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SUPPORTING INFECTIOUS DISEASE RESEARCH

Salmonella enterica subsp. enterica, Strain 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD_059/060_Kan

Catalog No. NR-42840

For research use only. Not for human use.

Contributor:

Michael McClelland, Professor, Scientific Director, Vaccine Research Institute of San Diego, San Diego, California, USA

Manufacturer:

BEI Resources

Product Description:

Production in the 96-well format has increased risk of crosscontamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources does not confirm or validate individual mutants provided by the contributor.

The *Salmonella enterica* (*S. enterica*) subsp. *enterica*, strain 14028s (serovar Typhimurium) targeted single-gene deletion (SGD) mutant library contains a total of 3,773 individual genes deleted simultaneously across two collections of mutants differentiated by kanamycin or chloramphenicol resistance.^{1,2} The kanamycin-resistant mutant collection contains 3517 mutants distributed among 11 96-well plates, in which a single gene is replaced by a cassette conferring the kanamycin resistance gene, and includes 9 double mutants that contain both kanamycin and chloramphenicol cassettes. Deletions were confirmed by the depositor.^{1,2}

Genes were targeted for deletion by primers designed to preserve the first and last 30 bases of each deleted gene.² Gene replacement followed a modified Lambda-Red technique, with an added T7 RNA polymerase promoter positioned in plasmid <u>pCLF3</u> to generate a gene-specific transcript from the *Salmonella* genome directly downstream of each mutant.²⁻⁴ Detailed information about each mutant is shown in Table 1.

Note: The strain designation on the plate, strain CDC 6516-60, is incorrect. The correct strain designation is strain 14028s. *S. enterica* subsp. *enterica*, strain 14028s was originally known as strain 14028. A variant of the original strain with a rough colony morphology was designated 14028r and the original smooth strain was renamed 14028s. Strain 14028 is a descendent of strain CDC 6516-60, which was isolated from pools of hearts and livers of 4week-old chickens.⁵ The complete genome of *S. enterica* subsp. *enterica*, strain 14028s (GenBank: <u>CP001363.1</u>) and plasmid (GenBank: <u>CP001362.1</u>) sequences are available.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 50 μL of culture in Luria Bertani (LB) broth containing 60 $\mu g/mL$ kanamycin supplemented with 10% glycerol.

Packaging/Storage:

NR-42840 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

<u>Media</u>: LB broth or agar containing 60 μg/mL kanamycin <u>Incubation</u>: Temperature: 37°C Atmosphere: Aerobic <u>Propagation</u>: 1. Scrape top of frozen well with a pipette tip a

- 1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
- 2. Incubate the plates at 37°C for 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Salmonella enterica* subsp. *enterica*, Strain 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD_059/060_Kan, NR-42840."

Biosafety Level: 2

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. <u>Biosafety in</u> <u>Microbiological and Biomedical Laboratories</u>. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

Disclaimers:

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References:

1. McClelland, M., Personal Communication.

- Porwollik, S., et al. "Defined Single-Gene and Multi-Gene Deletion Mutant Collections in *Salmonella enterica* sv Typhimurium." <u>PLoS One</u> 9 (2014): e99820. PubMed: 25007190.
- Santiviago, C. A., et al. "Analysis of Pools of Targeted Salmonella Deletion Mutants Identifies Novel Genes Affecting Fitness during Competitive Infection in Mice." <u>PLoS Pathog.</u> 5 (2009): e1000477. PubMed: 19578432.
- Datsenko, K. A. and B. L. Wanner. "One-step Inactivation of Chromosomal Genes in *Escherichia coli* K-13 Using PCR Products." <u>Proc. Natl. Acad. Sci. USA</u> 97 (2000): 6640-6645. PubMed: 10829079.
- Jarvik, T., et al. "Short-Term Signatures of Evolutionary Change in the Salmonella enterica Serovar Typhimurium 14028 Genome." <u>J. Bacteriol.</u> 192 (2010): 560-567. PubMed: 19897643.

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Table 1: S. enterica subsp. enterica, Strain 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD_059/060_Kan^{1,2}

Well Position	Gene Type	Gene Start	Gene End	Target Gene (Locus Tag)	Deleted Region Start	Deleted Region End	Gene Strand	Description
A01	CDS	1525050	1525946	STM14_1737	1525080	1525915	-	Putative aldo/keto reductase
A02	CDS	1531083	1532204	STM14_1744	1531113	1532173	-	Anhydro-N-acetylmuramic acid kinase
A03	CDS	1524760	1524999	STM14_1736	1524790	1524968	-	Putative oxidoreductase
A04	CDS	1524058	1524657	STM14_1735	1524088	1524626	+	Putative transcriptional repressor
A05	CDS	1436576	1437409	STM14_1637	1436606	1437378	+	Hypothetical protein
A06	CDS	1455097	1456215	STM14_1657	1455127	1456184	+	Putative inner membrane protein
A07	CDS	1433549	1434991	STM14_1633	1433579	1434960	-	Hypothetical protein
A08	CDS	1416287	1417045	STM14_1611	1416317	1417014	-	Putative outer membrane protein
A09	CDS	1384916	1385467	STM14_1574	1384946	1385436	-	Hypothetical protein
A11	CDS	1410051	1411442	STM14_1604	1410081	1411411	+	Kinase/transporter-like protein
B01	CDS	1933939	1934517	STM14_2207	1933969	1934486	-	Hypothetical protein
B02	CDS	1380462	1380740	STM14_1568	1380492	1380709	-	Putative cytoplasmic protein
B03	CDS	1377451	1378335	STM14_1563	1377481	1378304	+	Aldose 1-epimerase
B04	CDS	1371804	1373738	STM14_1558	1371834	1373707	+	Putative serine protein kinase
B05	CDS	1370395	1371681	STM14_1556	1370425	1371650	+	Hypothetical protein
B07	CDS	1364878	1366062	STM14_1547	1364908	1366031	+	Putative amino acid/amine transport protein
B09	CDS	1996485	1997804	STM14_2299	1996515	1997773	+	Hypothetical protein
B10	CDS	2005190	2005930	STM14_2310	2005220	2005899	+	Hypothetical protein
B11	CDS	1992889	1993758	STM14_2295	1992919	1993727	-	DNA-binding transcriptional regulator HexR
B12	CDS	1943495	1944115	STM14_2216	1943525	1944084	-	Hypothetical protein
C01	CDS	1955391	1955975	STM14_2234	1955421	1955944	+	Putative nucleotide-binding protein
C02	CDS	1956017	1957300	STM14_2235	1956047	1957269	-	Putative inner membrane protein
C03	CDS	1959980	1961419	STM14_2237	1960055	1961388	-	rRNA (cytosine-C(5)-)-methyltransferase RsmF
C04	CDS	2052017	2052769	STM14_2369	2052047	2052738	+	Putative amino-acid ABC transporter ATP-binding protein YecC
C05	CDS	2008612	2009178	STM14_2314	2008642	2009147	-	Hypothetical protein
C06	CDS	2050772	2050996	STM14_2367	2050802	2050965	-	Hypothetical protein
C07	CDS	2013195	2013764	STM14_2320	2013225	2013733	+	Hypothetical protein
C08	CDS	2010482	2011225	STM14_2317	2010512	2011194	-	Putative SAM-dependent methyltransferase
C09	CDS	2011222	2012193	STM14_2318	2011252	2012162	-	Putative enzyme
C10	CDS	2052766	2053434	STM14_2370	2052796	2053403	+	Putative ABC-type amino acid transporter permease component

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Product Information Sheet for NR-42840

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C11 CDS 2065417 206417 206418 TM14_2355 2065177 2064167 Hypothetical protein D01 CDS 2053267 2004498 STM14_2371 2063485 2054410 - D-cysteline desutPhytase D02 CDS 2165780 2168607 Hypothetical protein - Putative innor membrane protein D03 CDS 213302 2169807 TM14_2686 2134868 - Putative innor membrane protein D04 CDS 213302 2169807 TM14_2682 2274869 - Putative innor membrane protein D06 CDS 2274869 STM14_2622 2274869 - Putative innor membrane protein D07 CDS 2267081 277142 227350 - Putative innor membrane protein D10 CDS 22670781 2770200 STM14_2622 226412 2273550 - Putative informembrane protein D11 CDS 22670781 2770200 STM14_2662 2206507 - Putative innor me	Well Position	Gene Type	Gene Start	Gene End	Target Gene (Locus Tag)	Deleted Region Start	Deleted Region End	Gene Strand	Description
C12 CDS 208387 2084107 + Hypothetical protein D01 CDS 2053455 2064441 STM4 2560 2168700 Plattive inner membrane protein D02 CDS 2166780 2166838 STM4 2650 216801 Plattive inner membrane protein D04 CDS 216500 15144286 2133932 2136664 Plattive inner membrane protein D05 CDS 216500 15144 2465 216500 15144 2465 216500 15144 2465 216500 15144 2465 2274691 Multidrog diffux system protein 1616 D06 CDS 22737281 STM4 2826 227051 Plattive behydrates 201610 1161 2016 201610 216690 11414 248576 228567 Plattive behydrates 201610 1161 201610 216102 220721 227381 STM14 248576 2305661 2406101 1161 230567 Plattive behydrates 2016102 230507 2305601 2305700	C11	CDS	2065147	2066412	STM14_2385	2065177	2066381	-	Putative inner membrane protein
DD1 CDS 2053465 2054441 STM14 2271 2053485 2054471 + Deckstein membrane protein D02 CDS 2169779 218673 STM14 2660 2196971 + Putative innon acid transport protein D04 CDS 2133902 115535 STM14 2546 2136034 + Putative innon acid transport protein D05 CDS 2165200 115535 STM14 2544 2200709 + Putative innor membrane protein D07 CDS 2249481 2245481 2249482 2270420 STM14 2621 2270320 STM14 2621 2270320 STM14 2622 2270321 STM14 2622 2270321 ZTM14 2622 2270321 ZTM14 2632 2270321 ZTM14	C12	CDS	2083287	2084198	STM14_2410	2083317	2084167	+	Hypothetical protein
DD2 CD5 2186780 2186803 Filter Putative inner membrane protein D04 CD5 218730 2184603 STM14 2486 2133932 2134668 Putative inner membrane protein D05 CD5 2186302 2134669 STM14 2486 2186302 Putative anino acid transport protein D06 CD5 218903 STM14 2486 2186304 Putative dehydrates D07 CD5 2270201 2271281 2272462 228462 Putative dehydrates D08 CD5 2270201 2271281 Putative infinit membrane protein D11 CD5 2270201 227231 2272326 Putative brotes E01 CD5 2280561 STM14 226529 2280641 Putative brotes E02 CD5 2306013 STM14 2682 2306542 2306491 Putative brotes E03 CD5 2308031 STM14 2682 230454 Putative brotes Putative brotes Putative brotes	D01	CDS	2053455	2054441	STM14_2371	2053485	2054410	+	D-cysteine desulfhydrase
D03 CDS 219379 2198743 2198742 + Putative amino acid transport protein D04 CDS 2133002 2146668 STM14 2485 2185230 2186686 + Hypothetical protein D06 CDS 2199883 2200807 STM14 2242 2263645 - Multidrug efflux system protein Multidrug efflux system subunit MdE D07 CDS 2264441 2264442 2264442 2264442 - Multidrug efflux system subunit MdB D10 CDS 22670763 STM14 22632 227028 - Multidrug efflux system subunit MdB D11 CDS 2205203 STM14 22632 2282697 - Putative proteins Putative proteins D12 CDS 2305601 STM14 2664 2305677 228569 + Putative sensor transe Putative sensor transe E04 CDS 2306013 2307601 STM14 2662 2304431 + Putative ABC-type proline/glycline betaine transport	D02	CDS	2185780	2186838	STM14_2550	2185810	2186807	+	Putative inner membrane protein
D04 CDS 213402 2134690 FTM14, 2465 213302 2134668 - Putative inner membrane protein D05 CDS 218500 218500 Putative dehydratene protein D06 CDS 2273278 2274690 STM14 2627 227300 2274761 Putative dehydratene protein D08 CDS 2264473 2264732 227300 2274761 Putative chapcrone D09 CDS 2267081 STM14 2625 2270102 2270161 Putative inner membrane protein D10 CDS 22670781 2270200 STM14 2625 2281671 Putative inner membrane protein D11 CDS 2280561 STM14 2662 230527 2306951 Putative wor-component response-regulatory protein E04 CDS 2308051 STM14 2662 2306542 2310431 Putative Wor-component response-regulatory protein E06 CDS 2305251 2310462 STM14 2661 230642 230441 Putative ABC-type proline/glycine betaine transport E05 CDS	D03	CDS	2197379	2198743	STM14_2560	2197409	2198712	+	Putative amino acid transport protein
DD6 CD5 2185200 218535 STM14_2548 215230 2165204 + Hypothecical protein DD6 CD5 22199863 STM14_2624 220308 - Multidrug efflux system protein D06 CD5 2248448 2266468 STM14_2622 2248492 2268647 - Putative chaperone D06 CD5 2264478 2266648 STM14_2625 227010 227142 - Putative chaperone D01 CD5 2267078 STM14_2625 227021 2272326 - Multidrug efflux system subunit Md15 D12 CD5 2206605 STM14_2641 228569 - Putative wor-component response-regulatory protein E04 CD5 2306013 STM14_2662 230643 2307667 + Putative wor-component response-regulatory protein E04 CD5 2306013 STM14_2662 230643 2307667 + Putative MaC-type proline/glycine betaine transport E04 CD5 2306013 STM14_2662 230643 23107	D04	CDS	2133902	2134699	STM14_2485	2133932	2134668	-	Putative inner membrane protein
Do6 CDS 2109983 2200807 STM14_2664 2200776 + Putative delydratese D07 CDS 2273782 STM14_2627 222308 2274690 STM14_2627 Putative chaperone D08 CDS 2284044 2265365 STM14_2627 Putative chaperone D10 CDS 2287078 2277080 STM14_2665 2270169 - Multidrug efflux system subunit Md16 D11 CDS 2287078 2277081 STM14_2666 2203642 - Putative protesse E01 CDS 2286465 STM14_2664 2200586 + Putative adc-type proliner(synothese transport E04 CDS 2306911 STM14_2666 2309454 2312514 + Putative adc-type proliner(synothese transport E06 CDS 2329645 STM14_2667 2309454 2312514 + Putative adc-type proliner(synothese transport E06 CDS 2342964 STM14_2717 232519 259247 + Putative adc-type proliner(synothese transport	D05	CDS	2185200	2185535	STM14_2548	2185230	2185504	+	Hypothetical protein
D07 CDS 2273278 2274690 STM14_282 22874690	D06	CDS	2199983	2200807	STM14_2564	2200013	2200776	+	Putative dehydratase
D06 CDS 2284044 2285366 STM14_2852 2285365 - Putative chaperone D09 CDS 2285478 S27078 227009 STM14_2852 2270169 - Multidrug efflux system subunit Md12 D11 CDS 2285778 2270381 STM14_2862 220231 2271285 - Multidrug efflux system subunit Md12 D12 CDS 2285586 STM14_2862 2203527 2305865 + Putative processe E02 CDS 2305297 2306018 STM14_2862 2305832 2305805 + Putative secomponent response-regulatory protein E04 CDS 2308600 STM14_2662 2306830 2309500 + Putative secomponent system permease component E05 CDS 2305215 STM14_2669 2310582 STM14_277 2332302 2349405 STM14_277 2332302 + Putative table membrane protein E06 CDS 2325405 STM14_277 2332302 234017 - Putative table memembrane pro	D07	CDS	2273278	2274690	STM14_2627	2273308	2274659	-	Multidrug efflux system protein MdtE
D09 CDS 228478 2284878 2284878 2284878 2284878 2284878 228478 228478 228478 228478 228478 2270200 TM4 2625 227010 2270200 TM4 2625 227016 2270201	D08	CDS	2264044	2265396	STM14_2622	2264122	2265365	-	Putative chaperone
D10 CDS 2267076 2270201 STM14_2662 227021 STM14_2662 227021 STM14_2664 2282567 - Multidrug efflux system subunit MdtC D11 CDS 22824057 IstM14_2664 2282567 - Putative processe E01 CDS 2286465 STM14_2662 2305327 2305985 + Putative Asc-type proline/glycine betaine transport E02 CDS 23066015 STM14_2666 2306830 2309500 + Putative Asc-type proline/glycine betaine transport E04 CDS 2309515 STM14_2669 2311663 2312514 + Putative Asc-type proline/glycine betaine transport E06 CDS 2310462 STM14_2669 2311658 2312514 + Putative Tansport protein E07 CDS 23252160 2352483 STM14_2707 2335114 2351201 - S-domydutation ascore S-monydutation ascore Putative Tansport protein E08 CDS 23253084 2374863 STM14_2741 2336027 2326101 - </td <td>D09</td> <td>CDS</td> <td>2254878</td> <td>2256458</td> <td>STM14_2615</td> <td>2254908</td> <td>2256427</td> <td>-</td> <td>Putative inner membrane protein</td>	D09	CDS	2254878	2256458	STM14_2615	2254908	2256427	-	Putative inner membrane protein
D11 CDS 2270201 2273281 STM14_2664 2273260 - Multidug price Multidug with system subunit MdtC D12 CDS 2285596 STM14_2641 2285596 - Putative protease E01 CDS 2285566 STM14_2661 2305327 2305985 + Putative Brochemotent E03 CDS 2308000 STM14_2666 2308604 2307667 + Putative Brochemotent Putative	D10	CDS	2267078	2270200	STM14_2625	2267108	2270169	-	Multidrug efflux system subunit MdtB
D12 CDS 228/237 228/256 Year Putative protease E01 CDS 2286665 STM14_2662 2305327 2305985 + Putative Maccomponent response-regulatory protein E02 CDS 2306013 STM14_2662 2305327 2305985 + Putative ABC-type proline/glycine betaine transport E04 CDS 2308600 STM14_2661 2309643 2309640 + Putative ABC-type proline/glycine betaine transport E05 CDS 2309515 2310462 STM14_2667 2309546 2310431 + Putative ABC-type proline/glycine betaine transport E06 CDS 2309505 STM14_2767 2382130 2382701 - Schornydjutathion hydrolase E08 CDS 2330524 STM14_2773 2382102 2362816 - Elongation factor P E11 CDS 2368054 STM14_273 2380302 2364017 - Putative ABC-type dipplide/digoppide/nic/kl <ttr> F01 CDS 2369587 2370681 STM14_2741 2363062 2364017</ttr>	D11	CDS	2270201	2273281	STM14_2626	2270231	2273250	-	Multidrug efflux system subunit MdtC
E01 CDS 2286566 2286565 STM14_2661 2286541 - Lipid knase E02 CDS 2306016 STM14_2662 2306327 230586 + Putative Servor knase E03 CDS 2308001 STM14_2663 2306404 2307667 + Putative Servor knase E04 CDS 2308515 2310462 STM14_2666 2308800 2309560 + Putative Servor knase E06 CDS 2310428 STM14_2667 2309545 2310431 + Putative Servor knase E07 CDS 2325631 STM14_2777 2343025 231412 - Putative Enchroponent respondent E09 CDS 2342995 2343428 STM14_2774 2362076 2362781 - Futative Enchroponent respondent E10 CDS 236648 STM14_2741 2369017 - Putative Anchroponent respondent respondent respondent respondent respondent respondent respondent re	D12	CDS	2281237	2282598	STM14_2634	2281267	2282567	-	Putative protease
E02 CDS 23063297 2306016 STM14_2662 2305327 2305985 + Putative Mo-component response-regulatory protein YehT E03 CDS 2308000 STM14_2663 2308000 2309601 + Putative sensor kinase E04 CDS 2308000 2309515 STM14_2663 2308800 + Putative sensor kinase E05 CDS 2309515 2310462 STM14_2667 2309545 2310431 + Putative ABC-type proline/glycine betaine transport system perimeses component E06 CDS 2315465 STM14_2707 2352130 2352932 + Putative ABC-type proline/glycine betaine transport system perimetransport protein E06 CDS 2352402 2349025 2349025 2349026 236211 - Putative ABC-type Proline/glycine betaine transport system perimetars or protein E10 CDS 2369042 2364048 STM14_2719 2363012 - Putative ABC-type Inder/not component F01 CDS 2369062 2370661 STM14_2742 237011 2371676	E01	CDS	2285566	2286465	STM14_2641	2285596	2286434	-	Lipid kinase
E03 CDS 2308013 2307667 + Putative sensor kinase E04 CDS 2308800 2309513 STM14_2662 2308800 2309500 + Putative ABC-type proline/glycine betaine transport E05 CDS 2309515 2310462 STM14_2667 2309545 2310431 + Putative ABC-type proline/glycine betaine transport E06 CDS 2315245 STM14_2717 2352130 2352932 + Putative DNA-binding transcriptional regulator E06 CDS 2342995 2341682 231142 2351142 235114 236017 Putative cobalamin biosynthetic protein E10 CDS 2369587 2370681 STM14_274 2370765 Putative ABC-type dipeptide/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokelg/lokepetad/lokelg/lokelg/lokepetad/lokelg/lokepetad/lokelg/	E02	CDS	2305297	2306016	STM14_2662	2305327	2305985	+	Putative two-component response-regulatory protein YehT
E04 CDS 2308800 2309501 STM14_2666 2308830 2309500 + Putative ABC-type proline/glycine betaine transport system permease component E05 CDS 2310462 STM14_2667 2309545 2310431 + Putative ABC-type proline/glycine betaine transport system ATPase component E06 CDS 2311628 23115245 STM14_2717 2352130 2352932 + Putative transport protein E07 CDS 2352042 2344395 STM14_2717 2353114 2352932 + Putative transport protein E10 CDS 2363062 236448 STM14_2713 2362076 2362076 - Putative cobalamin biosynthetic protein F01 CDS 2369587 2370681 STM14_2741 2369617 2370650 - Putative cobalamin biosynthetic protein F02 CDS 2370681 STM14_2742 2370711 2371676 - Putative ABC-type dipeptide/icid/glogeptide/ic/cle F04 CDS 2376101 2377661 STM14_2742 23771313 2373641	E03	CDS	2306013	2307800	STM14_2663	2306043	2307667	+	Putative sensor kinase
Los Losses Losses Losses Losses Losses Losses Losses Putative ABC-type proline/typic inc betaine transport E05 CDS 231042 STM14_2667 2309545 2310431 + System ATPase component E06 CDS 2315281 Statta Putative Tarsport protein E07 CDS 2352905 STM14_2707 235310 2352932 + Putative Tarsport system premease component E08 CDS 2352932 StM14_2707 2353041 - Duative Inner membrane protein E10 CDS 2362139 2362491 StM14_2741 2369027 2360401 - Putative ABC-type dipertide/loigopetide/loikel F01 CDS 2369587 2370681 STM14_2742 2370711 2371675 - Putative ABC-type dipertide/loigopetide/loikel F02 CDS 2370681 2371708 STM14_2742 2371738 2373266 - Putative ADC-type dipertide/loigopetide/loikel F03 CDS 2373012 23776451 STM14_2742	F04	CDS	2308800	2300531	STM14 2666	2308830	2309500	+	Putative ABC-type proline/glycine betaine transport
E05 CDS 2309515 231042 STM14_2667 2309545 2310431 + Putative ABC-type proline/glycine betaine transport system ATPase component E06 CDS 2311628 231152	204	000	2000000	2000001	2000	2000000	2000000		system permease component
E06 CDS 2311628 23112445 STM14 2707 2352103 + Putative transport protein E07 CDS 2352092 + Putative transport protein Feature E08 CDS 2353084 2354133 STM14 2707 2343025 2343701 - S-formylglutathione hydrolase E09 CDS 2363084 2364133 STM14 2713 2362016 - Elongation factor P E10 CDS 2365182 2364048 STM14 2731 2366017 - Putative colarismi biosynthetic protein F01 CDS 2369587 2370681 STM14 2741 2369617 2370650 - Putative colarismi biosynthetic/ickel transport system permease transport system permease component F02 CDS 2371081 237142 2377112 2377366 - Putative colarismi biosynthetic/ickel transport system Parmease component F03 CDS 237301 2373301 237331 2373614 + Putative conspontent F04 CDS 2376011 2377864 STM	E05	CDS	2309515	2310462	STM14_2667	2309545	2310431	+	Putative ABC-type proline/glycine betaine transport system ATPase component
E07 CDS 2352100 2352903 STM14 2717 2352130 2352932 + Putative DNA-binding transcriptional regulator E08 CDS 2345905 2343820 - Putative inner membrane protein E10 CDS 2362139 2362249 STM14 2733 2362076 2362818 - Putative cobalamin biosynthetic protein E11 CDS 2360867 2370681 STM14_2741 2369617 2370650 Putative cobalamin biosynthetic protein F01 CDS 2360867 2370681 STM14_2742 2370711 2371675 - Putative ABC-type dipeptide/nickel transport system premease component F02 CDS 237108 2373297 STM14_2743 2371738 2373264 - Putative ABC-type dipeptide/nickel transport system ATPase component F03 CDS 237101 2377861 STM14_2743 237331 2373814 + Hypothetical protein F04 CDS 237301 2377861 STM14_2773 2380024 2380410 - Hypoth	E06	CDS	2311628	2312545	STM14_2669	2311658	2312514	+	Putative transport protein
E08 CDS 2343952 STM14_2707 2343025 2343701	E07	CDS	2352100	2352963	STM14_2717	2352130	2352932	+	Putative DNA-binding transcriptional regulator
E09 CDS 2353084 2354114 219 2353114 2354102	E08	CDS	2342995	2343852	STM14_2707	2343025	2343701	-	S-formylglutathione hydrolase
E10 CDS 2362139 2362049 STM14_2733 2362076 2362818 - Elongation factor P E11 CDS 2363062 2364048 STM14_2734 2363092 2364017 - Putative cobalamin biosynthetic protein F01 CDS 2369687 2370681 STM14_2741 2369617 2370650 - Putative cabalamin biosynthetic protein F02 CDS 2370681 STM14_2742 2370711 2371675 - Putative ABC-type dipeptide/oligopeptide/nickel transport system permease component F03 CDS 2373045 STM14_2742 237331 2373614 + Hypothetical protein F04 CDS 237301 2373645 STM14_2748 2376131 2373830 - Putative ABC-type transport system ATPase component F05 CDS 2376101 2377861 STM14_2752 2379057 238003 + Nucleoid-associated protein MdpA F07 CDS 2454575 STM14_2751 2360442 2345010 - Hypothetical protein	E09	CDS	2353084	2354133	STM14_2719	2353114	2354102	-	Putative inner membrane protein
E11 CDS 2363062 2364048 STM14_2734 2363092 2364017 Putative cobalamin biosynthetic protein F01 CDS 2369687 2370681 STM14_2741 2369617 2370650 - Putative cABC-type dipeptide/oligopeptide/nickel transport system permease F02 CDS 2370681 2371706 STM14_2742 237173 2371675 - Putative cABC-type dipeptide/oligopeptide/nickel transport system permease component F03 CDS 237301 2373645 STM14_2748 237331 2373614 + Hypothetical protein F04 CDS 237301 2377861 STM14_2748 2371738 2377830 - Putative cABC-type transport system ATPase component F05 CDS 2370027 2380341 STM14_2752 2370677 2380034 + Nucleid-associated protein helicase F06 CDS 2380241 S380441 STM14_2821 2454180 2445454 - Putative inore membrane protein F07 CDS 2485476 STM14_2874 2493577 2494730 </td <td>E10</td> <td>CDS</td> <td>2362139</td> <td>2362849</td> <td>STM14_2733</td> <td>2362076</td> <td>2362818</td> <td>-</td> <td>Elongation factor P</td>	E10	CDS	2362139	2362849	STM14_2733	2362076	2362818	-	Elongation factor P
F01 CDS 2369587 2370681 STM14_2741 2369617 2370650 Putative ABC-type dipeptide/oligopeptide/nickel transport system permease F02 CDS 2370681 2371706 STM14_2742 2370711 2371675 Putative ABC-type dipeptide/oligopeptide/nickel transport system permease component F03 CDS 2371070 STM14_2743 2371378 2373266 Putative ABC-type dipeptide/oligopeptide/nickel transport system permease F04 CDS 237301 2373645 STM14_2742 237311 2373674 Putative ABC-type dipeptide/oligopeptide/nickel transport system permease F05 CDS 2370101 2377861 STM14_2748 237311 2373730 Putative ATP-dependent helicase F06 CDS 2380101 2377861 STM14_2748 237614 Putative ATP-dependent helicase F08 CDS 245150 2454575 STM14_2812 2430471 2480470 Putative ATP-dependent helicase F10 CDS 249547 944730 STM14_2876 249576 2494730 Aminotransferase AlaT F11	E11	CDS	2363062	2364048	STM14_2734	2363092	2364017	-	Putative cobalamin biosynthetic protein
F02 CDS 2370681 2371706 STM14_2742 2370711 2371675 Putative ABC-type dipeptide/oligopeptide/nickel transport system ATPase component F03 CDS 2371708 2373297 STM14_2743 2371378 2373266 Putative ABC-type dipeptide/oligopeptide/nickel transport system ATPase component F04 CDS 2373611 2373615 STM14_2742 2373331 2373614 + Hypothetical protein F05 CDS 2376101 2377861 STM14_2752 2380034 + Nucleoid-associated protein NdpA F07 CDS 2450214 2380411 STM14_2753 2380244 2380410 + Hypothetical protein F08 CDS 2453292 245376 STM14_2872 2453357 2497300 - Aminotransferase AlaT F10 CDS 2495347 2494761 STM14_2874 2498377 2494730 - Aminotransferase AlaT F11 CDS 249546 2497372 STM14_2874 249566 249731 + Hypothetical protein <tr< td=""><td>F01</td><td>CDS</td><td>2369587</td><td>2370681</td><td>STM14_2741</td><td>2369617</td><td>2370650</td><td>-</td><td>Putative ABC-type dipeptide/oligopeptide/nickel transport system permease</td></tr<>	F01	CDS	2369587	2370681	STM14_2741	2369617	2370650	-	Putative ABC-type dipeptide/oligopeptide/nickel transport system permease
F03 CDS 2371708 2373297 STM14_2743 2371738 2373266 Putative ABC-type transport system ATPase component F04 CDS 237301 2373645 STM14_2744 2373331 2376101 + Hypothetical protein F05 CDS 2376101 2377861 STM14_2752 2379057 2380003 + Nucleoid-associated protein NdpA F06 CDS 2380241 2380411 STM14_2753 2380244 2380410 - Hypothetical protein F07 CDS 2464150 2454575 STM14_2832 2453180 2453444 - Putative NTP pyrophosphohydrolase F08 CDS 245329 245376 STM14_2874 2493577 2494730 - Aminotransferase AlaT F10 CDS 2495562 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2544262 545265 STM14_2874 2547244 254824 + Hypothetical protein G02 CDS 25472	F02	CDS	2370681	2371706	STM14_2742	2370711	2371675	-	Putative ABC-type dipeptide/oligopeptide/nickel transport system permease component
F04 CDS 2373301 2373645 STM14_2744 2373331 2373614 + Hypothetical protein F05 CDS 2376101 2377861 STM14_2748 2379057 2380003 + Hucleoid-associated protein helicase F06 CDS 2380214 2380441 STM14_2753 2380244 2380410 - Hypothetical protein F07 CDS 2380214 2380441 STM14_2753 2380244 2380410 - Hypothetical protein F08 CDS 2454150 2454575 STM14_2831 245359 245395 + Putative inner membrane protein F10 CDS 2493577 2494761 STM14_2876 2493576 2497341 + Putative inner membrane protein F11 CDS 2498119 2498613 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2547214 2548146 STM14_2878 2498149 2498542 + Hypothetical protein G02 <t< td=""><td>F03</td><td>CDS</td><td>2371708</td><td>2373297</td><td>STM14_2743</td><td>2371738</td><td>2373266</td><td>-</td><td>Putative ABC-type transport system ATPase component</td></t<>	F03	CDS	2371708	2373297	STM14_2743	2371738	2373266	-	Putative ABC-type transport system ATPase component
F05 CDS 2376101 2377861 STM14 2748 2376131 2377830 Putative ATP-dependent helicase F06 CDS 2379027 2380034 STM14 2752 2379057 2380033 + Nucleoid-associated protein NdpA F07 CDS 2380244 2380244 2380244 2380410 - Hypothetical protein F08 CDS 2453150 STM14 2833 2453359 2453446 - Putative Inner membrane protein F10 CDS 245327 2494761 STM14 287 2493577 2494730 - Aminotransferase AlaT F11 CDS 2498613 STM14 287 2493577 2494731 + Putative Inter membrane protein G01 CDS 2498613 STM14 287 2493577 2494734 + Hypothetical protein G02 CDS 2544456 2545265 STM14 291 2544448 2545264 + Hypothetical protein G02	F04	CDS	2373301	2373645	STM14 2744	2373331	2373614	+	Hypothetical protein
F06 CDS 2379027 2380034 STM14_2752 2379057 2380003 + Nucleoid-associated protein NdpA F07 CDS 2380214 2380241 STM14_2753 2380244 2380410 - Hypothetical protein F08 CDS 2454150 2454575 STM14_2832 24534180 2454544 - Putative NTP pyrophosphohydrolase F09 CDS 2453329 2453329 2453329 2453329 2453345 + Putative inner membrane protein F10 CDS 2493547 2494761 STM14_2874 2493577 2494730 - Aminotransferase AlaT F11 CDS 2498513 STM14_2874 2493576 2497341 + Putative inner membrane protein G01 CDS 2547214 254486 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 251571 2511122 STM14_2832 2510601 2511091 + Phosphodiesterase G04 CDS <	F05	CDS	2376101	2377861	STM14 2748	2376131	2377830	-	Putative ATP-dependent helicase
F07 CDS 2380214 2380441 STM14_2753 2380244 2380410 - Hypothetical protein F08 CDS 2454150 2454575 STM14_2832 2454180 2454544 - Putative NTP pyrophosphohydrolase F09 CDS 2453329 2453376 STM14_2831 2453359 2453345 + Putative inner membrane protein F10 CDS 2493547 2493772 STM14_2876 2493577 2494730 - Aminotransferase AlaT F11 CDS 2493547 2494761 STM14_2876 2495576 2497341 + Putative response regulator F12 CDS 2498119 2498612 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2544456 2545265 STM14_2931 2544486 254524 + Hypothetical protein G02 CDS 2517271 2511122 STM14_2893 2511001 2511071 + Phosphodiesterase G03 CDS <td>F06</td> <td>CDS</td> <td>2379027</td> <td>2380034</td> <td>STM14 2752</td> <td>2379057</td> <td>2380003</td> <td>+</td> <td>Nucleoid-associated protein NdpA</td>	F06	CDS	2379027	2380034	STM14 2752	2379057	2380003	+	Nucleoid-associated protein NdpA
F08 CDS 2454150 2454575 STM14_2832 2454180 2454544 - Putative NTP pyrophosphohydrolase F09 CDS 2453329 2453976 STM14_2831 2453359 2453945 + Putative inner membrane protein F10 CDS 2493547 2494761 STM14_2876 2493577 2494730 - Aminotransferase AlaT F11 CDS 2495546 2497372 STM14_2876 2495576 2497341 + Putative response regulator F12 CDS 2498119 2498613 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2547214 2548146 STM14_2934 2547244 2548061 + N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase G02 CDS 2510571 2511122 STM14_2893 2510601 2511701 + Putative glutathione S-transferase G04 CDS 2511178 2511805 STM14_2896 2511208 2511791 + Putative glutathione S	F07	CDS	2380214	2380441	STM14 2753	2380244	2380410	-	Hypothetical protein
F09 CDS 2453329 2453359 2453359 2453945 + Putative inner membrane protein F10 CDS 2493547 2494761 STM14_2874 2493577 2494730 - Aminotransferase AlaT F11 CDS 2495546 2497372 STM14_2876 2495576 2497311 + Putative response regulator F12 CDS 249819 2498613 STM14_2876 2495576 2497341 + Putative response regulator G01 CDS 2544456 2545265 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 2547214 2548146 STM14_2934 2547244 2548061 + Mosphate Mosphat Mosphat Mosphate <td>F08</td> <td>CDS</td> <td>2454150</td> <td>2454575</td> <td>STM14 2832</td> <td>2454180</td> <td>2454544</td> <td>-</td> <td>Putative NTP pyrophosphohydrolase</td>	F08	CDS	2454150	2454575	STM14 2832	2454180	2454544	-	Putative NTP pyrophosphohydrolase
F10 CDS 2493547 2494761 STM14_2874 2493577 2494730 - Aminotransferase AlaT F11 CDS 2495546 2497372 STM14_2876 2495576 2497341 + Putative response regulator F12 CDS 2498119 2498613 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2544456 2545265 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 2547214 2548146 STM14_2893 2547244 2548061 + N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase G03 CDS 2510571 2511122 STM14_2893 2510601 2511091 + Phosphodiesterase G04 CDS 2511971 2511822 STM14_2894 2511208 2512581 - Putative glutathione S-transferase G06 CDS 2512738 2513631 STM14_2896 2512581 - Putative sugar nucleotide epimerase G0	F09	CDS	2453329	2453976	STM14 2831	2453359	2453945	+	Putative inner membrane protein
F11 CDS 2495546 2497372 STM14_2876 249576 2497341 + Putative response regulator F12 CDS 2498119 2498613 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2544456 2545265 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 2547214 2548146 STM14_2934 2547244 2548061 + Ms-glutamine S-adenosyl-L-methionine-dependent methyltransferase G03 CDS 2510571 2511122 STM14_2893 2510601 2511091 + Phosphodiesterase G04 CDS 2511178 2511822 STM14_2894 2511208 2511791 + Putative glutathione S-transferase G05 CDS 2512178 2511803 STM14_2896 2512768 2513600 - Putative glutathione S-transferase G06 CDS 2543800 2543831 STM14_2929 2543630 2543844 + Putative glutathione S-transferase <td>F10</td> <td>CDS</td> <td>2493547</td> <td>2494761</td> <td>STM14 2874</td> <td>2493577</td> <td>2494730</td> <td>-</td> <td>Aminotransferase AlaT</td>	F10	CDS	2493547	2494761	STM14 2874	2493577	2494730	-	Aminotransferase AlaT
F12 CDS 2498119 2498613 STM14_2878 2498149 2498582 + Hypothetical protein G01 CDS 2544456 2545265 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 2547214 2548146 STM14_2934 2547244 2548061 + N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase G03 CDS 2510571 2511122 STM14_2893 2510601 25111091 + Phosphodiesterase G04 CDS 2511178 2511822 STM14_2895 2511208 2511791 + Putative glutathione S-transferase G05 CDS 2511965 2512612 STM14_2896 2512581 - Putative glutathione S-transferase G06 CDS 2513631 STM14_2929 2543630 2543844 + Putative cytoplasmic protein G08 CDS 2543908 2544456 STM14_2937 2548632 - Hypothetical protein G10 CDS 2567557 <td>F11</td> <td>CDS</td> <td>2495546</td> <td>2497372</td> <td>STM14 2876</td> <td>2495576</td> <td>2497341</td> <td>+</td> <td>Putative response regulator</td>	F11	CDS	2495546	2497372	STM14 2876	2495576	2497341	+	Putative response regulator
G01 CDS 2544456 2545265 STM14_2931 2544486 2545234 + Hypothetical protein G02 CDS 2547214 2548146 STM14_2934 2547244 2548061 + N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase G03 CDS 2510571 2511122 STM14_2893 2510601 2511091 + Phosphodiesterase G04 CDS 2511178 2511822 STM14_2894 2511208 2511791 + Putative glutathione S-transferase G06 CDS 2511785 25112612 STM14_2896 2512768 2513600 - Putative glutathione S-transferase G07 CDS 2543600 2543875 STM14_2929 2543630 2543844 + Putative sugar nucleotide epimerase G08 CDS 2548312 2548863 STM14_2937 2549687 2551773 + Hypothetical protein G10 CDS 2549657 2568795 STM14_2937 2549687 2551773 + Multipha	F12	CDS	2498119	2498613	STM14 2878	2498149	2498582	+	Hypothetical protein
G02 CDS 2547214 2548146 STM14_2934 2547244 2548061 + N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase G03 CDS 2510571 2511122 STM14_2893 2510601 2511091 + Phosphodiesterase G04 CDS 2511178 2511822 STM14_2894 2511208 2511791 + Putative glutathione S-transferase G05 CDS 2511965 2512612 STM14_2895 2511995 2512581 - Putative glutathione S-transferase G06 CDS 2512738 2513631 STM14_2896 2512768 2513600 - Putative glutathione S-transferase G07 CDS 2543600 2543875 STM14_2929 2543630 2543844 + Putative cytoplasmic protein G08 CDS 2548312 2548863 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2937 2549687 2551773 +<	G01	CDS	2544456	2545265	STM14 2931	2544486	2545234	+	Hypothetical protein
G03 CDS 2510571 2511122 STM14_2893 2510601 2511091 + Phosphodiesterase G04 CDS 2511178 2511822 STM14_2894 2511208 2511791 + Putative glutathione S-transferase G05 CDS 2511965 2512612 STM14_2895 2511995 2512581 - Putative glutathione S-transferase G06 CDS 2512738 2513631 STM14_2896 2512768 2513600 - Putative glutathione S-transferase G07 CDS 2543600 2543875 STM14_2929 2543630 2543844 + Putative cytoplasmic protein G08 CDS 2543908 2544456 STM14_2930 2543938 2544425 + Putative cytoplasmic protein G09 CDS 2548312 2548863 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2930 2549638 2590305 - Putative Na+-depend	G02	CDS	2547214	2548146		2547244	2548061	+	N5-glutamine S-adenosyl-L-methionine-dependent
G04 CDS 251178 2511822 STM14_2894 2511208 2511791 + Putative glutathione S-transferase G05 CDS 2511965 2512612 STM14_2895 2511995 2512581 - Putative glutathione S-transferase G06 CDS 2512738 2513631 STM14_2896 2512768 2513600 - Putative glutathione S-transferase G07 CDS 2543600 2543875 STM14_2929 2543630 2543844 + Putative cytoplasmic protein G08 CDS 2543908 2544456 STM14_2930 2543938 2544425 + Putative cytoplasmic protein G09 CDS 2548312 2548863 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit G10 CDS 2567557 2568795 STM14_2954 2567587 2568764 + Aminotransferase H02 CDS 2589338 2590305 - Putative Na+-dependent transporter H03 CDS	G03	CDS	2510571	2511122	STM14 2893	2510601	2511091	+	Phosphodiesterase
G05 CDS 2511965 2512612 STM14_2895 2511995 2512581 - Putative glutathione's during of the second of the secon	G04	CDS	2511178	2511822	STM14 2894	2511208	2511791	+	Putative glutathione S-transferase
G06 CDS 2512738 2513631 STM14_2896 2512768 2513600 - Putative sugar nucleotide epimerase G07 CDS 2543600 2543875 STM14_2929 2543630 2543804 + Putative sugar nucleotide epimerase G08 CDS 2543908 2544866 STM14_2930 2543938 2544425 + Putative cytoplasmic protein G09 CDS 2548312 2548863 STM14_2935 2548342 2548832 - Hypothetical protein G10 CDS 2549657 2551804 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2930 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohy	G05	CDS	2511965	2512612	STM14 2895	2511995	2512581	-	Putative glutathione S-transferase
G07 CDS 2543600 2543875 STM14_2929 2543630 2543844 + Putative cytoplasmic protein G08 CDS 2543908 2544456 STM14_2930 2543938 2544425 + Putative cytoplasmic protein G09 CDS 2548312 2548863 STM14_2935 2548342 2548832 - Hypothetical protein G10 CDS 2549657 2551804 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2934 2567587 2568764 + Aminotransferase H02 CDS 2589338 2590336 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase	G06	CDS	2512738	2513631	STM14_2896	2512768	2513600	-	Putative sugar nucleotide epimerase
G08 CDS 2543908 2544456 STM14_2930 2543938 2544425 + Putative cytoplasmic protein G09 CDS 2548312 2548863 STM14_2935 2548342 254832 - Hypothetical protein G10 CDS 2549657 2551804 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2934 2568767 2568764 + Aminotransferase H02 CDS 2589338 2590336 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3059 261026 2661354 - Putative arsenate reductase <t< td=""><td>G07</td><td>CDS</td><td>2543600</td><td>2543875</td><td>STM14 2929</td><td>2543630</td><td>2543844</td><td>+</td><td>Putative cytoplasmic protein</td></t<>	G07	CDS	2543600	2543875	STM14 2929	2543630	2543844	+	Putative cytoplasmic protein
G09 CDS 2548312 2548863 STM14_2935 2548342 2548322 - Hypothetical protein G10 CDS 2549657 2551804 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2934 2567587 2568764 + Aminotransferase H02 CDS 2589338 2590336 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate reductase <td>G08</td> <td>CDS</td> <td>2543908</td> <td>2544456</td> <td>STM14 2930</td> <td>2543938</td> <td>2544425</td> <td>+</td> <td>Putative cytoplasmic protein</td>	G08	CDS	2543908	2544456	STM14 2930	2543938	2544425	+	Putative cytoplasmic protein
G10 CDS 2549657 2551804 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2937 2549687 2551773 + Multifunctional fatty acid oxidation complex subunit alpha H01 CDS 2567557 2568795 STM14_2954 2567587 2568764 + Aminotransferase H02 CDS 2589338 2590336 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate	G09	CDS	2548312	2548863	STM14 2935	2548342	2548832	-	Hypothetical protein
H01 CDS 2567557 2568795 STM14_2954 2567587 2568764 + Aminotransferase H02 CDS 2589338 2590336 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate reductase	G10	CDS	2549657	2551804	STM14_2937	2549687	2551773	+	Multifunctional fatty acid oxidation complex subunit
HO2 CDS 258036 CTM14_2080 2580368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_2980 2589368 2590305 - Putative Na+-dependent transporter H03 CDS 2648886 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate reductase	H01	CDS	2567557	2568795	STM14 2954	2567587	2568764	+	Aminotransferase
H03 CDS 2648866 2649242 STM14_3045 2648916 2649211 - Hypothetical protein H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate reductase	H02	CDS	2589338	2590336	STM14_2980	2589368	2590305	-	Putative Na+-dependent transporter
H04 CDS 2638641 2639216 STM14_3038 2638671 2639185 + Putative pyrophosphohydrolase H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661385 STM14_3059 2661056 2661354 - Putative arsenate reductase	H03	CDS	2648886	2649242	STM14_2000	2648916	2649211	-	Hypothetical protein
H05 CDS 2710249 2711415 STM14_3097 2710279 2711384 + Hypothetical protein H06 CDS 2661026 2661056 2661354 - Putative arsenate reductase	H04	CDS	2638641	2639216	STM14_3038	2638671	2639185	+	Putative pyrophosphohydrolase
H06 CDS 2661026 2661385 STM14 3059 2661056 2661354 - Putative arsenate reductase	H05	CDS	2710249	2711415	STM14_3097	2710279	2711384	+	Hypothetical protein
	H06	CDS	2661026	2661385	STM14_3059	2661056	2661354	-	Putative arsenate reductase

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Product Information Sheet for NR-42840

SUPPORTING INFECTIOUS DISEASE RESEARCH

Well Position	Gene Type	Gene Start	Gene End	Target Gene (Locus Tag)	Deleted Region Start	Deleted Region End	Gene Strand	Description
H07	CDS	2661412	2662137	STM14_3060	2661442	2662106	+	DNA replication initiation factor
H08	CDS	2704600	2705778	STM14_3091	2704630	2705747	+	Outer membrane protein assembly complex subunit YfgL
H09	CDS	2705789	2706409	STM14_3092	2705819	2706378	+	Putative inner membrane protein
H10	CDS	2755627	2756964	STM14_3141	2755657	2756933	+	Putative transcriptional regulator
H11	CDS	2766121	2766756	STM14_3149	2766151	2766725	+	Hypothetical protein
H12	CDS	2732323	2732646	STM14_3116	2732353	2732615	+	Iron-sulfur cluster assembly protein

¹All information in this table was provided by the depositor at the time of deposition. ²Construction of each listed mutant has been confirmed either by PCR or by an array indicating a functional T7 promoter in the correct location and orientation. Mutants that did not produce such a signal on the array, or did not yield the expected mutant product during PCR, are not listed.