Supporting Information

Plasma treatment causes structural modifications in lysozyme, with possible applications for cancer treatment

Table S1: Amino acids affected in control lysozyme at pH 2 and 7. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn, and Pro) were chosen as variable oxidation sites for the analysis with Mascot and Sequest.

Identifying	Annotated Sequence	Modifications	Master	Protein Accessions	m/z [Da]	MH+ [Da]	DeltaM
Node			Protein				[ppm]
			Accessions				
Sequest				B8YJT7; Q6LEL2;			
HT				P00698; B8YJN9;			
	[R].cELAAAMK.[R]	C1(Carbamidomethyl)	B8YJT7	B8YK79; B8YJP1	893.33335	893.33335	-99.15
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.75001	1428.49275	-110.23
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.83335	1428.65941	6.43
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.83335	1428.65941	6.43

Sequest			B8YJT7; P00698;			
HT			B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]	B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest			B8YJT7; P00698;			
HT			B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]	B8YJT7	B8YJP1	715.00001	1428.99275	239.75
Sequest			B8YJT7; P00698;			
HT			B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]	B8YJT7	B8YJP1	714.83335	1428.65941	6.43
Sequest						
HT	[R].NTDGSTDYGILQINSR.[W]	B8YJT7	P00698; B8YK79	585.50001	1754.48547	370.81
Sequest						
HT	[R].NTDGSTDYGILQINSR.[W]	B8YJT7	P00698; B8YK79	877.75002	1754.49276	374.96
Sequest						
HT	[R].NTDGSTDYGILQINSR.[W]	B8YJT7	P00698; B8YK79			

Table S2: Number of CAP-induced oxidations and type of amino acids affected by plasma-treated lysozyme at pH 7. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn, and Pro) were chosen as variable oxidation sites for the analysis with Mascot and Sequest.

Identifying	Annotated Sequence	Modifications	Master	Protein Accessions	m/z [Da]	MH+ [Da]	DeltaM
Node	_		Protein				[ppm]
			Accessions				
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7	877.83335	1754.65942	469.99
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7	877.50002	1753.99276	89.88
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7	877.75002	1754.49276	374.96

Sequest				P00698; B8YJT7;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	В8ҮК79	663.50001	1325.99275	273.12
Sequest		W7(Oxidation);		P00698; B8YJT7;			
HT	[R].GYSLGNwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	671.33334	1341.65941	25.2
Sequest	T			B8YJT7; P00698;	$\prod_{i=1}^{n}$		
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDyGILQINSR.[W]	Y8(Oxidation)	B8YJT7	B8YJT7	885.50002	1769.99276	91.94
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	715.00001	1428.99275	239.75
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7	877.25002	1753.49276	-195.21
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				B8YJT7; Q6LEL2;			
HT				P00698; B8YJN9;			
	[R].cELAAAMK.[R]	C1(Carbamidomethyl)	B8YJT7	B8YK79; B8YJP1	893.58335	893.58335	180.67
Sequest	T			B8YJT7; P00698;	$\prod_{i=1}^{n}$		
HT				B8YJN9; B8YK79;			
	[K].GTDVQAWIR.[G]		B8YJT7	B8YJP1	1045.50002	1045.50002	-40.65

Table S3: Number of CAP-induced oxidations and type of amino acids affected by plasma-treated lysozyme at pH 2. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn, and Pro) were chosen as variable oxidation sites for the analysis with Mascot and Sequest.

Identifying	Annotated Sequence	Modifications	Master	Protein Accessions	m/z [Da]	MH+ [Da]	DeltaM
Node	-		Protein				[ppm]
			Accessions				
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7	877.58335	1754.15942	184.91
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDyGILQINSR.[W]	Y8(Oxidation)	B8YJT7	B8YJT7	885.41668	1769.82609	-2.23
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].fESNFNTQATNR.[N]	F1(Oxidation)	B8YJT7	B8YJP1	722.91668	1444.82608	125.25
Sequest				P00698; B8YK79;			
HT	[R].NTDGSTDYGILQInSR.[W]	N14(Oxidation)	B8YJT7	B8YJT7	885.41668	1769.82609	-2.23
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNfNTQATNR.[N]	F5(Oxidation)	B8YJT7	B8YJP1	722.83335	1444.65942	9.88
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.83335	1428.65941	6.43
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79; B8YJT7	663.25001	1325.49275	-104.05

Table S4: Oxidized amino acids in control lysozyme peptide at pH 2. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn and Pro) were chosen for analysis. Samples were analyzed with Mascot and Sequest algorithms.

Identifying	Annotated Sequence	Modifications	Master	Protein	m/z [Da]	MH+ [Da]	DeltaM
Node			Protein	Accessions			[ppm]
			Accessions				
Sequest HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7;	877.50002	1753.99276	89.88
(A7)				P00698			
Sequest HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7;	663.50001	1325.99275	273.12
(A7)				P00698			
Sequest HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7;	663.58334	1326.15941	398.85
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	714.83335	1428.65941	6.43
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	715.16668	1429.32608	473.07
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	714.91668	1428.82608	123.09
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	715.00001	1428.99275	239.75
(A7)				P00698			

Table S5: Oxidized amino acids in control lysozyme peptide at pH 7. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn and Pro) were chosen for analysis. Samples were analyzed with Mascot and Sequest algorithms.

Identifying	Annotated Sequence	Modifications	Master	Protein	m/z [Da]	MH+ [Da]	DeltaM
Node			Protein	Accessions			[ppm]
			Accessions				

Sequest HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7;	877.50002	1753.99276	89.88
(A7)				P00698			
Sequest HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7;	663.50001	1325.99275	273.12
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	715.16668	1429.32608	473.07
(A7)				P00698			
Sequest HT	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJT7;	715.00001	1428.99275	239.75
(A7)				P00698			

Table S6: Oxidized amino acids in plasma-treated lysozyme peptide at pH 7. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn and Pro) were chosen for analysis. Samples were analyzed with Mascot and Sequest algorithms.

Identifying	Annotated Sequence	Modifications	Master	Protein	m/z [Da]	MH+ [Da]	DeltaM
Node			Protein	Accessions			[ppm]
			Accessions				
Sequest							
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	P00698; B8YK79	877.75002	1754.49276	374.96
Sequest							
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	P00698; B8YK79	585.33334	1753.98547	85.72
Sequest		C3(Carbamidomethyl);		B8YJT7; P00698;			
HT		C7(Carbamidomethyl);		B8YJN9; B8YK79;			
	[R].NLcNIPcSALLSSDITASVNcAK.[K]	C21(Carbamidomethyl)	B8YJT7	B8YJP1	836.75002	2508.23549	18.5
Sequest							
HT	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	P00698; B8YK79	877.83335	1754.65942	469.99
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	663.41668	1325.82608	147.4
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09

Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	715.00001	1428.99275	239.75
Sequest		N6(Oxidation);					
HT		W7(Oxidation);		P00698; B8YJN9;			
	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	679.33334	1357.65941	28.65
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	663.50001	1325.99275	273.12
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.83335	1428.65941	6.43
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	663.41668	1325.82608	147.4
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	663.41668	1325.82608	147.4
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	715.08335	1429.15941	356.41
Sequest				P00698; B8YJN9;			
HT	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	663.50001	1325.99275	273.12
Sequest		N6(Oxidation);					
HT		W7(Oxidation);		P00698; B8YJN9;			
	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	679.33334	1357.65941	28.65
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].IVSDGNGMNAWVAWR.[N]		B8YJT7	B8YJP1	838.50002	1675.99276	114.46
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09

ã							
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.83335	1428.65941	6.43
Sequest		W7(Oxidation);		P00698; B8YJN9;			
HT	[R].GYSLGNwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	671.41668	1341.82608	149.43
Sequest		W7(Oxidation);		P00698; B8YJN9;			
HT	[R].GYSLGNwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YK79	671.41668	1341.82608	149.43
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	714.91668	1428.82608	123.09
Sequest				B8YJT7; P00698;			
HT				B8YJN9; B8YK79;			
	[K].FESNFNTQATNR.[N]		B8YJT7	B8YJP1	1428.4167	1428.4167	-163.46
Sequest				B8YJT7; Q6LEL2;			
HT		C1(Carbamidomethyl);		P00698; B8YJN9;			
	[R].cELAAAmK.[R]	M7(Oxidation)	B8YJT7	B8YK79; B8YJP1	909.50002	909.50002	91.45

Table S7: Oxidized amino acids in plasma-treated lysozyme peptide at pH 2. Eight amino acids (Met, Tyr, Asp, Phe, His, Trp, Asn and Pro) were chosen for analysis. Samples were analyzed with Mascot and Sequest algorithms.

Identifying	Annotated Sequence	Modifications	Master	Protein Accessions	m/z [Da]	MH+	Delta
Node	_		Protein			[Da]	М
			Accessions				[ppm]
						1769.8	
Sequest HT (A7)	[R].NTDGSTDyGILQINSR.[W]	Y8(Oxidation)	B8YJT7	B8YJT7; P00698	885.41668	2609	-2.23
						1754.4	
Sequest HT (A7)	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7; P00698	585.50001	8547	370.81
						1753.6	-
Sequest HT (A7)	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7; P00698	877.33335	5942	100.18

						1754.6	
Sequest HT (A7)	[R].NTDGSTDYGILQINSR.[W]		B8YJT7	B8YJT7; P00698	877.83335	5942	469.99
				B8YJT7; P00698; B8YJN9;		1428.8	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.91668	2608	123.09
		N6(Oxidation);					
		W7(Oxidation);				1357.8	
Sequest HT (A7)	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7; P00698; B8YK79	679.41668	2608	151.42
		N6(Oxidation);					
		W7(Oxidation);				1357.6	
Sequest HT (A7)	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7; P00698; B8YK79	679.33334	5941	28.65
						1770.6	
Sequest HT (A7)	[R].NTDGSTDyGILQINSR.[W]	Y8(Oxidation)	B8YJT7	B8YJT7; P00698	885.83335	5942	468.62
				B8YJT7; P00698; B8YJN9;		1428.9	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	715.00001	9275	239.75
				B8YJT7; P00698; B8YJN9;		1429.3	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	715.16668	2608	473.07
				B8YJT7; P00698; B8YJN9;		1429.3	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	715.16668	2608	473.07
				B8YJT7; P00698; B8YJN9;		1428.6	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.83335	5941	6.43
				B8YJT7; P00698; B8YJN9;		1429.2	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	715.14166	7605	438.05
				B8YJT7; P00698; B8YJN9;		1428.9	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	715.00001	9275	239.75
						1325.8	
Sequest HT (A7)	[R].GYSLGNWVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7, P00698; B8YJN9	663.41668	2608	147.4
		N6(Oxidation);					
		W7(Oxidation);				1358.1	
Sequest HT (A7)	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7; P00698; B8YJN9	679.58334	5941	396.94
		W7(Oxidation);				1341.6	
Sequest HT (A7)	[R].GYSLGNwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7; P00698; B8YJN9	671.33334	5941	25.2

				B8YJT7; P00698; B8YJN9;		1428.8	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.91668	2608	123.09
				B8YJT7; P00698; B8YJN9;		1428.4	-
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.75001	9275	110.23
				B8YJT7; P00698; B8YJN9;		1428.4	-
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.75001	9275	110.23
				B8YJT7; P00698; B8YJN9;		1428.8	
Sequest HT (A7)	[K].FESNFNTQATNR.[N]		B8YJT7	B8YK79; B8YJP1	714.91668	2608	123.09
		N6(Oxidation);					
		W7(Oxidation);				1358.1	
Sequest HT (A7)	[R].GYSLGnwVcAAK.[F]	C9(Carbamidomethyl)	B8YJT7	B8YJT7; P00698; B8YJN9	679.58334	5941	396.94
				B8YJT7; P00698; B8YJN9;		1061.9	
Sequest HT (A7)	[K].GTDVQAwIR.[G]	W7(Oxidation)	B8YJT7	B8YK79; B8YJP1	531.50001	9274	428.91
				B8YJT7; P00698; B8YJN9;		1045.6	
Sequest HT (A7)	[K].GTDVQAWIR.[G]		B8YJT7	B8YK79; B8YJP1	523.33334	594	111.79
				B8YJT7; P00698; B8YJN9;		1061.8	
Sequest HT (A7)	[K].GTDVQAwIR.[G]	W7(Oxidation)	B8YJT7	B8YK79; B8YJP1	531.41667	2607	271.9
				B8YJT7; P00698; B8YJN9;		1045.9	
Sequest HT (A7)	[K].GTDVQAWIR.[G]		B8YJT7	B8YK79; B8YJP1	523.50001	9274	430.61
				B8YJT7; P00698; B8YJN9;		1045.8	
Sequest HT (A7)	[K].GTDVQAWIR.[G]		B8YJT7	B8YK79; B8YJP1	523.41667	2607	271.2



Figure S1. Cell viability analysis as a function of time, of HACAT (a), SK-MEL-2 (b) and G361 (c) cells, treated with plasma-treated lysozyme solutions. Results are presented as means \pm SEM (n = 3). Statistically significant differences are indicated as ** p < 0.01, and *** p < 0.001 between untreated lysozyme and corresponding treated groups. Significance was determined using student's t-test.



Figure S2. Comparison analysis of plasma-treated and untreated lysozyme solution under different conditions. (a-c) Viability assays of HACAT (a), SK-MEL-2 (b) and G361 (c) cells treated as indicated in the x-axis. ns = not significant. Results are presented as means \pm SEM (n = 3). Statistically significant difference are indicated as * p < 0.05, ** p < 0.01, and *** p < 0.001 between untreated lysozyme and corresponding treated groups. Significance was determined using student's t-test.