGA KGEVGPAGSPGSNGAPG*	7xOxidation [P16; P17; P23; P26; P34; P38; P44]	Collagen alpha-1(III) chain	12.16	7.72	13.76	13.59	within
e025949	EVGKPGERGLHGEFGLPGAGPRGERGPP GESGAAGPTGPIG*	3xOxidation [P5; P17; P19]	Collagen alpha-2(I) chain	8.12	2.65	11.71	11.25	within
e025951	PSAQGGSAEEEEEDGAEESTLKDSSEKDG LSEVDTVAADP	none	E3 ubiquitin-protein ligase HECW1	11.85	7.64	13.43	13.69	up
e215804	TSGQSSTFDQEGSSTGQSSSHGQHGS GS SQSSSYGQQGSGSG	none	Homerin	9.12	3.13	12.73	10.1	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e025956	GEPGRDGVPGGPGMRGMPGSPGGPGSD GKPGPPGSQGSESRPGP*	2xOxidation [P]	Collagen alpha-1(III) chain	10.16	3.34	14.92	14.63	within
e215806	SGASGERGPPGPMGPPGLAGPPGESGRE GAPGAEGSPGRDGSPGA*	2xOxidation [P31; P37]	Collagen alpha-1(I) chain	9.65	3.03	14.31	13.86	within
e105090	PEGGKGAAGPPGPPGAAGTPGLQGMPGE RGLGLSPGPKGDKGEPG*	1xAcetylation [N-Term]; 1xOxidation [P]	Collagen alpha-1(III) chain	7.71	1.36	10.54	7.69	within
e103507	HSKEVSEAEPGGGSSGDSGPPEESGQEM MEEKEIRKS	none	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	6.87	2.24	12.61	11.66	within
e025972	ARGNDGQPGPAGPPGPVGPAGGPGFPGA PGAKGEAGPTGARGPEGA*	3xOxidation [P13; P14; P16]	Collagen alpha-1(II) chain	5.53	0.87	11.35	7.85	within
e025983	SPGTPAPAAEETMTNSPGTPAPAAEETMTT SPGTPAPAAEET	none	Tumor necrosis factor receptor superfamily member 10C	11.41	6.7	13.09	13.57	up
e105194	DGQPGPKGNVGPQGEPGPPGQQGNPGA QGLPGPQGAIGPPGE*	11xOxidation [P4; P6; P12; P16; P18; P19; P25; P31; P33; P39; P40]	Collagen alpha-1(V) chain	11.17	6.56	13.28	13.52	up
e215822	VIKGARDSHAGLYMWHLVGHQRNNRQVTL EVSGAEP	none	Secreted and transmembrane protein 1	6.02	1.29	12.55	5.69	within
e025994	KDLHDDDEDEEMLETADGESMNTESNQG STPSDQQ	none	Protein phosphatase inhibitor 2 family member B	11.83	6.67	14.97	13.65	within
e104538	PQGPSGLPGIPGEEGKEGRDGKPGPPGEP GKAGEPGLPGPE*	9xOxidation [P1; P4; P8; P11; P23; P25; P26; P29; P35]	Collagen alpha-1(XXII) chain	11.17	5.88	13.4	13.47	up
e103659	GLGGNFAAQMAGGFDEKAGGAQLGVMQG PMGPMGPRGPPGPAG*	2xOxidation [P39; P]	Collagen alpha-1(II) chain	10.54	5.09	12.8	12.08	within
e026007	EQTPLYSADPNAIDTDYYPGGYDIESDFPPP PEDFP	none	Protocadherin Fat 1	6.95	2.56	11.2	8.76	within
e026010	GEPGRDGNPGSDGLPGRDGSPGGKGDRG ENGSPGAPGAPGHGPG*	2xOxidation [P]	Collagen alpha-1(III) chain	7.02	1.2	10.74	7.79	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026015	GGAEPGADSAEGDVGDDGDFGAGVNKD GGSRVVVQMEEVAR	none	Matrix metalloproteinase-15	6.36	2.84	8.43	8.57	up
e026017	QTFPIQDPDQMHSTSDPSHRSSSELMSEML EYDRS	none	Coagulation factor V	6.59	1.89	9.74	9.12	within
e026037	QGPPGPPGRDGTGPRDGEPPGDEGKPG GDTGPPQGFPGTPGD*	4xOxidation [P4; P6; P7; P13]	Collagen alpha-1(XVIII) chain	9.69	5.18	12.16	10.58	within
e026038	GETGPHGYKGMVGAIGATGPPGEEGPRGP PGRAGEKGDEGSPG*	1xOxidation [P]	Collagen alpha-2(IX) chain	9.02	4.31	11.72	10.48	within
e026041	GEAGRPGSSGSPSGDEGQPGEPGPPGEKG EAGDEGNPGPDGAPGE*	3xOxidation [P6; P11; P18]	Collagen alpha-1(VI) chain	12.38	6.35	15.34	15.42	up
e101983	GNSGEKGDQGFQGGQPGFPGPPGPPGFPG KVGSPGPPGPQAEK*	3xOxidation [P18; P20; P21]	Collagen alpha-1(XVI) chain	6.88	1.83	10.33	9.59	within
e215837	GELGPQGPTGPPGAKGQEGAHPGAAG NPGAPGHVGAHPGSPGPPGS*	2xOxidation [P33; P39]	Collagen alpha-1(XXII) chain	6.52	2.03	9.6	9.29	within
e026047	DADLADGVSGGEGKGGSDGGGSHRKEGE EADAPGVIPGIVGAVV	none	CD99 antigen	14.4	10.92	16.05	16.02	within
e026049	RGREGPMGPRGEAGPPGSGEKGERGAAG EPGPHGPPGVPGSVG*	3xOxidation [P6; P9; P15]	Collagen alpha-1(XVII) chain	13.68	11.14	15.23	15.33	up
e215839	PGFPGERGQKDEGPPGISIPGPPGLDGQ PGAPGLPGPPGPAG*	7xOxidation [P4; P15; P16; P21; P23; P24; P30]	Collagen alpha-5(IV) chain	11.47	7.85	13.78	13.06	within
e026057	EEKAVADTRDQADGSRASVDSGSSEEQGG SSRALVSTLVP	none	Polymeric immunoglobulin receptor	11.41	5.8	13.93	14.24	up
e026062	RGENGSPGAPGAPGHPGPPGVPGPAGKS GDRGESGPAGPAGAPGPAG*	2xOxidation [P10; P13]	Collagen alpha-1(III) chain	10.27	4.31	12.86	14.12	up
e026076	VTGIRGRPGPAGPPGSGQPRGERGPKGRP GPRGPQGIDGEP*	3xOxidation [P25; P29; P31]	Collagen alpha-2(V) chain	4.86	0.35	14.69	6.36	within
e215847	ERGEQGRDGPPLPGTPGPPGPPGPKVSV DEPGPGLSGEQGP*	3xOxidation [P10; P11; P14]	Collagen alpha-1(VII) chain	7.03	2.98	10.88	9.79	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e206564	GAVGEKGEPGEAGEPGLPGEGGPPGPKG ERGEKGESGPSGAAGPP*	1xOxidation [P]	Collagen alpha-1(V) chain	5.27	0.06	10.85	4.22	within
e215851	DKGESGPSGPAGPTGARGAPGDRGEPGP PGPAGFAGPPGADGQP*	10xOxidation [P7; P10; P13; P20; P26; P28; P29; P31; P37; P38]	Collagen alpha-1(I) chain	10.63	5.47	12.94	12.87	within
e026095	RGNDGARGSDGQPPGPPPGTAGFPGSP GAKGEVGPAGSPGSNGA*	7xOxidation [P13; P15; P16; P18; P19; P25; P28]	Collagen alpha-1(III) chain	10.09	5.12	12.37	11.69	within
e215852	RSGSGSQSPSYGRHSGSGRSSSSGRHG SGSGQSSGFHKSSS	none	Hornerin	8.32	3.96	11.3	10.4	within
e026099	GPRGPPGPAGAPGPQGFQGNPGEPGEPG VSGPMGPRGPPGPPG*	12xOxidation [P5; P6; P8; P12; P14; P21; P24; P27; P32; P35; P38; P39]	Collagen alpha-1(II) chain	10.79	5.44	13.27	11.63	within
e026102	FAEEKAVADTRDQADGSRASVDSGSSEEQ GGSSRALVSTL	none	Polymeric immunoglobulin receptor	10.58	3.92	14.7	11.98	within
e215857	KGDQGPDPGSPGSPGPAGPAGPPGYG PQGEPLQGTQGVPGAPG*	1xOxidation [P]	Collagen alpha-3(IV) chain	9.07	3.02	14.25	10.28	within
e215858	GDVTAEEAAGASPAKANGQENGHVKSNGD LSPKGEGESPPVN	none	MARCKS-related protein	7.22	3.18	13.57	10.37	within
e215859	PGKDGPPGPAGNTGAPGSPGVSGPKGDA GQPGEKGSPGAQGPAGP*	3xOxidation [P42; P43; P]	Collagen alpha-1(III) chain	5.67	0.0	11.88	6.23	within
e099792	GNDGARGSDGQPPGPPPGTAGFPGSPG AKGEVGPAGSPGSNGAPG*	8xOxidation [P15; P17; P18; P24; P27; P35; P39; P]	Collagen alpha-1(III) chain	8.99	4.15	12.04	11.92	within
e026120	GEGGEAEAPAAEGGKDEAAGGAAAAAAEA GAASGEQAAAPGEEAAAGE	none	Myristoylated alanine-rich C-kinase substrate	9.61	4.65	12.5	12.36	within
e101938	GPPGEKGETGDVGQMGPPGPPGPRGSPG APGADGPQGPPGGIGNPG*	1xOxidation [P30]	Collagen alpha-1(V) chain	6.59	1.73	9.9	9.55	within
e215862	AGYPGPAGPPGPPGPPGTSGHPGSPGSP GYQPPGEPGQAGPSGPP*	3xOxidation [P6; P9; P]	Collagen alpha-1(III) chain	8.71	2.59	12.37	11.95	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026126	SKGESGNKGEPGSAGPQQPPGPSGEEGKRGPNGEAGSAGPPGPPG*	3xOxidation [P16; P19; P]	Collagen alpha-2(I) chain	8.66	4.33	12.2	11.92	within
e026131	PGERGETGPPGPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGP*	3xOxidation [P9; P10; P]	Collagen alpha-1(II) chain	9.55	4.47	12.65	11.76	within
e101781	VGEVGAAGEAGGTGEAGATGEAGAAGEAGGAGEAGGVGEAGAAGEAGGAGEA	none	Paraneoplastic antigen Ma6E	12.05	5.3	14.52	13.3	within
e215865	GPPGIAGMSGKPGAPGPPGVPGEPPERGPVGDIGFPGPEGPSGKP*	1xOxidation [P2]	Collagen alpha-1(XIX) chain	5.92	0.08	12.44	2.2	within
e215866	SGSGNPNPQGWPGAWGNQAGAGGYPGASYPGAYPGQAPPGAY	none	Galectin-3	11.92	6.05	14.38	13.02	within
e026138	GPPGEPGPAGQDGPDPKDDGEPGQTGSPGPTGEPGPSGPPGK*	9xOxidation [P14; P15; P24; P30; P32; P36; P38; P41; P42]	Collagen alpha-1(V) chain	4.35	1.08	10.98	3.61	within
e102780	EKAVADTRDQADGSRASVDSGSSEEQGGSRLVSTLVPLG	none	Polymeric immunoglobulin receptor	7.23	3.03	11.54	5.53	within
e026153	ERGETGPPGPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQG*	2xOxidation [P23; P41]	Collagen alpha-1(II) chain	12.77	8.67	14.6	14.46	within
e026155	PGPAGPPGPPGPPGTSGHPGSPGSPGYQGPPGEPGQAGPSGPPGPPG*	3xOxidation [P6; P]	Collagen alpha-1(III) chain	12.35	8.14	14.1	14.61	up
e026160	VEEDVQEEQSKEASDPESNEEEGDSSGGE DTEESDSPD	none	Nucleolar protein 14	7.0	1.93	11.47	8.44	within
e100317	SEGARGAPGPAGPPGDPGLMGERGEDGPAAGNGTEGFPGFPGYP*	4xOxidation [P10; P13; P14; P17]	Collagen alpha-1(VI) chain	10.07	4.18	12.29	11.34	within
e026163	GPSGAPGADGPQGGPPGGIGNPGAVGEKEGEPGEAGEPGLPGEGGPPGP*	4xOxidation [P36; P39; P44; P45]	Collagen alpha-1(V) chain	12.39	9.07	14.12	13.7	within
e026169	GAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPPGP*	2xOxidation [P45; P]	Collagen alpha-1(I) chain	7.84	2.94	10.83	4.58	within
e026170	NGHVKNVDASPAAAESGAKEELQANGSA PAADKEEPAAAGSGA	none	Myristoylated alanine-rich C-kinase substrate	9.2	3.99	11.38	10.85	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e206595	GTTPSPVPTTSTISVPTTSTTSASTTSTTSAS TTSTTSGPGTTP	none	Mucin-5AC	9.06	1.58	11.66	11.2	within
e100925	PPGPVGPSPGKDGANGIPGPIGPPGPRGRS GETGPAGPPGNPGPP*	11xOxidation [P1; P2; P4; P7; P17; P19; P22; P23; P25; P34; P37]	Collagen alpha-1(II) chain	7.21	2.85	11.0	7.84	within
e101963	EGPKGSKGERGYPGIPGEKGDEGLQGIPGI PGAPGPTGPPGL*	8xOxidation [P13; P16; P28; P31; P34; P36; P39; P40]	Collagen alpha-1(XIX) chain	6.09	1.79	9.54	8.41	within
e096355	SKGESGNKGEPGSAGPQGPSPGSGEKG RGPNGEAGSAGPPGPPG*	5xOxidation [P11; P16; P19; P20; P22]	Collagen alpha-2(I) chain	11.04	6.63	12.82	13.03	up
e026186	GPMGPPGLAGPPGESGREGAPGAEGSPG RDGSPGAKGDRGETGPA*	4xOxidation [P12; P21; P27; P33]	Collagen alpha-1(I) chain	10.6	5.78	12.23	12.9	up
e099850	VGPPGPPGPPGPPGPPSAGFDFSFLPQPP QEKAHDGGRYY*	3xOxidation [P4; P6; P13]	Collagen alpha-1(I) chain	7.44	3.56	10.14	10.77	up
e104711	RPGSSGSPGDEGQPGEPGPPGEKGEAGD EGNPGPDGAPGERGGPG*	1xOxidation [P]	Collagen alpha-1(VI) chain	10.04	4.06	12.92	7.61	within
e215884	PGLAGTAGEPGRDGNPGSDGLPGRDGSP GGKGDRGENGSPGAPGAP	none	Collagen alpha-1(III) chain	8.4	1.29	13.34	12.56	within
e026197	NPGPVGFPGDPGPPGEPGAGQDGVGGD KGEDGDPGQPGPPGSPG*	6xOxidation [P4; P8; P11; P13; P14; P17]	Collagen alpha-1(XI) chain	9.86	3.91	12.42	8.66	within
e104264	KGNPGPVGFPGDPGPPGEGGPRGQDGAK GDRGEDGEPGQPGSPG*	2xOxidation [P6; P10]	Collagen alpha-2(XI) chain	8.99	3.51	11.87	13.02	up
e026198	SPGERGETGPPGPAGFPAGQNGEPGG KGERGAPGEKGEKGPPG*	2xOxidation [P43; P44]	Collagen alpha-1(III) chain	7.9	2.39	13.24	8.53	within
e105511	GERGGPGGPGPQGPKNGETGPQGPPG PTGPGGDKGDTGPPGPQ*	8xOxidation [P11; P14; P15; P23; P26; P27; P29; P]	Collagen alpha-1(III) chain	9.69	4.35	12.5	7.66	within
e026215	SKGESGNKGEPGSAGPQGPSPGSGEKG RGPNGEAGSAGPPGPP*	10xOxidation [P11; P16; P19; P20; P22; P31; P40; P41; P43; P44]	Collagen alpha-2(I) chain	9.3	4.17	12.25	9.15	within
e026221	QQTGGRGGGRGGYEHSSYGGRGHEQG GGRGGRGYDHGGRGG	none	Protein FAM98A	6.49	2.2	9.7	8.53	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026222	GPSGSPGKDGPPGPAGNTGAPGSPGVSG PKGDAGQPGEKGSPGAQGP*	7xOxidation [P12; P14; P21; P24; P29; P36; P42]	Collagen alpha-1(III) chain	6.38	2.54	9.73	7.54	within
e026233	GLYHTGANVESFSSSTRPGQMEISFLPEFGI SSADNAFT	none	Lengsin	5.87	2.09	10.97	10.27	within
e103535	ERGEQGPAGSPGFQGLPGPAGPPGEAGK PGEQGVPGDLGAPGPSG*	5xOxidation [P19; P22; P23; P]	Collagen alpha-1(I) chain	10.32	5.02	13.19	12.4	within
e215902	GLAGYPGPAGPPGPPGPGTSGHPGSPGS PGYQGPPEPGQAGPSGP*	3xOxidation [P8; P11; P12]	Collagen alpha-1(III) chain	10.11	4.94	12.85	11.72	within
e026245	VEVSETADNSTNDIADDSTYVTADNPTDDT ATQPNFPGGN	none	BEN domain-containing protein 2	7.29	2.26	10.34	10.2	within
e104999	GEIGEPGQKGSKGDKGNGPPGPPGLQGP VGAPGIAGGDGEPGPR*	2xOxidation [P33; P42]	Collagen alpha-1(XI) chain	9.35	5.47	12.47	11.4	within
e215905	DAGAPGAPGGKGDAGAPGERGPPGLAGA PGLRGGAGPPGPEGGKAAGP*	6xOxidation [P17; P22; P23; P29; P37; P38]	Collagen alpha-1(III) chain	13.79	9.13	16.11	14.37	within
e026250	EEKAVADTRDQADGSRASVDSGSSEEQGG SSRALVSTLVPL	none	Polymeric immunoglobulin receptor	13.94	9.24	16.12	14.34	within
e026252	VGEKGEPGEAGNPGPPGEAGVGGPKGER GEKGEGAPPGAAGPPGAK*	3xOxidation [P24; P36; P37]	Collagen alpha-1(XI) chain	13.55	10.09	15.35	13.29	within
e215907	GPRGEPGTPGSPGPAGASGNPGTDGIPGA KGSAGAPGIAGAPGFPGPR*	2xOxidation [P42; P]	Collagen alpha-1(II) chain	13.47	9.93	15.33	13.39	within
e026264	SNGADLSGVTEEAPLKLKSAVHKAVLTIDEK GTEAAGAMFL	none	Alpha-1-antitrypsin	3.57	0.06	12.52	9.91	within
e215917	SMGPVGGPPGAGERGHPGAPGSPGSPGL PGVPGSMGDMVNYDEI*	2xOxidation [P]	Collagen alpha-1(XVI) chain	12.97	9.17	15.19	14.53	within
e215920	DVGPMGPPGPPGPRGPQGPNGADGPQGP PGSVGSGVGGVGEKGEPGE*	2xOxidation [P28; P29]	Collagen alpha-1(XI) chain	12.54	8.91	14.57	14.31	within
e026273	FQGEPPGQGEPPGDRGLKGDNGVGQP GLPGAPGQGGAPGPPGL*	3xOxidation [P40; P42; P]	Collagen alpha-2(VIII) chain	9.19	4.31	11.15	10.71	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215924	AGAEDRMAGAPMAAAVQPAEVTVEVGEDLHMHQVRDREM	none	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 9	6.88	3.67	10.04	10.4	up
e026296	GREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPA*	2xOxidation [P12; P18]	Collagen alpha-1(I) chain	8.51	4.32	11.7	10.8	within
e215931	SRGENGPTGAVGFAGPQQPDGQPGVKGEPGEPGQKGDAGSPGPQG*	3xOxidation [P]	Collagen alpha-2(V) chain	9.87	5.02	12.51	9.84	within
e026299	PAGKDGEAGAQQPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEA*	2xOxidation [P13; P]	Collagen alpha-1(I) chain	10.09	4.0	12.68	12.62	within
e026303	RGFGGASGGYSSSGGFGGGFGGGSGGGFGGGYGSGFGGFGGFGGGAGGGDG	none	Keratin, type I cytoskeletal 9	9.07	3.51	12.2	13.5	up
e026306	ELVAEPADPEEAKSTEDQEENEEDKEEEEKEEDSEE	none	Coiled-coil domain-containing protein 136	7.15	2.66	11.14	10.88	within
e215936	GSPGGPGAAGFPGARGLPGPPGSNGNPGPPGPSGSPGKDGPPGPAGNT*	7xOxidation [P20; P21; P27; P29; P30; P32; P36]	Collagen alpha-1(III) chain	7.93	3.28	11.13	10.83	within
e215938	PGPAGSKGESGNKGEPGSAGPQGPGPSGEEGKRGNGEAGSAGPPG*	2xOxidation [P3; P16]	Collagen alpha-2(I) chain	6.33	1.34	10.08	10.61	up
e026314	TVNFGDTEEAKKQINDYVEKGTQGGKIVDLVKELDRDT	none	Alpha-1-antitrypsin	9.53	0.0	15.57	10.61	within
e100829	GFPDGPDPGPPGEPGPAGQDGPDPKGGDDGEPGQTGSPGPTGEPGPSG*	4xOxidation [P]	Collagen alpha-1(V) chain	10.43	5.49	13.22	14.74	up
e026319	EPGADGEAGRPGSSGSPSGDEGQPGEPGPGEKGEGAGDEGNPGPDGA*	1xOxidation [P23]	Collagen alpha-1(VI) chain	10.41	5.05	13.37	14.61	up
e026325	GAPGFPGARGPSGPQGPGGPPGPKGNSEPGAPGSKGDTGAKGEPGPV	none	Collagen alpha-1(I) chain	4.92	1.11	10.83	8.31	within
e102424	QTGPRGEMGQPGPSGERGLAGPPGREGIPGPLGPPGPPGSGVGP*	7xOxidation [P11; P13; P22; P23; P29; P31; P34]	Collagen alpha-1(VII) chain	11.44	6.09	14.3	11.35	within
e026350	EEKAVADTRDQADGSRASVDSGSSEEQGGSSRALVSTLVPLG	none	Polymeric immunoglobulin receptor	15.52	10.22	17.48	14.54	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026354	GDFGLKGEPGRKGEKGEPADPGPPGEPGRGPRGVPGPEGEPPG*	3xOxidation [P24; P27; P]	Collagen alpha-2(VI) chain	15.07	10.85	16.77	14.35	within
e026364	TASTADSETTSASTTGSETTTASTTSSETTTASTEGSETTVST	none	Mucin-22	7.73	2.68	11.41	8.55	within
e026369	GPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTGSPGPAG*	2xOxidation [P35; P39]	Collagen alpha-1(II) chain	10.63	6.03	12.81	11.33	within
e215959	PGPVGPAGGPGFPGAPGAKGEAGPTGAR GPEGAQGPRGEPGTGSPGP*	4xOxidation [P6; P10; P]	Collagen alpha-1(II) chain	10.23	4.59	12.74	11.06	within
e102782	AEEKAVADTRDQADGSRASVDSGSSEEQGSSRALVSTLVPL	none	Polymeric immunoglobulin receptor	8.5	3.45	12.21	11.73	within
e026380	KANDESNEHSDVIDSQELSKVSREFHSHEFHSHEDM	none	Osteopontin	7.26	1.71	12.35	10.05	within
e026381	ARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPRGSEGPQG*	3xOxidation [P22; P]	Collagen alpha-1(I) chain	11.16	5.71	13.59	12.63	within
e026382	IGTDGTPGAKGPTGSPGTSGPPGSAGPPGSPGPQGSTGPQGIRGQPGD*	2xOxidation [P]	Collagen alpha-2(V) chain	10.63	4.71	12.68	12.09	within
e026405	ARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPRGSEGPQG*	4xOxidation [P22; P23; P]	Collagen alpha-1(I) chain	12.21	7.54	14.11	13.18	within
e026408	KGDRGENGSPGAPGAPGHPGPPGPVGPA GKSGDRGESGPAGPAGAPGP*	4xOxidation [P24; P27; P39; P42]	Collagen alpha-1(III) chain	11.9	7.62	13.65	12.74	within
e026409	GQPGSMGLPGPKGSSGDPGKPGGEAGNAGVPGQRGAPGKDGEVGPSPGP*	3xOxidation [P]	Collagen alpha-2(V) chain	9.07	3.26	12.44	10.94	within
e215968	GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPG*	9xOxidation [P9; P11; P18; P20; P21; P23; P24; P]	Collagen alpha-1(I) chain	12.01	6.8	15.31	5.07	down
e026430	FAEEKAVADTRDQADGSRASVDSGSSEEQGGSSRALVSTLVP	none	Polymeric immunoglobulin receptor	8.83	2.75	13.02	13.71	up
e026433	GERGETGPPGPAGFAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGP*	3xOxidation [P18; P24; P42]	Collagen alpha-1(II) chain	7.71	2.23	10.94	8.54	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e215977	GQQQGNPGLGTPWVHGYPGNSAGSFG MNPQGAPWGQGGNGGPPN	none	Dermokine	6.13	2.87	9.25	6.72	within
e026439	GAKGEAGPQGPRGSEGPQGVGEPPG PAGAAGPAGNPGADGQPGAK*	3xOxidation [P35; P39; P]	Collagen alpha-1(I) chain	5.13	1.3	11.73	4.57	within
e215978	PPGTAGFPSPGAKGEVGPAGSPGSNGAP GQRGEPGPQGHAGAQQPPG*	4xOxidation [P19; P23; P29; P35]	Collagen alpha-1(III) chain	10.71	6.22	12.74	9.28	within
e215979	ARGNDGATGAAGPPGPTGPAGPPGFPGAV GAKGEAGPQGPRGSEGPQ*	9xOxidation [P14; P16; P19; P22; P23; P26; P37; P40; P]	Collagen alpha-1(I) chain	10.53	5.24	12.87	9.91	within
e105109	GPTGARGAPGDRGEPGPPGPAGFAGPPG ADGQPGAKGEPGDAGAKGD*	9xOxidation [P2; P9; P15; P17; P18; P20; P26; P27; P33]	Collagen alpha-1(I) chain	7.33	3.01	11.73	7.19	within
e026452	IQDPRLFAEEKAVADTRDQADGSRASVDSG SSEEQGGSSRA	none	Polymeric immunoglobulin receptor	11.02	5.24	13.95	14.03	up
e102885	GTPGVAGPSGEPGMPGKDGQNGVPLDG QKGEAGRNGAPGEKGPNG*	5xOxidation [P12; P15; P24; P39; P]	Collagen alpha-3(IX) chain	9.84	5.56	12.89	13.49	up
e099797	AEEKAVADTRDQADGSRASVDSGSSEEQG GSSRALVSTLVPLG	none	Polymeric immunoglobulin receptor	10.05	5.38	12.87	9.25	within
e215987	GPPGPAGFAGPPGADGQPGAKGEQGEAG QKGDAGAPGPQGPSGAPGPQG*	3xOxidation [P41; P45; P]	Collagen alpha-1(II) chain	14.64	11.93	16.23	15.78	within
e026466	AGARGNDGATGAAGPPGPTGPAGPPGF GAVGAKGEAGPQGPRGSEGP*	10xOxidation [P15; P16; P18; P21; P24; P25; P28; P39; P42; P48]	Collagen alpha-1(I) chain	14.31	11.75	15.81	15.59	within
e026467	PGPAGFAGPPGADGQPGAKGEPGDAGAK GDAGPPGPAGPAGPPGPIGNV*	8xOxidation [P22; P33; P34; P36; P39; P42; P43; P45]	Collagen alpha-1(I) chain	7.83	1.38	11.55	5.82	within
e026470	GETLGADSDLSSNAGDGPGEGBSVHLASS RGTLSDSEIETNSATS	none	MAP kinase-activating death domain protein	12.47	8.02	14.01	11.76	within
e026477	PRGPPGSAGAPGKDGLNGLPGPIGPPGPR GRTGDAGVPVGPVPPGPPG*	2xOxidation [P]	Collagen alpha-1(I) chain	6.14	0.25	14.87	3.15	within
e026489	VDAEGPAGDSVDAEGRVGDSVEAGDPAG DGVEAGVPAGDSVEAEGPA	none	Chloride intracellular channel protein 6	14.41	11.78	15.67	15.95	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026490	GPPGPPGPRGPAGPNGADGPQGPPGGVG NLGPPGEKGEPEGESGSPGIQ*	3xOxidation [P]	Collagen alpha-2(XI) chain	6.44	0.4	12.33	6.44	within
e026492	QPGVMGFPGPKGNDGAPGKNGERGGPGG PGPQQPPGKNGETGPQG*	10xOxidation [P2; P8; P10; P17; P26; P29; P31; P34; P35; P43]	Collagen alpha-1(III) chain	14.14	11.95	15.33	15.73	up
e026493	APGERGETGPPGPAGFAGPPGADGQPGA KGEQGEAGQKGDAGAPGPQG*	1xOxidation [P]	Collagen alpha-1(II) chain	5.89	1.66	12.61	6.19	within
e026496	SPGAKGEVGPAGSPGSNGAPQQRGEGP QGHAGAQQPPGPPGINGSP*	10xOxidation [P2; P10; P14; P20; P26; P28; P37; P38; P40; P41]	Collagen alpha-1(III) chain	12.5	8.03	13.83	9.92	within
e026497	TYDLYTIPKDADSQNPDAPGKRSSGLTAV WVARNRFAV	none	Coatomer subunit alpha	3.66	0.61	8.35	2.23	within
e215999	QPDPPAPFTPSPLPRLANQDSRPVFTSPTP AMAAVPTQPQS	none	Seizure protein 6 homolog	10.38	4.8	13.25	12.07	within
e099960	GAPGQPGMAGVDGPPGPKGNMGPQGEP GPPGQQGNPGPQGLPGPQG*	3xOxidation [P3; M8; P17]	Collagen alpha-1(XI) chain	5.42	0.14	12.34	10.74	within
e026518	QGLPGPPGEKGENGDVGPMGPPGPPGPR GPQGPNGADGPQGPPGSVG*	3xOxidation [P4; P6; P7]	Collagen alpha-1(XI) chain	10.45	2.43	15.42	12.35	within
e216009	GERGGPGGPGPQGPPEGKNGETGPQGP PTGPGGDKGDTGPPGPQGLQ*	1xOxidation [P9]	Collagen alpha-1(III) chain	9.36	1.64	14.21	11.52	within
e026522	TGPPGPVGSPLPGAIGTDGTPGAKGPTG SPGTSGPPGSAGPPGSPGPQG*	8xOxidation [P4; P6; P10; P13; P22; P27; P31; P]	Collagen alpha-2(V) chain	8.24	3.3	13.12	12.72	within
e026527	PSEGGSSSTMYVSGPPGPPGPPGPPGIS SSGQEIQQYISEYM*	3xOxidation [P16; P18; P19]	Collagen alpha-1(XVII) chain	12.06	7.34	14.69	9.9	within
e026530	GFGSGYGGGFGGGFGGGRGMGGGFGGA GGFGGAGGFGGAGGFGGPGGFGGSGGF	none	Keratin, type II cytoskeletal 3	11.81	6.46	14.35	10.39	within
e026533	KGEKGEPGADGEAGRPGSSGSPSGDEGQP GEPGPPGEKGEAGDEGNP*	3xOxidation [P7; P16; P21]	Collagen alpha-1(VI) chain	7.7	3.12	11.45	8.32	within
e026540	PQVQYHNDKYISNTSGEDEKTHPGFQQMP EDKEDESE	none	Dystonin	8.21	3.02	11.92	12.38	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e206759	GAPGQPGMAGVDGPPGPKGNMGPPQGEPPGGQQGNPGPQGLPGPQGP*	4xOxidation [P3; P6; P14; P47]	Collagen alpha-1(XI) chain	4.16	1.23	8.82	4.83	within
e105208	GEVGPAAGSPGSGAPGQRGEPGPQGHAGAQGPPGPPGINGSPPGKGEMG*	1xOxidation [P33]	Collagen alpha-1(III) chain	8.68	3.25	11.28	10.04	within
e026556	GRTGPPGPGSGISGPPGPPGPAGKEGLRGP RGDQQPVGRTGEVGAVGP*	3xOxidation [P20; P29; P35]	Collagen alpha-2(I) chain	5.54	2.75	13.19	4.15	within
e026563	GPQGGPPGPPGRDGTGRDGEPPGDPGEDG KPGDTGPQGFPGTGPDV*	7xOxidation [P6; P8; P9; P15; P21; P24; P]	Collagen alpha-1(XVIII) chain	11.9	6.16	14.3	10.63	within
e216023	YRGDEGPPGSEGARGAPGAPGPPGDPGL MGERGEDGPAGNGTEGF*	6xOxidation [P7; P8; P17; P19; P22; P23]	Collagen alpha-1(VI) chain	11.38	5.6	14.09	9.09	within
e216027	GDQGNIGKIGETGPVGLPGEVGMTGSIGEK GERGSPGLGPQGEK*	3xOxidation [P18; P36; P38]	Collagen alpha-1(XXIV) chain	6.88	2.96	11.55	7.27	within
e300025	KANDESNEHSDVIDSQELSKVSREFHSHEF HSHEDML	none	Osteopontin	7.92	0.73	12.88	9.96	within
e026572	AIQDPRLFAEEKAVADTRDQADGSRASVDS GSSEEQGGSSRA	none	Polymeric immunoglobulin receptor	12.37	7.47	15.18	15.09	within
e026574	PPGSNGNPGPPGSPGSGKDGPPGPAGN TGAPGSPGVSGPKGDAGQPGE*	8xOxidation [P11; P13; P17; P22; P23; P25; P32; P35]	Collagen alpha-1(III) chain	8.7	3.77	12.69	10.33	within
e026578	EGPQQQRGETGPPGPVGSPLPGAIGTDG TPGAKGPTGSPGTSGPPGSA*	3xOxidation [P12; P13; P15]	Collagen alpha-2(V) chain	11.05	5.87	14.79	14.11	within
e026580	VGEKGDGRGMMGPPGVGPKGSMGHGPM PGGMGTPGEPGPQGPPGS*	11xOxidation [P12; P13; P16; P18; P25; P28; P34; P37; P39; P42; P43]	Collagen alpha-1(XXVII) chain	14.09	9.4	16.71	16.86	up
e026581	AGEAGAAGEGGAAGEAGGAGEAGGVGEA GAAGEAGGAGEAGGVGEAGAAGEAGGAG E	none	Paraneoplastic antigen Ma6E	7.81	3.37	11.46	10.36	within
e216034	FSGALPDDEDVVGPGQESDDFELSGSGDL DDLEDSMIGPEVV	none	Syndecan-4	14.12	9.45	16.71	16.87	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026584	VQQIEMESKEPDDQDAPDEHESPPPEDA PLYPHSPGSQ	none	Ubiquitin carboxyl-terminal hydrolase 9X	14.16	9.81	16.66	16.84	up
e026586	LTPTPTAAMPETSEGAGKEEDVGIGDYD YVPSEDYYTP*	4xOxidation [P5; P10; P12; P33]	Collagen alpha-1(V) chain	12.83	8.6	15.08	14.56	within
e100911	GDPGVSGIDGSPGEKGDPGDVGGPGPPG ASGEPGAPPPGKRGPSGHMG*	3xOxidation [P33; P36; P38]	Collagen alpha-3(V) chain	6.28	2.69	12.79	8.45	within
e026592	GLAGYPGPAGPPGPPPGTSGHPGSPGS PGYQGPPEPGQAGPSGPP*	10xOxidation [P6; P8; P11; P12; P14; P15; P17; P18; P24; P27]	Collagen alpha-1(III) chain	7.96	3.57	11.76	12.25	up
e103208	PGDDGPKGSPGPVGFPGDPGPPGEPGA GQDGGPKGDDGEPGQTG*	6xOxidation [P1; P6; P10; P12; P16; P19]	Collagen alpha-1(V) chain	12.5	6.88	15.54	12.0	within
e105035	AGQDGPBGDKGDDGEPGQTGSPGPTGEP GPSGPPGKRPPGAGPEG*	9xOxidation [P22; P24; P28; P30; P33; P34; P39; P40; P42]	Collagen alpha-1(V) chain	12.71	8.08	15.64	11.97	within
e026613	GDPGSPGSPGAPGAGPPGYGPQGEPL QGTQGVGPAGPPGEAGPRGE*	3xOxidation [P22; P26; P35]	Collagen alpha-3(IV) chain	8.26	3.18	11.67	11.87	up
e026617	LQDEERSFFPTMEEMFGGGAADDYGKAGP PEDEGDPKAGAGP	none	Proline-rich protein 12	9.43	4.74	12.26	8.81	within
e216041	KGDRGENGSPGAPGAPGHPGPPGPVGPA GKSGDRGESGPAGPAGAPGPA*	7xOxidation [P13; P16; P19; P21; P22; P24; P27]	Collagen alpha-1(III) chain	8.43	3.8	12.01	11.56	within
e102010	TSGHPGSPGSPGYQGPPEPGQAGPSGP PGPPGAIGSPGAGKDGESG*	11xOxidation [P8; P11; P16; P17; P20; P25; P28; P29; P31; P32; P37]	Collagen alpha-1(III) chain	7.79	2.67	11.6	8.22	within
e026622	FGGGYGGGGFGGGGFGGGGFGGGGIGG GGFGGFGSGGGFGGGGFGGGGYGGGY GP	none	Keratin, type II cytoskeletal 1	8.45	2.34	12.38	9.69	within
e104616	PQTPHTTHSPPTAGSPVPSTGPVTATSFHA TTTYPTPSHPETT	none	Mucin-6	9.23	4.95	12.66	8.08	within
e105099	GEAGRPGSSGSPGDEGQPGEPGPPGEKG EAGDEGNPGPDGAPGERGGP*	1xOxidation [P]	Collagen alpha-1(VI) chain	5.36	2.17	12.35	10.15	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026623	FAEEKAVADTRDQADGSRASVDSGSSEEQ GGSSRALVSTLVPL	none	Polymeric immunoglobulin receptor	11.95	6.62	14.96	14.63	within
e026624	GPPGEPGPAGQDGP PGDKGDDGEPGQTG SPGPTGEPGSPGPPGKRGP*	8xOxidation [P15; P24; P30; P32; P36; P38; P41; P42]	Collagen alpha-1(V) chain	8.24	3.19	12.23	11.98	within
e026625	GPRGLPGTPGTDGPKGASGPAGPPGAQG PPGLQGMPGERGAAGIAGPK*	8xOxidation [P2; P6; P9; P14; P20; P23; P24; P29]	Collagen alpha-1(II) chain	12.46	6.2	15.04	14.62	within
e026639	APGDRGEPGPPGPAGFAGPPGADGQPGA KGEPGDAGAKGDAGPPGPAGPA*	5xOxidation [P20; P26; P32; P43; P]	Collagen alpha-1(I) chain	7.33	1.61	12.61	5.42	within
e102257	TEAAPMPETSEGAGKEEDVGIGDYDYVPSE DYYPSPYDD*	2xOxidation [P7; P28]	Collagen alpha-1(V) chain	10.57	4.99	14.31	10.2	within
e300155	ADASEAHSSSRGEAGAPGEEDIQGPTKA DTEKWAEGGHSRE	none	Secretogranin-1	7.39	2.91	11.41	11.14	within
e100154	AGATGEAGAAGEAGGAGEAGGVGEAGAA GEAGGAGEAGAAGEGGAAGEAGGAGEAG GV	none	Paraneoplastic antigen Ma6E	6.85	3.1	11.25	11.51	up
e026658	PQNQEPQSQPTESLYDYEPYYDVMTTG TTPDYQDP*	3xOxidation [P20; P21; P32]	Collagen alpha-2(XI) chain	11.26	5.86	14.14	14.04	within
e026661	VEEVVEGVAGEEDHHDEQEEHGEENAE AEGQHDEHDE	none	E3 ubiquitin-protein ligase UBR5	11.22	5.54	14.1	14.06	within
e026665	DITVSSVHTSDLSSFEEDTEEEVVTSDSMEE GEITSDDEE	none	Biorientation of chromosomes in cell division protein 1-like 1	10.15	3.69	13.19	10.81	within
e026667	PPGDDGPKGNPGPVGFPGDPGPPGEPGP AGQDGVGGDKGEDGDPGQP*	7xOxidation [P20; P22; P23; P26; P]	Collagen alpha-1(XI) chain	11.85	5.75	14.88	15.06	up
e026670	TSGFGQHRSSSGQYSGFGQHSGSGQSS GFGQHGTGSGQYSGFGQ	none	Filaggrin-2	11.5	5.6	14.7	14.98	up
e026672	GPTGPGGDKGDTGPPGPQGLQLPGTGG PPGENGKPGEPGPKGDAGAPGA*	3xOxidation [P36; P39; P41]	Collagen alpha-1(III) chain	10.54	5.09	12.33	11.29	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e216058	ARGNDGATGAAGPPGPTGPAGPPGFPGAV GAKGEAGPQGPRGSEGPQGV*	8xOxidation [P16; P19; P22; P23; P26; P37; P40; P]	Collagen alpha-1(I) chain	10.33	5.7	12.27	11.01	within
e099501	GEKGEPGPPGFGLPGKQKAGERGLKGQ KGDAGNPGDPGTPGTTGR*	3xOxidation [P8; P9; P14]	Collagen alpha-1(XVI) chain	7.29	2.09	13.76	8.92	within
e216060	GFPGSKGDPGSPGPPGPAGIATKGLNGPT GPPGPPGPRGHSGEPLPGP*	2xOxidation [P17; P28]	Collagen alpha-1(X) chain	5.83	1.62	13.39	12.45	within
e216066	IGEAGQPNGEAEQPNGDADEPDGAGIEDP EERAEPEGKAEPP	none	Paternally-expressed gene 3 protein	9.5	2.94	12.96	9.42	within
e026689	SRLGGDEDEGYEEEEEDENSQRSEDDDDSETE KPEADDPKDN	none	SAP30-binding protein	8.98	2.84	13.45	10.53	within
e216067	GQTGNRGPSPGSRGSPGAPGPPGPPGSHVI GIKGDKGSMGHPGPKGPPG*	2xOxidation [P23; P24]	Collagen alpha-3(IV) chain	3.59	0.21	10.69	4.6	within
e026692	KGDRGENGSPGAPGAPGHGPPGPVGP GKSGDRGESGPAGPAGAPGAGS*	2xOxidation [P]	Collagen alpha-1(III) chain	13.78	9.19	16.0	14.46	within
e026694	GPRGLPGTPGTDGPKGASGPAGPPGAQG PPGLQGMPGERGAAGIAGPKG*	8xOxidation [P2; P6; P9; P14; P20; P23; P24; P29]	Collagen alpha-1(II) chain	13.42	8.68	15.55	14.17	within
e216073	TVNFGDTEEAKKQINDYVEKGTQGGKIVDLV KELDRDTVF	none	Alpha-1-antitrypsin	4.55	1.08	12.87	9.02	within
e026706	GAEGRQGEKGAKGEAGAEGPPGKTGPVG PQGPAKPGPEGLRGIPGPV*	2xOxidation [P45; P]	Collagen alpha-1(XI) chain	9.29	0.0	15.25	9.28	within
e026742	GSEGARGAPGPAGPPGDPGLMGERGEDG PAGNGTEGFPFGPYGNR*	3xOxidation [P18; P29; P38]	Collagen alpha-1(VI) chain	11.06	6.81	12.85	11.46	within
e026745	GPPGKNGETGPQGPPGPTGPGGDKGDTG PPGPQGLQGLPGTGGPPGEN*	11xOxidation [P3; P11; P14; P15; P17; P20; P29; P30; P32; P39; P44]	Collagen alpha-1(III) chain	11.0	7.35	12.5	13.32	up
e026750	RGSDGQPGPPGPPGTAGFPGSPGAKGEV GPAGSPGSNGAPQGRGEPGPQG*	2xOxidation [P]	Collagen alpha-1(III) chain	9.37	3.52	13.27	5.46	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026763	PGPVGSPGERGSAGTAGPIGLPGRPGPQG PPGPAGEKGAPGEKGPQGPAG*	4xOxidation [P25; P27; P30; P31]	Collagen alpha-1(XI) chain	5.79	1.49	10.03	4.13	within
e216097	RDGSPGGKGDRENGSPGAPGAPGHPPG PGPVGPAGKSGDRGESGPAGPA*	3xOxidation [P20; P23; P26]	Collagen alpha-1(III) chain	8.77	3.82	11.17	11.29	up
e026770	RGEPPPPGAGFAGPPGADGQPGAKGEP GDAGAKGDAGPPGPAGPAGPPGP*	7xOxidation [P28; P39; P40; P42; P45; P48; P49]	Collagen alpha-1(I) chain	8.42	3.35	10.95	11.37	up
e026772	KGESGPSGPAGPTGARGAPGDRGEPGP GPAGFAGPPGADGQPGAKGEP*	10xOxidation [P9; P12; P19; P25; P27; P28; P30; P36; P37; P43]	Collagen alpha-1(I) chain	4.27	0.0	9.58	7.89	within
e026773	LFAEEKAVADTRDQADGSRASVDSGSSEE QGGSSRALVSTLVPL	none	Polymeric immunoglobulin receptor	8.54	2.96	13.1	12.47	within
e026776	GVRGEPGPPGPAGAAGPAGNPGADGQPG AKGANGAPGIAGAPGFPARGPSGP*	1xOxidation [P]	Collagen alpha-1(I) chain	9.05	2.67	13.51	11.74	within
e105756	MRGMPGSPGGPGSDGKPGPPGSQGESG RPGPPGSPGRQPGVMGFPG*	5xOxidation [P20; P29; P31; P32; P34]	Collagen alpha-1(III) chain	7.08	2.54	9.97	8.81	within
e216099	EPGPAGSKGESGNKGEPGSAGPQGP SGEEGKRGPNGEAGSAGPPGPP*	1xOxidation [P]	Collagen alpha-2(I) chain	5.29	1.9	8.59	8.52	within
e026789	QGGGAGPTGPPGEPDGPMPGPIGSRGP EGPPGKPGEDGEGRNGNP*	9xOxidation [P17; P19; P22; P28; P31; P32; P35; P41; P47]	Collagen alpha-2(V) chain	5.76	0.79	9.57	10.33	up
e103267	TAGEPGRDGNPGSDGLPGRDGSPGGKGD RGENGSPGAPGAPGHPGPPGP*	6xOxidation [P17; P23; P35; P38; P41; P44]	Collagen alpha-1(III) chain	5.92	0.29	9.58	7.82	within
e026795	PRGSPGERGETGPPGPAGFPAGPQNGE PGGKGERGAPGEKGEPP*	11xOxidation [P1; P5; P13; P14; P16; P20; P23; P29; P38; P46; P47]	Collagen alpha-1(III) chain	5.22	0.99	9.67	10.32	up
e026796	GSKGESGNKGEPGSAGPQGPSPGEEG KRGPNGEAGSAGPPGPPGLR*	10xOxidation [P12; P17; P20; P21; P23; P32; P41; P42; P44; P45]	Collagen alpha-2(I) chain	5.04	1.31	9.62	10.18	up
e026801	ESGREGAPGAEGSPGRDGSPGAKGDRGE TGPAGPPGAPGAPGAPVGPAG*	6xOxidation [P14; P20; P31; P34; P35; P38]	Collagen alpha-1(I) chain	9.85	5.38	12.05	11.73	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e216106	GERGPPGPMGPPGLAGPPGESGREGAPG AEGSPGRDGSPPGAKGDRGETG*	3xOxidation [P27; P33; P39]	Collagen alpha-1(I) chain	10.5	5.12	12.34	12.07	within
e216108	GSVGDPGMEGPMGQREGPMGPRGEA GPPGSGEKGERGAAGEPGPH*	2xOxidation [P44; P46]	Collagen alpha-1(XVII) chain	8.25	3.34	10.4	10.74	up
e102508	TAGEPGRDGNPGSDGLPGRDGSPPGKGD RGENGSPGAPGAPGHPGPPGP*	7xOxidation [P11; P17; P23; P35; P38; P41; P44]	Collagen alpha-1(III) chain	6.82	1.46	11.07	7.66	within
e026807	DGNPGSDGLPGRDGSPPGKGDRGENGSP GAPGAPGHPGPPGPVGPAGKSG*	8xOxidation [P10; P16; P28; P31; P34; P37; P39; P40]	Collagen alpha-1(III) chain	6.41	1.85	10.98	10.14	within
e026810	ESGREGAPGAEGSPGRDGSPPGAKGDRGE TGPAGPPGAPGAPGAPGPVGPAG*	7xOxidation [P20; P31; P34; P35; P38; P41; P44]	Collagen alpha-1(I) chain	10.01	5.35	12.19	12.1	within
e026812	GEKGDQGPDPGSPGSPGAPGAPGPPG YGPQGEPLQGTQGVGPAGPPG*	3xOxidation [P18; P20; P23]	Collagen alpha-3(IV) chain	11.08	6.74	13.41	13.79	up
e026816	LFAEEKAVADTRDQADGSRASVDSGSSEE QGGSSRALVSTLVPLG	none	Polymeric immunoglobulin receptor	10.37	4.23	14.46	12.65	within
e026817	PAGPPGFPGAVGAKGEAGPQGPGRGSEGP QGVREGEPPGPAGAAGPAGNPGA*	2xOxidation [P37; P38]	Collagen alpha-1(I) chain	10.81	4.29	14.32	12.6	within
e026819	TAGEPGRDGNPGSDGLPGRDGSPPGKGD RGENGSPGAPGAPGHPGPPGP*	8xOxidation [P5; P11; P17; P23; P35; P38; P41; P44]	Collagen alpha-1(III) chain	5.89	1.07	11.18	9.82	within
e026822	GQQPSQSAFGSGTTNSSSAFQFGSSTTN FNFTNNSPSGVFTFGA	none	Nuclear pore complex protein Nup153	6.73	1.61	10.97	10.36	within
e026828	VDKASESSDPSAYQNQPGSSEAVSPGDM AGSASWGAVSSLNDVSN	none	Ubiquitin carboxyl-terminal hydrolase 42	7.17	1.89	11.5	12.16	up
e026831	AIPVAQDLNAPSDWDSRGKDSYETSQLDD QSAETHSHKQSR	none	Osteopontin	6.92	0.42	12.13	5.85	within
e100778	GEKGDPLPGEPLQGRPGELGPQGPTG PPGAKQGEAGHAPGAAGNPG*	9xOxidation [P9; P12; P18; P23; P26; P29; P30; P42; P48]	Collagen alpha-1(XXII) chain	7.88	3.37	10.53	9.77	within
e026841	MRGMPGSPGGPGSDGKGPSPGSGESG RPGPPGSPGPRGQPGVMGFPG*	10xOxidation [P8; P11; P17; P19; P20; P29; P31; P32; P34; P37]	Collagen alpha-1(III) chain	8.35	3.04	10.59	9.36	within

a: Distribution in healthy female

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e216125	PGRDGARGAPGAVGAPGPAGATGDRGEA GAAGPAGPAGPRGSPGERGEVGPAG*	3xOxidation [P16; P18; P33]	Collagen alpha-2(I) chain	4.44	0.14	8.42	3.31	within
e216126	GDRGGGYGGDRGGGYGGDRGGGYGGDR GGYGGDRGGGYGGDRGGYGGDRG	none	TATA-binding protein-associated factor 2N	5.13	1.38	10.47	3.2	within
e104273	DPADASEAHESSSRGEAGAPGEEDIQGPT KADTEKWAEGGGHSRE	none	Secretogranin-1	8.71	3.57	12.47	11.95	within
e026854	DEVEDNDNDSEMERPVNRGGSRRRVSL DGSDSESSSASSPL	none	Protein AF-9	6.6	1.24	10.11	13.11	up
e026869	FGQHRPGSGQSSGFGQYSGSGQSSGFG QHSGTGKSSGFAQHEYR	none	Filaggrin-2	7.38	0.1	11.05	8.19	within
e026871	TVNFGDTEEAKKQINDYVEKGTQGKIVDLV KELDRDTVFAL	none	Alpha-1-antitrypsin	5.0	0.07	12.0	8.05	within
e026876	MQGPMGPMGPRGPPGPAGAPGPQGFQG NPGEPEGVSGPMGPRGPPG*	11xOxidation [P13; P14; P16; P20; P22; P29; P32; P35; P40; P43; P46]	Collagen alpha-1(II) chain	11.35	7.47	12.94	13.23	up
e026888	TGTEDSDDALLKMTISQQEFGRGTGLPDLSS MTEEEQIAYAMQ	none	26S proteasome non-ATPase regulatory subunit 4	3.48	0.17	12.8	5.11	within
e026889	QGPPGKNGETGPQGPPGPTGPGGDKGDT GPPGPQGLQGLPGTGPPGENGK*	2xOxidation [P21; P30]	Collagen alpha-1(III) chain	9.67	3.77	12.53	11.82	within
e216128	WGPVPGASGFRISWSTGSGPESSQTLPPD STATDITGLQPGTTYQ*	3xOxidation [P5; P20; P27]	Collagen alpha-1(VII) chain	9.74	4.79	12.53	11.89	within
e103787	DTSAAGSSEQPRAGSSTPGDAPPAVAEVQ GRSDGSGESAQPPEDSSPPA	none	E3 ubiquitin-protein ligase HUWE1	5.66	0.29	10.19	5.3	within
e026893	KGDQGPDPGSPGSPGAPGAPPPGYG PQGEPLQGTQGVPGAPGPPGEA*	9xOxidation [P13; P16; P18; P21; P24; P25; P29; P33; P42]	Collagen alpha-3(IV) chain	7.09	2.14	12.29	9.53	within
e026895	GRVGDSVDAEGPAGDSVDAEGLDNIQA EGPAGDSVDAEGRVGDSVDA	none	Chloride intracellular channel protein 6	5.77	0.06	10.01	6.17	within

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e216131	GAAGPPGPAGPAGERGEQQAPGPSGFQG LPGPPGPPGEGGKPGDQGVPEAGA*	3xOxidation [P]	Collagen alpha-1(II) chain	13.23	8.2	15.53	15.16	within
e026899	EPGPPGSEGLPGPPGPAGPRGERGPQGN SGEKGDQGFQGGQPGFPGPPGP*	1xOxidation [P25]	Collagen alpha-1(XVI) chain	13.46	9.16	15.62	15.17	within
e026902	PGRDGVPGGPGMRGMPGSPGGPGSDGK PGPPGSQGESGRPGPPGPSGRGQ*	2xOxidation [P19; P22]	Collagen alpha-1(III) chain	11.98	5.68	14.0	12.09	within
e105451	GEHGPPGPPGPIGPVQPGAAGADGEPGA RGPPQHFGAKGDEGTRGFNGP*	3xOxidation [P11; P14; P18]	Collagen alpha-2(XI) chain	10.32	4.8	13.18	12.57	within
e026911	PTTSTTSAPITSTTSGPGSTPSPVPTTSTTS APTTSTTSASTASTTSGPGT	none	Mucin-5AC	10.02	5.0	12.65	12.49	within
e026912	GGSGGSYGGGSGSGGGSGGGYGGGSGG GHSGGSGGGHSGGSGGNYGGGSGSGGG SGGGYGGGS	none	Keratin, type I cytoskeletal 9	10.98	6.83	12.68	12.49	within
e216138	EVVEEYEEEEQEEAAVEEEEDWREDEDEQ EEAAEEDAEA	none	Troponin T, cardiac muscle	11.26	6.8	12.94	13.02	up
e102807	GPPGPAGAPGDKGESGPSGPAGPTGARG APGDRGEPGPPGPAGFAGPPGADGQ*	8xOxidation [P3; P5; P9; P17; P20; P23; P30; P36]	Collagen alpha-1(I) chain	10.35	3.98	13.49	5.92	within
e216141	PPGPPGRDGTGRDGEPPGDPGEDGKPGD TGPQGFPGTGPDVGPKGDKGD*	3xOxidation [P35; P38; P43]	Collagen alpha-1(XVIII) chain	6.99	2.28	10.96	8.43	within
e105753	DKGPPGPVGPSPGNGPVGEPGPEGPAGN DGTPGRDGAVERGERDRGDPGA*	8xOxidation [P11; P16; P20; P22; P25; P32; P]	Collagen alpha-2(V) chain	7.08	2.39	10.74	8.08	within
e216147	SSSVRRGSSYSSTMSTGGGGAGSLGAGG AFGEAAGDRGPYGTIDGPGGGYGAA*	1xOxidation [P]	Collagen alpha-1(XVII) chain	9.42	4.52	11.16	11.43	up
e216149	GPIGPPGPPGLMGPPGPPGLPGPKGNMGL NFQGPKEKGEQGLQGPPGPP*	2xOxidation [P]	Collagen alpha-5(IV) chain	7.39	1.77	12.57	9.32	within
e105169	GYPGLSGEKSPGQKGSRLDGYQGPDG PRGPKGEAGDPGPPGLPAYSP*	2xOxidation [P26; P29]	Collagen alpha-2(IV) chain	5.67	1.23	11.66	8.92	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e206996	HEALQRITTLTVTGPPGPPGPQGLQGPKGE QGSPGIPGMDGEQGLKGS*	2xOxidation [P21; P27]	Collagen alpha-1(XXV) chain	6.18	0.0	11.15	5.57	within
e216155	YGKDLMEKVKSPELQAEAKSYFEKSKEQLT PLIKKAGTELVN	none	Apolipoprotein A-II	2.91	0.0	7.38	2.17	within
e103827	DPGPPGEPGPAGQDGVGGDKGEDGDPGQ PGPPGPSGEAGPPGPPGKRGPFGA*	9xOxidation [P31; P32; P34; P40; P41; P43; P44; P49; P50]	Collagen alpha-1(XI) chain	10.43	3.39	13.67	13.5	within
e216156	VIPPTENEHDEHDENNAEASAELSNEGVMN HRSEEERTVETQ	none	Radixin	11.05	4.88	14.13	14.13	up
e026952	DNQREEAADNQRAEAPADQRSQGTDNHR EEAADNQRAEAPADQ	none	Coiled-coil domain-containing protein 8	7.34	3.38	10.84	12.41	up
e026955	GENGHPGSPGEKGEKGETGQAGSPGEKG EAGEKGNPGAEPVGLPGEPPG*	3xOxidation [P36; P41; P44]	Collagen alpha-1(XIII) chain	6.88	2.51	9.84	10.61	up
e026960	GLAGTAGEPGRDGNPGSDGLPGRDGSFG GKGDRGENGSPGAPGAPGHPGPPG*	4xOxidation [P27; P39; P42; P]	Collagen alpha-1(III) chain	6.48	0.78	11.6	10.66	within
e103878	GNDGAPGKNGERGGPGGPGPQGGPKN GETGPQGGPPTGPGDKGDTGPPGP*	6xOxidation [P32; P35; P36; P38; P41; P50]	Collagen alpha-1(III) chain	6.95	1.94	11.26	6.97	within
e104461	GPPGEGRAGEPGTAGPTGPPGVPGSPGIT GPPGPPGPPGPPGAPGAFDETGIA*	11xOxidation [P19; P20; P23; P26; P31; P32; P34; P35; P37; P38; P40]	Collagen alpha-2(VIII) chain	9.48	4.19	11.9	11.9	up
e026966	PGPPGVVGPQGPTGETGPMGERGHGPP GPPGEQGLPGLAGKEGTGKDPG*	11xOxidation [P3; P4; P9; P12; P18; P25; P27; P28; P30; P31; P37]	Collagen alpha-1(V) chain	9.01	3.66	11.45	11.74	up
e216160	EDAGAGGEDVGAGGEDAGAGGEDAGAGG EDAGPGGEDAGAGGEDAGPGGEDAGAGG ED	none	Golgin subfamily A member 6-like protein 2	13.54	9.34	15.48	16.35	up
e026977	IAGPRGSPGERGETGPPGPAGFPAGPQGN GEPGKGGERGAPGEKGEPPG*	10xOxidation [P4; P8; P16; P17; P19; P23; P26; P32; P41; P49]	Collagen alpha-1(III) chain	8.59	4.33	12.85	8.4	within

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e026978	ERGGPGGPGPQGPPGKNGETGPQGPPGP TGPGGDKGDTGPPGPQGLQGLPGT*	8xOxidation [P25; P26; P28; P31; P40; P41; P43; P50]	Collagen alpha-1(III) chain	6.35	2.08	11.95	8.51	within
e100368	PPGESGREGAPGAEGSPGRDGSPGAKGD RGETGPAGPPGAPGAPGAPGVGPAG*	8xOxidation [P17; P23; P34; P37; P38; P41; P44; P47]	Collagen alpha-1(I) chain	10.06	4.39	12.38	12.17	within
e026982	AGPTGARGAPGDRGEPGPPGAGFAGPP GADGQPGAKGEPGDAGAKGDAGPPGP*	8xOxidation [P16; P18; P19; P21; P27; P28; P34; P]	Collagen alpha-1(I) chain	10.01	4.5	12.22	11.98	within
e026986	GLAGTAGEPGRDGNPGSDGLPGRDGSPG GKGDRGENGSPGAPGAPGHPGPPGP*	6xOxidation [P9; P15; P21; P27; P39; P42]	Collagen alpha-1(III) chain	9.49	1.48	13.5	11.71	within
e026987	QPGEPGPPGPKGPTGDDGPKGNPGPVGF PGDPGPPGEGGPRGQDGAKGDRG*	6xOxidation [P23; P25; P29; P]	Collagen alpha-2(XI) chain	5.09	0.0	8.83	6.84	within
e026990	APGAEGSPGRDGSPGAKGDRGETGPAGP PGAPGAPGAPGVGPAGKSGDRGET*	11xOxidation [P2; P8; P14; P25; P28; P29; P32; P35; P38; P40; P43]	Collagen alpha-1(I) chain	9.93	2.61	13.47	11.95	within
e026991	GVMQGPMPGMPGRGPPGAPAGPQGF QGNPGEPEGVSGPMGPRGPPGP*	7xOxidation [P24; P31; P34; P37; P42; P45; P48]	Collagen alpha-1(II) chain	8.9	3.58	12.72	11.77	within
e100304	NPGSRGENGPTGAVGFAGPQGPDPGQPGV KGEPGEPGQKGDAGSPGPQGLAGS*	6xOxidation [P22; P26; P32; P35; P44; P46]	Collagen alpha-2(V) chain	10.0	4.0	12.04	11.85	within
e216165	PGPVGFPGDPGPPGEPGAGQDGVGGDK GEDGDPGQPGPPGSGEAGPPGPPGK*	2xOxidation [P]	Collagen alpha-1(XI) chain	10.49	4.68	12.27	12.14	within
e027002	GDPGAFGLKGEKGEAGDEAGRPGSSG PSGDEGQPGEPGPPGEKGEAGDEG*	3xOxidation [P3; P15; P24]	Collagen alpha-1(VI) chain	9.84	4.16	13.33	13.05	within
e027004	EGFPGFPGYPGNRGAPGNGTKGYPLKG DEGEAGDPGDDNNDIAPRG*	5xOxidation [P7; P10; P16; P25; P37]	Collagen alpha-1(VI) chain	7.11	1.5	10.32	10.12	within
e027012	LLHDHELLAKLKALEDREVWELLQEADKTAE ENKDQSQVYD	none	Coiled-coil domain-containing protein 141	9.96	3.99	13.49	11.74	within
e216169	PPGDDGPKGNPGPVGFPGDPGPPGEPGP AGQDGVGGDKGEDGDPGQPGPPGPSG	none	Collagen alpha-1(XI) chain	11.13	6.64	12.97	13.08	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e027015	PGPVGFPGDPGPPGEPGPAGQDGVGGDK GEDGDPGQPGPPGPSGEAGPPGPPGK*	3xOxidation [P16; P18; P34]	Collagen alpha-1(XI) chain	11.56	7.63	13.14	12.99	within
e103278	GLAGTAGEPGRDGNPGSDGLPGRDGSPG GKGDRGENGSPGAPGAPGHPGPPGP*	8xOxidation [P9; P15; P21; P27; P39; P42; P45; P48]	Collagen alpha-1(III) chain	8.61	2.05	13.14	11.38	within
e216172	GPPGSNGPVGEPGPEGPAGNDGTPGRDG AVGERGDRGDPGPAGLPGSQGAPGT*	6xOxidation [P14; P17; P24; P39; P41; P45]	Collagen alpha-2(V) chain	8.05	3.0	11.74	11.66	within
e106774	GGAGPTGPPGEPGDPGPMGPIGSRGPEG PPGKPGEDGEPRNGNPGEVGFAG*	8xOxidation [P15; P17; P20; P26; P29; P30; P33; P39]	Collagen alpha-2(V) chain	5.62	0.97	10.73	6.61	within
e104196	GPPGESGREGAPGAEGSPGRDGSPGAKG DRGETGPAGPPGAPGAPGAPGPVGPAG*	8xOxidation [P18; P24; P35; P38; P39; P42; P45; P48]	Collagen alpha-1(I) chain	11.28	6.88	13.39	13.32	within
e027021	PVGAAGPAGPNGPPGPAGSRGDGGPPGM TGFPGAAGRTGPPGPSGISGPPGPPGP*	12xOxidation [P1; P7; P10; P13; P14; P16; P25; P26; P32; P40; P41; P43]	Collagen alpha-2(I) chain	11.88	7.83	13.67	13.61	within
e100793	GLAGTAGEPGRDGNPGSDGLPGRDGSPG GKGDRGENGSPGAPGAPGHPGPPGP*	9xOxidation [P9; P15; P21; P27; P39; P42; P45; P48; P50]	Collagen alpha-1(III) chain	7.44	1.72	12.02	10.23	within
e102314	GPSGEPGKQGAPGASGDRGPPGPVGP LTGPAGEPGREGSPGADGPPGRDGAA*	8xOxidation [P6; P12; P20; P21; P23; P26; P27; P32]	Collagen alpha-1(II) chain	9.68	3.81	12.34	11.95	within
e027032	PSGEKGETGDVGPMGPPGPPGPRGPAGP NGADGPQGPPEGVGNLGPGEKGEPEG*	3xOxidation [P38; P46; P47]	Collagen alpha-2(XI) chain	10.0	4.06	12.82	11.7	within
e100244	LAGTAGEPGRDGNPGSDGLPGRDGSPGG KGDRGENGSPGAPGAPGHPGPPGPV*	9xOxidation [P8; P14; P20; P26; P38; P41; P44; P47; P49]	Collagen alpha-1(III) chain	6.26	1.32	10.59	9.47	within
e216180	GETGDVGPMGPPGPPGPRGPAGPNGADG PQGPPEGVGNLGPGEKGEPEGESGSPG*	3xOxidation [P33; P41; P42]	Collagen alpha-2(XI) chain	7.82	2.85	11.48	10.24	within
e216181	GPAGPTGARGAPGDRGEPGPPGPAGFAG PPGADGQPGAKGEPGDAGAKGDAGPPG*	11xOxidation [P5; P12; P18; P20; P21; P23; P29; P30; P36; P42; P53]	Collagen alpha-1(I) chain	8.8	3.16	11.13	12.41	up
e027040	SGQSSSYGQHESASHHASGRGRHSGSG QSPGHGQRGSGSGQSPSYGRHG	none	Hornerin	7.18	2.31	10.62	11.94	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e216187	RVLRENADSLQASLRPHADELKAKIDQNVE ELKGRLTPYADEF	none	Apolipoprotein A-IV	8.93	2.39	13.63	14.28	up
e103559	SDKPDMAEIEKFDKSKLKKTTETQEKNPLPS KETIEQEKQAGES*	1xAcetylation [S1]	Thymosin beta-4	11.52	5.9	16.78	13.12	within
e216190	GKTGPPGPAGQDGRPGPPGPPGARGQAG VMGFPGPKGAAGEPGKAGERGVPGPPG*	1xOxidation [P]	Collagen alpha-1(I) chain	11.59	4.85	16.8	13.07	within
e027064	LPGMIGSPGLPGSKGATGDIFGAENGAPGE QGLQGLTGHKGFLGDSGLPLK*	3xOxidation [P8; P11; P28]	Collagen alpha-6(IV) chain	10.04	4.83	14.14	11.6	within
e096406	EIENKAIQDPRLFAEEKAVADTRDQADGSR ASVDSGSSEEQGGSSRA	none	Polymeric immunoglobulin receptor	9.67	4.29	12.45	12.4	within
e027066	GQKGDAGAPGPQGSPGAPGPQGPTGVTG PKGARGAQGPPGATGFPGAAGRVPGPS*	7xOxidation [P14; P18; P20; P23; P29; P38; P39]	Collagen alpha-1(II) chain	9.38	3.92	12.46	12.02	within
e101945	EDAGAAREDAGAGGDDVGAGREDAGAGG EDVGAGGEDAGAGGEDAGAGGEDAGPGG ED	none	Golgin subfamily A member 6-like protein 2	13.88	10.82	15.68	15.74	up
e216199	GEGSSGGGGRGGGSFGGGYGGGSSGGG SSGGGHGGGHGGSSGGGYGGGSSGGGS SGGGYGGGSSSG	none	Keratin, type I cytoskeletal 10	14.28	11.23	16.14	16.06	within
e099923	ARGNDGARGSDGQPGPPGPPGTAGFPGS PGAKEVGPAAGSPGSGNAPGQRGEPGP*	8xOxidation [P19; P20; P26; P29; P37; P41; P47; P53]	Collagen alpha-1(III) chain	10.11	3.67	12.69	12.32	within
e098508	HSGSRASRQTRNDEQSGDGSRRHSGSRH HEASSRADSSGHSQVGQQQS	none	Filaggrin	10.75	5.06	12.99	12.73	within
e098509	GESGSPGIQGEFVGKPRGERGEKGESG QPGEPPGPKGPTGDDGPKGNPG*	9xOxidation [P6; P12; P17; P30; P33; P35; P36; P38; P41]	Collagen alpha-2(XI) chain	9.1	3.24	12.28	12.0	within
e098515	ARGNDGARGSDGQPGPPGPPGTAGFPGS PGAKEVGPAAGSPGSGNAPGQRGEPGP*	9xOxidation [P17; P19; P20; P26; P29; P37; P41; P47; P53]	Collagen alpha-1(III) chain	10.02	4.38	12.46	13.36	up
e098516	FAESGQSSGQFQGRPSEVWSQWQSQHH GQQSGEQHSHQQPGQTEV	none	Aryl hydrocarbon receptor nuclear translocator 2	5.0	0.7	8.62	10.43	up

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e098517	AGGPGFPGAPGAKGEAGPTGARGPEGAQ GPRGEPGTPGSPGPAGASGNPGTDGIPGA *	10xOxidation [P7; P10; P18; P24; P30; P34; P37; P40; P42; P49]	Collagen alpha-1(II) chain	10.94	5.4	12.87	13.33	up
e216209	AGPRGSPGERGETGPPGPAGFPAGPQN GEPGGKGERGAPGEKGEPPGVAGP*	12xOxidation [P3; P7; P15; P16; P18; P22; P25; P31; P40; P48; P49; P54]	Collagen alpha-1(III) chain	9.68	3.76	12.4	12.74	up
e103715	NDGQPGPAGPPGPVGPAGGPGFPGAPGA KGEAGPTGARGPEGAQGRGEPGTPGSP*	9xOxidation [P16; P20; P23; P26; P34; P40; P46; P50; P53]	Collagen alpha-1(II) chain	6.11	0.0	9.59	9.31	within
e098521	AALNSKDAALATALGDKKSLEGLDLKDQI AQLEASLAAAKQLADET	none	Lamin-B1	10.35	0.49	15.81	14.83	within
e216210	KNEEELIKLIEQFPESFFTIKDQENQKLNQF FQELGLKNVV	none	Transcription termination factor 2, mitochondrial	8.0	0.0	15.52	14.41	within
e102618	LPGLAGTAGEPGRDGNPGSDGLPGRDGSP GGKGRGGENGSPGAPGAPGHPGPPGP*	8xOxidation [P11; P17; P23; P29; P41; P44; P47; P50]	Collagen alpha-1(III) chain	6.7	0.0	10.8	10.37	within
e105306	AQEGKAAATPESQEPQAKGAEASASEEE AGPQATEPSTPSGPESGPTPASAE	none	MARCKS-related protein	6.79	1.83	10.61	10.53	within
e216219	GPGFPGAPGAKGEAGPTGARGPEGAQGP RGEPGTPGSPGPAGASGNPGTDGIPGAK*	12xOxidation [P2; P5; P8; P16; P22; P28; P32; P35; P38; P40; P47; P53]	Collagen alpha-1(II) chain	6.66	1.69	10.49	10.53	up
e098538	GAPGIPGTRGPIGPPGIPGFGSKGDPGSP GPPGPAGIATKGLNGPTGPPGPPGPRG*	3xOxidation [P35; P46; P49]	Collagen alpha-1(X) chain	2.38	0.0	6.87	5.0	within
e216224	ARGPPGLRGDPGFEGERGKPLPGEKGEA GDPGRPGDLGPVGYQGMKGEKGS*	2xOxidation [P]	Collagen alpha-1(VI) chain	6.16	0.0	12.89	8.58	within
e101521	PHQPNHQPSFLTSPQDLASSPMEEDEQHS EADEPPSDEPLSDDPLSP	none	Methylcytosine dioxygenase TET1	8.05	2.84	11.09	11.52	up
e098548	EQTPEKPPSSSAPPSAPQSLPEPVAHSS SAESESTSDSDSSDSESESSS	none	AF4/FMR2 family member 1	8.36	3.78	11.11	11.48	up

a: Distribution in healthy female

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e098551	AEGPPGPTGQAGEPGPRGLLGPRGSPGPTGRPGVTGIDGAPGAKGNVGPPGEPGPPG*	4xOxidation [P22; P26; P28; P32]	Collagen alpha-3(V) chain	5.05	0.1	12.68	10.49	within
e104378	GQMGPPGPPGPRGPGSAPGADGPQGPPG GIGNPGAVGEKGEPGEAGEPGLPGEGGPP G*	9xOxidation [P18; P23; P26; P27; P33; P42; P48; P51; P]	Collagen alpha-1(V) chain	9.31	1.13	11.68	11.82	up
e098562	EPGYSEGTRPGPPGPTGDPGLPGDMGKK GEMGQGPGLHGPAGPEGAPGSPGSPG *	2xOxidation [P12; P13]	Collagen alpha-3(IV) chain	11.31	5.78	13.25	13.24	within
e101413	ELSAAAIKRIVATAKASGKKLQKVTLKVS P GIILTDNLNQLIENVSI	none	Low density lipoprotein receptor adapter protein 1	8.84	3.92	11.68	12.43	up
e098563	GEKGENGDVGPMPGPPGPRGPQGPN G ADGPQGPSPGVS G G VGEKGEPGEAGN P*	4xOxidation [P26; P32; P35; P36]	Collagen alpha-1(XI) chain	11.04	5.06	13.05	13.14	up
e098567	AARAAPAAPADPD SGATPEDPD SGTAPAD PD SGAFAADPD SGAAPAAPADPD SGAAPD	none	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	5.56	0.83	9.22	3.79	within
e106402	GQMGPPGPPGPRGPGSAPGADGPQGPPG GIGNPGAVGEKGEPGEAGEPGLPGEGGPP G*	10xOxidation [P14; P18; P23; P26; P27; P33; P42; P48; P51; P56]	Collagen alpha-1(V) chain	10.09	4.46	12.26	12.42	up
e098569	ARGNDGARGSDGQPGPPGPGTAGFPGS PGAKGEVGPAGSPG SNGAPGQ RGEPGPQ G*	9xOxidation [P17; P19; P20; P26; P29; P37; P41; P47; P53]	Collagen alpha-1(III) chain	12.1	7.18	13.84	14.12	up
e098570	RGAAGEPGRDGVPGGPGMRGMPGSPGG PGSDGKPGPPGSQGESRGP PPGSPGPR G*	12xOxidation [P13; P16; P22; P25; P28; P34; P36; P37; P46; P48; P49; P51]	Collagen alpha-1(III) chain	11.79	7.77	13.68	14.24	up
e102537	AIQDPRLF AEEKAVADTRDQADGSRASVDS GS SEEQGGSSRALVSTLVPLG	none	Polymeric immunoglobulin receptor	6.72	1.01	13.21	9.8	within
e216227	PGTSGHPGSPGSPGYQGPPGEPGQAGPS GPPGPPGAIGSPGAGKDGESRGP RPG E *	8xOxidation [P22; P27; P30; P31; P33; P34; P39; P42]	Collagen alpha-1(III) chain	10.77	6.65	13.08	13.36	up

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e216228	PGEEGKRGPRGDPGTGPPGPVGERGAPGNRGFPDGLPGPKGAQGERGPVGSS*	2xOxidation [P28; P34]	Collagen alpha-2(V) chain	7.91	2.82	13.15	9.57	within
e098571	DGPKGNPGPVGFPGDPGPPGEPGAGQDGVGGDKGEDGDPGQPPGPSGEAGPPGPP*	3xOxidation [P3; P7; P9]	Collagen alpha-1(XI) chain	8.37	0.0	10.84	11.24	up
e100038	PPGSNGNPGPPGPSGSPGKDGPAGNPGAGSPGVSGPKGDAGQPGKEKSPGAQGPP*	9xOxidation [P22; P23; P25; P32; P35; P40; P47; P53; P58]	Collagen alpha-1(III) chain	9.61	4.12	11.95	12.54	up
e216230	EPRSPGGYTPQSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPSYSPTSPSY	none	DNA-directed RNA polymerase II subunit RPB1	8.12	2.84	11.58	11.85	up
e098573	SSHYGQHGSGSRQSSGHGRQGSGSGQSPSRGRHGSGLGHSSSHGQHGSGSGRSS	none	Hornerin	7.34	1.46	11.39	7.19	within
e101064	PTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSPNYSPTSPSYSPTSPSYSP	none	DNA-directed RNA polymerase II subunit RPB1	7.98	2.72	10.91	12.0	up
e098575	PPGEKGENGDVGMGPPGPPGPRGPQGPNGADGPQGPSPSVGSVGGVGEKGEPEGA G*	8xOxidation [P20; P22; P25; P28; P34; P37; P38; P53]	Collagen alpha-1(XI) chain	8.77	2.47	11.7	11.94	up
e098578	DDGPKGSPGPVGFPGDPGPPGEPGAGQDGPPGDKGDDGEPGQTGSPGPTGEPGPS GP*	2xOxidation [P]	Collagen alpha-1(V) chain	6.18	1.22	10.64	9.54	within
e100385	QGPGASGERGPPGPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPPGAKGDRGETGPA*	3xOxidation [P15; P18; P19]	Collagen alpha-1(I) chain	6.54	1.43	12.01	13.12	up
e098580	PGTDVFMGPPGSPGEDGPAGEPPGPEGQPGVDGATGLPMKGEKGARGPNGSVGE*	1xOxidation [P51]	Collagen alpha-1(XV) chain	5.5	0.58	11.47	12.3	up
e098583	SSPVQQGLGGQAQQQPNSANMASLSAMGKSPLSQGDSSAPSLPKQAASTSGPTPAA	none	CREB-binding protein	7.82	1.73	11.14	10.29	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098586	EAREAANGDSDGPSYMSSLSYLADSTLSEE MSQFDFSTGVQSYSSSQD	none	DNA-dependent protein kinase catalytic subunit	4.5	0.0	12.62	11.39	within
e098592	NSSNPAPPPGEGADDLEGEFTEETIRNLDE NYYDPYYDPTSSPSEIGPG*	5xOxidation [P9; P35; P39; P]	Collagen alpha-1(V) chain	4.58	0.0	11.56	11.1	within
e098593	GQHSGSGSQSSGFGQHSGSGSQSSGFG QHESRSGQSSYGQHSSGSSQSSGYGQHGS	none	Filaggrin-2	4.28	0.0	10.91	11.35	up
e098595	PPGTSGHPGSPGSPGYQGPPGEPGQAGP SGPPGPPGAIGPSGPAGKDGESGRPRGPE*	12xOxidation [P14; P19; P20; P23; P28; P31; P32; P34; P35; P40; P43; P53]	Collagen alpha-1(III) chain	7.45	2.54	10.38	9.51	within
e106444	PTGLPGDLGPPGDPGVSGIDGSPGEKGDP GDVGGPGPPGASGEPGAPGPPGKRGPSTHMG*	8xOxidation [P1; P5; P10; P11; P14; P23; P29; P35]	Collagen alpha-3(V) chain	5.4	0.0	12.42	10.88	within
e098611	PSDGMVGGGPPAPHMQNQMNGQMPGPN HMPMQGPGPNQLNMTNSSMNPSSSH	none	Protein SSXT	8.01	0.0	13.94	13.67	within
e098612	MDTEMSIDIDHNLTPTLDSMSYGMNPQTG SENSLLDEDDYFLNSGDLAGI	none	Zinc finger MYM-type protein 4	7.67	0.47	13.54	13.84	up
e098613	GDDGPKGNPGPVGFPGDPGPPGEGGPRG QDGAKGDRGEDGEPGQPGSPGPTGENGP PG*	10xOxidation [P15; P18; P20; P21; P26; P42; P45; P48; P50; P56]	Collagen alpha-2(XI) chain	4.88	0.0	8.76	12.11	up
e103739	SAPITSTTSGPGSTPSPVPTTSTTSAPTST TSASTSTSGPGTTPSPVPTTSTTSAPT	none	Mucin-5AC	4.5	0.0	11.22	9.71	within
e098617	GDKGESGSPGAGPTGARGAPGDRGEPG PPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP*	1xOxidation [P]	Collagen alpha-1(I) chain	4.52	1.11	11.27	8.46	within
e098622	ESGREGAPGAEGSPGRDGSPGAKGDRGE TGPAGPPGAPGAPGAPGVGPAGKSGDR GETGP*	7xOxidation [P20; P31; P34; P35; P38; P41; P44]	Collagen alpha-1(I) chain	7.61	2.51	10.75	10.76	up

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098633	SGVLASGDSTSGDPTSSEPSSSDAASGDA TSGDAPSGDVSPGDATSGDATADDLSSGD PTSS	none	Activating transcription factor 7-interacting protein 1	10.65	2.98	12.84	13.03	up
e098635	PGKNGETGPQGPPGPTGPGGDKGDTGPP GPQQLQGLPGTGGPPGENGKPGEPGPKG DAGAP*	9xOxidation [P27; P28; P30; P37; P42; P43; P49; P52; P54]	Collagen alpha-1(III) chain	7.71	0.09	13.6	9.59	within
e098647	SSGGYGGGLGGFGGGSFRGSYSSSFSGGS YGGIFGGGSFGGGSFGGGSFGGGGFGGG GFGGGFGGGFG	none	Keratin, type I cytoskeletal 10	4.96	0.0	10.34	2.1	within
e216249	SLGKGPGPRTDVGAPFGPQGHRDVPFSPD EMVPPSMNSQSGTIGPDHLDHMTPEQ	none	B-cell CLL/lymphoma 9 protein	7.39	3.46	11.35	9.65	within
e098663	GEKGEQGEDGKAEGPPGPPGDRGPVGDR GDRGEPGDPGYPGQEGVQLRGKPGQQG QP*	2xOxidation [P52; P58]	Collagen alpha-1(XXVII) chain	7.12	1.86	10.31	11.21	up
e098667	TNSEFSTVSSGSIATNSESSTTSSGASTAT NSESSTPSSGASTATNSDSSTTSSGASTAT N	none	Mucin-21	9.69	1.04	13.75	6.08	within
e098669	SASRQTRNEEQSGDGRHSGSRHHEASS QADSSRHSQVGQGQSSGPRTSRNQGSS	none	Filaggrin	3.63	0.0	7.74	5.58	within
e098681	GKQGPPSGASGERGPPGPMGPPGLAGPPG ESGREGAPGAEGSPGRDGSFGAKGDRGE TGPAGPPG*	11xOxidation [P14; P15; P17; P20; P21; P26; P27; P36; P42; P48; P59]	Collagen alpha-1(I) chain	6.04	1.0	9.95	10.43	up
e098687	RGERGMPLPGPAGTPGKVGPTGATGDK GPPGPVGPSPGNGPVGEPGPEGPAGNDG TPGRDGAV*	11xOxidation [P7; P10; P12; P16; P21; P30; P31; P33; P36; P37; P42]	Collagen alpha-2(V) chain	8.62	1.34	11.3	12.2	up
e098692	GPPGEPGPPGPPGPPGHLTAALGDMGHY DESMPDPLPEFTEDQAAPDDKNKTDPGVH A*	2xOxidation [P]	Collagen alpha-2(V) chain	7.62	1.38	14.2	11.79	within

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e207302	GAAGPPGPKGPPGDDGPKGSPGPVGFPG DPGPPGEPGAGQDGPBGDKGDDGEPGQ TGSPGPTGEPGP*	11xOxidation [P8; P11; P12; P17; P21; P23; P27; P30; P32; P33; P36]	Collagen alpha-1(V) chain	7.78	1.9	11.95	11.64	within
e102084	HPGPQGPKGQKGSVGDPGMEGPMGQRG REGPMGRGEAGPPGSGEKGERGAAGEP GPHGPPGVP*	8xOxidation [P17; P22; P31; P34; P40; P41; P55; P57]	Collagen alpha-1(XVII) chain	9.61	3.05	13.13	13.14	up
e098717	GPPGEKGETGDVGQMGPPGPPGPRGPSG APGADGPQGPPGGIGNPGAVGEKGEPEGEA GEPGLPGEGGPPG*	3xOxidation [P]	Collagen alpha-1(V) chain	11.19	5.4	14.18	14.98	up
e098758	PHSTGPTGGSSAETETDSFSLPEEYFTPAP SPGDQSSGSTIWLEGGTPMDALQIAEDTL QTL	none	BLOC-3 complex member HPS1	6.39	0.69	10.98	12.38	up
e216256	SGQSPSPSRGRHSGSGQSSSYSPYGSG SGWSSSRGPYESGSSHSSGLGHRESRSG QSSGYGQHGS	none	Hornerin	7.61	1.35	13.3	8.5	within
e098770	TENPEEGVTPGPDNEERLAATAAGEAEALA SMPGEVEASGVAPGELDLSMSAQLGEEA TVGPSSD*	5xOxidation [P10; P12; P33; P43; P63]	Collagen alpha-1(XV) chain	8.62	1.65	16.03	6.6	within
e216271	DISGRASGLPSGTELSGQASGSPDVSGEIP GLFGVSGQPSGFPDTSGETSGVTELSGLSS GQPGISGEASGVLYGTSQPFG	none	Aggrecan core protein	3.95	0.0	12.16	10.89	within
e098813	SLLAPLRLDADPSLQVRQEESEIKTLNNK FASIDKVRFLEQQNKLETKWTLLQEKS KSSRLPDI	none	Keratin, type II cytoskeletal 7	13.71	2.18	15.99	17.15	up
e098815	RASLTRTPSRASLTMTPSRASLTRTPSTASL TGTPPTASLTRTPPTASLTRSPPTASLTRTP STASLTRMPSTASLTRK	none	Uncharacterized protein DKFZp434B061	13.38	2.52	16.41	17.07	up
e098816	AVGLHTGEVRTARALLDRDALKQRLVVVVQ DHGQPPLSATVTLTVAVADSIPDVLADLGS KPSADPDDSGLTLYLVVA	none	Protocadherin gamma-A4	14.08	4.25	16.52	17.03	up

a: Distribution in healthy female

fidAuswertung	Sequence	Modification	Protein Name	median ^a	2.5% ^a	97.5% ^a	Your Result	Range
e098820	QDVVKA AVA VLSPEEFMVLLDSVLPESAH RLKSSIGLINEKAADKLGSTQIVKILTQDTPE FFIDQGHAKVAQLI	none	BPI fold-containing family B member 1	12.54	1.93	15.91	16.68	up
e098826	SYDVKSGVAVGGLAGYPGAGPPGPPGPP GTSGHPGSPGSPGYQGPPGEPGQAGPSG PPGPPGAIGPSGPAGKDGESGRPGRPGER GLPGP*	1xOxidation [P]	Collagen alpha-1(III) chain	2.98	0.0	8.16	4.97	within
e098831	HLTPEPDIVASTKKPVPARPPPTNFPPPRP PPPSRPAPPPRKRKSELEFETLKTDPIDVPK ENITSDSLLTASM	none	WD repeat-containing protein 44	9.44	0.38	13.7	7.74	within
e098835	GGMQIFVKTLTGKTITLEVEPSDTIENVKAKI QDKEGIPPDQQLIFAGKQLEDGRTLSDYNI QKESTLHLVLR	none	Polyubiquitin-B	10.75	2.35	14.21	16.06	up