

Supporting Information

Mass Spectrometry-based proteomic approach in *Oenococcus oeni* (*O. oeni*) enological starter

Anna Napoli^{1}, Donatella Aiello¹, Gilda Aiello¹, Maria Stella Cappello², Leonardo Di Donna¹,
Fabio Mazzotti¹, Stefano Materazzi³, Marco Fiorillo¹, Giovanni Sindona¹*

¹Department of Chemistry and Chemical Technologies, University of Calabria, Italy

²CNR, Institute of Science of Food Production (ISPA), Lecce, Italy.

³ Department of Chemistry, “Sapienza” University of Rome, Italy

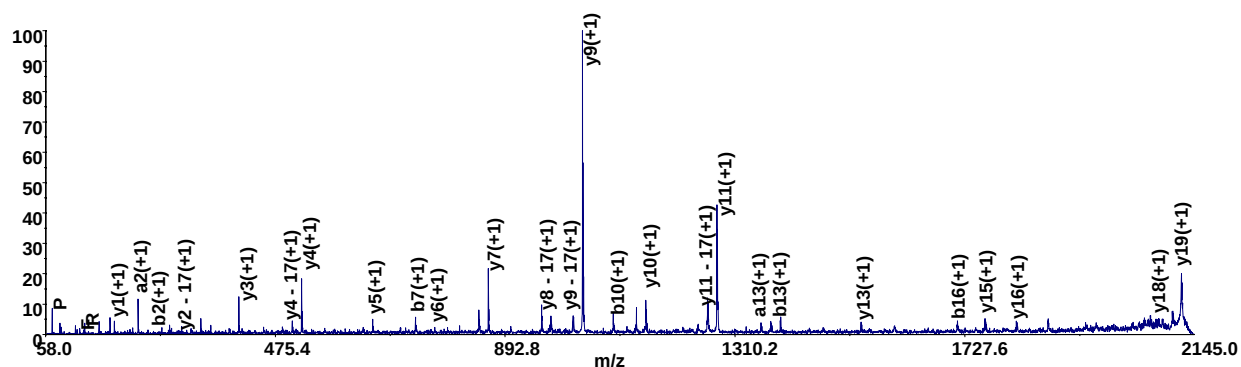
Corresponding Author: Prof. Anna Napoli

Department of Chemistry and Chemical Technologies, University of Calabria,

Via P. Bucci, Cubo 12/D, 87036 Arcavacata di Rende (CS), Italia.

e-mail: amc.napoli@unical.it; Fax: +39 0984 493307

**Supporting information Figure 1: (a) MS/MS spectrum of the ion specie of m/z 2121.83;
(b) sequence identification by data base search**



MASCOT SEARCH RESULTS

Database : NCBI nr (26682258 sequences; 9281362451 residues)

Taxonomy : Firmicutes (gram-positive bacteria) (3757491 sequences)

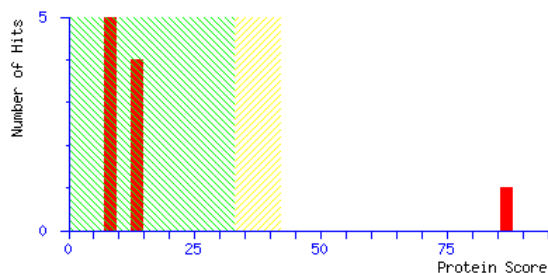
Significant hits: [gi|116491770](#) putative phosphoketolase [Oenococcus oeni PSU-1]

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 33 indicate peptides with significant homology

Individual ions scores > 42 indicate identity or extensive homology ($p < 0.05$).



Peptide Summary Report

1. [gi|116491770](#) Mass: 92249 Total Score: 87 Peptides matched: 1 putative phosphoketolase [Oenococcus oeni PSU-1]

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Peptide
1	2121.83	2120.82	2120.95	-62.45	1	87	1	GWGGPKFDEDGNPIENSFR

Proteins matching the same set of peptides:

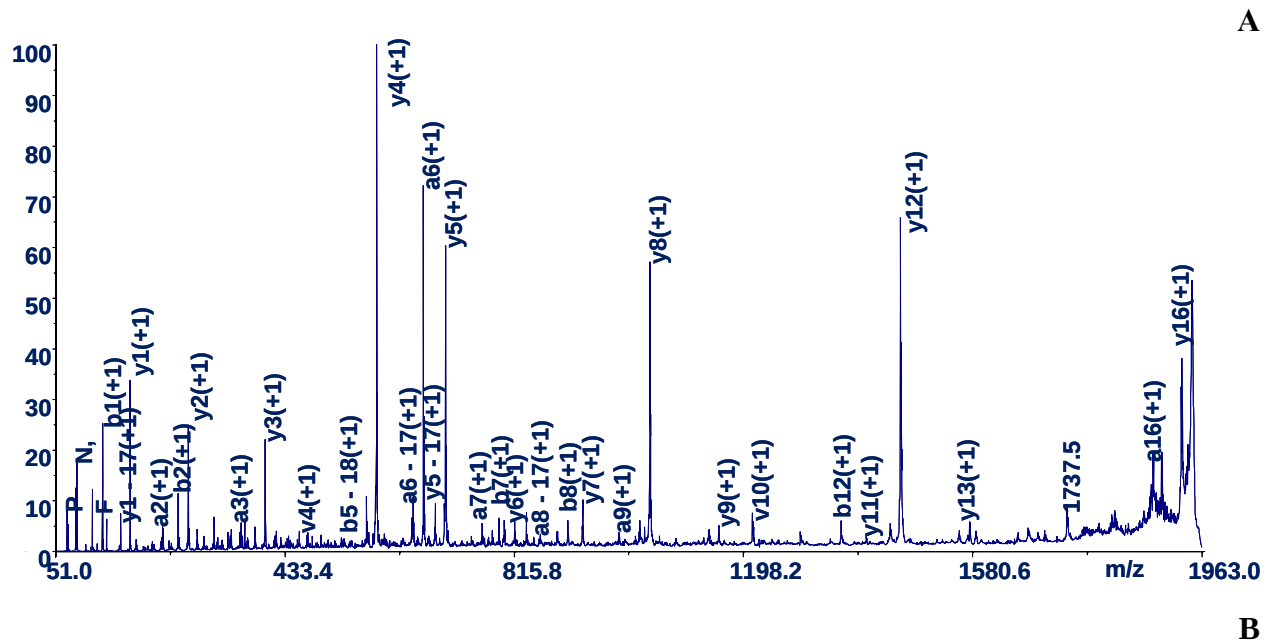
[gi|488909596](#) Mass: 92259 Total Score: 87 Peptides Matches: 1 phosphoketolase [Oenococcus oeni]

[gi|488909958](#) Mass: 92277 Total Score: 87 Peptides Matches: 1 phosphoketolase [Oenococcus oeni]

[gi|488913637](#) Mass: 92250 Total Score: 87 Peptides Matches: 1 phosphoketolase [Oenococcus oeni]

[gi|495019210](#) Mass: 92275 Total Score: 87 Peptides Matches: 1 phosphoketolase [Oenococcus kitaharae].

Supporting information Figure 2: (a) MS/MS spectrum of the ion specie of m/z 1946.97;
(b) sequence identification by data base search.



MASCOT SEARCH RESULTS

Database : NCBI nr (26682258 sequences; 9281362451 residues)

Taxonomy : Firmicutes (gram-positive bacteria) (3757491 sequences)

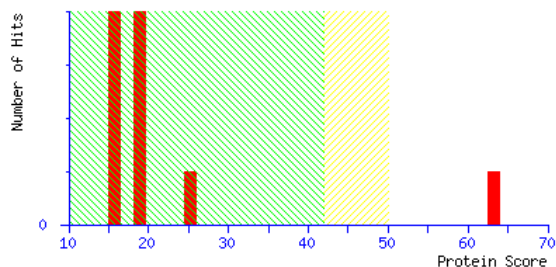
Significant hits: [gi116490597](#) alcohol dehydrogenase [Oenococcus oeni PSU-1]

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 42 indicate peptides with significant homology.

Individual ions scores > 50 indicate identity or extensive homology ($p < 0.05$).



Peptide Summary Report

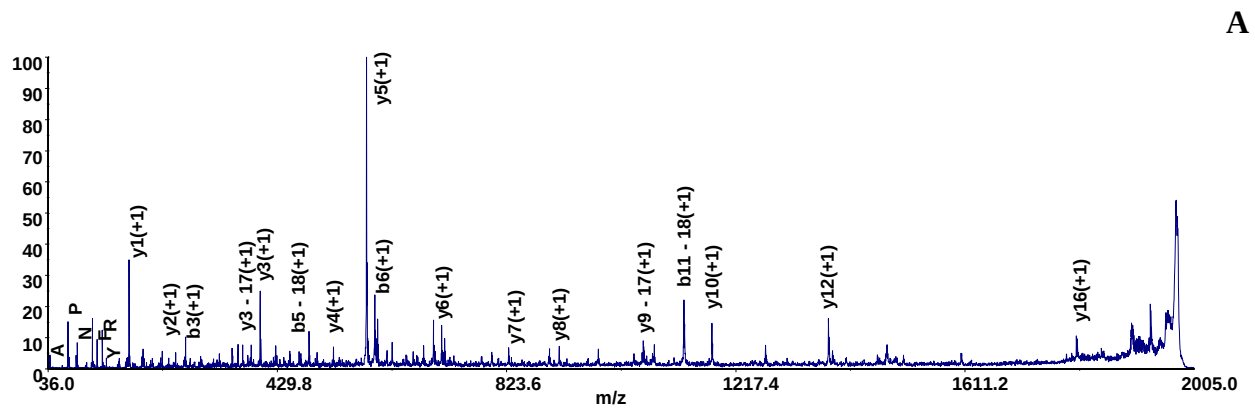
1. [gi116490597](#) Mass: 40895 Total Score: 63 Peptides Matches: 1 alcohol dehydrogenase [Oenococcus oeni PSU-1]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Peptide
1	1946.97	1945.96	1945.95	4.80	1	63	1	EKNDGFVDLIDDWKPR

Proteins matching the same set of peptides:

[gi|488905980](#) **Mass:** 37464 **Total Score:** 63 **Peptides Matches:** 1 alcohol dehydrogenase [Oenococcus oeni]
[gi|488907272](#) **Mass:** 40017 **Total Score:** 63 **Peptides Matches:** 1 alcohol dehydrogenase [Oenococcus oeni]
[gi|488911902](#) **Mass:** 40865 **Total Score:** 63 **Peptides Matches:** 1 alcohol dehydrogenase [Oenococcus oeni]
[gi|488912609](#) **Mass:** 40923 **Total Score:** 63 **Peptides Matches:** 1 alcohol dehydrogenase [Oenococcus oeni]
[gi|488915487](#) **Mass:** 39989 **Total Score:** 63 **Peptides Matches:** 1 alcohol dehydrogenase [Oenococcus oeni]

Supporting information Figure 3:(a) MS/MS spectrum of the ion specie of m/z 1973.90;
(b) sequence identification by data base search.



B

MASCOT SEARCH RESULTS

Database : SwissProt (540546 sequences; 192006283 residues)

Taxonomy : Firmicutes (gram-positive bacteria) (68260 sequences)

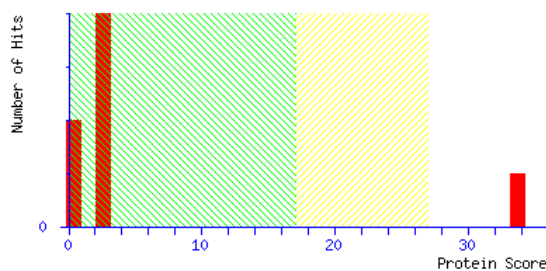
Significant hits: [ENO](#) [OENOB](#) Enolase OS=Oenococcus oeni

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 17 indicate peptides with significant homology.

Individual ions scores > 27 indicate identity or extensive homology ($p < 0.05$).



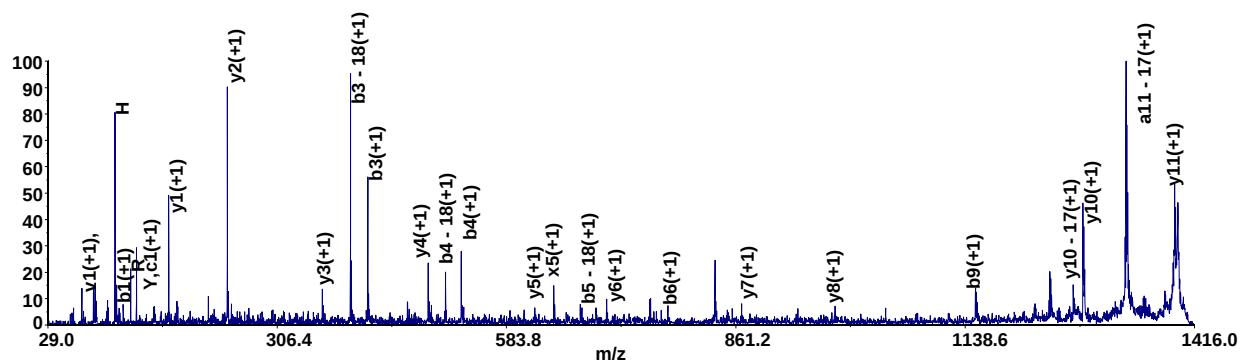
Peptide Summary Report

1. [ENO](#) [OENOB](#) Mass: 48419 Total Score: 34 Peptides Matches: 1 Enolase OS=Oenococcus oeni (strain ATCC BAA-331 / PSU-1)

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Peptide
1	1973.90	1972.89	1972.88	6.3	0	35	1	GNPTVEAEVYSEDGFFGR

**Supporting information Figure 4: (a) MS/MS spectrum of the ion specie of m/z 1396.66;
(b) sequence identification by data base search**

A



MASCOT SEARCH RESULTS

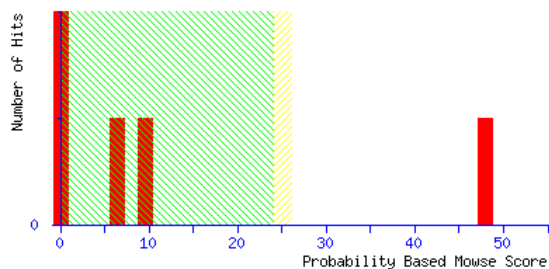
Database : NCBIInr (1411415 sequences; 454141287 residues)

Taxonomy : Firmicutes (gram-positive bacteria) (3757491 sequences)

Significant hits: [gi23038375](#) Glyceraldehyde-3-phosphate dehydrogenase

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 24 indicate peptides with significant homology ($p < 0.05$). Individual ions scores > 26 indicate identity or extensive homology ($p < 0.05$).



Peptide Summary Report

1. [gi23038375](#) Mass: 37097 Total score: 48 Peptides matched: 1 Glyceraldehyde-3-phosphate dehydrogenase [Oenococcus oeni MCW]

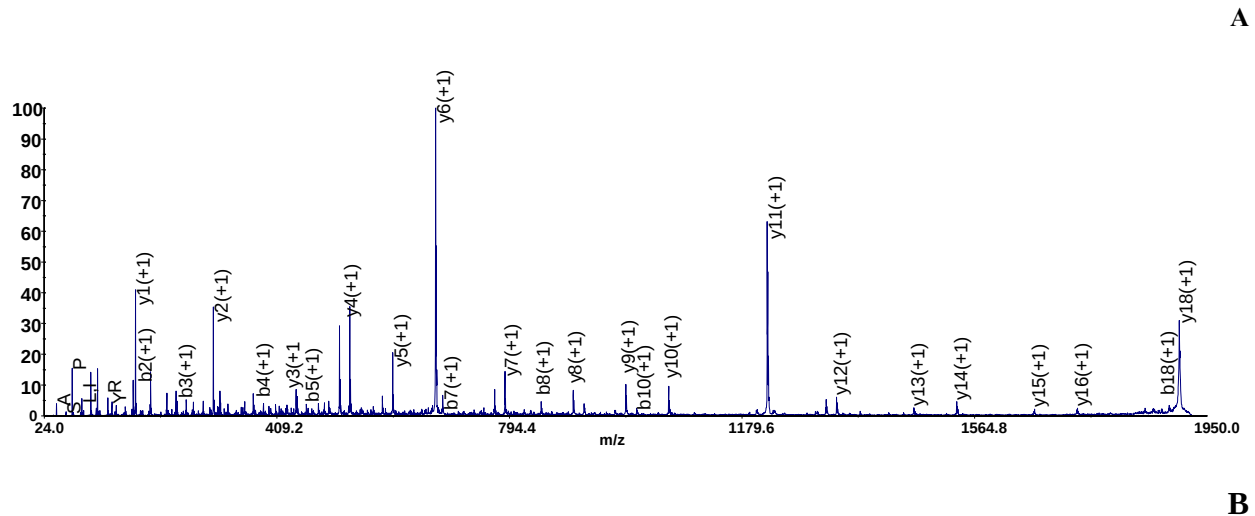
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Peptide
1	1396.66	1395.65	1395.64	7.2	1	48	1	DYHIYSEKDAR

Proteins matching the same set of peptides:

[gi21399047](#) Mass: 48837 Total score: 9 Peptides matched: 1 Peptidase_M48, [Bacillus anthracis A2012]

[gi21363093](#) Mass: 88649 Total score: 0 Peptides matched: 1 Xylulose-5-phosphate phosphoketolase

Supporting information Figure 5: (a) MS/MS spectrum of the ion specie of m/z 1904.90; (b) sequence identification by data base search.



MASCOT SEARCH RESULTS

Database : NCBI nr (26682258 sequences; 9281362451 residues)

Taxonomy : Firmicutes (gram-positive bacteria) (68260 sequences)

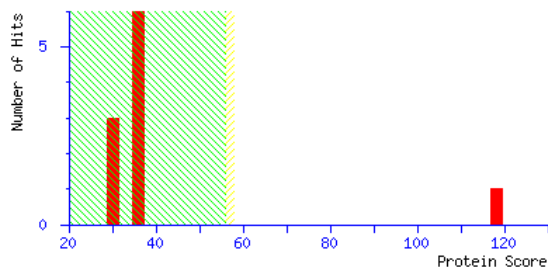
Significant hits: [gi|116490839](#) elongation factor Tu [Oenococcus oeni PSU-1]

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 56 indicate peptides with significant homology.

Individual ions scores > 58 indicate identity or extensive homology ($p < 0.05$).



Peptide Summary Report

1. [gi|116490839](#) Mass: 43597 Total Score: 118 Peptides Matches: 1 elongation factor Tu [Oenococcus oeni PSU-1]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Peptide
1	1904.91	1903.90	1903.89	6.5	0	118	1	GLAQAQDYASIDAAPEER

Proteins matching the same set of peptides:

[gi|488906257](#) Mass: 44198 Total Score: 118 Peptides Matches: elongation factor Tu [Oenococcus oeni]

[gi|495021022](#) Mass: 43713 Total Score: 118 Peptides Matches: 1 elongation factor Tu [Oenococcus kitaharae]

Supporting information Figure 6: Protein sequence coverage of Zn-dependent alcohol dehydrogenase [*Oenococcus oeni* PSU-1]. Matched peptides are shown in bold

1	MLNYR DLMVF	LFATKEGIKI	FK ESRELKMK	AAVVR EKNDG	FVDLIDDWKP
51	REL GFGDALV	DVEYCGLCHT	DLHCASGDFG	DPNTLGERNG	DFRRVVGHEG
101	VGIVSKLGEG	ADQYLKVGDR	VSIAWFYDAC	GVCDYCVSGN	ETFCRKVR NS
151	GYTVDGAMAQ	QVVVDAKYAV	KVPEGLDPAQ	ASSITCAGVT	MYKSLKVGET
201	KPGQWVSVHG	AGGLGNLAVQ	YAHNVFGAHV	VAIDGNPDKL	EAAK EGGAEV
251	LINRKQPGID	VAAEVQKDTG	GVHNAQVTAV	NDAAFQQAVD	SLRPMGKLVA
301	VALPQGDMEL	NIVK TVLDGI	EVRGSLVGTR	ADLKEAFQFG	AEGKVTPIVE
351	KVDLNDINDV	IEEMKEGTIT	GRKVDFDTHM		

Supporting information Table 1: Peptides identified of *O. oeni* by MS/MS data processing.

The identification was performed using Protein Pilot Paragon Method. The MS/MS data were processed using a mass tolerance of 10 ppm and 0.2 Da for the precursor and fragment ions, respectively.

			m/z	PM	Phosphosite
		Amino acid metabolism/catabolism			
1	Q04D18	Pyruvate oxidase			
	1	21-41 EVYGLPGDSVDTTVDALRRQK	2319.21	d → Q(20)	
	2	122-131 LFDDVAVFNR	1195.62		
	3	202-215 NSQKPIALIGLGAK	1409.85		
2	Q04DB8	2-keto-4-methylthiobutyrate/aminotransferase/fructokinase			
	1	54-66 AIGVSSFQPIELR	1345.77		
	2	146-159 FIGDLGHPMGHVR	1564.80		
	3	230-246 IVFGGGVVSpEEFLKKVR	1944.07		S(238)
3	Q04GE6	Zn-dependent alcohol dehydrogenase			
	1	36-51 EKNDGFVDLIDDWKPR	1946.97		
	2	36-51 EKNQGFVDLIDDWKPR	1960.00	D → Q(39)	
	3	36-51 EKNDGFVDLIDDWKPR	1946.98	d → N(38)	
	4	36-51 EKNDGFVDLIDDWQPR	1946.93	K → Q(49)	
	5	36-51 EpyroKNDGFVDLIDDWKPR	1928.96		
	6	149-167 NSGYTVDGAMAQQVVVDAK	1952.94		
	7	245-254 EGGAEVLINR	1057.57		
	8	287-297 EpyroAVDSLRLPMGK	1184.62		
	9	315-323 TVLDGIEVR	1001.56		
	10	315-323 TVNDGIEVR	1002.53	L → N(317)	
	11	324-334 GSLVGTRADLK	1116.65		
	12	331-351 ADLKEAFQFGAEGKVTPIVEK	2277.22	d → Q(338)	
	13	335-344 EAFQFGAEGK	1083.52	D → E(335)	
	14	345-372 VTPIVEKVDLNDINDVIEEMKEGTITGR	3127.64		
	15	345-372 VTPIVEKVDLNDINDVIEEMKEGTITGR	3128.66	d → N(355)	
	16	352-372 DDLNDINDVIEEMKEGTpITGR	2457.09	V → D(352)	T(368)
	18	373-380 KVFDFTHM	1023.51		
	19	373-380 KVFDFTHm	1040.51		
4	Q04EB7	1,3-propanediol dehydrogenase			
	1	62-77 SGVDYVVYNEVEPNPK	1808.88		
	2	78-90 IHNIKEVKTLYEK	1613.95		
	3	233-244 EAVANGHNLQAR	1280.87	d → N(237)	
	4	382-390 IFQEAYDAK	1084.54		
5	Q04GX2	Lactaldehyde dehydrogenase			

	1	290-302	VYVQEDIAEEFTK	1570.77		
	2	290-303	VYVQEDIAEEFTKK	1699.88	d→Q(293)	
	3	361-373	GYFYPATVVTNVK	1458.77		
6		Q04GQ8	Glyceraldehyde-3-phosphate dehydrogenase			
	1	77-87	DYHIYSEKDAR	1396.66		
	2	113-123	AQAHIDAGAKR	1137.62		
	3	198-213	SSKKRTNRTAASNTIP	1731.97		
	4	206-220	TAASNTIPHSTGAAK	1426.73		
	5	221-239	AIGLVVPEVDGKLNGHAQR	1974.12	d→N(234)	
	6	221-239	AIGLV <u>C</u> PEVDGKLNGHAQR	1977.05	V→C(226)	
	7	240-250	VAVVDG <u>Sp</u> VTEL	1168.57		S(46)
	8	240-256	VAVVDGSVTELTTILSK	1731.98		
	9	316-332	TVSWYDNEYGFTSNMVR	2068.92		
7		Q04EF1	NAD-dependent aldehyde dehydrogenase			
	1	16-27	KYDFSTQDDIER	1516.70		
	2	28-37	AL <u>Sp</u> QGH <u>Tp</u> LYKK	1405.64		S(30), T(34)
	3	39-56	WRNGPLDKRVA <u>Tp</u> LHTIAK	2157.15	d→N(41)	T(50)
	4	127-140	AVEPWNFPYYQIMR	1813.88		
	5	200-210	VQGVALTGSER	1116.61		
	6	269-282	FIVADNLYDEFLTR	1715.88		
8		Q04EJ8	Acetaldehyde dehydrogenase/alcoholdehydrogenase			
	1	250-258	AAEDLLL <u>Sp</u> KR	1195.61		S(257)
	2	302-323	IADFVFSDKHAVNGPVAGMSGR	2275.14		
	3	311-323	HAVNGPVAGM <u>Sp</u> GR	1332.60		S(321)
	4	324-335	WIAEHAGVTLPK	1321.73		
	5	516-528	ILEQFELRPDQVK	1614.90		
	6	884-891	<u>Epyro</u> PNLAEIR	923.50		
	7	884-891	QPNLAEIR	940.53		
9		Q04D72	Cystein synthase			
	1	139-154	NSYVPLQFQNPNPDIYYR	2299.13		
10		Q04DQ5	S-ribosylhomocysteine lyase			
	1	125-128	GNFK	465.25		
	2	141-154	VILDEGISSDPFER	1576.79		
11		Q04D47	CTP synthase			
	1	32-44	LLK <u>Sp</u> RGLAVTVQK	1492.87		S(35)
	2	278-291	ANLSQWGALVDRIR	1598.86		
	3	334-349	SINSEMLTDNNVAEKL	1777.87		
	4	349-364	LAGIDGVIVPGGFGPR	1524.86		
	5	365-377	GIEGMISAIKYAR	1408.76		
	6	452-465	TAEAYNNVSEISER	1583.75	d→N(458)	
12		Q04FD8	Phenylalanine—tRNA ligase alpha subunit			
	1	14-31	VSVEIDK <u>SSpSp</u> VDLIENIR	2163.00		S(22), S(23)
	2	171-179	TQTSAMQAR	993.48		
			Glycolysis and pyruvate and carbohydrate metabolism			
13		Q04FG3	6-phosphogluconate dehydrogenase decarboxylating			
	1	17-25	NLALNVESR	1016.56	d→N(21)	

	2	26-34	GYTVAIFNR	1040.56		
	3	51-62	LIPSFTIEDFVK	1408.78		
	4	147-157	EAYELVRPIFE	1365.72		
	5	147-162	EAYELVRPIFEQIAAK	1877.02		
	6	193-206	GDEELIDE <u>Tp</u> YNIMR	1777.74		T (201)
	7	226-242	GELDSYLIEITADILTR	1922.02		
	8	268-290	WSSGDALEVQVPQSVITEAVYAR	2505.27		
	9	335-346	IMSYAQGFELR	1442.72		
	10	339-350	AQGFEQLRFAAK	1365.73		
	11	419-437	AGVPVPALSAAVIYFDSYR	1996.06		
	12	419-437	AGVPVPALSAAVIYFDSYR	1978.08	Dehyd S (427)	
	13	430-437	VIYFDSYR	1062.53		
	14	438-450	SEVL PANLIQAQR	1438.81		
	15	451-460	DYFGAHTYQR	1257.58		
14		Q04G42	Phosphoglycerate kinase			
	1	20-36	VDFNVPIKDG VIGNDNR	1871.97		
		Q04DH2	Enolase			
	1	1-16	MSLIASIYAREVLD <u>Sp</u> R	1885.94		S(15),Dehyd S (6)
	2	2-10	SLIASIYAR	993.58		
	3	17-34	GNPTVEAEVYSEDGFFGR	1973.90		
	4	17-34	GN <u>T</u> TVEAEVYSEDGFFGR	1977.89	P→T(19)	
	5	17-34	GNPTVEAEVY <u>Sp</u> EDGFFGR	2053.87		S(27)
	6	35-52	GIVPSGASTGEHEAVELR	1808.92		
	7	83-106	FDVADQQRGIDLAMIALDG <u>Tp</u> PNKGK	2626.31	d→N(103)	T(101)
15		Q04F61	Pyruvate kinase			
	1	56-73	KTGKLIGFMLDTKGAEIR	1978.13		
	2	177-198	DKSDIEFGLEQGIDFIAASFVR	2457.25		
16		Q04G44	Glucosio-6-phosphato isomerase			
	1	37-60	TGVGNEMEDWLTLPDYDKEEFAR	2802.28		
	2	106-121	EGLPEVYFVGTSASGR	1668.83		
	3	122-133	YIDDVIDLIGNR	1405.74		
	4	163-172	KYGKEEASKR	1195.65		
	5	196-205	FVVPDGIGGR	1016.56		
	6	241-256	DEDILNKPSILYAIYR	1923.03		
17		Q04D23	Phosphoketolase			
	1	2-24	AANAPAVDYYDSTEYLELVDKWWR	2754.26		N-Acetyl
	2	70-77	FIYAHENR	1049.52		
	3	95-104	GGQVMVTNSYL	1168.57		
	4	213-224	GWKISNPTIFSR	1405.76		
	5	233-242	FFEGLGWSPR	1195.60		
	6	262-271	LFDQAIEDIK	1191.64		
	7	279-297	ENNKYQDGTIPAWPVIIAR	2185.15		
	8	301-319	GWGG <u>V</u> KFDEDDGNPIENSFR	2123.02	P→V(305)	
	9	307-319	FDEDGNPIENSFR	1539.67		
	10	437-447	FFGPDETMSNR	1300.57		
	11	463-476	IKFPNDALLAPEGR	1540.86		

12	477-499	IIDSQSEHEAEGWLEGYTLTGR	2604.28		
13	512-533	VVDSMINEYFKWIRQADAEPWR	2754.33	d→N(518)	
14	526-533	QADAEPWR	972.46		
15	526-533	<u>Epyro</u> ADAEPWR	955.43		
16	576-591	<u>Epyro</u> YLPADGNELLAVASR	1699.87		
17	576-591	QYLPADGNELLAVASR	1716.89		
18	571-598	QNYIRQYLPADGNELLAVASRALVDRQK	3202.66	d→N(572)	
19	579-596	PADGNELLAVA <u>Sp</u> RALVDR	1946.98		S(590)
20	587-596	AVASRALVDR	1057.61		
21	671-681	FHYVNVVELGR	1332.71		
22	714-729	GFHGFEDLIEAIFYER	1942.94		
23	740-751	EDGDITTQYDMR	1443.61		
24	790-799	ILDKHFEVTR	1257.70		
18	Q04H39	Mannose-6phospate isomerase, type 1			
1	137-153	QELSDWVYRGDWDKLLR	2179.10		
2	151-175	LLRKVPVKAGDFVYVP <u>Sp</u> GTHALNK	2802.55		T(167)
3	212-222	<u>EpyroSp</u> IDVT <u>Tp</u> VPFR	1405.58		S(213), T(18)
19	Q04HE3	Glucose 6-phosphate-1-dehydrogenase			
1	159-178	TAEELQNQLESGFSDDQIFR	2327.08		
2	212-226	NVQVTLAEQLGVEER	1684.89		
3	266-281	AAKNTVF <u>Sp</u> KLK <u>Q</u> YDER	1977.99	M→Q(277)	S(273)
4	302-322	SYTEEPNVPADSKNDTYVAGR	2314.06	d→N(308)	
5	323-338	LQFENDRW <u>Tp</u> GVPFYIR	2121.00	d→N(327)	T(331)
20	Q04HF5	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase			
1	47-60	GIQFDQAYTSVLTR	1598.82		
2	166-179	VMPFWEDKIAPDLR	1716.89		
3	174-194	IAPDLRAGKNVIAAHGNSLR	2186.27		
21	Q04G34	Phosphoenolpyruvate-protein phosphotransferase			
1	133-141	ADIRDIKR	1057.62		
2	247-254	KVGEYFAR	969.52		
3	285-301	DLDSVIESGAEGIGLFR	1777.90		
4	355-363	EDNPFLGYR	1110.53		
5	385-405	ASVYGNLWIMFPMIATLPEFR	2457.25	d→N(390)	
6	561-575	DTNQEVIDLKNSIK	1715.93		
22	Q04GQ0	Phosphoglycerate dehydrogenase-like dehydrogenase			
1	42-59	NAAGADGVVVYQQLPYTR	1921.99		
23	Q04HJ9	Aldo/ketoreductase related enzym			
1	19-29	PAIGLGTYLVR	1159.69		
2	30-46	GGQGVDQILSAIEDGYR	1777.88		
3	47-65	LIDTSTNYDSEGAVGEAIR	2010.97		
4	139-152	SIGVSNFLPEHLDR	1583.01		
5	185-196	GIVSEAWSPLGR	1271.68		
6	244-266	SNIDIFDFSLTSSEIEQINALNR	2626.32		
7	267-283	SDGRVDGQDPNTYEEFD	1943.80		
		Other			
24	Q04FQ4	Elongation factor Tu			

	1	2-9	AEKEHYER	1061.51		
	2	36-58	VLSEKGLAQADYASIDAAPEER	2461.23		
	3	41-58	GLAQADYASIDAAPEER	1904.90		
	4	61-76	GITINTAHVEYETDKR	1846.93		
	5	92-118	NMITGAAQMDGAILVVAATDGMPMPQTR	2729.35		
	6	136-156	LNKTDLVDDPELIDLVE <u>m</u> EV	2457.29	d→N(137)	
	7	139-156	TDLVDDPELIDLVE <u>m</u> EV	2117.07		
	8	157-173	ELLSEYDFPGDDIPVIR	1977.98		
	9	179-206	ALQGDPEQEKVILHLMDDVIDEYIPTPVR	3218.69		
	10	207-225	DVDKPFLMPVEDVFTITGR	2179.12		
	11	267-282	TLDLGEAGDNIGALLR	1627.87		
	12	283-291	GIDRDGVER	1016.52		
	13	326-332	FTNYRPQ	925.46		
25		Q04ED6	Elongation Factor G			
	1	87-104	VNIIDTPGHVDFTIEVER	2054.07		
	2	171-191	AIQWPIGAEDDFAGVIDLIQR	2327.22		
	3	616-635	VSIVSPIDNLGDVMGHVSAR	2066.08		
26		Q04G77	50S ribosomal protein L29			
	1	30-42	FQQAAGQLENTAR	1433.72		
27		P94898	Heat shock protein Hsp18			
	1	31-38	DGLWESAR	933.45		
	2	94-99	DKKNNVVR	972.56		
28		Q04E64	60 kDa chaperonin			
	1	3-13	KEVRFSEDARTR	1493.79		
	2	7-14	F <u>S</u> pEDARTR	1061.45		S(8)
	3	36-57	NVVLEQSYGTPITITNDGV ^{TI} AK	2320.22		
	4	105-116	NVTAGANPVGIR	1168.65		
	5	119-137	IEKATAAAVAGLNKNSHEV	1923.04		
	6	167-195	VGHDGVITIEESKGIE ^{TE} LDVVEGMQFDR	3202.57		
	7	180-195	GIE ^{TE} LDVVEGMQFDR	1837.87		
	8	225-243	IGNIQDILPVLQSVVEQGR	2078.17		
	9	267-282	G <u>Tp</u> FNVA ^{AV} KAPGFGDR	1686.81		T(268)
	10	285-308	AQL <u>M</u> DI ^{AI} L ^{TG} ATV ^{VT} EDLGLQLK	2513.40	Q→M (288)	
	11	309-320	DVTIDQLGQANR	1329.68		
	12	309-320	DV <u>Tp</u> IDQLGQANR	1409.65		T(311)
	13	309-325	DVTIDQLGQANRVTITK	1872.00		
	14	394-402	IEDALNATR	1002.52		
	15	426-440	KVADSLQGDVATGAR	1487.79		
	16	427-451	VADSLQGDVAT <u>Tp</u> GARIVLRAL ^{EE} PLR	2729.46		T(437)
	17	427-440	VADSLQGDVATGAR	1359.70		
	18	452-467	<u>Epyro</u> IVENAGLEGSVIAQR	1666.88		
	19	452-467	QIVENAGLEGSVIAQR	1684.92	d→N(456)	
	20	452-467	<u>L</u> IVENAGLEGSVIAQR	1668.93	Q→L(452)	
29		Q04EE1	Chaperone protein DnaK			
	1	26-34	IITNPDGGR	942.51		
	2	84-95	EYRP ^{EE} ISAMIL	1450.73		

	3	270-282	AQFNQLTADLVER	1504.78		
30		Q04GA6	ATP-binding subunit of Clp protease and DnaK/DnaJ chaperones			
	1	307-319	AAVDYSVQYIPQR	1509.77		
	2	568-579	LTDGQGNVVNFK	1291.67		
31		Q04G51	30S ribosomal protein S9			
	1	21-33	LTPG <u>Sp</u> GKITINNR	1451.75	d→N(32)	S(25)
	2	34-45	SFEEYIPAANLR	1409.72		
	3	86-99	ALLQVDPDFRPALK	1582.91		
32		Q04G86	30S ribosomal protein S10			
	1	32-46	TGAQVVGPIPLPTER	1534.87		
	2	73-88	LID <u>M</u> VNPTDK <u>Tp</u> VDS <u>Sp</u> LR	1976.89	L→M (76)	T(83), S(86)
33		Q04G81	30S ribosomal protein S19			
	1	28-37	KPVIRTW <u>Sp</u> RR	1378.75		S(35)
	2	71-78	LGEFVPTR	918.51		
34		Q04EQ1	Cyclopropane-fatty-acyl-phospholipid synthase			
	1	5-13	TIYRRL <u>Sp</u> R	1257.69		S(12)
	2	84-92	<u>S</u> AGSFLTDK	925.47	N→S(84)	
	3	334-341	VFDQTAQR	964.49		
35		Q04G20	ATP synthase subunit beta			
	1	23-35	KLPDINNALKVQR	1509.90	d→N(29)	
	2	56-67	TIAMDSTDGLTR	1280.62		
	3	71-89	VLDTGAPIEVPVGEA <u>Tp</u> LGR	1974.00		T(86)
	4	136-145	VIDLLEPYLR	1230.72		
	5	236-251	DQEGKDVLLFIDNIFR	1922.01		
	6	252-265	FTQ <u>P</u> GSEV <u>Sp</u> ALLGR	1541.74	A→P(255)	S(560)
36		Q04G23	ATP synthase subunit delta			
	1	27-40	VLSELQVIELVFER	1673.95		
	2	142-159	NVVDPNV <u>I</u> EGVILTAG <u>Sp</u> K	1923.00	A→F(250)	S(158)
37		Q04EY2	Putative Uncharacterized protein			
	1	59-69	LAEQDYNGYR	1391.63		
38		Q04H48	Putative Uncharacterized protein			
	1	23-37	NIDSLNADEDKNVER	1731.82		
	2	23-37	NIDSLNADEDKNVER	1732.83	d→N(28)	
39		Q04HG0	Predicted GTPase, probable translation factor			
	1	301-318	SGMKAPQVAGIIHSDFER	1942.99		
40		Q04GT1	Uvr ABC system protein A			
	1	537-553	DLGNTLVVVEHDEDTMR	1942.93		
	2	712-723	GLFAQTNEAKMR	1365.70		
41		Q04H97	Transcription-repair coupling factor			
	1	779-796	QLRANVDVLTATPIPR	1978.15		
	2	980-988	LA <u>m</u> RDLSIR	1090.62		
42		Q04F00	Exonuclease RecJ			
	1	307-315	SEIAKQVEH	1040.54		
			DNA Binding			
43		Q04HR5	DNA polymerase III subunit beta			
		87-95	HLSSDKVEI	1027.54		

		127-149	LDDANTINIPSELIDIIGETIR	2512.32	
44	Q04F53		Bacterial nucleoid protein Hbs		
	1	43-54	VQLIGFGNFEVR	1378.75	
	2	45-54	LIGFGNFEVR	1151.63	
45	Q04GT5		NAD/NADP transhydrogenase alpha subunit		
	1	109-121	AGVTSLAFELLPR	1373.78	
46	Q04HR4		S4-like RNA binding protein		
	1	35-52	ENANSFFVNGE <u>S</u> pENRRGR	2162.95	S(46)
47	Q04HJ7		Putative Uncharacterized protein		
	1	2-19	ADKKDEQEKVNNKKDEEAK	2132.09	
48	Q04GM3		Serine—tRNA ligase		
	1	114-127	VPVGPDDSYNVEQR	1574.75	