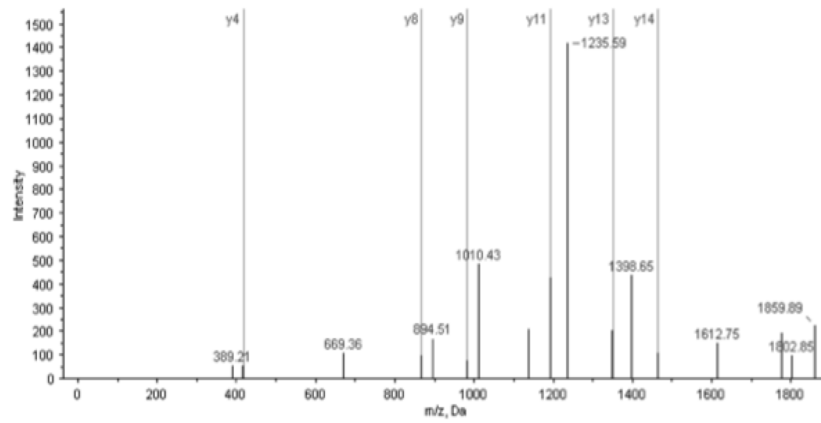


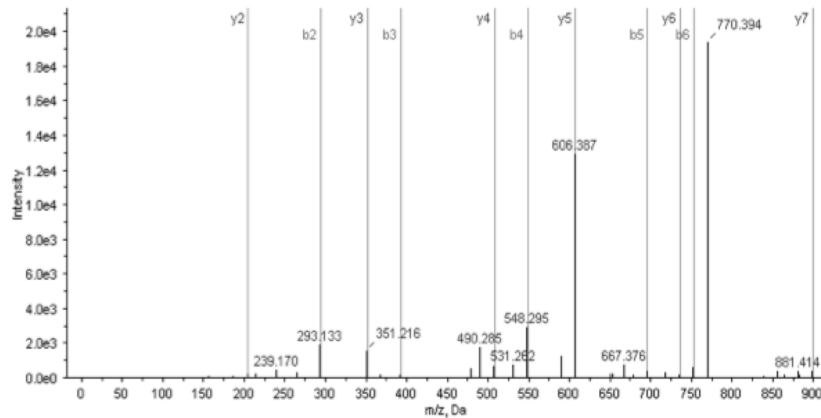
1. Q16-K33

Residue	b	y
Q	112.0393	1901.9491
L	225.1234	1790.9171
T	326.1710	1677.8330
I	439.2551	1576.7853
N(Dea)	554.2821	1463.7013
G	611.3035	1348.6743
V	710.3719	1291.6529
P	807.4247	1192.5844
D	922.4516	1095.5317
D	1037.4786	980.5005
S	1124.5106	865.4778
F	1271.5790	778.4458
T	1372.6267	631.3774
I	1485.7108	530.3297
N	1599.7537	417.2456
V	1698.8221	303.2027
G	1755.8436	204.1343
K	1883.9385	147.1128



2. Y42-K48

Residue	b	y
Y	164.0706	898.4781
E	293.1132	735.4148
V	392.1816	606.3722
R	548.2827	507.3038
F	695.3511	351.2027
G	752.3726	204.1343
K	880.4676	147.1128



3 (1). A49-K61

Residue	b	y
G	58.0287	1479.7182
N	172.0717	1422.6967
E	301.1143	1308.6538
Q(Dea)	430.1569	1179.6112
S	517.1889	1050.5686
V	616.2573	963.5366
I	729.3414	864.4682
I	842.4254	751.3841
M	973.4659	638.3000
S	1060.4979	507.2595
C(CAM)	1220.5286	420.2275
I	1333.6126	260.1969
K	1461.7076	147.1128

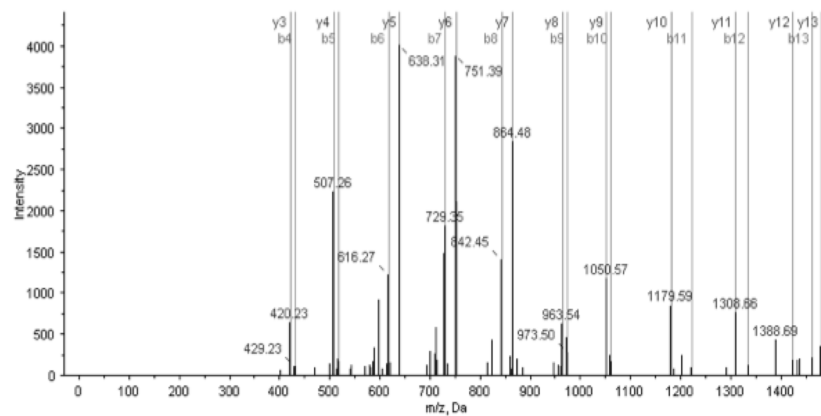
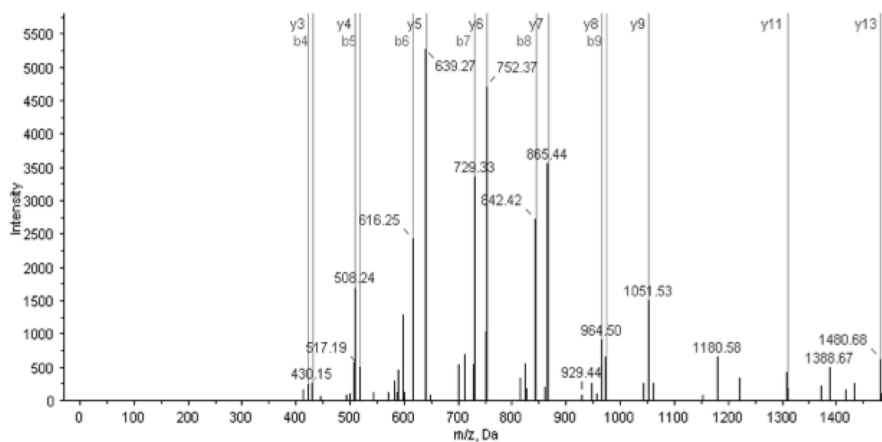


FIGURE S3. Nano LC-MS/MS analysis of Con II-tagged Con-P.

MALDI TOF MS/MS analysis was achieved by using an AB SCIEX TOF/TOF 5800 Analyzer after digested with *Achromobacter* protease I and subsequently separated by a nano-LC system. ProteinPilot software with the Paragon method was used for identification. As a result, the 27 peptide fragments were detected with 95% confidence intervals, and 82.3% of rCon-P sequence was covered with non-redundant 10 peptide fragments including QLTINGVPDDSFITNVGK (16-33), YEVRFGK (42-48), ANEQSVIIMSCIK (49-61), DG VVLHTQTETSPFPQK (62-78), SRSFEVSIS (79-87), INSHVMYFSN (97-106), FSNSLDAQDYDIWSHGK (104-121), and VSIEGISIN (122-130). The typical spectra of 10 fragments used for identifying Con-P sequence are shown.

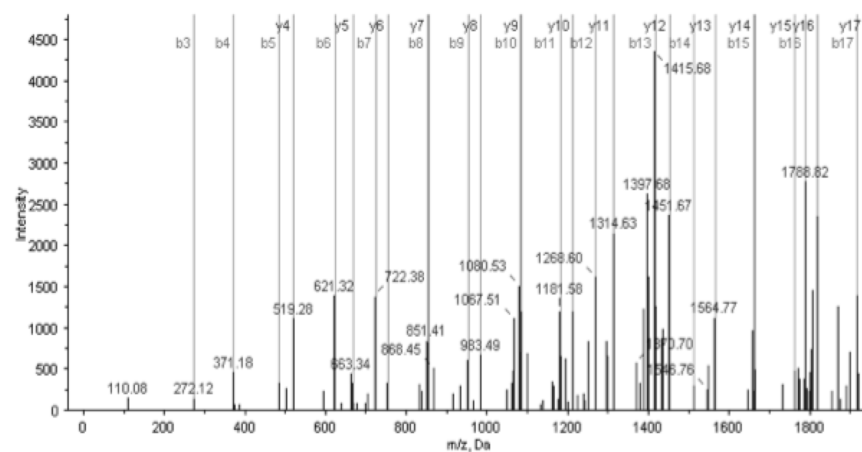
3 (2). A49-K61

Residue	b	y
A	72.0444	1480.7022
T	173.0921	1409.6651
E	302.1347	1308.6174
Q	430.1932	1179.5748
S	517.2253	1051.5162
V	616.2937	964.4842
I	729.3777	865.4158
I	842.4618	752.3317
M	973.5023	639.2477
S	1060.5343	508.2072
C(CAM)	1220.5650	421.1751
I	1333.6490	261.1445
K	1462.6916	148.0604



4. D62-K78

Residue	b	y
D	116.0342	1933.9654
G	173.0557	1818.9385
V	272.1241	1761.9170
V	371.1925	1662.8486
L	484.2766	1563.7802
H	621.3355	1450.6961
T	722.3832	1313.6372
Q	850.4417	1212.5895
T	951.4894	1084.5310
E	1080.5320	983.4833
T	1181.5797	854.4407
S	1268.6117	753.3930
F	1415.6801	666.3610
P	1512.7329	519.2926
F	1659.8013	422.2398
Q	1787.8599	275.1714
K	1915.9549	147.1128



5. S79-S87

Residue	b	y
S	88.0393	1011.5106
R	244.1404	924.4785
S	331.1724	768.3774
F	478.2409	681.3454
E	607.2835	534.2770
V	706.3519	405.2344
S	793.3839	306.1660
I	906.4680	219.1339
S	993.5000	106.0499

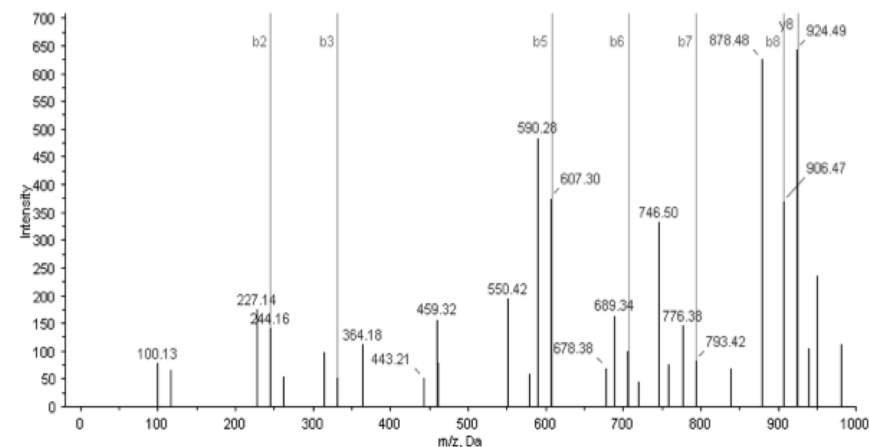
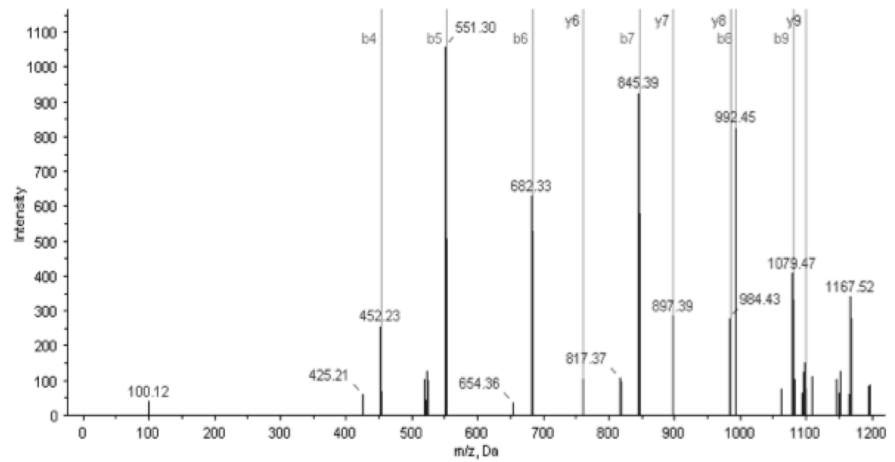


Figure S3 continued.

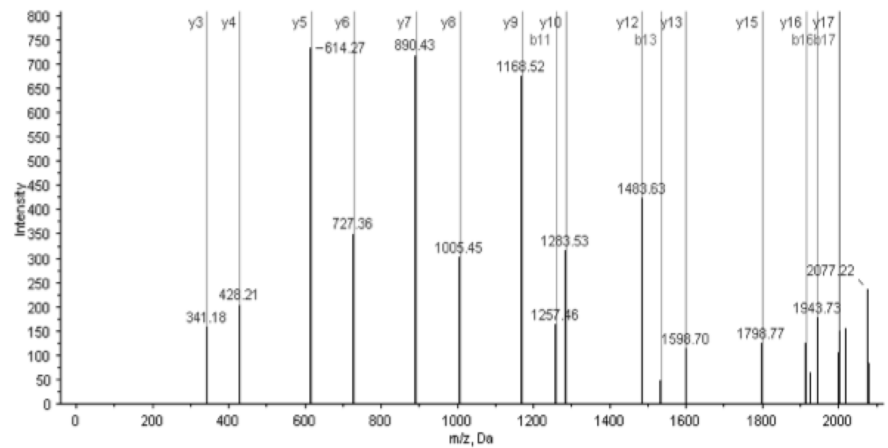
6. I97-N106

Residue	b	y
I	114.0913	1211.5514
N	228.1343	1098.4673
S	315.1663	984.4244
H	452.2252	897.3923
V	551.2936	760.3334
M	682.3341	661.2650
Y	845.3974	530.2245
F	992.4658	367.1612
S	1079.4979	220.0928
N	1193.5408	133.0608



F104-K121

Residue	b	y
F	148.0757	2146.9352
S	235.1077	1999.8668
N	349.1506	1912.8348
S	436.1827	1798.7919
L	549.2667	1711.7598
D	664.2927	1598.6758
A	735.3308	1483.6488
Q(Dea)	864.3734	1412.6117
D	979.4003	1283.5691
Y	1142.4637	1168.5422
D	1257.4906	1005.4789
Y	1420.5539	890.4519
I	1533.6380	727.3886
W	1719.7173	614.3045
S	1806.7493	428.2252
H	1943.8082	341.1932
G	2000.8297	204.1343
K	2128.9247	147.1128



V122-N130

Residue	b	y
V	100.0757	953.4914
S	187.1077	854.4230
I	300.1918	767.3910
E (NaX)	451.2163	654.3069
G	508.2378	503.2824
I	621.3218	446.2609
S	708.3539	333.1769
I	821.4379	246.1448
N	935.4809	133.0608

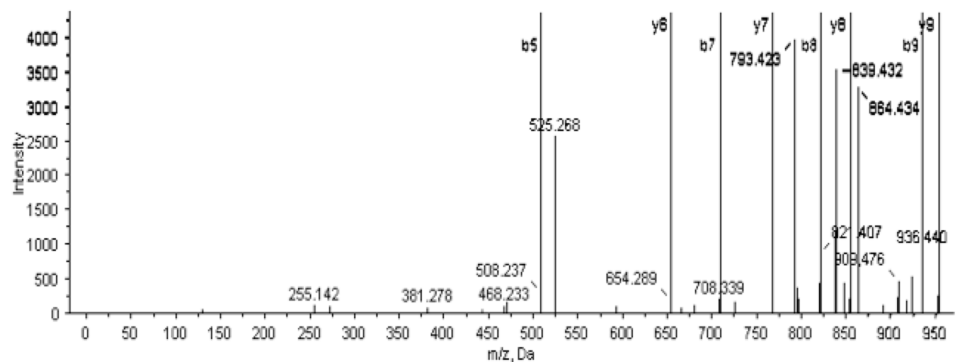


FIGURE S3 continued.