

SUPPLEMENTARY INFORMATION

Prosinecki et al. 2006 A proteomic approach towards the selection of proteins with enhanced intrinsic conformational stability

Supplementary Table. MALDI MS and MS/MS signal assignments. The table shows the peptide masses and the corresponding sequences identifying the Superoxide Dismutase, the Hypothetical DNA-binding protein 7e and the Ferredoxin reported in figure 5. The last three columns show the MS/MS assignments (a, b and y series) for the above proteins.

Protein	MALDI TOF spectrum		MALDI TOF/TOF spectrum			
	m/z	Peptide sequence	Fragment type	m/z	sequence	
Superoxide Dismutase	1098.663	(74-83) GLVFNINGHK				
	1119.591	(10-18) YELPPLPYK				
	1247.703	(9-18) KYELPPLPYK				
	1447.800	(29-40) DIIDVHYNGHHK				
	1649.858	(59-73) GEITSGQYDIQGLLR	b3	300.155	GEI	
			b4	401.203	GEIT	
			b5	488.235	GEITS	
			b7	673.315	GEITSGQ	
			b8	836.378	GEITSGQY	
			b9	951.405	GEITSGQYD	
			b10	1064.489	GEITSGQYDI	
			b14	1249.570	GEITSGQYDIQGLLR	
			y1	175.118	R	
			y3	401.287	RLL	
			y4	458.287	RLLG	
			y5	586.367	RLLGQ	
			y6	699.451	RLLGQI	
			y7	814.478	RLLGQID	
			y8	977.541	RLLGQIDY	
			y10	1162.621	RLLGQIDYQG	
		y11	1249.653	RLLGQIDYQGS		
		y13	1463.785	RLLGQIDYQGSTI		
		y15	1649.849	RLLGQIDYQGSTIEG		
	2032.821	(56-73) IIRGEITSGQYDIQGLLR				
	2363.409	(9-28) KYELPPLPYKVDALPEYISK				
	2469.394	(98-101) GGKPGGALADLIDKQYGSFDFKFK				
Hypothetical DNA-binding protein	1001.519	(43-52) GAVSEKDAPK				
	1019.540	(53-60) ELLQMLEK + Met ox	b1	130.050	E	
			b2	243.134	EL	
			b3	356.218	ELL	
			b4	484.277	ELLQ	
			b5	631.312	ELLQM	
			b6	744.396	ELLQM	
			y1	147.112	K	
			y2	276.155	KE	
			y3	389.239	KEL	
			y4	536.274	KELM	
			y5	664.333	KELMQ	
			y6	777.417	KELMQL	
			y8	1019.540	KELMQLLE	
		1290.558	(29-39) MISFITYDDNGK			
		1306.651	(29-39) + Met ox			
Ferredoxin	834.406	GPDINYR				
	1077.748	QVVGEGHSGHK	b6	650.093	QVVGEGH	
			y4	428.167	KHGS	
			y5	565.188	KHGS	
			y7	751.279	KHGSHEG	
			y10	1077.587	KHGSHEGVVQ	
			y9b8	665.861	VVGEGHSG	
			y8b9	703.831	VVGEGHSGH	