

Copper pretreatment augments ultraviolet B toxicity in the cyanobacterium *Anabaena doliolum*: a proteomic analysis of cell death

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Accessory publication

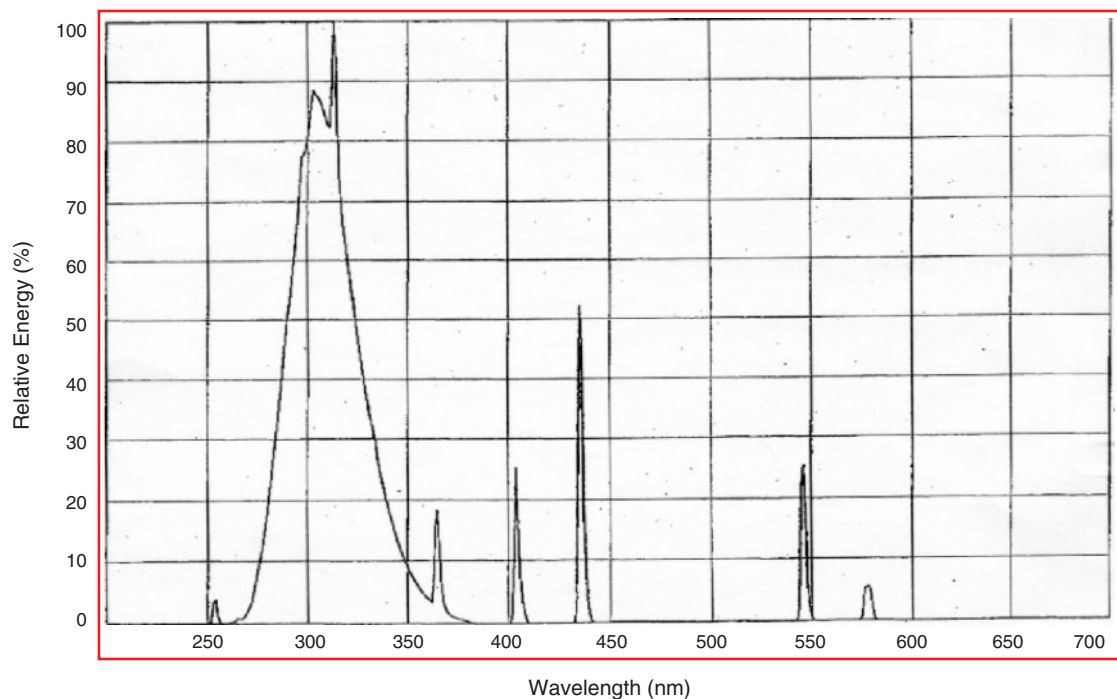


Fig. S1. Spectra of the UV-B lamp used to give artificial UV-B radiation.

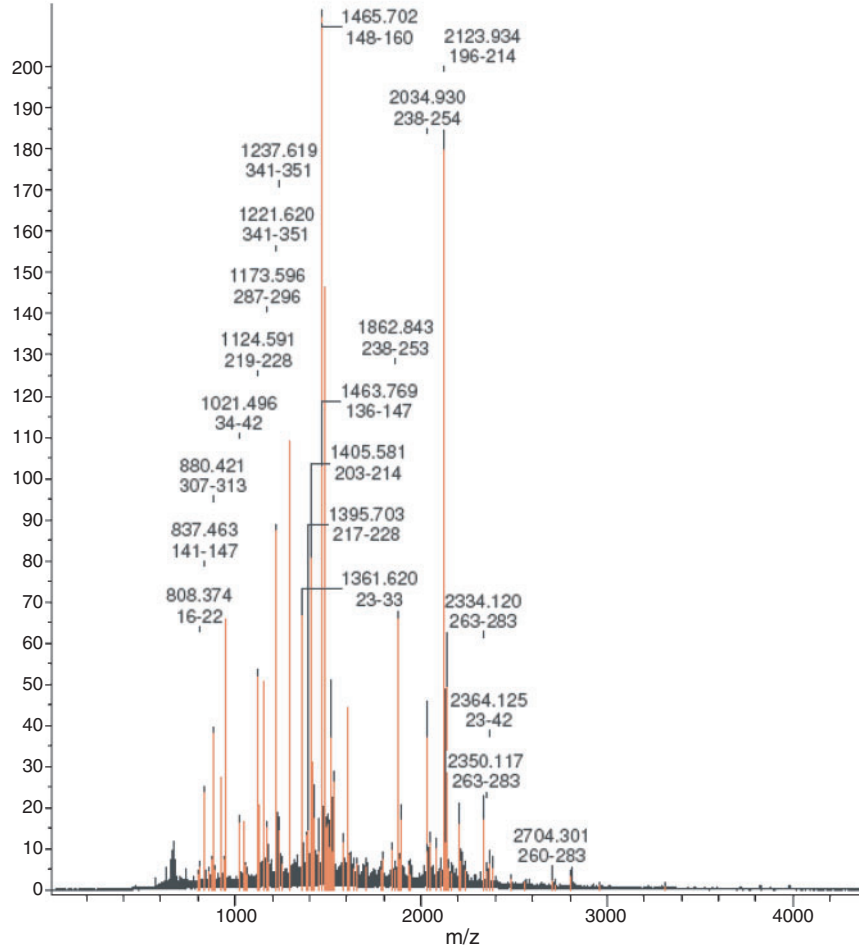
Spectrum Analysis Report

Date: 09/21/2006 Time: 16:51

FileName: K:\COMMERCIAL 2006\September\BHU\UV-3-1\O_A17\1\1SRef.pdata\1\1r

Sequence Name: ribulose 1,5-bisphosphate carboxylase/oxygenase large chain [imported] - Nostoc sp. (:
Parentmass: 1000.000
Mass Error: 998.992
MH+ (mono): 1.008
MH+ (avg): 1.008
Threshold (a.i.): 0.000
Tolerance (Da): 1.000
Number of Peaks: 95
Above Threshold: 95
Assigned Peaks: 0
Not assigned Peaks: 95

[Abs. Int. * 1000]

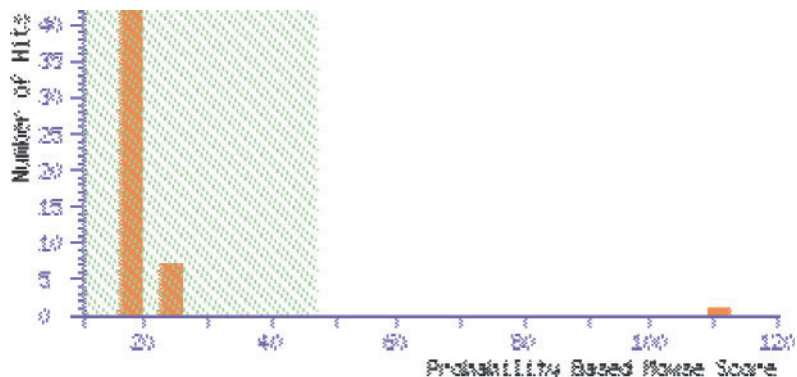


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Fig. S2. MALDI-TOF MS/MS spectrum of RuBisCo large chain tryptic peptide (spot no. 7, see Table 3).

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 47 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

1. AD2321 **Mass:** 38659 **Score:** 111 **Queries matched:** 6
 phosphoribulokinase [imported] - Nostoc sp. (strain PCC 7120)

Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/>	<u>44</u>	625.65	1249.29	1249.63	-0.34	0	38	0.61	1	R.YEDVLAAINSR.K
	<u>50</u>	533.65	1597.93	1597.86	0.07	0	(16)	87	3	K.YQGELTQLLLQHR.E
	<u>51</u>	533.82	1598.44	1597.86	0.58	0	19	40	3	K.YQGELTQLLLQHR.E
<input checked="" type="checkbox"/>	<u>58</u>	899.86	1797.71	1798.02	-0.32	0	(21)	24	1	R.EFADVVLQVLPPTNLIK.D
<input checked="" type="checkbox"/>	<u>59</u>	600.25	1797.73	1798.02	-0.30	0	36	0.77	1	R.EFADVVLQVLPPTNLIK.D
<input checked="" type="checkbox"/>	<u>61</u>	1015.23	2028.45	2028.00	0.45	0	22	18	1	R.EYPGSNNGTGFFQVLTGLK.M

Fig. S3. LC-MS of Phosphoribulokinase tryptic peptide (spot no. 1, see Table 3).

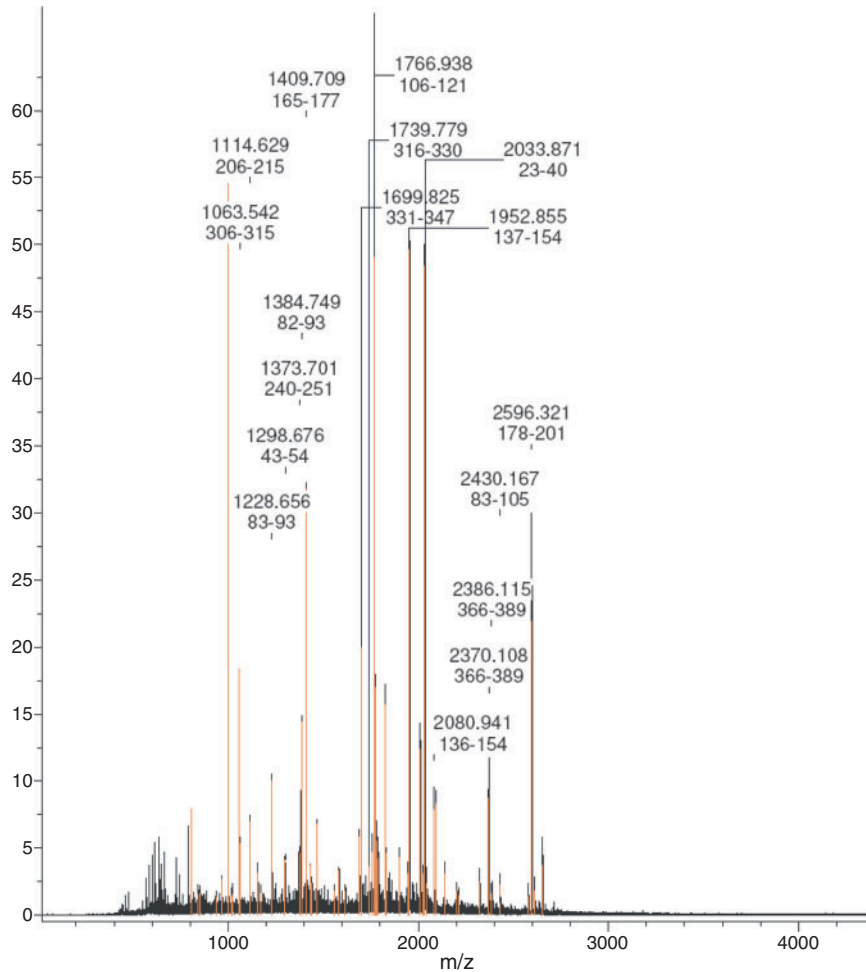
Spectrum Analysis Report

Date: 11/27/2006 Time: 14:07

FileName: K:\COMMERCIAL 2006\november\BHU\LCRA\1\0_C24\1\1SRef\data\1\1r

Sequence Name: phosphoglycerate kinase [imported] - Nostoc sp. (strain PCC 7120)
Parentmass: 1000.000
Mass Error: 998.992
MH+ (mono): 1.008
MH+ (avg): 1.008
Threshold (a.i.): 0.000
Tolerance (Da): 1.000
Number of Peaks: 58
Above Threshold: 58
Assigned Peaks: 0
Not assigned Peaks: 58

[Abs. Int. * 1000]



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Fig. S4. MALDI-TOF MS/MS spectrum of phosphoglycerate kinase tryptic peptide (spot no. 5, see Table 3).

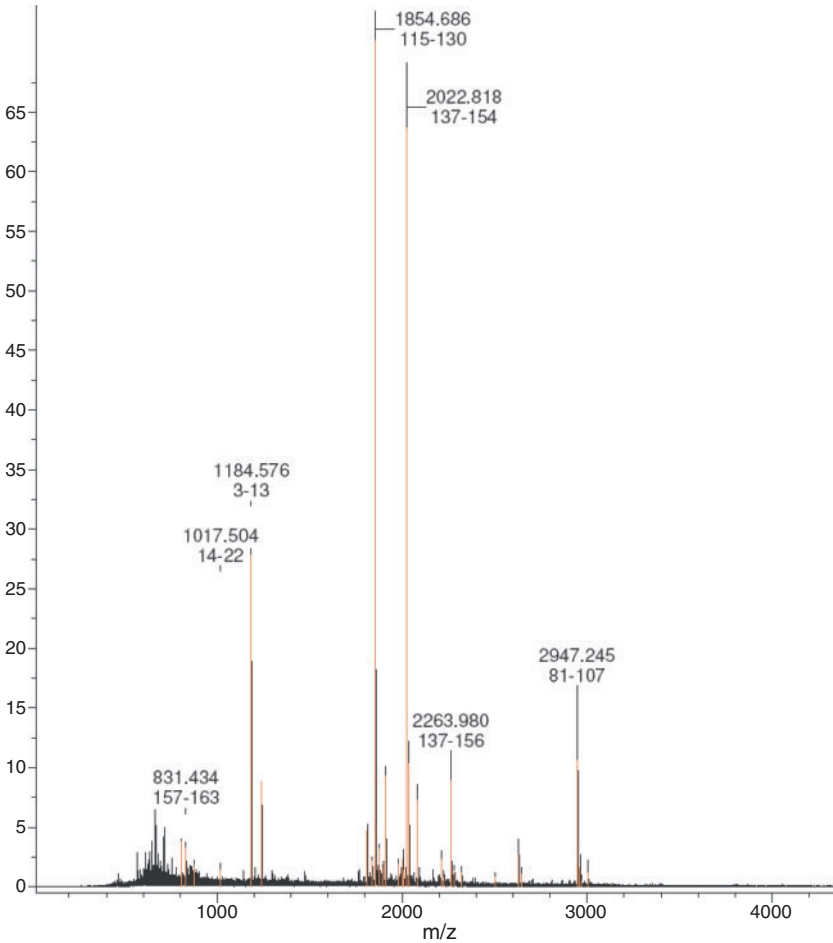
Spectrum Analysis Report

Date: 11/27/2006 Time: 15:51

FileName: K:\COMMERCIAL 2006\november\BHU\LCRA\3-1\0_D23\1\1SRef\data\1\1r

Sequence Name: flavodoxin - Anabaena sp. (PCC 7119) (fragment)
Parentmass: 1000.000
Mass Error: 998.992
MH+ (mono): 1.008
MH+ (avg): 1.008
Threshold (a.i.): 0.000
Tolerance (Da): 1.000
Number of Peaks: 30
Above Threshold: 30
Assigned Peaks: 0
Not assigned Peaks: 30

[Abs. Int. * 1000]

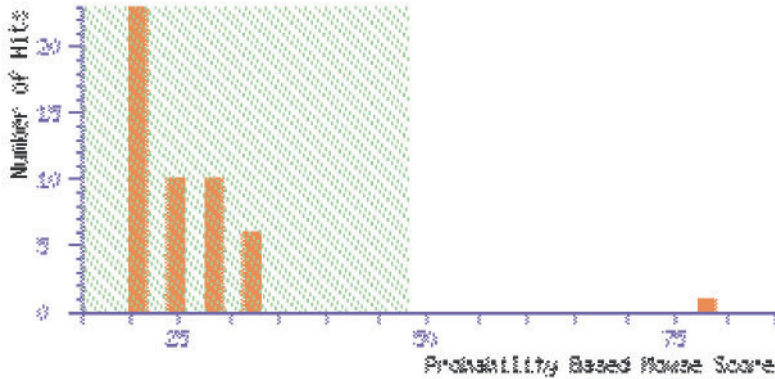


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Fig. S5. MALDI-TOF MS/MS spectrum of flavodoxin tryptic peptide (spot no. 2, see Table 3).

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 48 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

1. CUAI **Mass:** 11154 **Score:** 78 **Queries matched:** 2
plastocyanin - *Anabaena variabilis*

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> <u>25</u>	487.29	972.57	972.56	0.00	0	36	1.3	1	K.GLLVFEPAK.L
<input checked="" type="checkbox"/> <u>50</u>	563.64	1687.90	1687.90	-0.01	0	44	0.12	1	K.VPPHNVVFDALNPAK.S

Proteins matching the same set of peptides:

AB1839 **Mass:** 14667 **Score:** 78 **Queries matched:** 2
plastocyanin precursor [imported] - *Nostoc* sp. (strain PCC 7120)

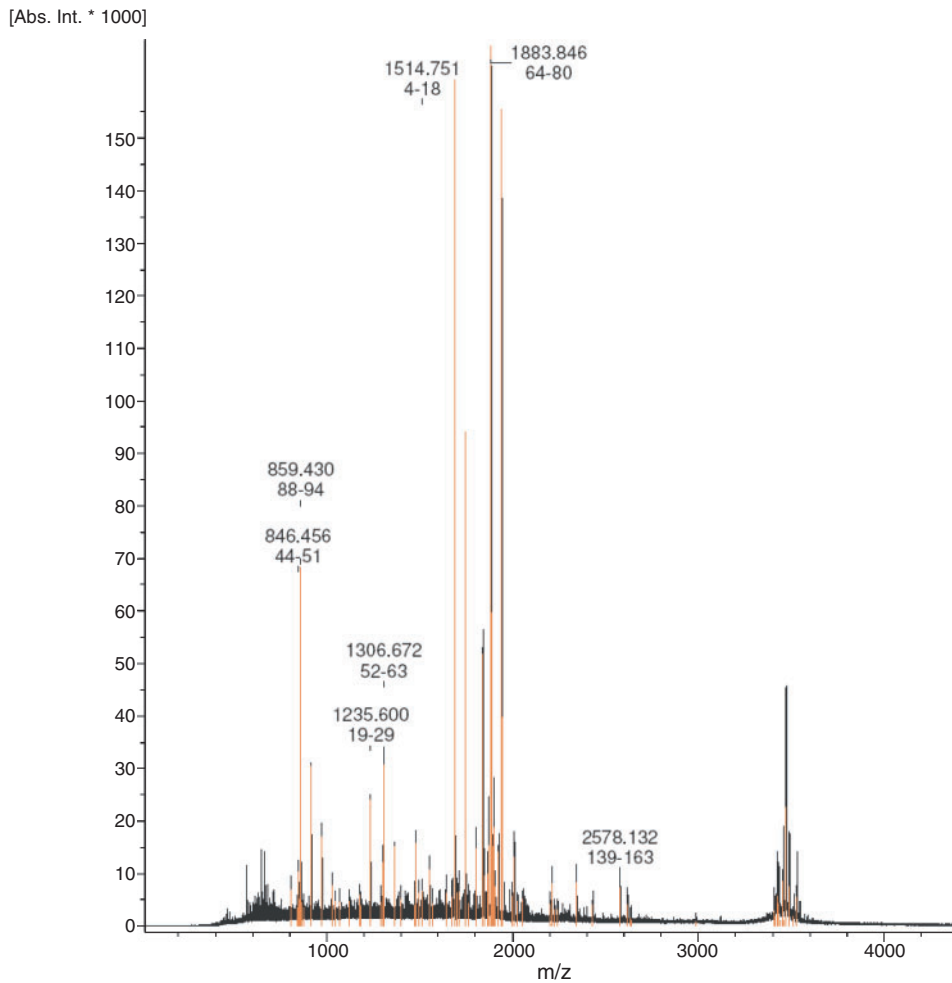
Fig. S6. LC-MS of plastocyanin tryptic peptide (spot no. 6, see Table 3).

Spectrum Analysis Report

Date: 11/27/2006 Time: 16:22

FileName: K:\COMMERCIAL 2006\november\BHU\LCRA\CS-2\0_E22\1\1SRef\data\1\1r

Sequence Name:	phycocyanin alpha chain - Anabaena sp.
Parentmass:	1000.000
Mass Error:	998.992
MH+ (mono):	1.008
MH+ (avg):	1.008
Threshold (a.i.):	0.000
Tolerance (Da):	1.000
Number of Peaks:	80
Above Threshold:	80
Assigned Peaks:	0
Not assigned Peaks:	80



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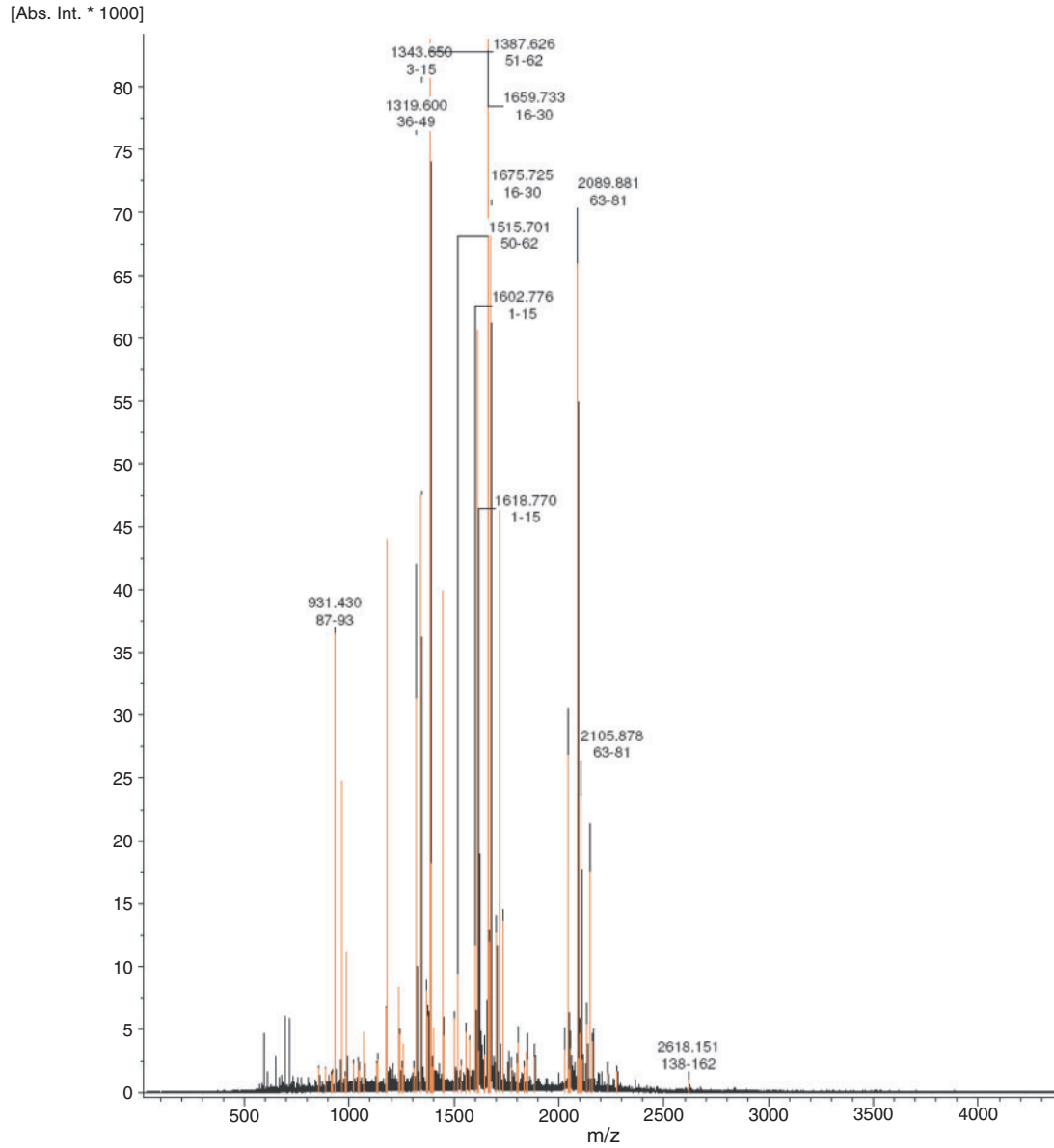
Fig. S7. MALDI-TOF MS/MS spectrum of phycocyanin α -chain tryptic peptide (spot no. 3, see Table 3).

Spectrum Analysis Report

Date: 03/23/2006 Time: 12:43

FileName: \\Flex-pc2\D:\data\userdata\COMMERCIAL 2006\March\BHU\BHU-c\0_E2\1\1SR\1\data\1\1r

Sequence Name:	phycoerythrocyanin alpha chain - Anabaena sp. (strain PCC 7120)		
Parentmass:	1000.000	Mass Error:	998.992
MH+ (mono):	1.008	MH+ (avg):	1.008
Threshold (a.i.):	0.000	Tolerance (Da):	1.000
Number of Peaks:	83	Above Threshold:	83
Assigned Peaks:	0	Not assigned Peaks:	83



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Fig. S8. MALDI-TOF MS/MS spectrum of phycoerythrocyanin α -chain tryptic peptide (spot no. 12, see Table 3).

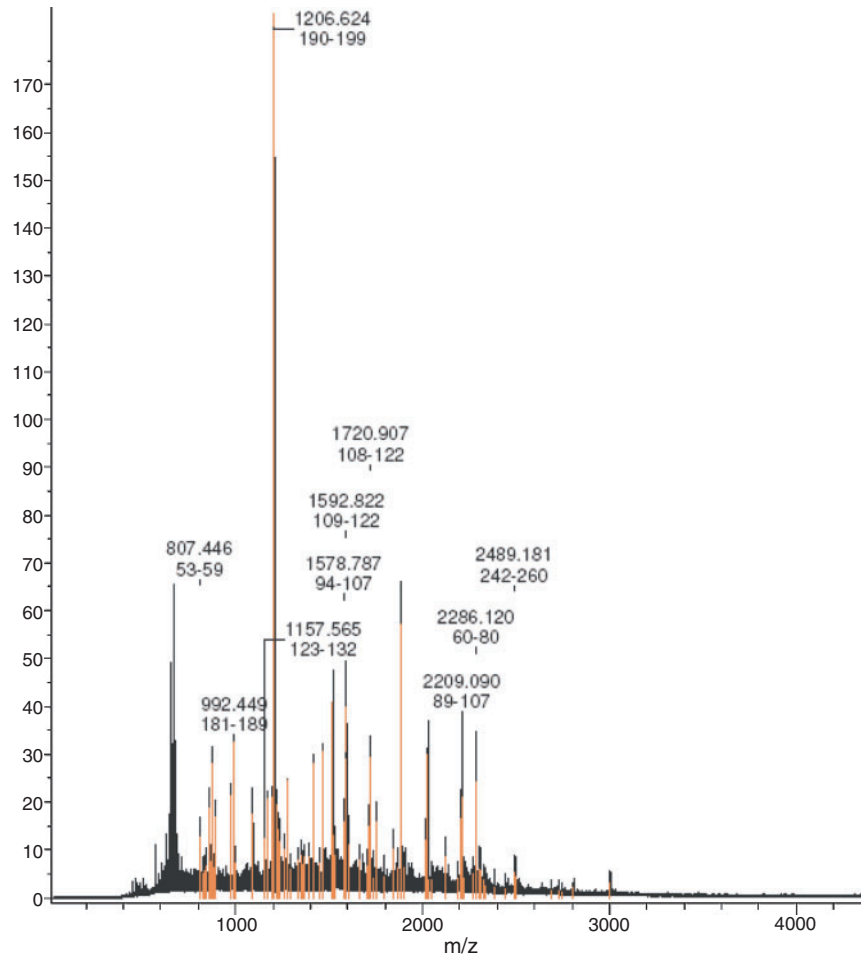
Spectrum Analysis Report

Date: 09/21/2006 Time: 16:57

FileName: K:\COMMERCIAL 2006\September\BHU\UV-4.0_A18.1\1SRef.pdata\1\1r

Sequence Name:	superoxide dismutase [imported] - Nostoc sp. (strain PCC 7120)
Parentmass:	1000.000
Mass Error:	998.992
MH+ (mono):	1.008
MH+ (avg):	1.008
Threshold (a.i.):	0.000
Tolerance (Da):	1.000
Number of Peaks:	87
Above Threshold:	87
Assigned Peaks:	0
Not assigned Peaks:	87

[Abs. Int. * 1000]



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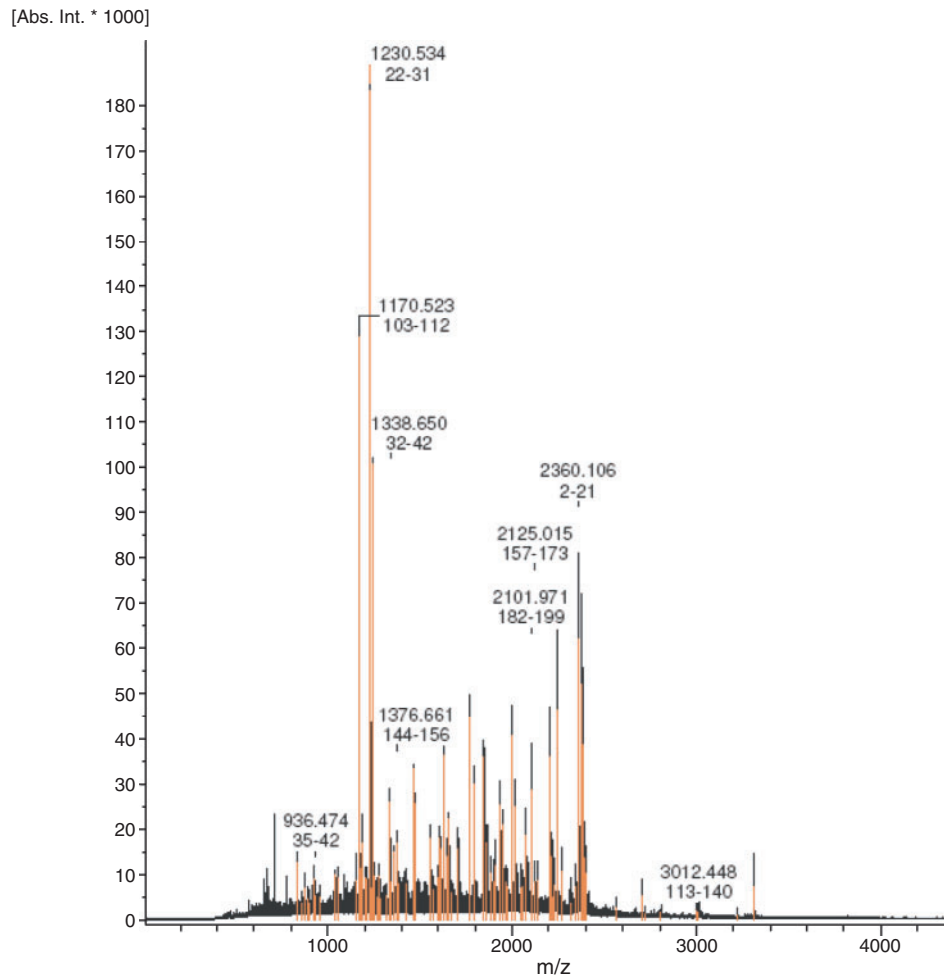
Fig. S9. MALDI-TOF MS/MS spectrum of superoxide dismutase tryptic peptide (spot no. 10, see Table 3).

Spectrum Analysis Report

Date: 09/21/2006 Time: 17:00

FileName: K:\COMMERCIAL 2006\September\BHU\UV-5\0_A19\1\1SRef.pdata\1\1r

Sequence Name:	iron superoxide dismutase [imported] - Nostoc sp. (strain PCC 7120)
Parentmass:	1000.000
Mass Error:	998.992
MH+ (mono):	1.008
MH+ (avg):	1.008
Threshold (a.i.):	0.000
Tolerance (Da):	1.000
Number of Peaks:	100
Above Threshold:	100
Assigned Peaks:	0
Not assigned Peaks:	100



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Fig. S10. MALDI-TOF MS/MS spectrum of iron superoxide dismutase tryptic peptide (spot no. 9, see Table 3).

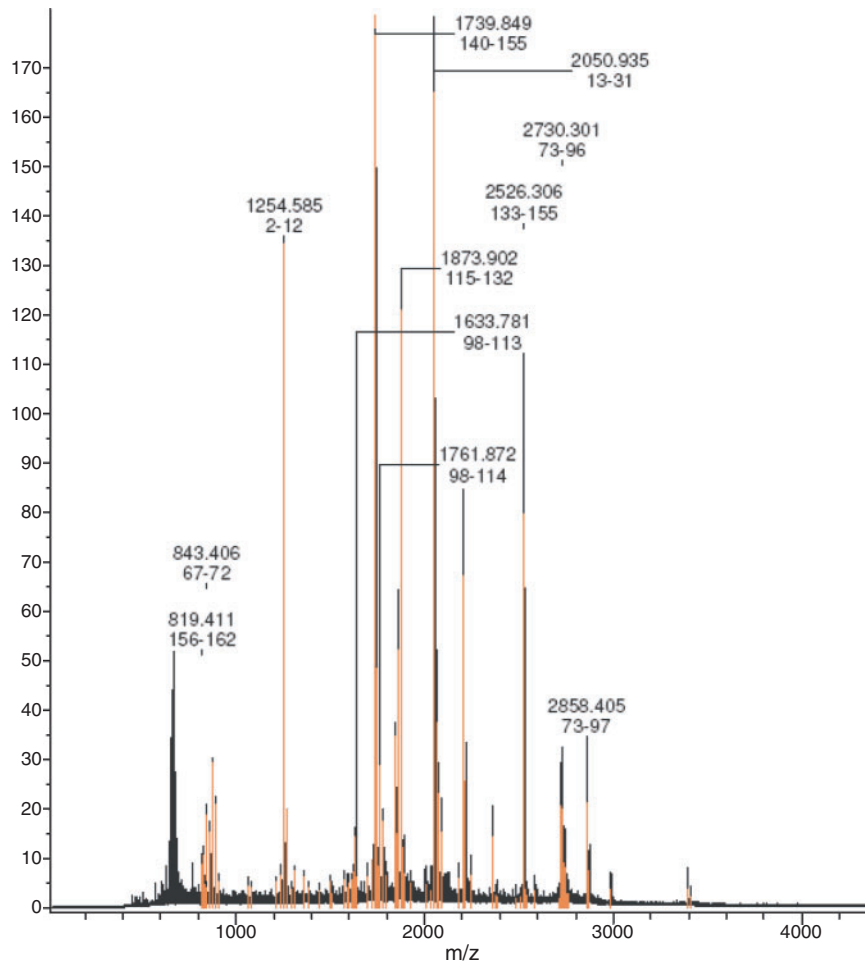
Spectrum Analysis Report

Date: 09/21/2006 Time: 16:41

FileName: K:\COMMERCIAL 2006\September\BHU\UV-2\0_A16\2\1SRef.pdata\1\1r

Sequence Name: peroxiredoxin [imported] - Nostoc sp. (strain PCC 7120)
Parentmass: 1000.000
Mass Error: 998.992
MH+ (mono): 1.008
MH+ (avg): 1.008
Threshold (a.i.): 0.000
Tolerance (Da): 1.000
Number of Peaks: 83
Above Threshold: 83
Assigned Peaks: 0
Not assigned Peaks: 83

[Abs. Int. * 1000]



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Fig. S11. MALDI-TOF MS/MS spectrum of peroxiredoxin tryptic peptide (spot no. 8, see Table 3).

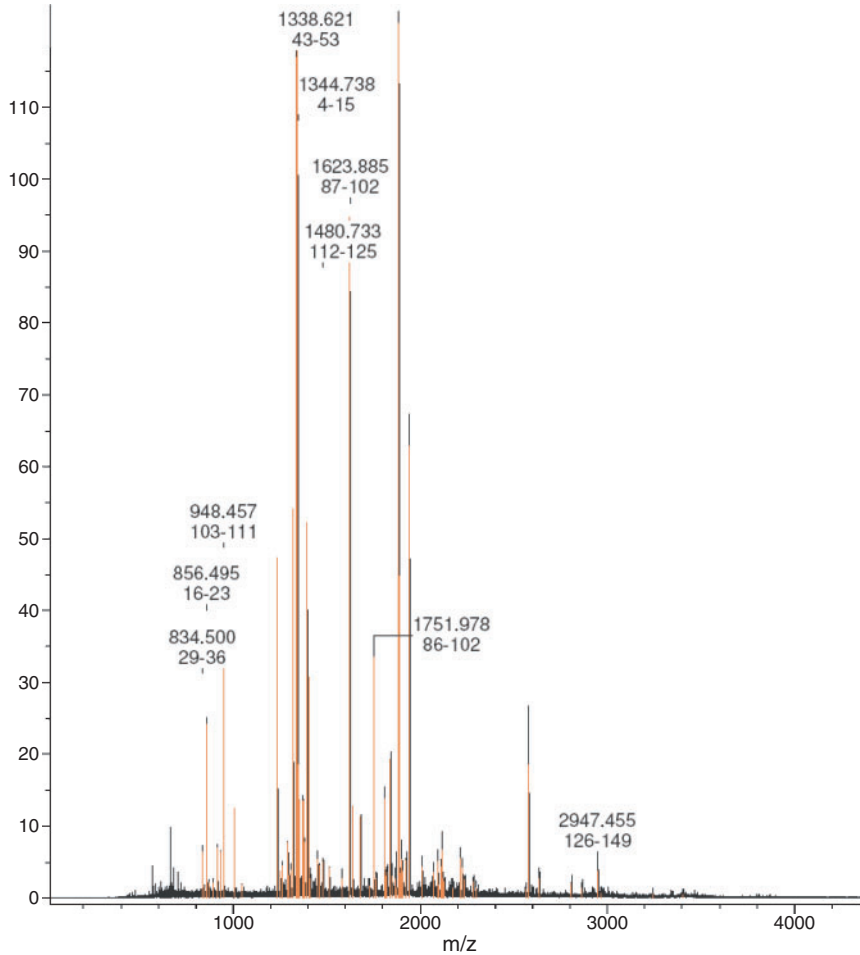
Spectrum Analysis Report

Date: 11/27/2006 Time: 14:13

FileName: K:\COMMERCIAL 2006\november\BHULCRA\60_E23\1\1SRef\data\1\1r

Sequence Name:	Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase) (Nucleoside-2-P kin
Parentmass:	1000.000
Mass Error:	998.992
MH+ (mono):	1.008
MH+ (avg):	1.008
Threshold (a.i.):	0.000
Tolerance (Da):	1.000
Number of Peaks:	82
Above Threshold:	82
Assigned Peaks:	0
Not assigned Peaks:	82

[Abs. Int. * 1000]



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Fig. S12. MALDI-TOF MS/MS spectrum of nucleoside diphosphate kinase tryptic peptide (spot no. 4, see Table 3).

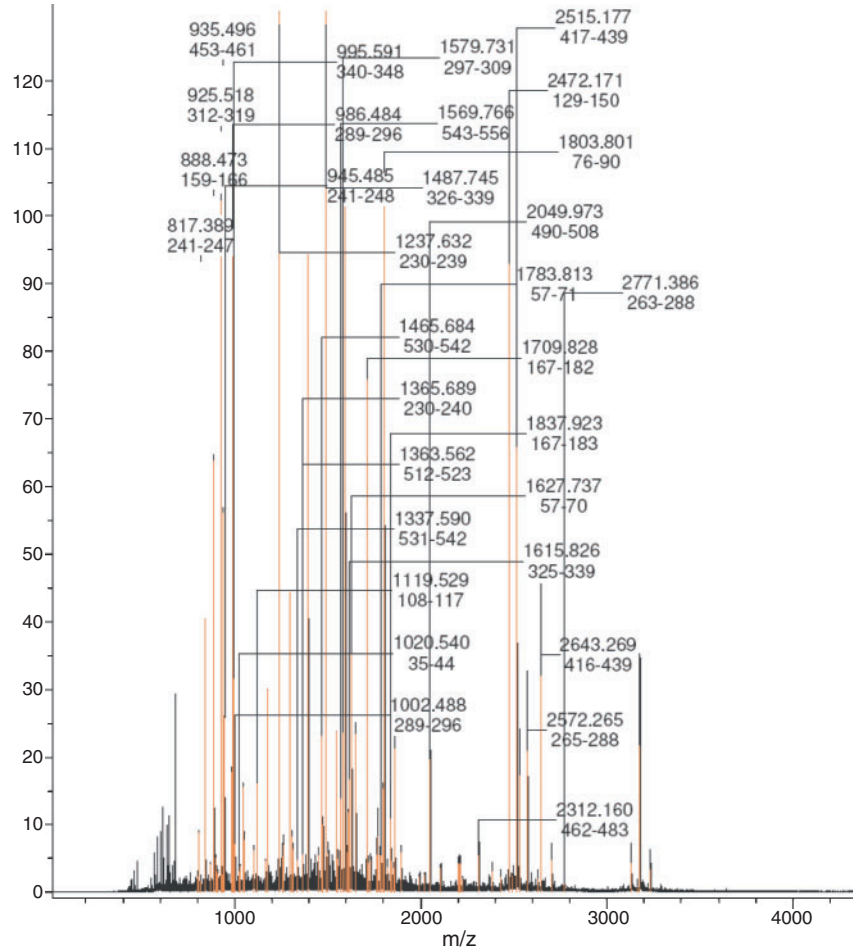
Spectrum Analysis Report

Date: 11/27/2006 Time: 14:10

FileName: K:\COMMERCIAL 2006\november\BHULCRA\1C40_D24\1\1SRef\data\1\1r

Sequence Name: DnaK-type molecular chaperone [imported] - Nostoc sp. (strain PCC 7120)
Parentmass: 1000.000
Mass Error: 998.992
MH+ (mono): 1.008
MH+ (avg): 1.008
Threshold (a.i.): 0.000
Tolerance (Da): 1.000
Number of Peaks: 100
Above Threshold: 100
Assigned Peaks: 0
Not assigned Peaks: 100

[Abs. Int. * 1000]



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Fig. S13. MALDI-TOF MS/MS spectrum of DnaK-Type molecular chaperone tryptic peptide (spot no. 11, see Table 3).