

Supporting Information

for

A multi-technique analysis of gelatin biodegradation on core-shell nanoparticles surface by *Alteromonas macleodii* extracellular proteases

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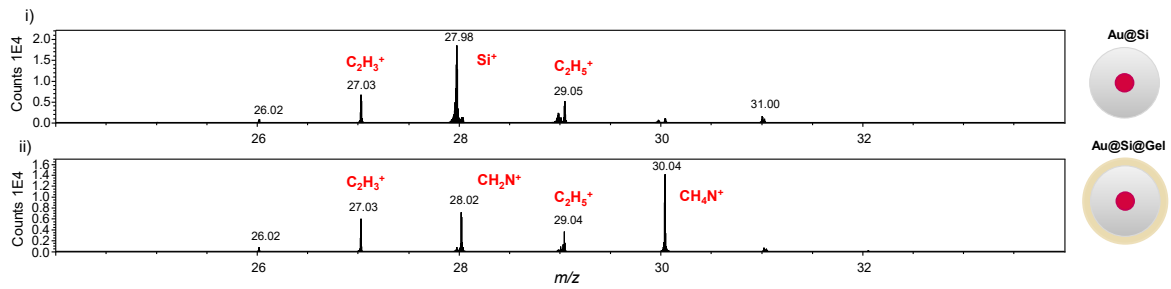


Figure S1 ToF-SIMS spectra in positive polarity of core-shell nanoparticles before biodegradation for i) Au@Si and ii) Au@Si@Gel, over 24 to 34 m/z range; the characteristic peaks are labelled in red.

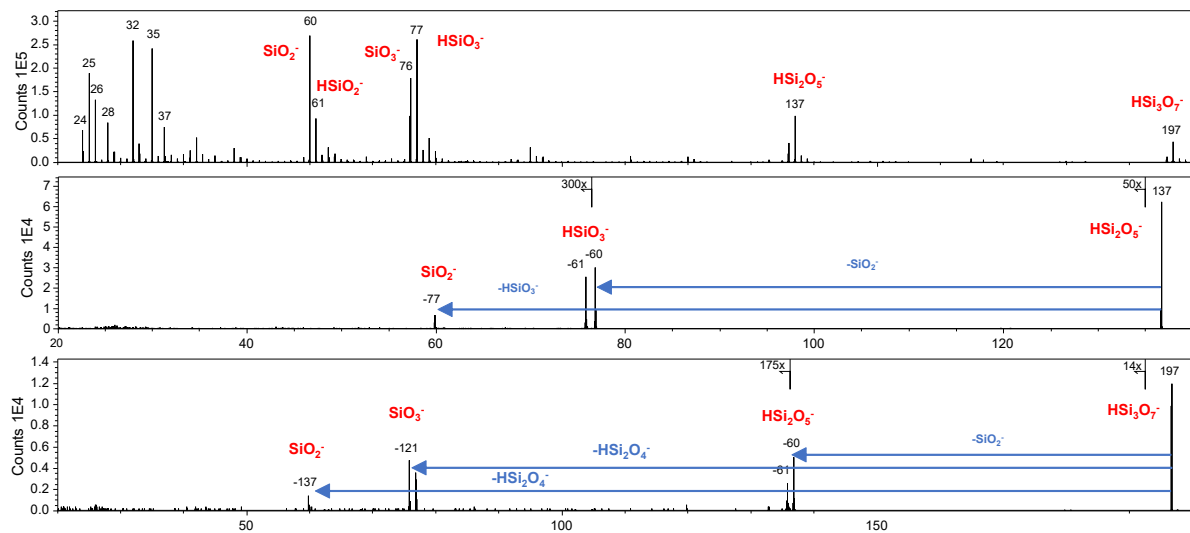


Figure S2 ToF-SIMS Tandem MS of Au@Si@Gel incubated 60 min in the culture medium. The middle spectrum shows the fragmentation of the precursor ion m/z 136.93, confirmed as HSi₂O₅⁻. The bottom spectrum shows the fragmentation of the precursor ion m/z 196.9, confirmed as HSi₃O₇⁻.

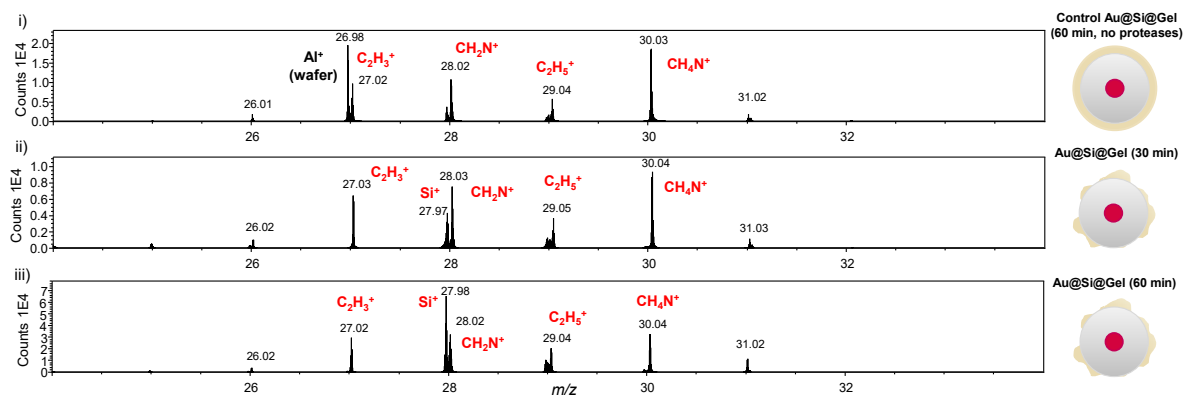


Figure S3 ToF-SIMS spectra of incubated nanoparticles in the positive polarity. i) control Au@Si@Gel incubated 60 min without proteases, ii) Au@Si@Gel incubated 30 min and iii) Au@Si@Gel incubated 60 min over 24 to 34 m/z range; the characteristic peaks are labelled in red.

Table S1 XPS quantitative analyses of nanoparticles before and after biodegradation with binding Energies (eV) and atomic percent concentrations (At.%) of a) type A gelatin, b) Au@Si before biodegradation, c) Au@Si@Gel before biodegradation, d) control Au@Si@Gel incubated 60 min without proteases, e) Au@Si@Gel incubated 30 min and f) Au@Si@Gel incubated 60 min.

a

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.48	30.28	C-C, C-H C-O, C-N O=C-(N,O)
	286.3	1.29	18.96	
	288.06	1.38	16.11	
			65.35	
N 1s	398.46	1.71	1.53	N=C-NH, N-C N-C=O
	399.96	1.61	16.5	
			18.03	
O 1s	531.48	1.64	13.35	O=C-(N,O) O-C=O
	532.78	1.8	3.28	
			16.63	

b

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.6	2.77	C-C C-O C=O
	286.43	1.6	1.37	
	288.57	1.6	0.6	
			4.74	
O 1s	532.97	1.73	57.82	O-Si, O-C, O=C
Si 2p	103.65	1.77	37.44	SiO₂

c

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.48	14.09	C-C, C-H C-O, C-N O=C-(N,O)
	286.22	1.4	13.43	
	288.08	1.6	11.08	
			38.6	
N 1s	398.54	1.8	0.46	N=C-NH, N-C N-C=O
	400.04	1.66	11.03	
			11.49	
O 1s	531.36	1.59	6.97	O=C-(N,O) O-Si, O-C=O
	532.67	1.67	25.5	
			32.47	
Si 2p	103.41	1.64	17.45	SiO₂

d

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.57	14.61	C-C, C-H C-O, C-N O=C-(N,O)
	286.24	1.32	9.61	
	288.02	1.6	9.55	
			33.77	
N 1s	399.98	1.65	9.32	N=C-NH, N-C N-C=O
O 1s	531.22	1.8	7.44	O=C-(N,O) O-Si, O-C=O
	532.57	1.73	30.17	
			37.61	
Si 2p	103.37	1.65	19.29	SiO₂

e

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.6	11.54	C-C, C-H C-O, C-N O=C-(N,O)
	286.28	1.26	5.87	
	288.06	1.47	5.71	
			23.12	
N 1s	399.96	1.61	6.05	N=C-NH, N-C N-C=O
O 1s	531.05	1.8	6.54	O=C-(N,O) O-Si, O-C=O
	532.53	1.58	38.51	
			45.05	
Si 2p	103.26	1.6	25.79	SiO₂

f

Orbitals	Position	FWHM	At. %	Assignments
C 1s	285	1.6	4.69	C-C, C-H C-O, C-N O=C-(N,O)
	286.49	1.6	3.09	
	288.39	1.6	1.61	
			9.39	
N 1s	400.04	1.92	1.93	N=C-NH, N-C N-C=O
O 1s	531.62	1.29	2.02	O=C-(N,O) O-Si, O-C=O
	532.69	1.46	52.95	
			54.97	
Si 2p	103.37	1.61	33.71	SiO₂

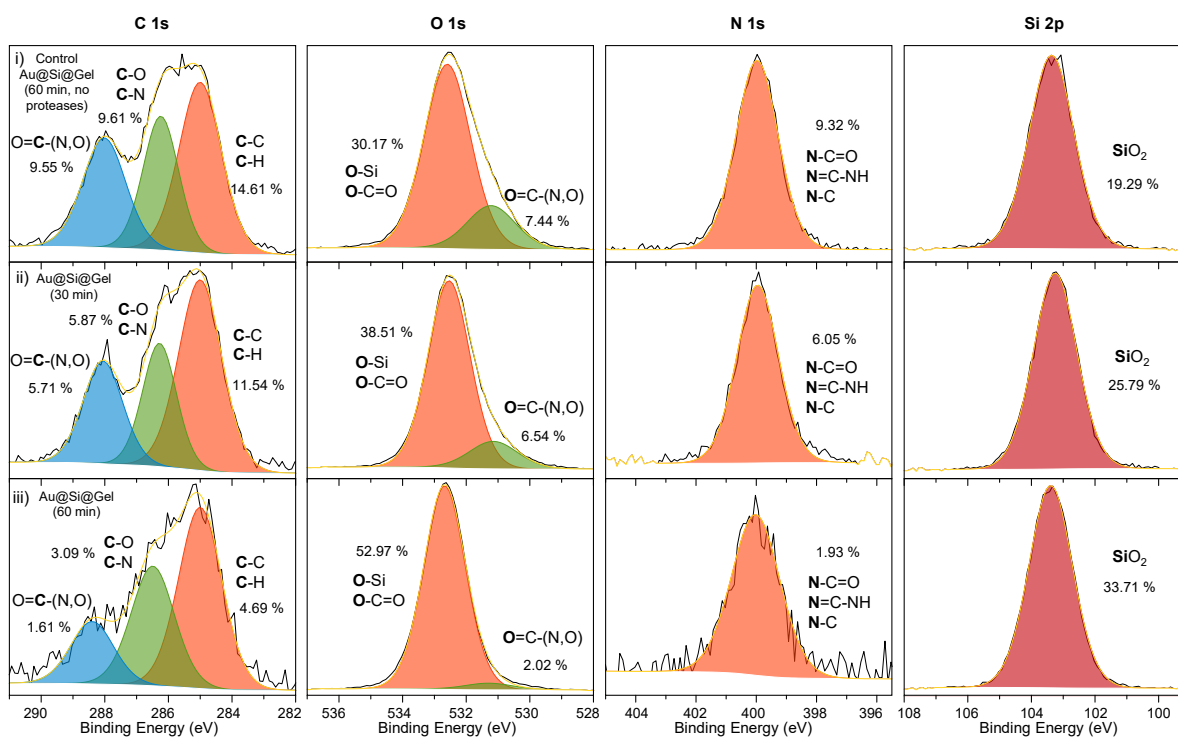


Figure S4 XPS C 1s, O 1s, N 1s and Si 2p core peaks spectra of i) control Au@Si@Gel incubated 60 min without proteases, ii) Au@Si@Gel incubated 30 min and iii) Au@Si@Gel incubated 60 min with the At.% for all components.

Table S2 List of peptides de novo sequenced from the MS/MS data from the LC-ESI-MS/MS analysis of the positive gelatin control digested by trypsin. P represents hydroxyproline. N represents deamidated asparagine. M represents oxidized methionine.

Peptide Sequence	m/z	Charge	Accession number	Protein	E-value	Identity	PepNovo+ Score
TGETGASGPPGFAGEK	1478.68	1	F1SFA7	Collagen type I alpha 2 chain	4.2E-10	100%	190.56
GPPGESGAAGPAGPIGSR	775.88	2	F1SFA7	Collagen type I alpha 2 chain	5.1E-12	100%	174
GEPGPAGLPGPPGER	1435.68	1	A0A5G2QQE9	Collagen type I alpha 1 chain	2.5E-9	100%	163.6
GEPGNIGFPGPK	1201.58	1	F1SFA7	Collagen type I alpha 2 chain	1E-6	100%	162.2
GSAGPPGATGFPGAAGR	730.35	2	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	160.5
GDGGPPGATGFPGAAGR	729.34	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-11	100%	159.11
GPPGESGAAGPAGPIGSR	1550.76	1	F1SFA7	Collagen type I alpha 2 chain	5.1E-12	100%	156.68
GPPGPMGPPGLAGPPGESGR	916.93	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	155.51
TGETGASGPPGFAGEK	739.84	2	F1SFA7	Collagen type I alpha 2 chain	4.2E-1	100%	155.25
GAAGLPGVAGAPGLPGPR	1562.83	1	F1SFA7	Collagen type I alpha 2 chain	7.8E-12	100%	154.88
GETGPAGPAGPVGPVGAR	1546.8	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.6E-12	100%	154.59
GDGGPPGATGFPGAAGR	737.34	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-11	100%	153.33
GPPGPMGPPGLAGPPGESGR	900.94	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	151.47
GPPGAVGNPVGNGAPGEAGR	874.42	2	F1SFA7	Collagen type I alpha 2 chain	2.6E-14	100%	147.43
GSAGPPGATGFPGAAGR	722.35	2	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	145.93
GSAGPPGATGFPGAAGR	1459.69	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	145.71
PGADGVAGPK	442.73	2	A0A5G2QQE9	Collagen type I alpha 1 chain	6.5E-4	100%	145.48
PGPAGAAGAPGPQGAAGVGPAGK	858.94	2	F1SFA7	Collagen type I alpha 2 chain	3.4E-15	100%	144.22
GPAGPPGPPGAAGTGLQGMPGER	1095.52	2	A0A286ZQ85	Collagen type III alpha 1 chain	4.1E-19	100%	143.13
GFSGLDGAK	851.43	1	A0A5G2QQE9	Collagen type I alpha 2 chain	9.6E-3	100%	142.41
GLPGVAGSVGEPGPL	1338.69	1	F1SFA7	Collagen type I alpha 2 chain	9.9E-9	100%	142.31
PGPAGAAGAPGPQGAAGVGPAGK	850.94	2	F1SFA7	Collagen type I alpha 2 chain	3.4E-15	100%	140.65
TGQPGAVGPAGIR	1180.64	1	F1SFA7	Collagen type I alpha 2 chain	2.8E-7	100%	140.19
GFPGSPGNVGPAGK	1273.62	1	F1SFA7	Collagen type I alpha 2 chain	1.9E-8	100%	138.5
GPAGAPGTPGPQGIAGQR	802.91	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.2E-12	100%	138.22
GSDGQPGPPGPPGTAGFPGSPGAK	1085.49	2	A0A286ZQ85	Collagen type III alpha 1 chain	4.4E-19	100%	138.11
GVPGPPGAVGPAGK	1192.63	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.2E-8	100%	137.48
GPPGPMGPPGLAGPPGESGR	908.94	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	136.92
GEVGPAGPNFAGPAGAAGQP GAK	1034.49	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-18	100%	136.74
GFPGSPGNVGPAGK	1273.62	1	F1SFA7	Collagen type I alpha 2 chain	1.9E-8	100%	136.63
TGQPGAVGPAGIR	1196.64	1	F1SFA7	Collagen type I alpha 2 chain	2.8E-7	100%	136.4
PGPPGAVGPAGK	518.77	2	A0A5G2QQE9	Collagen type I alpha 1 chain	2.7E-6	100%	136.07
PGPAGLPGPPGER	625.31	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.8E-7	100%	136.06

Peptide Sequence	m/z	Charge	Accession number	Protein	E-value	Identity	PepNovo+ Score
TGETGASGPPGFAGEK	1478.68	1	F1SFA7	Collagen type I alpha 2 chain	4.2E-10	100%	190.56
GPPGESGAAGPAGPIGSR	775.88	2	F1SFA7	Collagen type I alpha 2 chain	5.1E-12	100%	174
GEPGPAGLPGPPGER	1435.68	1	A0A5G2QQE9	Collagen type I alpha 1 chain	2.5E-9	100%	163.6
GEPGNIGFPGPK	1201.58	1	F1SFA7	Collagen type I alpha 2 chain	1E-6	100%	162.2
GSAGPPGATGFPGAAGR	730.35	2	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	160.5
GDGGPPGATGFPGAAGR	729.34	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-11	100%	159.11
GPPGESGAAGPAGPIGSR	1550.76	1	F1SFA7	Collagen type I alpha 2 chain	5.1E-12	100%	156.68
GPPGPMGPPGLAGPPGESGR	916.93	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	155.51
TGETGASGPPGFAGEK	739.84	2	F1SFA7	Collagen type I alpha 2 chain	4.2E-1	100%	155.25
GAAGLPVAGAPGLPGPR	1562.83	1	F1SFA7	Collagen type I alpha 2 chain	7.8E-12	100%	154.88
GETGPAGPAGVPVPGAR	1546.8	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.6E-12	100%	154.59
GDGGPPGATGFPGAAGR	737.34	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-11	100%	153.33
GPPGPMGPPGLAGPPGESGR	900.94	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	151.47
GPPGAVGNPGVNGAPGEAGR	874.42	2	F1SFA7	Collagen type I alpha 2 chain	2.6E-14	100%	147.43
GSAGPPGATGFPGAAGR	722.35	2	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	145.93
GSAGPPGATGFPGAAGR	1459.69	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.4E-11	100%	145.71
PGADGVAGPK	442.73	2	A0A5G2QQE9	Collagen type I alpha 1 chain	6.5E-4	100%	145.48
PGPAGAAGAPGPQGA VGPAGK	858.94	2	F1SFA7	Collagen type I alpha 2 chain	3.4E-15	100%	144.22
GPAGPPGPPGAAGT PGLQGMP GER	1095.52	2	A0A286ZQ85	Collagen type III alpha 1 chain	4.1E-19	100%	143.13
GFSGLDGAK	851.43	1	A0A5G2QQE9	Collagen type I alpha 2 chain	9.6E-3	100%	142.41
GLPGVAGSVGEPGPL	1338.69	1	F1SFA7	Collagen type I alpha 2 chain	9.9E-9	100%	142.31
PGPAGAAGAPGPQGA VGPAGK	850.94	2	F1SFA7	Collagen type I alpha 2 chain	3.4E-15	100%	140.65
TGQPGAVGPAGIR	1180.64	1	F1SFA7	Collagen type I alpha 2 chain	2.8E-7	100%	140.19
GFPGSPGNVGPAGK	1273.62	1	F1SFA7	Collagen type I alpha 2 chain	1.9E-8	100%	138.5
GPAGAPGTPGPQGIAGQR	802.91	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.2E-12	100%	138.22
GSDGQPGPPGPGTAGFP GSP GAK	1085.49	2	A0A286ZQ85	Collagen type III alpha 1 chain	4.4E-19	100%	138.11
GVPGPPGAVGPAGK	1192.63	1	A0A5G2QQE9	Collagen type I alpha 1 chain	3.2E-8	100%	137.48
GPPGPMGPPGLAGPPGESGR	908.94	2	A0A5G2QQE9	Collagen type I alpha 1 chain	5.8E-15	100%	136.92
GEVGPAGPNGFAGPAGAAGQP GAK	1034.49	2	F1SFA7	Collagen type I alpha 2 chain	2.2E-18	100%	136.74
GFPGSPGNVGPAGK	1273.62	1	F1SFA7	Collagen type I alpha 2 chain	1.9E-8	100%	136.63
TGQPGAVGPAGIR	1196.64	1	F1SFA7	Collagen type I alpha 2 chain	2.8E-7	100%	136.4
PGPPGAVGPAGK	518.77	2	A0A5G2QQE9	Collagen type I alpha 1 chain	2.7E-6	100%	136.07
PGPAGLPGPPGER	625.31	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.8E-7	100%	136.06

Table S3 List of peptides de novo sequenced from the MS/MS data from the LC-ESI-MS/MS analysis of the supernatant of Au@Si@Gel nanoparticles incubated in the culture medium for 60 minutes. P represents hydroxyproline.

Peptide Sequence	m/z	Charge	Accession number	Protein	E-value	Identity	PepNovo+ Score
GVQGGKGEQGPAGPPGFQ	842.41	2	F1SFA7	Collagen type I alpha 2 chain	6.4E-13	100%	115.17
GAPGTAGPSGSPGLPGERGAA	890.43	2	F1SFA7	Collagen type I alpha 2 chain	8.4E-15	100%	113.52
DFGYEGDFYR	634.76	2	F1SFA7	Collagen type I alpha 2 chain	3.6E-5	100%	106.52
GISGPPGPPGPA	1035.51	1	F1SFA7	Collagen type I alpha 2 chain	2E-6	100%	101.6
GKEGPAGLPGID	563.79	2	F1SFA7	Collagen type I alpha 2 chain	5.3E-6	100%	94.53
PGLPGPR	363.2	2	F1SFA7	Collagen type I alpha 2 chain	5E-1	100%	93.86
GSVGEPPGL	828.41	1	F1SFA7	Collagen type I alpha 2 chain	1.1E-2	100%	89.04
GAPGTAGPSGSPGLPGERGAA	898.43	2	F1SFA7	Collagen type I alpha 2 chain	8.4E-15	100%	88.99
GEVGSAGPPGPPGLR	690.35	2	F1SFA7	Collagen type I alpha 2 chain	3.8E-9	100%	86.13
GYEGDFYR	503.72	2	F1SFA7	Collagen type I alpha 2 chain	9.6E-3	100%	82.03
GILGAPGFL	860.49	1	F1SFA7	Collagen type I alpha 2 chain	8.3E-3	100%	77.88
GPSGSPGLPGERGAA	663.33	2	F1SFA7	Collagen type I alpha 2 chain	8.2E-9	100%	77.31
GLMGPRGPPGAVGAPGPQ	824.42	2	F1SFA7	Collagen type I alpha 2 chain	7.3E-13	100%	76.24
DFGYEGDF	949.36	1	F1SFA7	Collagen type I alpha 2 chain	1.5E-2	100%	75.06
GLTGSPGSPGPDGKTGPFGPA	926.44	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.8E-15	100%	73.48
GFPGSPGNVGPA	544.75	2	F1SFA7	Collagen type I alpha 2 chain	2E-6	100%	71.55
GANGDRGEAGPAGPAGPAGPR	611.3	3	F1SFA7	Collagen type I alpha 2 chain	3.4E-15	100%	69.91
GAPGLPGPR	853.45	1	F1SFA7	Collagen type I alpha 2 chain	5.1E-3	100%	69.45
GPTGPPGPIGSVGAPGPK	779.91	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.2E-12	100%	68.68
GEVGLPGVS	830.43	1	F1SFA7	Collagen type I alpha 2 chain	1.5E-2	100%	66.57
GDQGPVGRGTGETGASGPPGFA	965.95	2	F1SFA7	Collagen type I alpha 2 chain	1.4E-15	100%	66.45
GAAGATGARGL	451.25	2	F1SFA7	Collagen type I alpha 2 chain	1.9E-4	100%	65.34
DFGYEGDFY	1112.42	1	F1SFA7	Collagen type I alpha 2 chain	5.7E-4	100%	63.44
GPRGFPGSPGNVGPA	699.84	2	F1SFA7	Collagen type I alpha 2 chain	1.1E-9	100%	62.48
GAAGLPGVA	728.39	1	F1SFA7	Collagen type I alpha 2 chain	2.2E-2	100%	60.98
GGGYDFGYE	964.37	1	F1SFA7	Collagen type I alpha 2 chain	1.3E-3	100%	59.99

Table S4 List of peptides de novo sequenced from the MS/MS data from the LC-ESI-MS/MS analysis of the supernatant of Au@Si@Gel nanoparticles incubated in the culture medium for 30 minutes. P represents hydroxyproline.

Peptide Sequence	m/z	Charge	Accession number	Protein	E-value	Identity	PepNovo+ Score
GAPGTAGPSGSPGLPGERGAA	890.43	2	F1SFA7	Collagen type I alpha 2 chain	8.4E-15	100%	124.67
GVQGGKGEQGPAGPPGFQ	842.41	2	F1SFA7	Collagen type I alpha 2 chain	6.4E-13	100%	119.25
DFGYEGDFYR	634.76	2	F1SFA7	Collagen type I alpha 2 chain	3.6E-5	100%	119.20
GISGPPGPPGPA	1035.51	1	F1SFA7	Collagen type I alpha 2 chain	2E-6	100%	93.61
GSVGEPPGL	828.41	1	F1SFA7	Collagen type I alpha 2 chain	1.1E-2	100%	99.13
PGLPGPR	363.2	2	F1SFA7	Collagen type I alpha 2 chain	5E-1	100%	92.95
GYEGDFYR	503.72	2	F1SFA7	Collagen type I alpha 2 chain	9E-3	100%	91.53
GKEGPAGLPID	563.79	2	F1SFA7	Collagen type I alpha 2 chain	5.3E-6	100%	87.35
GAAGATGARGL	451.25	2	F1SFA7	Collagen type I alpha 2 chain	1.9E-4	100%	85.80
GPSGSPGLPGERGAA	663.33	2	F1SFA7	Collagen type I alpha 2 chain	8.2E-9	100%	83.44
GGGYDFGYE	964.37	1	F1SFA7	Collagen type I alpha 2 chain	1.3E-3	100%	79.08
GEQGPAGPPGFQ	579.26	2	F1SFA7	Collagen type I alpha 2 chain	1E-6	100%	76.53
GLTGSPGSPGPDGKTGPPGPA	926.44	2	A0A5G2QQE9	Collagen type I alpha 1 chain	1.8E-15	100%	76.30
GLMGRPPGAVGAPGPQ	824.42	2	F1SFA7	Collagen type I alpha 2 chain	7.3E-13	100%	72.24
GPSGSPGLPGERGAA	655.33	2	F1SFA7	Collagen type I alpha 2 chain	8.2E-9	100%	71.76
GGGYDFGY	835.33	1	F1SFA7	Collagen type I alpha 2 chain	1.4E-2	100%	61.16
GEVGSAGPPGPPGLR	690.35	2	F1SFA7	Collagen type I alpha 2 chain	3.8E-9	100%	71.22
GILGAPGFL	860.49	1	F1SFA7	Collagen type I alpha 2 chain	8.3E-3	100%	70.96
DFGYEGDF	949.36	1	F1SFA7	Collagen type I alpha 2 chain	1.5E-2	100%	70.92
GDQGPVGRGTGETGASGPPGFA	965.95	2	F1SFA7	Collagen type I alpha 2 chain	1.4E-15	100%	68.36
AGPPGPPGLR	475.76	2	F1SFA7	Collagen type I alpha 2 chain	3.2E-4	100%	68.25
DFGYEGDFY	1112.42	1	F1SFA7	Collagen type I alpha 2 chain	5.7E-4	100%	62.98
GEVGLPGVS	830.43	1	F1SFA7	Collagen type I alpha 2 chain	1.5E-2	100%	59.85

F1SFA7_PIG - Collagen type I alpha 2 chain. Coverage 305/1365 → 22.34 %

MLSFVDTRLLLLAVTSLATCQSLQEATARKGPTGDRGRPRGERGPPGPPGRDGDGIPGPPGPPGPPGPPGLGNNFAAQYDGGKGVG
AGPGMGLMGRPPGAVGAPGQGFQGPAGEPEGPGQTGPAGARGPPGPPGKAGEDGHPGKPRPGERGVVGPQGARGFPPT
GLPGFKGIRGHNLGLDGLKQPGAPVKGEPGAPGENGTGQTGARGLPGERGRVGPAGARGNDGVSVPVGPAGPIGSAGPPGF
PGAPGPKGELGPVGNPAGPAGPRGEVGLPGVSGPVGPPGNPGANLPGAKGAAGLPGVAGAPLPGPRGIPGPAAGAATGARG
LVGEPGAGSKGESGKGEPPGAAGPQPPGPSGEEGKRGNPEVGSAGPPGPPGLGNPGRSLPGADGRAGVMGPPGSRGPTG
PAGVVRGPNDSGRPEPEGLMGRGFPSPGNVGPAGKEGPAAGLPGIDGRPGPIGPAGARGEPGNIGFPPGKGTGDPGKNGEKGHA
GLAGARCAPGPDGNGAQQPPGQGVQGGKEQGPAGPPGFQGLPGPAGTAGEVGVKPGERGIPEFGLPGPAGPRGERGPPGES
GAAGPAGPIGSRGPSPPGPDGNKGEVGLGAPGTAGPSGSPGLPGERGAAGIPGGKGEKGETGLRGDVGSPGRDARGAPAVGA
PGPAGANGDRGEAGPAGPAGPRGSPGERGEVGPAGPNFAGPAGAAGQPGAKGERGKPKGENGPVGTGPVGAAGPAGP
NGPPGAGSRGDDGGPPGATGFPGAAGRIGPPGPSISGPPGPPGAGKEGLRGRDQGPVGRITGASGPPGFAGEKGPSGEP
GTAGPPGTPGPGQILGAPGFLGLPGSRGERCLPGVAGSVGEPGLGIAGPPGARPPGAVGNPVGNGAGEAGRDGNPDSGPPGR
DQAGHKGERGYPGNPPGAGAAGAPGQGA/GPAGKHGNGEPGAGSVGPAGAVGFRGPSGPGQIRGEKGEKGDGPRGLPL
KGHNLQGLPLAGHHDQAGPVPVGPAGPRGPAGSPGAGKDGRTGQPGAVGPAIGRGSQGSQGPAGPPGPPGPPGPPGSGG
GYDFGYEGDFYRADQPRSPSLRPKDYEVDA TLKSLNNQIETLLTEPSRKNPARTCRDLRLSHPEWSSGYWIDPNQGCMTDAIKVYC
DFSTGETCIRQPENIPAKNWRNSKVKKHWLGETINGGTQFEYNMEGVTTKEMATQLAFMRLLANHASQNTIYHCKNSIAYMDEETGN
LKKAVILQGSNDVELVAEGNSRFTYTVLVDGCSKKTNEWRTIIEYKTNKPSRLPILDIAPLDIGDADQEVSDVGVPCFK

A0A5G2QE9_PIG - Collagen type I alpha 1 chain. Coverage 219/1451 → 15.09 %

MFSFVDRLLLLAATALLTHGQEEGQEEGQQGQEEIPPVTCVQNGRLYHDRDWWKPVPCQICVCDNGNVLCDDDVICDEIKNCPSARV
PAGECCPVCPEGEVSPDQETTGVGPKGDTGPRGPRGSPGPPGRDGPQGLPGLPGLPGLPGLGNNFAPQLSYGYDEKSA
GISVPGMGPSPGRGLPGLPAGPQGFQGPGEPEGASGPMGPRGPPGPPGKNGDDGEAGKGRPGERGPPGQARGPLP
TAGLPGMKGHRGFSCLDGAAGDAGAPAGPKGEPGSPGANGAGQMGPRGLPGERGRPPGPAAGTGPAGPPGAVGAKGEAG
PQARGSEGPQGVREGEPPGPAAGPAGNPAGDQPGGKANGAPGIAGAPGFPGARGPSGPPGPPGPKGNSGEPGAPG
SKGDTGAKGEPGPTGVQPPGPAEEGKRGARPEGPAGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGAPGKSGP
EAGRPGEAGLPGAKLGTSPGSPGDKTGPPGAGQDGRPPGPPGARQOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVG
PAGKDGEAGAQQPPGAPGAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVGDLGAPGSPGARGERGFGERGVQGGPP
PAGPRGANGAPNDGAKGDAGAPGAGSQGAPLQGMGERGAAGLPGPKGDRGDAGPKGADGAPKDGVRGLTGPVPPGPA
PGDKGETGPSGAPGTARGAPDRGEPGPPGPAFAGPPGADGQPGAKGEPGDAGAKGDAGPPGAPGTGPPGPIGSVGPAGPK
GARBSAGPPGATGPPGAAGRVPPPGPSNAGPPGPPGAGKEGSKGRPETGPAGRPGEAGPPGPPGAGEKSGPADGPAGAP
GTPGPGQIAGQGVVGLPQGRGERGFPGLGSPGEPGKQSPGSPGERGPPGPMGPPGLAGPPGESGRGEGAPGAEKSPGRDGP
GKGDREGSEGPAGPPGAPGAPGVPVGPAGKSGDRGETGPAGPAGVGPVGPARGPAGPQGRDGETGEQDGRGKHRGFS
GLQGGPPGPPGSPGEGQPSGASGAPGPPGPPGSAGAPGKDG LNLGPIGPPGPRGRTGDAGVPVPPGPPGPPGPPGPPSGGDFD
FLPQPPQEKAHDGGRYRADDANVVRDRDLEVDTLKSLSQIENIRSPGSRKNPARTCRDLKMSHSDWKSGEYWIDPNQGCNLD
KVFCNMETGETCVYPTQPSVPPQKNWYISKNPDKRHWYGESMTDGFQFEYGGESDPADVAIQLTFLRLMSTEASQNTIYHCKNSVA
YMDQQTGNLKKALLQGSNEIIRAEGNSRFTYSVIYDGTSTHTGAWGKTVEYKTTKTSRLPIIDVAPLDVGPADQEFIDLSPVCF

A0A286ZQ85_PIG - Collagen type III alpha 1 chain. Coverage 135/1467 → 9.20 %

DMTSFVQKGTWLLFALLHPTVILAQQQEAIEGGCSHLGQSYADRDVWKPEPCQICVCDSGSVLCDDDIICDDQELDCPNPEIPFGECCAVC
PQPPTATPRPPNGHGPQPKGDPGPPGIPGRNDPGLPGQPGSPGSPGPPGICESCPTGGQNYSPQYESYDVKAGVAGGGIGGYPG
PAGPPGPPGPPGVSGHPGAPGSPGYQPPGEPGQAGPAGPPGPPGAIGPSGPAKDGESGRPGRGERGLPGPPGLGAPAMPGF
PGMKGHRGFDGRNGEKDGTGAPGLKGENLPGENGAPGPMGPRGAPGERGRPLGAAGARGNDGARSSDQGPFPGPPGPTAGF
PGSPGAKGEVGPAGSPGSPGQQRGEPGQGHAGAAAGPPGPPGNSGSPGGKEMGPAGIPGAPGLMGARGPPGPPGTNAGAPGQ
RGAAGEPGKNGAKGEPGRGERGEAGSPGIPGPKGEDGKDGSPGEPGANGLPGAAGERGMPPGFRGAPGANGLPGEKGPAGERGGP
GPAGPRVAGEPGRDGVPPGGLRGMPPGSPGSDGKPPGSPGQGESGRPPGSPGPRGQGVMGFPGPKNGDAPGKNGE
RGGPGGGLPGLPGLNGETGPQPPGPTGPGDKGDTGPPGQQLQGLPGTSGPPGENGKPGEPGPKGEAGAPGIPGKGDGSA
PGERGPPGAVGSPGPRGAGPPGPEGGKGPAGPPGPPGAAGTGLQGMPPGERGSSGSPGPKGDKGDPGSGADGAPKDGPRG
PTGPIGPPGAPQPDKGESGAPGLPIAGPRGGGERGEHPPGAPGFPAGPQNGEPGAKGERGAPGKGGGPPGIAGQPPGTT
GPPGPPGPPGQVKGERSPPGGGAAGFPGGRLPGPPGNSNGNPPGSSGPPGKDGPPGPPGSSGAPGSPVSGPKGDAGQPGEK
GSPGPPGPPGAPGPGISGITGARLAGPPGMPGARGSPGQGVKGENKPPGSLNGERGPPGQGLPLGAGAAGEPGRDGNP
SDGLPGRDGPAGSKDRGENSPGAPGAPGHPGPPGVPVGPAGKNGDRGETGPAGPAGAPGAGSRGAPGQGRGDKGETGERG
ANGIKGHRGFPGNPAGSPGAGHQQAVGSPGAPGRPVGSPGPPGKDGASGHPGPIGPPGPRGNGRGERGSESPGHPGQPP
PGPPGAPGCCGGAAAIAGVGEKAGGFAPYYGDEPMDFKINTDEIMTSLKSVNGQIESLISPDGSRKNPARNCRDLKFCHEPKSGE
YVVDPNQGCMDAIKVFNCNMETGETCISASPSTVPRKNWWTDSGAEKYYVWFGESMNGGFQFSYGNPELPEVDLVDQLAFLRLSSR
ASQNTIYHCKNSIAYMEHASGNVKKALRLMGSNEGEFKAEGNSKFTYTVLEDGCTKHTGEWVKTVFEYRTRKAVRLPIVDIAPYDGGPD
QEFADIGPVCFL

Figure S5 Protein coverage of the three proteins found in the positive trypsin-digested gelatin control. The identified peptides for Collagen type I alpha 2 chain protein had a 22.34 % protein coverage, for Collagen type I alpha 1 chain had a 15.09 % coverage and for Collagen type III alpha 1 chain had a 9.20 % coverage.

F1SFA7_PIG - Collagen type I alpha 2 chain. Coverage 223/1365 → 16.34 %

MLSFVDTRLLLLAVTSLCATCQSLQEATARKGPTGDRGRPRGERGPPGPPGRDGDGIPGPPGPPGPPGPPGLGGNFAAQYDGKGV
GAGPGPMGLMCPRGPPGAVGAPGPGFQGPAGEPEGEPGQTGPAGARGPPGPKAGEDGHPGKPRGERGVVGPQGARGFP
GTPGLPGFKIRGHNLGLDGLKGGPAGPVKGEPAENGTPGQTGARGLPGERGRVAGPAGARGNDGSGVGPVGPAGPIGSA
GPPGFPGAPGPKGELGPVGNPAGPAGPRGEVGLPGVS
GPVGPNGPANGPLGAKGAAGLPGVAGAPGLGPR
GIPGPA
GAAGATGARGLVGEPPAGSKGESGKGEPAAGPQGGPPGSGEEGRGN
GEVGSAGPPGPPGLR
GNPGRSLPGADGRAGVMGP
PGSRGPTGPAVGRPNNGDSGRPGEPGLM
GPRGFPGSPGNVGPAGKEGAPGLPGID
GRPGPIGPAGARGEPGNIGFPGPKGPTGDP
GKNGEKGHAGLAGARGAPDPGNNGAQGGPPGQ
VQGGKGEQGPAGPPGFQ
GLPGPAGTAGEVGPGERGIPGEFGLPGPAGP
RGERGPPGESGAAGPAGPIGSRGSPGPPGPDGNKGEVGLGAPGTAGPSGSPGLPGERGAA
GIPGGKGEKGETGLRGDVGSPGR
DGARGAPAVGAPGA
GANGDRGEAGPAGPAGPR
GSPGERGEVGPAGPNGFAGPAGAAGQPAGKGERGTKGPKGENGPVG
PTGPVGAAGPAGPNGPPGAGSRGDGPPGATGFPGAAGRIGPPGSPGISGPPGPPGAGKEGLRGR
GDQGPVGRGTGETGASC
PPGFA
GKGPSEPGTAGPPGTPGPO
GILGAPGFL
GLPGSRGERGLPGVA
GSVGEPPGL
GIAGPPGARGPPGAVGNPVGNGAPGE
AGRDGNPDSGPPGRDQAGHKGERGYPGNPAGAAAGPQGAAGVGPAGKHGNGRGEPPAGSVGPAGAVGPRGSPGQIR
GEKGEVGDGKPRGLPGLKGHNLQGLPGLAGHHGDQAGPVPVGPAGPRGAPSPGAGKDGRTGQPAVGPAGIRGSQGSQGP
AGPPGPPGPPGPPGSP
CGGYDFGYEGDFYR
ADQPRSPSLRPKYEV DATLTKSLNNQIETLLTPEGSRKNPARTCRDLRLSHPEWS
SGYYWIDPNQCTMDAIVYCDFSTGETCIRQENIPAKNWRNSKVKKHVWLGETINGGTQFEYNMEGVTTKEMATQLAFMRLLAN
HASQNITYHCKNSIAYMDEETGNLKKAVILQGSNDVELVAEGNSRFTYTVLVDGCSKKTNEWKRKTIIYKTNKPSRLPILDIAPLDIGDAD
QEVSVDPVPCFK

A0A5G2QQE9_PIG - Collagen type I alpha 1 chain. Coverage 39/1451 → 2.69 %

MFSFVDRLLLLLAATALLTHGQEEGQEEGQQQEEEDIPPVTCVQNGLRYHHRDWWKPVPCQICVCDNGNVLCDDDVICDEIKNCPARS
VPAGECCPVCPEGEVSPTDQETTGVGPKGDTGPRGPRGSPGPPGRDGIQGPGLGPPGPPGPPGPPGLGGNFAPQLSYGYDEK
SAGISVPGPMGSPGRGLPGPPGAPGQGFQGGPEGEPGASGPMGPRGPPGPKNGDDGEAGKPRGERGPPGQGARG
LPGTAGLPGMKGHRGFSGLDGAKGDAGAPGKGEPSGGENGAPGQMGPRGLPGERGRGPPGAPGTPAGPPGFPAGVGA
GEAGPQARGSEGPQVRGEPGPPGAGAAGPAGNPAGDQGGKANGAPGAPGFPGARGPSGQGPSGPPGPKGNSGE
PGAPGSKGDTGAKGEPGPTGVQGGPAGEEKRGARGEPGAGLPGPPGERGGPGSRGFPGADGVAAGPKGAGERGSPGAP
PKGSPGEAGRPEAGLPGAK
GLTGSPGSPGPDGKTGPPGPA
GQDGRGPPGPPGARGQAGVMGFPGKGAAGEPGKAGERGVP
GPPGAVGPAGKDGEAGAQQPPGAPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPEQGVPGDLGAPGSPGARGERGFPGE
RGVQGGPPGAPPRGANGAPNDGAKGDAGAPGAPGAPGLQGMGERGAAGLPGPKGDRGDAGPKGADGAPKDGVRGLT
GPIGPPGAPAGPDKGETGSPGAPGPTGARGAPDRGEPGPPGAPGAGPPGADGQPGAKGEPGDAGAKGDAGPPGPA
GPTGFP
GPIGSPVAGP
GARGSAGPPGATGFPGAAGRVP
GPPGSPGNAGPPGPPGAPGKEGSKGPRGETGPAGRPG
EAGPPGPPGAPGK
GSPGADGAPAGP
GTPGQGIAGQRGVVGLPGQRGERGFPLPGSPGEPGKQGPSGSPGERGPPGPMGPPGLAGPPGESGREGA
PGAEGSPGRD
GAPGKDRGESGAPPPGAPGAPGAPGVPAGKSGDRGETGPAGPAGVGPVGARFAGPQGPGRGDKGETG
EQGDRGK
GHRGFSGLQGGPPGSPGEGQGPSGASGAPGPRGPPGSAAGPKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPG
PPGPPGPPSGGDFD
SFLPQPPQEK
AHDGGRYRADDANVVRDRDLEVD
TTLKSLSQIENIR
SPEGSRKNPARTCRDLK
MCHSDWK
SGEY
WIDPNQGNLDAIKVFCN
METGETCVYPTQPSVPK
NWIYISK
NPKDKRHVVYGES
MTDGFQFEYGGEGSD
PADVAIQLTFLRL
MSTEASQNITYHCKNSVAYMDQQTGNLKKALLLQGSNEIEIRAEGNSRFTYSVIYDGTSTHTGAWGKTIVIEYKTTKTSRLPIIDVAPLDV
GAPDQEFIDLSPVCF

Figure S6 Protein coverage of the two proteins found in the supernatant of Au@Si@Gel nanoparticles incubated in culture medium for 60 min. The identified peptides for Collagen type I alpha 2 chain protein had a 16.34 % coverage and for Collagen type I alpha 1 chain had a 2.69 % coverage. Peptides corresponding to Collagen type III alpha 1 chain were not found in this sample.