



MASCOT Search Results

Protein View: tr|A0A0F6B5H4|A0A0F6B5H4_SALT1

Outer membrane receptor FepA OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=iroN PE=3 SV=1

Database: Salmonella_typhimurium_LT2
Score: 105
Expect: 3.1e-007
Nominal mass (M_r): 79438
Calculated pI: 5.90

Sequence similarity is available as [an NCBI BLAST search of tr|A0A0F6B5H4|A0A0F6B5H4_SALT1 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 42
Mass values matched: 15

Protein sequence coverage: 26%

Matched peptides shown in **bold red**.

1	MGMRVKKFIW	LITVVSTGVN	SPLSAAESTD	DNGETMVVES	TAEQVLKQQP
51	GVSIIITR DDI	QKNPPVNDLA	DIIR KMPGVN	LTGNSASGTR	GNNRQIDIRG
101	MGPENTLVLI	DGVPVTSR NS	VRYSWRGERD	TRGDTNWVPP	EMVER IEVIR
151	GPAAARY YGS	AAGGVVNIIT	KRPTNDWHGS	LSLYTNQPES	SKEGDTRRGN
201	FSLSGPLAGD	TLTMRLYGNL	NRTDADSWDI	NSSAGTKNAA	GR EGVTNKDI
251	NSVFSWKMP	QQILD FEAGY	SR QGNIIYAGD	TQNSTNAVT	KSLAQSGRET
301	NRLYRQNYGL	THNGIWDWGQ	SR LGFYYEKT	DNTRMNEGLS	GGGEGRITND
351	QTFTTNRLTS	YR TSGEVNV	VIWLFEQTLT	VGAEWNRDEL	NDPSSTSLTV
401	KDSNIAGIPG	SAANRSSKNK	SEISALYVED	NIEPMAGTNI	IPGLRFDYLS
451	ESGSNFSPSL	NLSQELGEYV	KVKAGIARAF	KAPNLYQTSE	GYLLYSKNG
501	CPKDITSGGC	YLVGNKNLDP	EISIN KEIGL	EFTVDDYHAS	VTYFR NDYQN
551	KIVAGDQIIG	RSASGAYVLQ	WQNGGKALIE	GIEASMAVPL	MPDRLNWNNTN
601	ATYMIASEQK	DTGNPLSIIP	KYTVNTFLDW	TITSALSANV	NWTLYGKQKP
651	RTHAESRSEE	TKGLSG KALG	AYSLVGANVN	YDINKNLR LN	VGISNIFDKQ
701	IYRSAEGANT	YNEPGRAYYA	GVTASF		

Unformatted sequence string: **726 residues** (for pasting into other applications).

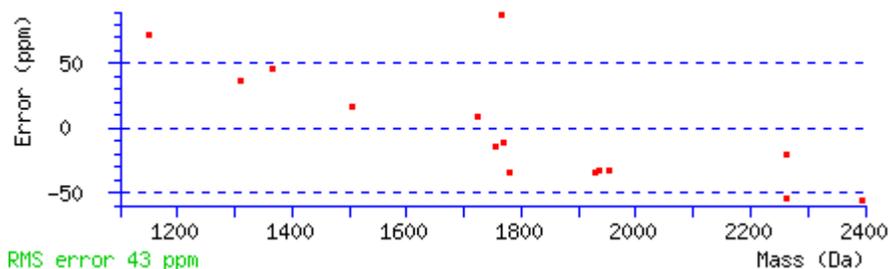
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
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Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
58 - 74	1935.9494	1934.9421	1935.0061	-33.1	1	R.DDIQKNPPVNDLADIIR.K
100 - 118	1954.9609	1953.9537	1954.0194	-33.6	0	R.GMGPENTLVLIDGVPTSR.N
146 - 156	1152.7677	1151.7604	1151.6775	72.0	1	R.IEVIRGPAAAR.Y
243 - 257	1723.8807	1722.8734	1722.8577	9.11	1	R.EGVTNKDINSVFSWK.M
258 - 272	1755.8110	1754.8037	1754.8298	-14.8	0	K.MTPQQILDFEAGYSR.Q
258 - 272	1771.8130	1770.8057	1770.8247	-10.7	0	K.MTPQQILDFEAGYSR.Q + Oxidation (M)
323 - 334	1506.7481	1505.7408	1505.7150	17.1	1	R.LGFYYEKTDNTR.M
330 - 346	1766.9272	1765.9200	1765.7649	87.8	1	K.TDNTRMNEGLSGGEGR.I + Oxidation (M)
347 - 357	1310.6825	1309.6752	1309.6263	37.4	0	R.ITNDQTFITTNR.L
347 - 362	1930.8944	1929.8872	1929.9545	-34.9	1	R.ITNDQTFITTNRLLTSYR.T
527 - 545	2262.0257	2261.0184	2261.0641	-20.2	0	K.EIGLEFTVDDYHASVTFYFR.N
668 - 688	2265.0756	2264.0684	2264.1913	-54.3	1	K.ALGAYSLVGANVNYDINKNLR.L
689 - 703	1779.9136	1778.9063	1778.9679	-34.6	1	R.LNVGISNIFDKQIYR.S
704 - 716	1365.6654	1364.6581	1364.5956	45.8	0	R.SAEGANTYNEPGR.A
704 - 726	2395.9433	2394.9360	2395.0716	-56.6	1	R.SAEGANTYNEPGRAYVAGVTASF.-

No match to: 1202.6934, 1367.7158, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1728.8183, 1764.8373, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2319.0381, 2398.9797, 2453.9716, 2998.3197



Mascot: <http://www.matrixscience.com/>

1930.8944, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2192.0176, 2244.0164, 2262.0257, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

4. [tr|Q8ZKJ0|Q8ZKJ0_SALTY](#) Mass: 17041 Score: 37 Expect: 1.8 Matches: 4
Cytoplasmic protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM4215 PE=1 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|-------------------------------------|
| 1755.8110 | 1754.8037 | 1754.9461 | -81.14 | 1 | 15 | 1 | -.METLSVIHTVANRLR.E + Oxidation (M) |
| 1785.8290 | 1784.8217 | 1784.8251 | -1.87 | 16 | 31 | 0 | R.ELNPFMDIHISSTDAK.V |
| 2054.9787 | 2053.9714 | 2054.0102 | -18.90 | 14 | 31 | 1 | R.LRELNPMDIHISSTDAK.V |
| 2265.0756 | 2264.0684 | 2264.2852 | -95.76 | 68 | 88 | 1 | R.ISATVIVPQISDAINALDRLR.R |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1930.8944, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2192.0176, 2244.0164, 2262.0257, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197
5. [tr|A0A0F6BB10|A0A0F6BB10_SALT1](#) Mass: 37714 Score: 36 Expect: 2.8 Matches: 5
L-idonate 5-dehydrogenase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=idnD PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|--|
| 1771.8130 | 1770.8057 | 1770.9013 | -53.94 | 14 | 28 | 1 | K.RAVAVTEQNIWNNK.G |
| 1906.9695 | 1905.9623 | 1905.7556 | 108 | 98 | 111 | 0 | K.YCLQHEENHCTEMR.F |
| 1935.9494 | 1934.9421 | 1934.8774 | 33.4 | 112 | 128 | 0 | R.FFGSAMYFFPHVDGGFTR.F |
| 2395.9433 | 2394.9360 | 2395.1595 | -93.30 | 260 | 282 | 0 | K.GVMVQVGMGGAVPNFPMVMVISK.E + Oxidation (M) |
| 2998.3197 | 2997.3124 | 2997.4870 | -58.24 | 260 | 287 | 1 | K.GVMVQVGMGGAVPNFPMVMVISKEISLK.G + 3 Oxidation (M) |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1930.8944, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2398.9797, 2453.9716
6. [tr|Q8ZK22|Q8ZK22_SALTY](#) Mass: 37714 Score: 36 Expect: 2.8 Matches: 5
L-idonate 5-dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=idnD PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|--|
| 1771.8130 | 1770.8057 | 1770.9013 | -53.94 | 14 | 28 | 1 | K.RAVAVTEQNIWNNK.G |
| 1906.9695 | 1905.9623 | 1905.7556 | 108 | 98 | 111 | 0 | K.YCLQHEENHCTEMR.F |
| 1935.9494 | 1934.9421 | 1934.8774 | 33.4 | 112 | 128 | 0 | R.FFGSAMYFFPHVDGGFTR.F |
| 2395.9433 | 2394.9360 | 2395.1595 | -93.30 | 260 | 282 | 0 | K.GVMVQVGMGGAVPNFPMVMVISK.E + Oxidation (M) |
| 2998.3197 | 2997.3124 | 2997.4870 | -58.24 | 260 | 287 | 1 | K.GVMVQVGMGGAVPNFPMVMVISKEISLK.G + 3 Oxidation (M) |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1930.8944, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2398.9797, 2453.9716
7. [tr|A0A0F6B7K8|A0A0F6B7K8_SALT1](#) Mass: 16477 Score: 34 Expect: 4.3 Matches: 4
Zinc-responsive transcriptional regulator OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=zntR PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|--------------------------------------|
| 1798.8146 | 1797.8074 | 1797.8646 | -31.82 | 33 | 47 | 1 | R.TEGGFRLYTENDLQR.L |
| 1836.8843 | 1835.8770 | 1835.8043 | 39.6 | 24 | 38 | 1 | K.QQMDHEVTRTEGGFR.L + Oxidation (M) |
| 1930.8944 | 1929.8872 | 1929.9942 | -55.45 | 90 | 105 | 1 | R.LQEVEARIAELQTMQR.S + Oxidation (M) |
| 2192.0176 | 2191.0103 | 2191.0691 | -26.85 | 66 | 83 | 1 | R.ELLSIRIDPEHHTCQESK.S |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1812.8393, 1855.8316, 1906.9695, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197
8. [tr|Q8ZLM3|Q8ZLM3_SALTY](#) Mass: 16477 Score: 34 Expect: 4.3 Matches: 4
Zn(II)-responsive transcriptional regulator OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=zntR PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|--------------------------------------|
| 1798.8146 | 1797.8074 | 1797.8646 | -31.82 | 33 | 47 | 1 | R.TEGGFRLYTENDLQR.L |
| 1836.8843 | 1835.8770 | 1835.8043 | 39.6 | 24 | 38 | 1 | K.QQMDHEVTRTEGGFR.L + Oxidation (M) |
| 1930.8944 | 1929.8872 | 1929.9942 | -55.45 | 90 | 105 | 1 | R.LQEVEARIAELQTMQR.S + Oxidation (M) |
| 2192.0176 | 2191.0103 | 2191.0691 | -26.85 | 66 | 83 | 1 | R.ELLSIRIDPEHHTCQESK.S |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1812.8393, 1855.8316, 1906.9695, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197
9. [tr|A0A0F6AZ78|A0A0F6AZ78_SALT1](#) Mass: 37727 Score: 30 Expect: 9.9 Matches: 5
VirK-like protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ybjX PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|-------------------------------------|
| 1779.9136 | 1778.9063 | 1778.9454 | -22.01 | 306 | 321 | 0 | R.YALLDSVVEQVPATFKR |
| 1836.8843 | 1835.8770 | 1836.0556 | -97.26 | 84 | 98 | 1 | R.LPIRLHRPYMAVNIK.R + Oxidation (M) |
| 1930.8944 | 1929.8872 | 1929.8502 | 19.2 | 100 | 114 | 0 | R.DFALDALCFHYQMR.Q + Oxidation (M) |
| 1935.9494 | 1934.9421 | 1935.0466 | -53.96 | 306 | 322 | 1 | R.YALLDSVVEQVPATFKR.- |
| 2011.9754 | 2010.9681 | 2010.9907 | -11.22 | 220 | 236 | 0 | R.IVMEALCQFAQVQAEK.I |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1855.8316, 1906.9695, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197
10. [tr|H9L481|H9L481_SALTY](#) Mass: 37727 Score: 30 Expect: 9.9 Matches: 5
Homolog of virK OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ybjX PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|-------------------------------------|
| 1779.9136 | 1778.9063 | 1778.9454 | -22.01 | 306 | 321 | 0 | R.YALLDSVVEQVPATFKR |
| 1836.8843 | 1835.8770 | 1836.0556 | -97.26 | 84 | 98 | 1 | R.LPIRLHRPYMAVNIK.R + Oxidation (M) |
| 1930.8944 | 1929.8872 | 1929.8502 | 19.2 | 100 | 114 | 0 | R.DFALDALCFHYQMR.Q + Oxidation (M) |
| 1935.9494 | 1934.9421 | 1935.0466 | -53.96 | 306 | 322 | 1 | R.YALLDSVVEQVPATFKR.- |
| 2011.9754 | 2010.9681 | 2010.9907 | -11.22 | 220 | 236 | 0 | R.IVMEALCQFAQVQAEK.I |
- No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1855.8316, 1906.9695, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197
11. [tr|A0A0F6B2L4|A0A0F6B2L4_SALT1](#) Mass: 32173 Score: 28 Expect: 16 Matches: 4
DNA-binding transcriptional regulator HexR OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yebK PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|----------|-----------|-----------|-----|-------|-----|------|---------|
|----------|-----------|-----------|-----|-------|-----|------|---------|

1906.9695 1905.9623 1905.9407 11.3 131 - 149 0 K.IAFFGLGSSAAVAHDAMNK.F
 1930.8944 1929.8872 1929.9652 -40.43 1 - 16 1 -.MNMLEKVVQSLEHLK.S + Oxidation (M)
 2395.9433 2394.9360 2395.2165 -117.12 32 - 53 0 R.SIHLSIAMLAQEANVSEPTVNR.F + Oxidation (M)
 2998.3197 2997.3124 2997.3662 -17.93 84 - 110 1 R.NVDEDDSVVEAYTGKIFESAMASLDHVR.Q
No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2398.9797, 2453.9716

12. [tr|Q8ZNW1|Q8ZNW1_SALTY](#) Mass: 32173 Score: 28 Expect: 16 Matches: 4
 Transcriptional regulator OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yebK PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1906.9695	1905.9623	1905.9407	11.3	131	- 149	0	K.IAFFGLGSSAAVAHDAMNK.F
1930.8944	1929.8872	1929.9652	-40.43	1	- 16	1	-.MNMLEKVVQSLEHLK.S + Oxidation (M)
2395.9433	2394.9360	2395.2165	-117.12	32	- 53	0	R.SIHLSIAMLAQEANVSEPTVNR.F + Oxidation (M)
2998.3197	2997.3124	2997.3662	-17.93	84	- 110	1	R.NVDEDDSVVEAYTGKIFESAMASLDHVR.Q

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2398.9797, 2453.9716

13. [sp|P58696|SYN_SALTY](#) Mass: 52718 Score: 28 Expect: 16 Matches: 6
 Asparagine--tRNA ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=asnS PE=3 SV=2

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1691.9146	1690.9073	1690.8382	40.9	400	- 414	1	R.LDVLDDARMAEMGLNK.E + Oxidation (M)
1707.8197	1706.8124	1706.8331	-12.14	400	- 414	1	R.LDVLDDARMAEMGLNK.E + 2 Oxidation (M)
1779.9136	1778.9063	1778.8853	11.8	425	- 440	1	R.RYGTVPVHSGFGLGFER.L
1993.9284	1992.9212	1992.9139	3.64	97	- 114	0	K.VEVAGVWVEDPDTYFMAAK.R + Oxidation (M)
2011.9754	2010.9681	2011.0448	-38.12	265	- 281	1	R.LAEAMLVYFVNAVLEER.A + Oxidation (M)
2054.9787	2053.9714	2054.0830	-54.34	376	- 396	0	K.TVAAMDVLAPGIGIIGGSQR.E

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1930.8944, 1935.9494, 1954.9609, 1963.9793, 1997.9709, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

14. [tr|A0A0F6AZF2|A0A0F6AZF2_SALT1](#) Mass: 52718 Score: 28 Expect: 16 Matches: 6
 Asparagine--tRNA ligase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=asnS PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1691.9146	1690.9073	1690.8382	40.9	400	- 414	1	R.LDVLDDARMAEMGLNK.E + Oxidation (M)
1707.8197	1706.8124	1706.8331	-12.14	400	- 414	1	R.LDVLDDARMAEMGLNK.E + 2 Oxidation (M)
1779.9136	1778.9063	1778.8853	11.8	425	- 440	1	R.RYGTVPVHSGFGLGFER.L
1993.9284	1992.9212	1992.9139	3.64	97	- 114	0	K.VEVAGVWVEDPDTYFMAAK.R + Oxidation (M)
2011.9754	2010.9681	2011.0448	-38.12	265	- 281	1	R.LAEAMLVYFVNAVLEER.A + Oxidation (M)
2054.9787	2053.9714	2054.0830	-54.34	376	- 396	0	K.TVAAMDVLAPGIGIIGGSQR.E

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1930.8944, 1935.9494, 1954.9609, 1963.9793, 1997.9709, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

15. [tr|A0A0F6BAF4|A0A0F6BAF4_SALT1](#) Mass: 29400 Score: 27 Expect: 19 Matches: 4
 Transcriptional activator OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=adiY PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1930.8944	1929.8872	1929.9618	-38.70	83	- 99	0	R.NADPLLNTANCLTPDIFR.V
1993.9284	1992.9212	1992.9574	-18.21	100	- 117	1	R.VAARYSAMEAPDEIVSER.T
1997.9709	1996.9636	1997.0330	-34.77	145	- 161	1	R.SRISDSVYVHIQSDIHK.D
2262.0257	2261.0184	2261.1548	-60.31	162	- 181	1	K.DWNLSAVASCLCLSPSLKK.K

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1935.9494, 1954.9609, 1963.9793, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

16. [tr|Q8ZKE4|Q8ZKE4_SALTY](#) Mass: 29400 Score: 27 Expect: 19 Matches: 4
 Transcriptional activator of adIA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=adiY PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1930.8944	1929.8872	1929.9618	-38.70	83	- 99	0	R.NADPLLNTANCLTPDIFR.V
1993.9284	1992.9212	1992.9574	-18.21	100	- 117	1	R.VAARYSAMEAPDEIVSER.T
1997.9709	1996.9636	1997.0330	-34.77	145	- 161	1	R.SRISDSVYVHIQSDIHK.D
2262.0257	2261.0184	2261.1548	-60.31	162	- 181	1	K.DWNLSAVASCLCLSPSLKK.K

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1935.9494, 1954.9609, 1963.9793, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

17. [tr|A0A0F6B6W2|A0A0F6B6W2_SALT1](#) Mass: 31287 Score: 27 Expect: 21 Matches: 4
 3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=icc PE=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1624.7961	1623.7888	1623.9308	-87.40	2	- 16	1	M.ESLLTLPAGEARVR.I
1755.8110	1754.8037	1754.8224	-10.63	261	- 275	1	R.LQDTRFRPDTASEGY.-
1771.8130	1770.8057	1770.9662	-90.59	1	- 16	1	-.MESLLTLPAGEARVR.I + Oxidation (M)
1836.8843	1835.8770	1835.9853	-59.00	245	- 260	1	R.TLELRANGVLETEVHR.L

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1764.8373, 1766.9272, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1855.8316, 1906.9695, 1930.8944, 1935.9494, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

18. [tr|Q8ZLZ6|Q8ZLZ6_SALTY](#) Mass: 31287 Score: 27 Expect: 21 Matches: 4
 3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1624.7961	1623.7888	1623.9308	-87.40	2	- 16	1	M.ESLLTLPAGEARVR.I
1755.8110	1754.8037	1754.8224	-10.63	261	- 275	1	R.LQDTRFRPDTASEGY.-
1771.8130	1770.8057	1770.9662	-90.59	1	- 16	1	-.MESLLTLPAGEARVR.I + Oxidation (M)
1836.8843	1835.8770	1835.9853	-59.00	245	- 260	1	R.TLELRANGVLETEVHR.L

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1728.8183, 1764.8373, 1766.9272, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1855.8316, 1906.9695, 1930.8944, 1935.9494,

1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2262.0257, 2265.0756, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

19. [tr|A0A0F6AZT2|A0A0F6AZT2_SALT1](#) Mass: 34672 Score: 26 Expect: 24 Matches: 4

Curved DNA-binding protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=cbpA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1728.8183	1727.8110	1727.8440	-19.12	5	-	19	0	K.DYYAIMGVKPTDDLK.T
1935.9494	1934.9421	1934.9374	2.46	46	-	61	1	R.FKEVAEAEWVLSDEQR.R
2262.0257	2261.0184	2261.0959	-34.29	1	-	19	1	-.MELKDYYAIMGVKPTDDLK.T + 2 Oxidation (M)
2265.0756	2264.0684	2264.2238	-68.67	263	-	282	1	K.HTGDLYAIKIVMPPKPEK.T

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1930.8944, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

20. [sp|P63263|CBPA_SALTY](#) Mass: 34672 Score: 26 Expect: 24 Matches: 4

Curved DNA-binding protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cbpA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1728.8183	1727.8110	1727.8440	-19.12	5	-	19	0	K.DYYAIMGVKPTDDLK.T
1935.9494	1934.9421	1934.9374	2.46	46	-	61	1	R.FKEVAEAEWVLSDEQR.R
2262.0257	2261.0184	2261.0959	-34.29	1	-	19	1	-.MELKDYYAIMGVKPTDDLK.T + 2 Oxidation (M)
2265.0756	2264.0684	2264.2238	-68.67	263	-	282	1	K.HTGDLYAIKIVMPPKPEK.T

No match to: 1152.7677, 1202.6934, 1310.6825, 1365.6654, 1367.7158, 1506.7481, 1624.7961, 1634.9028, 1664.8952, 1688.8426, 1691.9146, 1707.8197, 1723.8807, 1755.8110, 1764.8373, 1766.9272, 1771.8130, 1779.9136, 1785.8290, 1798.8146, 1812.8393, 1836.8843, 1855.8316, 1906.9695, 1930.8944, 1954.9609, 1963.9793, 1993.9284, 1997.9709, 2011.9754, 2054.9787, 2192.0176, 2244.0164, 2319.0381, 2395.9433, 2398.9797, 2453.9716, 2998.3197

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 120 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 42

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: tr|Q8ZNL0|Q8ZNL0_SALTY

Outer membrane porin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cirA PE=3 SV=1

Database: Salmonella_typhimurium_LT2
Score: 191
Expect: 7.9e-016
Nominal mass (M_r): 73838
Calculated pI: 5.46

Sequence similarity is available as [an NCBI BLAST search of tr|Q8ZNL0|Q8ZNL0_SALTY against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 56
Mass values matched: 19

Protein sequence coverage: 33%

Matched peptides shown in **bold red**.

```

1 MFRFNPFV RV GLCMSAVTLA WPVAAATDDG ETMVVTASAI EQNLKDAPAS
51 ISVITQODLQ RRPVQNLKDV LKEVPGVQLT NEGDNRKGV S IRGLDSSYTL
101 ILIDGKRVNS RNAVFRHND F DLNWI PVDAI ERIEVVRGPM S SLYGSDALG
151 GVVNIITKKI GQKWHG SVTV DSTIQEHRDR GDTYNGQFFT S GPLIDGVLG
201 MKAYGSLAKR EKDEQQSSAT TATGETPRIE GFTSRDGNVE FAWTPNENHD
251 VTAGYGFDRQ DRDSDSL DKN RLERQNYALS HNGRWDLGNS ELKFYGEKVE
301 NKNPGNSSPI TSESNSIDGK YVLPLASVNQ FLTFGGEWRH DKLSDAVNLT
351 GGSSTKTSAS QYALFLEDEW RIFEPLALTT GIRMDDHETY GDHWSPRAYL
401 VYNATDTLTV KGGWATAFKA PSSLQLSPDW ATNSCRGGCR IVGSPDLKPE
451 TSESWELGLY YRGEEGILEG VEASVTFRN DVDNRISISR TPDVNAAPGY
501 SNFVG FETNS RGQRVPVFRY YNVNKARIQG VETELKVPFN EAWKLSLNYT
551 YNDGRDVSNG GNKPLSDLPF HTANGTLDWK PVQLEDWSFY VSGNYTGRKR
601 ADSATAKTPG GYVVDWTGAA WQATKNV KLR AGVLNVGDKD LKRDDYGYTE
651 DGRRYFMAVD YRF

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Unformatted sequence string: **663 residues** (for pasting into other applications).

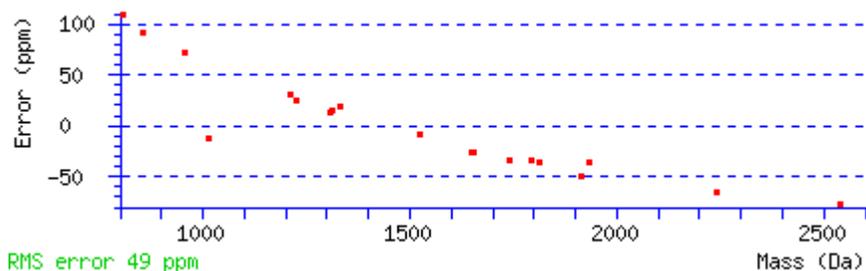
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
46 - 61	1741.8493	1740.8420	1740.9006	-33.7	0	K.DAPASISVITQODLQ.R
62 - 68	854.5987	853.5914	853.5134	91.4	0	R.RPVQNLK.D

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
62 - 72	1309.8125	1308.8052	1308.7878	13.3	1	R.RPVQNLKDVLK.E
73 - 86	1527.7254	1526.7182	1526.7325	-9.38	0	K.EVPGVQLTNEGDNR.K
73 - 87	1655.7911	1654.7839	1654.8275	-26.3	1	K.EVPGVQLTNEGDNRK.G
93 - 107	1650.8614	1649.8541	1649.8988	-27.1	1	R.GLDSSYTLILIDGKR.V
211 - 228	1935.8201	1934.8128	1934.8817	-35.6	1	R.EKDEQQSSATTATGETPR.I
229 - 235	809.5031	808.4958	808.4079	109	0	R.IEGFTSR.D
357 - 371	1815.7886	1814.7813	1814.8475	-36.5	0	K.TSASQYALFLEDEWR.I
372 - 383	1330.7971	1329.7899	1329.7656	18.2	0	R.IFEPLALTTGIR.M
420 - 436	1915.8372	1914.8299	1914.9258	-50.1	0	K.APSLLQLSPDWATNSCR.G
441 - 462	2539.0746	2538.0673	2538.2642	-77.6	0	R.IVGSPDLKPETSESWELGLYYR.G
463 - 479	1793.8303	1792.8230	1792.8843	-34.2	0	R.GEEGILEGVEASVTTFR.N
491 - 511	2242.8912	2241.8839	2242.0291	-64.8	0	R.TPDVNAAPGYSNFGVFETNSR.G
512 - 519	958.6268	957.6195	957.5508	71.7	1	R.GQRVPVFR.Y
528 - 536	1016.5490	1015.5417	1015.5550	-13.1	0	R.IQGVETELK.V
545 - 555	1315.6483	1314.6410	1314.6204	15.7	0	K.LSLNYTYNDGR.D
655 - 663	1211.5924	1210.5852	1210.5481	30.6	1	R.YFMAVDYRF.-
655 - 663	1227.5800	1226.5728	1226.5430	24.2	1	R.YFMAVDYRF.- + Oxidation (M)

No match to: 524.3198, 568.2942, 606.4785, 615.5242, 617.5106, 770.4837, 1142.5755, 1143.5355, 1163.5946, 1179.6276, 1342.7532, 1352.7658, 1372.7829, 1384.7942, 1387.7851, 1456.7632, 1502.6656, 1521.7196, 1570.7894, 1637.7870, 1648.7893, 1707.8022, 1753.8368, 1755.8824, 1759.7655, 1763.7901, 1829.7859, 1871.8122, 1929.8145, 2044.8419, 2204.4013, 2226.9067, 2255.9108, 2258.9162, 2265.8751, 2299.9009, 2411.9466



Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P06179|FLIC_SALTY

Flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)
OX=99287 GN=fliC PE=1 SV=4

Database: Salmonella_Typhi_LT2
Score: 68
Expect: 0.00028
Nominal mass (M_r): 51581
Calculated pI: 4.79

Sequence similarity is available as [an NCBI BLAST search of P06179|FLIC_SALTY against nr.](#)

Search parameters

MS data file: peaklist_12.xml
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 88
Mass values matched: 12

Protein sequence coverage: 36%

Matched peptides shown in **bold red**.

1 **MAQVINTNSL SLLTQNNLNK SQSALGTAIE RLSSGLRINS** AKDDAAGQAI
51 ANRFTANIKG LTQASRNAND **GISIAQTTEG ALNEINNNLQ RVRELAVQSA**
101 **NSTNSQSDLD SIQAEITQRL NEIDRVSGQT** QFNGVKVLAQ DNTLTIQVGA
151 NDGETIDIDL **KQINSQTLGL DTLNVQQKYK** VSDTAATVTG YADTTIALDN
201 STFK**ASATGL GGTDQK**IDGD LKFDDTTGKY YAK**VTVTGGT GK**DGYEVS
251 DKTNGEVTLA GGATSPLTGG LPATATEDVK NVQVANADLT EAKAALTAAG
301 VTGTASVVKM SYTDNNGKTI DGGLAVKVD DYYSATQNKD GSISINTTKY
351 TADDGTSKTA LNKLGADGK TEVVSIGGKT YAASKAEGHN FKAQPDIAEA
401 AATTTENPLQ **KIDAALQVD TLRSDLGAVQ** NR**FNSAITNL GNTVNNL TSA**
451 **RSRIEDSDYA TEVSNMSRAQ ILQQAGTSVL AQANQVPQNV LSLLR**

Unformatted sequence string: **495 residues** (for pasting into other applications).

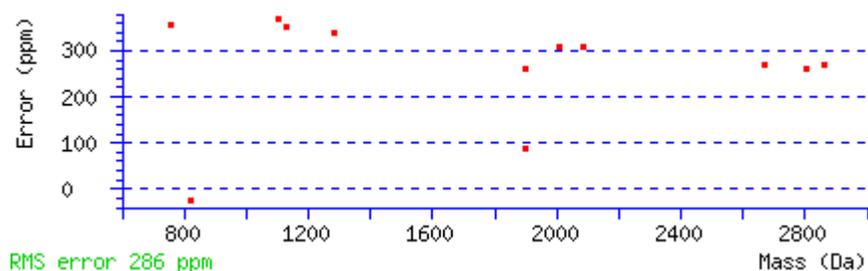
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
2 - 20	2085.7717	2084.7645	2084.1225	308	0	M.AQVINTNSLSLLTQNNLNK.S
21 - 31	1132.9962	1131.9889	1131.5884	354	0	K.SQSALGTAIER.L
67 - 91	2671.0261	2670.0188	2669.3004	269	0	R.NANDGISIAQTTEGALNEINNNLQR.V
94 - 119	2806.0854	2805.0782	2804.3424	262	0	R.ELAVQSANSTNSQSDLDLSIQAEITQR.L
120 - 125	759.6703	758.6631	758.3922	357	0	R.LNEIDR.V
162 - 178	1900.1819	1899.1746	1899.0061	88.7	0	K.QINSQTLGLDTLNVQQK.Y

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
162 - 178	1900.5092	1899.5019	1899.0061	261	0	K.QINSQTLGLDITLNVQOK.Y
205 - 216	1105.9583	1104.9510	1104.5411	371	0	K.ASATGLGGTDQK.I
234 - 242	819.4356	818.4283	818.4498	-26.2	0	K.VTVTGGTGK.D
412 - 423	1286.1462	1285.1390	1284.7038	339	0	K.IDAALAQVDTLR.S
433 - 451	2007.6425	2006.6352	2006.0181	308	0	R.FNSAITNLGNTVNNLTSAR.S
469 - 495	2861.3657	2860.3584	2859.5930	268	0	R.AQILQQAGTSVLAQANQVPQNVLSLLR.-

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 768.8820, 774.6613, 792.7436, 810.6292, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2065.8123, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2705.8262



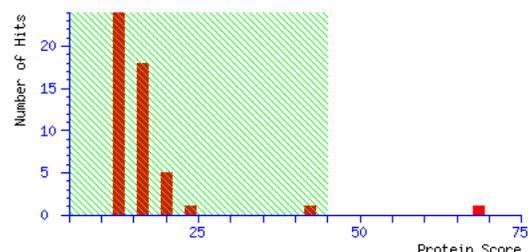
Mascot: <http://www.matrixscience.com/>

MASCOT SEARCH RESULTS

User : mrlabs
 Email : mrlabs7389@gmail.com
 Search title : Sample_12
 MS data file : peaklist_12.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 30 Jul 2024 at 09:16:42 GMT
 Top Score : 68 for [P06179|FLIC_SALTY](#), Flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flic PE=1 SV=4

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)

Significance threshold $p < 0.05$ Max. number of hits

Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P06179 FLIC_SALTY	51581	68	Flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flic PE=1 SV=4
2. P52616 FLJB_SALTY	52504	42	Phase 2 flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fljB PE=1 SV=2
3. P37462 ALKB_SALTY	24000	23	Alpha-ketoglutarate-dependent dioxygenase AlkB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=alkB PE=1 SV=1
4. P15931 FLGJ_SALTY	34363	22	Peptidoglycan hydrolase FlgJ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgJ PE=1 SV=1
5. P0A287 RMUC_SALTY	54611	20	DNA recombination protein RmuC OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rmuC PE=1 SV=1
6. P54698 RCSA_SALTY	23458	20	Transcriptional regulatory protein RcsA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rcaA PE=1 SV=1
7. P0A289 RNH_SALTY	17670	19	Ribonuclease HI OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rnhA PE=3 SV=1
8. P66974 TRMJ_SALTY	26768	19	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=trmJ PE=1 SV=1
9. Q8ZKR2 AIRSK_SALTY	34786	18	Aminoimidazole riboside kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM4066 PE=1 SV=1
10. D0ZLR9 DGAR_SALTY	105953	17	Transcriptional regulatory protein DagR OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=dgaR PE=1 SV=1
11. P74840 PRPD_SALTY	54152	17	2-methylcitrate dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=prpD PE=1 SV=1
12. P26417 FLIL_SALTY	17148	17	Flagellar protein Flil OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flil PE=3 SV=1
13. P0A172 SKP_SALTY	17894	17	Chaperone protein Skp OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=skp PE=1 SV=1
14. Q8ZR43 HTRR_SALTY	22017	17	Transcriptional regulator RamR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ramR PE=1 SV=1
15. P37430 NUSA_SALTY	55562	17	Transcription termination/antitermination protein NusA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nusA PE=1 SV=1
16. P39434 SLT_SALTY	73801	16	Soluble lytic murein transglycosylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slyT PE=1 SV=1
17. P67912 HLDD_SALTY	34941	16	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=hlhA PE=1 SV=1
18. P59696 T200_SALTY	18231	16	Transposase for insertion sequence element IS200 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=t200 PE=1 SV=1
19. Q9L914 DCUP_SALTY	39363	16	Uroporphyrinogen decarboxylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=hemE PE=1 SV=1
20. Q8ZQ02 SLRP_SALTY	87274	16	E3 ubiquitin-protein ligase SlrP OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slrP PE=1 SV=1

Results List

1. [P06179|FLIC_SALTY](#) Mass: 51581 Score: 68 Expect: 0.00028 Matches: 12
 Flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flic PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
759.6703	758.6631	758.3922	357	120	- 125	0	R.LNEIDR.V
819.4356	818.4283	818.4498	-26.25	234	- 242	0	K.VTVTGGTGK.D
1105.9583	1104.9510	1104.5411	371	205	- 216	0	K.ASATGLGGTDQK.I
1132.9962	1131.9889	1131.5884	354	21	- 31	0	K.SQSALGTAIER.L
1286.1462	1285.1390	1284.7038	339	412	- 423	0	K.IDAALAQVDTLR.S
1900.1819	1899.1746	1899.0061	88.7	162	- 178	0	K.QINSQTLGLDTLNVQK.Y
1900.5092	1899.5019	1899.0061	261	162	- 178	0	K.QINSQTLGLDTLNVQK.Y
2007.6425	2006.6352	2006.0181	308	433	- 451	0	R.FNSAITNLGNTVNNLTSAR.S
2085.7717	2084.7645	2084.1225	308	2	- 20	0	M.AQVINTNSLSLLTQNNLNK.S
2671.0261	2670.0188	2669.3004	269	67	- 91	0	R.NANDGISIAQTTEGALNEINNLR.V
2806.0854	2805.0782	2804.3424	262	94	- 119	0	R.ELAVQSANSTNSQSLDLSIQAEITQR.L
2861.3657	2860.3584	2859.5930	268	469	- 495	0	R.AQILQAGTSVLAQANVQPQNVLSLR.-

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 768.8820, 774.6613, 792.7436, 810.6292, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706,

1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2065.8123, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2705.8262

2. [P52616|FLJB_SALTY](#) Mass: 52504 Score: 42 Expect: 0.13 Matches: 8

Phase 2 flagellin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fljB PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
759.6703	758.6631	758.3922	357	120	- 125	0	R.LNEIDR.V
823.4167	822.4094	822.3508	71.3	228	- 234	0	K.FDADNNK.Y
994.5035	993.4962	993.4801	16.2	272	- 281	0	K.TTMPAGATTK.T + Oxidation (M)
1132.9962	1131.9889	1131.5884	354	21	- 31	0	K.SQSALGTAIER.L
2085.7717	2084.7645	2084.1225	308	2	- 20	0	M.AQVINTNSLSLLTQNNLNK.S
2671.0261	2670.0188	2669.3004	269	67	- 91	0	R.NANDGISIAQTTEGALNEINNNLQR.V
2806.0854	2805.0782	2804.3424	262	94	- 119	0	R.ELAVQSANSTNSQSDLSIQAEITQR.L
2861.3657	2860.3584	2859.5930	268	480	- 506	0	R.AQILQQAGTSVLAQANQVQPNVLSLLR.-

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 842.8293, 848.6038, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2705.8262

3. [P37462|ALKB_SALTY](#) Mass: 24000 Score: 23 Expect: 9.8 Matches: 4

Alpha-ketoglutarate-dependent dioxygenase AlkB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=alkB PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.4227	605.4154	605.3173	162	122	- 127	0	R.YAPGAK.L
715.4630	714.4557	714.3660	126	162	- 167	0	R.SDPIQR.I
1249.3043	1248.2970	1248.5710	-219.40	194	- 204	0	K.AGFHPMTGEFR.Y
2806.0854	2805.0782	2804.2391	299	48	- 73	0	R.QMVTGGYMTSAMVAMTNCGALGWTTDR.H

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2861.3657

4. [P15931|FLGJ_SALTY](#) Mass: 34363 Score: 22 Expect: 13 Matches: 6

Peptidoglycan hydrolase FlgJ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgJ PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
656.2935	655.2862	655.4017	-176.24	159	- 164	0	R.LSLPAR.L
1456.5835	1455.5762	1455.6924	-79.82	39	- 50	0	R.QVEGMFVQMLK.S + Oxidation (M)
1488.2366	1487.2293	1487.6823	-304.47	39	- 50	0	R.QVEGMFVQMLK.S + 3 Oxidation (M)
1729.7589	1728.7516	1728.9046	-88.48	7	- 22	0	K.LLASAAWDAQSLNELK.A
1839.2871	1838.2798	1837.8581	229	214	- 230	0	K.GPVTIEITTEYENGEAK.K
2211.6995	2210.6922	2210.1331	253	116	- 134	0	K.FSLETVNSYQNALTLQVLR.K

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

5. [P0A287|RMUC_SALTY](#) Mass: 54611 Score: 20 Expect: 20 Matches: 6

DNA recombination protein RmuC OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rnuC PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
715.4630	714.4557	714.4276	39.4	427	- 433	0	R.LGLVEIK.R
759.6703	758.6631	758.4174	324	253	- 259	0	K.DVVIDAK.M
810.6292	809.6219	809.4144	256	26	- 32	0	K.AHADQIR.A
819.4356	818.4283	818.3671	74.8	362	- 367	0	R.YEHQSR.N
1638.4940	1637.4867	1637.7971	-189.48	385	- 399	0	R.LFVDDMSAIGQSLDK.A
2399.8494	2398.8421	2399.3498	-211.60	2	- 25	0	M.DITLMISAVVALAAGAVIGWLATK.A + Oxidation (M)

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

6. [P54698|RCSA_SALTY](#) Mass: 23458 Score: 20 Expect: 20 Matches: 4

Transcriptional regulatory protein RcsA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rcaA PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
774.6613	773.6540	773.4647	245	100	- 106	0	K.NLLISSK.S
823.4167	822.4094	822.3905	23.0	141	- 147	0	R.TESSMLR.M
1609.3949	1608.3876	1608.7930	-251.98	194	- 207	0	R.LTDNVNTEGIFVNMNR.- + Oxidation (M)
1651.1450	1650.1377	1650.7494	-370.54	148	- 161	0	R.MWMGEGQTIQISDR.M

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 792.7436, 810.6292, 819.4356, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

7. [P0A289|RNH_SALTY](#) Mass: 17670 Score: 19 Expect: 23 Matches: 3

Ribonuclease HI OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rnhA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
774.6613	773.6540	773.4072	319	100	- 105	0	K.NVDLWK.R
1411.1356	1410.1283	1409.7204	289	76	- 86	0	R.QEITQWIHNWK.K
2477.8357	2476.8284	2477.2009	-150.38	4	- 27	0	K.QVEIFTDGSCSLGNPGGYGAIRL.Y

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2671.0261, 2705.8262, 2806.0854, 2861.3657

8. [P66974|TRMJ_SALTY](#) Mass: 26768 Score: 19 Expect: 26 Matches: 4
tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=trmJ PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.4227	605.4154	605.2843	217	95	- 99	0	R.ECGLK.S
774.6613	773.6540	773.4218	300	1	- 6	0	-.MLQNI.R.I
1225.5845	1224.5772	1224.6325	-45.16	85	- 94	0	R.TLPWPLMDPR.E
1882.6255	1881.6182	1880.9785	340	186	- 201	0	R.FYGHLEQTLTSTGFIR.E

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

9. [Q8ZKR2|AIRSK_SALTY](#) Mass: 34786 Score: 18 Expect: 29 Matches: 4
Aminimidazole riboside kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM4066 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
614.3611	613.3539	613.3224	51.4	207	- 210	0	R.YYLR.D
1627.2775	1626.2702	1625.8665	248	7	- 21	0	K.VVWIGDASVDLVPEK.Q
2085.7717	2084.7645	2085.0954	-158.70	78	- 97	0	R.LDADLTSALVIVNLTADGER.S
2235.8264	2234.8191	2235.0749	-114.43	121	- 138	0	R.QYEWYFSSIGLTDPRP.E

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2150.8479, 2211.6995, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

10. [D0ZLR9|DGAR_SALTY](#) Mass: 105953 Score: 17 Expect: 34 Matches: 8
Transcriptional regulatory protein DagR OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=dgaR PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
614.3611	613.3539	613.3911	-60.74	878	- 882	0	R.IVINR.K
1267.1986	1266.1913	1266.6278	-344.60	740	- 749	0	R.MVILDYNEVR.S + Oxidation (M)
1267.5372	1266.5300	1266.6278	-77.25	740	- 749	0	R.MVILDYNEVR.S + Oxidation (M)
1488.2366	1487.2293	1486.7086	350	363	- 375	0	R.LAEMSVNPTPEQR.L + Oxidation (M)
1540.5765	1539.5693	1539.6455	-49.51	867	- 877	0	R.FLIHCCMVVER.I + Oxidation (M)
1600.5422	1599.5350	1599.8654	-206.55	256	- 270	0	R.LICATTEPVGSALLR.T
2085.7717	2084.7645	2085.1735	-196.17	127	- 147	0	R.AAVLYPHGLHVLTPGSGVGK.T
2399.8494	2398.8421	2398.2678	239	819	- 839	0	R.FISALTMESIIINHISVLPQR.I + Oxidation (M)

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1492.0393, 1566.6804, 1582.5706, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

11. [P74840|PRPD_SALTY](#) Mass: 54152 Score: 17 Expect: 35 Matches: 6
2-methylcitrate dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=prpd PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
630.3571	629.3498	629.3497	0.20	130	- 136	0	R.NAVAAGK.A
1249.3043	1248.2970	1248.5815	-227.86	254	- 263	0	K.TWGFYDVFSFK.G
1839.2871	1838.2798	1837.9172	197	469	- 483	0	R.LEQMPVNEYLDLYVI.-
1986.4994	1985.4921	1985.0218	237	192	- 209	0	R.DEILNAVSLAWVDGQSLR.T
1986.6616	1985.6543	1985.0218	319	192	- 209	0	R.DEILNAVSLAWVDGQSLR.T
1994.5728	1993.5655	1992.9768	295	269	- 284	0	R.FQRPYGSYVMENVLFK.I + Oxidation (M)

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

12. [P26417|FLIL_SALTY](#) Mass: 17148 Score: 17 Expect: 36 Matches: 3
Flagellar protein Flil OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flil PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1132.9962	1131.9889	1131.5924	350	91	- 99	0	R.LNEYLPPEVR.S
1294.4711	1293.4638	1293.7292	-205.17	129	- 141	0	K.ETLAAPLVAGQPK.Q
1638.4940	1637.4867	1636.9189	347	142	- 155	0	K.QVTVDLVYAFILR.-

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

1286.1462, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

13. [P0A1Z2|SKP_SALTY](#) Mass: 17894 Score: 17 Expect: 36 Matches: 4

Chaperone protein Skp OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=skp PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.4227	605.4154	605.3207	156	71	-	75	0 R.LQSMK.A
634.3081	633.3008	633.2718	45.9	109	-	113	0 R.SNEER.N
1986.4994	1985.4921	1986.0608	-286.34	4	-	23	0 K.WLLAAGLGLAMVTSQAQADK.I
1986.6616	1985.6543	1986.0608	-204.66	4	-	23	0 K.WLLAAGLGLAMVTSQAQADK.I

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 614.3611, 615.7364, 630.3571, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

14. [Q8ZR43|HTHTR_SALTY](#) Mass: 22017 Score: 17 Expect: 38 Matches: 4

Transcriptional regulator RamR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ramR PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
634.3081	633.3008	633.3333	-51.34	77	-	82	0 R.SITDAK.M
774.6613	773.6540	773.4283	292	108	-	114	0 R.QLAVSEK.L
1638.4940	1637.4867	1637.7211	-143.12	64	-	76	0 K.QDLCQSMIMELDR.S
1960.7357	1959.7284	1959.9744	-125.48	87	-	102	0 R.FIWNYSIVSGLNHPAR.H

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

15. [P37430|NUSA_SALTY](#) Mass: 55562 Score: 17 Expect: 39 Matches: 4

Transcription termination/antitermination protein NusA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nusA PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1378.5457	1377.5384	1377.7326	-140.96	205	-	215	0 R.SKPEMLIELFR.I + Oxidation (M)
1882.6255	1881.6182	1881.9367	-169.22	308	-	325	0 K.HTMDIAVEAGNLQAIGR.N + Oxidation (M)
2705.8262	2704.8189	2705.1981	-140.16	82	-	104	0 R.FEDESINVGDYVEDQIESVTFDR.I
2806.0854	2805.0782	2804.2910	281	457	-	482	0 R.GVCTLEDLADQIGDDLADIEGLTDEK.A

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1900.1819, 1900.5092, 1960.7357, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

16. [P39434|SLT_SALTY](#) Mass: 73801 Score: 16 Expect: 43 Matches: 6

Soluble lytic murein transglycosylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slt PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
759.6703	758.6631	758.4075	337	283	-	288	0 R.DIVAWR.L
848.6038	847.5965	847.4552	167	105	-	111	0 R.FVNELAR.R
1294.4711	1293.4638	1293.6466	-141.28	573	-	585	0 R.IFASAAAYNGPGR.V
1351.5415	1350.5342	1350.5874	-39.36	633	-	643	0 K.EALMSDSEWQR.R
1492.0393	1491.0320	1490.7081	217	61	-	71	0 K.DYPLYPLEYR.K
2235.8264	2234.8191	2234.0909	326	449	-	467	0 R.YAFNQHWDLSSVQATIAGK.L

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

17. [P67912|HLDD_SALTY](#) Mass: 34941 Score: 16 Expect: 45 Matches: 5

ADP-L-glycerol-D-manno-heptose-6-epimerase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=hlDD PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
560.3840	559.3767	559.2966	143	18	-	22	0 K.ALNDK.G
1456.5835	1455.5762	1455.5798	-2.49	88	-	98	0 K.YMMDNNYQYSK.E
1488.2366	1487.2293	1487.5697	-228.82	88	-	98	0 K.YMMDNNYQYSK.E + 2 Oxidation (M)
1540.5765	1539.5693	1539.7681	-129.16	272	-	284	0 R.YQAFTQADLTNLR.N
1755.7000	1754.6927	1754.8298	-78.12	294	-	308	0 K.TVAEGVTEYMAWLNLR.D + Oxidation (M)

No match to: 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

18. [P59696|T200_SALTY](#) Mass: 18231 Score: 16 Expect: 46 Matches: 3

Transposase for insertion sequence element IS200 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tnpA1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
684.6204	683.6131	683.3715	354	6	-	11	0 K.SLAHTR.W
715.4630	714.4557	714.4388	23.7	36	-	42	0 R.AVGSILR.K

1249.3043 1248.2970 1248.5883 -233.23 72 - 82 0 K.MSVSSFMGYLK.G

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 695.3472, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1986.4994, 1986.6616, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

19. [Q9L9I4|DCUP_SALTY](#) Mass: 39363 Score: 16 Expect: 46 Matches: 5

Uroporphyrinogen decarboxylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=heme PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1249.3043	1248.2970	1248.7078	-328.92	188	-	198	0	K.SVTLYLNAQIK.A
1638.4940	1637.4867	1637.7184	-141.46	218	-	229	0	R.DYQQFSLYMHK.I + Oxidation (M)
1986.4994	1985.4921	1984.9928	252	112	-	129	0	K.LPIPDPEGELGYMNAVR.T + Oxidation (M)
1986.6616	1985.6543	1984.9928	333	112	-	129	0	K.LPIPDPEGELGYMNAVR.T + Oxidation (M)
2671.0261	2670.0188	2669.3047	268	137	-	162	0	K.GEVPLIGFSGSPWTLATYVMEGSSK.A

No match to: 560.3840, 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1138.4381, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1396.1864, 1411.1356, 1411.4263, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1582.5706, 1600.5422, 1609.3949, 1627.2775, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2211.6995, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2705.8262, 2806.0854, 2861.3657

20. [Q8ZQ02|SLRP_SALTY](#) Mass: 87274 Score: 16 Expect: 53 Matches: 8

E3 ubiquitin-protein ligase SlrP OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slrP PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
560.3840	559.3767	559.2714	188	161	-	165	0	K.EAANR.E
1138.4381	1137.4308	1137.5700	-122.30	620	-	629	0	R.ESLSLTTMTR.D
1396.1864	1395.1791	1394.6976	345	1	-	12	0	-.MFNITNIQSTAR.H
1411.4263	1410.4190	1410.6925	-193.91	1	-	12	0	-.MFNITNIQSTAR.H + Oxidation (M)
1582.5706	1581.5633	1581.8515	-182.19	260	-	273	0	R.LPSALQSLDLFHNK.I
1986.4994	1985.4921	1984.9234	287	533	-	549	0	R.ETVFIAMNATISCEDR.V + Oxidation (M)
1986.6616	1985.6543	1984.9234	368	533	-	549	0	R.ETVFIAMNATISCEDR.V + Oxidation (M)
2211.6995	2210.6922	2211.0742	-172.79	550	-	568	0	R.VTLAYHQMQEATLVHDAER.G

No match to: 568.4212, 574.3776, 576.7371, 592.3998, 606.4227, 614.3611, 615.7364, 630.3571, 634.3081, 654.2974, 656.2935, 662.9393, 684.6204, 695.3472, 715.4630, 759.6703, 768.8820, 774.6613, 792.7436, 810.6292, 819.4356, 823.4167, 842.8293, 848.6038, 994.5035, 1036.4569, 1052.0515, 1064.0465, 1078.4246, 1105.9583, 1132.9962, 1165.9988, 1189.9401, 1207.6920, 1225.5845, 1249.3043, 1267.1986, 1267.5372, 1283.0823, 1286.1462, 1294.4711, 1309.5243, 1336.4221, 1351.5415, 1378.5457, 1411.1356, 1429.5258, 1438.4973, 1456.5835, 1488.2366, 1492.0393, 1540.5765, 1566.6804, 1600.5422, 1609.3949, 1627.2775, 1638.4940, 1651.1450, 1729.7589, 1755.7000, 1771.7156, 1797.8961, 1839.2871, 1882.6255, 1900.1819, 1900.5092, 1960.7357, 1994.5728, 2007.6425, 2065.8123, 2085.7717, 2150.8479, 2235.8264, 2371.9548, 2399.8494, 2477.8357, 2671.0261, 2705.8262, 2806.0854, 2861.3657

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : \pm 371.5 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 0
 Number of queries : 88

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P26466|LAMB_SALTY

Maltoporin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)
OX=99287 GN=lamB PE=1 SV=2

Database: Salmonella_Typhi_LT2
Score: 76
Expect: 4.9e-005
Nominal mass (M_r): 50631
Calculated pI: 4.87

Sequence similarity is available as [an NCBI BLAST search of P26466|LAMB_SALTY against nr.](#)

Search parameters

MS data file: peaklist_3.xml
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 66
Mass values matched: 11

Protein sequence coverage: 31%

Matched peptides shown in **bold red**.

```

1  MMITLRKLPL AVAVAAGVMS AQAMAVDFHG YARSGIGWTG SGGEQQCFQA
51 TGAQSKYRLG NECETYAELK LGQEVWKEGD KSFYFDTNVA YSVNQNDWE
101 STDPAFREAN VQGKNLIEWL PGSTIWAGKR FYQRHDVHMI DFYYWDISGP
151 GAGIENIDLG FGKLSLAATR STEAGGSYTF SSQNIYDEVK DTANDVFDVR
201 LAGLQTNPDG VLELGVVDYGR ANTTDGYKLA DGASKDGWMF TAEHTQSMLK
251 GYNKFVVQYA TDAMTTQGKG QARGSDGSSS FTEELSDGTK INYANKVINN
301 NGNMWRILDH GAISLGDKWD LMYVGMQNI DWDNNLGTEW WTVGVRPMYK
351 WTPIMSTLLE VGYDNVSQQ TGDRNNQYKI TLAQQWQAGD SIWSRPAIRI
401 FATYAKWDEK WGYIKGDGNI SRYAAATNSG ISTNSRGDSD EWTFGAQMEI
451 WW

```

Unformatted sequence string: **452 residues** (for pasting into other applications).

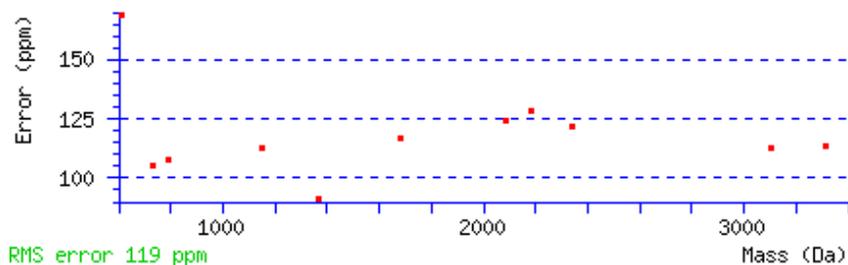
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
34 - 56	2342.3325	2341.3252	2341.0394	122	0	R.SGIGWTGSGGEQQCFQATGAQSK.Y
82 - 107	3101.7053	3100.6980	3100.3475	113	0	K.SFYFDTNVAYSVNQNDWESTDPAFR.E
115 - 129	1685.1019	1684.0947	1683.8984	117	0	K.NLIEWLPGSTIWAGK.R
131 - 134	613.4128	612.4056	612.3020	169	0	R.FYQR.H
164 - 170	731.5178	730.5105	730.4337	105	0	K.LSLAATR.S
171 - 190	2183.2573	2182.2500	2181.9702	128	0	R.STEAGGSYTFSSQNIYDEVK.D
171 - 200	3315.8687	3314.8614	3314.4851	114	1	R.STEAGGSYTFSSQNIYDEVKDTANDVFDVR.L

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
191 - 200	1151.6626	1150.6553	1150.5255	113	0	K.DTANDVFDVR.L
201 - 220	2087.3357	2086.3284	2086.0695	124	0	R.LAGLQTNPDGVLELGVDYGR.A
368 - 374	791.4495	790.4422	790.3569	108	0	K.SQQTGDR.N
400 - 410	1371.8195	1370.8122	1370.6870	91.3	1	R.IFATYAKWDEK.W

No match to: 592.2010, 606.2520, 663.3585, 684.3077, 717.4303, 842.6016, 964.5684, 1021.5976, 1170.7046, 1234.7214, 1282.8002, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2126.2590, 2144.3513, 2235.4358, 2304.4600, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3158.7300, 3218.8752, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398



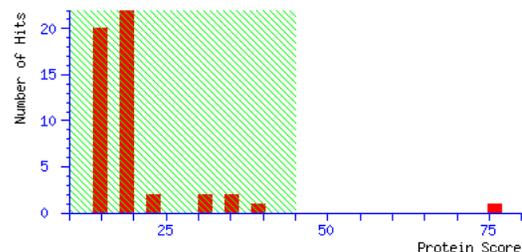
Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

User : MR Labs
 Email : mr1labs7389@gmail.com
 Search title : Sample_3
 MS data file : peaklist_3.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 15 Jul 2024 at 07:34:27 GMT
 Top Score : 76 for **P26466|LAMB_SALTY**, Maltoporin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lamb PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)

Significance threshold $p < 0.05$ Max. number of hits

Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P26466 LAMB_SALTY	50631	76	Maltoporin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lamb PE=1 SV=2
2. Q8ZNA5 FADL_SALTY	47445	40	Long-chain fatty acid transport protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=
3. Q8ZK31 SYV_SALTY	108563	37	Valine--tRNA ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=valS PE=3 SV=1
4. P40676 SLYA_SALTY	16469	36	Transcriptional regulator SlyA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slyA PE=
5. P0A2P0 RHLB_SALTY	47291	33	ATP-dependent RNA helicase RhlB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rhlB PE=
6. P07800 CHEZ_SALTY	23905	32	Protein phosphatase CheZ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cheZ PE=1 SV=1
7. Q9L646 NRDD_SALTY	80820	23	Anaerobic ribonucleoside-triphosphate reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=
8. Q56121 RF3_SALTY	59810	22	Peptide chain release factor 3 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=prfC PE=
9. P0A1Q8 HEM3_SALTY	33921	21	Porphobilinogen deaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=hemC PE=3 SV=
10. P0CL14 MRDA_SALTY	69903	20	Peptidoglycan D,D-transpeptidase MrdA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=m
11. P74876 DPO3X_SALTY	70894	20	DNA polymerase III subunit tau OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dnaX PE=
12. Q8ZN25 MURQ_SALTY	31083	20	N-acetylmuramic acid 6-phosphate etherase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287
13. Q06961 TDCD_SALTY	43919	19	Propionate kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tdcD PE=1 SV=2
14. P26392 RMLD_SALTY	32705	19	dTDP-4-dehydroorhamnose reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rfdB P
15. Q8ZQW2 KDPB_SALTY	72267	19	Potassium-transporting ATPase ATP-binding subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) O
16. P0A2C1 RNH2_SALTY	21550	19	Ribonuclease HII OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rnhB PE=3 SV=1
17. Q8ZPV2 ASTC_SALTY	44146	19	Succinylornithine transaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=astC PE=
18. P08002 PDXB_SALTY	41558	19	Erythronate-4-phosphate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=p
19. Q8ZKE6 PHNO_SALTY	18035	19	Aminoalkylphosphonate N-acetyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287
20. P37178 PT1P_SALTY	83916	19	Phosphoenolpyruvate-dependent phosphotransferase system OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700

Results List

1. [P26466|LAMB_SALTY](#) Mass: 50631 Score: 76 Expect: 4.9e-005 Matches: 11
 Maltoporin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lamb PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
613.4128	612.4056	612.3020	169	131	- 134	0	R.FYQR.H
731.5178	730.5105	730.4337	105	164	- 170	0	K.LSLAATR.S
791.4495	790.4422	790.3569	108	368	- 374	0	K.SQQTGDR.N
1151.6626	1150.6553	1150.5255	113	191	- 200	0	K.DTANDVFDVR.L
1371.8195	1370.8122	1370.6870	91.3	400	- 410	1	R.IFATYAKWDEK.W
1685.1019	1684.0947	1683.8984	117	115	- 129	0	K.NLIEWLPGSTIWAGK.R
2087.3357	2086.3284	2086.0695	124	201	- 220	0	R.LAGLQTPDGVLELGVGYGR.A
2183.2573	2182.2500	2181.9702	128	171	- 190	0	R.STEAGGSYTFSSQNIYDEVK.D
2342.3325	2341.3252	2341.0394	122	34	- 56	0	R.SGIGWTGSSGGEQQCFQATGAQSK.Y
3101.7053	3100.6980	3100.3475	113	82	- 107	0	K.SFYFDTNVAVSNQQNDWESTDPAFR.E
3315.8687	3314.8614	3314.4851	114	171	- 200	1	R.STEAGGSYTFSSQNIYDEVKDTANDVFDVR.L

No match to: 592.2010, 606.2520, 663.3585, 684.3077, 717.4303, 842.6016, 964.5684, 1021.5976, 1170.7046, 1234.7214, 1282.8002, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2126.2590, 2144.3513, 2235.4358, 2304.4600, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3158.7300, 3218.8752, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

2. [Q8ZNA5|FADL_SALTY](#) Mass: 47445 Score: 40 Expect: 0.17 Matches: 10
Long-chain fatty acid transport protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fadL PE=3 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--|
| 1170.7046 | 1169.6973 | 1169.5941 | 88.2 | 234 | - 242 | 1 | K.NNRYALTYR.S |
| 1419.8948 | 1418.8875 | 1418.7154 | 121 | 251 | - 263 | 0 | K.GNYSDLPPIAINR.F |
| 1587.9663 | 1586.9590 | 1586.7689 | 120 | 357 | - 371 | 0 | R.TGIAFDSPVPAQNR.S |
| 1916.1786 | 1915.1713 | 1914.9264 | 128 | 161 | - 177 | 0 | R.LNEAWSFGLGFDVAVYR.A |
| 1999.1714 | 1998.1641 | 1997.9159 | 124 | 341 | - 356 | 0 | R.IALGTYYDDNNTFR.T |
| 2517.5310 | 2516.5237 | 2516.2336 | 115 | 372 | - 393 | 1 | R.SISIPDQDRFWSAGTTYAFNK.D |
| 2749.6885 | 2748.6812 | 2748.4446 | 86.1 | 183 | - 210 | 0 | R.FAGDLQLVAAQNPALAPVAGQIPSDTK.I |
| 2753.6489 | 2752.6417 | 2752.3649 | 101 | 297 | - 319 | 0 | R.VAPQWAIHYSLAYTWSQFQELK.A |
| 3598.2148 | 3597.2076 | 3596.7610 | 124 | 264 | - 296 | 0 | R.FNLPIPTATGGATQSGYLTLNLPMEWVSGYNR.V |
| 3614.2231 | 3613.2159 | 3612.7559 | 127 | 264 | - 296 | 0 | R.FNLPIPTATGGATQSGYLTLNLPMEWVSGYNR.V + Oxidation (M) |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1234.7214, 1282.8002, 1371.8195, 1569.9546, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 2006.1919, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2663.5623, 2720.5835, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3641.2495, 3809.3398
3. [Q8ZK31|SYV_SALTY](#) Mass: 108563 Score: 37 Expect: 0.39 Matches: 12
Valine--tRNA ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=valS PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|--|
| 606.2520 | 605.2447 | 605.3067 | -102.44 | 128 | - 131 | 1 | R.QMRR.L + Oxidation (M) |
| 717.4303 | 716.4230 | 716.3704 | 73.4 | 94 | - 100 | 0 | K.IAAEEGK.T |
| 1282.8002 | 1281.7929 | 1281.6106 | 142 | 519 | - 528 | 0 | R.MIMTMHFVK.D |
| 1419.8948 | 1418.8875 | 1418.7518 | 95.7 | 906 | - 918 | 1 | R.IEGLKLSNEGFVAR.A |
| 1569.9546 | 1568.9473 | 1568.6745 | 174 | 581 | - 593 | 1 | K.RTGNMMQPMMAEK.I + 3 Oxidation (M) |
| 1842.1445 | 1841.1373 | 1840.9505 | 101 | 293 | - 308 | 0 | R.HALPMINILTFDGDIRE + Oxidation (M) |
| 1860.1655 | 1859.1583 | 1859.1033 | 29.6 | 242 | - 257 | 1 | R.YQSLIGKFKVILPLVNR.R |
| 2056.2139 | 2055.2066 | 2054.9765 | 112 | 259 | - 277 | 1 | R.IPIVGDHADMKEGTGCVK.I |
| 2342.3325 | 2341.3252 | 2341.1485 | 75.5 | 72 | - 92 | 0 | K.NTLWQVGDHAGIATQMVVER.K + Oxidation (M) |
| 3598.2148 | 3597.2076 | 3596.7475 | 128 | 519 | - 548 | 1 | R.MIMTMHFVKDENGKQPVPFHTVYMTGLIR.D + 2 Oxidation (M) |
| 3614.2231 | 3613.2159 | 3612.7424 | 131 | 519 | - 548 | 1 | R.MIMTMHFVKDENGKQPVPFHTVYMTGLIR.D + 3 Oxidation (M) |
| 3809.3398 | 3808.3326 | 3808.8465 | -134.92 | 498 | - 528 | 1 | R.QFHPTSMVSGFDIIFWIAIRMMIMTMHFVK.D + 3 Oxidation (M) |
- No match to: 592.2010, 613.4128, 663.3585, 684.3077, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1371.8195, 1587.9663, 1611.9919, 1685.1019, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3641.2495
4. [P40676|SLYA_SALTY](#) Mass: 16469 Score: 36 Expect: 0.45 Matches: 5
Transcriptional regulator SlyA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=slyA PE=1 SV=3
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--|
| 731.5178 | 730.5105 | 730.4589 | 70.7 | 90 | - 95 | 1 | R.IKLTEK.A |
| 842.6016 | 841.5943 | 841.5286 | 78.0 | 12 | - 17 | 1 | R.LVRIWR.A |
| 1842.1445 | 1841.1373 | 1840.9353 | 110 | 96 | - 111 | 1 | K.ADALIAEMEEVIHKTR.G + Oxidation (M) |
| 1916.1786 | 1915.1713 | 1914.9621 | 109 | 129 | - 144 | 1 | K.LIAKLEHNMILHSHD. - + Oxidation (M) |
| 2056.2139 | 2055.2066 | 2055.0558 | 73.4 | 92 | - 109 | 1 | K.LTEKADALIAEMEEVIHK.T + Oxidation (M) |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 791.4495, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
5. [P0A2P0|RHLB_SALTY](#) Mass: 47291 Score: 33 Expect: 1 Matches: 7
ATP-dependent RNA helicase RhlB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rhlB PE=3 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|---|
| 613.4128 | 612.4056 | 612.3344 | 116 | 82 | - 86 | 0 | K.VNQPR.A |
| 1170.7046 | 1169.6973 | 1169.6669 | 26.0 | 259 | - 268 | 1 | R.AIIFANTKHR.C |
| 1930.2207 | 1929.2134 | 1928.8812 | 172 | 267 | - 282 | 1 | K.HRCEDIWGLHAADGHR.V |
| 2183.2573 | 2182.2500 | 2182.1027 | 67.5 | 186 | - 204 | 1 | R.MPPAAQRLNMLFSATLSYR.V + Oxidation (M) |
| 2304.4600 | 2303.4527 | 2303.2460 | 89.7 | 27 | - 47 | 1 | K.KGFYNTPIQALALPLTLAGR.D |
| 2807.6565 | 2806.6492 | 2806.4977 | 54.0 | 145 | - 169 | 1 | R.LIDYAKQNHINLGAIVVLDADR.M |
| 3550.2068 | 3549.1995 | 3548.7358 | 131 | 48 | - 80 | 1 | R.DVAGQAQTGTGKTMAFILTSTFHYLLSHPAIDDR.K |
- No match to: 592.2010, 606.2520, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2235.4358, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
6. [P07800|CHEZ_SALTY](#) Mass: 23905 Score: 32 Expect: 1.3 Matches: 5
Protein phosphatase CheZ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=chez PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--------------------------|
| 1419.8948 | 1418.8875 | 1418.7010 | 131 | 151 | - 161 | 1 | K.RMMDVIQIEI.R |
| 1949.1753 | 1948.1680 | 1947.9426 | 116 | 196 | - 214 | 0 | K.AGVVASQDQVDDLLDLSLGF.- |
| 2087.3357 | 2086.3284 | 2086.0187 | 148 | 1 | - 20 | 0 | -.MMQPSIKPADEGSAGDIIR.I |
| 2183.2573 | 2182.2500 | 2182.0324 | 99.7 | 69 | - 88 | 1 | R.ALNSVEASQPHQDAMEKEAK.A |
| 2235.4358 | 2234.4285 | 2234.2569 | 76.8 | 162 | - 180 | 1 | R.QLLMVLLENIEQPSARPKR.E |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
7. [Q9L646|NRDD_SALTY](#) Mass: 80820 Score: 23 Expect: 8.8 Matches: 7
Anaerobic ribonucleoside-triphosphate reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nrdd PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
717.4303	716.4230	716.4293	-8.79	673	-	678	1 R.VSVTRR.V
842.6016	841.5943	841.5385	66.3	20	-	26	1 R.IKEAIRL.A
1282.8002	1281.7929	1281.6829	85.8	76	-	85	1 K.QLARAYIEYR.H
2069.2405	2068.2332	2067.9935	116	342	-	359	1 K.FGDPNYDIKQLALECASK.R
2087.3357	2086.3284	2085.9504	181	386	-	403	0 R.SFLGVWENENGEQIHDGR.N
2932.6340	2931.6268	2931.4760	51.4	54	-	79	1 R.SQVDINEIQTAVENQLMSGPYKQLAR.A
3101.7053	3100.6980	3100.5930	62.9	556	-	583	1 R.LDTAEFGVPGVTDKGYTNSFHLDVEK.K

No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 731.5178, 791.4495, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2949.6680, 3084.6946, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

8. [Q56121|RF3_SALTY](#) Mass: 59810 Score: 22 Expect: 13 Matches: 5

Peptide chain release factor 3 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=prfc PE=3 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1371.8195	1370.8122	1370.5595	184	57	-	66	1 K.SDWMEKQR.G + 2 Oxidation (M)
1918.2118	1917.2045	1917.0005	106	164	-	180	1 K.IGCAPITWPIGCGKLFK.G
1930.2207	1929.2134	1929.0207	99.9	15	-	32	1 R.TFAIISHPDAGKTTITEK.V
3348.9749	3347.9676	3347.6667	89.9	488	-	517	1 R.KNETQLALDGGDNLYIAPTVMNLTQER.Y + Oxidation (M)
3641.2495	3640.2422	3640.6926	-123.71	354	-	386	0 R.SHVEEAYPGDILGHNHGTIQIGDTFTQEGEMMK.F + Oxidation (M)

No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3809.3398

9. [P0A108|HEM3_SALTY](#) Mass: 33921 Score: 21 Expect: 15 Matches: 6

Porphobilinogen deaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=hmc PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
592.2010	591.1937	591.2799	-145.70	233	-	237	0 R.AMNTR.L
1170.7046	1169.6973	1169.6880	7.93	2	-	11	1 M.LDNVLR.IATR.Q
2144.3513	2143.3440	2143.1022	113	113	-	132	1 K.YHSLDDLPAAGSIVGTSSLR.Q
2183.2573	2182.2500	2182.1126	63.0	25	-	44	0 K.DALMATHPGLTVELVPMVTR.G + 2 Oxidation (M)
2304.4600	2303.4527	2303.2346	94.7	207	-	227	1 R.LDDARTQALLAPLNSQTALR.V
2749.6885	2748.6812	2748.3719	113	106	-	131	1 R.DAFVSNKYHSLDDLPAAGSIVGTSSLR.R

No match to: 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2235.4358, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

10. [P0CL14|MRDA_SALTY](#) Mass: 69903 Score: 20 Expect: 17 Matches: 6

Peptidoglycan D,D-transpeptidase MrdA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mrda PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1569.9546	1568.9473	1568.7875	102	78	-	90	0 R.NVTWYDIIVTPYK.I
1685.1019	1684.0947	1683.8614	139	50	-	64	1 R.SNENDIKMLPVAPTR.G
2056.2139	2055.2066	2055.0133	94.0	190	-	208	1 K.GLAENYAADHNIGKQGIER.Y
2087.3357	2086.3284	2086.0695	124	100	-	117	1 K.QLTPIVDLSPDDISDFRR.A
3101.7053	3100.6980	3100.4886	67.6	267	-	295	0 R.AAVLVEDPHDGSVLAMVSMPSYDPNPFVK.G + Oxidation (M)
3614.2231	3613.2159	3613.7763	-155.07	400	-	431	1 R.IDTMLSQFGYKPTGIDLNEEYDGLLPSRAWK.Q

No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

11. [P74876|DPO3X_SALTY](#) Mass: 70894 Score: 20 Expect: 18 Matches: 6

DNA polymerase III subunit tau OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dnaX PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
791.4495	790.4422	790.4119	38.4	313	-	318	1 R.MRELAR.T + Oxidation (M)
964.5684	963.5611	963.5501	11.4	2	-	9	1 M.SYQVLARK.W
1419.8948	1418.8875	1418.7517	95.7	603	-	614	1 R.QAIYEEKLAQAR.E
1587.9663	1586.9590	1586.8165	89.8	106	-	119	1 R.DLLDNVQYAPARGR.F
1842.1445	1841.1373	1840.9804	85.2	347	-	362	1 R.MGVEMTLRLALAFHPR.M
2235.4358	2234.4285	2234.1947	105	142	-	161	1 K.TLEPPAHVKFLLATTDPOK.L

No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

12. [Q8ZN25|MURO_SALTY](#) Mass: 31083 Score: 20 Expect: 20 Matches: 4

N-acetylmuramic acid 6-phosphate etherase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=murQ PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.6016	841.5943	841.4658	153	43	-	50	0 K.ATLPDVAR.A
1419.8948	1418.8875	1418.7122	124	238	-	250	1 R.ACRMVVEATGIGR.E
1916.1786	1915.1713	1915.0084	85.1	241	-	258	1 R.MVVEATGIGREEAEALLK.Q
1999.1714	1998.1641	1997.9948	84.7	197	-	215	1 K.SGTAQKMLNMISTGAMVK.F + 2 Oxidation (M)

No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

13. [Q06961|TDCD_SALTY](#) Mass: 43919 Score: 19 Expect: 22 Matches: 6
Propionate kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tdcD PE=1 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-------|------|--|
| 1021.5976 | 1020.5903 | 1020.4526 | 135 | 285 | - 292 | 0 | K.AWHEGHER.A |
| 1973.2067 | 1972.1994 | 1972.0840 | 58.5 | 266 | - 284 | 1 | K.ESGLLGISGLSSDLRVLEK.A |
| 1994.2230 | 1993.2157 | 1993.0013 | 108 | 1 | - 18 | 0 | -.MNEFPVVLVINCSSSIK.F |
| 2183.2573 | 2182.2500 | 2182.1303 | 54.9 | 364 | - 383 | 0 | R.IISANPSQVICAIVPTNEEK.M |
| 2235.4358 | 2234.4285 | 2234.1920 | 106 | 110 | - 130 | 1 | R.RVSLAPLPHNYANLSGIDAAR.H |
| 3809.3398 | 3808.3326 | 3808.6875 | -93.19 | 215 | - 250 | 1 | R.NQSVSDTSMGMTPLGLEMMGTRSGDVFVGAMAWIAK.E + 3 Oxidation (M) |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495
14. [P26392|RMLD_SALTY](#) Mass: 32705 Score: 19 Expect: 22 Matches: 4
dTDP-4-dehydroharnose reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rfBD PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|-----------------------|
| 731.5178 | 730.5105 | 730.3974 | 155 | 45 | - 51 | 0 | K.GVAETVR.K |
| 1151.6626 | 1150.6553 | 1150.5917 | 55.3 | 159 | - 168 | 1 | K.GNNFAKTLMLR.L |
| 1611.9919 | 1610.9847 | 1610.8351 | 92.8 | 138 | - 150 | 1 | K.ALQDNCPKHLIFR.T |
| 1918.2118 | 1917.2045 | 1917.0796 | 65.2 | 52 | - 69 | 1 | R.KLRPDIIVNAAHTAVDK.A |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
15. [Q8Z0W2|KDPB_SALTY](#) Mass: 72267 Score: 19 Expect: 22 Matches: 6
Potassium-transporting ATPase ATP-binding subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=kdpB PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-------|------|---|
| 717.4303 | 716.4230 | 716.3817 | 57.7 | 396 | - 402 | 0 | K.GSVDAIR.R |
| 731.5178 | 730.5105 | 730.3973 | 155 | 92 | - 98 | 0 | K.AQANSLK.G |
| 1419.8948 | 1418.8875 | 1418.7122 | 124 | 383 | - 394 | 1 | R.MSGINIDNRMIR.K |
| 1918.2118 | 1917.2045 | 1917.0068 | 103 | 309 | - 326 | 1 | K.TGTITLGNRQASDFIPAR.G |
| 2056.2139 | 2055.2066 | 2055.2456 | -18.98 | 426 | - 446 | 0 | R.LGATPLVVVEGAHLVGIALK.D |
| 3348.9749 | 3347.9676 | 3347.6555 | 93.2 | 467 | - 499 | 1 | K.TVMITGDNRLTAAIAAEAGVDFLAEATPEAK.L + Oxidation (M) |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
16. [P0A2C1|RNH2_SALTY](#) Mass: 21550 Score: 19 Expect: 23 Matches: 4
Ribonuclease HII OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rnhB PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|---|
| 1587.9663 | 1586.9590 | 1586.8627 | 60.7 | 125 | - 140 | 1 | K.GDSRVAEISAASILAK.V |
| 1842.1445 | 1841.1373 | 1840.9175 | 119 | 112 | - 128 | 1 | R.CPELPPVPSMAVVKGDSR.V |
| 3315.8687 | 3314.8614 | 3314.7519 | 33.0 | 94 | - 124 | 1 | R.AVAGLHIAPEYVLIDGNRCPPELPPVPSMAVVK.G |
| 3331.9414 | 3330.9341 | 3330.7468 | 56.2 | 94 | - 124 | 1 | R.AVAGLHIAPEYVLIDGNRCPPELPPVPSMAVVK.G + Oxidation (M) |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
17. [Q8ZPV2|ASTC_SALTY](#) Mass: 44146 Score: 19 Expect: 24 Matches: 4
Succinylornithine transaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=astC PE=2 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|--|
| 1918.2118 | 1917.2045 | 1916.9480 | 134 | 375 | - 392 | 0 | R.FAPALNVSDDEIATGLDR.F |
| 1999.1714 | 1998.1641 | 1998.0316 | 66.3 | 295 | - 311 | 1 | K.VLDIINTPEMQNVRQR.H + Oxidation (M) |
| 2087.3357 | 2086.3284 | 2086.0748 | 122 | 71 | - 88 | 1 | R.FWHIINGYNTNEPALRLAK.K |
| 3809.3398 | 3808.3326 | 3808.8578 | -137.89 | 167 | - 203 | 0 | R.HAAYNDLNSASALIDTNCVIVPEVQEGGVIPATK.A |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 2006.1919, 2056.2139, 2069.2405, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495
18. [P60802|PDXB_SALTY](#) Mass: 41558 Score: 19 Expect: 24 Matches: 4
Erythronate-4-phosphate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pdxB PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--------------------------------------|
| 842.6016 | 841.5943 | 841.4406 | 183 | 321 | - 327 | 1 | R.RDDAPLR.K |
| 1611.9919 | 1610.9847 | 1610.7796 | 127 | 1 | - 13 | 1 | -.MKILVDENMPYAR.E + 2 Oxidation (M) |
| 1842.1445 | 1841.1373 | 1840.9683 | 91.8 | 180 | - 195 | 1 | K.DGPYKTLHLAEDTLIR.R |
| 3558.1548 | 3557.1475 | 3556.8050 | 96.3 | 45 | - 78 | 1 | R.SVTKVNESLLSGPTINFGTATAGTDHVEAWLK.Q |
- No match to: 592.2010, 606.2520, 613.4128, 663.3585, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1419.8948, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398
19. [Q8ZKE6|PHNO_SALTY](#) Mass: 18035 Score: 19 Expect: 26 Matches: 4
Aminoalkylphosphonate N-acetyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=phnO PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|----------|----------|----------|-----|-------|-----|------|---------|
|----------|----------|----------|-----|-------|-----|------|---------|

663.3585	662.3512	662.3607	-14.44	1	-	5	0	-.MILMR.R
1151.6626	1150.6553	1150.5519	89.9	141	-	149	1	R.EGYKQSHFR.F
1419.8948	1418.8875	1418.6646	157	7	-	17	1	R.REDVMPVCELR.H + Oxidation (M)
3315.8687	3314.8614	3314.5765	85.9	18	-	45	1	R.HATTEDTDSVYALICELKLNELDYQAFR.D

No match to: 592.2010, 606.2520, 613.4128, 684.3077, 717.4303, 731.5178, 791.4495, 842.6016, 964.5684, 1021.5976, 1170.7046, 1234.7214, 1282.8002, 1371.8195, 1569.9546, 1587.9663, 1611.9919, 1685.1019, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1916.1786, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2304.4600, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

20. [P37178|PT1P_SALTY](#) Mass: 83916 Score: 19 Expect: 26 Matches: 8
 Phosphoenolpyruvate-dependent phosphotransferase system OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ptsP PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
613.4128	612.4056	612.3820	38.6	60	-	64	1 K.KPRGR.T
791.4495	790.4422	790.5065	-81.26	699	-	704	1 R.VKYLLR.H
1234.7214	1233.7142	1233.6023	90.7	718	-	728	0 R.SLEAQMATEVR.H
1282.8002	1281.7929	1281.6928	78.1	81	-	92	0 R.LAEPINLADAQK.H
1569.9546	1568.9473	1568.7504	126	437	-	450	0 K.VMLNAGLSPEHEEK.L + Oxidation (M)
1685.1019	1684.0947	1683.9559	82.4	527	-	540	0 R.ITLDQPEIFLIQVR.A
1916.1786	1915.1713	1914.9985	90.2	575	-	591	1 R.AGREVEEMIGYAIKPR.I
2304.4600	2303.4527	2303.1150	147	718	-	737	1 R.SLEAQMATEVRHQVAAFMER.R

No match to: 592.2010, 606.2520, 663.3585, 684.3077, 717.4303, 731.5178, 842.6016, 964.5684, 1021.5976, 1151.6626, 1170.7046, 1371.8195, 1419.8948, 1587.9663, 1611.9919, 1842.1445, 1860.1655, 1876.1610, 1892.1362, 1894.0756, 1918.2118, 1930.2207, 1933.1796, 1949.1753, 1973.2067, 1994.2230, 1999.1714, 2006.1919, 2056.2139, 2069.2405, 2087.3357, 2126.2590, 2144.3513, 2183.2573, 2235.4358, 2342.3325, 2517.5310, 2663.5623, 2720.5835, 2749.6885, 2753.6489, 2797.6963, 2807.6565, 2932.6340, 2949.6680, 3084.6946, 3101.7053, 3158.7300, 3218.8752, 3315.8687, 3331.9414, 3348.9749, 3550.2068, 3558.1548, 3598.2148, 3614.2231, 3641.2495, 3809.3398

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 200 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 66
 Selected for scoring : 48

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P0A263|OMPC_SALTY

Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1

Database: Salmonella_Typhi_LT2
 Score: 55
 Expect: 0.0058
 Nominal mass (M_r): 41214
 Calculated pI: 4.63

Sequence similarity is available as [an NCBI BLAST search of P0A263|OMPC_SALTY against nr.](#)

Search parameters

MS data file: peaklist_4.xml
 Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
 Fixed modifications: **Carbamidomethyl (C)**
 Variable modifications: **Oxidation (M)**
 Mass values searched: 78
 Mass values matched: 12

Protein sequence coverage: 39%

Matched peptides shown in **bold red**.

```

1 MKVKVLSLLV PALLVAGAAN AAEIYNK DGN KLDLFGKVDG LHYFSDDKGS
51 DGDQTYMRIG FKGETQVNDQ LTGYQWEYQ IQGNQTEGSN DSWTRVAFAG
101 LKFADAGSFD YGRNYGVTYD VTSWTDVLPE FGGDTYGADN FMQQRGNGYA
151 TYRNTDFFGL VDGLDFALQY QGKNGSVSGE NTNGRSLNQ NGDGYGGS LT
201 YAIGEGFSVG GAITTSKRTA DQNNTANARL YGNGDRATVY TGGLKYDANN
251 IYLAAQYSQT YNATRFGTSN GSNPSTSYGF ANKAAQNFEV A QYQDFGLR
301 PSVAYLQSKG KDISNGYGAS YGDQDIVKYV DVGATYYFNK NMSTYVDYKI
351 NLLDKNDFTR DAGINTDDIV ALGLVYQF
  
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Unformatted sequence string: **378 residues** (for pasting into other applications).

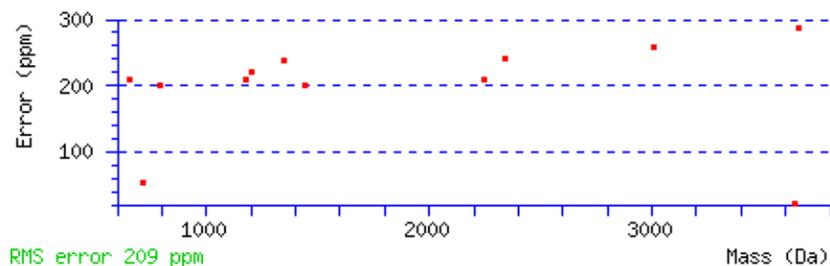
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
103 - 113	1205.7891	1204.7818	1204.5149	222	0	K.FADAGSFDYGR.N
114 - 145	3646.6877	3645.6805	3645.5995	22.2	0	R.NYGVTYDVTSWTDVLPEFGGDTYGADNFMQQR.G
114 - 145	3663.6531	3662.6458	3661.5944	287	0	R.NYGVTYDVTSWTDVLPEFGGDTYGADNFMQQR.G + Oxidation (M)
154 - 173	2248.5625	2247.5552	2247.0848	209	0	R.NTDFGLVDGLDFALQYQK.N
219 - 229	1175.7850	1174.7778	1174.5327	209	0	R.TADQNNTANAR.L
230 - 236	794.5391	793.5318	793.3719	202	0	R.LYGNGDR.A
246 - 265	2340.6538	2339.6465	2339.0818	241	0	K.YDANNIYLAAQYSQTYNATR.F
284 - 309	3006.2944	3005.2872	3004.5083	259	0	K.AQNFEVVAQYQDFGLRPSVAYLQSK.G
329 - 340	1439.9731	1438.9659	1438.6769	201	0	K.YVDVGATYYFNK.N
350 - 355	715.4736	714.4664	714.4276	54.3	0	K.INLLDK.N

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
350 - 360	1349.0420	1348.0347	1347.7146	237	1	K.INLLDKNDFTR.D
356 - 360	652.4406	651.4333	651.2976	208	0	K.NDFTR.D

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 667.3455, 668.3666, 669.3725, 712.3618, 776.4191, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1193.7748, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811



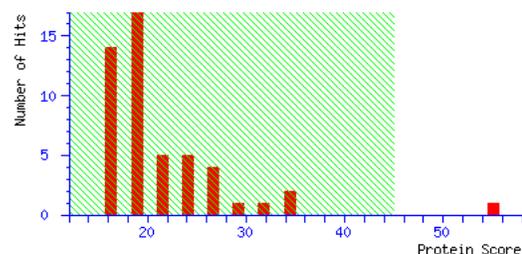
Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

User : MR Labs
 Email : mr1abs7389@gmail.com
 Search title : Sample_4
 MS data file : peaklist_4.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 15 Jul 2024 at 07:47:04 GMT
 Top Score : 55 for [P0A263|OMP_C_SALTY](#), Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)

Significance threshold $p < 0.05$ Max. number of hits

Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P0A263 OMP_C_SALTY	41214	55	Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1
2. D0ZX01 OMPD_SALT1	39655	34	Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompD PE=1 SV=1
3. P37592 OMPD_SALTY	39655	34	Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompD
4. P14567 DPO3A_SALTY	130820	32	DNA polymerase III subunit alpha OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dnaE P
5. Q8ZMS4 ENDPH_SALTY	93684	28	Probable replication endonuclease from prophage-like region OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=endPH
6. Q8ZKW2 RAVA_SALTY	56896	27	ATPase RuvA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ravA PE=3 SV=1
7. D0ZWR9 SCTC2_SALT1	54193	27	SPI-2 type 3 secretion system secretin OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sctC2 PE=
8. Q8ZPB3 OPGD_SALTY	62586	27	Glucans biosynthesis protein D OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mdoD PE=
9. P02936 OMPA_SALTY	37606	26	Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2
10. P66746 RUVA_SALTY	22189	25	Holliday junction branch migration complex subunit RuvA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ruvA
11. Q8ZNB9 TRUA_SALTY	30424	24	tRNA pseudouridine synthase A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=truA PE=3
12. P40784 YCDD_SALTY	21045	23	Tail fiber assembly protein homolog from lambdoid prophage Fels-1 OS=Salmonella typhimurium (strain LT2 / SGSC1412
13. Q8ZL65 SADB_SALTY	25947	23	Inner membrane lipoprotein SadB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sadB PE
14. P22253 PNCB_SALTY	45974	23	Nicotinate phosphoribosyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pn
15. P10503 PUTA_SALTY	144741	22	Bifunctional protein PutA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=putA PE=2 SV=
16. Q8ZQW2 KDPB_SALTY	72267	22	Potassium-transporting ATPase ATP-binding subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) O
17. Q8ZKH9 PLSB_SALTY	91455	22	Glycerol-3-phosphate acyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pl
18. Q7CPI8 BCSF_SALTY	7304	21	Cellulose biosynthesis protein BcsF OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=bcs
19. P67557 OPGG_SALTY	57808	20	Glucans biosynthesis protein G OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mdoG PE=
20. P63603 AROL_SALTY	19905	20	Shikimate kinase 2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=aroL PE=3 SV=1

Results List

1. [P0A263|OMP_C_SALTY](#) Mass: 41214 Score: 55 Expect: 0.0058 Matches: 12
 Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1

Observed	Mr(expt)	Mr(calcd)	ppm	Start	End	Miss	Peptide
652.4406	651.4333	651.2976	208	356	- 360	0	K.NDFTR.D
715.4736	714.4664	714.4276	54.3	350	- 355	0	K.INLLDK.N
794.5391	793.5318	793.3719	202	230	- 236	0	R.LYNGNDR.A
1175.7850	1174.7778	1174.5327	209	219	- 229	0	R.TADQNNTANAR.L
1205.7891	1204.7818	1204.5149	222	103	- 113	0	K.FADAGSFDYGR.N
1349.0420	1348.0347	1347.7146	237	350	- 360	1	K.INLLDKNDFTR.D
1439.9731	1438.9659	1438.6769	201	329	- 340	0	K.YVDVGATYFFNK.N
2248.5625	2247.5552	2247.0848	209	154	- 173	0	R.NTDFGLVDGLDFALQYQGK.N
2340.6538	2339.6465	2339.0818	241	246	- 265	0	K.YDANNIYLAQYSQTYNATR.F
3006.2944	3005.2872	3004.5083	259	284	- 309	0	K.AQNFVEVAQYQDFGLRPSVAYLQSK.G
3646.6877	3645.6805	3645.5995	22.2	114	- 145	0	R.NYGVTYDVTSWTDVLPFEGGDTYGADNFMQQR.G
3663.6531	3662.6458	3661.5944	287	114	- 145	0	R.NYGVTYDVTSWTDVLPFEGGDTYGADNFMQQR.G + Oxidation (M)

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 667.3455, 668.3666, 669.3725, 712.3618, 776.4191, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1193.7748, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

2. [D0ZX01|OMPD_SALTY](#) Mass: 39655 Score: 34 Expect: 0.7 Matches: 9
Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompD PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--|
| 868.6127 | 867.6054 | 867.4450 | 185 | 149 | - 156 | 0 | R.TTGVATYR.N |
| 1058.7227 | 1057.7154 | 1057.5556 | 151 | 229 | - 238 | 0 | K.NAEVWAAGLK.Y |
| 1280.9110 | 1279.9037 | 1279.6296 | 214 | 334 | - 344 | 0 | K.INLLDDSDFTK.A |
| 1297.8484 | 1296.8411 | 1296.5411 | 231 | 105 | - 115 | 0 | K.FADYGSFDYGR.N |
| 2219.5527 | 2218.5455 | 2218.0695 | 215 | 157 | - 176 | 0 | R.NTDFFLVEGLNFAAQYQGGK.N |
| 2390.6392 | 2389.6319 | 2389.0863 | 228 | 63 | - 82 | 0 | K.GETQINDQLTGFQQWEYEFK.G |
| 2807.1331 | 2806.1258 | 2805.4126 | 254 | 273 | - 296 | 0 | K.TQNFEAVAQYQDFGLRPSIAYLK.S |
| 3424.5625 | 3423.5552 | 3423.4804 | 21.9 | 180 | - 212 | 1 | R.DGAYESNGDGFGLSATYIEYEGFVGVAAYAKSDR.T |
| 3683.7490 | 3682.7417 | 3681.6723 | 290 | 116 | - 148 | 0 | R.NYGVAYDIGAWTDVLPFFGGDTWTQTDVFMTR.T |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1282.9219, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2248.5625, 2340.6538, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
3. [P37592|OMPD_SALTY](#) Mass: 39655 Score: 34 Expect: 0.7 Matches: 9
Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompD PE=1 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-------|------|--|
| 868.6127 | 867.6054 | 867.4450 | 185 | 149 | - 156 | 0 | R.TTGVATYR.N |
| 1058.7227 | 1057.7154 | 1057.5556 | 151 | 229 | - 238 | 0 | K.NAEVWAAGLK.Y |
| 1280.9110 | 1279.9037 | 1279.6296 | 214 | 334 | - 344 | 0 | K.INLLDDSDFTK.A |
| 1297.8484 | 1296.8411 | 1296.5411 | 231 | 105 | - 115 | 0 | K.FADYGSFDYGR.N |
| 2219.5527 | 2218.5455 | 2218.0695 | 215 | 157 | - 176 | 0 | R.NTDFFLVEGLNFAAQYQGGK.N |
| 2390.6392 | 2389.6319 | 2389.0863 | 228 | 63 | - 82 | 0 | K.GETQINDQLTGFQQWEYEFK.G |
| 2807.1331 | 2806.1258 | 2805.4126 | 254 | 273 | - 296 | 0 | K.TQNFEAVAQYQDFGLRPSIAYLK.S |
| 3424.5625 | 3423.5552 | 3423.4804 | 21.9 | 180 | - 212 | 1 | R.DGAYESNGDGFGLSATYIEYEGFVGVAAYAKSDR.T |
| 3683.7490 | 3682.7417 | 3681.6723 | 290 | 116 | - 148 | 0 | R.NYGVAYDIGAWTDVLPFFGGDTWTQTDVFMTR.T |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1282.9219, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2248.5625, 2340.6538, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
4. [P14567|DPO3A_SALTY](#) Mass: 130820 Score: 32 Expect: 1.2 Matches: 15
DNA polymerase III subunit alpha OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dnaE PE=3 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|--------|------|--|
| 592.2476 | 591.2403 | 591.3228 | -139.42 | 869 | - 873 | 1 | R.TDTKK.L |
| 614.2392 | 613.2319 | 613.3799 | -241.27 | 24 | - 29 | 0 | K.TGPLVK.K |
| 634.4214 | 633.4141 | 633.2905 | 195 | 136 | - 141 | 0 | R.MGDVGR.C |
| 804.4407 | 803.4335 | 803.4575 | -29.91 | 615 | - 621 | 1 | R.GMKDLIK.R |
| 902.5742 | 901.5669 | 901.4909 | 84.3 | 119 | - 125 | 0 | R.DWLVELK.E |
| 994.3445 | 993.3373 | 993.5131 | -176.97 | 725 | - 733 | 1 | R.SVFEAGAKK.N |
| 1175.7850 | 1174.7778 | 1174.6016 | 150 | 733 | - 743 | 1 | K.KNGIDGLAMK.I |
| 1193.7748 | 1192.7675 | 1192.6452 | 103 | 363 | - 375 | 0 | R.GSGAGSLVAYALK.I |
| 2031.4553 | 2030.4480 | 2030.0507 | 196 | 11 | - 29 | 1 | R.VHSDYSIMDGLAKTGPLVK.K |
| 2033.4734 | 2032.4661 | 2032.0266 | 216 | 536 | - 553 | 1 | K.HPVTQFDKSDVEYAGLVK.F |
| 2219.5527 | 2218.5455 | 2218.1131 | 195 | 840 | - 860 | 1 | K.GVGEGPIEAIIDARNQGGYFR.E |
| 2340.6538 | 2339.6465 | 2340.2148 | -242.82 | 1047 | - 1068 | 1 | R.ILVISGQVSFDDFSGGLKMTAR.E |
| 2390.6392 | 2389.6319 | 2389.9865 | -148.36 | 776 | - 796 | 0 | K.AHYPAEFMAAVMTADMNTEK.V + 3 Oxidation (M) |
| 2895.1831 | 2894.1758 | 2893.3640 | 281 | 142 | - 165 | 1 | R.CLLRGNQALVEECVAFYEAHFDR.Y |
| 3006.2944 | 3005.2872 | 3004.4487 | 279 | 474 | - 499 | 1 | K.AFEAEPQLPEIYEAEDEVRALDMAR.K |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 606.3871, 623.3754, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 872.6952, 884.5612, 1036.3574, 1058.7227, 1064.2002, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2200.5593, 2216.6750, 2248.5625, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2864.1743, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
5. [Q8ZMS4|ENDPH_SALTY](#) Mass: 93684 Score: 28 Expect: 3 Matches: 10
Probable replication endonuclease from prophage-like region OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM2729 PE=3
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|--|
| 560.2399 | 559.2327 | 559.2714 | -69.30 | 104 | - 107 | 0 | R.EQQR.F |
| 614.2392 | 613.2319 | 613.3184 | -140.96 | 84 | - 88 | 0 | R.DPVQR.E |
| 634.4214 | 633.4141 | 633.3962 | 28.3 | 470 | - 474 | 1 | R.KFAIR.E |
| 668.3666 | 667.3593 | 667.4017 | -63.51 | 95 | - 100 | 0 | R.LISHAK.T |
| 715.4736 | 714.4664 | 714.4136 | 73.8 | 730 | - 735 | 1 | R.RELAAR.L |
| 1297.8484 | 1296.8411 | 1296.5202 | 248 | 274 | - 282 | 0 | R.MLCADWRCR.K |
| 1349.0420 | 1348.0347 | 1347.6783 | 264 | 478 | - 489 | 1 | R.EELGNTGPRFK.S |
| 2807.1331 | 2806.1258 | 2806.4510 | -115.88 | 588 | - 614 | 1 | R.LDAVLAADAGCFATYIMKQGGVLPVR.K |
| 3683.7490 | 3682.7417 | 3683.8318 | -295.90 | 32 | - 65 | 0 | K.AVNPYLDPAEVAPESALSNIALLYAADNEQEQLR.R |
| 3726.7932 | 3725.7859 | 3726.6958 | 293 | 664 | - 697 | 1 | K.AVDVQEAADQACAPWTRGNMCPAENLNQKEK.D |
- No match to: 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 623.3754, 644.1973, 652.4406, 667.3455, 669.3725, 712.3618, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3690.6987, 3774.8674, 3790.8430, 3879.8811
6. [Q8ZKN2|RAVA_SALTY](#) Mass: 56896 Score: 27 Expect: 3.6 Matches: 8
ATPase Rava OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rava PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
634.4214	633.4141	633.2904	195	494	-	498	1 R.QAKQC.-
668.3666	667.3593	667.3442	22.6	61	-	65	0 K.FAFQR.A
669.3725	668.3652	668.3354	44.6	459	-	463	0 R.QQHTR.F
715.4736	714.4664	714.4500	22.9	53	-	58	1 K.SLIARR.L
794.5391	793.5318	793.3606	216	138	-	144	0 R.NGAFFEEK.I
1280.9110	1279.9037	1279.7751	101	270	-	281	0 R.DAVAPIDLILLK.D
2790.1184	2789.1111	2789.5626	-161.83	26	-	52	1 R.SHAIRLRLAALSQGESVFLGPPGPIAK.S
3599.5999	3598.5926	3597.7423	236	464	-	493	1 R.FSEQQHCLFIHSDWLGRIEASLQDVGGEQIR.Q

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 712.3618, 776.4191, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

- [D0ZWR9|SCTC2_SALTI](#) Mass: 54193 Score: 27 Expect: 3.6 Matches: 9
 SPI-2 type 3 secretion system secretin OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sctC2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.3871	605.3799	605.3207	97.8	1	-	5	0 -.MNVNK.R + Oxidation (M)
872.6952	871.6879	871.5127	201	366	-	373	1 K.LQGEKVAK.L
1282.9219	1281.9146	1281.6816	182	172	-	183	0 K.DSAVSVSIYTLK.Y
1641.2277	1640.2204	1640.0752	88.5	6	-	19	1 K.RLILILLFILTAK.S
2248.5625	2247.5552	2247.1470	182	118	-	136	1 R.FIHYLRSQNILSSPQCEVK.E
2790.1184	2789.1111	2789.3218	-75.52	172	-	195	1 K.DSAVSVSIYTLKYATAMDTQYQYR.D + Oxidation (M)
2895.1831	2894.1758	2893.3553	284	301	-	328	0 K.IAFNTGLNDGGASGFSTVISDTSNFMVR.L + Oxidation (M)
3006.2944	3005.2872	3005.4553	-55.95	300	-	328	1 K.KIAFNTGLNDGGASGFSTVISDTSNFMVR.L
3599.5999	3598.5926	3597.8712	200	266	-	299	1 R.QQMIEISVKIIDVNAGDINQLGIDWGTAVSLGGK.K + Oxidation (M)

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1297.8484, 1349.0420, 1439.9731, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
- [Q8ZPB3|OPGD_SALTY](#) Mass: 62586 Score: 27 Expect: 3.8 Matches: 10
 Glucans biosynthesis protein D OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mDoD PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
566.2863	565.2790	565.3046	-45.37	517	-	520	0 R.MFLR.C
592.2476	591.2403	591.2911	-85.83	1	-	4	1 -.MNR.R + Oxidation (M)
667.3455	666.3382	666.2973	61.4	544	-	548	0 R.YVDDR.I
1439.9731	1438.9659	1438.7568	145	399	-	411	1 K.AIKAGDTLAFNYR.L
1803.2269	1802.2197	1801.9145	169	253	-	267	1 K.SQVIMDVENHLYARK.D
2033.4734	2032.4661	2031.8785	289	432	-	450	0 R.TGMGGFPEGWAPGEHYDPK.W
2200.5593	2199.5520	2199.9823	-195.58	271	-	289	1 K.QLGIAPMTSMFSCGNERR.V + 2 Oxidation (M)
2790.1184	2789.1111	2788.3068	288	336	-	358	1 K.GFGLLQDRDFSHYQDVMGWYK.R
3063.3223	3062.3150	3062.4306	-37.76	517	-	541	1 R.MFLRCQGEAISETWLYQYFPPAPDK.R + Oxidation (M)
3599.5999	3598.5926	3597.6789	254	6	-	41	1 R.FIKGSMAMAAVCGSSGASLFSQAFAAESDIADGK.I + 2 Oxidation (M)

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1641.2277, 2031.4553, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3424.5625, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
- [P02936|OMPA_SALTY](#) Mass: 37606 Score: 26 Expect: 4.2 Matches: 7
 Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
872.6952	871.6879	871.5127	201	333	-	339	1 R.RVEIEVK.G
1214.9086	1213.9013	1213.6125	238	322	-	332	0 R.AALIDLAPDR.R
1264.9457	1263.9384	1263.6460	231	256	-	267	0 K.DGSVVVLGFTDR.I
1641.2277	1640.2204	1639.8094	251	104	-	117	0 K.LGYPITDLDLVYTR.L
2033.4734	2032.4661	2031.9102	274	303	-	321	0 R.GMGESNPVTGNTCDNVKPR.A
2616.9348	2615.9275	2615.2868	245	139	-	163	0 K.DHDTGVSPVFAGGIEYAITPEIATR.L
3424.5625	3423.5552	3422.6855	254	164	-	194	0 R.LEYQWNNIGDANTIGTRPDNGLLSVGVSYR.F

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1803.2269, 2031.4553, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
- [P66746|RUVA_SALTY](#) Mass: 22189 Score: 25 Expect: 6.3 Matches: 5
 Holliday junction branch migration complex subunit RuvA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ruvA PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
565.3261	564.3188	564.3020	29.9	130	-	133	1 K.DRFK.G
614.2392	613.2319	613.4024	-277.86	2	-	6	1 M.IGRRLR.G
712.3618	711.3545	711.4643	-154.26	113	-	119	1 K.LPGIGKK.T
1205.7891	1204.7818	1204.6485	111	120	-	129	1 K.TAERLIVEMK.D + Oxidation (M)
2787.0510	2786.0437	2786.4749	-154.72	78	-	104	1 K.TNGVGPKLALAILSGMSAQFVNAVER.E + Oxidation (M)

No match to: 560.2399, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

11. [Q8ZNB9|TRUA_SALTY](#) Mass: 30424 Score: 24 Expect: 8.4 Matches: 6
tRNA pseudouridine synthase A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=truA PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|-------------------------------|
| 652.4406 | 651.4333 | 651.3340 | 152 | 111 | - 116 | 0 | R.FSATAR.R |
| 1297.8484 | 1296.8411 | 1296.6727 | 130 | 118 | - 126 | 1 | R.YRYIYNHR.L |
| 2200.5593 | 2199.5520 | 2200.1012 | -249.58 | 2 | - 22 | 1 | M.SGQQSSAVYKIALGIEYDGSK.Y |
| 2216.6750 | 2215.6678 | 2215.1419 | 237 | 39 | - 58 | 1 | K.LEKALSQVANEPINVFCAGR.T |
| 2397.6675 | 2396.6602 | 2397.2804 | -258.73 | 127 | - 147 | 1 | R.LRPAVLAKGVTHYVPLDAER.M |
| 2787.0510 | 2786.0437 | 2786.4715 | -153.50 | 206 | - 231 | 0 | R.NIVGSLLEVGAHNPESWIAELLAAR.D |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
12. [P40784|YCDL_SALTY](#) Mass: 21045 Score: 24 Expect: 8.4 Matches: 5
Tail fiber assembly protein homolog from lambdoid prophage Fels-1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ycdD P
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|---|
| 560.2399 | 559.2327 | 559.3329 | -179.31 | 9 | - 13 | 0 | K.AQTIK.I |
| 634.4214 | 633.4141 | 633.2970 | 185 | 130 | - 135 | 0 | R.EAEGTK.S |
| 3646.6877 | 3645.6805 | 3644.6829 | 274 | 73 | - 107 | 0 | R.GETVYDITTTGNQMYISEPGLPENVTSPVSGGGYK.K |
| 3774.8674 | 3773.8602 | 3772.7778 | 287 | 73 | - 108 | 1 | R.GETVYDITTTGNQMYISEPGLPENVTSPVSGGGYK.W |
| 3790.8430 | 3789.8357 | 3788.7727 | 281 | 73 | - 108 | 1 | R.GETVYDITTTGNQMYISEPGLPENVTSPVSGGGYK.W + Oxidation (M) |
- No match to: 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
13. [Q8ZL65|SADB_SALTY](#) Mass: 25947 Score: 23 Expect: 9.4 Matches: 5
Inner membrane lipoprotein SADB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sadB PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-------|------|---|
| 634.4214 | 633.4141 | 633.2970 | 185 | 40 | - 44 | 0 | K.EQETK.I |
| 2219.5527 | 2218.5455 | 2218.1555 | 176 | 172 | - 191 | 0 | K.MDSTIELLPGAWNTVTLTK.G + Oxidation (M) |
| 2390.6392 | 2389.6319 | 2389.2199 | 172 | 203 | - 223 | 1 | K.IGIDMENVIFDSIQPINDTKK.K |
| 3030.2285 | 3029.2212 | 3028.6518 | 188 | 165 | - 191 | 1 | K.QLLLNTKMDSTIELLPGAWNTVTLTK.G + Oxidation (M) |
| 3424.5625 | 3423.5552 | 3423.6924 | -40.05 | 7 | - 35 | 1 | K.FIPLLALGFTFFLSGCDYFADKHLVEEMK.E + Oxidation (M) |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
14. [P22253|PNCB_SALTY](#) Mass: 45974 Score: 23 Expect: 9.6 Matches: 7
Nicotinate phosphoribosyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pncB PE=1 SV=2
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|---|
| 565.3261 | 564.3188 | 564.3132 | 9.96 | 179 | - 182 | 1 | R.RFSR.E |
| 1214.9086 | 1213.9013 | 1213.6489 | 208 | 358 | - 368 | 0 | K.LVECNKGPVAK.L |
| 1225.4161 | 1224.4089 | 1224.7091 | -245.16 | 107 | - 116 | 1 | K.LNIRLTGPWR.E |
| 1297.8484 | 1296.8411 | 1296.5735 | 206 | 282 | - 293 | 0 | R.HDSGDPVWAGEK.A |
| 1349.0420 | 1348.0347 | 1347.7047 | 245 | 321 | - 331 | 1 | K.AVELYRHFASR.V |
| 2549.8513 | 2548.8440 | 2548.3512 | 193 | 117 | - 137 | 0 | R.EVIMWEVPLLAVISELVVHHR.S + Oxidation (M) |
| 2787.0510 | 2786.0437 | 2786.3520 | -110.64 | 154 | - 177 | 1 | K.LVDFALTANLDMRSRFLMDFGTR.R + Oxidation (M) |
- No match to: 560.2399, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811
15. [P10503|PUTA_SALTY](#) Mass: 144741 Score: 22 Expect: 11 Matches: 16
Bifunctional protein PutA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=putA PE=2 SV=4
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|--------|------|---|
| 592.2476 | 591.2403 | 591.3380 | -165.22 | 1240 | - 1244 | 0 | R.VQFAK.A |
| 606.3871 | 605.3799 | 605.2955 | 139 | 917 | - 921 | 0 | R.CSALR.V |
| 652.4406 | 651.4333 | 651.2976 | 208 | 340 | - 344 | 0 | R.AQYDR.V |
| 776.4191 | 775.4118 | 775.4374 | -33.04 | 18 | - 24 | 1 | R.IKMAASR.I |
| 794.5391 | 793.5318 | 793.4004 | 166 | 2 | - 9 | 0 | M.GTTTGMVK.L |
| 795.5314 | 794.5242 | 794.3415 | 230 | 247 | - 253 | 0 | K.GVDMAMR.L + Oxidation (M) |
| 872.6952 | 871.6879 | 871.5677 | 138 | 428 | - 434 | 1 | R.LMIRLVK.G |
| 1036.3574 | 1035.3501 | 1035.5059 | -150.40 | 345 | - 352 | 0 | R.VMEELYPR.L |
| 1058.7227 | 1057.7154 | 1057.4941 | 209 | 337 | - 344 | 1 | R.YSRAQYDR.V |
| 2200.5593 | 2199.5520 | 2199.0668 | 221 | 610 | - 629 | 1 | R.DLYGEGRINSAGLDLANEHR.L |
| 2248.5625 | 2247.5552 | 2247.1681 | 172 | 254 | - 274 | 1 | R.LMGGEQVFTGETIAQALANARK.L |
| 2696.0813 | 2695.0740 | 2695.3581 | -105.38 | 387 | - 409 | 1 | K.LCFEPPELAGWNGIFVQYQYKRC |
| 3030.2285 | 3029.2212 | 3029.5682 | -114.54 | 1029 | - 1055 | 1 | R.YNRNQLAELIEQINASGYGLTLGVHTR.I |
| 3642.9509 | 3641.9437 | 3642.8504 | -248.93 | 645 | - 677 | 1 | K.WQAKPVLQEPVADGEMTPVINPAEPKDIVGWR.E + Oxidation (M) |
| 3663.6531 | 3662.6458 | 3661.9203 | 198 | 570 | - 604 | 1 | R.IADATLPLDELVDVPEAVEKLAQQEQAGIPHPK.I |
| 3690.6987 | 3689.6915 | 3689.8830 | -51.92 | 145 | - 178 | 1 | R.AGMVQLLQEFSLSSQEGVALMCLAEALLRIPDK.A + Oxidation (M) |
- No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 804.4407, 868.6127, 884.5612, 902.5742, 994.3445, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2216.6750, 2219.5527, 2340.6538, 2390.6392,

2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3646.6877, 3683.7490, 3726.7932, 3774.8674, 3790.8430, 3879.8811

16. [Q8Z0W2|KDPB_SALTY](#) Mass: 72267 Score: 22 Expect: 12 Matches: 9

Potassium-transporting ATPase ATP-binding subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=kdpB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
560.2399	559.2327	559.2867	-96.58	29	32	0	R.AQWR.N
565.3261	564.3188	564.3020	29.9	103	107	0	K.TAFAR.R
592.2476	591.2403	591.3414	-170.89	462	466	1	R.KMGIK.T + Oxidation (M)
634.4214	633.4141	633.3598	85.7	457	461	0	R.FAQLR.K
795.5314	794.5242	794.3779	184	567	572	0	K.QMLMTR.G + Oxidation (M)
1205.7891	1204.7818	1204.6234	131	282	293	0	R.MLGANVIATSGR.A + Oxidation (M)
2200.5593	2199.5521	2199.1028	204	567	586	1	K.QMLMTRGSLTTFSIANDVAK.Y + Oxidation (M)
2216.6750	2215.6678	2215.0977	257	567	586	1	K.QMLMTRGSLTTFSIANDVAK.Y + 2 Oxidation (M)
3726.7932	3725.7859	3725.7996	-3.66	168	202	1	R.ESGGDFASVTGGTRILSDWLVIACSVNPGETFLLDR.M

No match to: 566.2863, 568.3034, 576.6311, 606.3871, 614.2392, 623.3754, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3774.8674, 3790.8430, 3879.8811

17. [Q8ZKH9|PLSB_SALTY](#) Mass: 91455 Score: 22 Expect: 13 Matches: 13

Glycerol-3-phosphate acyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=plsB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
623.3754	622.3682	622.3075	97.5	162	166	0	R.DSFVR.F
1175.7850	1174.7778	1174.5037	233	175	184	1	R.RMADEHGTDK.I + Oxidation (M)
1205.7891	1204.7818	1204.7180	53.0	754	764	0	K.AVFSLSLTLR.D
1225.4161	1224.4089	1224.7078	-244.07	590	600	0	K.DTIGDIIILPR.E
1641.2277	1640.2204	1639.9369	173	695	709	1	R.TLQLLAAGARETLQR.Y
2248.5625	2247.5552	2248.0793	-233.14	657	675	1	R.WEREELASVIDALASEMQR.Q + Oxidation (M)
2390.6392	2389.6319	2390.2384	-253.77	611	631	0	R.NNIAHMLIMPSLMAAIIHQHR.R + Oxidation (M)
2531.8457	2530.8384	2530.3446	195	611	632	1	R.NNIAHMLIMPSLMAAIIHQHR.R
2864.1743	2863.1670	2863.4942	-114.26	412	437	0	R.GGTRPITLVPIYIGYEHVMEVGTAK.E
2989.2437	2988.2364	2988.5266	-97.12	24	50	0	K.SIPAEPAQELGDLTSRPIMVLPYNSK.A
3006.2944	3005.2872	3004.5215	255	24	50	0	K.SIPAEPAQELGDLTSRPIMVLPYNSK.A + Oxidation (M)
3030.2285	3029.2212	3029.4586	-78.35	244	269	1	K.AQQNAIALMEEIAANFSYEMIRLTD.R + 2 Oxidation (M)
3646.6877	3645.6805	3644.8451	229	601	631	1	R.EQAVLMTYYRNNIAHMLIMPSLMAAIIHQHR.R + Oxidation (M)

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1193.7748, 1214.9086, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2340.6538, 2397.6675, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2895.1831, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

18. [Q7CPI8|BCSF_SALTY](#) Mass: 7304 Score: 21 Expect: 15 Matches: 3

Cellulose biosynthesis protein BcsF OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=bcsF PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
560.2399	559.2327	559.3329	-179.31	58	62	1	K.VKADK.K
668.3666	667.3593	667.3878	-42.66	27	31	1	R.HLSLR.I
3424.5625	3423.5552	3422.8611	203	2	30	1	M.MTISDVIQIILFCALIFFPLGLYARHSLR.R + Oxidation (M)

No match to: 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 606.3871, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2565.8599, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

19. [P67557|OPGG_SALTY](#) Mass: 57808 Score: 20 Expect: 18 Matches: 7

Glucans biosynthesis protein G OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mdoG PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
560.2399	559.2327	559.3329	-179.31	479	483	1	K.VKDAK.K
565.3261	564.3188	564.2876	55.4	2	5	1	M.MKMR.W
606.3871	605.3799	605.3021	129	408	413	0	R.STGDVK.Q
668.3666	667.3593	667.2999	89.0	378	382	0	K.EMNFK.Y
712.3618	711.3545	711.3230	44.4	1	5	1	-MMKMR.W + Oxidation (M)
1297.8484	1296.8411	1296.6714	131	123	134	1	K.DTVKDLGFAGFK.V
2565.8599	2564.8526	2564.2718	226	439	463	0	K.LPPDTPVAQTSIGDNGEIVDSNVR.Y

No match to: 566.2863, 568.3034, 576.6311, 592.2476, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 669.3725, 715.4736, 776.4191, 794.5391, 795.5314, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2549.8513, 2616.9348, 2696.0813, 2769.4771, 2787.0510, 2790.1184, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

20. [P63603|AROL_SALTY](#) Mass: 19905 Score: 20 Expect: 18 Matches: 4

Shikimate kinase 2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arol PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.3871	605.3799	605.2744	174	90	93	0	R.YMHR.V
795.5314	794.5242	794.3810	180	175	181	0	R.LQGDVYT.-
2549.8513	2548.8440	2549.3336	-192.05	111	133	0	R.LEAPEADRLPTLTGKPLSEEV.R
2790.1184	2789.1111	2789.4447	-119.58	61	88	0	R.ETAALAEVAPSTVVATGGGIILTEYNR.R

No match to: 560.2399, 565.3261, 566.2863, 568.3034, 576.6311, 592.2476, 614.2392, 623.3754, 634.4214, 644.1973, 652.4406, 667.3455, 668.3666, 669.3725, 712.3618, 715.4736, 776.4191, 794.5391, 804.4407, 868.6127, 872.6952, 884.5612, 902.5742, 994.3445, 1036.3574, 1058.7227, 1064.2002, 1175.7850, 1193.7748, 1205.7891, 1214.9086, 1225.4161, 1264.9457, 1280.9110, 1282.9219, 1297.8484, 1349.0420, 1439.9731, 1641.2277, 1803.2269, 2031.4553, 2033.4734, 2200.5593, 2216.6750, 2219.5527, 2248.5625, 2340.6538, 2390.6392, 2397.6675, 2531.8457, 2565.8599, 2616.9348, 2696.0813,

2769.4771, 2787.0510, 2807.1331, 2864.1743, 2895.1831, 2989.2437, 3006.2944, 3030.2285, 3063.3223, 3424.5625, 3599.5999, 3635.7212, 3642.9509, 3646.6877, 3663.6531, 3683.7490, 3690.6987, 3726.7932, 3774.8674, 3790.8430, 3879.8811

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 300 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 78
Selected for scoring : 71

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P02936|OMPA_SALTY

Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2

Database: Salmonella_Typhi_LT2
 Score: 95
 Expect: 6.1e-007
 Nominal mass (M_r): 37606
 Calculated pI: 5.60

Sequence similarity is available as [an NCBI BLAST search of P02936|OMPA_SALTY against nr.](#)

Search parameters

MS data file: peaklist_6.xml
 Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
 Fixed modifications: **Carbamidomethyl (C)**
 Variable modifications: **Oxidation (M)**
 Mass values searched: 65
 Mass values matched: 13

Protein sequence coverage: 61%

Matched peptides shown in **bold red**.

```

1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYA GAKLGWSQYH DTGFIHNDGP
51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGDNIN GAYKAQGVQL
101 TAKLGYPITD DLVDYTRLGG MVWRADTKSN VPGGPSTKDH DTGVSPVFAG
151 GIEYAITPEI ATRLEYQWTN NIGDANTIGT RPDNGLLSVG VSYRFGQGEA
201 APVVAPAPAP APEVQTKHFT LKSDVLFNFN KSTLKPEGQQ ALDQLYSOLS
251 NLDPKDGSVV VLGFTDRIGS DAYNQLSEK RAQSVVDYLI SKGIPSDKIS
301 ARGMGESNPV TGNTCDNVKP RAALIDCLAP DRRVEIEVKG VKDVVTQPQA

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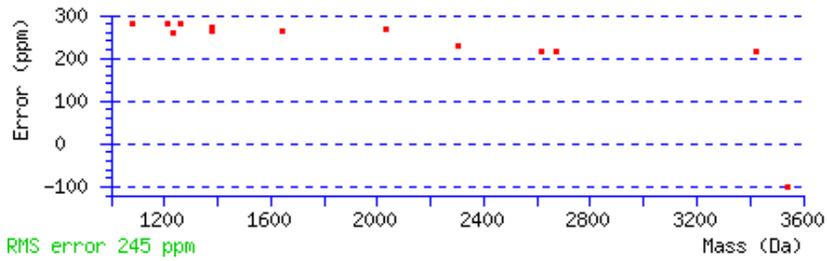
Unformatted sequence string: **350 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
104 - 117	1641.2485	1640.2413	1639.8094	263	0	K.LGYPITDDLVDYTR.L
118 - 128	1233.9594	1232.9521	1232.6336	258	1	R.LGGMVWRADTK.S
129 - 163	3540.4058	3539.3985	3539.7533	-100	1	K.SNVPGGPSTKDHDTGVSPVFAGGIEYAITPEIATR.L
139 - 163	2616.8557	2615.8484	2615.2868	215	0	K.DHDTGVSPVFAGGIEYAITPEIATR.L
164 - 194	3424.4331	3423.4258	3422.6855	216	0	R.LEYQWTNIGDANTIGTRPDNGLLSVGVSYR.F
195 - 217	2303.7295	2302.7222	2302.1957	229	0	R.FGQGEAAPVVAPAPAPAPEVQTK.H
223 - 231	1083.8506	1082.8433	1082.5397	280	0	K.SDVLFNFNK.S
232 - 255	2673.9441	2672.9368	2672.3657	214	0	K.STLKPEGQQALDQLYSQSLNLDPK.D
256 - 267	1265.0081	1264.0008	1263.6460	281	0	K.DGSVVVLGFTDR.I
268 - 280	1382.0330	1381.0257	1380.6521	271	0	R.IGSDAYNQLSEK.R
281 - 292	1379.1334	1378.1261	1377.7616	265	1	K.RAQSVVDYLISK.G
303 - 321	2033.4601	2032.4528	2031.9102	267	0	R.GMGESNPVTGNTCDNVKPR.A
322 - 332	1214.9586	1213.9513	1213.6125	279	0	R.AALIDCLAPDR.R

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1116.9061, 1205.8615, 1246.9989, 1283.0033, 1297.9064, 1487.1834, 1623.2347, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2663.8237, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3633.4744, 3790.5007



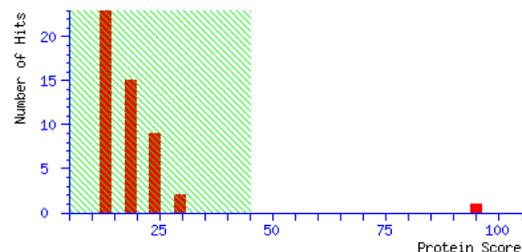
Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

User : MR Labs
 Email : mr1abs7389@gmail.com
 Search title : Sample_6
 MS data file : peaklist_6.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 15 Jul 2024 at 08:03:50 GMT
 Top Score : 95 for **P02936|OMPA_SALTY**, Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)
 Significance threshold $p < 0.05$ Max. number of hits
 Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P02936 OMPA_SALTY	37606	95	Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2
2. P37924 FIMD_SALTY	95354	31	Outer membrane usher protein FimD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimD P
3. Q9L7R4 YIHO_SALTY	53011	30	Putative sulfoquinovose importer OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yiho P
4. Q8ZRB6 COF_SALTY	30483	25	HMP-PP phosphatase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cof PE=3 SV=1
5. Q8ZM06 DKGA_SALTY	31090	25	2,5-diketo-D-gluconic acid reductase A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=d
6. P41784 SCTF1_SALTY	8851	24	SPI-1 type 3 secretion system needle filament protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sctF1
7. P63343 FTSH_SALTY	70898	24	ATP-dependent zinc metalloprotease FtsH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ftsh
8. Q8ZKZ7 TORA_SALTY	95295	22	Trimethylamine-N-oxide reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tora P
9. P0A263 OMPC_SALTY	41214	22	Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1
10. Q9KTB9 SIFB_SALTY	36683	22	Secreted effector protein SifB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sifB PE=3
11. P26978 PUR9_SALTY	57830	22	Bifunctional purine biosynthesis protein PurH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pur9
12. Q8ZQB7 MUKF_SALTY	50487	22	Chromosome partition protein MukF OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mukF P
13. Q8ZPQ1 SUF6_SALTY	15864	20	Cysteine desulfuration protein SufE OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sufE
14. Q8ZJX4 YJJB_SALTY	17161	20	Probable succinate transporter subunit YjJB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yjJB
15. P0A2R0 SOXR_SALTY	17093	19	Redox-sensitive transcriptional activator SoxR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=soxR
16. Q8ZKP3 GLPK_SALTY	56313	19	Glycerol kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=glpK PE=3 SV=3
17. Q8ZHF5 CYSN_SALTY	53300	18	Sulfate adenyllyltransferase subunit 1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cysN
18. P0AA02 NUSG_SALTY	20532	18	Transcription termination/antitermination protein NusG OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nusG
19. Q8ZNV2 SYD_SALTY	65910	18	Aspartate--tRNA ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=aspS PE=3 SV=1
20. P64209 GCH1_SALTY	24869	17	GTP cyclohydrolase 1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=foI1 PE=3 SV=2

Results List

1. [P02936|OMPA_SALTY](#) Mass: 37606 Score: 95 Expect: 6.1e-007 Matches: 13
 Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1083.8506	1082.8433	1082.5397	280	223	- 231	0	K.SDVLFNFNK.S
1214.9586	1213.9513	1213.6125	279	322	- 332	0	R.AALIDCLAPDR.R
1233.9594	1232.9521	1232.6336	258	118	- 128	1	R.LGGMWRADTK.S
1265.0081	1264.0008	1263.6460	281	256	- 267	0	K.DGSVVVLGFTDR.I
1379.1334	1378.1261	1377.7616	265	281	- 292	1	K.RAQSVVDYLISK.G
1382.0330	1381.0257	1380.6521	271	268	- 280	0	R.IGSDAYNQLSEK.R
1641.2485	1640.2413	1639.8094	263	104	- 117	0	K.LGYPIITDDLIVYTR.L
2033.4601	2032.4528	2031.9102	267	303	- 321	0	R.GMGESNPVTGNTCDNVKPR.A
2303.7295	2302.7222	2302.1957	229	195	- 217	0	R.FGQQEAAVPVAPAPAPEVQTK.H
2616.8557	2615.8484	2615.2868	215	139	- 163	0	K.DHDTGVSPVFAGGIEYAIATPEIATR.L
2673.9441	2672.9368	2672.3657	214	232	- 255	0	K.STLKEPQQALDQLYSLSNLDPK.D
3424.4331	3423.4258	3422.6855	216	164	- 194	0	R.LEYQWNTNIGDANTIGTRPDNGLLSVGVSYR.F
3540.4058	3539.3985	3539.7533	-100.23	129	- 163	1	K.SNVPGGPSTKDHTDGVSPVFAGGIEYAIATPEIATR.L

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1116.9061, 1205.8615, 1246.9989, 1283.0033, 1297.9064, 1487.1834, 1623.2347, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2663.8237, 2720.8564, 2748.9087, 2806.9880,

2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3633.4744, 3790.5007

2. [P37924|FIMD_SALTY](#) Mass: 95354 Score: 31 Expect: 1.4 Matches: 9
 Outer membrane usher protein FimD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimD PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1283.0033	1281.9960	1281.6717	253	363	-	373	1 R.VKYDLVAGDFR.S
1623.2347	1622.2275	1621.7633	286	98	-	111	0 K.SGGLMPCFTPEWIK.R
1949.4026	1948.3953	1947.9301	239	727	-	742	1 K.TDWRGYAVMPYATVYR.Y
1965.4363	1964.4290	1963.9251	257	727	-	742	1 K.TDWRGYAVMPYATVYR.Y + Oxidation (M)
2340.6221	2339.6148	2339.1030	219	76	-	97	1 R.NDEFVATQDIRFEAGAVGTGDK.S
2616.8557	2615.8484	2616.2972	-171.54	192	-	214	1 R.GTSDSDSYFLSLLSGLNYGPWRLR.N
2673.9441	2672.9368	2673.2857	-130.50	272	-	295	1 R.LYSSDNMYPDSLQGYAPTVRGIAR.T
3006.1321	3005.1248	3005.3064	-60.41	648	-	676	0 R.SSSNGYSGSASASWQATYGLTGVGVNYDR.D
3424.4331	3423.4258	3423.8013	-109.67	4	-	35	1 K.TTWFAGRFPGYVSPSSVALSVLAALCPLTSR.G

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1641.2485, 1845.5233, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2663.8237, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

3. [Q9L7R4|YIHO_SALTY](#) Mass: 53011 Score: 30 Expect: 1.8 Matches: 5
 Putative sulfoquinovose importer OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yiho PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1641.2485	1640.2413	1639.8716	225	1	-	14	1 -.MSNHDPDLTKLSLR.E + Oxidation (M)
1949.4026	1948.3953	1948.9605	-289.98	61	-	77	0 K.FFTAFTDMLTGVLLDSR.R + Oxidation (M)
2340.6221	2339.6148	2340.2698	-279.87	236	-	256	0 R.NPPLLVCVANLCTLAAFNIK.L
2673.9441	2672.9368	2672.4263	191	414	-	436	0 R.QLIFLWPCGLAIIAALTMGFFYK.L
3513.4495	3512.4422	3511.6940	213	116	-	146	0 K.TAFATVLFMFLFGLFYSLMNCSYGAMVPAITK.N + 3 Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3540.4058, 3633.4744, 3790.5007

4. [Q8ZRB6|COF_SALTY](#) Mass: 30483 Score: 25 Expect: 5.8 Matches: 7
 HMP-PP phosphatase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cof PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1214.9586	1213.9513	1213.6302	265	160	-	169	0 R.IQLNEALEER.A
2235.6926	2234.6854	2234.0175	299	81	-	99	0 R.QDLDPQVADTMHHAWDR.A
2303.7295	2302.7222	2302.0908	274	170	-	189	0 R.AHLCFSAVDCELEVLPLGCNK.G
2516.8809	2515.8736	2515.1770	277	1	-	22	1 -.MARLAAFDMGTLMPDHLGLR.E + 3 Oxidation (M)
3393.5344	3392.5271	3391.6197	268	100	-	129	0 R.ASMHVFNDNGWFTGQIPELLQAHVYSGFR.Y
3409.5044	3408.4971	3407.6146	259	100	-	129	0 R.ASMHVFNDNGWFTGQIPELLQAHVYSGFR.Y + Oxidation (M)
3498.5037	3497.4964	3497.7105	-61.21	160	-	189	1 R.IQLNEALEERAHLCFSAVDCELEVLPLGCNK.G

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3404.3062, 3424.4331, 3449.4070, 3513.4495, 3540.4058, 3633.4744, 3790.5007

5. [Q8ZM06|DKGA_SALTY](#) Mass: 31090 Score: 25 Expect: 6.1 Matches: 3
 2,5-diketo-D-gluconic acid reductase A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dkgA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1205.8615	1204.8542	1204.6101	203	171	-	180	0 R.QLHAWNATHK.I
1994.4729	1993.4656	1993.9956	-265.80	44	-	62	1 R.SIDTATAYQNEEGVGKALK.A
2235.6926	2234.6854	2234.1742	229	129	-	147	1 K.EGLVKSIGVGNFIHHLQR.L

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

6. [P41784|SCTF1_SALTY](#) Mass: 8851 Score: 24 Expect: 7.5 Matches: 2
 SPI-1 type 3 secretion system needle filament protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sctF1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1641.2485	1640.2413	1639.7552	296	1	-	15	0 -.MATPWSGYLDDVSAK.F
1994.4729	1993.4656	1992.9640	252	16	-	33	0 K.FDTGVNDLQQTVEALDK.L

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

7. [P63343|FTSH_SALTY](#) Mass: 70898 Score: 24 Expect: 8 Matches: 8
 ATP-dependent zinc metalloprotease FtsH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ftsH PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1083.8506	1082.8433	1082.5318	288	379	-	387	0 R.VVSMVEFEK.A + Oxidation (M)
1283.0033	1281.9960	1281.6639	259	379	-	389	1 R.VVSMVEFEKAK.D + Oxidation (M)
2235.6926	2234.6854	2234.2198	208	66	-	84	1 R.YTTYIPIPNPKLLDNLTK.N
2249.6855	2248.6783	2248.0901	262	562	-	580	1 R.QILTDNMIDILHAMKDALMK.Y + 3 Oxidation (M)
2325.6763	2324.6690	2324.1028	244	576	-	595	1 K.DALMKYETIDAPQIDLMAR.R + Oxidation (M)
2340.6221	2339.6148	2340.0977	-206.37	576	-	595	1 K.DALMKYETIDAPQIDLMAR.R + 2 Oxidation (M)
2616.8557	2615.8484	2616.2424	-150.59	400	-	423	1 R.SMVMTEAQKESTAYHEAGHAIIGR.L
3006.1321	3005.1248	3004.5005	208	204	-	232	1 K.AIAGEAKVPFFFTISGSDVFEMFVGVGASR.V + Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081,

1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2301.2268, 2303.7295, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

8. [Q8ZKZ7|TORA_SALTY](#) Mass: 95295 Score: 22 Expect: 11 Matches: 6

Trimethylamine-N-oxide reductase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=torA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1265.0081	1264.0008	1263.6533	275	224	-	234	0	K.TIVLWGSDMVK.N + Oxidation (M)
2211.6321	2210.6248	2211.2449	-280.45	14	-	35	0	R.FLAQLGLTVAGMLGPSLLTPR.S
2303.7295	2302.7222	2303.1328	-178.28	701	-	720	1	R.LHSQLCESETLRQQYAVGGK.E
3006.1321	3005.1248	3004.4427	227	520	-	545	1	R.FADIVLPATTQFERNDLDQFGNHSNR.G
3424.4331	3423.4258	3422.7358	202	421	-	453	1	K.GIILSGFSGSTVPPVHDSTDYKGYSSSTIPIAR.F
3633.4744	3632.4671	3631.7823	189	603	-	631	1	K.GRGIHLPIFEVFWNQEQYIEFDHPQMFVR.H

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3790.5007

9. [P0A263|OMPC_SALTY](#) Mass: 41214 Score: 22 Expect: 12 Matches: 4

Outer membrane porin C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompC PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1205.8615	1204.8542	1204.5149	282	103	-	113	0	K.FADAGSFDYGR.N
2340.6221	2339.6148	2339.0818	228	246	-	265	0	K.YDANNIYLAQYSQTYNATR.F
3006.1321	3005.1248	3004.5083	205	284	-	309	0	K.AQNFVVAQYQDFGLRPSVAYLQSK.G
3790.5007	3789.4935	3788.6575	221	63	-	95	0	K.GETQVNDQLTGYGQWEYIQGNQTEGSNDSWTR.V

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744

10. [Q9KIB9|SIFB_SALTY](#) Mass: 36683 Score: 22 Expect: 12 Matches: 3

Secreted effector protein SifB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sifB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1994.4729	1993.4656	1993.8840	-209.83	35	-	50	1	K.DFFCDTORSTADQYIK.E
2235.6926	2234.6854	2234.0711	275	178	-	196	1	K.NIEETLIAMAEKGNLCKDWK.E
2673.9441	2672.9368	2672.1900	279	81	-	101	1	R.GNFHFQHYKDAECQYTNLCKI.D

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

11. [P26978|PUR9_SALTY](#) Mass: 57830 Score: 22 Expect: 13 Matches: 5

Bifunctional purine biosynthesis protein PurH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=purH PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1845.5233	1844.5160	1843.9931	284	338	-	354	0	R.QFVEVIAIAPSATEEALK.I
2673.9441	2672.9368	2672.1925	279	224	-	245	1	K.QDMRYGENSHQQAIFYEENVK.E + Oxidation (M)
3424.4331	3423.4258	3423.6331	-60.54	228	-	258	1	R.YGENSHQQAIFYEENVKESAVATAQQVQGK.A
3498.5037	3497.4964	3496.6868	232	470	-	504	1	K.GSAMASDAFFPFRDGDIAAAVGVSCVIPPQGSIR.D
3513.4495	3512.4422	3512.6817	-68.19	470	-	504	1	K.GSAMASDAFFPFRDGDIAAAVGVSCVIPPQGSIR.D + Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

12. [Q8Z0B7|MUKF_SALTY](#) Mass: 50487 Score: 22 Expect: 13 Matches: 4

Chromosome partition protein MukF OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mukF PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1487.1834	1486.1761	1485.7576	282	187	-	198	1	K.DDIAQLLNKDW.R.A
1994.4729	1993.4656	1993.9931	-264.55	1	-	17	1	-.MSEFSQTVPELVAVARK.N + Oxidation (M)
3006.1321	3005.1248	3004.4025	240	303	-	327	1	R.QSVQTYFDDPWALTYANADRLDMR.D + Oxidation (M)
3424.4331	3423.4258	3423.5889	-47.63	43	-	73	1	R.LDGESEGLVDAFRHSVDAFEQTSSETIGVR.A

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

13. [Q8ZPQ1|SUFE_SALTY](#) Mass: 15864 Score: 20 Expect: 20 Matches: 2

Cysteine desulfuration protein SufE OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sufE PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
2303.7295	2302.7222	2303.2273	-219.30	24	-	42	1	K.VLYIIEELGQRLAELNPQDR.N
2340.6221	2339.6148	2339.1375	204	43	-	61	1	R.NPQNTIHGCQSQVIVMRR.N + Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

14. [Q8ZJX4|YJJB_SALTY](#) Mass: 17161 Score: 20 Expect: 21 Matches: 3

Probable succinate transporter subunit YjJB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yjJB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
2340.6221	2339.6148	2339.1905	181	112	-	131	0	K.ISHLGYSEPMITLLTNFLK.A + 2 Oxidation (M)

2600.9146 2599.9073 2599.3794 203 87 - 111 0 K.VFTVAIVPMPFGISAYTAMISAVK.I + Oxidation (M)
 2616.8557 2615.8484 2615.3743 181 87 - 111 0 K.VFTVAIVPMPFGISAYTAMISAVK.I + 2 Oxidation (M)
No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

15. [P0A2R0|SOXR_SALTY](#) Mass: 17093 Score: 19 Expect: 22 Matches: 2
 Redox-sensitive transcriptional activator SoxR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=soxR PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2235.6926	2234.6854	2234.2059	215	21	41	1	R.SGVAVSALHFYESKGLITSR.N
2340.6221	2339.6148	2338.9763	273	114	133	1	R.DELDGCIGCGCLSRSDCPLR.N

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

16. [Q8ZKP3|GLPK_SALTY](#) Mass: 56313 Score: 19 Expect: 26 Matches: 4
 Glycerol kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=glpK PE=3 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1233.9594	1232.9521	1232.6183	271	109	118	1	R.TADICEQLKR.D
1994.4729	1993.4656	1994.0367	-286.40	391	408	1	R.DVLEAMQDSGIRLHALR.V
2340.6221	2339.6148	2339.0054	261	259	279	1	K.EGMKANTYGTGCFMLMNTGEK.A
3006.1321	3005.1248	3005.3978	-90.83	179	203	1	R.VHVTDYTNASRTMLFNIHDLDDWDD.M

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

17. [Q8ZMF5|CYSN_SALTY](#) Mass: 53300 Score: 18 Expect: 26 Matches: 4
 Sulfate adenylyltransferase subunit 1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cysN PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1265.0081	1264.0008	1263.6459	281	90	100	0	R.EQGITIDVAYR.Y
1845.5233	1844.5160	1844.9414	-230.58	424	440	1	R.LSNVTGVMGMRVRELDER.G
1994.4729	1993.4656	1993.9633	-249.58	185	201	0	R.EDYLTFAEQLPGDLDIR.F
2303.7295	2302.7222	2303.0951	-161.90	300	320	0	K.EEACAGEAITLVNDDIDISR.G

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

18. [P0AA02|NUSG_SALTY](#) Mass: 20532 Score: 18 Expect: 28 Matches: 3
 Transcription termination/antitermination protein NusG OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nusG PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2303.7295	2302.7222	2302.1740	238	85	106	1	R.SVPRVMFGIGGTSDRPAPISDK.E + Oxidation (M)
2600.9146	2599.9073	2599.2662	247	32	53	0	K.LHNMEELFGEVMPTEEVVEIR.G
2616.8557	2615.8484	2615.2611	225	32	53	0	K.LHNMEELFGEVMPTEEVVEIR.G + Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

19. [Q8ZNV2|SYD_SALTY](#) Mass: 65910 Score: 18 Expect: 30 Matches: 5
 Aspartate--tRNA ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=aspS PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2117.6223	2116.6150	2117.1555	-255.26	538	556	1	R.LTMLLTGTDNIRDVIAFPK.T
2340.6221	2339.6148	2339.1104	216	226	245	0	R.QPEFTQIDVETSFMTPAQVR.E + Oxidation (M)
2597.8306	2596.8233	2596.2228	231	464	489	0	K.TAPEGAVANAYDMVINGYEVGGGSVR.I
2616.8557	2615.8484	2616.3233	-181.48	187	208	1	K.FYALPQSPQLFKQLLMSGFDR.Y
3540.4058	3539.3985	3539.6431	-69.11	425	455	0	K.WAPLWIDFPMFEDDGGGLTAMHHPFTAPR.D

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

20. [P64209|GCH1_SALTY](#) Mass: 24869 Score: 17 Expect: 36 Matches: 4
 GTP cyclohydrolase 1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=foI1E PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1265.0081	1264.0008	1263.6935	243	7	18	0	K.EAALVHDALVAR.G
2211.6321	2210.6248	2210.1001	237	19	37	1	R.GLETPLRPPMEDLDNETRK.S
3409.5044	3408.4971	3407.6887	237	37	66	1	R.KSLIAGHMTEIMQLLNLDLSDSLMETPHR.I
3424.4331	3423.4258	3423.6836	-75.29	37	66	1	R.KSLIAGHMTEIMQLLNLDLSDSLMETPHR.I + Oxidation (M)

No match to: 615.6252, 684.4383, 768.7656, 770.6706, 842.7556, 1051.9963, 1083.8506, 1116.9061, 1205.8615, 1214.9586, 1233.9594, 1246.9989, 1265.0081, 1283.0033, 1297.9064, 1379.1334, 1382.0330, 1487.1834, 1623.2347, 1641.2485, 1845.5233, 1949.4026, 1965.4363, 1994.4729, 2033.4601, 2117.6223, 2211.6321, 2218.5791, 2235.6926, 2249.6855, 2301.2268, 2303.7295, 2325.6763, 2340.6221, 2399.6104, 2448.7646, 2501.7976, 2516.8809, 2549.7861, 2571.8135, 2578.3474, 2597.8306, 2600.9146, 2616.8557, 2663.8237, 2673.9441, 2720.8564, 2748.9087, 2806.9880, 2932.9246, 3006.1321, 3289.3862, 3332.2683, 3349.3062, 3387.5405, 3393.5344, 3404.3062, 3409.5044, 3424.4331, 3449.4070, 3498.5037, 3513.4495, 3540.4058, 3633.4744, 3790.5007

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 300 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 65
Selected for scoring : 14

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P0A261|TSX_SALTY

Nucleoside-specific channel-forming protein Tsx OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tsx PE=3 SV=1

Database: Salmonella_Typhi_LT2
Score: 89
Expect: 2.2e-006
Nominal mass (M_r): 32758
Calculated pI: 4.96

Sequence similarity is available as [an NCBI BLAST search of P0A261|TSX_SALTY against nr.](#)

Search parameters

MS data file: peaklist_8.xml
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 94
Mass values matched: 14

Protein sequence coverage: 62%

Matched peptides shown in **bold red**.

1 MKKTL LAVSA ALALTSSFTA NAAENDQPQY LSDWWHQSVN VVGSYHTRFS
 51 **PKLNNDVYLE YEAF AKKDFE DFYGYIDIPK** TFDWGNNGNDK **GIWSDGSPLF**
 101 **MEIEPRFSID KLTGADLSFG PFKEWYFANN YIYDMGDNKA SRQSTWYMGL**
 151 **GTDIDTGLPM GLSLNVYAKY QWQNYGASNE NEWDGYRFKV KYFVPITDLW**
 201 **GKLSYIGFT NFDWGS DLGD DPNRTS NSIA SSHILALNYD HWHYSV VARY**
 251 FHNGGQWQNG AKLWNWGDGDF SAKSTGWGGY LVVGYNF

Unformatted sequence string: **287 residues** (for pasting into other applications).

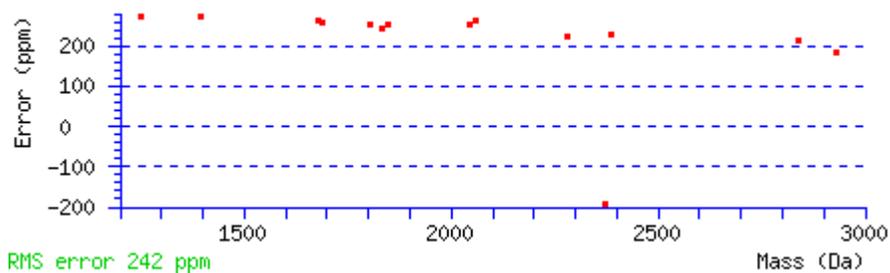
Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
53 - 66	1689.2509	1688.2436	1687.8093	257	0	K.LNNDVYLEYEAF AK.K
67 - 80	1807.3342	1806.3270	1805.8665	255	1	K.KDWDFYGYIDIPK.T
68 - 80	1679.2188	1678.2115	1677.7715	262	0	K.DWDFYGYIDIPK.T
91 - 106	1834.3252	1833.3179	1832.8767	241	0	K.GIWSDGSPLFMEIEPR.F
91 - 106	1850.3451	1849.3378	1848.8716	252	0	K.GIWSDGSPLFMEIEPR.F + Oxidation (M)
112 - 123	1252.9999	1251.9926	1251.6499	274	0	K.LTGADLSFGPFK.E
124 - 139	2043.3737	2042.3664	2041.8516	252	0	K.EWYFANNIYDMGDNK.A
124 - 139	2059.3972	2058.3899	2057.8465	264	0	K.EWYFANNIYDMGDNK.A + Oxidation (M)

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
124 - 142	2372.5693	2371.5621	2372.0168	-192	1	K.EWYFANNYIYDMGDNKASR.Q + Oxidation (M)
143 - 169	2931.9609	2930.9537	2930.4194	182	0	R.QSTWYMGLGTDIDTGLPMGLSLNVIYAK.Y
170 - 187	2280.4438	2279.4366	2278.9304	222	0	K.YQWQNYGASNENEWDGYR.F
192 - 203	1396.1125	1395.1053	1394.7235	274	0	K.YFVPITDLWGGK.L
204 - 224	2389.6150	2388.6077	2388.0659	227	0	K.LSYIGFTNFDWGSDDLGDPPNR.T
225 - 249	2842.0085	2841.0013	2840.3994	212	0	R.TSNSIASSHILALNYDHWHSVVAR.Y

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2883.0608, 2899.0327, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392



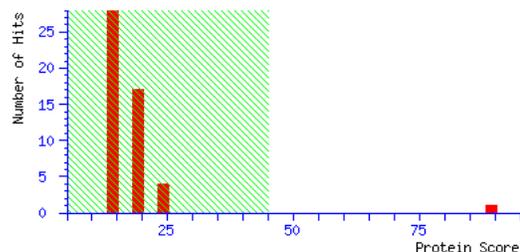
Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

User : MR Labs
 Email : mr1abs7389@gmail.com
 Search title : Sample_8
 MS data file : peaklist_8.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 15 Jul 2024 at 08:41:07 GMT
 Top Score : 89 for [P0A261|TSX_SALTY](#), Nucleoside-specific channel-forming protein Tsx OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)

Significance threshold $p < 0.05$ Max. number of hits

Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P0A261 TSX_SALTY	32758	89	Nucleoside-specific channel-forming protein Tsx OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=9
2. Q8ZL65 SADB_SALTY	25947	25	Inner membrane lipoprotein SadB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sadB PE=
3. Q8ZR03 LIPB_SALTY	23993	25	Octanoyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lipB PE=3 SV=2
4. Q9F0N8 IRAM_SALTY	13902	23	Anti-adaptor protein IraM OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=iram PE=1 SV=1
5. Q8ZPR4 YDIB_SALTY	31545	22	Quinate/shikimate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ydib PE=
6. P60190 SPRT_SALTY	19459	22	Protein SprT OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sprt PE=3 SV=1
7. P02936 OMPA_SALTY	37606	21	Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2
8. P0A2R6 DUSB_SALTY	36166	20	tRNA-dihydrouridine synthase B OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dusB PE=3
9. P04942 CHEB_SALTY	37642	20	Protein-glutamate methyltransferase/protein-glutamine glutaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / AT
10. Q8ZRX5 CAID_SALTY	28145	20	Carnitiny-CoA dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=caid PE=3 SV=
11. P23924 MG1A_SALTY	56613	19	Galactose/methyl galactoside import ATP-binding protein MglA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC
12. Q9ZV2 EUTA_SALTY	49724	19	Ethanolamine ammonia-lyase reactivase EutA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287
13. Q7C056 MENB_SALTY	32129	19	1,4-dihydroxy-2-naphthoyl-CoA synthase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=m
14. P60428 RL2_SALTY	29916	19	Large ribosomal subunit protein uL2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rp1B
15. Q8ZQN4 RLMF_SALTY	34574	19	Ribosomal RNA large subunit methyltransferase F OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=9
16. Q8ZND6 PTA_SALTY	77572	18	Phosphate acetyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pta PE=1 SV=
17. P0A1D7 CLPP_SALTY	23276	18	ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99
18. Q8ZR43 HTHR_SALTY	22017	18	Transcriptional regulator RamR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ramR PE=1
19. P66643 RS9_SALTY	14817	18	Small ribosomal subunit protein uS9 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rpsI
20. Q8ZK33 ARCA_SALTY	45875	17	Arginine deiminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arca PE=3 SV=1

Results List

1. [P0A261|TSX_SALTY](#) Mass: 32758 Score: 89 Expect: 2.2e-006 Matches: 14
 Nucleoside-specific channel-forming protein Tsx OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=tsx PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1252.9999	1251.9926	1251.6499	274	112	- 123	0	K.LTGADLSFGPFK.E
1396.1125	1395.1053	1394.7235	274	192	- 203	0	K.YVFPITDLWGGK.L
1679.2188	1678.2115	1677.7715	262	68	- 80	0	K.KDWFDFYGYIDIPK.T
1689.2509	1688.2436	1687.8093	257	53	- 66	0	K.LNNDVYLEEAFK.K
1807.3342	1806.3270	1805.8665	255	67	- 80	1	K.KDWFDFYGYIDIPK.T
1834.3252	1833.3179	1832.8767	241	91	- 106	0	K.GIWSGDGSLPFMEIEPR.F
1850.3451	1849.3378	1848.8716	252	91	- 106	0	K.GIWSGDGSLPFMEIEPR.F + Oxidation (M)
2043.3737	2042.3664	2041.8516	252	124	- 139	0	K.EWYFANNIYIDMGDNK.A
2059.3972	2058.3899	2057.8465	264	124	- 139	0	K.EWYFANNIYIDMGDNK.A + Oxidation (M)
2280.4438	2279.4366	2278.9304	222	170	- 187	0	K.YQWQNYGASNEWDGGR.F
2372.5693	2371.5621	2372.0168	-191.69	124	- 142	1	K.EWYFANNIYIDMGDNKASR.Q + Oxidation (M)
2389.6150	2388.6077	2388.0659	227	204	- 224	0	K.LSYIGFTNFDWGSGLGDDPNR.T
2842.0085	2841.0013	2840.3994	212	225	- 249	0	R.TSNSIASSHILALNYDHWHSVVAR.Y
2931.9609	2930.9537	2930.4194	182	143	- 169	0	R.QSTWYMLGTDIDTGLPMLSLNVYAK.Y

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2086.4060, 2150.5496, 2204.4160,

2235.6609, 2262.4353, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2883.0608, 2899.0327, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

2. [Q8ZL65|SADB_SALTY](#) Mass: 25947 Score: 25 Expect: 6.2 Matches: 5

Inner membrane lipoprotein SADB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sadb PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
2262.4353	2261.4280	2261.1249	134	203	-	222	0	K.IGIDMENVIFDSIQPINDTK.K
2389.6150	2388.6077	2389.2199	-256.23	203	-	223	1	K.IGIDMENVIFDSIQPINDTKK.K
2842.0085	2841.0013	2840.4248	203	4	-	28	1	K.NGKFIPLLALGFTFFLSCDYFADK.H
3409.5366	3408.5293	3407.6974	244	7	-	35	1	K.FIPLLALGFTFFLSCDYFADKHLVEEMK.E
3424.4839	3423.4766	3423.6924	-63.01	7	-	35	1	K.FIPLLALGFTFFLSCDYFADKHLVEEMK.E + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

3. [Q8ZR03|LIPB_SALTY](#) Mass: 23993 Score: 25 Expect: 6.5 Matches: 4

Octanoyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lipB PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
684.4216	683.4144	683.2948	175	1	-	5	0	-MYQDK.I
1877.3440	1876.3367	1875.9513	205	55	-	71	0	K.AEHILMPGDIPVVQSDR.G
2086.4060	2085.3987	2085.1510	119	195	-	213	0	R.LLANILALLNPPPEYIAA.-
2931.9609	2930.9537	2930.4895	158	6	-	30	1	K.IILVRQLGLQPYEAIQSAMHNFTDMR.D

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

4. [Q9F0N8|IRAM_SALTY](#) Mass: 13902 Score: 23 Expect: 8.8 Matches: 4

Anti-adaptor protein Iram OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=iram PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
2478.6218	2477.6145	2478.1018	-196.63	91	-	111	0	K.SEACSPYFEECLVSVCPFLTR.N
2581.7935	2580.7862	2581.3291	-210.31	29	-	50	0	R.LTLWYQADVMPGSIIPFNK.G + Oxidation (M)
2616.8638	2615.8565	2615.3741	184	5	-	28	1	K.VVDTVISPTGVSFSCIHSLKNLR.L
2806.9824	2805.9751	2806.4034	-152.60	1	-	25	1	-MEWKVVDTVISPTGVSFSCIHSLK.N

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

5. [Q8ZPR4|YDIB_SALTY](#) Mass: 31545 Score: 22 Expect: 12 Matches: 5

Quinate/shikimate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ydib PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
606.4691	605.4618	605.3537	179	164	-	169	0	K.AVAFAK.R
634.4969	633.4896	633.3632	200	58	-	62	1	K.ALKMR.G + Oxidation (M)
2369.4521	2368.4449	2368.3148	54.9	124	-	149	1	R.GKTMVLLGAGGAATAIGAQAIEIGIK.E
2579.5068	2578.4996	2578.2407	100	63	-	86	1	R.GTGVSMPNKQLACEYVDELTPAAK.L
2725.8398	2724.8326	2724.2993	196	33	-	57	0	K.AGLPYTYMAFEVDNTTFASAIIEGLK.A + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

6. [P60190|SPRT_SALTY](#) Mass: 19459 Score: 22 Expect: 13 Matches: 4

Protein SprT OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sprt PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1396.1125	1395.1053	1394.8180	206	6	-	17	1	R.LPIAIQQAVMRR.L
1641.2290	1640.2217	1639.7842	267	44	-	58	0	R.GTSAGTAWLESYEIR.L
1850.3451	1849.3378	1849.8855	-296.06	98	-	112	1	K.EWKMMMSLVGVPAR.R + 2 Oxidation (M)
2372.5693	2371.5621	2372.1015	-227.41	125	-	142	1	R.NTFPYHCQQHQHQLTVRR.H

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

7. [P02936|OMPA_SALTY](#) Mass: 37606 Score: 21 Expect: 16 Matches: 5

Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompA PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1264.9937	1263.9864	1263.6460	269	256	-	267	0	K.DGSVVVLGFTDR.I
1641.2290	1640.2217	1639.8094	251	104	-	117	0	K.LGYPIITDDLVDVYTR.L
2616.8638	2615.8565	2615.2868	218	139	-	163	0	K.DHDTGVSPVFAGGIEYAITPEIATR.L

3424.4839 3423.4766 3422.6855 231 164 - 194 0 R.LEYQWNTNIGDANTIGTRPDNGLLSVGVSYR.F

3541.4392 3540.4319 3539.7533 192 129 - 163 1 K.SNVPGGPSTKDHDTGVSPVFFAGGIEYAITPEIATR.L

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065

8. [P0A2RG|DUSB_SALTY](#) Mass: 36166 Score: 20 Expect: 17 Matches: 5

tRNA-dihydrouridine synthase B OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dusB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1689.2509	1688.2436	1687.9257	188	193	-	208	0 K.VSIPIIANGDITNPHK.A
2725.8398	2724.8326	2724.3436	179	150	-	173	1 R.NCVEIAQLAEDCGIQALTIHGRTR.A
2748.4651	2747.4578	2747.4330	9.05	211	-	235	1 R.AVLDTYADALMIGRAAQRPIWFR.E
3206.1235	3205.1163	3204.8737	75.7	109	-	139	1 K.LAGSALLQYPLDKVLSILIGVVNAVDPVTLK.I
3326.1658	3325.1585	3324.4407	216	27	-	55	1 R.TLCYEMAGLTVSEMMSSNPVWESDKSR.L + 2 Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

9. [P04042|CHEB_SALTY](#) Mass: 37642 Score: 20 Expect: 18 Matches: 6

Protein-glutamate methyltransferase/protein-glutamine glutaminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cheB PE=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
634.4969	633.4896	633.3632	200	1	-	5	1 -.MSKIR.V
650.4960	649.4888	649.3581	201	1	-	5	1 -.MSKIR.V + Oxidation (M)
2389.6150	2388.6077	2388.2869	134	74	-	95	1 R.LRPMPVVMVSLTGKGEVTLR.A + 2 Oxidation (M)
2725.8398	2724.8326	2725.2979	-170.75	48	-	70	1 K.FNPDVLTLDVEMPRMDGLDFLEK.L + 2 Oxidation (M)
3326.1658	3325.1585	3325.7758	-185.60	173	-	202	1 R.HVLQPLPLSSPAVITITQHPMPGFTRFAER.L
3409.5366	3408.5293	3408.7672	-69.79	96	-	126	1 R.ALELGAIDFVTKPQLGIREGLMAYSEMIAEK.V + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3415.2065, 3424.4839, 3541.4392

10. [Q8ZRXS|CAID_SALTY](#) Mass: 28145 Score: 20 Expect: 18 Matches: 4

Carnitiny-CoA dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=caid PE=3 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1641.2290	1640.2217	1639.8790	209	149	-	163	0 K.LLPPAIVNEMVMTRGR.R
1850.3451	1849.3378	1849.0672	146	191	-	208	0 R.ELAQLVNSAPLAIALK.E
1995.3813	1994.3741	1994.1057	135	146	-	163	1 R.LPKLLPRAIVNEMVMTRGR.R + Oxidation (M)
2389.6150	2388.6077	2388.3125	124	2	-	22	1 M.SESLHTRNGPILEITLDRPK.A

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

11. [P23924|MGLA_SALTY](#) Mass: 56613 Score: 19 Expect: 22 Matches: 6

Galactose/methyl galactoside import ATP-binding protein MglA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mglA PE=1 S

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
634.4969	633.4896	633.3486	223	22	-	27	0 K.SFPGVK.A
2280.4438	2279.4366	2279.1290	135	1	-	21	1 -.MGSTISPPSGEYLLEMRGINK.S
2293.4514	2292.4441	2292.1896	111	84	-	103	0 K.EALENGISMVHQELNLVLQR.S
2372.5693	2371.5621	2372.2488	-289.49	348	-	368	1 R.RSTGIYAYLDIGFNLSINIR.N
2478.6218	2477.6146	2477.2411	151	326	-	347	1 K.KINNHTANEAINHGFAVTEER.R
3206.1235	3205.1163	3205.6190	-156.82	76	-	103	1 K.EVDFHSAKEALENGISMVHQELNLVLQR.S

No match to: 560.3074, 568.3801, 606.4691, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2389.4651, 2398.4651, 2446.6294, 2472.5049, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

12. [Q9ZFY2|EUTA_SALTY](#) Mass: 49724 Score: 19 Expect: 22 Matches: 6

Ethanolamine ammonia-lyase reactivase EutA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=euta PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1508.0737	1507.0665	1506.8194	164	31	-	43	1 R.AAVSQVPRYEFIK.R
1689.2509	1688.2436	1687.8828	214	296	-	309	1 R.LREMNVQFPAQTVR.A
1807.3342	1806.3270	1806.0403	159	382	-	398	0 R.YAALLTVINALTAFVAR.Y
2472.5049	2471.4976	2471.1937	123	145	-	167	1 R.MCRVLNIDIGGGTSNYALFDAGK.V
2489.5005	2488.4932	2489.2009	-284.31	189	-	211	0 R.VVYAHQPGQMIIDEVFGSDTAR.A
2806.9824	2805.9751	2806.4793	-179.65	440	-	467	1 R.AGDYIDITGTLFSGSVVPTVKSIAFFS.-

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702,

2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2478.6218, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

13. [Q7CQ56|MENB_SALTY](#) Mass: 32129 Score: 19 Expect: 24 Matches: 4

1,4-dihydroxy-2-naphthoyl-CoA synthase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=menB PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1807.3342	1806.3270	1806.8327	-279.93	217	-	230	1 R.WCREMLQNSPMALR.C + Oxidation (M)
2086.4060	2085.3987	2085.0102	186	159	-	178	1 K.VGSFDGGWASVYMARIVGQK.K
2806.9824	2805.9751	2805.3855	210	55	-	80	1 K.EMIQALADARYDDNVGVIITLGEQDK.A
3117.0977	3116.0904	3115.5860	162	189	-	216	1 R.QYDAQQALDMLVNTVPLADLEKETVR.W

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5068, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

14. [P60428|RL2_SALTY](#) Mass: 29916 Score: 19 Expect: 25 Matches: 7

Large ribosomal subunit protein uL2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rlpB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
842.7554	841.7482	841.5134	279	204	-	212	1 R.VLKGAGAAR.W
1514.1390	1513.1318	1512.7355	262	190	-	203	0 R.ATLGEVGNAEHMLR.V + Oxidation (M)
1689.2509	1688.2436	1687.7485	293	222	-	238	0 R.GTAMNPVDHPHGGEGR.N
1807.3342	1806.3270	1805.9458	211	134	-	150	0 R.NIPVGVSTVHNVEMKPGK.G
2150.5496	2149.5423	2149.9712	-199.50	222	-	242	1 R.GTAMNPVDHPHGGEGRNFQK.H + Oxidation (M)
2389.6150	2388.6077	2388.2696	142	134	-	156	1 R.NIPVGVSTVHNVEMKPGKGGQLAR.S
2663.8152	2662.8079	2662.3683	165	126	-	150	1 K.AGNTLPMRNPVGVSTVHNVEMKPGK.G + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1605.1729, 1641.2290, 1679.2188, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5068, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

15. [Q8ZQ4|RLMF_SALTY](#) Mass: 34574 Score: 19 Expect: 25 Matches: 5

Ribosomal RNA large subunit methyltransferase F OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rlmF PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1282.9873	1281.9800	1281.7081	212	164	-	175	0 K.DPAAIFGTGIHK.N
1492.0540	1491.0467	1490.7888	173	1	-	13	1 -.MSAQKPLGHPRRN.H
1508.0737	1507.0665	1506.7837	188	1	-	13	1 -.MSAQKPLGHPRRN.H + Oxidation (M)
2389.6150	2388.6077	2388.2954	131	246	-	265	1 R.QVLWFTTLVSRGENLPLLYR.A
2931.9609	2930.9537	2930.5054	153	58	-	83	0 K.ALLAHFYAVTHWIDIPPGLCPPVGR.A

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5068, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

16. [Q8ZND6|PTA_SALTY](#) Mass: 77572 Score: 18 Expect: 26 Matches: 11

Phosphate acetyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pta PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
634.4969	633.4896	633.3268	257	26	-	30	1 R.AMERK.G
650.4960	649.4888	649.3217	257	26	-	30	1 R.AMERK.G + Oxidation (M)
1282.9873	1281.9800	1281.6288	274	262	-	271	0 R.SIPHMLEHFR.A + Oxidation (M)
1605.1729	1604.1656	1603.8062	224	669	-	683	0 R.SADLISIGPMLQGMK.K + Oxidation (M)
1875.3273	1874.3200	1874.8568	-286.31	585	-	603	0 R.VAMLSYSTGTSGAGSDVEK.V + Oxidation (M)
1877.3440	1876.3367	1875.9036	231	84	-	99	0 K.DVLMEEIANYHANTK.D + Oxidation (M)
2043.3737	2042.3664	2042.0765	142	665	-	683	1 K.AVQRSADLISIGPMLQGMK.K
2059.3972	2058.3899	2058.0714	155	665	-	683	1 K.AVQRSADLISIGPMLQGMK.K + Oxidation (M)
2389.6150	2388.6077	2388.1817	178	615	-	636	0 K.RPDLMDIGPLQYDAAMVADVAK.S
2446.6294	2445.6221	2445.2751	142	692	-	714	0 R.GALVDDIVYTIATLAIQASQQQQ.-
2616.8638	2615.8565	2616.4707	-234.74	1	-	25	1 -.MSRIIMLPTGTSGVLSVSLGVIR.A + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5068, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

17. [P0A1D7|CLPP_SALTY](#) Mass: 23276 Score: 18 Expect: 30 Matches: 4

ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=clpP PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2352.4702	2351.4629	2352.1063	-273.51	161	-	180	1 K.GRMNEMAHHTGQSLEQIER.D + Oxidation (M)
2369.4521	2368.4449	2368.1011	145	161	-	180	1 K.GRMNEMAHHTGQSLEQIER.D + 2 Oxidation (M)
2931.9609	2930.9537	2931.4042	-153.65	1	-	26	1 -.MSYSGERDNLAPHMLVPMVIEQTSR.G
3415.2065	3414.1993	3414.7203	-152.59	42	-	71	0 R.VIFLTGQVEDHMANLIVAQMLFLEAENPEK.D + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1834.3252, 1850.3451, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5068, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3424.4839, 3541.4392

18. [Q8ZR43|HHTHR_SALTY](#) Mass: 22017 Score: 18 Expect: 30 Matches: 3

Transcriptional regulator RamR OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ramR PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
606.4691	605.4618	605.3020	264	6	10	1	K.SEDKK.Q
634.4969	633.4896	633.3333	247	77	82	0	R.SITDAK.M
3541.4392	3540.4319	3539.9059	149	11	46	1	K.QALLEAATQIAQSGIAASTAVIARNAGVAEGTLFR.Y

No match to: 560.3074, 568.3801, 650.4960, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839

19. [P66643|RS9_SALTY](#) Mass: 14817 Score: 18 Expect: 31 Matches: 4

Small ribosomal subunit protein uS9 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rpsI PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
650.4960	649.4888	649.3548	206	101	106	0	K.AGFVTR.D
1786.3160	1785.3088	1784.9528	199	46	60	1	R.MVVRQPLELVDMEK.L
1807.3342	1806.3270	1805.8730	251	81	95	1	R.HGITRALMEYDESLR.G + Oxidation (M)
2262.4353	2261.4280	2261.2229	90.7	50	68	1	R.QPLELVDMEKLDLYITVK.G + Oxidation (M)

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1508.0737, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2579.5068, 2581.7935, 2598.6797, 2616.8638, 2663.8152, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2883.0608, 2899.0327, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3415.2065, 3424.4839, 3541.4392

20. [Q8ZK33|ARCA_SALTY](#) Mass: 45875 Score: 17 Expect: 35 Matches: 9

Arginine deiminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arcA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1508.0737	1507.0665	1506.8406	150	375	389	0	K.AGITVLPPIGDELGR.G
2235.6609	2234.6536	2234.0889	253	28	46	0	R.LTPSNCQELLFDDVLSVER.A
2280.4438	2279.4366	2279.0827	155	158	177	0	R.DTSCWIYNGVINSINMAKPAR.Q
2579.5068	2578.4996	2579.2373	-286.03	158	179	1	R.DTSCWIYNGVINSINMAKPARQ.R.E + Oxidation (M)
2663.8152	2662.8079	2662.4153	147	226	250	1	R.GAVLIGMSERTTPQGVFLAQLFK.H
2883.0608	2882.0535	2882.4208	-127.41	134	157	0	K.NMVDVTHDINDFIMKPLPNHLFTR.D + Oxidation (M)
2899.0327	2898.0254	2898.4157	-134.64	134	157	0	K.NMVDVTHDINDFIMKPLPNHLFTR.D + 2 Oxidation (M)
3415.2065	3414.1993	3413.7116	143	343	371	1	R.EQWNDANNVLTLRPGVVGYERNIWTNEK.Y
3541.4392	3540.4319	3540.8060	-105.64	310	342	1	R.TQESTLVHALETALGIDQVRLITGGDAFEAER.E

No match to: 560.3074, 568.3801, 606.4691, 634.4969, 663.5013, 684.4216, 698.5597, 741.4453, 804.5068, 842.7554, 1052.0278, 1252.9999, 1264.9937, 1272.9283, 1278.0363, 1282.9873, 1297.8931, 1371.9962, 1396.1125, 1485.1072, 1492.0540, 1514.1390, 1605.1729, 1641.2290, 1679.2188, 1689.2509, 1716.1390, 1718.1329, 1786.3160, 1794.5973, 1807.3342, 1834.3252, 1850.3451, 1875.3273, 1877.3440, 1923.3407, 1939.3589, 1966.3507, 1977.3616, 1995.3813, 2003.5532, 2043.3737, 2059.3972, 2086.4060, 2150.5496, 2204.4160, 2235.6609, 2262.4353, 2280.4438, 2293.4514, 2310.4243, 2338.4863, 2352.4702, 2369.4521, 2372.5693, 2389.6150, 2398.4651, 2446.6294, 2472.5049, 2478.6218, 2489.5005, 2581.7935, 2598.6797, 2616.8638, 2670.8091, 2698.5469, 2725.8398, 2748.4651, 2806.9824, 2825.9910, 2842.0085, 2931.9609, 3006.1333, 3102.1394, 3117.0977, 3130.0725, 3148.1089, 3174.1228, 3190.1462, 3206.1235, 3290.4988, 3326.1658, 3332.2830, 3369.3054, 3409.5366, 3424.4839

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 300 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 94
 Selected for scoring : 40

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: P40131|FLGA_SALTY

Flagella basal body P-ring formation protein FlgA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgA PE=1 SV=1

Database: Salmonella_Typhi_LT2
 Score: 46
 Expect: 0.042
 Nominal mass (M_r): 23655
 Calculated pI: 10.39

Sequence similarity is available as [an NCBI BLAST search of P40131|FLGA_SALTY against nr.](#)

Search parameters

MS data file: peaklist_9.xml
 Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
 Fixed modifications: **Carbamidomethyl (C)**
 Variable modifications: **Oxidation (M)**
 Mass values searched: 100
 Mass values matched: 11

Protein sequence coverage: 68%

Matched peptides shown in **bold red**.

1 MQTLK**RGFAV AALLFSPLTM AQDINAQLTT WFSQRLAGFS DEVVVTLRSS**
 51 **PNLLPSCEQP AFSMTGSAKL WGNVNVVARC ANEKRYLQVN VQATGNYVAV**
 101 **AAP⁺IARGGKL TPANVTLKRG RLDQLPPRTV LDIRQIQDAV SLRDLAPGQP**
 151 **VQLTMIRQAW RVKAGQRVQV IANGEGFSVN AEGQAMNNA VAQNARVRMT**
 201 **SGQIVSGTVD SDGNILINL**

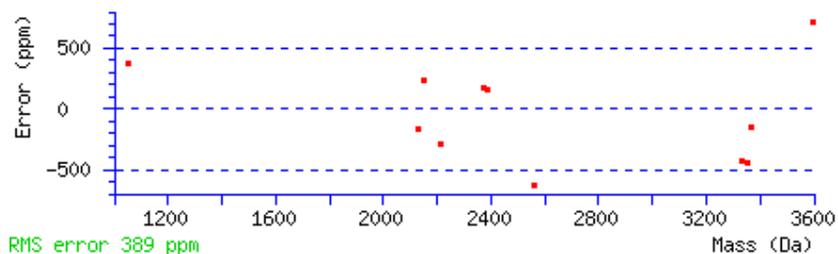
Unformatted sequence string: **219 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
6 - 35	3352.2449	3351.2376	3352.7390	-448	1	K.RGFAVAALLFSPLTMAQDINAQLTTWFSQR.L
6 - 35	3369.2581	3368.2508	3368.7340	-143	1	K.RGFAVAALLFSPLTMAQDINAQLTTWFSQR.L + Oxidation (M)
36 - 69	3598.3555	3597.3482	3594.7698	717	1	R.LAGFSDEVVVTLRSPNLLPSCEQPAFSMTGSAK.L
49 - 79	3332.2227	3331.2154	3332.6282	-424	1	R.SSPNLLPSCEQPAFSMTGSAKLWGNVNVVAR.C + Oxidation (M)
85 - 106	2374.7117	2373.7044	2373.2917	174	1	K.RYLQVNVQATGNYVAVAAP⁺IAR.G
86 - 106	2217.5588	2216.5516	2217.1906	-288	0	R.YLQVNVQATGNYVAVAAP⁺IAR.G
120 - 128	1051.9971	1050.9898	1050.5934	377	1	R.GRLDQLPPR.T
135 - 157	2563.7852	2562.7779	2564.3745	-623	1	R.QIQDAVSLRDLAPGQPVQLTMIR.Q + Oxidation (M)
197 - 219	2389.6138	2388.6065	2388.2319	157	1	R.VRMTSGQIVSGTVDSDGNILINL.-
199 - 219	2133.7046	2132.6973	2133.0624	-171	0	R.MTSGQIVSGTVDSDGNILINL.-
199 - 219	2150.5637	2149.5564	2149.0573	232	0	R.MTSGQIVSGTVDSDGNILINL.- + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2399.5691, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3750.4011



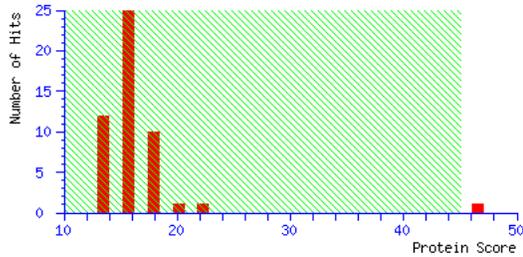
Mascot: <http://www.matrixscience.com/>

MASCOT SEARCH RESULTS

User : MR Labs
 Email : mr1labs7389@gmail.com
 Search title : Sample_9
 MS data file : peaklist_9.xml
 Database : Salmonella_Typhi_LT2 Typhi_LT2_20240715 (1873 sequences; 608672 residues)
 Timestamp : 30 Jul 2024 at 06:53:57 GMT
 Top Score : 46 for [P40131|FLGA_SALTY](#), Flagella basal body P-ring formation protein FlgA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 45 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Preferred taxonomy

Index

Accession	Mass	Score	Description
1. P40131 FLGA_SALTY	23655	46	Flagella basal body P-ring formation protein FlgA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgA PE=1 SV=1
2. Q8ZRK5 CAID_SALTY	28145	21	Carnitiny-CoA dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=caid PE=3 SV=
3. P64162 FTSB_SALTY	11568	20	Cell division protein FtsB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ftsB PE=3 SV=
4. Q8ZKP3 GLPK_SALTY	56313	19	Glycerol kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=glpK PE=3 SV=3
5. P26319 FIMZ_SALTY	23532	18	Fimbriae Z protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimZ PE=3 SV=1
6. P58533 DTD_SALTY	16029	18	D-aminoacyl-tRNA deacylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=dtl PE=3 SV=1
7. D0ZX01 OMP_D_SALTY	39655	18	Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompD PE=1 SV=1
8. P37592 OMP_D_SALTY	39655	18	Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompD PE=1 SV=1
9. Q8ZRU7 MURE_SALTY	53538	17	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=murG PE=1 SV=1
10. Q8ZRN9 LPXB_SALTY	42823	17	Lipid-A-disaccharide synthase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lpxB PE=3 SV=1
11. Q8ZPU9 ASTB_SALTY	49389	17	N-succinylarginine dihydrolase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=astB PE=2 SV=1
12. P05989 ILVC_SALTY	54249	17	Ketol-acid reductoisomerase (NADP(+)) OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ilvC PE=1 SV=1
13. Q7COK5 YDGT_SALTY	8375	17	Transcription modulator YdgT OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ydgT PE=1 SV=1
14. Q7CPQ7 GATY_SALTY	31131	17	D-tagatose-1,6-bisphosphate aldolase subunit GatY OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=gatY PE=1 SV=1
15. P03062 RAVA_SALTY	56896	17	ATPase Rava OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rava PE=3 SV=1
16. P67286 YBJQ_SALTY	11487	17	UPF0145 protein YbjQ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ybjQ PE=3 SV=1
17. D0ZNR9 SCTC2_SALTY	54193	16	SPI-2 type 3 secretion system secretin OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sctC2 PE=2 SV=1
18. P03062 LPL_SALTY	3101	16	leu operon leader peptide OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=leuL PE=4 SV=1
19. Q8ZK33 ARCA_SALTY	45875	16	Arginine deiminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arcA PE=3 SV=1
20. Q7CR64 YAEH_SALTY	15142	16	UPF0325 protein YaeH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yaeH PE=3 SV=1

Results List

1. [P40131|FLGA_SALTY](#) Mass: 23655 Score: 46 Expect: 0.042 Matches: 11
 Flagella basal body P-ring formation protein FlgA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgA PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1051.9971	1050.9898	1050.5934	377	120	128	1	R.GRLDQLPPR.T
2133.7046	2132.6973	2133.0624	-171.14	199	219	0	R.MTSGQIVSGTVSDGNILINL.-
2150.5637	2149.5564	2149.0573	232	199	219	0	R.MTSGQIVSGTVSDGNILINL.- + Oxidation (M)
2217.5588	2216.5516	2217.1906	-288.21	86	106	0	R.YLQVNVQATGNYVAVAAPIAR.G
2374.7117	2373.7044	2373.2917	174	85	106	1	K.RYLQVNVQATGNYVAVAAPIAR.G
2389.6138	2388.6065	2388.2319	157	197	219	1	R.VRMTSGQIVSGTVSDGNILINL.-
2563.7852	2562.7779	2564.3745	-622.60	135	157	1	R.QIQDAVSLRDLAPGQVQLTMIR.Q + Oxidation (M)
3332.2227	3331.2154	3332.6282	-423.93	49	79	1	R.SSPNLLPSCSQPAFMSMTGSAKLWGNVNVVAR.C + Oxidation (M)
3352.2449	3351.2376	3352.7390	-447.83	6	35	1	K.RGFAVAALLFSPLTMAQDINAQLTTFWFSQR.L
3369.2581	3368.2508	3368.7340	-143.43	6	35	1	K.RGFAVAALLFSPLTMAQDINAQLTTFWFSQR.L + Oxidation (M)
3598.3555	3597.3482	3594.7698	717	36	69	1	R.LAGFSDVSVVTLRSPNLLPSCSQPAFMSMTGSAK.L

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2399.5691, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3750.4011

2. [Q8ZRK5|CAID_SALTY](#) Mass: 28145 Score: 21 Expect: 14 Matches: 8
Carnitiny-CoA dehydratase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=caid PE=3 SV=3
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide | |
|-----------|-----------|-----------|---------|-------|-----|------|---------|--|
| 1335.2451 | 1334.2378 | 1334.6500 | -308.81 | 179 | - | 190 | 0 | R.VVVSQSELMESAR.E |
| 1640.2776 | 1639.2703 | 1639.8790 | -371.15 | 149 | - | 163 | 0 | K.LLPPAIVNEMVMTGR.R |
| 1994.4568 | 1993.4495 | 1994.1057 | -329.04 | 146 | - | 163 | 1 | R.LPKLLPPAIVNEMVMTGR.R + Oxidation (M) |
| 2150.5637 | 2149.5564 | 2148.1902 | 636 | 10 | - | 29 | 1 | R.NGPILITLDRPKANAIDAK.T |
| 2173.5159 | 2172.5086 | 2173.0626 | -254.94 | 23 | - | 42 | 1 | K.ANAIDAKTSFAMGEAFLNFR.D |
| 2189.5266 | 2188.5193 | 2189.0575 | -245.85 | 23 | - | 42 | 1 | K.ANAIDAKTSFAMGEAFLNFR.D + Oxidation (M) |
| 2217.5588 | 2216.5516 | 2215.0368 | 684 | 30 | - | 48 | 1 | K.TSFAMGEAFLNFRDPELR.V |
| 2389.6138 | 2388.6065 | 2388.3125 | 123 | 2 | - | 22 | 1 | M.SESHLTRNGPILITLDRPK.A |
- No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2153.5410, 2184.6348, 2200.5488, 2211.6138, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011
3. [P64162|FTSB_SALTY](#) Mass: 11568 Score: 20 Expect: 17 Matches: 5
Cell division protein FtsB OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ftsB PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide | |
|-----------|-----------|-----------|---------|-------|-----|------|---------|---|
| 2374.7117 | 2373.7044 | 2373.0877 | -582.41 | 50 | - | 70 | 0 | R.NDQLFAEIDDLNGGQEAIEER.A |
| 2389.6138 | 2388.6065 | 2389.4177 | -339.51 | 4 | - | 23 | 0 | K.LTLLLLALLVWLQYSLWFGK.N |
| 2399.5691 | 2398.5618 | 2398.1838 | 158 | 73 | - | 93 | 1 | R.NELSMTPKGETFYRLVPDASK.R + Oxidation (M) |
| 2705.7573 | 2704.7500 | 2705.5746 | -304.77 | 1 | - | 23 | 1 | -.MGKLTLLLLALLVWLQYSLWFGK.N |
| 3332.2227 | 3331.2154 | 3331.8485 | -190.02 | 4 | - | 31 | 1 | K.LTLLLLALLVWLQYSLWFGKNGIHDYSR.V |
- No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011
4. [Q8ZKP3|GLPK_SALTY](#) Mass: 56313 Score: 19 Expect: 25 Matches: 13
Glycerol kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=glpK PE=3 SV=3
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide | |
|-----------|-----------|-----------|---------|-------|-----|------|---------|--|
| 768.7584 | 767.7511 | 767.3966 | 462 | 484 | - | 489 | 1 | R.YSGWKK.A |
| 1335.2451 | 1334.2378 | 1333.6626 | 431 | 470 | - | 480 | 0 | R.EFRPGIETTER.N |
| 1835.4911 | 1834.4838 | 1834.8744 | -212.89 | 174 | - | 189 | 1 | K.MTQGRVHVDTYTNASR.T |
| 1839.3707 | 1838.3635 | 1838.7637 | -217.70 | 264 | - | 279 | 0 | K.NTYGTGCFMLMNTGEK.A + Oxidation (M) |
| 1994.4568 | 1993.4495 | 1994.0367 | -294.48 | 391 | - | 408 | 1 | R.DVLEAMQADSGIRLHALR.V |
| 2109.4949 | 2108.4876 | 2108.9612 | -224.57 | 319 | - | 336 | 1 | R.DEMKLSIDAFDSEYFATK.V |
| 2125.4988 | 2124.4915 | 2124.9561 | -218.65 | 319 | - | 336 | 1 | R.DEMKLSIDAFDSEYFATK.V + Oxidation (M) |
| 2153.5410 | 2152.5337 | 2152.9592 | -197.59 | 264 | - | 282 | 1 | K.NTYGTGCFMLMNTGEKAVK.S + 2 Oxidation (M) |
| 2340.6150 | 2339.6077 | 2339.0054 | 257 | 259 | - | 279 | 1 | K.EGMAKNYGTGCFMLMNTGEK.A |
| 2389.6138 | 2388.6065 | 2386.9902 | 677 | 259 | - | 279 | 1 | K.EGMAKNYGTGCFMLMNTGEK.A + 3 Oxidation (M) |
| 2638.8320 | 2637.8248 | 2637.3068 | 196 | 380 | - | 403 | 1 | R.ATLESIAAYQTRDVLEAMQADSGIR.L |
| 2815.8660 | 2814.8587 | 2814.3721 | 173 | 190 | - | 212 | 1 | R.TMLFNHIDLDDDKMLDLVDIPR.A |
| 3006.1233 | 3005.1160 | 3005.3978 | -93.75 | 179 | - | 203 | 1 | R.VHVDTYTNASRTMLFNHIDLDDDKM |
- No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011
5. [P26319|FIMZ_SALTY](#) Mass: 23532 Score: 18 Expect: 30 Matches: 8
Fimbriae Z protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimZ PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide | |
|-----------|-----------|-----------|---------|-------|-----|------|---------|--|
| 1588.2262 | 1587.2189 | 1587.8216 | -379.59 | 26 | - | 39 | 1 | K.NSNIQVVLKTDSSR.T |
| 1835.4911 | 1834.4838 | 1834.9797 | -270.25 | 1 | - | 16 | 0 | -.MKPASVIIMDEHPVIR.M |
| 2150.5637 | 2149.5564 | 2149.1783 | 176 | 192 | - | 210 | 1 | K.LGLHSIVELIDYAKSHELL.- |
| 2235.6978 | 2234.6905 | 2235.1568 | -208.65 | 160 | - | 179 | 1 | R.YLANGMSKEIAEQLLSNK.T |
| 2691.8560 | 2690.8487 | 2690.4863 | 135 | 2 | - | 25 | 1 | M.KPASVIIMDEHPVIRMSIEVLLGK.N + Oxidation (M) |
| 2705.7573 | 2704.7500 | 2706.4812 | -639.63 | 2 | - | 25 | 1 | M.KPASVIIMDEHPVIRMSIEVLLGK.N + 2 Oxidation (M) |
| 2806.9954 | 2805.9881 | 2805.5318 | 163 | 1 | - | 25 | 1 | -.MKPASVIIMDEHPVIRMSIEVLLGK.N |
| 3572.3103 | 3571.3030 | 3568.7548 | 714 | 109 | - | 139 | 1 | K.DLNDIYNAVKKMILSGSYFFPSETLNFISNTR.T |
- No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011
6. [P58533|DTD_SALTY](#) Mass: 16029 Score: 18 Expect: 30 Matches: 5
D-aminoacyl-tRNA deacylase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ddd PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide | |
|-----------|-----------|-----------|-----|-------|-----|------|---------|-------------------|
| 1166.0479 | 1165.0406 | 1164.6073 | 372 | 45 | - | 53 | 1 | R.LCERVLGYR.I |
| 1441.1334 | 1440.1261 | 1439.7409 | 268 | 49 | - | 61 | 1 | R.VLGYRIFSDADGK.M |

2747.9395 2746.9322 2747.3912 -167.09 62 - 87 0 K.MNLNVQQAGGSVLLVVSQFTLAADTER.G
 2789.8696 2788.8624 2790.3184 -521.81 88 - 112 1 R.GMRPFSFGGAAPDRAQALYEFYVER.C + Oxidation (M)
 3598.3555 3597.3482 3596.7781 159 54 - 87 1 R.IFSDADGKMNLNVQQAGGSVLLVVSQFTLAADTER.G + Oxidation (M)
No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8516, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3750.4011

7. [D0ZXQ1|OMPD_SALT1](#) Mass: 39655 Score: 18 Expect: 33 Matches: 10

Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=ompD PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.7885	867.7812	867.4450	388	149	156	0	R.TTGVATYR.N
1297.9083	1296.9010	1296.5411	278	105	115	0	K.FADYGSFYDGR.N
1640.2776	1639.2703	1638.8253	272	348	362	0	K.VSTDNIVAVGLNYQF.-
2217.5588	2216.5516	2218.0695	-684.35	157	176	0	R.NTDFFLVEGLNFAAQYQGK.N
2220.6372	2219.6299	2218.0695	704	157	176	0	R.NTDFFLVEGLNFAAQYQGK.N
2389.6138	2388.6065	2389.0863	-200.81	63	82	0	K.GETQINDQLTGFQWMEYEFK.G
2581.8191	2580.8118	2580.1517	256	32	54	1	K.LDLYGKVAHQHYFSDDDNGSDGDK.T
2806.9954	2805.9881	2805.4126	205	273	296	0	K.TQNFVAQAQYQDFGLRPSIAYLK.S
3070.1433	3069.1360	3067.5040	532	149	176	1	R.TTGVATYRNTDFFLVEGLNFAAQYQGK.N
3425.3232	3424.3160	3423.4804	244	180	212	1	R.DGAYESNGDGFGLSATYEGFVGVAAYAKSDR.T

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2399.5691, 2563.7852, 2597.7852, 2610.7830, 2616.8516, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

8. [P37592|OMPD_SALTY](#) Mass: 39655 Score: 18 Expect: 33 Matches: 10

Outer membrane porin protein OmpD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ompD PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.7885	867.7812	867.4450	388	149	156	0	R.TTGVATYR.N
1297.9083	1296.9010	1296.5411	278	105	115	0	K.FADYGSFYDGR.N
1640.2776	1639.2703	1638.8253	272	348	362	0	K.VSTDNIVAVGLNYQF.-
2217.5588	2216.5516	2218.0695	-684.35	157	176	0	R.NTDFFLVEGLNFAAQYQGK.N
2220.6372	2219.6299	2218.0695	704	157	176	0	R.NTDFFLVEGLNFAAQYQGK.N
2389.6138	2388.6065	2389.0863	-200.81	63	82	0	K.GETQINDQLTGFQWMEYEFK.G
2581.8191	2580.8118	2580.1517	256	32	54	1	K.LDLYGKVAHQHYFSDDDNGSDGDK.T
2806.9954	2805.9881	2805.4126	205	273	296	0	K.TQNFVAQAQYQDFGLRPSIAYLK.S
3070.1433	3069.1360	3067.5040	532	149	176	1	R.TTGVATYRNTDFFLVEGLNFAAQYQGK.N
3425.3232	3424.3160	3423.4804	244	180	212	1	R.DGAYESNGDGFGLSATYEGFVGVAAYAKSDR.T

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2399.5691, 2563.7852, 2597.7852, 2610.7830, 2616.8516, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

9. [Q8ZRZU|MURE_SALTY](#) Mass: 53538 Score: 17 Expect: 34 Matches: 15

UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=mu

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
768.7584	767.7511	767.3450	529	479	484	0	R.LDYSDR.V
1588.2262	1587.2189	1586.7801	277	276	289	1	K.AEAVEYHDRGATIR.F
1835.4911	1834.4838	1833.9077	314	440	456	1	R.VMEGRAEAVTNAIMQAK.D + Oxidation (M)
1994.4568	1993.4495	1992.9476	252	94	110	1	R.LSALAGRIFYHEPSENMR.L + Oxidation (M)
2150.5637	2149.5564	2150.9981	-670.23	467	484	1	K.GHEDYQIVGTQRLDYSDR.V
2153.5410	2152.5337	2150.9981	714	467	484	1	K.GHEDYQIVGTQRLDYSDR.V
2340.6150	2339.6077	2341.2246	-690.61	423	444	1	R.AIINDILAGMLDAGQVRVMEGR.A
2374.7117	2373.7044	2373.2144	206	423	444	1	R.AIINDILAGMLDAGQVRVMEGR.A + 2 Oxidation (M)
2399.5691	2398.5618	2397.2322	555	418	439	1	R.TEEPRAIINDILAGMLDAGQVR.V + Oxidation (M)
2691.8560	2690.8487	2691.2724	-157.46	226	248	1	K.WMLYSTHHGQAIIVNADDEVGRR.W
2709.8667	2708.8594	2707.2674	588	226	248	1	K.WMLYSTHHGQAIIVNADDEVGRR.W + Oxidation (M)
2841.9858	2840.9786	2842.3555	-484.45	69	93	1	K.DEASDGEIREMHGVPVYVLSQLNER.L
3458.2544	3457.2471	3456.9782	77.8	303	335	1	R.LMGAFNVSNLLALATLALLGYPLDLLKTAAR.L
3525.3823	3524.3750	3524.7796	-114.78	336	367	1	R.LQPVCGRMEVFTAPGKPTVVVYDAHTPDALK.E.A
3541.3293	3540.3221	3540.7745	-127.79	336	367	1	R.LQPVCGRMEVFTAPGKPTVVVYDAHTPDALK.E.A + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2399.5691, 2563.7852, 2597.7852, 2610.7830, 2616.8516, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

10. [Q8ZRZU|MURE_SALTY](#) Mass: 42823 Score: 17 Expect: 35 Matches: 10

Lipid-A-disaccharide synthase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=lpxB PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1441.1334	1440.1261	1439.7748	244	295	305	1	R.MKPFTFWLAKR.L + Oxidation (M)
1839.3707	1838.3635	1839.0254	-359.96	221	236	1	R.QRYPDLEVVPLVNAK.R

2035.4794	2034.4721	2034.0932	186	244	- 262	1	K.IKAEVADPLAVHLLDGMAR.E + Oxidation (M)
2109.4949	2108.4876	2107.0983	659	202	- 220	1	R.GAEVEMLSADFLKTAQLLR.Q + Oxidation (M)
2563.7852	2562.7779	2562.4493	128	2	- 27	0	M.AAQRPLTIALVAGETSGDILGAGLIR.A
2705.7573	2704.7500	2705.4309	-251.66	326	- 349	1	K.ELLQEECEPQKLAELPLLANGK.T
2709.8667	2708.8594	2709.4847	-230.78	1	- 27	0	-.MAAQRPLTIALVAGETSGDILGAGLIR.A + Oxidation (M)
3006.1233	3005.1160	3005.7059	-196.26	1	- 30	1	-.MAAQRPLTIALVAGETSGDILGAGLIRALK.A
3369.2581	3368.2508	3369.6263	-408.21	263	- 294	1	R.EAMIASDAALLASGTAALCEMLAKCPMVVGYR.M
3384.2881	3383.2808	3385.6212	-691.27	263	- 294	1	R.EAMIASDAALLASGTAALCEMLAKCPMVVGYR.M + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2061.4875, 2069.7756, 2087.5403, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3409.3721, 3425.3232, 3458.2544, 3525.3242, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

11. [Q8ZPU9|ASTB_SALTY](#) Mass: 49389 Score: 17 Expect: 35 Matches: 12

N-succinylarginine dihydrolase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=astB PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1223.0487	1222.0414	1221.6830	293	125	- 135	0	K.VHLTVANLNK.F
1282.9894	1281.9821	1281.7292	197	139	- 150	0	R.ALEAPVTEALLR.A
1335.2451	1334.2378	1334.5707	-249.42	355	- 367	0	R.ESMANGGGPACLR.L + Oxidation (M)
1588.2262	1587.2189	1587.7610	-341.38	355	- 369	1	R.ESMANGGGPACLR.L.R.V
2389.6138	2388.6065	2390.1511	-646.23	379	- 400	0	R.AVNPVAMNDALFTALNAWADR.Y
2563.7852	2562.7779	2562.2471	207	378	- 400	1	R.RAVNPVAMNDALFTALNAWADR.Y + Oxidation (M)
2581.8191	2580.8118	2582.4121	-619.70	51	- 74	0	K.ALADAGFPQAVIPHPERPFIPALR.Q
2747.9395	2746.9322	2748.3970	-532.99	422	- 447	1	R.EALDVLTRLLDLGSSVYFQQTGAADG.-
2841.9858	2840.9786	2841.5476	-200.25	49	- 74	1	K.MKALADAGFPQAVIPHPERPFIPALR.Q
3384.2881	3383.2808	3384.6912	-416.69	281	- 312	0	R.VDGFMAIEVPAGEVSVSDAVATYLFNSQLSR.N
3525.3823	3524.3750	3523.6804	197	1	- 32	1	-.MTAHEVNFVGLVGLTHHYAGLSFGNEASTRHR.F
3541.3293	3540.3221	3539.6753	183	1	- 32	1	-.MTAHEVNFVGLVGLTHHYAGLSFGNEASTRHR.F + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1297.9083, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2789.8696, 2806.9954, 2815.8660, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3409.3721, 3425.3232, 3458.2544, 3525.3242, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

12. [P05989|ILVC_SALTY](#) Mass: 54249 Score: 17 Expect: 36 Matches: 15

Ketol-acid reductoisomerase (NADP(+)) OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ilvC PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
568.3654	567.3581	567.2540	184	163	- 166	0	R.EEYK.R
842.7435	841.7362	841.3687	437	20	- 25	1	K.CRFMGR.D + Oxidation (M)
1335.2451	1334.2378	1334.7082	-352.39	203	- 215	0	R.AGVLESSFVAEVK.S
1372.0110	1371.0037	1371.6605	-478.82	1	- 11	0	-.MANYFNLTNLR.Q + Oxidation (M)
1640.2776	1639.2703	1638.8512	256	110	- 123	1	K.QHSDVVRVQPLMK.D + Oxidation (M)
2031.4807	2030.4734	2029.0561	699	39	- 57	1	K.KVVIVGCGAQLNQLNMR.D + Oxidation (M)
2069.7756	2068.7684	2070.0529	-620.56	349	- 366	1	K.IGEQEYFDKGVLMIAVVK.A
2087.5403	2086.5330	2086.0479	233	349	- 366	1	K.IGEQEYFDKGVLMIAVVK.A + Oxidation (M)
2563.7852	2562.7779	2563.2741	-193.58	168	- 192	0	R.GFGVPTLIAVHPENDPQEGMAIAK.A + Oxidation (M)
2698.9661	2697.9588	2699.1302	-433.99	303	- 326	1	K.HMDDIISGEFSSGMMADWANDDKK.L
2705.7573	2704.7500	2703.3803	507	167	- 192	1	K.RGFGVPTLIAVHPENDPQEGMAIAK.A
2733.9468	2732.9395	2731.1200	666	303	- 326	1	K.HMDDIISGEFSSGMMADWANDDKK.L + 2 Oxidation (M)
2747.9395	2746.9322	2747.1149	-66.53	303	- 326	1	K.HMDDIISGEFSSGMMADWANDDKK.L + 3 Oxidation (M)
3525.3823	3524.3750	3525.7576	-392.12	168	- 202	1	R.GFGVPTLIAVHPENDPQEGMAIAKAWAAATGGHR.A
3541.3293	3540.3221	3541.7525	-403.87	168	- 202	1	R.GFGVPTLIAVHPENDPQEGMAIAKAWAAATGGHR.A + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2035.4794, 2061.4875, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2709.8667, 2725.8169, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3242, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

13. [QZCQK5|YDGT_SALTY](#) Mass: 8375 Score: 17 Expect: 37 Matches: 4

Transcription modulator YdgT OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ydgT PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1282.9894	1281.9821	1281.7081	214	2	- 11	1	M.TVQDYLLKFR.K
1530.1479	1529.1407	1529.7991	-430.39	56	- 68	0	R.LFDVGVQVPSVWR.Y
3053.2410	3052.2337	3054.3964	-708.06	22	- 46	1	K.LFDHLYNTLTDMDIVNMYRAADHR.R + Oxidation (M)
3070.1433	3069.1360	3070.3913	-408.83	22	- 46	1	K.LFDHLYNTLTDMDIVNMYRAADHR.R + 2 Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3242, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

14. [QZCP07|GATY_SALTY](#) Mass: 31131 Score: 17 Expect: 40 Matches: 8

D-tagatose-1,6-bisphosphate aldolase subunit GatY OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=gatY PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2117.7065	2116.6993	2118.0456	-635.64	100	- 118	0	R.SVMIDGSHFPFEENVALVK.S
2133.7046	2132.6973	2134.0405	-629.41	100	- 118	0	R.SVMIDGSHFPFEENVALVK.S + Oxidation (M)

2173.5159 2172.5086 2172.0885 193 167 - 188 0 R.TGIDSLAVAIGTAHGMAYAAEPK.L
 2189.5266 2188.5193 2188.0834 199 167 - 188 0 R.TGIDSLAVAIGTAHGMAYAAEPK.L + Oxidation (M)
 2581.8191 2580.8118 2579.2603 602 127 - 150 1 R.YDTSVEALGLRGGIEDLLVWDSK.D
 2616.8618 2615.8545 2616.3031 -171.45 138 - 161 1 R.LGGIEDLLVWDSKDALYTNPQQAR.E
 2747.9395 2746.9322 2745.3982 559 94 - 118 1 K.VMAGIRSVMDIGSHFFFEENVALVK.S
 2789.8696 2788.8624 2790.4010 -551.42 162 - 188 1 R.EFVARTGIDSLAVAIGTAHGMAYAAEPK.L + Oxidation (M)
No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2125.4988, 2150.5637, 2153.5410, 2184.6348, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2597.7852, 2610.7830, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

15. [Q8ZK2|RAVA_SALTY](#) Mass: 56896 Score: 17 Expect: 40 Matches: 11

ATPase RavA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ravA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1372.0110	1371.0037	1370.7266	202	323	-	333	1 R.RLQLQQQQSDK.T
1530.1479	1529.1407	1529.8249	-447.23	1	-	13	1 -.MAHPHLLAERTSR.L
1643.1958	1642.1885	1641.8283	219	432	-	447	0 R.LALPGTAEDSMPAEIK.Q
2235.6978	2234.6905	2236.1667	-660.17	100	-	118	0 R.LTTGYLPEAEIVFLDEIWK.A
2374.7117	2373.7044	2375.1856	-623.61	149	-	170	0 R.LLVAASNELPEADSSLEALYDR.M
2725.8169	2724.8096	2723.4177	511	399	-	423	1 R.GKLNIGGFAQTLNMEVDNAQHLVVR.D
2789.8696	2788.8624	2789.5626	-251.01	26	-	52	1 R.SHAIRLCLLAALSSEVFLGPPGIK.S
3070.1433	3069.1360	3070.4917	-441.51	432	-	458	1 R.LALPGTAEDSMPAEIKQQLETLENDWR.Q + Oxidation (M)
3409.3721	3408.3648	3408.7572	-115.12	401	-	431	1 K.LNGIGFAQTLNMEVDNAQHLVVRDISLQGR.L
3425.3232	3424.3160	3424.7521	-127.36	401	-	431	1 K.LNGIGFAQTLNMEVDNAQHLVVRDISLQGR.L + Oxidation (M)
3598.3555	3597.3482	3597.7423	-109.54	464	-	493	1 R.FSEQQHCLFHSDWLGRIEASLDQVGEQIR.Q

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1441.1334, 1487.1772, 1578.1509, 1588.2262, 1640.2776, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2280.4924, 2332.6294, 2340.6150, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2733.9468, 2747.9395, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3750.4011

16. [P67286|YBJQ_SALTY](#) Mass: 11487 Score: 17 Expect: 40 Matches: 4

UPF0145 protein YbjQ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=ybjQ PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1051.9971	1050.9898	1051.5298	-513.53	47	-	55	1 R.SGAYEKELR.K
3369.2581	3368.2508	3367.6891	167	71	-	104	1 K.ALGADAVVIGIDIDYETVKGDSMLMVSVSATVAVK.T
3384.2881	3383.2808	3383.6841	-119.17	71	-	104	1 K.ALGADAVVIGIDIDYETVKGDSMLMVSVSATVAVK.T + Oxidation (M)
3458.2544	3457.2471	3456.7235	151	2	-	33	0 M.QFSTTPTLEGGQIVEYCGVVTGEAILGANIFR.D

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3409.3721, 3425.3232, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

17. [D0ZWR9|SCTC2_SALT1](#) Mass: 54193 Score: 16 Expect: 44 Matches: 11

SPI-2 type 3 secretion system secretin OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sctC2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1282.9894	1281.9821	1281.6816	234	172	-	183	0 K.DSAVSVSIYTLK.Y
1441.1334	1440.1261	1440.7613	-440.82	359	-	370	1 K.NITFYTKLQGEK.V
1487.1772	1486.1700	1486.8719	-472.07	371	-	384	1 K.VAKLESITGSLLR.V
1640.2776	1639.2703	1639.9621	-421.81	156	-	170	1 R.ISQLASVLDNALIKR.K
1643.1958	1642.1885	1641.9414	151	374	-	388	1 K.LESITGSLLRVTPR.L
2061.4875	2060.4803	2059.0983	671	258	-	274	1 K.LITLEDQRQQMIEISVK.I + Oxidation (M)
2616.8618	2615.8545	2617.2442	-530.98	214	-	239	0 K.TSVPSTSTNNGSPATQALPMFAADPR.Q
2789.8696	2788.8624	2789.3218	-164.71	172	-	195	1 K.DSAVSVSIYTLKYATAMDTQYQYR.D + Oxidation (M)
2841.9858	2840.9786	2839.5477	504	143	-	169	1 K.AVEVSGVSPCLTRISQLASVLDNALIKR.R
3006.1233	3005.1160	3005.4553	-112.89	300	-	328	1 K.KIAFTGLNDGGASGFSTVISDTSNFMVR.L
3598.3555	3597.3482	3597.8712	-145.38	266	-	299	1 R.QQMEISVKIIDVNDAGDINQLGIDWGTAVSLGGK.K + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2806.9954, 2815.8660, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

18. [P03062|LPL_SALTY](#) Mass: 3101 Score: 16 Expect: 45 Matches: 3

leu operon leader peptide OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=leuL PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
2069.7756	2068.7684	2068.2309	260	2	-	19	1 M.SHIVRFTGLLLLNAFIVR.G
2200.5488	2199.5416	2199.2714	123	1	-	19	1 -.MSHIVRFTGLLLLNAFIVR.G
2217.5588	2216.5516	2215.2663	580	1	-	19	1 -.MSHIVRFTGLLLLNAFIVR.G + Oxidation (M)

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2153.5410, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2374.7117, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

19. [Q8ZK33|ARCA_SALTY](#) Mass: 45875 Score: 16 Expect: 46 Matches: 14

Arginine deiminase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arca PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
868.7885	867.7812	867.5429	275	257	- 264	0	R.VIAVELPK.H
1051.9971	1050.9898	1051.4249	-413.82	396	- 403	0	R.CMSCPLER.D
1643.1958	1642.1885	1641.8726	192	118	- 133	0	R.HLSGGLTYGEIPASIK.N
1650.1978	1649.1905	1648.8825	187	236	- 250	0	R.TTPQGVFLAQALFK.H
2153.5410	2152.5337	2153.0840	-255.58	95	- 113	1	R.LGPTFAADIRAWLADMPHR.E + Oxidation (M)
2235.6978	2234.6905	2234.8889	269	28	- 46	0	R.LTPSNCQELLFDDVLSVER.A
2280.4924	2279.4852	2279.0827	177	158	- 177	0	R.DTSCWIYNGVSINPAKPAR.Q
2389.6138	2388.6065	2390.1900	-662.50	27	- 46	1	R.LTPSNCQELLFDDVLSVER.A
2563.7852	2562.7779	2563.2424	-181.21	158	- 179	1	R.DTSCWIYNGVSINPAKPAR.Q
2581.8191	2580.8118	2579.2373	610	158	- 179	1	R.DTSCWIYNGVSINPAKPAR.Q
2616.8618	2615.8545	2617.4275	-600.95	4	- 26	1	K.HFVGSEIGQLRSVMLHRPNLSLK.R
2663.8267	2662.8194	2662.4153	152	226	- 250	1	R.GAVLIGMSERTTPQGVFLAQALFK.H
2678.8311	2677.8238	2678.4102	-218.93	226	- 250	1	R.GAVLIGMSERTTPQGVFLAQALFK.H + Oxidation (M)
3541.3293	3540.3221	3540.8060	-136.67	310	- 342	1	R.TQESTLVHALETALGIDQVRLITGGDAFAER.E

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 882.8126, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1335.2451, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2332.6294, 2340.6150, 2374.7117, 2399.5691, 2597.7852, 2610.7830, 2638.8320, 2670.8516, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

20. [Q7CR64|YAEH_SALTY](#) Mass: 15142 Score: 16 Expect: 48 Matches: 4

UPF0325 protein YaeH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yaeH PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1335.2451	1334.2378	1334.7194	-360.81	55	- 67	1	R.KTVVADGIGQGYK.E
2109.4949	2108.4876	2109.0953	-288.14	106	- 124	1	R.HLESVVANKISEIEADLDK.L
2125.4988	2124.4915	2123.0204	693	1	- 18	1	-.MYDNKSLGITNPEIEDR.Y + Oxidation (M)
2374.7117	2373.7044	2372.2336	620	56	- 77	1	K.TVVADGIGQGYKEVQEISPNLR.Y

No match to: 568.3654, 568.7900, 596.8179, 768.7584, 842.7435, 868.7885, 882.8126, 1051.9971, 1152.0350, 1166.0479, 1223.0487, 1229.9471, 1278.0420, 1282.9894, 1297.9083, 1372.0110, 1441.1334, 1487.1772, 1530.1479, 1578.1509, 1588.2262, 1640.2776, 1643.1958, 1650.1978, 1707.2756, 1835.4911, 1839.3707, 1860.3849, 1874.4060, 1963.5680, 1994.4568, 2031.4807, 2035.4794, 2061.4875, 2069.7756, 2087.5403, 2109.4949, 2117.7065, 2125.4988, 2133.7046, 2150.5637, 2173.5159, 2184.6348, 2189.5266, 2200.5488, 2211.6138, 2217.5588, 2220.6372, 2235.6978, 2280.4924, 2332.6294, 2340.6150, 2389.6138, 2399.5691, 2563.7852, 2581.8191, 2597.7852, 2610.7830, 2616.8618, 2638.8320, 2663.8267, 2670.8516, 2678.8311, 2691.8560, 2698.9661, 2705.7573, 2709.8667, 2725.8169, 2733.9468, 2747.9395, 2789.8696, 2806.9954, 2815.8660, 2841.9858, 2933.9133, 2990.0242, 3006.1233, 3043.5889, 3053.2410, 3070.1433, 3117.0610, 3163.1846, 3290.3687, 3332.2227, 3352.2449, 3369.2581, 3384.2881, 3409.3721, 3425.3232, 3458.2544, 3525.3823, 3541.3293, 3557.3242, 3572.3103, 3578.3208, 3598.3555, 3750.4011

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 717.5 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 100
 Selected for scoring : 50

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: tr|A0A0F6AWA9|A0A0F6AWA9_SALT1

TraT complement resistance protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=traT PE=3 SV=1

Database: Salmonella_typhimurium_LT2
 Score: 68
 Expect: 0.0018
 Nominal mass (M_r): 26209
 Calculated pI: 8.99

Sequence similarity is available as [an NCBI BLAST search of tr|A0A0F6AWA9|A0A0F6AWA9_SALT1 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
 Fixed modifications: **Carbamidomethyl (C)**
 Variable modifications: **Oxidation (M)**
 Mass values searched: 13
 Mass values matched: 5

Protein sequence coverage: 19%

Matched peptides shown in **bold red**.

1 MKMKKIMMVT LVSSTLALSG CGAMSTAIKK RNLEVKTQMS QTIWLDPSS E
 51 RTVYLQVKNT SDKDMSDLQS LIAKDIQAKG YTVVTSPDKA YYWIQANVLK
 101 ADKMDLRESQ GWLNRGYEGA LSGAALGAGI TAYNSNSAGA TLGVGLAAGL
 151 VGMAADAMVE DINYTMITDV QISER**TKATV TTDNVAALRQ** GTSGAK**IQTS**
 201 **TETGNQHKYQ TRVVS**NANKV **NLKFEEAKPV LEEQLAKS**IA NIL

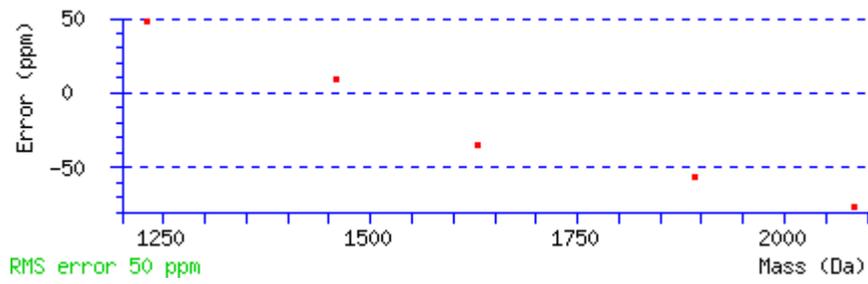
Unformatted sequence string: **243 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
176 - 189	1460.8198	1459.8125	1459.7995	8.96	1	R.TKATVTTDNVAALR.Q
178 - 189	1231.7230	1230.7157	1230.6568	47.9	0	K.ATVTTDNVAALR.Q
197 - 212	1891.8182	1890.8109	1890.9184	-56.8	1	K.IQTSTETGNQHKYQTR.V
220 - 237	2084.9996	2083.9923	2084.1517	-76.5	1	K.VNLKFEEAKPVLEEQLAK.S
224 - 237	1630.8118	1629.8045	1629.8613	-34.9	0	K.FEEAKPVLEEQLAK.S

No match to: 568.3147, 825.2004, 841.1862, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498



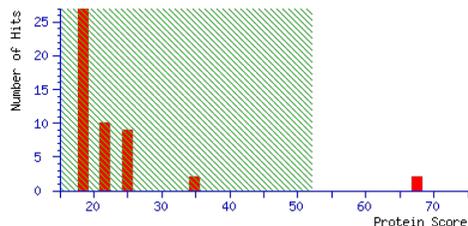
Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

User : raju
 Email : raju.r@fountomics.com
 Search title : Sample 4
 Database : Salmonella typhimurium LT2 typhimurium LT2_04012025 (9918 sequences; 2883936 residues)
 Timestamp : 4 Jan 2025 at 18:55:24 GMT
 Top Score : 68 for [tr|AOAOF6AWA9|AOAOF6AWA9_SALT1](#), TraT complement resistance protein OS=Salmonella typhimurium (strain 14028s / SGSC 2

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 52 are significant ($p < 0.05$).



Protein Summary Report

Format As [Help](#)
 Significance threshold $p <$ Max. number of hits
 Preferred taxonomy

Overview Table

Click on column header to jump to entry in results list.
 Move mouse over any indicator to highlight identical peptides.
 Click on an indicator to see details of individual match.
 Use check boxes to select sub-set of queries for new search.

Mouse over:

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<input checked="" type="checkbox"/> 568.3147 (1+)																				
<input checked="" type="checkbox"/> 825.2004 (1+)																				
<input checked="" type="checkbox"/> 841.1862 (1+)																				
<input checked="" type="checkbox"/> 1231.7230 (1+)																				
<input checked="" type="checkbox"/> 1460.8198 (1+)																				
<input checked="" type="checkbox"/> 1630.8118 (1+)																				
<input checked="" type="checkbox"/> 1640.7788 (1+)																				
<input checked="" type="checkbox"/> 1891.8182 (1+)																				
<input checked="" type="checkbox"/> 1904.8052 (1+)																				
<input checked="" type="checkbox"/> 1948.8261 (1+)																				
<input checked="" type="checkbox"/> 1982.0991 (1+)																				
<input checked="" type="checkbox"/> 2084.9996 (1+)																				
<input checked="" type="checkbox"/> 2797.2498 (1+)																				

Index

Accession	Mass	Score	Description
1. tr AOAOF6AWA9 AOAOF6AWA9_SALT1	26209	68	TraT complement resistance protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX
2. tr Q93GL9 Q93GL9_SALT1	26209	68	TraT complement resistance protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC
3. sp P40722 SOPD_SALT1	36460	34	Secreted effector protein SopD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 7007
4. tr AOAOF6B616 AOAOF6B616_SALT1	36460	34	Secreted effector protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 G
5. sp Q9ZF31 IF2_SALT1	97514	24	Translation initiation factor IF-2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC
6. tr AOAOF6B771 AOAOF6B771_SALT1	97514	24	Translation initiation factor IF-2 OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX
7. tr AOAOF6B6R0 AOAOF6B6R0_SALT1	32323	23	Putative glutathione S-transferase YghU OS=Salmonella typhimurium (strain 14028s / SGSC 226
8. tr Q8ZM21 Q8ZM21_SALT1	32323	23	Glutathione S-transferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) O
9. tr AOAOF6AZI6 AOAOF6AZI6_SALT1	26023	23	Bacteriophage virulence determinant OS=Salmonella typhimurium (strain 14028s / SGSC 2262) O
10. tr AOAOF6B537 AOAOF6B537_SALT1	25938	23	Type III secretion system effector protease GogA OS=Salmonella typhimurium (strain 14028s /
11. tr Q8ZMY7 Q8ZMY7_SALT1	25915	23	Gifsy-1 prophage protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX
12. sp P07800 CHEZ_SALT1	23905	23	Protein phosphatase CheZ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX
13. tr AOAOF6B2P8 AOAOF6B2P8_SALT1	23905	23	Protein phosphatase CheZ OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN
14. tr AOAOF6B805 AOAOF6B805_SALT1	19748	23	Glucokinase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=gntK PE=3
15. tr Q7CPK4 Q7CPK4_SALT1	19748	23	Glucokinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=g
16. tr AOAOF6AZJ3 AOAOF6AZJ3_SALT1	75538	23	ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain 14028s / S
17. tr Q8ZQ94 Q8ZQ94_SALT1	75538	23	ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain LT2 / SGSC
18. tr AOAOF6BA47 AOAOF6BA47_SALT1	37971	22	Putative cytoplasmic protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=58885
19. tr Q8ZKJ7 Q8ZKJ7_SALT1	37971	22	Cytoplasmic protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=9928
20. tr AOAOF6B7H8 AOAOF6B7H8_SALT1	32235	20	Ribosomal protein L11 methyltransferase OS=Salmonella typhimurium (strain 14028s / SGSC 226

Results List

1. [tr|A0A0F6AWA9|A0A0F6AWA9_SALT1](#) Mass: 26209 Score: 68 Expect: 0.0018 Matches: 5
TraT complement resistance protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=traT PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1231.7230	1230.7157	1230.6568	47.9	178	-	189	0	K.ATVITDVAALR.Q
1460.8198	1459.8125	1459.7995	8.96	176	-	189	1	R.TKATVTTDVAALR.Q
1630.8118	1629.8045	1629.8613	-34.86	224	-	237	0	K.FEEAKPVLEEQLAK.S
1891.8182	1890.8109	1890.9184	-56.84	197	-	212	1	K.IQTSTETGNQHKYQTR.V
2084.9996	2083.9923	2084.1517	-76.49	220	-	237	1	K.VNLKFEAKPVLEEQLAK.S

No match to: 568.3147, 825.2004, 841.1862, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498
2. [tr|Q93GL9|Q93GL9_SALTY](#) Mass: 26209 Score: 68 Expect: 0.0018 Matches: 5
TraT complement resistance protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=traT PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1231.7230	1230.7157	1230.6568	47.9	178	-	189	0	K.ATVITDVAALR.Q
1460.8198	1459.8125	1459.7995	8.96	176	-	189	1	R.TKATVTTDVAALR.Q
1630.8118	1629.8045	1629.8613	-34.86	224	-	237	0	K.FEEAKPVLEEQLAK.S
1891.8182	1890.8109	1890.9184	-56.84	197	-	212	1	K.IQTSTETGNQHKYQTR.V
2084.9996	2083.9923	2084.1517	-76.49	220	-	237	1	K.VNLKFEAKPVLEEQLAK.S

No match to: 568.3147, 825.2004, 841.1862, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498
3. [sp|P40722|SOPD_SALTY](#) Mass: 36460 Score: 34 Expect: 3.5 Matches: 3
Secreted effector protein SopD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=sopD PE=1 SV=2

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1891.8182	1890.8109	1890.9774	-88.06	87	-	102	0	R.LQHLACPAHQDLFTIK.M
1948.8261	1947.8188	1948.0088	-97.52	142	-	157	1	R.EERQLFLQICEVIGSK.M
2084.9996	2083.9923	2084.0724	-38.46	158	-	174	1	K.MTWHPELLQESISTLRK.E + Oxidation (M)

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1982.0991, 2797.2498
4. [tr|A0A0F6B616|A0A0F6B616_SALT1](#) Mass: 36460 Score: 34 Expect: 3.5 Matches: 3
Secreted effector protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sopD PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1891.8182	1890.8109	1890.9774	-88.06	87	-	102	0	R.LQHLACPAHQDLFTIK.M
1948.8261	1947.8188	1948.0088	-97.52	142	-	157	1	R.EERQLFLQICEVIGSK.M
2084.9996	2083.9923	2084.0724	-38.46	158	-	174	1	K.MTWHPELLQESISTLRK.E + Oxidation (M)

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1982.0991, 2797.2498
5. [sp|Q9ZF31|IF2_SALTY](#) Mass: 97514 Score: 24 Expect: 44 Matches: 4
Translation initiation factor IF-2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=infB PE=3 SV=2

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1460.8198	1459.8125	1459.7606	35.6	393	-	406	0	R.APVVVTIMGHVDHGK.T
1640.7788	1639.7715	1639.8141	-25.97	596	-	609	1	K.GDIVLCGFYGRV.R.A
1891.8182	1890.8109	1890.8564	-24.06	852	-	868	1	K.DDVNEVRNGMECGIGVK.N
2797.2498	2796.2426	2796.3786	-48.65	341	-	366	0	K.LGAMATINQVIDQETAQLVAEEMGHK.V

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1630.8118, 1904.8052, 1948.8261, 1982.0991, 2084.9996
6. [tr|A0A0F6B771|A0A0F6B771_SALT1](#) Mass: 97514 Score: 24 Expect: 44 Matches: 4
Translation initiation factor IF-2 OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=infB PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1460.8198	1459.8125	1459.7606	35.6	393	-	406	0	R.APVVVTIMGHVDHGK.T
1640.7788	1639.7715	1639.8141	-25.97	596	-	609	1	K.GDIVLCGFYGRV.R.A
1891.8182	1890.8109	1890.8564	-24.06	852	-	868	1	K.DDVNEVRNGMECGIGVK.N
2797.2498	2796.2426	2796.3786	-48.65	341	-	366	0	K.LGAMATINQVIDQETAQLVAEEMGHK.V

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1630.8118, 1904.8052, 1948.8261, 1982.0991, 2084.9996
7. [tr|A0A0F6B6R0|A0A0F6B6R0_SALT1](#) Mass: 32323 Score: 23 Expect: 45 Matches: 2
Putative glutathione S-transferase YghU OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yghU PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1982.0991	1981.0918	1980.9766	58.2	17	-	36	0	K.SGGGAFANINRPVSGPTHDK.T
2797.2498	2796.2426	2796.3732	-46.73	11	-	36	1	K.VWTWDKSGGGAFANINRPVSGPTHDK.T

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1891.8182, 1904.8052, 1948.8261, 2084.9996
8. [tr|Q8ZM21|Q8ZM21_SALTY](#) Mass: 32323 Score: 23 Expect: 45 Matches: 2
Glutathione S-transferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yghU PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1982.0991	1981.0918	1980.9766	58.2	17	-	36	0	K.SGGGAFANINRPVSGPTHDK.T
2797.2498	2796.2426	2796.3732	-46.73	11	-	36	1	K.VWTWDKSGGGAFANINRPVSGPTHDK.T

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1891.8182, 1904.8052, 1948.8261, 2084.9996
9. [tr|A0A0F6AZI6|A0A0F6AZI6_SALT1](#) Mass: 26023 Score: 23 Expect: 45 Matches: 2
Bacteriophage virulence determinant OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=gtgA PE=1 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1891.8182	1890.8109	1890.9224	-58.97	27	-	42	0	K.VFPDLPEHQDNPSQLR.L
2084.9996	2083.9923	2084.0538	-29.52	88	-	105	1	R.EVLSRILEDAYTQSGTFR.R

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498
10. [tr|A0A0F6B537|A0A0F6B537_SALT1](#) Mass: 25938 Score: 23 Expect: 45 Matches: 2
Type III secretion system effector protease Goga OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_3198 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1891.8182	1890.8109	1890.9224	-58.97	27	-	42	0	K.VFPDLPEHQDNPSQLR.L
2084.9996	2083.9923	2084.0538	-29.52	88	-	105	1	R.EVLSRILEDAYTQSGTFR.R

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498
11. [tr|Q8ZMY7|Q8ZMY7_SALTY](#) Mass: 25915 Score: 23 Expect: 45 Matches: 2
Gifsy-1 prophage protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM2614 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1891.8182	1890.8109	1890.9224	-58.97	27	-	42	0	K.VFPDLPEHQDNPSQLR.L
2084.9996	2083.9923	2084.0538	-29.52	88	-	105	1	R.EVLSRILEDAYTQSGTFR.R

No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2797.2498

12. [sp|P07800|CHEZ_SALTY](#) Mass: 23905 Score: 23 Expect: 45 Matches: 2
Protein phosphatase CheZ OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cheZ PE=1 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|----------------------------|
| 1630.8118 | 1629.8045 | 1629.7846 | 12.2 | 181 | - | 195 | 0 R.ENESLLNGPQVDTSK.A |
| 1948.8261 | 1947.8188 | 1947.9426 | -63.54 | 196 | - | 214 | 0 K.AGVVASQDQVDDLLDLSLGF.- |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1640.7788, 1891.8182, 1904.8052, 1982.0991, 2084.9996, 2797.2498
13. [tr|A0A0F6B2P8|A0A0F6B2P8_SALT1](#) Mass: 23905 Score: 23 Expect: 45 Matches: 2
Protein phosphatase CheZ OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=cheZ PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|----------------------------|
| 1630.8118 | 1629.8045 | 1629.7846 | 12.2 | 181 | - | 195 | 0 R.ENESLLNGPQVDTSK.A |
| 1948.8261 | 1947.8188 | 1947.9426 | -63.54 | 196 | - | 214 | 0 K.AGVVASQDQVDDLLDLSLGF.- |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1640.7788, 1891.8182, 1904.8052, 1982.0991, 2084.9996, 2797.2498
14. [tr|A0A0F6B805|A0A0F6B805_SALT1](#) Mass: 19748 Score: 23 Expect: 47 Matches: 2
Gluconokinase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=gntK PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-----|------|-----------------------|
| 1231.7230 | 1230.7157 | 1230.7370 | -17.24 | 82 | - | 92 | 1 K.ISLIVCSALKK.H |
| 1891.8182 | 1890.8109 | 1891.0203 | -110.73 | 96 | - | 111 | 1 R.DLLREGPNLSFIYLK.G |
- No match to: 568.3147, 825.2004, 841.1862, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2084.9996, 2797.2498
15. [tr|Q7CPK4|Q7CPK4_SALTY](#) Mass: 19748 Score: 23 Expect: 47 Matches: 2
Gluconokinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=gntK PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-----|------|-----------------------|
| 1231.7230 | 1230.7157 | 1230.7370 | -17.24 | 82 | - | 92 | 1 K.ISLIVCSALKK.H |
| 1891.8182 | 1890.8109 | 1891.0203 | -110.73 | 96 | - | 111 | 1 R.DLLREGPNLSFIYLK.G |
- No match to: 568.3147, 825.2004, 841.1862, 1460.8198, 1630.8118, 1640.7788, 1904.8052, 1948.8261, 1982.0991, 2084.9996, 2797.2498
16. [tr|A0A0F6AZJ3|A0A0F6AZJ3_SALT1](#) Mass: 75538 Score: 23 Expect: 53 Matches: 3
ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_1173 PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------------------------|
| 1460.8198 | 1459.8125 | 1459.6831 | 88.7 | 463 | - | 475 | 1 R.EGAEYKYVTTGDK.Q |
| 1630.8118 | 1629.8045 | 1629.7886 | 9.77 | 627 | - | 641 | 0 R.LDDASQSTFYLTAAK.G |
| 1948.8261 | 1947.8188 | 1947.9104 | -47.01 | 493 | - | 509 | 0 R.QAIINDMMMLTDVPMK.L |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1640.7788, 1891.8182, 1904.8052, 1982.0991, 2084.9996, 2797.2498
17. [tr|Q8ZQ94|Q8ZQ94_SALTY](#) Mass: 75538 Score: 23 Expect: 53 Matches: 3
ATP-dependent Clp protease proteolytic subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM1033 PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------------------------|
| 1460.8198 | 1459.8125 | 1459.6831 | 88.7 | 463 | - | 475 | 1 R.EGAEYKYVTTGDK.Q |
| 1630.8118 | 1629.8045 | 1629.7886 | 9.77 | 627 | - | 641 | 0 R.LDDASQSTFYLTAAK.G |
| 1948.8261 | 1947.8188 | 1947.9104 | -47.01 | 493 | - | 509 | 0 R.QAIINDMMMLTDVPMK.L |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1640.7788, 1891.8182, 1904.8052, 1982.0991, 2084.9996, 2797.2498
18. [tr|A0A0F6BA47|A0A0F6BA47_SALT1](#) Mass: 37971 Score: 22 Expect: 64 Matches: 4
Putative cytoplasmic protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_5059 PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|---------------------------------|
| 1640.7788 | 1639.7715 | 1639.8570 | -52.12 | 158 | - | 171 | 1 R.VTQYAEITDVAFLKR.L |
| 1904.8052 | 1903.7979 | 1903.9581 | -84.11 | 62 | - | 77 | 1 R.WVNEWYPGKGDTLALR.L |
| 2084.9996 | 2083.9923 | 2084.1001 | -51.74 | 96 | - | 116 | 0 K.IDISAPPSTVNIDGIATSVSK.A |
| 2797.2498 | 2796.2426 | 2796.4004 | -56.44 | 71 | - | 95 | 1 K.GDTLALRLGYQGEDLLDCGIYVIDK.I |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1891.8182, 1948.8261, 1982.0991
19. [tr|Q8ZKJ7|Q8ZKJ7_SALTY](#) Mass: 37971 Score: 22 Expect: 64 Matches: 4
Cytoplasmic protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM4208 PE=4 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|---------------------------------|
| 1640.7788 | 1639.7715 | 1639.8570 | -52.12 | 158 | - | 171 | 1 R.VTQYAEITDVAFLKR.L |
| 1904.8052 | 1903.7979 | 1903.9581 | -84.11 | 62 | - | 77 | 1 R.WVNEWYPGKGDTLALR.L |
| 2084.9996 | 2083.9923 | 2084.1001 | -51.74 | 96 | - | 116 | 0 K.IDISAPPSTVNIDGIATSVSK.A |
| 2797.2498 | 2796.2426 | 2796.4004 | -56.44 | 71 | - | 95 | 1 K.GDTLALRLGYQGEDLLDCGIYVIDK.I |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1460.8198, 1630.8118, 1891.8182, 1948.8261, 1982.0991
20. [tr|A0A0F6B7H8|A0A0F6B7H8_SALT1](#) Mass: 32235 Score: 20 Expect: 90 Matches: 2
Ribosomal protein L11 methyltransferase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=prmA PE=3 SV=1
- | Observed | Mr (expt) | Mr (calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|------|-------|-----|------|---------------------|
| 1460.8198 | 1459.8125 | 1459.6943 | 81.0 | 87 | - | 97 | 1 K.IEQLEDKDWER.E |
| 1948.8261 | 1947.8188 | 1947.8145 | 2.24 | 94 | - | 107 | 1 K.DWEREWMDNFHFM.R |
- No match to: 568.3147, 825.2004, 841.1862, 1231.7230, 1630.8118, 1640.7788, 1891.8182, 1904.8052, 1982.0991, 2084.9996, 2797.2498

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 120 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 13
 Selected for scoring : 10

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: sp|P26319|FIMZ_SALTY

Fimbriae Z protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimZ PE=3 SV=1

Database: Salmonella_typhimurium_LT2
Score: 64
Expect: 0.0044
Nominal mass (M_r): 23532
Calculated pI: 9.20

Sequence similarity is available as [an NCBI BLAST search of sp|P26319|FIMZ_SALTY against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 774
Mass values matched: 26

Protein sequence coverage: 80%

Matched peptides shown in **bold red**.

1 **MKPASVIIMD EHPIVRMSIE VLLGKNSNIQ VVLKTDDSR** AIEYLRTYPV
 51 **DLVILDIELP GTDGF⁺TLLKR IKSIQEHTRI LFLSSKSEAF YAGRAIRAGA**
 101 **NGFVSKRKDL NDIYNAVKMI LSGYSFFPSE TLNFISNTRT** PKGGHDMPL
 151 **SNREVTVLRY LANGMSNKEI AEQLLSNKT ISAHKANIFS** KLGLHSIVEL
 201 **IDYAKSHELL**

Unformatted sequence string: **210 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

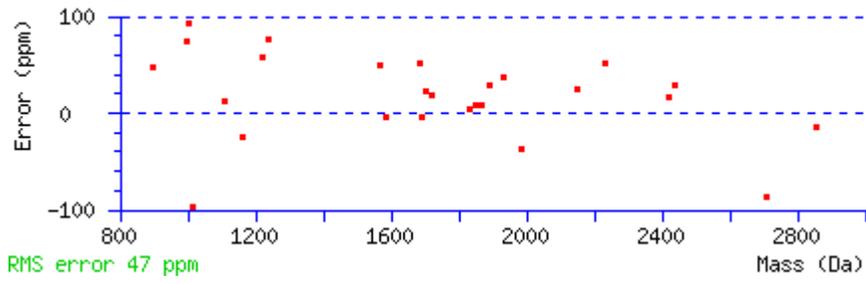
Show predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
1 - 16	1835.9939	1834.9866	1834.9797	3.74	0	-.MKPASVIIMDEHPIVR.M
1 - 16	1851.9967	1850.9894	1850.9746	8.00	0	-.MKPASVIIMDEHPIVR.M + Oxidation (M)
1 - 16	1867.9921	1866.9848	1866.9696	8.16	0	-.MKPASVIIMDEHPIVR.M + 2 Oxidation (M)
1 - 25	2854.4853	2853.4780	2853.5166	-13.5	1	-.MKPASVIIMDEHPIVRMSIEVLLGK.N + 3 Oxidation (M)
2 - 16	1704.9842	1703.9769	1703.9392	22.1	0	M.KPASVIIMDEHPIVR.M
2 - 16	1720.9735	1719.9662	1719.9342	18.7	0	M.KPASVIIMDEHPIVR.M + Oxidation (M)
2 - 25	2707.2569	2706.2496	2706.4812	-85.6	1	M.KPASVIIMDEHPIVRMSIEVLLGK.N + 2 Oxidation (M)
17 - 34	1985.0742	1984.0669	1984.1391	-36.3	1	R.MSIEVLLGKNSNIQVVLK.T

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
26 - 34	1014.4957	1013.4885	1013.5869	-97.1	0	K.NSNIQVVLK.T
26 - 39	1588.8224	1587.8151	1587.8216	-4.12	1	K.NSNIQVVLKTTDDSR.T
71 - 79	1111.6346	1110.6273	1110.6145	11.5	1	R.IKSIQEHTR.I
80 - 94	1688.9864	1687.9791	1687.8933	50.8	1	R.ILFLSSKSEAFYAGR.A
87 - 94	900.4641	899.4568	899.4137	47.9	0	K.SEAFYAGR.A
87 - 97	1240.7387	1239.7314	1239.6360	77.0	1	K.SEAFYAGRAIR.A
98 - 107	1006.6371	1005.6298	1005.5356	93.7	1	R.AGANGFVSKR.K
109 - 118	1164.5603	1163.5530	1163.5822	-25.1	0	K.DLNDIYNAVK.M
119 - 139	2424.2299	2423.2227	2423.1831	16.3	0	K.MILSGYSFFPSETLNFISNTR.T
119 - 139	2440.2555	2439.2482	2439.1780	28.8	0	K.MILSGYSFFPSETLNFISNTR.T + Oxidation (M)
143 - 153	1220.6298	1219.6225	1219.5516	58.1	0	K.GGHDMPLSNR.E
143 - 159	1934.0397	1933.0324	1932.9588	38.1	1	K.GGHDMPLSNREVTVLR.Y + Oxidation (M)
154 - 168	1694.8817	1693.8744	1693.8821	-4.55	1	R.EVTVLRYLANGMSNK.E
160 - 168	997.5510	996.5438	996.4698	74.2	0	R.YLANGMSNK.E
160 - 179	2236.2783	2235.2711	2235.1568	51.1	1	R.YLANGMSNKEIAEQLLLSNK.T
169 - 185	1895.1157	1894.1085	1894.0523	29.6	1	K.EIAEQLLLSNKTISAHK.A
192 - 205	1570.9610	1569.9537	1569.8766	49.1	0	K.LGLHSIVELIDYAK.S
192 - 210	2150.2402	2149.2330	2149.1783	25.4	1	K.LGLHSIVELIDYAKSHELL.-

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 1007.6064, 1008.4141, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417,

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3239.6938, 3370.3906, 3428.3914



Mascot: <http://www.matrixscience.com/>

1570.9610	1569.9537	1569.8766	49.1	192	-	205	0	K.LGLHSIVELIDYAK.S
1588.8224	1587.8151	1587.8216	-4.12	26	-	39	1	K.NSNIQVVLKTDSSR.T
1688.9864	1687.9791	1687.8933	50.8	80	-	94	1	R.LFLSSKSEAFYAGR.A
1694.8817	1693.8744	1693.8821	-4.55	154	-	168	1	R.EVTVLRLYLANGMSNK.E
1704.9842	1703.9769	1703.9392	22.1	2	-	16	0	M.KPASVIIMDEHPIVR.M
1720.9735	1719.9662	1719.9342	18.7	2	-	16	0	M.KPASVIIMDEHPIVR.M + Oxidation (M)
1835.9939	1834.9866	1834.9797	3.74	1	-	16	0	-.MKPASVIIMDEHPIVR.M
1851.9967	1850.9894	1850.9746	8.00	1	-	16	0	-.MKPASVIIMDEHPIVR.M + Oxidation (M)
1867.9921	1866.9848	1866.9696	8.16	1	-	16	0	-.MKPASVIIMDEHPIVR.M + 2 Oxidation (M)
1895.1157	1894.1085	1894.0523	29.6	169	-	185	1	K.EIAEQQLLSNKTISAHK.A
1934.0397	1933.0324	1932.9588	38.1	143	-	159	1	K.GGHHMPLSNREVTVLR.Y + Oxidation (M)
1985.0742	1984.0669	1984.1391	-36.35	17	-	34	1	R.MSIEVLLGKNSNIQVVLK.T
2150.2402	2149.2330	2149.1783	25.4	192	-	210	1	K.LGLHSIVELIDYAKSHELL.-
2236.2783	2235.2711	2235.1568	51.1	160	-	179	1	R.YLANGMSNKETAQQLLSNK.T
2424.2299	2423.2227	2423.1831	16.3	119	-	139	0	K.MILSGYSFFPSETLNFISNTR.T
2440.2555	2439.2482	2439.1780	28.8	119	-	139	0	K.MILSGYSFFPSETLNFISNTR.T + Oxidation (M)
2707.2569	2706.2496	2706.4812	-85.58	2	-	25	1	M.KPASVIIMDEHPIVRMSIEVLLGK.N + 2 Oxidation (M)
2854.4853	2853.4780	2853.5166	-13.53	1	-	25	1	-.MKPASVIIMDEHPIVRMSIEVLLGK.N + 3 Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 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3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6398, 3370.3906, 3428.3914								

2. [tr|A0A0F6AY36|A0A0F6AY36_SALT1](#) Mass: 23532 Score: 64 Expect: 0.0044 Matches: 26

Transcriptional regulator FimZ OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=fimZ PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
900.4641	899.4568	899.4137	47.9	87	-	94	0	K.SEAFYAGR.A
997.5510	996.5438	996.4698	74.2	160	-	168	0	R.YLANGMSNK.E
1006.6371	1005.6298	1005.5356	93.7	98	-	107	1	R.AGANGFVSKR.K
1014.4957	1013.4885	1013.5869	-97.15	26	-	34	0	K.NSNIQVVLK.T
1111.6346	1110.6273	1110.6145	11.5	71	-	79	1	R.IKSIQEHTR.I
1164.5603	1163.5530	1163.5822	-25.08	109	-	118	0	K.DLNDIYNAV.K
1220.6298	1219.6225	1219.5516	58.1	143	-	153	0	K.GGHHMPLSNR.E
1240.7387	1239.7314	1239.6360	77.0	87	-	97	1	K.SEAFYAGR.AIR.A
1570.9610	1569.9537	1569.8766	49.1	192	-	205	0	K.LGLHSIVELIDYAK.S
1588.8224	1587.8151	1587.8216	-4.12	26	-	39	1	K.NSNIQVVLKTDSSR.T
1688.9864	1687.9791	1687.8933	50.8	80	-	94	1	R.LFLSSKSEAFYAGR.A
1694.8817	1693.8744	1693.8821	-4.55	154	-	168	1	R.EVTVLRLYLANGMSNK.E
1704.9842	1703.9769	1703.9392	22.1	2	-	16	0	M.KPASVIIMDEHPIVR.M
1720.9735	1719.9662	1719.9342	18.7	2	-	16	0	M.KPASVIIMDEHPIVR.M + Oxidation (M)
1835.9939	1834.9866	1834.9797	3.74	1	-	16	0	-.MKPASVIIMDEHPIVR.M
1851.9967	1850.9894	1850.9746	8.00	1	-	16	0	-.MKPASVIIMDEHPIVR.M + Oxidation (M)

1867.9921	1866.9848	1866.9696	8.16	1	-	16	0	-	M.KPASVIIMDEHPVIR.M + 2 Oxidation (M)
1895.1157	1894.1085	1894.0523	29.6	169	-	185	1	K.EIAEQLLLSNKTISAHK.A	
1934.0397	1933.0324	1932.9588	38.1	143	-	159	1	K.GGHHMPLSNREVTVLR.Y + Oxidation (M)	
1985.0742	1984.0669	1984.1391	-36.35	17	-	34	1	R.MSIEVLLGKNSNIQVVLK.T	
2150.2402	2149.2330	2149.1783	25.4	192	-	210	1	K.LGLHSIVLEIDYAKSHELL.-	
2236.2783	2235.2711	2235.1568	51.1	160	-	179	1	R.YLANGMSNKEIAEQLLSNK.T	
2424.2299	2423.2227	2423.1831	16.3	119	-	139	0	K.MILSGYFFPSETLNFISNTR.T	
2440.2555	2439.2482	2439.1780	28.8	119	-	139	0	K.MILSGYFFPSETLNFISNTR.T + Oxidation (M)	
2707.2569	2706.2496	2706.4812	-85.58	2	-	25	1	M.KPASVIIMDEHPVIRMSIEVLLGK.N + 2 Oxidation (M)	
2854.4853	2853.4780	2853.5166	-13.53	1	-	25	1	-M.KPASVIIMDEHPVIRMSIEVLLGK.N + 3 Oxidation (M)	
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5599, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 1007.6064, 1008.4141, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 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1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9054, 1426.9024, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7834, 1430.8129, 1432.8150, 1434.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 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1788.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1836.5255, 1836.5255, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1842.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1899.9957, 1905.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2015.0906, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1930, 2200.1785, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2222.2371, 2234.1094, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2287.2528, 2294.7813, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2413.4904, 2429.3032, 2432.0943, 2432.0943, 2432.0943, 2433.8928, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117,									

3.

[sp|P63223|GMHA_SALTY](#) Mass: 21054 Score: 39 Expect: 1.3 Matches: 17
 Phosphoheptose isomerase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=gmhA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
608.3639	607.3566	607.2999	93.3	136	-	140	1	R.EKGMV.K + Oxidation (M)
731.4891	730.4818	730.4589	31.3	141	-	147	0	K.VITLTKG.D
829.4593	828.4521	828.4817	-35.79	130	-	137	1	K.AIAAAREK.G
880.5598	879.5525	879.5178	39.5	171	-	177	0	R.IQEIHK.V
1076.5905	1075.5832	1075.5332	46.5	152	-	161	0	K.MAGTADIEIR.V
1088.5680	1087.5608	1087.6237	-57.90	141	-	151	1	K.VITLTKGDKGK.M
1152.5762	1151.5689	1151.5683	0.49	23	-	32	0	K.DDANIHAIQR.A
1347.6516	1346.6443	1346.7558	-82.74	33	-	46	1	R.AAVLLADSPFKAGGK.V
1676.8532	1675.8460	1675.8417	2.57	8	-	22	0	R.NELNEAAETLANFLK.D
1821.9672	1820.9599	1821.0797	-65.82	178	-	192	1	K.VIHILQLIEKEMVK.- + Oxidation (M)
1859.9930	1858.9858	1858.9636	11.9	111	-	129	0	R.EGDVLLGISTSGNSGNVIK.A
2180.2331	2179.2258	2179.3456	-54.97	171	-	188	1	R.IQEIHKVIHILQLIEK.E
2413.4904	2412.4832	2412.2972	77.1	111	-	135	1	R.EGDVLLGISTSGNSGNVIKAIIAAR.E
2465.1886	2464.1813	2464.2597	-31.81	2	-	22	1	M.YQDLIRNELNEAAETLANFLK.D
2612.4159	2611.4086	2611.2951	43.5	1	-	22	1	-M.YQDLIRNELNEAAETLANFLK.D + Oxidation (M)
2810.4221	2809.4148	2809.3994	5.49	8	-	32	1	R.NELNEAAETLANFLKDDANIHAIQR.A
2824.4995	2823.4922	2823.2276	93.7	47	-	71	1	K.VLSCGNGSHCDAMFAEELTGRYR.E
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169,								

789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8474, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9917, 1819.9817, 1820.9674, 1822.9879, 1823.9744, 1824.9911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1851.9967, 1853.0172, 1854.0166, 1857.0792, 1858.9889, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0762, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1645, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0632, 2015.0906, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2020.9998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2287.2528, 2294.7843, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2424.2299, 2429.3032, 2432.0943, 2433.8928, 2440.2555, 2441.2124, 2442.1767, 2443.2146, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2577.4476, 2578.1790, 2593.3455, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2733.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2819.3966, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914

4.

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
608.3639	607.3566	607.2999	93.3	136	-	140	1 R.EKGMV.K + Oxidation (M)
731.4891	730.4818	730.4589	31.3	141	-	147	0 K.VITLTGK.D
829.4593	828.4521	828.4817	-35.79	130	-	137	1 K.AIAAAREK.G
880.5598	879.5525	879.5178	39.5	171	-	177	0 R.IQEIHK.V
1076.5905	1075.5832	1075.5332	46.5	152	-	161	0 K.MAGTADIEI.R.V
1088.5680	1087.5608	1087.6237	-57.90	141	-	151	1 K.VITLTGKGGK.M
1152.5762	1151.5689	1151.5683	0.49	23	-	32	0 K.DDANIHAIQ.R.A
1347.6516	1346.6443	1346.7558	-82.74	33	-	46	1 R.AAVLLADSPFKAGG.V
1676.8532	1675.8460	1675.8417	2.57	8	-	22	0 R.NELNEAAETLANFLK.D
1821.9672	1820.9599	1821.0797	-65.82	178	-	192	1 K.VIHILIQLEIKEMV.K + Oxidation (M)
1859.9930	1858.9858	1858.9636	11.9	111	-	129	0 R.EGDVLLGISTSGNSGVNIK.A
2180.2331	2179.2258	2179.3456	-54.97	171	-	188	1 R.IQEIHKVHILIQLEI.K.E
2413.4904	2412.4832	2412.2972	77.1	111	-	135	1 R.EGDVLLGISTSGNSGVNIKATAAAR.E
2465.1886	2464.1813	2464.2597	-31.81	2	-	22	1 M.YQDLIRNELNEAAETLANFLK.D
2612.4159	2611.4086	2611.2951	43.5	1	-	22	1 -.MYQDLIRNELNEAAETLANFLK.D + Oxidation (M)
2810.4221	2809.4148	2809.3994	5.49	8	-	32	1 R.NELNEAAETLANFLKDDANIHAIQ.R.A
2824.4995	2823.4922	2823.2276	93.7	47	-	71	1 K.VLSCGNGSHCDAMHFAEELTGRY.R
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 14							

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5. [sp|P0A1B5|AROF_SALTY](#) Mass: 38974 Score: 35 Expect: 2.9 Matches: 24

Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
609.3424	608.3351	608.3030	52.7	275	-	278	1 K.DYRR.R.Q
801.4429	800.4357	800.4140	27.0	4	-	10	0 K.DALNNVR.I
1014.4957	1013.4885	1013.5869	-97.15	42	-	51	0 R.GIISDIIAGR.D
1057.6003	1056.5931	1056.5676	24.1	2	-	10	1 M.QKDALNNVR.I
1382.8490	1381.8417	1381.7677	53.5	42	-	54	1 R.GIISDIIAGRDP.R.L
1491.7085	1490.7012	1490.7147	-9.07	188	-	202	0 K.NGTGSLATAINAMR.A
1507.8137	1506.8064	1506.7096	64.2	188	-	202	0 K.NGTGSLATAINAMR.A + Oxidation (M)
1549.8304	1548.8232	1548.6878	87.4	239	-	252	0 K.APNYSADVAQCEK.E
1610.8721	1609.8648	1609.8617	1.96	94	-	106	1 R.VYFEKPRITVGVK.G
1637.9067	1636.8994	1636.8494	30.5	79	-	93	0 K.ALAAEVSDSLVLV.MR.V
1801.1041	1800.0968	1799.9530	79.9	25	-	41	0 K.AAFPLSLAQEAQIAQSR.G
2015.0906	2014.0834	2013.9466	67.9	107	-	125	0 K.GLINDPHMDGSDVFEAGLK.I
2287.2528	2286.2455	2286.0661	78.5	322	-	341	0 K.YGVSVDACISWEMTDALLR.E
2326.2005	2325.1933	2325.0729	51.8	167	-	187	1 R.TTESQTHREMSGLSMPVGF.K.N + 2 Oxidation (M)
2371.2952	2370.2879	2370.1638	52.4	107	-	128	1 K.GLINDPHMDGSDVFEAGLK.IAR.Q + Oxidation (M)
2443.2146	2442.2074	2442.2424	-14.35	4	-	24	1 K.DALNNVRITDQVLMTEPQLK.A + Oxidation (M)
2556.2672	2555.2599	2555.2625	-1.01	55	-	76	1 R.LLVVCGPCSIHDPETALEYARR.F
2557.2535	2556.2463	2556.3410	-37.05	79	-	100	1 K.ALAAEVSDSLVLV.MRVYFEKPR.T
2703.3952	2702.3879	2702.3010	32.2	101	-	125	1 R.TTVGWKGLINDPHMDGSDVFEAGLK.I + Oxidation (M)
2703.4537	2702.4465	2702.3010	53.8	101	-	125	1 R.TTVGWKGLINDPHMDGSDVFEAGLK.I + Oxidation (M)
2762.2851	2761.2778	2761.2171	0.63	318	-	341	1 R.SEMKYGVSVTDACISWEMTDALLR.E
2778.3752	2777.3679	2777.2710	34.9	318	-	341	1 R.SEMKYGVSVTDACISWEMTDALLR.E + Oxidation (M)
2810.4221	2809.4148	2809.3415	26.1	322	-	345	1 K.YGVSVDACISWEMTDALLREIHK.D + Oxidation (M)
2926.5030	2925.4957	2925.2804	73.6	253	-	277	1 K.EMEQAGLRSLMVDCSHGNSNKDYR.R + 2 Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2281, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1474.7804, 1484.8008, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1515.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8844, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1677.9625, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 16							

1729.8514	1733.9702	1735.9066	1740.9185	1744.0412	1744.9492	1747.9953	1752.9310	1754.4304	1770.9978	1773.0229	1782.8800
1784.0138	1784.3559	1784.9049	1798.9803	1801.9998	1802.9835	1811.9675	1812.6380	1812.9202	1813.0155	1818.0005	1818.9971
1819.9817	1820.9674	1821.9672	1822.9879	1823.9744	1824.5911	1824.9739	1826.0116	1832.0143	1833.0029	1834.0035	1834.9935
1835.9939	1836.5255	1836.5255	1837.0417	1838.0402	1839.0195	1840.0281	1840.9886	1843.0146	1843.9968	1844.9852	1845.9752
1846.9746	1848.0317	1849.0138	1850.0083	1850.9851	1851.9967	1853.0172	1854.0166	1857.0792	1857.9971	1858.9889	1859.9930
1860.9842	1861.9950	1862.9844	1864.0104	1865.0186	1866.0053	1866.9934	1867.9921	1870.9054	1874.0316	1875.0189	1875.9869
1877.0347	1878.0964	1879.0377	1880.0500	1880.9728	1882.0132	1887.9463	1889.5385	1889.9832	1895.1157	1899.9957	1906.0393
1908.9901	1909.9951	1920.3227	1921.5187	1921.9343	1924.0376	1925.9303	1926.1751	1927.2787	1927.6857	1934.0397	1935.0489
1936.1319	1943.0314	1948.0470	1949.0554	1950.1053	1951.1198	1952.0482	1966.0732	1979.0134	1980.0905	1983.1378	1984.0749
1985.0742	1993.1465	1994.1027	1997.0170	1998.0895	1999.1204	2003.0372	2006.0662	2016.0953	2016.9429	2017.0145	2017.7316
2019.1348	2029.5998	2040.5629	2054.0346	2054.5547	2059.0789	2061.1910	2063.1081	2064.0574	2065.0866	2066.1219	2067.0702
2078.2417	2080.0997	2100.1475	2101.1968	2102.7230	2102.7663	2122.1075	2126.0141	2136.4216	2150.2402	2151.1171	2153.3052
2154.0620	2167.3962	2172.2670	2178.1433	2179.0839	2180.2331	2182.2199	2183.2148	2190.9589	2193.9478	2195.1606	2196.1686
2197.1533	2198.2097	2199.1933	2200.1785	2204.0553	2208.0806	2212.1239	2214.3019	2221.7770	2222.0633	2222.0633	2227.2371
2234.1094	2236.2783	2250.1605	2251.2520	2259.1965	2260.2760	2263.3634	2294.7843	2325.1694	2327.1367	2328.1809	2329.1377
2338.3237	2342.1769	2343.0658	2344.1959	2353.9617	2354.3651	2362.0220	2372.2452	2374.5358	2379.2761	2401.4648	2403.0948
2406.5304	2410.3282	2413.4904	2424.2299	2429.3032	2432.0943	2432.0943	2433.8928	2440.2555	2441.2124	2442.1767	2465.1886
2467.1581	2483.5250	2487.4560	2503.2901	2508.3816	2538.3152	2547.5415	2555.2801	2564.5540	2575.1049	2575.6610	2577.4476
2578.1790	2593.8455	2612.4159	2613.2655	2614.2147	2626.8232	2637.4086	2649.3814	2665.3769	2689.9414	2699.0236	2702.5323
2704.3054	2705.3609	2707.2569	2710.4371	2717.8868	2721.3467	2722.3532	2723.3682	2724.3431	2725.3270	2726.3894	2727.4008
2729.2636	2730.3089	2733.4188	2735.2590	2738.4027	2739.3788	2740.3914	2741.3626	2742.3583	2743.3617	2744.3622	2745.4238
2747.7878	2748.5760	2753.4750	2754.3483	2755.4058	2756.4252	2757.7074	2758.3385	2761.3770	2763.3717	2765.5077	2770.3374
2770.4562	2772.3758	2777.3133	2782.4481	2807.4718	2808.5260	2809.4385	2819.3966	2824.4995	2841.5703	2854.4853	2855.4945
2856.3831	2867.5253	2871.4151	2873.4266	2941.3713	3013.4550	3050.5328	3174.0607	3174.7819	3222.8141	3224.5749	3224.6849

6. [tr|A0A0F6B5A1|A0A0F6B5A1_SALT1](#) Mass: 38974 Score: 35 Expect: 2.9 Matches: 24

Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=aroF PE=3 SV=1

Observed	Mr (exp)	Mr (calc)	ppm	Start	End	Miss	Peptide
609.3424	608.3351	608.3030	52.7	275	-	278	1 K.DYRR.Q
801.4429	800.4357	800.4140	27.0	4	-	10	0 K.DALNNVR.I
1014.4957	1013.4885	1013.5869	-97.15	42	-	51	0 R.GIISDIAGR.D
1057.6003	1056.5931	1056.5676	24.1	2	-	10	1 M.QKDALNNVR.I
1382.8490	1381.8417	1381.7677	53.5	42	-	54	1 R.GIISDIAGRDRP.L
1491.7085	1490.7012	1490.7147	-9.07	188	-	202	0 K.NGTDGSLATAINAMR.A
1507.8137	1506.8064	1506.7096	64.2	188	-	202	0 K.NGTDGSLATAINAMR.A + Oxidation (M)
1549.8304	1548.8232	1548.6878	87.4	239	-	252	0 K.APNYSADVAQCEK.E
1610.8721	1609.8648	1609.8617	1.96	94	-	106	1 R.VYFEKPRTTVGWK.G
1637.9067	1636.8994	1636.8494	30.5	79	-	93	0 K.ALAAEVSDSLVLVLR.V
1801.1041	1800.0968	1799.9530	79.9	25	-	41	0 K.AAFPLSLAQEAQIAQSR.G
2015.0906	2014.0834	2013.9466	67.9	107	-	125	0 K.GLINDPHMDGSDVEAGLK.I
2287.2528	2286.2455	2286.0661	78.5	322	-	341	0 K.YGVSVTDACISWEMTDALLR.E
2326.2005	2325.1933	2325.0729	51.8	167	-	187	1 R.TTESQTHREMSGLSMPVGFKN + 2 Oxidation (M)
2371.2952	2370.2879	2370.1638	52.4	107	-	128	1 K.GLINDPHMDGSDVEAGLK.IAR.Q + Oxidation (M)
2443.2146	2442.2074	2442.2424	-14.35	4	-	24	1 K.DALNNVRITDEQVLMTPPEQLK.A + Oxidation (M)
2556.2672	2555.2599	2555.2625	-1.01	55	-	76	1 R.LLVVCGPCSIHDPETALEYARR.F
2557.2535	2556.2463	2556.3410	-37.05	79	-	100	1 K.ALAAEVSDSLVLVLRVYFEKPR.T
2703.3952	2702.3879	2702.3010	32.2	101	-	125	1 R.TTVGKGLINDPHMDGSDVEAGLK.I + Oxidation (M)
2703.4537	2702.4465	2702.3010	53.8	101	-	125	1 R.TTVGKGLINDPHMDGSDVEAGLK.I + Oxidation (M)
2762.2851	2761.2778	2761.2761	0.63	318	-	341	1 R.SEMKYGVSVDACISWEMTDALLR.E
2778.3752	2777.3679	2777.2710	34.9	318	-	341	1 R.SEMKYGVSVDACISWEMTDALLR.E + Oxidation (M)
2810.4221	2809.4148	2809.3415	26.1	322	-	345	1 K.YGVSVTDACISWEMTDALLREIHK.D + Oxidation (M)
2926.5030	2925.4957	2925.2804	73.6	253	-	277	1 K.EMEAGLRPSLMLVDCSHGNSKDYR.R + 2 Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 610.4027, 611.4267, 612.3107, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1734, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.1338, 936.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.1100, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5394, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6893, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6647, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 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1784.9049, 1798.9803, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1851.9967, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.							

2154.0620	2167.3962	2172.2670	2178.1433	2179.0839	2180.2331	2182.2199	2183.2148	2190.9589	2193.9478	2195.1606	2196.1686
2197.1533	2198.2097	2199.1933	2200.1785	2204.0553	2208.0806	2212.1239	2214.3019	2221.7770	2222.0633	2222.0633	2227.2371
2234.1094	2236.2803	2250.1605	2251.2520	2259.1965	2260.2760	2263.3634	2294.7843	2325.1694	2327.1367	2328.1809	2329.1377
2338.3237	2342.1769	2343.0658	2344.1959	2353.9617	2354.3651	2362.0220	2372.2452	2374.5358	2379.2761	2401.4648	2403.0948
2406.5304	2410.3282	2413.4904	2424.2299	2429.3032	2432.0943	2432.0943	2432.0943	2440.2555	2441.2124	2442.1767	2465.1886
2467.1581	2483.8520	2487.4560	2503.2901	2508.3816	2538.3152	2547.5415	2555.2801	2564.5540	2575.1049	2575.6610	2577.4476
2578.1790	2593.3455	2612.4159	2613.2655	2614.2147	2626.8232	2637.4086	2649.3814	2665.3769	2689.9414	2699.0236	2702.5323
2704.3054	2705.3609	2707.2569	2710.4371	2717.8868	2721.3467	2722.3532	2723.3682	2724.3431	2725.3270	2726.3894	2727.4008
2729.2636	2730.3089	2733.4188	2735.2590	2738.4027	2739.3788	2740.3914	2741.3626	2742.3583	2743.3617	2744.3622	2745.4238
2747.7878	2748.5760	2753.4750	2754.3483	2755.4058	2756.4252	2757.7074	2758.3385	2761.3770	2763.3717	2765.5077	2770.3374
2770.4562	2772.3758	2777.3133	2782.4481	2807.4718	2808.5260	2809.4385	2819.3966	2824.4995	2841.5703	2854.4853	2855.4945
2856.3831	2867.5253	2871.4151	2873.4266	2941.3713	3013.4550	3050.5328	3174.0607	3174.7819	3222.8141	3224.5749	3224.6849

7. [sp|O31042|PDUE_SALTY](#) Mass: 19189 Score: 35 Expect: 3 Matches: 21

Propanediol dehydratase small subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pduE PE=1 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
730.4027	729.3954	729.4385	-59.02	88	94	0	R.LQASIAK.D
829.4593	828.4521	828.4705	-22.27	81	87	0	R.ITPPTLR.L
1007.6064	1006.5991	1006.5083	90.2	158	166	0	R.EAAGLYVER.K
1135.5390	1134.5317	1134.5339	-1.90	2	11	0	M.NTDAIESMVR.D
1151.5598	1150.5525	1150.5553	-2.39	99	107	1	R.DRLAMNFER.A
1157.6254	1156.6182	1156.5724	39.6	108	118	0	R.AAELTAVPDDR.I
1157.6580	1156.6507	1156.5724	67.7	108	118	0	R.AAELTAVPDDR.I
1500.7849	1499.7777	1499.7467	20.6	134	146	0	K.EELLAIADLENNR.Y
1520.8752	1519.8679	1519.8510	11.1	119	130	0	R.ILEIYNALRPYR.S
1540.8317	1539.8244	1539.8984	-48.05	81	94	1	R.ITPPTLRQLQASIAK.D
1705.9736	1704.9664	1704.8465	70.3	2	16	1	M.NTDAIESMVRDVLRS.M
1721.9486	1720.9413	1720.8414	58.1	2	16	1	M.NTDAIESMVRDVLRS.M + Oxidation (M)
1782.8800	1781.8727	1781.9100	-20.95	40	54	1	K.VSDYPLANKHPEWVK.T
1824.9739	1823.9666	1823.9352	17.2	151	166	1	K.ICAAFVREAAAGLYVER.K
1837.0417	1836.0344	1836.0257	4.75	119	133	1	R.ILEIYNALRPYRSTK.E
1843.0146	1842.0073	1841.8690	75.1	17	36	0	R.MNSLQGDAPAAAAGGTSR.S
1853.0172	1852.0100	1851.8819	69.2	1	16	1	-M.NTDAIESMVRDVLRS.M + Oxidation (M)
1858.9889	1857.9816	1857.8639	63.4	17	36	0	R.MNSLQGDAPAAAAGGTSR.S + Oxidation (M)
2019.1348	2018.1275	2017.9891	68.6	101	118	1	R.LAMNFERRAELTAVPDDR.I
2410.3282	2409.3209	2409.1846	56.6	60	80	1	K.TLDDFTLENLNSKVTQADM.R
2429.3032	2428.2959	2428.1765	49.2	12	36	1	R.DVLSRMSLQGDAPAAAAGGTSR.S + Oxidation (M)

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.0514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4588, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 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1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1851.9967, 1854.0166, 1857.0792, 1857.9971, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9991, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 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2441.2124, 2442.1767, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2564.5540, 2575.1049, 2575.6610, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.3952, 2704.3054, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2929.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
730.4027	729.3954	729.4385	-59.02	88	94	0	R.LQASIAK.D
829.4593	828.4521	828.4705	-22.27	81	87	0	R.ITPETLR.L
1007.6064	1006.5991	1006.5083	90.2	158	166	0	R.EAAGLYVER.K
1135.5390	1134.5317	1134.5339	-1.90	2	11	0	M.NTDAIESMVR.D
1151.5598	1150.5525	1150.5553	-2.39	99	107	1	R.DRLAMNFER.A
1157.6254	1156.6182	1156.5724	39.6	108	118	0	R.AAELTAVPDDR.I
1157.6580	1156.6507	1156.5724	67.7	108	118	0	R.AAELTAVPDDR.I
1500.7849	1499.7777	1499.7467	20.6	134	146	0	K.EELLAIADLENR.Y
1520.8752	1519.8679	1519.8510	11.1	119	130	0	R.ILEIYNALRPYR.S
1540.8317	1539.8244	1539.8984	-48.05	81	94	1	R.ITPETLR.LQASIAK.D
1705.9736	1704.9664	1704.8465	70.3	2	16	1	M.NTDAIESMVRDVLRSR.M
1721.9486	1720.9413	1720.8414	58.1	2	16	1	M.NTDAIESMVRDVLRSR.M + Oxidation (M)
1782.8800	1781.8727	1781.9100	-20.95	40	54	1	K.VSDYPLANKHPEWVK.T
1824.9739	1823.9666	1823.9352	17.2	151	166	1	K.ICAAFVREAGLYVER.K
1837.0417	1836.0344	1836.0257	4.75	119	133	1	R.ILEIYNALRPYRSTK.E
1843.0146	1842.0073	1841.8690	75.1	17	36	0	R.MNSLQGDAPAAAPAGGTSR.S
1853.0172	1852.0100	1851.8819	69.2	1	16	1	-MNTDAIESMVRDVLRSR.M + Oxidation (M)
1858.9889	1857.9816	1857.8639	63.4	17	36	0	R.MNSLQGDAPAAAPAGGTSR.S + Oxidation (M)
2019.1348	2018.1275	2017.9891	68.6	101	118	1	R.LAMNFERRAELTAVPDDR.I
2410.3282	2409.3209	2409.1846	56.6	60	80	1	K.TLDDFTLENLVSNKVTQDMR.I
2429.3032	2428.2959	2428.1765	49.2	12	36	1	R.DVLSRNMNSLQGDAPAAAPAGGTSR.S + Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1152.5762, 1153.5354, 1154.6056, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7400, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1527.8749, 1528.7873, 1529.8371, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9335, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1784.0138, 1784.0138, 1784.9049, 1798.9803, 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3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914							

9. [tr|A0A0F6B8X0|A0A0F6B8X0_SAL1](#) Mass: 13704 Score: 34 Expect: 3.9 Matches: 10

Putative inner membrane protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yidG PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1135.5390	1134.5317	1134.6437	-98.69	111	120	0	R.QLIAFIGNFI.-
1153.5354	1152.5281	1152.5523	-20.99	10	19	0	R.QNDPGLQMER.L
1448.8400	1447.8327	1447.8221	7.33	27	40	0	R.TLLGYGALMALAVR.H
2015.0906	2014.0834	2014.0021	40.4	10	26	1	R.QNDPGLQPERTSLAWFR.T
2197.1533	2196.1460	2196.3398	-88.25	91	110	0	K.FLISLAVLSLAILFAVTHIR.Q
2200.1785	2199.1712	2199.0379	60.6	72	90	1	R.NLMDVAHSDFSETHVVR.D
2326.2005	2325.1933	2325.2667	-31.59	20	40	1	R.TSLAWFRTLLGYGALMALAVR.H + Oxidation (M)
2440.2555	2439.2482	2439.4617	-87.52	89	110	1	R.DKFLISLAVLSLAILFAVTHIR.Q
2577.4476	2576.4403	2576.2442	76.1	67	88	1	R.YTLRNLMDVAHSDFSETHVVR.D
2593.3455	2592.3382	2592.2391	38.2	67	88	1	R.YTLRNLMDVAHSDFSETHVVR.D + Oxidation (M)

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.0665, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1162.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1545.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1570.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9988, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1851.9967, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2660, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2198.2097, 2199.1933, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2287.2528, 2294.7843, 2325.1694, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2413.4904, 2424.2219, 2429.3032, 2432.0943, 2432.0943, 2433.8928, 2441.2124, 2442.1767, 2443.2146, 2465.1866, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2578.1790, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3529, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3899, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6396, 3370.3906, 3428.3914

10. [tr|Q8ZL06|Q8ZL06 SALTY](#) Mass: 13704 Score: 34 Expect: 3.9 Matches: 10

Inner membrane protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=yidG PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1135.5390	1134.5317	1134.6437	-98.69	111	120	0	R.QLIAFIGNFI.-
1153.5354	1152.5281	1152.5523	-20.99	10	19	0	R.QNDPGLQPER.T
1448.8400	1447.8327	1447.8221	7.33	27	40	0	R.TLLGYGALMALAVR.H
2015.0906	2014.0834	2014.0021	40.4	10	26	1	R.QNDPGLQPRTSLAWFR.T
2197.1533	2196.1460	2196.3398	-88.25	91	110	0	K.FLISLAVLSLALLFAVTHIR.Q
2200.1785	2199.1712	2199.0379	60.6	72	90	1	R.NLMDVAHSDSFETHVVRD.K.F
2326.2005	2325.1933	2325.2667	-31.59	20	40	1	R.TSLAWFRLLGYGALMALAVR.H + Oxidation (M)
2440.2555	2439.2482	2439.4617	-87.52	89	110	1	R.DKFLISLAVLSLALLFAVTHIR.Q
2577.4476	2576.4403	2576.2442	76.1	67	88	1	R.YTLRNLMDVAHSDSFETHVVR.D
2593.3455	2592.3382	2592.2391	38.2	67	88	1	R.YTLRNLMDVAHSDSFETHVVR.D + Oxidation (M)

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.0665, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1162.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 127

1442.8905, 1443.8092, 1444.7555, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1517.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9633, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.9739, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.9939, 1836.9939, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1851.9967, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0070, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2198.2097, 2199.1933, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2287.2528, 2294.7843, 2325.1694, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2413.4904, 2424.2299, 2429.3032, 2432.0943, 2432.0943, 2433.8928, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2578.1790, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914

11. [tr|AOA0F6B792|AOA0F6B792_SAL11](#) Mass: 10884 Score: 30 Expect: 11 Matches: 9
 DNA-binding transcriptional regulator Nlp OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=nlp PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
743.5209	742.5136	742.4589	73.8	49	55	0	K.GELIIAK.A
909.3293	908.3220	908.4022	-88.24	21	29	0	K.GTSMMAESR.R
1037.4828	1036.4756	1036.4971	-20.80	20	29	1	K.KGTSMMAESR.R
1589.8670	1588.8598	1588.8725	-8.05	5	18	0	K.LIDWHPADIIAGLR.K
1934.0397	1933.0324	1933.0421	-5.01	2	18	1	M.ESKLIIDWHPADIIAGLR.K
2065.0866	2064.0793	2064.0826	-1.58	1	18	1	-M.ESKLIIDWHPADIIAGLR.K
2180.2331	2179.2258	2179.0963	59.4	56	73	1	K.ALGTPEFWIWPVSRVHDFP.T
2236.2783	2235.2711	2235.2415	13.2	49	68	1	K.GELIIAKALGTPEFWIWPVSRV.Y
2637.4086	2636.4013	2636.4649	-24.12	31	55	1	R.NGLSSTLANALTRFPWKGELIIAK.A
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4169, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 744.2361, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 913.5616, 915.2224, 915.2470, 916.5075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1144, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5633, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.1971, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 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1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9633, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 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1936.1319, 1943.0314, 1948.0749, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2015.0906, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589,							

2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636,
 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878,
 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374,
 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703,
 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819,
 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914

12. [tr|H9L4B3|H9L4B3_SALTY](#) Mass: 10884 Score: 30 Expect: 11 Matches: 9

Regulatory factor of maltose metabolism OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nlp PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
743.5209	742.5136	742.4589	73.8	49	55	0	K.GELIIAK.A
909.3293	908.3220	908.4022	-88.24	21	29	0	K.GTSMMAAESR.R
1037.4828	1036.4756	1036.4971	-20.80	20	29	1	K.KGTSMMAAESR.R
1589.8670	1588.8598	1588.8725	-8.05	5	18	0	K.LIDWHPADIIAGLR.K
1934.0397	1933.0324	1933.0421	-5.01	2	18	1	M.ESKLIWHPADIIAGLR.K
2065.0866	2064.0793	2064.0826	-1.58	1	18	1	-.MESKLIWHPADIIAGLR.K
2180.2331	2179.2258	2179.0963	59.4	56	73	1	K.ALGTPEWVWPSRYHDFR.T
2236.2783	2235.2711	2235.2415	13.2	49	68	1	K.GELIIAKALGTPEWVWPSR.Y
2637.4086	2636.4013	2636.4649	-24.12	31	55	1	R.NGLSSSTLANALTRPWPKGELIIAK.A

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497,
 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694,
 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542,
 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160,
 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419,
 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891,
 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192,
 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 839.1542,
 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770,
 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764,
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 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217,
 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499,
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 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598,
 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603,
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 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221,
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 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905,
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 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817,
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 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744,
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 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343,
 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198,
 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204,
 2003.0372, 2006.0622, 2015.0906, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547,
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 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0806, 2212.1238,
 2224.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3642, 2287.2528,
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 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2413.4904, 2424.2299, 2429.3032,
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 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878,
 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374,
 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703,
 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819,
 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914

13. [tr|A0A0F6B999|A0A0F6B999_SALTI](#) Mass: 34440 Score: 29 Expect: 11 Matches: 24

Porphobilinogen deaminase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=hemC PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
674.4337	673.4264	673.3759	75.0	182	187	0	R.LGLESR.I
901.5182	900.5109	900.5141	-3.59	155	163	1	R.GNVGTRLGK.L
959.6182	958.6109	958.5308	83.6	152	160	1	R.SLRGNVGT.R.L
1057.6003	1056.5931	1056.6066	-12.84	70	78	0	K.ELEIALLEK.R
1141.7127	1140.7054	1140.6390	58.2	50	60	0	R.GDVILDTPLAK.V
1148.5345	1147.5272	1147.5768	-43.15	233	242	1	R.VTAERAMNTR.L
1164.5603	1163.5530	1163.5717	-16.02	233	242	1	R.VTAERAMNTR.L + Oxidation (M)
1264.7488	1263.7415	1263.6493	73.0	2	12	0	M.TVTSMLDNVLR.I + Oxidation (M)
1277.7255	1276.7182	1276.6048	88.9	107	117	1	R.EDPRDAFVSNK.Y
1377.8030	1376.7957	1376.6823	82.4	306	318	0	R.AILTEVYNGETPA.-
1411.8307	1410.8234	1410.6847	98.3	1	12	0	-.MTVTSMLDNVLR.I + 2 Oxidation (M)
1540.8317	1539.8244	1539.8198	3.01	17	29	0	R.QSPALWQAHYVK.Q
1690.0239	1689.0166	1688.9243	54.6	2	16	1	M.TVTSMLDNVLR.IATR.Q
1705.9736	1704.9664	1704.9192	27.6	2	16	1	M.TVTSMLDNVLR.IATR.Q + Oxidation (M)
1733.9702	1732.9629	1732.9584	2.61	217	232	0	R.TQALLAPLNHSQTALR.V

1820.9674	1819.9602	1819.9648	-2.56	1	-	16	1	-.MTVTSMLDNVLR.IATR.Q
1837.0417	1836.0344	1835.9597	40.7	1	-	16	1	-.MTVTSMLDNVLR.IATR.Q + Oxidation (M)
1853.0172	1852.0100	1851.9547	29.9	1	-	16	1	-.MTVTSMLDNVLR.IATR.Q + 2 Oxidation (M)
2059.0789	2058.0716	2058.1361	-31.31	161	-	180	1	R.LGKLDNGDYDAILAVAGLK.R
2151.1171	2150.1099	2150.1228	-6.02	30	-	49	0	K.DALMATHPGLTVELVPMVTR.G
2183.2148	2182.2075	2182.1126	43.5	30	-	49	0	K.DALMATHPGLTVELVPMVTR.G + 2 Oxidation (M)
2429.3032	2428.2959	2428.1540	58.4	283	-	305	0	R.GSPEQAEQMGISLAEELLENGAR.A
2777.3133	2776.3061	2776.4178	-40.24	190	-	216	1	R.TALPPDVSPLPAVGGQAVGIECRLLDDAR.T
2926.5030	2925.4957	2925.4729	7.82	80	-	106	1	R.ADIAVHSMKDPVPAFPDGLGLVTICER.E + Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 804.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.3986, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2274, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.5727, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1142.6196, 1147.5494, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8407, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8714, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7833, 1529.8371, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0338, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1850.0083, 1850.9851, 1851.9967, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.1032, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2877, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2015.0066, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2021.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5610, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2287.2528, 2294.7843, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2410.3282, 2413.4904, 2424.2299, 2432.0943, 2432.0943, 2433.8928, 2440.2555, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5762, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4560, 2772.3758, 2778.3752, 2782.4481, 2807.4718, 2808.5620, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914								

14. [tr|A0A0F6B4I7|A0A0F6B4I7_SAL1](#) Mass: 14076 Score: 29 Expect: 14 Matches: 9
YfeK family protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yfeK PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
801.4429	800.4357	800.4868	-63.90	68	74	1	R.LKLGNTN.R	
1179.6547	1178.6474	1178.5819	55.6	77	86	0	R.IDTAEQFIDK.V	
1838.0402	1837.0330	1837.0899	-31.02	10	26	0	K.IVCAVAVALLTLPAWAK.L	
1950.1053	1949.0981	1948.9173	92.7	53	69	1	R.NGDahnCEEAVSHLR.LK.L	
1966.0732	1965.0659	1965.1849	-60.54	9	26	1	K.KIVCAVAVALLTLPAWAK.L	
2015.0906	2014.0834	2013.9643	59.1	106	123	0	K.SDENAQPYLHALIAETDK.N	
2410.3282	2409.3209	2409.2176	42.9	102	123	1	K.IPGKSDENAQPYLHALIAETDK.N	
2440.2555	2439.2482	2439.1349	46.4	47	67	1	K.DLTFVRNGDAHNCEEAVSHLR.L	
2758.3385	2757.3312	2757.5363	-74.39	10	34	1	K.IVCAVAVALLTLPAWAKLNAHEEAR.I	
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 804.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.3986, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2274, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 11								

1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1332.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8824, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 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1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1837.0417, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1849.0138, 1850.0083, 1850.0882, 1850.9851, 1851.9967, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1867.9921, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.0964, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1951.1198, 1952.0482, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2016.0953, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0860, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2706, 2263.3634, 2287.2528, 2294.7843, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.0948, 2406.5304, 2413.4904, 2424.2299, 2429.3032, 2432.0943, 2432.0943, 2433.8928, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2575.6610, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2727.4008, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2743.3617, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3774, 2770.4562, 2772.3758, 2778.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5303, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914

15. [tr|A0A0F6B4V7|A0A0F6B4V7_SALT1](#) Mass: 13983 Score: 28 Expect: 17 Matches: 12

Iron-sulfur cluster assembly scaffold protein IscU OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=nifU PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1142.6196	1141.6123	1141.5516	53.2	7	15	0	K.VIDHYENPR.N
1159.6699	1158.6627	1158.6244	33.0	79	89	1	K.GKSLDEQAQATK.N
1230.6414	1229.6341	1229.5888	36.9	47	57	0	K.VNDEGIEDAR.F
1553.8347	1552.8274	1552.7984	18.6	90	103	0	K.NTDIADELELPPVK.I
1712.9796	1711.9723	1711.9104	36.1	43	57	1	K.LQIKVNDDEGIEDAR.F
1720.9735	1719.9662	1719.8216	84.1	2	15	1	M.AYSEKVIDHYENPR.N
1851.9967	1850.9895	1850.8621	68.8	1	15	1	-.MAYSEKVIDHYENPR.N
1867.9921	1866.9848	1866.8570	68.4	1	15	1	-.MAYSEKVIDHYENPR.N + Oxidation (M)
2016.0953	2015.0880	2014.9670	60.1	60	78	0	K.TYGGSAIASSLVTEWVK.G
2727.4008	2726.3935	2726.1371	94.0	16	42	0	R.NVGSFDNDDNVSGSMVGPACGDVVK.L
2743.3617	2742.3545	2742.1320	81.1	16	42	0	R.NVGSFDNDDNVSGSMVGPACGDVVK.L + Oxidation (M)
3225.7104	3224.7031	3224.4537	77.3	16	46	1	R.NVGSFDNDDNVSGSMVGPACGDVVKLQIK.V + Oxidation (M)

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4574, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1332.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8153, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8824, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9052, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1464.8874, 1471.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.

1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1985.0742, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2015.0906, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2284.2528, 2294.7843, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.9948, 2406.5304, 2410.3282, 2413.4904, 2424.2299, 2429.3032, 2432.0943, 2432.0943, 2433.8928, 2440.2555, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3239.6938, 3370.3906, 3428.3914

16. [tr|Q7CQ11|Q7CQ11_SALTY](#) Mass: 13983 Score: 28 Expect: 17 Matches: 12

Iron-sulfur cluster assembly scaffold protein IscU OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nifu PE=

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1142.6196	1141.6123	1141.5516	53.2	7	15	0	K.VIDHYENPR.N
1159.6699	1158.6627	1158.6244	33.0	79	89	1	K.KGSLDEQAQAIK.N
1230.6414	1229.6341	1229.5888	36.9	47	57	0	K.VNDEGIIDAR.F
1553.8347	1552.8274	1552.7984	18.6	90	103	0	K.NTDIADLELLELPVK.I
1712.9796	1711.9723	1711.9104	36.1	43	57	1	K.LQIKVNDIIEEDAR.F
1720.9735	1719.9662	1719.8216	84.1	2	15	1	M.AYSEKVIDHYENPR.N
1851.9967	1850.9895	1850.8621	68.8	1	15	1	-.MAYSEKVIDHYENPR.N
1867.9921	1866.9848	1866.8570	68.4	1	15	1	-.MAYSEKVIDHYENPR.N + Oxidation (M)
2016.0953	2015.0880	2014.9670	60.1	60	78	0	K.TYCGSVAIDSSSLVTEWVK.G
2727.4008	2726.3935	2726.1371	94.0	16	42	0	R.NVGSFDNDDNVGSGMVGAPACGDVVK.L
2743.3617	2742.3545	2742.1320	81.1	16	42	0	R.NVGSFDNDDNVGSGMVGAPACGDVVK.L + Oxidation (M)
3225.7104	3224.7031	3224.4537	77.3	16	46	1	R.NVGSFDNDDNVGSGMVGAPACGDVVKLQIK.V + Oxidation (M)
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4435, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 844.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.1338, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6132, 959.6132, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5394, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6200, 1157.6580, 1157.8279, 1158.7864, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6303, 1226.3409, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7040, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1403.8470, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 1410.8154, 1411.1634, 1411.8307, 1412.8608, 1413.8631, 1414.8717, 1415.8822, 1416.8634, 1417.8661, 1418.2417, 1418.7763, 1419.2144, 1420.1293, 1421.8757, 1422.8766, 1423.8520, 1424.8858, 1425.9052, 1426.9054, 1427.8797, 1428.2709, 1428.8517, 1428.8517, 1429.7833, 1430.8129, 1432.8150, 1436.8839, 1438.8871, 1439.9008, 1440.8874, 1441.9221, 1442.8905, 1443.8092, 1444.7555, 1448.8400, 1451.8844, 1452.8106, 1453.8585, 1454.8821, 1462.8416, 1463.9175, 1469.8713, 1470.9038, 1473.9917, 1484.7804, 1485.1008, 1487.8231, 1488.8226, 1490.0624, 1491.7085, 1492.8214, 1498.9405, 1500.7849, 1507.8137, 1512.9808, 1513.9817, 1514.7099, 1514.9344, 1516.8498, 1518.8473, 1520.8752, 1527.8749, 1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9089, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1718.9693, 1720.0046, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9313, 1752.9313, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9670, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 1836.5255, 1836.5255, 1837.0417, 1838.0402, 1839.0195, 1840.0281, 1840.9886, 1843.0146, 1843.9968, 1844.9852, 1845.9752, 1846.9746, 1848.0317, 1849.0138, 1850.0083, 1850.9851, 1853.0172, 1854.0166, 1857.0792, 1857.9971, 1858.9889, 1859.9930, 1860.9842, 1861.9950, 1862.9844, 1864.0104, 1865.0186, 1866.0053, 1866.9934, 1870.9054, 1874.0316, 1875.0189, 1875.9869, 1877.0347, 1878.9644, 1879.0377, 1880.0500, 1880.9728, 1882.0132, 1887.9463, 1889.5385, 1889.9832, 1895.1157, 1899.9957, 1906.0393, 1908.9901, 1909.9951, 1920.3227, 1921.5187, 1921.9343, 1924.0376, 1925.9303, 1926.1751, 1927.2787, 1927.6857, 1934.0397, 1935.0489, 1936.1319, 1943.0314, 1948.0470, 1949.0554, 1950.1053, 1951.1198, 1952.0482, 1966.0732, 1979.0134, 1980.0905, 1983.1378, 1984.0749, 1985.0742, 1993.1465, 1994.1027, 1997.0170, 1998.0895, 1999.1204, 2003.0372, 2006.0662, 2015.0906, 2016.9429, 2017.0145, 2017.7316, 2019.1348, 2029.5998, 2040.5629, 2054.0346, 2054.5547, 2059.0789, 2061.1910, 2063.1081, 2064.0574, 2065.0866, 2066.1219, 2067.0702, 2078.2417, 2080.0997, 2100.1475, 2101.1968, 2102.7230, 2102.7663, 2122.1075, 2126.0141, 2136.4216, 2150.2402, 2151.1171, 2153.3052, 2154.0620, 2167.3962, 2172.2670, 2178.1433, 2179.0839, 2180.2331, 2182.2199, 2183.2148, 2190.9589, 2193.9478, 2195.1606, 2196.1686, 2197.1533, 2198.2097, 2199.1933, 2200.1785, 2204.0553, 2208.0806, 2212.1239, 2214.3019, 2221.7770, 2222.0633, 2222.0633, 2227.2371, 2234.1094, 2236.2783, 2250.1605, 2251.2520, 2259.1965, 2260.2760, 2263.3634, 2284.2528, 2294.7843, 2325.1694, 2326.2005, 2327.1367, 2328.1809, 2329.1377, 2338.3237, 2342.1769, 2343.0658, 2344.1959, 2353.9617, 2354.3651, 2362.0220, 2371.2952, 2372.2452, 2374.5358, 2379.2761, 2401.4648, 2403.9948, 2406.5304, 2410.3282, 2413.4904, 2424.2299, 2429.3032, 2432.0943, 2432.0943, 2433.8928, 2440.2555, 2441.2124, 2442.1767, 2443.2146, 2465.1886, 2467.1581, 2483.8520, 2487.4560, 2503.2901, 2508.3816, 2538.3152, 2547.5415, 2555.2801, 2556.2672, 2557.2535, 2564.5540, 2575.1049, 2577.4476, 2578.1790, 2593.3455, 2612.4159, 2613.2655, 2614.2147, 2626.8232, 2637.4086, 2649.3814, 2665.3769, 2689.9414, 2699.0236, 2702.5323, 2703.3952, 2703.4537, 2704.3054, 2705.3609, 2707.2569, 2710.4371, 2717.8868, 2721.3467, 2722.3532, 2723.3682, 2724.3431, 2725.3270, 2726.3894, 2729.2636, 2730.3089, 2733.4188, 2735.2590, 2738.4027, 2739.3788, 2740.3914, 2741.3626, 2742.3583, 2744.3622, 2745.4238, 2747.7878, 2748.5760, 2753.4750, 2754.3483, 2755.4058, 2756.4252, 2757.7074, 2758.3385, 2761.3770, 2762.2851, 2763.3717, 2765.5077, 2770.3374, 2770.4562, 2772.3758, 2777.3133, 2778.3752, 2782.4481, 2807.4718, 2808.5260, 2809.4385, 2810.4221, 2819.3966, 2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3239.6938, 3370.3906, 3428.3914							

17. [tr|A0A0F6B787|A0A0F6B787_SALTY](#) Mass: 4839 Score: 28 Expect: 18 Matches: 7

Uncharacterized protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_3987 PE=4 SV=1

Observed	Mr (expt)</
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841.5049	840.4976	840.4202	92.1	18 - 24	1	K.EHNKTGR.K
1690.0239	1689.0166	1688.8522	97.4	2 - 17	0	M.HLLPDGGANASYLAYK.E
1820.9674	1819.9602	1819.8927	37.1	1 - 17	0	-M.HLLPDGGANASYLAYK.E
1837.0417	1836.0344	1835.8876	80.0	1 - 17	0	-M.HLLPDGGANASYLAYK.E + Oxidation (M)
2198.2097	2197.2024	2197.0916	50.5	2 - 21	1	M.HLLPDGGANASYLAYKEHNNK.T
2329.1377	2328.1304	2328.1321	-0.70	1 - 21	1	-M.HLLPDGGANASYLAYKEHNNK.T
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.3179, 741.4923, 742.7356, 743.2661, 743.5209, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 871.1103, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 888.4984, 892.5764, 893.1075, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.2822, 947.5394, 948.5407, 949.5245, 956.6032, 959.6182, 960.5483, 961.5681, 969.4670, 973.1694, 975.0095, 986.5468, 987.6194, 988.9217, 995.5197, 997.5510, 1006.6371, 1007.6064, 1008.4141, 1014.4957, 1019.0822, 1037.4828, 1044.2024, 1044.5366, 1046.5266, 1047.1504, 1050.1499, 1051.1541, 1057.6003, 1059.6460, 1060.1151, 1060.6413, 1066.1512, 1067.1422, 1068.1551, 1076.5905, 1082.1112, 1082.6322, 1083.1170, 1084.1131, 1085.5653, 1087.0616, 1087.6503, 1088.5680, 1091.3210, 1096.7263, 1098.0888, 1098.6034, 1099.1046, 1099.6526, 1100.0657, 1100.5508, 1100.7811, 1103.6703, 1110.5485, 1111.6346, 1112.5399, 1113.6640, 1113.6640, 1121.5729, 1122.7527, 1124.5651, 1124.8226, 1126.6178, 1130.7286, 1135.5390, 1136.7624, 1137.6144, 1139.5547, 1140.5255, 1141.7127, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6012, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1274.6321, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 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1528.7873, 1529.8371, 1540.8317, 1541.8622, 1542.8542, 1546.5351, 1549.8304, 1550.9376, 1552.8392, 1553.8347, 1554.8484, 1555.9044, 1556.8513, 1557.8329, 1558.8575, 1559.9098, 1560.8677, 1561.3153, 1567.7611, 1570.9610, 1571.8841, 1572.9041, 1573.8709, 1574.8713, 1576.0440, 1576.0769, 1576.1502, 1584.8908, 1588.8224, 1589.8670, 1590.8569, 1592.6682, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1617.8471, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 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2824.4995, 2841.5703, 2854.4853, 2855.4945, 2856.3831, 2867.5253, 2871.4151, 2873.4266, 2926.5030, 2941.3713, 3013.4550, 3050.5328, 3174.0607, 3174.7819, 3222.8141, 3224.5749, 3224.6849, 3224.6849, 3224.8117, 3225.7104, 3239.6938, 3370.3906, 3428.3914						

18. [tr|A0A0F6B4R6|A0A0F6B4R6_SALT1](#) Mass: 59062 Score: 26 Expect: 25 Matches: 25

GMP synthase [glutamine-hydrolyzing] OS=Salmonella typhimurica (strain 14028s / SGSC 2262) OX=588858 GN=guaA PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
741.3179	740.3106	740.3817	-95.98	2 - 7	0		M.TENIHK.H
888.4984	887.4911	887.4171	83.5	1 - 7	0		-M.TENIHK.H + Oxidation (M)
1037.4828	1036.4756	1036.5342	-56.56	466 - 473	0		K.YDWVVSRLR.A
1059.6460	1058.6387	1058.5356	97.4	221 - 229	1		R.IREQVGGDK.V
1124.5651	1123.5579	1123.5444	12.0	419 - 426	1		K.EYCDLLRR.A
1141.7127	1140.7054	1140.6615	38.5	213 - 222	1		K.IIDDAVARIR.E
1274.6321	1273.6248	1273.6774	-41.29	367 - 377	1		K.EMKMLVEPLK.E
1403.8470	1402.8397	1402.7894	35.9	370 - 381	1		K.MGLVPEPLKELF.D
1520.8752	1519.8679	1519.7817	56.7	254 - 266	0		K.NLTCVFDVNGLLR.L
1570.9610	1569.9537	1569.8587	60.5	496 - 509	1		R.VSNRIINEVNGISR.V
1617.8471	1616.8399	1616.8158	14.9	294 - 308	1		R.FLSALAGENDPEAKR.K
1837.0417	1836.0344	1836.0145	10.8	10 - 25	0		R.IILLDFGSQYTLVAR.R
1864.0104	1863.0031	1863.0142	-5.96	310 - 325	1		K.IIGRVFVEVFDEEALK.L
1874.0316	1873.0243	1872.9384	45.9	174 - 188	1		K.RFYGVQFHEVTHTR.Q
1889.9832	1888.9759	1889.0193	-22.96	250 - 266	1		R.AIGKMLTCVFDVNGLLR.L
1993.1465	1992.1392	1992.1156	11.8	10 - 26	1		R.IILLDFGSQYTLVAR.R.V
1994.1027	1993.0955	1992.9550	70.5	197 - 212	1		R.FVRDICQCEALWTFK.I
2178.1433	2177.1360	2177.1004	16.3	331 - 351	0		K.WLAQGTIYDPVIESAASATGK.A
2222.0633	2221.0561	2221.1678	-50.31	444 - 464	1		K.VSQAFTVFLPVRVSGVMGDGR.K
2222.0633	2221.0561	2221.1678	-50.31	444 - 464	1		K.VSQAFTVFLPVRVSGVMGDGR.K
2338.3237	2337.3164	2337.1100	88.3	29 - 47	0		R.ELGVYCELWAWDVTEAQR.D
2410.3282	2409.3209	2409.3414	-8.49	230 - 253	1		K.VILGLSGGVSDSVTAMLLHRAIGK.N + Oxidation (M)
2593.3455	2592.3382	2592.2795	22.7	27 - 47	1		R.VRELGVYCELWAWDVTEAQR.D
2726.3894	2725.3821	2725.4439	-22.66	331 - 356	1		K.WLAQGTIYDPVIESAASATGKAHVIR.S
2762.2851	2761.2778	2761.4174	-50.54	326 - 351	1		K.LEDVKWLAQGTIYDPVIESAASATGK.A
No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694,							

635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 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1140.5255, 1142.6196, 1147.5494, 1148.5345, 1151.5598, 1152.5762, 1153.5354, 1154.6056, 1157.6254, 1157.6580, 1157.8279, 1158.7864, 1159.6699, 1161.5205, 1163.5460, 1164.2443, 1164.5603, 1166.6869, 1171.4275, 1173.5508, 1177.5595, 1178.6102, 1179.6547, 1194.6374, 1196.6591, 1199.0366, 1220.6298, 1221.4632, 1221.6904, 1223.6903, 1226.3409, 1230.6414, 1240.7387, 1242.8126, 1252.7994, 1261.8111, 1264.7488, 1267.7764, 1272.3057, 1272.6873, 1276.6473, 1277.7255, 1278.7447, 1279.6311, 1285.6990, 1293.7090, 1310.1513, 1324.7514, 1325.7197, 1333.6322, 1336.7595, 1337.7480, 1338.1407, 1343.7598, 1344.6947, 1346.4682, 1346.7232, 1347.3684, 1347.6516, 1349.6450, 1355.4671, 1358.1153, 1359.0890, 1359.7407, 1370.1862, 1370.7538, 1371.2297, 1372.3281, 1372.6906, 1373.7610, 1374.3532, 1375.1354, 1377.8030, 1382.8490, 1383.8151, 1384.8221, 1388.9408, 1389.6718, 1393.7926, 1400.8690, 1401.8674, 1402.8721, 1405.8573, 1406.0370, 1406.3968, 1406.6964, 1407.0191, 1407.7036, 1407.7784, 1408.0553, 1410.0426, 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1592.6882, 1598.9120, 1604.8327, 1605.8724, 1606.8493, 1607.8258, 1610.8721, 1612.9648, 1618.1937, 1620.8700, 1621.9171, 1622.8355, 1623.8444, 1623.8444, 1624.8877, 1626.4516, 1627.9045, 1628.8204, 1632.8607, 1634.8545, 1635.8515, 1636.8546, 1637.9067, 1643.8072, 1655.9905, 1672.0654, 1673.9782, 1674.8508, 1676.8532, 1677.9262, 1679.9309, 1687.9901, 1688.9864, 1690.0239, 1690.9803, 1692.0375, 1693.0172, 1694.8817, 1695.9014, 1697.8900, 1703.9811, 1704.9842, 1705.9736, 1706.9522, 1707.9418, 1712.9796, 1718.9693, 1720.0046, 1720.9735, 1721.9486, 1726.9935, 1727.7899, 1727.8361, 1729.8514, 1733.9702, 1735.9066, 1740.9185, 1744.0412, 1744.9492, 1747.9953, 1752.9310, 1754.4304, 1770.9978, 1773.0229, 1782.8800, 1784.0138, 1784.3559, 1784.9049, 1798.9803, 1801.1041, 1801.9998, 1802.9835, 1811.9675, 1812.6380, 1812.9202, 1813.0155, 1818.0005, 1818.9971, 1819.9817, 1820.9674, 1821.9672, 1822.9879, 1823.9744, 1824.5911, 1824.9739, 1826.0116, 1832.0143, 1833.0029, 1834.0035, 1834.9935, 1835.9939, 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19. [sp|Q8ZN60|GUAA_SALTY](#) Mass: 59078 Score: 26 Expect: 25 Matches: 25

GMP synthase [glutamine-hydrolyzing] OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=guaA PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
741.3179	740.3106	740.3817	-95.98	2	7	0	M.TENIHK.H
888.4984	887.4911	887.4171	83.5	1	7	0	- .MTENIHK.H + Oxidation (M)
1037.4828	1036.4756	1036.5342	-56.56	466	473	0	K.YDWWVSLR.A
1059.6460	1058.6387	1058.5356	97.4	221	229	1	R.IREQVGGDK.V
1124.5651	1123.5579	1123.5444	12.0	419	426	1	K.EYCDLLRR.A
1141.7127	1140.7054	1140.6615	38.5	213	222	1	K.IIDDAVARIR.E
1274.6321	1273.6248	1273.6774	-41.29	367	377	1	K.EMKMGVLEPLK.E
1403.8470	1402.8397	1402.7894	35.9	370	381	1	K.MGLVLEPLKELFK.D
1520.8752	1519.8679	1519.7817	56.7	254	266	0	K.NLTCVFDNGLLR.L
1570.9610	1569.9537	1569.8587	60.5	496	509	1	R.VSNRIINEVNGISR.V
1617.8471	1616.8399	1616.8158	14.9	294	308	1	R.FLSALAGENDPEAKR.K
1837.0417	1836.0344	1836.0145	10.8	10	25	0	R.LILIDFGSQYQLVAR.R
1864.0104	1863.0031	1863.0142	-5.96	310	325	1	K.IIGRVFVVFDEEALK.L
1874.0316	1873.0243	1872.9384	45.9	174	188	1	K.RFYGVQFHEVTHTR.Q
1889.9832	1888.9759	1889.0193	-22.96	250	266	1	R.AIGKNLTCVFDNGLLR.L
1993.1465	1992.1392	1992.1156	11.8	10	26	1	R.LLILIDFGSQYQLVARR.V
1994.1027	1993.0955	1992.9550	70.5	197	212	1	R.FVRDIQCCEALWTPAK.I
2178.1433	2177.1360	2177.1004	16.3	331	351	0	K.WLAQGTIYDPVIESAASATGK.A
2222.0633	2221.0561	2221.1678	-50.31	444	464	1	K.VSQAFTVFLPVRVSGVMGDGR.K
2222.0633	2221.0561	2221.1678	-50.31	444	464	1	K.VSQAFTVFLPVRVSGVMGDGR.K
2338.3237	2337.3164	2337.1100	88.3	29	47	0	R.ELGVYCELWAWDVTEAQR.D
2410.3282	2409.3209	2409.3414	-8.49	230	253	1	K.VILGLSGGVSSVTMALLHRAIGK.N + Oxidation (M)
2593.3455	2592.3382	2592.2795	22.7	27	47	1	R.VRELGVYCELWAWDVTEAQR.D
2726.3894	2725.3821	2725.4439	-22.66	331	356	1	K.WLAQGTIYDPVIESAASATGKAHVIK.S
2762.2851	2761.2778	2761.4174	-50.54	326	351	1	K.LEDVKWLAQGTIYDPVIESAASATGK.A

No match to: 600.3852, 605.4023, 606.2971, 606.3251, 607.2868, 608.3639, 609.3424, 610.4027, 611.4267, 612.3107, 612.3107, 613.4497, 614.4557, 617.2606, 617.4666, 618.2989, 618.4100, 621.4671, 622.4900, 623.4040, 624.3960, 626.4053, 628.2436, 629.4189, 634.2694, 635.2736, 635.3858, 640.2891, 641.4497, 642.4315, 644.1559, 645.1839, 650.1724, 651.1962, 652.2023, 653.1990, 657.4514, 658.4542, 659.4486, 666.1350, 667.1394, 668.1636, 671.5041, 672.1823, 672.4075, 674.4337, 678.5273, 679.5260, 682.1103, 683.0983, 684.1160, 684.3146, 685.4689, 686.4443, 688.2323, 690.2508, 700.4895, 701.4379, 702.4805, 704.4984, 705.5065, 706.5287, 709.3508, 710.4419, 710.4419, 711.4430, 712.3728, 713.4954, 714.4930, 717.4764, 720.5994, 721.3751, 721.3751, 722.9277, 729.4858, 730.4027, 731.4891, 735.4394, 736.4609, 740.5189, 741.4923, 742.7356, 743.2661, 743.5209, 745.4865, 755.2952, 758.5047, 769.5308, 771.5642, 781.5192, 782.5169, 789.5907, 799.4200, 801.4429, 804.3734, 808.4436, 823.2324, 829.4593, 831.3839, 835.4872, 837.3986, 837.4389, 839.1542, 840.1659, 841.5049, 842.6039, 843.6059, 844.3603, 848.5075, 855.1180, 855.5918, 856.1271, 856.5793, 857.1094, 857.4954, 858.4770, 861.1434, 862.1563, 863.1604, 871.1103, 872.1119, 873.1511, 877.1086, 878.1229, 879.1425, 880.5598, 885.4855, 892.5764, 893.0750, 893.5403, 894.1223, 895.1084, 896.1147, 899.4577, 900.4641, 901.5182, 903.5221, 904.7232, 909.0609, 909.3293, 913.5616, 915.2224, 915.2470, 916.3075, 916.5175, 931.1426, 932.1338, 932.1338, 932.6551, 938.1048, 945.6557, 946.5703, 947.1144, 947.1541, 947.2822,

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Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 774
Selected for scoring : 466

Mascot: <http://www.matrixscience.com/>



MASCOT Search Results

Protein View: tr|A0A0F6AYQ2|A0A0F6AYQ2_SALT1

Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=pal PE=3 SV=1

Database: Salmonella_typhimurium_LT2
Score: 99
Expect: 1.2e-006
Nominal mass (M_r): 18910
Calculated pI: 6.29

Sequence similarity is available as [an NCBI BLAST search of tr|A0A0F6AYQ2|A0A0F6AYQ2_SALT1 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M)**
Mass values searched: 13
Mass values matched: 7

Protein sequence coverage: 33%

Matched peptides shown in **bold red**.

1 MQLNKVLKGL MIALPVMAlA ACSSNKNASN DGSEGGMLNG AGTGMDANGN
 51 GNMSSEEQAR LQMQLQQNN IVYFDLDKYD IR**SDFAAMLDAHANFLRSNP**
 101 **SYKVTVEGHA DERGTPEYNI SLGERR**ANAV KMYLQKGVS ADQISIVSYG
 151 **KEKPAVLGHD EAAYAK**NRRA VLVY

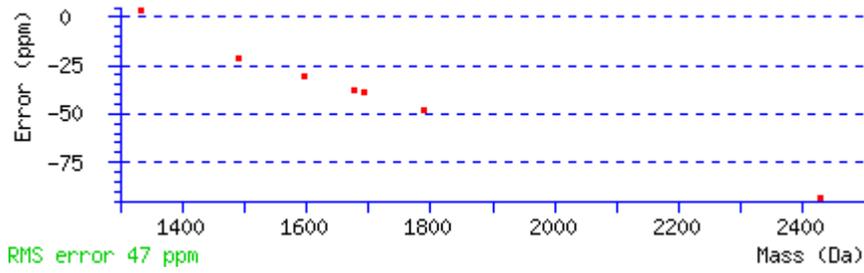
Unformatted sequence string: **174 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
83 - 97	1678.7373	1677.7300	1677.7933	-37.7	0	R.SDFAAMLDAHANFLR.S
83 - 97	1694.7292	1693.7219	1693.7882	-39.2	0	R.SDFAAMLDAHANFLR.S + Oxidation (M)
98 - 113	1788.7647	1787.7575	1787.8438	-48.3	1	R.SNPSYKVTVEGHADER.G
104 - 125	2428.9414	2427.9341	2428.1619	-93.8	1	K.VTVEGHADERGTPEYNISLGER.R
114 - 125	1335.6590	1334.6517	1334.6466	3.81	0	R.GTPEYNISLGER.R
114 - 126	1491.7229	1490.7157	1490.7477	-21.5	1	R.GTPEYNISLGERR.A
152 - 166	1598.7677	1597.7604	1597.8100	-31.0	0	K.EKPAVLGHDEAAYAK.N

No match to: 720.5636, 1056.6176, 1392.6734, 1630.7496, 1721.7299, 1845.7790



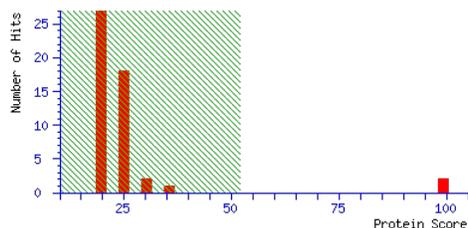
Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

User : raju
 Email : raju.r@fountomics.com
 Search title : Sample 5
 Database : Salmonella typhimurium LT2 typhimurium LT2_04012025 (9918 sequences; 2883936 residues)
 Timestamp : 4 Jan 2025 at 19:01:00 GMT
 Top Score : 99 for [tr|A0A0F6AYQ2|A0A0F6AYQ2_SALT1](#), Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain 14028s / SGSC

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 52 are significant ($p < 0.05$).



Protein Summary Report

Format As: [Help](#)
 Significance threshold $p <$ Max. number of hits
 Preferred taxonomy

Overview Table

Click on column header to jump to entry in results list.
 Move mouse over any indicator to highlight identical peptides.
 Click on an indicator to see details of individual match.
 Use check boxes to select sub-set of queries for new search.

Mouse over:

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<input checked="" type="checkbox"/> 720.5636 (1+)																				
<input checked="" type="checkbox"/> 1056.6176 (1+)																				
<input checked="" type="checkbox"/> 1335.6590 (1+)																				
<input checked="" type="checkbox"/> 1392.6734 (1+)																				
<input checked="" type="checkbox"/> 1491.7229 (1+)																				
<input checked="" type="checkbox"/> 1598.7677 (1+)																				
<input checked="" type="checkbox"/> 1630.7496 (1+)																				
<input checked="" type="checkbox"/> 1678.7373 (1+)																				
<input checked="" type="checkbox"/> 1694.7292 (1+)																				
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<input checked="" type="checkbox"/> 1788.7647 (1+)																				
<input checked="" type="checkbox"/> 1845.7790 (1+)																				
<input checked="" type="checkbox"/> 2428.9414 (1+)																				

Index

Accession	Mass	Score	Description
1. tr A0A0F6AYQ2 A0A0F6AYQ2_SALT1	18910	99	Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain 14028s / SGSC 2262)
2. tr Q7CQW9 Q7CQW9_SALTY	18910	99	Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATC
3. tr A0A0F6B6L6 A0A0F6B6L6_SALT1	4624	34	Uncharacterized protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=
4. tr A0A0F6BA75 A0A0F6BA75_SALT1	6053	30	Uncharacterized protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=
5. tr A0A0F6B3C0 A0A0F6B3C0_SALT1	38915	28	ATP phosphoribosyltransferase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=5888
6. tr A0A0F6B2J3 A0A0F6B2J3_SALT1	10545	27	Glycoside hydrolase family 19 protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262)
7. tr Q8ZNX7 Q8ZNX7_SALTY	10545	27	Glycoside hydrolase family 19 protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / AT
8. sp O31042 PDUE_SALTY	19189	26	Propanediol dehydratase small subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / AT
9. tr A0A0F6B387 A0A0F6B387_SALT1	19189	26	Propanediol dehydratase small subunit OS=Salmonella typhimurium (strain 14028s / SGSC 2262)
10. tr A0A0F6B436 A0A0F6B436_SALT1	74226	25	Bifunctional polymyxin resistance protein ArnA OS=Salmonella typhimurium (strain 14028s / S
11. sp O52325 ARNA_SALTY	74226	25	Bifunctional polymyxin resistance protein ArnA OS=Salmonella typhimurium (strain LT2 / SGSC
12. tr A0A0F6B6P1 A0A0F6B6P1_SALT1	14598	24	Anti-adaptor protein IraD OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 G
13. sp Q8ZM27 IRAD_SALTY	14598	24	Anti-adaptor protein IraD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) O
14. tr A0A0F6B0T2 A0A0F6B0T2_SALT1	17563	24	Lipoprotein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=nlpC PE=3 SV
15. tr Q8ZPS7 Q8ZPS7_SALTY	17563	24	Lipoprotein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nlp
16. tr A0A0F6AXY9 A0A0F6AXY9_SALT1	23037	23	Multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1 OS=Salmonel
17. tr Q8ZR91 Q8ZR91_SALTY	23037	23	Multifunctional acyl-CoA thioesterase I also functions as protease I, lysophospholipase(L(I)
18. tr A0A0F6B7K8 A0A0F6B7K8_SALT1	16477	23	Zinc-responsive transcriptional regulator OS=Salmonella typhimurium (strain 14028s / SGSC 2
19. tr Q8ZLM3 Q8ZLM3_SALTY	16477	23	Zn(II)-responsive transcriptional regulator OS=Salmonella typhimurium (strain LT2 / SGSC141
20. tr Q8ZPJ6 Q8ZPJ6_SALTY	90762	22	Dimethyl sulfoxide reductase, chain A1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / A

Results List

1. [tr|A0A0F6AYQ2|A0A0F6AYQ2_SALT1](#) Mass: 18910 Score: 99 Expect: 1.2e-006 Matches: 7
Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=pal PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.6466	3.81	114	-	125	0	R.GTPEYNISLGER.R
1491.7229	1490.7157	1490.7477	-21.50	114	-	126	1	R.GTPEYNISLGER.R.A
1598.7677	1597.7604	1597.8100	-31.05	152	-	166	0	K.EKPAVLGHDEAAYAK.N
1678.7373	1677.7300	1677.7933	-37.73	83	-	97	0	R.SDFAAMLDAHANFLR.S
1694.7292	1693.7219	1693.7882	-39.16	83	-	97	0	R.SDFAAMLDAHANFLR.S + Oxidation (M)
1788.7647	1787.7575	1787.8438	-48.31	98	-	113	1	R.SNPSYKVTVEGHADER.G
2428.9414	2427.9341	2428.1619	-93.80	104	-	125	1	K.VTVEGHADERGTPEYNISLGER.R

No match to: 720.5636, 1056.6176, 1392.6734, 1630.7496, 1721.7299, 1845.7790
2. [tr|Q7CQW9|Q7CQW9_SALTY](#) Mass: 18910 Score: 99 Expect: 1.2e-006 Matches: 7
Peptidoglycan-associated lipoprotein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pal PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.6466	3.81	114	-	125	0	R.GTPEYNISLGER.R
1491.7229	1490.7157	1490.7477	-21.50	114	-	126	1	R.GTPEYNISLGER.R.A
1598.7677	1597.7604	1597.8100	-31.05	152	-	166	0	K.EKPAVLGHDEAAYAK.N
1678.7373	1677.7300	1677.7933	-37.73	83	-	97	0	R.SDFAAMLDAHANFLR.S
1694.7292	1693.7219	1693.7882	-39.16	83	-	97	0	R.SDFAAMLDAHANFLR.S + Oxidation (M)
1788.7647	1787.7575	1787.8438	-48.31	98	-	113	1	R.SNPSYKVTVEGHADER.G
2428.9414	2427.9341	2428.1619	-93.80	104	-	125	1	K.VTVEGHADERGTPEYNISLGER.R

No match to: 720.5636, 1056.6176, 1392.6734, 1630.7496, 1721.7299, 1845.7790
3. [tr|A0A0F6B6L6|A0A0F6B6L6_SALT1](#) Mass: 4624 Score: 34 Expect: 4.4 Matches: 2
Uncharacterized protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_3757 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.7531	-75.97	16	-	27	1	K.GLSGITHRPNKR.S
1788.7647	1787.7575	1787.7827	-14.11	1	-	15	1	-.MLCCRYAMLPGSDAK.G + Oxidation (M)

No match to: 720.5636, 1056.6176, 1392.6734, 1491.7229, 1598.7677, 1630.7496, 1678.7373, 1694.7292, 1721.7299, 1845.7790, 2428.9414
4. [tr|A0A0F6BA75|A0A0F6BA75_SALT1](#) Mass: 6053 Score: 30 Expect: 9.7 Matches: 2
Uncharacterized protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_5088 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.6442	5.66	31	-	42	0	R.QPPFGDMFGLAR.Y
1491.7229	1490.7157	1490.7453	-19.84	30	-	42	1	R.RQPPFGDMFGLAR.Y

No match to: 720.5636, 1056.6176, 1392.6734, 1598.7677, 1630.7496, 1678.7373, 1694.7292, 1721.7299, 1788.7647, 1845.7790, 2428.9414
5. [tr|A0A0F6B3C0|A0A0F6B3C0_SALT1](#) Mass: 38915 Score: 28 Expect: 15 Matches: 3
ATP phosphoribosyltransferase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=hisG PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1491.7229	1490.7157	1490.7412	-17.14	6	-	17	1	R.HSDLPVHERMR.K + Oxidation (M)
1694.7292	1693.7219	1693.8940	-101.61	18	-	32	0	R.KPPDHLPGAFFLAR.D
2428.9414	2427.9341	2428.1477	-87.95	308	-	327	1	R.VAMHVSSETLFWETMEKLK.A + 2 Oxidation (M)

No match to: 720.5636, 1056.6176, 1335.6590, 1392.6734, 1598.7677, 1630.7496, 1678.7373, 1721.7299, 1788.7647, 1845.7790
6. [tr|A0A0F6B2J3|A0A0F6B2J3_SALT1](#) Mass: 10545 Score: 27 Expect: 18 Matches: 2
Glycoside hydrolase family 19 protein OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=STM14_2273 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.7306	-59.13	33	-	43	1	K.IRITGLENYTR.C
1694.7292	1693.7219	1693.8821	-94.60	35	-	49	1	R.ITGLENYTRCGVALK.L

No match to: 720.5636, 1056.6176, 1392.6734, 1491.7229, 1598.7677, 1630.7496, 1678.7373, 1721.7299, 1788.7647, 1845.7790, 2428.9414
7. [tr|Q8ZNX7|Q8ZNX7_SALTY](#) Mass: 10545 Score: 27 Expect: 18 Matches: 2
Glycoside hydrolase family 19 protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=STM1869a PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1335.6590	1334.6517	1334.7306	-59.13	33	-	43	1	K.IRITGLENYTR.C
1694.7292	1693.7219	1693.8821	-94.60	35	-	49	1	R.ITGLENYTRCGVALK.L

No match to: 720.5636, 1056.6176, 1392.6734, 1491.7229, 1598.7677, 1630.7496, 1678.7373, 1721.7299, 1788.7647, 1845.7790, 2428.9414
8. [sp|O31042|PDUE_SALTY](#) Mass: 19189 Score: 26 Expect: 24 Matches: 3
Propanediol dehydratase small subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pduE PE=1 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1630.7496	1629.7424	1629.8508	-66.56	74	-	87	1	K.VTAQDMRITPETLR.L
1721.7299	1720.7226	1720.8414	-69.01	2	-	16	1	M.NTDAIESMVRDVLRS.M + Oxidation (M)
2428.9414	2427.9341	2428.1765	-99.82	12	-	36	1	R.DVLSRMNSLQGDAPAAPAAGGTSR.S + Oxidation (M)

No match to: 720.5636, 1056.6176, 1335.6590, 1392.6734, 1491.7229, 1598.7677, 1678.7373, 1694.7292, 1788.7647, 1845.7790
9. [tr|A0A0F6B387|A0A0F6B387_SALT1](#) Mass: 19189 Score: 26 Expect: 24 Matches: 3
Propanediol dehydratase small subunit OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=pduE PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1630.7496	1629.7424	1629.8508	-66.56	74	-	87	1	K.VTAQDMRITPETLR.L
1721.7299	1720.7226	1720.8414	-69.01	2	-	16	1	M.NTDAIESMVRDVLRS.M + Oxidation (M)
2428.9414	2427.9341	2428.1765	-99.82	12	-	36	1	R.DVLSRMNSLQGDAPAAPAAGGTSR.S + Oxidation (M)

No match to: 720.5636, 1056.6176, 1335.6590, 1392.6734, 1491.7229, 1598.7677, 1678.7373, 1694.7292, 1788.7647, 1845.7790
10. [tr|A0A0F6B436|A0A0F6B436_SALT1](#) Mass: 74226 Score: 25 Expect: 34 Matches: 4
Bifunctional polymyxin resistance protein ArnA OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=yfBG PE=3 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide	
1056.6176	1055.6103	1055.5836	25.4	620	-	628	1	R.KPSIDNARR.C
1335.6590	1334.6517	1334.6111	30.4	629	-	639	0	R.CLGWEPISIAMR.D + Oxidation (M)
1491.7229	1490.7157	1490.7122	2.32	628	-	639	1	R.RCLGWEPISIAMR.D + Oxidation (M)
1630.7496	1629.7424	1629.8838	-86.81	150	-	164	0	R.VAIAQDDVALTLHKK.L

No match to: 720.5636, 1392.6734, 1598.7677, 1678.7373, 1694.7292, 1721.7299, 1788.7647, 1845.7790, 2428.9414
11. [sp|O52325|ARNA_SALTY](#) Mass: 74226 Score: 25 Expect: 34 Matches: 4
Bifunctional polymyxin resistance protein ArnA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=arnA PE=1 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
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