**Supporting Information**

**Enhanced Mutualistic Symbiosis between Soil Phages and Bacteria with Elevated Chromium-Induced Environmental Stress**

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**Table S1.** Physical chemical parameters of the soil samples

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Nitrate nitrogen | Ammonium nitrogen | pH | The organic matter | Total nitrogen | Total phosphorus | Total potassium | Alkaline hydrolysis nitrogen | Available phosphorus | Available potassium | Cadmium |
| mg/kg | mg/kg | g/kg | g/kg | g/kg | g/kg | mg/kg | mg/kg | mg/kg | mg/kg |
| L1 | 18.47 | 8.85 | 6.38 | 6.92 | 0.17 | 0.65  | 20.03 | 14.70 | 4.99  | 82.50 | 0.12 |
| L2 | 16.11 | 10.33 | 8.15 | 28.10 | 1.37 | 0.57  | 19.84 | 95.55 | 27.89  | 140.00 | 0.71 |
| L3 | 2.46 | 5.28 | 7.70 | 1.67 | 0.68 | 0.35  | 19.37 | 77.18 | 12.33  | 85.00 | 0.31 |
| Z1 | 15.07 | 5.58 | 8.89 | 14.57 | 0.89 | 0.85  | 21.07 | 40.43 | 13.17  | 190.00 | 0.25 |
| Z2 | 2.74 | 4.91 | 8.86 | 4.69 | 0.33 | 0.79  | 20.63 | 14.70 | 8.09  | 137.50 | 0.22 |
| Z3 | 0.94 | 5.55 | 8.85 | 2.72 | 0.21 | 0.64  | 19.51 | 18.38 | 5.18  | 112.50 | 0.17 |
| Z4 | 0.82 | 3.78 | 8.95 | 2.24 | 0.063 | 0.66 | 19.29 | 13.73 | 3.49 | 117.92 | 0.18 |
| Sample | CEC | DOC | Available sulfur | Total Chromium ( T Cr) | Available Cr | Available Cr(VI)  | Particles（%） | Soil type |
| cmol/kg | mg/kg | mg/kg | mg/kg | mg/kg | mg/kg | 2-0.05mm | 0.05-0.002mm | <0.002mm | US Standard |
| L1 | 14.92 | 207.56 | 159.22 | 44.92 | 0.11 | 0.04  | 64.69  | 27.11  | 8.21  | Sandy loam |
| L2 | 12.99 | 191.86 | 19.79 | 391.27 | 0.27 | 0.12  | 62.77  | 27.71  | 9.52  | Sandy loam |
| L3 | 11.37 | 40.12 | 12.72 | 261.27 | 6.76 | 6.64  | 70.71  | 15.00  | 14.29  | Sandy loam |
| Z1 | 8.02 | 62.79 | 38.10 | 374.27 | 0.91 | 0.13  | 13.86  | 72.64  | 13.50  | Silt loam |
| Z2 | 6.29 | 34.88 | 303.76 | 91.94 | 6.09 | 5.84 | 15.18  | 74.92  | 9.89  | Silt loam |
| Z3 | 5.18 | 27.91 | 383.34 | 644.57 | 413.84 | 361.60  | 19.38  | 72.11  | 8.51  | Silt loam |
| Z4 | 4.96 | 26.97 | 369.43 | 896.15 | 465.42 | 449.17 | 20.71 | 59.50 | 19.79 | Silt loam |

Note: Horizontal gradients of physicochemical properties were observed in both the LZ and ZY sites from the edge of detectable contamination to the epicenter of the Cr-contamination (show in **Fig.S1**). The concentrations of available Cr (defined as the total of exchangeable and soluble Cr) of taken samples were 0.11, 0.27, and 6.76 mg/kg in L1, L2, and L3 locations of LZ site, respectively (**Table S1**). The corresponding concentrations of available Cr were 0.91, 6.09, 413.84, and 465.42 mg/kg in Z1, Z2, Z3 and Z4 locations of ZY site, respectively (**Table S1**). Specifically, Cr (VI), which has been shown to have general biological toxicity, was the dominant species of Cr, and the concentrations of Cr (VI) and available Cr were highly positively correlated (R2 = 0.99, *p* < 0.01) (**Table S1**). Consistently, a decreasing gradient of total nitrogen, total organic matter, and total phosphorus were also observed from the edge of the contaminated site to the center (**Table S1**). Based on the Cr pollution level and nutrient conditions, these seven samples can be roughly divided into three groups: a slightly-contaminated group (L1, L2 and Z1), a moderately-contaminated group (L3 and Z2) and a severely-contaminated group (Z3 and Z4).

**Table S2.** Integrase family genes (annotated using PFAM)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| [PF00552](https://pfam.xfam.org/family?acc=PF00552) | PF14659 | PF13683 | PF14882 | PF13009 |
| PF00589 | PF13102 | PF07935 | PF12167 | PF14657 |
| PF00665 | PF13356 | PF09299 | PF12482 | PF13333 |
| PF02022 | PF16795 | PF12834 | PF18644 | PF13495 |
| PF02899 | PF17921 | PF12835 | PF18103 | PF09003 |
| PF02920 | PF18697 |  |  |  |

**Table S3.** Membrane transportor genes (annotated using KEGG)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| K01531 | K08151 | K08227 | K14696 | K17470 | K18936 | K07507 | K08220 | K14688 | K14718 | K18552 | K23254 | K01997 | K15555 |
| K01533 | K08152 | K08228 | K14697 | K17471 | K18989 | K07552 | K08221 | K14689 | K14719 | K18553 | K03322 | K01996 | K02073 |
| K01536 | K08153 | K08229 | K14700 | K17686 | K19364 | K07783 | K08222 | K14690 | K14720 | K18567 | K02051 | K01995 | K03523 |
| K01537 | K08154 | K08230 | K14701 | K18059 | K19478 | K07784 | K08223 | K11939 | K14990 | K18728 | K02044 | K01999 | K16783 |
| K02575 | K08156 | K08231 | K14702 | K18070 | K19541 | K07785 | K08169 | K12201 | K15102 | K23329 | K01990 | K02020 | K16784 |
| K02598 | K08157 | K08368 | K14704 | K18095 | K19542 | K07786 | K08170 | K12346 | K15113 | K23361 | K01992 | K07793 | K02071 |
| K03284 | K08158 | K08369 | K14706 | K18138 | K19552 | K05853 | K08171 | K13021 | K15115 | K23448 | K13896 | K07794 | K02072 |
| K03291 | K08159 | K08970 | K14708 | K18142 | K19576 | K06157 | K08172 | K13283 | K18833 | K23566 | K13895 | K07795 | K02047 |
| K03298 | K08160 | K08978 | K14709 | K18146 | K19577 | K06189 | K08173 | K13629 | K18887 | K23677 | K13894 | K11073 | K02045 |
| K03305 | K08161 | K09125 | K14710 | K18214 | K19578 | K06213 | K08174 | K15268 | K18888 | K24107 | K13893 | K07222 | K17207 |
| K03306 | K08162 | K09936 | K14711 | K18215 | K19585 | K06609 | K08175 | K15548 | K18889 | K24193 | K11103 | K11076 | K17205 |
| K03444 | K08163 | K10850 | K14712 | K18218 | K19594 | K06610 | K14430 | K16073 | K18890 | K24194 | K02067 | K11075 | K17206 |
| K03445 | K08164 | K11382 | K14713 | K18296 | K19646 | K06902 | K14637 | K16074 | K18891 | K21134 | K02066 | K11074 | K02030 |
| K03446 | K08165 | K11537 | K14714 | K18299 | K21133 | K08176 | K14638 | K16075 | K18892 | K18322 | K02013 | K03561 | K02052 |
| K03448 | K08166 | K11639 | K14715 | K18303 | K07122 | K08177 | K14640 | K16092 | K18893 | K22134 | K02015 | K03559 | K02053 |
| K03468 | K08167 | K11737 | K14716 | K18307 | K07191 | K08178 | K14683 | K16267 | K18894 | K22733 | K02016 | K02004 | K02054 |
| K05557 | K08168 | K11810 | K14717 | K18908 | K07238 | K08197 | K14684 | K16302 | K18899 | K22736 | K02000 | K02003 | K02055 |
| K05850 | K08224 | K14691 | K16788 | K18926 | K07240 | K08217 | K14685 | K16322 | K18902 | K23088 | K02001 | K02048 | K07225 |
| K07788 | K08225 | K14693 | K16789 | K18934 | K07241 | K08218 | K14686 | K16324 | K18324 | K23241 | K02002 | K15553 | K06076 |
| K07789 | K08226 | K14695 | K17469 | K18935 | K07243 | K08219 | K14687 | K16327 | K18326 | K23242 | K01998 | K15554 | K18480 |
| K02017 | K11535 | K03811 | K09690 | K20361 | K02043 | K07862 | K11734 | K02050 | K10126 | K10125 | K02029 | K02028 | K02049 |
| K02018 | K02019 | K03560 | K03562 | K17324 | K17325 | K17322 | K06214 | K04338 | K04337 | K11069 | K11070 | K11071 | K11072 |
| K10439 | K10441 | K10440 | K14347 | K17321 | K17323 |  |  |  |  |  |  |  |  |

**Table S4.** Reductase genes (annotated using KEGG)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| K15977 | K00342 | K17725 | K03951 | K03880 | K01118 | K00330 | K03968 | K11351 | K12972 | K13985 | K03939 | K03961 | K22470 |
| K00384 | K00341 | K12264 | K03942 | K03882 | K03611 | K09765 | K11353 | K11166 | K00528 | K00784 | K14737 | K03878 | K03949 |
| K00287 | K00340 | K08364 | K09008 | K03881 | K10680 | K09024 | K00383 | K11148 | K02164 | K06897 | K11170 | K03879 | K22182 |
| K00058 | K00339 | K11167 | K03947 | K03883 | K00297 | K06988 | K03937 | K18162 | K03673 | K14403 | K05361 | K07232 | K03956 |
| K00208 | K00338 | K11149 | K07305 | K03884 | K00077 | K14738 | K03950 | K03966 | K00067 | K16639 | K00121 | K01800 | K03946 |
| K00299 | K00337 | K14618 | K11147 | K00432 | K11209 | K14737 | K03959 | K03953 | K11752 | K01069 | K21456 | K01070 | K22366 |
| K00411 | K00336 | K03934 | K03935 | K01013 | K00344 | K10142 | K03944 | K03940 | K18979 | K00415 | K23790 | K00681 | K03952 |
| K00412 | K00335 | K00418 | K00381 | K00332 | K00380 | K19876 | K11164 | K00327 | K19784 | K00331 | K07007 | K00333 | K03958 |
| K00413 | K00334 | K00326 |  |  |  |  |  |  |  |  |  |  |  |

**Table S5.** Protein information of 4 viral contigs containing integrase genes (annotated by RAST)

|  |
| --- |
| Contig VC-2 |
| Feature ID | Type | Contig | Start | Stop | Frame | Strand | Length (bp) | Function |
| fig|6666666.691807.peg.1 | CDS | VC-2 | 3 | 146 | 3 | + | 144 | Glutathione-regulated potassium-efflux system protein KefC |
| fig|6666666.691807.peg.2 | CDS | VC-2 | 1047 | 157 | -3 | - | 891 | Transcriptional regulator, LysR family |
| fig|6666666.691807.peg.3 | CDS | VC-2 | 1094 | 1753 | 2 | + | 660 | Short-chain dehydrogenase |
| fig|6666666.691807.peg.4 | CDS | VC-2 | 1831 | 2289 | 1 | + | 459 | hypothetical protein |
| fig|6666666.691807.peg.5 | CDS | VC-2 | 3039 | 2365 | -3 | - | 675 | Putative periplasmic cytochrome type-C oxidoreductase signal peptide protein (EC 1.-.-.-) |
| fig|6666666.691807.peg.6 | CDS | VC-2 | 3156 | 4010 | 3 | + | 855 | ATPase associated with various cellular activities, AAA\_5 |
| fig|6666666.691807.peg.7 | CDS | VC-2 | 4019 | 4753 | 2 | + | 735 | Acetyltransferase, GNAT family |
| fig|6666666.691807.peg.8 | CDS | VC-2 | 4785 | 5972 | 3 | + | 1188 | VWA containing CoxE family protein |
| fig|6666666.691807.peg.9 | CDS | VC-2 | 6025 | 7899 | 1 | + | 1875 | Outer membrane component of TAM transport system |
| fig|6666666.691807.peg.10 | CDS | VC-2 | 7902 | 12221 | 3 | + | 4320 | Inner membrane component of TAM transport system |
| fig|6666666.691807.peg.11 | CDS | VC-2 | 12912 | 13058 | 3 | + | 147 | hypothetical protein |
| fig|6666666.691807.peg.12 | CDS | VC-2 | 14151 | 13114 | -3 | - | 1038 | Phage portal vertex protein GpQ |
| fig|6666666.691807.peg.13 | CDS | VC-2 | 16037 | 14148 | -2 | - | 1890 | Phage terminase, ATPase subunit GpP |
| fig|6666666.691807.peg.14 | CDS | VC-2 | 16157 | 17002 | 2 | + | 846 | Phage capsid scaffolding protein GpO |
| fig|6666666.691807.peg.15 | CDS | VC-2 | 17054 | 18064 | 2 | + | 1011 | Phage major capsid protein GpN |
| fig|6666666.691807.peg.16 | CDS | VC-2 | 18147 | 18866 | 3 | + | 720 | Phage terminase, endonuclease subunit GpM |
| fig|6666666.691807.peg.17 | CDS | VC-2 | 18975 | 19460 | 3 | + | 486 | Phage head completion protein |
| fig|6666666.691807.peg.18 | CDS | VC-2 | 19463 | 19687 | 2 | + | 225 | hypothetical protein |
| fig|6666666.691807.peg.19 | CDS | VC-2 | 19689 | 19940 | 3 | + | 252 | hypothetical protein |
| fig|6666666.691807.peg.20 | CDS | VC-2 | 19937 | 20521 | 2 | + | 585 | Phage lysozyme R (EC 3.2.1.17) |
| fig|6666666.691807.peg.21 | CDS | VC-2 | 20518 | 21099 | 1 | + | 582 | hypothetical protein |
| fig|6666666.691807.peg.22 | CDS | VC-2 | 21101 | 21637 | 2 | + | 537 | Phage tail completion protein GpR |
| fig|6666666.691807.peg.23 | CDS | VC-2 | 21641 | 22111 | 2 | + | 471 | hypothetical protein |
| fig|6666666.691807.peg.24 | CDS | VC-2 | 22182 | 22790 | 3 | + | 609 | Baseplate assembly protein V |
| fig|6666666.691807.peg.25 | CDS | VC-2 | 22787 | 23143 | 2 | + | 357 | Phage baseplate assembly protein |
| fig|6666666.691807.peg.26 | CDS | VC-2 | 23140 | 23994 | 1 | + | 855 | Phage baseplate assembly protein GpJ |
| fig|6666666.691807.peg.27 | CDS | VC-2 | 23994 | 24941 | 3 | + | 948 | hypothetical protein |
| fig|6666666.691807.peg.28 | CDS | VC-2 | 24945 | 25433 | 3 | + | 489 | hypothetical protein |
| fig|6666666.691807.peg.29 | CDS | VC-2 | 25441 | 27594 | 1 | + | 2154 | hypothetical protein |
| fig|6666666.691807.peg.30 | CDS | VC-2 | 27584 | 28618 | 2 | + | 1035 | hypothetical protein |
| fig|6666666.691807.peg.31 | CDS | VC-2 | 28630 | 29346 | 1 | + | 717 | hypothetical protein |
| fig|6666666.691807.peg.32 | CDS | VC-2 | 29350 | 30147 | 1 | + | 798 | hypothetical protein |
| fig|6666666.691807.peg.33 | CDS | VC-2 | 30150 | 30578 | 3 | + | 429 | hypothetical protein |
| fig|6666666.691807.peg.34 | CDS | VC-2 | 30746 | 31942 | 2 | + | 1197 | Phage tail sheath monomer GpFI |
| fig|6666666.691807.peg.35 | CDS | VC-2 | 31979 | 32488 | 2 | + | 510 | Phage major tail tube protein GpFII |
| fig|6666666.691807.peg.36 | CDS | VC-2 | 32623 | 32988 | 1 | + | 366 | hypothetical protein |
| fig|6666666.691807.peg.37 | CDS | VC-2 | 32997 | 33122 | 3 | + | 126 | hypothetical protein |
| fig|6666666.691807.peg.38 | CDS | VC-2 | 33115 | 35619 | 1 | + | 2505 | hypothetical protein |
| fig|6666666.691807.peg.39 | CDS | VC-2 | 35632 | 36096 | 1 | + | 465 | Phage tape measure |
| fig|6666666.691807.peg.40 | CDS | VC-2 | 36096 | 37175 | 3 | + | 1080 | Gene D protein |
| fig|6666666.691807.peg.41 | CDS | VC-2 | 37229 | 37495 | 2 | + | 267 | hypothetical protein |
| fig|6666666.691807.peg.42 | CDS | VC-2 | 37500 | 37772 | 3 | + | 273 | hypothetical protein |
| fig|6666666.691807.peg.43 | CDS | VC-2 | 37795 | 38184 | 1 | + | 390 | hypothetical protein |
| fig|6666666.691807.peg.44 | CDS | VC-2 | 38265 | 38585 | 3 | + | 321 | hypothetical protein |
| fig|6666666.691807.peg.45 | CDS | VC-2 | 38582 | 39457 | 2 | + | 876 | hypothetical protein |
| fig|6666666.691807.peg.46 | CDS | VC-2 | 39467 | 39712 | 2 | + | 246 | hypothetical protein |
| fig|6666666.691807.peg.47 | CDS | VC-2 | 39871 | 39719 | -1 | - | 153 | hypothetical protein |
| fig|6666666.691807.peg.48 | CDS | VC-2 | 40400 | 39927 | -2 | - | 474 | hypothetical protein |
| fig|6666666.691807.peg.49 | CDS | VC-2 | 41459 | 40494 | -2 | - | 966 | hypothetical protein |
| fig|6666666.691807.peg.50 | CDS | VC-2 | 42093 | 41521 | -3 | - | 573 | Transcriptional regulator, Xre family |
| fig|6666666.691807.peg.51 | CDS | VC-2 | 42176 | 42430 | 2 | + | 255 | hypothetical protein |
| fig|6666666.691807.peg.52 | CDS | VC-2 | 42441 | 42989 | 3 | + | 549 | Phage transcriptional activator Ogr/delta (ACLAME 74) |
| fig|6666666.691807.peg.53 | CDS | VC-2 | 43105 | 43515 | 1 | + | 411 | hypothetical protein |
| fig|6666666.691807.peg.54 | CDS | VC-2 | 43512 | 43670 | 3 | + | 159 | hypothetical protein |
| fig|6666666.691807.peg.55 | CDS | VC-2 | 43667 | 44080 | 2 | + | 414 | hypothetical protein |
| fig|6666666.691807.peg.56 | CDS | VC-2 | 44083 | 46005 | 1 | + | 1923 | Phage replication protein GpA, endonuclease |
| fig|6666666.691807.peg.57 | CDS | VC-2 | 46027 | 46254 | 1 | + | 228 | hypothetical protein |
| fig|6666666.691807.peg.58 | CDS | VC-2 | 46287 | 46490 | 3 | + | 204 | hypothetical protein |
| fig|6666666.691807.peg.59 | CDS | VC-2 | 46494 | 47180 | 3 | + | 687 | C-5 cytosine-specific DNA methylase family protein |
| fig|6666666.691807.peg.60 | CDS | VC-2 | 47177 | 47419 | 2 | + | 243 | hypothetical protein |
| fig|6666666.691807.peg.61 | CDS | VC-2 | 47424 | 47888 | 3 | + | 465 | hypothetical protein |
| fig|6666666.691807.peg.62 | CDS | VC-2 | 47885 | 48109 | 2 | + | 225 | hypothetical protein |
| fig|6666666.691807.peg.63 | CDS | VC-2 | 49221 | 48124 | -3 | - | 1098 | Phage integrase |
| fig|6666666.691807.peg.64 | CDS | VC-2 | 50900 | 52090 | 2 | + | 1191 | hypothetical protein |
| fig|6666666.691807.peg.65 | CDS | VC-2 | 52437 | 53918 | 3 | + | 1482 | Tyrosinase (EC 1.14.18.1) |
| fig|6666666.691807.peg.66 | CDS | VC-2 | 53928 | 54686 | 3 | + | 759 | Putative transmembrane protein |
| fig|6666666.691807.peg.67 | CDS | VC-2 | 55104 | 54706 | -3 | - | 399 | Transcriptional regulator |
| fig|6666666.691807.peg.68 | CDS | VC-2 | 55381 | 56040 | 1 | + | 660 | hypothetical protein |
| fig|6666666.691807.peg.69 | CDS | VC-2 | 57390 | 56053 | -3 | - | 1338 | Methyl-accepting chemotaxis sensor/transducer protein |
| fig|6666666.691807.peg.70 | CDS | VC-2 | 57424 | 57627 | 1 | + | 204 | hypothetical protein |
| fig|6666666.691807.peg.71 | CDS | VC-2 | 57694 | 58542 | 1 | + | 849 | hypothetical protein |
| fig|6666666.691807.peg.72 | CDS | VC-2 | 58628 | 59275 | 2 | + | 648 | Probable glutathione S-transferase (EC 2.5.1.18), YfcF homolog |
| fig|6666666.691807.peg.73 | CDS | VC-2 | 59299 | 59523 | 1 | + | 225 | hypothetical protein |
| fig|6666666.691807.peg.74 | CDS | VC-2 | 60090 | 59557 | -3 | - | 534 | hypothetical protein |
| fig|6666666.691807.peg.75 | CDS | VC-2 | 60533 | 62140 | 2 | + | 1608 | Methyl-accepting chemotaxis sensor/transducer protein |
| fig|6666666.691807.peg.76 | CDS | VC-2 | 63275 | 62244 | -2 | - | 1032 | Probable diguanylate cyclase YeaP |
| fig|6666666.691807.peg.77 | CDS | VC-2 | 64895 | 63444 | -2 | - | 1452 | Two-component system sensor histidine kinase |
| fig|6666666.691807.peg.78 | CDS | VC-2 | 65566 | 64892 | -1 | - | 675 | Two-component transcriptional response regulator, LuxR family |
| fig|6666666.691807.peg.79 | CDS | VC-2 | 66168 | 65764 | -3 | - | 405 | hypothetical protein |
| fig|6666666.691807.peg.80 | CDS | VC-2 | 67721 | 66204 | -2 | - | 1518 | Domain of unknown function / ABC transporter, ATP-binding protein |
| fig|6666666.691807.peg.81 | CDS | VC-2 | 69562 | 68009 | -1 | - | 1554 | Serine protease |
| fig|6666666.691807.peg.82 | CDS | VC-2 | 70026 | 69658 | -3 | - | 369 | Uncharacterized protein YfgD, not an arsenate reductase |
| fig|6666666.691807.peg.83 | CDS | VC-2 | 71374 | 70058 | -1 | - | 1317 | Xanthine permease |
| fig|6666666.691807.peg.84 | CDS | VC-2 | 72965 | 71580 | -2 | - | 1386 | Guanine deaminase (EC 3.5.4.3); Hydroxydechloroatrazine ethylaminohydrolase (EC 3.5.99.3) |
| fig|6666666.691807.peg.85 | CDS | VC-2 | 73986 | 73078 | -3 | - | 909 | Transcriptional regulator, LysR family |
| fig|6666666.691807.peg.86 | CDS | VC-2 | 75690 | 74044 | -3 | - | 1647 | Ferric iron ABC transporter, permease protein |
| fig|6666666.691807.peg.87 | CDS | VC-2 | 75840 | 77000 | 3 | + | 1161 | Ferric iron ABC transporter, ATP-binding protein |
| fig|6666666.691807.peg.88 | CDS | VC-2 | 77098 | 78519 | 1 | + | 1422 | FIG017431: Sigma factor-like phosphatase with CBS pair domains |
| fig|6666666.691807.peg.89 | CDS | VC-2 | 78516 | 79148 | 3 | + | 633 | FIG062788: hypothetical protein |
| fig|6666666.691807.peg.90 | CDS | VC-2 | 79184 | 79570 | 2 | + | 387 | hypothetical protein |
| fig|6666666.691807.peg.91 | CDS | VC-2 | 80072 | 79596 | -2 | - | 477 | Acetyltransferase, GNAT family |
| fig|6666666.691807.peg.92 | CDS | VC-2 | 80836 | 80087 | -1 | - | 750 | Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| fig|6666666.691807.peg.93 | CDS | VC-2 | 82134 | 80839 | -3 | - | 1296 | Dihydroorotase (EC 3.5.2.3) |
| fig|6666666.691807.peg.94 | CDS | VC-2 | 83341 | 82379 | -1 | - | 963 | Aspartate carbamoyltransferase (EC 2.1.3.2) |
| fig|6666666.691807.peg.95 | CDS | VC-2 | 83862 | 83344 | -3 | - | 519 | Pyrimidine operon regulatory protein PyrR |
| fig|6666666.691807.peg.96 | CDS | VC-2 | 84317 | 83859 | -2 | - | 459 | Putative pre-16S rRNA nuclease YqgF |
| fig|6666666.691807.peg.97 | CDS | VC-2 | 84913 | 84314 | -1 | - | 600 | UPF0301 protein YqgE |
| fig|6666666.691807.peg.98 | CDS | VC-2 | 84938 | 86419 | 2 | + | 1482 | Deoxyribodipyrimidine photolyase (EC 4.1.99.3) |
| fig|6666666.691807.peg.99 | CDS | VC-2 | 92886 | 86509 | -3 | - | 6378 | Response regulator receiver:CheW-like protein:ATP-binding region, ATPase-like:Hpt |
| fig|6666666.691807.peg.100 | CDS | VC-2 | 95189 | 92937 | -2 | - | 2253 | twitching motility protein PilJ |
| fig|6666666.691807.peg.101 | CDS | VC-2 | 95735 | 95208 | -2 | - | 528 | type IV pili signal transduction protein PilI |
| fig|6666666.691807.peg.102 | CDS | VC-2 | 96116 | 95751 | -2 | - | 366 | twitching motility protein PilH |
| fig|6666666.691807.peg.103 | CDS | VC-2 | 96514 | 96116 | -1 | - | 399 | twitching motility protein PilG |
| fig|6666666.691807.peg.104 | CDS | VC-2 | 96714 | 96562 | -3 | - | 153 | Rubredoxin |
| fig|6666666.691807.peg.105 | CDS | VC-2 | 96830 | 97789 | 2 | + | 960 | Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7) |
| fig|6666666.691807.peg.106 | CDS | VC-2 | 97882 | 99180 | 1 | + | 1299 | Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) |
| fig|6666666.691807.peg.107 | CDS | VC-2 | 99830 | 99231 | -2 | - | 600 | DNA-3-methyladenine glycosylase (EC 3.2.2.20) |
| fig|6666666.691807.peg.108 | CDS | VC-2 | 100309 | 99833 | -1 | - | 477 | Cytochrome c family protein |
| fig|6666666.691807.peg.109 | CDS | VC-2 | 101907 | 100309 | -3 | - | 1599 | IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) |
| fig|6666666.691807.peg.110 | CDS | VC-2 | 102185 | 101952 | -2 | - | 234 | DNA-binding protein Fis |
| fig|6666666.691807.peg.111 | CDS | VC-2 | 103252 | 102182 | -1 | - | 1071 | tRNA-dihydrouridine synthase DusB |
| fig|6666666.691807.peg.112 | CDS | VC-2 | 104004 | 103396 | -3 | - | 609 | hypothetical protein |
| fig|6666666.691807.peg.113 | CDS | VC-2 | 104112 | 104633 | 3 | + | 522 | probable membrane protein YPO3302 |
| fig|6666666.691807.peg.114 | CDS | VC-2 | 105595 | 104672 | -1 | - | 924 | Transcriptional regulator, LysR family |
| fig|6666666.691807.peg.115 | CDS | VC-2 | 105698 | 106402 | 2 | + | 705 | Pirin |
| fig|6666666.691807.peg.116 | CDS | VC-2 | 106511 | 107209 | 2 | + | 699 | Isochorismatase family |
| fig|6666666.691807.peg.117 | CDS | VC-2 | 107646 | 109544 | 3 | + | 1899 | Exoenzymes regulatory protein AepA precursor |
| fig|6666666.691807.peg.118 | CDS | VC-2 | 109556 | 110011 | 2 | + | 456 | Predicted membrane protein |
| fig|6666666.691807.peg.119 | CDS | VC-2 | 110001 | 111671 | 3 | + | 1671 | Uncharacterized MFS-type transporter |
| fig|6666666.691807.peg.120 | CDS | VC-2 | 112360 | 111722 | -1 | - | 639 | Two-component transcriptional response regulator, LuxR family |
| fig|6666666.691807.peg.121 | CDS | VC-2 | 113501 | 112353 | -2 | - | 1149 | Two-component system sensor histidine kinase |
| fig|6666666.691807.peg.122 | CDS | VC-2 | 114976 | 113657 | -1 | - | 1320 | CzcABC family efflux RND transporter, outer membrane protein |
| fig|6666666.691807.peg.123 | CDS | VC-2 | 118161 | 114988 | -3 | - | 3174 | CzcABC family efflux RND transporter, transmembrane protein |
| fig|6666666.691807.peg.124 | CDS | VC-2 | 119294 | 118158 | -2 | - | 1137 | CzcABC family efflux RND transporter, membrane fusion protein |
| fig|6666666.691807.peg.125 | CDS | VC-2 | 120835 | 119837 | -1 | - | 999 | BUG/TctC family periplasmic protein |
| fig|6666666.691807.peg.126 | CDS | VC-2 | 121888 | 120914 | -1 | - | 975 | BUG/TctC family periplasmic protein |
| fig|6666666.691807.peg.127 | CDS | VC-2 | 122869 | 121931 | -1 | - | 939 | 2-dehydropantoate 2-reductase (EC 1.1.1.169) |
| fig|6666666.691807.peg.128 | CDS | VC-2 | 124544 | 122898 | -2 | - | 1647 | Benzoylformate decarboxylase (EC 4.1.1.7) |
| fig|6666666.691807.peg.129 | CDS | VC-2 | 124675 | 125604 | 1 | + | 930 | Transcriptional regulator, LysR family |
| fig|6666666.691807.peg.130 | CDS | VC-2 | 126051 | 126833 | 3 | + | 783 | Oxidoreductase, short-chain dehydrogenase/reductase family |
| fig|6666666.691807.peg.131 | CDS | VC-2 | 127856 | 126861 | -2 | - | 996 | hypothetical protein |
| fig|6666666.691807.peg.132 | CDS | VC-2 | 128748 | 127867 | -3 | - | 882 | Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19) |
| fig|6666666.691807.peg.133 | CDS | VC-2 | 129823 | 128873 | -1 | - | 951 | Predicted NAD regulator in Alphaproteobacteria |
| fig|6666666.691807.peg.134 | CDS | VC-2 | 131170 | 130022 | -1 | - | 1149 | hypothetical protein |
| fig|6666666.691807.peg.135 | CDS | VC-2 | 131313 | 131167 | -3 | - | 147 | hypothetical protein |
| fig|6666666.691807.peg.136 | CDS | VC-2 | 132488 | 131601 | -2 | - | 888 | hypothetical protein |
| fig|6666666.691807.peg.137 | CDS | VC-2 | 133027 | 132485 | -1 | - | 543 | Colicin E2 tolerance protein CbrC-like protein |
| fig|6666666.691807.peg.138 | CDS | VC-2 | 134279 | 133185 | -2 | - | 1095 | GTP-binding and nucleic acid-binding protein YchF |
| fig|6666666.691807.peg.139 | CDS | VC-2 | 135215 | 134349 | -2 | - | 867 | probable iron-sulfur binding protein YPO1417 |
| fig|6666666.691807.peg.140 | CDS | VC-2 | 135321 | 135208 | -3 | - | 114 | hypothetical protein |
| fig|6666666.691807.peg.141 | CDS | VC-2 | 135382 | 136536 | 1 | + | 1155 | 2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase |
| fig|6666666.691807.peg.142 | CDS | VC-2 | 136681 | 137397 | 1 | + | 717 | Thiol:disulfide interchange protein DsbC |
| fig|6666666.691807.peg.143 | CDS | VC-2 | 137519 | 139441 | 2 | + | 1923 | Putative protease |
| fig|6666666.691807.peg.144 | CDS | VC-2 | 139537 | 140316 | 1 | + | 780 | Probable enoyl-CoA hydratase paaF (EC 4.2.1.17) |
| fig|6666666.691807.peg.145 | CDS | VC-2 | 140708 | 141745 | 2 | + | 1038 | hypothetical protein |
| fig|6666666.691807.peg.146 | CDS | VC-2 | 141855 | 142604 | 3 | + | 750 | hypothetical protein |
| fig|6666666.691807.peg.147 | CDS | VC-2 | 143833 | 142622 | -1 | - | 1212 | hypothetical protein |
| fig|6666666.691807.peg.148 | CDS | VC-2 | 144902 | 143817 | -2 | - | 1086 | Iron-regulated protein A precursor |
| fig|6666666.691807.peg.149 | CDS | VC-2 | 146398 | 144902 | -1 | - | 1497 | Probable thiol oxidoreductase with 2 cytochrome c heme-binding sites |
| fig|6666666.691807.peg.150 | CDS | VC-2 | 147699 | 146503 | -3 | - | 1197 | Iron-regulated protein A precursor |
| fig|6666666.691807.peg.151 | CDS | VC-2 | 150249 | 147949 | -3 | - | 2301 | TonB-dependent siderophore receptor |
| fig|6666666.691807.peg.152 | CDS | VC-2 | 150720 | 152012 | 3 | + | 1293 | Uncharacterized MFS-type transporter |
| fig|6666666.691807.peg.153 | CDS | VC-2 | 152504 | 152094 | -2 | - | 411 | hypothetical protein |
| fig|6666666.691807.peg.154 | CDS | VC-2 | 152876 | 152598 | -2 | - | 279 | hypothetical protein |
| fig|6666666.691807.peg.155 | CDS | VC-2 | 153917 | 153093 | -2 | - | 825 | DNA-binding domain of ModE / Molybdate-binding domain of ModE |
| fig|6666666.691807.peg.156 | CDS | VC-2 | 153907 | 154785 | 1 | + | 879 | Molybdenum ABC transporter, substrate-binding protein ModA |
| fig|6666666.691807.peg.157 | CDS | VC-2 | 154876 | 155556 | 1 | + | 681 | Molybdenum ABC transporter permease protein ModB |
| fig|6666666.691807.peg.158 | CDS | VC-2 | 155553 | 156683 | 3 | + | 1131 | Molybdenum ABC transporter ATP-binding protein ModC |
| fig|6666666.691807.peg.159 | CDS | VC-2 | 156736 | 157656 | 1 | + | 921 | Sulfur carrier protein FdhD |
| fig|6666666.691807.peg.160 | CDS | VC-2 | 157721 | 158131 | 2 | + | 411 | COG0012: Predicted GTPase, probable translation |
| fig|6666666.691807.peg.161 | CDS | VC-2 | 158288 | 159616 | 2 | + | 1329 | tRNA-i(6)A37 methylthiotransferase (EC 2.8.4.3) |
| fig|6666666.691807.peg.162 | CDS | VC-2 | 159827 | 162115 | 2 | + | 2289 | hypothetical protein |
| fig|6666666.691807.peg.163 | CDS | VC-2 | 162109 | 163329 | 1 | + | 1221 | Uncharacterized protein STM2133 |
| fig|6666666.691807.peg.164 | CDS | VC-2 | 163326 | 164000 | 3 | + | 675 | Putative inner membrane protein |
| fig|6666666.691807.peg.165 | CDS | VC-2 | 164418 | 164023 | -3 | - | 396 | hypothetical protein |
| fig|6666666.691807.peg.166 | CDS | VC-2 | 165071 | 164517 | -2 | - | 555 | Lipoprotein |
| fig|6666666.691807.peg.167 | CDS | VC-2 | 166559 | 165165 | -2 | - | 1395 | Signal recognition particle protein Ffh |
| fig|6666666.691807.peg.168 | CDS | VC-2 | 166596 | 166754 | 3 | + | 159 | hypothetical protein |
| fig|6666666.691807.peg.169 | CDS | VC-2 | 166827 | 170735 | 3 | + | 3909 | Probable sensor/response regulator hybrid protein (EC 2.7.3.-) |
| fig|6666666.691807.peg.170 | CDS | VC-2 | 170728 | 171654 | 1 | + | 927 | Two-component system response regulator protein |
| fig|6666666.691807.peg.171 | CDS | VC-2 | 171660 | 172556 | 3 | + | 897 | Inner membrane protein YpjD |
| fig|6666666.691807.peg.172 | CDS | VC-2 | 172553 | 172813 | 2 | + | 261 | hypothetical protein |
| fig|6666666.691807.peg.173 | CDS | VC-2 | 172816 | 174579 | 1 | + | 1764 | Multi-sensor signal transduction histidine kinase |
| fig|6666666.691807.peg.174 | CDS | VC-2 | 174579 | 176093 | 3 | + | 1515 | Two-component transcriptional response regulator, AtoC family |
| fig|6666666.691807.peg.175 | CDS | VC-2 | 176119 | 176721 | 1 | + | 603 | 1,6-anhydro-N-acetylmuramyl-L-alanine amidase |
| fig|6666666.691807.peg.176 | CDS | VC-2 | 177234 | 177082 | -3 | - | 153 | hypothetical protein |
| fig|6666666.691807.peg.177 | CDS | VC-2 | 177250 | 180168 | 1 | + | 2919 | Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1) |
| fig|6666666.691807.peg.178 | CDS | VC-2 | 180375 | 181469 | 3 | + | 1095 | Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1) |
| fig|6666666.691807.peg.179 | CDS | VC-2 | 181647 | 182606 | 3 | + | 960 | Low-complexity acidic protein, XCC2875 type |
| fig|6666666.691807.peg.180 | CDS | VC-2 | 183606 | 182704 | -3 | - | 903 | putative carbohydrate kinase |
| fig|6666666.691807.peg.181 | CDS | VC-2 | 184993 | 183641 | -1 | - | 1353 | Putative transmembrane protein |
| fig|6666666.691807.peg.182 | CDS | VC-2 | 185959 | 185069 | -1 | - | 891 | Ribosomal protein L11 methyltransferase |
| fig|6666666.691807.peg.183 | CDS | VC-2 | 187409 | 186045 | -2 | - | 1365 | Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14) |
| fig|6666666.691807.peg.184 | CDS | VC-2 | 188006 | 187542 | -2 | - | 465 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase |
| fig|6666666.691807.peg.185 | CDS | VC-2 | 188652 | 188152 | -3 | - | 501 | Cytochrome c-type biogenesis protein ResA |
| fig|6666666.691807.peg.186 | CDS | VC-2 | 189307 | 188699 | -1 | - | 609 | Predicted nucleotidyltransferase |
| fig|6666666.691807.peg.187 | CDS | VC-2 | 189563 | 189330 | -2 | - | 234 | hypothetical protein |
| fig|6666666.691807.peg.188 | CDS | VC-2 | 189552 | 190991 | 3 | + | 1440 | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) |
| fig|6666666.691807.peg.189 | CDS | VC-2 | 191392 | 191075 | -1 | - | 318 | hypothetical protein |
| fig|6666666.691807.peg.190 | CDS | VC-2 | 191640 | 192008 | 3 | + | 369 | Uncharacterized protein YqcC |
| fig|6666666.691807.peg.191 | CDS | VC-2 | 193223 | 192066 | -2 | - | 1158 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) |
| fig|6666666.691807.peg.192 | CDS | VC-2 | 194285 | 193665 | -2 | - | 621 | hypothetical protein |
| fig|6666666.691807.peg.193 | CDS | VC-2 | 195843 | 194383 | -3 | - | 1461 | TldD protein, part of TldE/TldD proteolytic complex |
| fig|6666666.691807.peg.194 | CDS | VC-2 | 197365 | 196196 | -1 | - | 1170 | Rod shape-determining protein RodA |
| fig|6666666.691807.peg.195 | CDS | VC-2 | 197578 | 198162 | 1 | + | 585 | Esterase YqiA |
| fig|6666666.691807.peg.196 | CDS | VC-2 | 198218 | 200284 | 2 | + | 2067 | Exoribonuclease II (EC 3.1.13.1) |
| fig|6666666.691807.peg.197 | CDS | VC-2 | 200333 | 201196 | 2 | + | 864 | TonB protein |
| fig|6666666.691807.peg.198 | CDS | VC-2 | 201235 | 202092 | 1 | + | 858 | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| fig|6666666.691807.peg.199 | CDS | VC-2 | 202100 | 202816 | 2 | + | 717 | Monofunctional biosynthetic peptidoglycan transglycosylase |
| fig|6666666.691807.peg.200 | CDS | VC-2 | 202834 | 203382 | 1 | + | 549 | Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4) |
| fig|6666666.691807.peg.201 | CDS | VC-2 | 203792 | 203376 | -2 | - | 417 | Esterase/lipase/thioesterase family protein |
| Contig VC-16 |
| Feature ID | Type | Contig | start | stop | Frame | Strand | Length(bp) | Function |
| fig|6666666.692453.peg.1 | CDS | VC-16 | 446 | 324 | -2 | - | 123 | hypothetical protein |
| fig|6666666.692453.peg.2 | CDS | VC-16 | 1178 | 447 | -2 | - | 732 | Autolysis response regulater LytR |
| fig|6666666.692453.peg.3 | CDS | VC-16 | 2232 | 1189 | -3 | - | 1044 | Autolysin sensor kinase (EC 2.7.3.-) |
| fig|6666666.692453.peg.4 | CDS | VC-16 | 2895 | 2236 | -3 | - | 660 | phospholipase/carboxylesterase family protein |
| fig|6666666.692453.peg.5 | CDS | VC-16 | 4871 | 2946 | -2 | - | 1926 | Glucans biosynthesis glucosyltransferase H (EC 2.4.1.-) |
| fig|6666666.692453.peg.6 | CDS | VC-16 | 5362 | 7407 | 1 | + | 2046 | Colicin I receptor precursor |
| fig|6666666.692453.peg.7 | CDS | VC-16 | 7638 | 7468 | -3 | - | 171 | hypothetical protein |
| fig|6666666.692453.peg.8 | CDS | VC-16 | 7852 | 8238 | 1 | + | 387 | FIG01112898: hypothetical protein |
| fig|6666666.692453.peg.9 | CDS | VC-16 | 10848 | 8317 | -3 | - | 2532 | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein) |
| fig|6666666.692453.peg.10 | CDS | VC-16 | 11952 | 11059 | -3 | - | 894 | UDP-glucose 4-epimerase (EC 5.1.3.2) |
| fig|6666666.692453.peg.11 | CDS | VC-16 | 13004 | 12051 | -2 | - | 954 | peptidase S41 |
| fig|6666666.692453.peg.12 | CDS | VC-16 | 12979 | 13476 | 1 | + | 498 | transcriptional regulator marR family |
| fig|6666666.692453.peg.13 | CDS | VC-16 | 14966 | 13482 | -2 | - | 1485 | hypothetical protein |
| fig|6666666.692453.peg.14 | CDS | VC-16 | 15125 | 14970 | -2 | - | 156 | hypothetical protein |
| fig|6666666.692453.peg.15 | CDS | VC-16 | 15211 | 15525 | 1 | + | 315 | Pyridoxamine 5&#39;-phosphate oxidase (EC 1.4.3.5) |
| fig|6666666.692453.peg.16 | CDS | VC-16 | 17008 | 15536 | -1 | - | 1473 | Permeases of the major facilitator superfamily |
| fig|6666666.692453.peg.17 | CDS | VC-16 | 17198 | 17755 | 2 | + | 558 | Transcriptional regulator, TetR family |
| fig|6666666.692453.peg.18 | CDS | VC-16 | 18121 | 17771 | -1 | - | 351 | Lactoylglutathione lyase (EC 4.4.1.5) |
| fig|6666666.692453.peg.19 | CDS | VC-16 | 18444 | 18244 | -3 | - | 201 | FIG01111417: hypothetical protein |
| fig|6666666.692453.peg.20 | CDS | VC-16 | 18633 | 22019 | 3 | + | 3387 | FIG01111736: hypothetical protein |
| fig|6666666.692453.peg.21 | CDS | VC-16 | 23276 | 22074 | -2 | - | 1203 | Bicyclomycin resistance protein |
| fig|6666666.692453.peg.22 | CDS | VC-16 | 23982 | 23530 | -3 | - | 453 | FIG01210133: hypothetical protein |
| fig|6666666.692453.peg.23 | CDS | VC-16 | 24448 | 25089 | 1 | + | 642 | Glutathione S-transferase (EC 2.5.1.18) |
| fig|6666666.692453.peg.24 | CDS | VC-16 | 25521 | 25114 | -3 | - | 408 | FIG01112641: hypothetical protein |
| fig|6666666.692453.peg.25 | CDS | VC-16 | 25990 | 25571 | -1 | - | 420 | HigA protein (antitoxin to HigB) |
| fig|6666666.692453.peg.26 | CDS | VC-16 | 26109 | 26501 | 3 | + | 393 | Inner membrane protein YqjF |
| fig|6666666.692453.peg.27 | CDS | VC-16 | 28295 | 26520 | -2 | - | 1776 | Beta-lactamase (EC 3.5.2.6) |
| fig|6666666.692453.peg.28 | CDS | VC-16 | 28943 | 29506 | 2 | + | 564 | putative; ORF located using Glimmer/Genemark |
| fig|6666666.692453.peg.29 | CDS | VC-16 | 29503 | 30018 | 1 | + | 516 | putative; ORF located using Glimmer/Genemark |
| fig|6666666.692453.peg.30 | CDS | VC-16 | 30311 | 31672 | 2 | + | 1362 | Integrase |
| fig|6666666.692453.peg.31 | CDS | VC-16 | 32286 | 31693 | -3 | - | 594 | Transcriptional regulator, XRE family |
| fig|6666666.692453.peg.32 | CDS | VC-16 | 32560 | 32706 | 1 | + | 147 | hypothetical protein |
| fig|6666666.692453.peg.33 | CDS | VC-16 | 33115 | 32726 | -1 | - | 390 | hypothetical protein |
| fig|6666666.692453.peg.34 | CDS | VC-16 | 33528 | 33755 | 3 | + | 228 | hypothetical protein |
| fig|6666666.692453.peg.35 | CDS | VC-16 | 33955 | 34437 | 1 | + | 483 | Error-prone repair protein UmuD |
| fig|6666666.692453.peg.36 | CDS | VC-16 | 34421 | 35671 | 2 | + | 1251 | Error-prone, lesion bypass DNA polymerase V (UmuC) |
| fig|6666666.692453.peg.37 | CDS | VC-16 | 36398 | 35718 | -2 | - | 681 | hypothetical protein |
| fig|6666666.692453.peg.38 | CDS | VC-16 | 37287 | 36379 | -3 | - | 909 | Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake |
| fig|6666666.692453.peg.39 | CDS | VC-16 | 38583 | 37621 | -3 | - | 963 | hypothetical protein |
| fig|6666666.692453.peg.40 | CDS | VC-16 | 39288 | 38602 | -3 | - | 687 | hypothetical protein |
| fig|6666666.692453.peg.41 | CDS | VC-16 | 39589 | 39290 | -1 | - | 300 | hypothetical protein |
| fig|6666666.692453.peg.42 | CDS | VC-16 | 46657 | 39644 | -1 | - | 7014 | Phage tail fiber protein |
| fig|6666666.692453.peg.43 | CDS | VC-16 | 47043 | 46648 | -3 | - | 396 | Phage peptidoglycan hydrolase (lysin) |
| fig|6666666.692453.peg.44 | CDS | VC-16 | 47504 | 47043 | -2 | - | 462 | Phage protein |
| fig|6666666.692453.peg.45 | CDS | VC-16 | 47623 | 47820 | 1 | + | 198 | hypothetical protein |
| fig|6666666.692453.peg.46 | CDS | VC-16 | 47979 | 47803 | -3 | - | 177 | hypothetical protein |
| fig|6666666.692453.peg.47 | CDS | VC-16 | 48420 | 48064 | -3 | - | 357 | Phage protein |
| fig|6666666.692453.peg.48 | CDS | VC-16 | 51194 | 48420 | -2 | - | 2775 | Phage tail length tape-measure protein 1 |
| fig|6666666.692453.peg.49 | CDS | VC-16 | 51830 | 51411 | -2 | - | 420 | hypothetical protein |
| fig|6666666.692453.peg.50 | CDS | VC-16 | 52588 | 51833 | -1 | - | 756 | hypothetical protein |
| fig|6666666.692453.peg.51 | CDS | VC-16 | 53080 | 52625 | -1 | - | 456 | hypothetical protein |
| fig|6666666.692453.peg.52 | CDS | VC-16 | 53387 | 53073 | -2 | - | 315 | hypothetical protein |
| fig|6666666.692453.peg.53 | CDS | VC-16 | 54160 | 53402 | -1 | - | 759 | FIG01217905: hypothetical protein |
| fig|6666666.692453.peg.54 | CDS | VC-16 | 55207 | 54206 | -1 | - | 1002 | elements of external origin; phage-related functions and prophages |
| fig|6666666.692453.peg.55 | CDS | VC-16 | 55984 | 55295 | -1 | - | 690 | hypothetical protein |
| fig|6666666.692453.peg.56 | CDS | VC-16 | 57348 | 55987 | -3 | - | 1362 | Head-tail preconnector protein GP5 |
| fig|6666666.692453.peg.57 | CDS | VC-16 | 58819 | 57338 | -1 | - | 1482 | Phage portal protein |
| fig|6666666.692453.peg.58 | CDS | VC-16 | 59027 | 58812 | -2 | - | 216 | hypothetical protein |
| fig|6666666.692453.peg.59 | CDS | VC-16 | 61023 | 59029 | -3 | - | 1995 | Terminase large subunit |
| fig|6666666.692453.peg.60 | CDS | VC-16 | 61594 | 61091 | -1 | - | 504 | Phage protein |
| fig|6666666.692453.peg.61 | CDS | VC-16 | 62075 | 61788 | -2 | - | 288 | hypothetical protein |
| fig|6666666.692453.peg.62 | CDS | VC-16 | 62559 | 62077 | -3 | - | 483 | hypothetical protein |
| fig|6666666.692453.peg.63 | CDS | VC-16 | 62999 | 62556 | -2 | - | 444 | hypothetical protein |
| fig|6666666.692453.peg.64 | CDS | VC-16 | 63496 | 63008 | -1 | - | 489 | Phage lysin |
| fig|6666666.692453.peg.65 | CDS | VC-16 | 64319 | 64984 | 2 | + | 666 | hypothetical protein |
| fig|6666666.692453.peg.66 | CDS | VC-16 | 65861 | 65094 | -2 | - | 768 | hypothetical protein |
| fig|6666666.692453.peg.67 | CDS | VC-16 | 66013 | 65861 | -1 | - | 153 | hypothetical protein |
| fig|6666666.692453.peg.68 | CDS | VC-16 | 67761 | 66010 | -3 | - | 1752 | Probable helicase |
| fig|6666666.692453.peg.69 | CDS | VC-16 | 68189 | 67758 | -2 | - | 432 | hypothetical protein |
| fig|6666666.692453.peg.70 | CDS | VC-16 | 68545 | 68189 | -1 | - | 357 | hypothetical protein |
| fig|6666666.692453.peg.71 | CDS | VC-16 | 69336 | 68545 | -3 | - | 792 | Phage-related protein |
| fig|6666666.692453.peg.72 | CDS | VC-16 | 69845 | 69333 | -2 | - | 513 | Helicase subunit of the DNA excision repair complex |
| fig|6666666.692453.peg.73 | CDS | VC-16 | 70375 | 69845 | -1 | - | 531 | hypothetical protein |
| fig|6666666.692453.peg.74 | CDS | VC-16 | 70916 | 70362 | -2 | - | 555 | hypothetical protein |
| fig|6666666.692453.peg.75 | CDS | VC-16 | 71940 | 70939 | -3 | - | 1002 | hypothetical protein |
| fig|6666666.692453.peg.76 | CDS | VC-16 | 72326 | 71940 | -2 | - | 387 | hypothetical protein |
| fig|6666666.692453.peg.77 | CDS | VC-16 | 72634 | 72323 | -1 | - | 312 | hypothetical protein |
| fig|6666666.692453.peg.78 | CDS | VC-16 | 73248 | 72646 | -3 | - | 603 | hypothetical protein |
| fig|6666666.692453.peg.79 | CDS | VC-16 | 73629 | 73357 | -3 | - | 273 | hypothetical protein |
| fig|6666666.692453.peg.80 | CDS | VC-16 | 74133 | 74537 | 3 | + | 405 | Phage protein |
| fig|6666666.692453.peg.81 | CDS | VC-16 | 74550 | 74960 | 3 | + | 411 | hypothetical protein |
| fig|6666666.692453.peg.82 | CDS | VC-16 | 75626 | 75168 | -2 | - | 459 | hypothetical protein |
| fig|6666666.692453.peg.83 | CDS | VC-16 | 75715 | 76230 | 1 | + | 516 | hypothetical protein |
| fig|6666666.692453.peg.84 | CDS | VC-16 | 76227 | 76511 | 3 | + | 285 | hypothetical protein |
| fig|6666666.692453.peg.85 | CDS | VC-16 | 76508 | 76732 | 2 | + | 225 | hypothetical protein |
| fig|6666666.692453.peg.86 | CDS | VC-16 | 76729 | 77001 | 1 | + | 273 | hypothetical protein |
| fig|6666666.692453.peg.87 | CDS | VC-16 | 76998 | 77261 | 3 | + | 264 | hypothetical protein |
| fig|6666666.692453.peg.88 | CDS | VC-16 | 77258 | 77452 | 2 | + | 195 | hypothetical protein |
| fig|6666666.692453.peg.89 | CDS | VC-16 | 77452 | 77697 | 1 | + | 246 | hypothetical protein |
| fig|6666666.692453.peg.90 | CDS | VC-16 | 77713 | 77937 | 1 | + | 225 | hypothetical protein |
| fig|6666666.692453.peg.91 | CDS | VC-16 | 77957 | 78163 | 2 | + | 207 | hypothetical protein |
| fig|6666666.692453.peg.92 | CDS | VC-16 | 78174 | 78626 | 3 | + | 453 | hypothetical protein |
| fig|6666666.692453.peg.93 | CDS | VC-16 | 78619 | 79182 | 1 | + | 564 | hypothetical protein |
| fig|6666666.692453.peg.94 | CDS | VC-16 | 79175 | 79423 | 2 | + | 249 | hypothetical protein |
| fig|6666666.692453.peg.95 | CDS | VC-16 | 79416 | 79622 | 3 | + | 207 | hypothetical protein |
| fig|6666666.692453.peg.96 | CDS | VC-16 | 79697 | 79945 | 2 | + | 249 | hypothetical protein |
| fig|6666666.692453.peg.97 | CDS | VC-16 | 79942 | 80514 | 1 | + | 573 | hypothetical protein |
| fig|6666666.692453.peg.98 | CDS | VC-16 | 80511 | 80921 | 3 | + | 411 | hypothetical protein |
| fig|6666666.692453.peg.99 | CDS | VC-16 | 80908 | 81162 | 1 | + | 255 | hypothetical protein |
| fig|6666666.692453.peg.100 | CDS | VC-16 | 82036 | 81368 | -1 | - | 669 | putative; ORF located using Glimmer/Genemark |
| fig|6666666.692453.peg.101 | CDS | VC-16 | 84028 | 82175 | -1 | - | 1854 | RNA polymerase sigma factor RpoD |
| fig|6666666.692453.peg.102 | CDS | VC-16 | 84559 | 84119 | -1 | - | 441 | D-tyrosyl-tRNA(Tyr) deacylase (EC 3.6.1.n1) |
| fig|6666666.692453.peg.103 | CDS | VC-16 | 84621 | 85541 | 3 | + | 921 | Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) |
| fig|6666666.692453.peg.104 | CDS | VC-16 | 85614 | 86750 | 3 | + | 1137 | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25) |
| fig|6666666.692453.peg.105 | CDS | VC-16 | 86826 | 87326 | 3 | + | 501 | FIG01112130: hypothetical protein |
| fig|6666666.692453.peg.106 | CDS | VC-16 | 87323 | 88861 | 2 | + | 1539 | Possibly related to ydbT |
| Contig VC-20 |
| Feature ID | Type | Contig | Start | Stop | Frame | Strand | Length(bp) | Function |
| fig|6666666.692451.peg.1 | CDS | VC-20 | 294 | 1532 | 3 | + | 1239 | Integrase |
| fig|6666666.692451.peg.2 | CDS | VC-20 | 1698 | 1522 | -3 | - | 177 | hypothetical protein |
| fig|6666666.692451.peg.3 | CDS | VC-20 | 1985 | 1698 | -2 | - | 288 | hypothetical protein |
| fig|6666666.692451.peg.4 | CDS | VC-20 | 2262 | 1987 | -3 | - | 276 | hypothetical protein |
| fig|6666666.692451.peg.5 | CDS | VC-20 | 2792 | 2262 | -2 | - | 531 | Phage protein |
| fig|6666666.692451.peg.6 | CDS | VC-20 | 3011 | 2847 | -2 | - | 165 | hypothetical protein |
| fig|6666666.692451.peg.7 | CDS | VC-20 | 3399 | 3028 | -3 | - | 372 | hypothetical protein |
| fig|6666666.692451.peg.8 | CDS | VC-20 | 3610 | 3416 | -1 | - | 195 | hypothetical protein |
| fig|6666666.692451.peg.9 | CDS | VC-20 | 3828 | 3610 | -3 | - | 219 | hypothetical protein |
| fig|6666666.692451.peg.10 | CDS | VC-20 | 4088 | 3828 | -2 | - | 261 | hypothetical protein |
| fig|6666666.692451.peg.11 | CDS | VC-20 | 4369 | 4097 | -1 | - | 273 | hypothetical protein |
| fig|6666666.692451.peg.12 | CDS | VC-20 | 5251 | 4451 | -1 | - | 801 | Phage protein |
| fig|6666666.692451.peg.13 | CDS | VC-20 | 5635 | 5303 | -1 | - | 333 | Translation elongation factors (GTPases) |
| fig|6666666.692451.peg.14 | CDS | VC-20 | 5914 | 6030 | 1 | + | 117 | hypothetical protein |
| fig|6666666.692451.peg.15 | CDS | VC-20 | 6460 | 5999 | -1 | - | 462 | hypothetical protein |
| fig|6666666.692451.peg.16 | CDS | VC-20 | 7178 | 6486 | -2 | - | 693 | merops peptidase family S24 |
| fig|6666666.692451.peg.17 | CDS | VC-20 | 7306 | 7482 | 1 | + | 177 | FIG00352411: hypothetical protein |
| fig|6666666.692451.peg.18 | CDS | VC-20 | 7491 | 7766 | 3 | + | 276 | hypothetical protein |
| fig|6666666.692451.peg.19 | CDS | VC-20 | 7812 | 8540 | 3 | + | 729 | Putative DNA-binding protein Roi of bacteriophage BP-933W |
| fig|6666666.692451.peg.20 | CDS | VC-20 | 8537 | 9379 | 2 | + | 843 | Replication protein O |
| fig|6666666.692451.peg.21 | CDS | VC-20 | 9370 | 9984 | 1 | + | 615 | hypothetical protein |
| fig|6666666.692451.peg.22 | CDS | VC-20 | 9981 | 10469 | 3 | + | 489 | hypothetical protein |
| fig|6666666.692451.peg.23 | CDS | VC-20 | 10466 | 10798 | 2 | + | 333 | hypothetical protein |
| fig|6666666.692451.peg.24 | CDS | VC-20 | 10803 | 11198 | 3 | + | 396 | FIG00353455: hypothetical protein |
| fig|6666666.692451.peg.25 | CDS | VC-20 | 11195 | 11557 | 2 | + | 363 | hypothetical protein |
| fig|6666666.692451.peg.26 | CDS | VC-20 | 11550 | 11984 | 3 | + | 435 | hypothetical protein |
| fig|6666666.692451.peg.27 | CDS | VC-20 | 11995 | 12408 | 1 | + | 414 | hypothetical protein |
| fig|6666666.692451.peg.28 | CDS | VC-20 | 12955 | 13068 | 1 | + | 114 | hypothetical protein |
| fig|6666666.692451.peg.29 | CDS | VC-20 | 13141 | 13530 | 1 | + | 390 | Phage protein |
| fig|6666666.692451.peg.30 | CDS | VC-20 | 13611 | 13784 | 3 | + | 174 | hypothetical protein |
| fig|6666666.692451.peg.31 | CDS | VC-20 | 13789 | 14007 | 1 | + | 219 | hypothetical protein |
| fig|6666666.692451.peg.32 | CDS | VC-20 | 14037 | 14219 | 3 | + | 183 | hypothetical protein |
| fig|6666666.692451.peg.33 | CDS | VC-20 | 14221 | 14439 | 1 | + | 219 | hypothetical protein |
| fig|6666666.692451.peg.34 | CDS | VC-20 | 14861 | 15352 | 2 | + | 492 | Phage terminase, small subunit |
| fig|6666666.692451.peg.35 | CDS | VC-20 | 15363 | 17078 | 3 | + | 1716 | Phage terminase, large subunit |
| fig|6666666.692451.peg.36 | CDS | VC-20 | 17078 | 18343 | 2 | + | 1266 | Phage portal protein |
| fig|6666666.692451.peg.37 | CDS | VC-20 | 18312 | 19157 | 3 | + | 846 | Prophage Clp protease-like protein |
| fig|6666666.692451.peg.38 | CDS | VC-20 | 19222 | 20430 | 1 | + | 1209 | Phage major capsid protein |
| fig|6666666.692451.peg.39 | CDS | VC-20 | 20480 | 20812 | 2 | + | 333 | TolA protein |
| fig|6666666.692451.peg.40 | CDS | VC-20 | 20822 | 21295 | 2 | + | 474 | hypothetical protein |
| fig|6666666.692451.peg.41 | CDS | VC-20 | 21296 | 21652 | 2 | + | 357 | Phage protein |
| fig|6666666.692451.peg.42 | CDS | VC-20 | 21634 | 22104 | 1 | + | 471 | hypothetical protein |
| fig|6666666.692451.peg.43 | CDS | VC-20 | 22101 | 22475 | 3 | + | 375 | Phage protein |
| fig|6666666.692451.peg.44 | CDS | VC-20 | 22576 | 23088 | 1 | + | 513 | Phage protein |
| fig|6666666.692451.peg.45 | CDS | VC-20 | 23160 | 23630 | 3 | + | 471 | Phage tail fibers |
| fig|6666666.692451.peg.46 | CDS | VC-20 | 23630 | 24067 | 2 | + | 438 | hypothetical protein |
| fig|6666666.692451.peg.47 | CDS | VC-20 | 24160 | 24291 | 1 | + | 132 | hypothetical protein |
| fig|6666666.692451.peg.48 | CDS | VC-20 | 24590 | 24288 | -2 | - | 303 | hypothetical protein |
| fig|6666666.692451.peg.49 | CDS | VC-20 | 24725 | 24904 | 2 | + | 180 | hypothetical protein |
| fig|6666666.692451.peg.50 | CDS | VC-20 | 24982 | 25815 | 1 | + | 834 | Phage Rha protein |
| fig|6666666.692451.peg.51 | CDS | VC-20 | 25896 | 26330 | 3 | + | 435 | hypothetical protein |
| fig|6666666.692451.peg.52 | CDS | VC-20 | 26389 | 28941 | 1 | + | 2553 | Phage tail length tape-measure protein 1 |
| fig|6666666.692451.peg.53 | CDS | VC-20 | 28951 | 29418 | 1 | + | 468 | hypothetical protein |
| fig|6666666.692451.peg.54 | CDS | VC-20 | 29419 | 29925 | 1 | + | 507 | hypothetical protein |
| fig|6666666.692451.peg.55 | CDS | VC-20 | 30138 | 30311 | 3 | + | 174 | hypothetical protein |
| fig|6666666.692451.peg.56 | CDS | VC-20 | 30268 | 33066 | 1 | + | 2799 | FIG00351590: hypothetical protein |
| fig|6666666.692451.peg.57 | CDS | VC-20 | 33121 | 35142 | 1 | + | 2022 | Phage tail fiber protein |
| fig|6666666.692451.peg.58 | CDS | VC-20 | 35144 | 35944 | 2 | + | 801 | hypothetical protein |
| fig|6666666.692451.peg.59 | CDS | VC-20 | 36091 | 36372 | 1 | + | 282 | Holin |
| fig|6666666.692451.peg.60 | CDS | VC-20 | 36369 | 37145 | 3 | + | 777 | N-acetylmuramoyl-L-alanine amidase, putative |
| fig|6666666.692451.peg.61 | CDS | VC-20 | 37142 | 37438 | 2 | + | 297 | hypothetical protein |
| fig|6666666.692451.peg.62 | CDS | VC-20 | 38098 | 37520 | -1 | - | 579 | hypothetical protein |
| fig|6666666.692451.peg.63 | CDS | VC-20 | 38830 | 38708 | -1 | - | 123 | Molybdopterin-guanine dinucleotide biosynthesis protein MobA |
| fig|6666666.692451.peg.64 | CDS | VC-20 | 40169 | 38952 | -2 | - | 1218 | Molybdopterin biosynthesis protein MoeA |
| fig|6666666.692451.peg.65 | CDS | VC-20 | 41089 | 40166 | -1 | - | 924 | Molybdenum cofactor biosynthesis protein MoaC / Molybdenum cofactor biosynthesis protein MoaB |
| fig|6666666.692451.peg.66 | CDS | VC-20 | 42110 | 41229 | -2 | - | 882 | Molybdenum cofactor biosynthesis protein MoaA |
| fig|6666666.692451.peg.67 | CDS | VC-20 | 42620 | 45034 | 2 | + | 2415 | Putative formate dehydrogenase oxidoreductase protein |
| fig|6666666.692451.peg.68 | CDS | VC-20 | 45140 | 45922 | 2 | + | 783 | Formate dehydrogenase chain D (EC 1.2.1.2) |
| fig|6666666.692451.peg.69 | CDS | VC-20 | 45980 | 46357 | 2 | + | 378 | DNA-binding domain of ModE |
| fig|6666666.692451.peg.70 | CDS | VC-20 | 46597 | 47379 | 1 | + | 783 | Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1) |
| fig|6666666.692451.peg.71 | CDS | VC-20 | 47382 | 48071 | 3 | + | 690 | Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) |
| fig|6666666.692451.peg.72 | CDS | VC-20 | 48076 | 48693 | 1 | + | 618 | Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) |
| fig|6666666.692451.peg.73 | CDS | VC-20 | 49128 | 48772 | -3 | - | 357 | transcriptional regulator, AraC family protein |
| fig|6666666.692451.peg.74 | CDS | VC-20 | 49826 | 49413 | -2 | - | 414 | FIG027190: Putative transmembrane protein |
| fig|6666666.692451.peg.75 | CDS | VC-20 | 49894 | 50718 | 1 | + | 825 | Transcriptional regulator, AraC family |
| fig|6666666.692451.peg.76 | CDS | VC-20 | 50885 | 51661 | 2 | + | 777 | Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases |
| fig|6666666.692451.peg.77 | CDS | VC-20 | 53106 | 51712 | -3 | - | 1395 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| fig|6666666.692451.peg.78 | CDS | VC-20 | 53234 | 54094 | 2 | + | 861 | Permease of the drug/metabolite transporter (DMT) superfamily |
| fig|6666666.692451.peg.79 | CDS | VC-20 | 54464 | 56347 | 2 | + | 1884 | putative Glutathione-regulated potassium-efflux system protein KefB |
| fig|6666666.692451.peg.80 | CDS | VC-20 | 58044 | 56467 | -3 | - | 1578 | FOG: GGDEF domain |
| fig|6666666.692451.peg.81 | CDS | VC-20 | 58368 | 58547 | 3 | + | 180 | hypothetical protein |
| fig|6666666.692451.peg.82 | CDS | VC-20 | 58924 | 58694 | -1 | - | 231 | hypothetical protein |
| fig|6666666.692451.peg.83 | CDS | VC-20 | 59221 | 59108 | -1 | - | 114 | Serine acetyltransferase (EC 2.3.1.30) |
| fig|6666666.692451.peg.84 | CDS | VC-20 | 60159 | 60377 | 3 | + | 219 | hypothetical protein |
| fig|6666666.692451.peg.85 | CDS | VC-20 | 61281 | 60685 | -3 | - | 597 | FIG00350032: hypothetical protein |
| fig|6666666.692451.peg.86 | CDS | VC-20 | 62069 | 61371 | -2 | - | 699 | Exodeoxyribonuclease X (EC 3.1.11.-) |
| fig|6666666.692451.peg.87 | CDS | VC-20 | 62561 | 63820 | 2 | + | 1260 | Lysophospholipase (EC 3.1.1.5) |
| fig|6666666.692451.peg.88 | CDS | VC-20 | 63977 | 65230 | 2 | + | 1254 | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| fig|6666666.692451.peg.89 | CDS | VC-20 | 65401 | 65805 | 1 | + | 405 | Regulator of nucleoside diphosphate kinase |
| fig|6666666.692451.peg.90 | CDS | VC-20 | 66118 | 66906 | 1 | + | 789 | putative tellurium resistant protein (KlaA/kilA) |
| fig|6666666.692451.peg.91 | CDS | VC-20 | 66926 | 68059 | 2 | + | 1134 | putative tellurique resistant protein (KlaB/TelA) |
| fig|6666666.692451.peg.92 | CDS | VC-20 | 68093 | 68479 | 2 | + | 387 | hypothetical protein; putative membrane protein |
| fig|6666666.692451.peg.93 | CDS | VC-20 | 68485 | 69018 | 1 | + | 534 | hypothetical protein; putative membrane protein |
| fig|6666666.692451.peg.94 | CDS | VC-20 | 69188 | 69835 | 2 | + | 648 | Alkyl hydroperoxide reductase protein F (EC 1.6.4.-) |
| Contig VC-22 |
| Feature ID | Type | Contig | Start | Stop | Frame | Strand | Length(bp) | Function |
| fig|6666666.692457.peg.1 | CDS | VC-22 | 746 | 405 | -2 | - | 342 | Phage minor tail protein |
| fig|6666666.692457.peg.2 | CDS | VC-22 | 1203 | 733 | -3 | - | 471 | hypothetical protein |
| fig|6666666.692457.peg.3 | CDS | VC-22 | 1171 | 1299 | 1 | + | 129 | hypothetical protein |
| fig|6666666.692457.peg.4 | CDS | VC-22 | 5179 | 1259 | -1 | - | 3921 | Phage tail length tape-measure protein 1 |
| fig|6666666.692457.peg.5 | CDS | VC-22 | 5645 | 5235 | -2 | - | 411 | hypothetical protein |
| fig|6666666.692457.peg.6 | CDS | VC-22 | 5860 | 5708 | -1 | - | 153 | hypothetical protein |
| fig|6666666.692457.peg.7 | CDS | VC-22 | 6333 | 5875 | -3 | - | 459 | Phage protein |
| fig|6666666.692457.peg.8 | CDS | VC-22 | 6888 | 6379 | -3 | - | 510 | Phage tail fibers |
| fig|6666666.692457.peg.9 | CDS | VC-22 | 7310 | 6942 | -2 | - | 369 | hypothetical protein |
| fig|6666666.692457.peg.10 | CDS | VC-22 | 7754 | 7311 | -2 | - | 444 | Phage protein |
| fig|6666666.692457.peg.11 | CDS | VC-22 | 8095 | 7736 | -1 | - | 360 | hypothetical protein |
| fig|6666666.692457.peg.12 | CDS | VC-22 | 8401 | 8096 | -1 | - | 306 | hypothetical protein |
| fig|6666666.692457.peg.13 | CDS | VC-22 | 9974 | 8472 | -2 | - | 1503 | Phage major capsid protein #Fam0024 |
| fig|6666666.692457.peg.14 | CDS | VC-22 | 10763 | 10038 | -2 | - | 726 | probable phage prohead protease, HK97 family |
| fig|6666666.692457.peg.15 | CDS | VC-22 | 12036 | 10753 | -3 | - | 1284 | Phage portal protein |
| fig|6666666.692457.peg.16 | CDS | VC-22 | 13871 | 12033 | -2 | - | 1839 | Phage terminase, large subunit |
| fig|6666666.692457.peg.17 | CDS | VC-22 | 14394 | 13882 | -3 | - | 513 | Phage Terminase Small Subunit |
| fig|6666666.692457.peg.18 | CDS | VC-22 | 14768 | 14538 | -2 | - | 231 | hypothetical protein |
| fig|6666666.692457.peg.19 | CDS | VC-22 | 15358 | 14771 | -1 | - | 588 | Phage holin |
| fig|6666666.692457.peg.20 | CDS | VC-22 | 16263 | 15802 | -3 | - | 462 | hypothetical protein |
| fig|6666666.692457.peg.21 | CDS | VC-22 | 18365 | 16599 | -2 | - | 1767 | DNA primase (bacterial type) |
| fig|6666666.692457.peg.22 | CDS | VC-22 | 19279 | 18362 | -1 | - | 918 | DNA primase (EC 2.7.7.-) |
| fig|6666666.692457.peg.23 | CDS | VC-22 | 19760 | 19272 | -2 | - | 489 | hypothetical protein |
| fig|6666666.692457.peg.24 | CDS | VC-22 | 20037 | 19807 | -3 | - | 231 | hypothetical protein |
| fig|6666666.692457.peg.25 | CDS | VC-22 | 20276 | 20995 | 2 | + | 720 | hypothetical protein |
| fig|6666666.692457.peg.26 | CDS | VC-22 | 21214 | 21339 | 1 | + | 126 | hypothetical protein |
| fig|6666666.692457.peg.27 | CDS | VC-22 | 21318 | 21533 | 3 | + | 216 | hypothetical protein |
| fig|6666666.692457.peg.28 | CDS | VC-22 | 21530 | 21853 | 2 | + | 324 | hypothetical protein |
| fig|6666666.692457.peg.29 | CDS | VC-22 | 21939 | 22136 | 3 | + | 198 | hypothetical protein |
| fig|6666666.692457.peg.30 | CDS | VC-22 | 22126 | 22587 | 1 | + | 462 | hypothetical protein |
| fig|6666666.692457.peg.31 | CDS | VC-22 | 22584 | 22778 | 3 | + | 195 | hypothetical protein |
| fig|6666666.692457.peg.32 | CDS | VC-22 | 22775 | 23287 | 2 | + | 513 | hypothetical protein |
| fig|6666666.692457.peg.33 | CDS | VC-22 | 23274 | 23507 | 3 | + | 234 | hypothetical protein |
| fig|6666666.692457.peg.34 | CDS | VC-22 | 23504 | 23752 | 2 | + | 249 | hypothetical protein |
| fig|6666666.692457.peg.35 | CDS | VC-22 | 24677 | 23727 | -2 | - | 951 | Integrase |
| fig|6666666.692457.peg.36 | CDS | VC-22 | 25576 | 24860 | -1 | - | 717 | Ribonuclease PH (EC 2.7.7.56) |
| fig|6666666.692457.peg.37 | CDS | VC-22 | 27077 | 25938 | -2 | - | 1140 | POSSIBLE LINOLEOYL-CoA DESATURASE (DELTA(6)-DESATURASE) |
| fig|6666666.692457.peg.38 | CDS | VC-22 | 28219 | 27197 | -1 | - | 1023 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 |
| fig|6666666.692457.peg.39 | CDS | VC-22 | 28394 | 29038 | 2 | + | 645 | Unsaturated fatty acid biosythesis repressor FabR, TetR family |
| fig|6666666.692457.peg.40 | CDS | VC-22 | 29736 | 29119 | -3 | - | 618 | Periplasmic thiol:disulfide interchange protein DsbA |
| fig|6666666.692457.peg.41 | CDS | VC-22 | 29966 | 30679 | 2 | + | 714 | 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) |
| fig|6666666.692457.peg.42 | CDS | VC-22 | 30679 | 31350 | 1 | + | 672 | Similar to phosphoglycolate phosphatase, clustered with ubiquinone biosynthesis SAM-dependent O-methyltransferase |
| fig|6666666.692457.peg.43 | CDS | VC-22 | 31612 | 32358 | 1 | + | 747 | Oxidoreductase, short-chain dehydrogenase/reductase family |
| fig|6666666.692457.peg.44 | CDS | VC-22 | 32586 | 32741 | 3 | + | 156 | hypothetical protein |
| fig|6666666.692457.peg.45 | CDS | VC-22 | 33023 | 33424 | 2 | + | 402 | putative signal peptide |
| fig|6666666.692457.peg.46 | CDS | VC-22 | 33623 | 33919 | 2 | + | 297 | conserved hypothetical protein; putative signal peptide |
| fig|6666666.692457.peg.47 | CDS | VC-22 | 34112 | 34474 | 2 | + | 363 | conserved hypothetical protein; putative signal peptide |
| fig|6666666.692457.peg.48 | CDS | VC-22 | 35230 | 36585 | 1 | + | 1356 | N-acetylglutamate synthase (EC 2.3.1.1) |
| fig|6666666.692457.peg.49 | CDS | VC-22 | 36921 | 37880 | 3 | + | 960 | Alkanesulfonates-binding protein |
| fig|6666666.692457.peg.50 | CDS | VC-22 | 37915 | 38907 | 1 | + | 993 | Alkanesulfonates-binding protein |
| fig|6666666.692457.peg.51 | CDS | VC-22 | 38930 | 40099 | 2 | + | 1170 | Alkanesulfonate monooxygenase (EC 1.14.14.5) |
| fig|6666666.692457.peg.52 | CDS | VC-22 | 40096 | 40917 | 1 | + | 822 | Alkanesulfonates transport system permease protein |
| fig|6666666.692457.peg.53 | CDS | VC-22 | 40927 | 41724 | 1 | + | 798 | Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB |
| fig|6666666.692457.peg.54 | CDS | VC-22 | 42445 | 43131 | 1 | + | 687 | Transcriptional regulator RutR of pyrimidine catabolism (TetR family) |
| fig|6666666.692457.peg.55 | CDS | VC-22 | 43801 | 43235 | -1 | - | 567 | 5&#39;-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9) |
| fig|6666666.692457.peg.56 | CDS | VC-22 | 43961 | 44503 | 2 | + | 543 | putative reductase |
| fig|6666666.692457.peg.57 | CDS | VC-22 | 44996 | 44730 | -2 | - | 267 | FIG00350327: hypothetical protein |
| fig|6666666.692457.peg.58 | CDS | VC-22 | 45799 | 45035 | -1 | - | 765 | Outer membrane protein assembly factor YaeT precursor |
| fig|6666666.692457.peg.59 | CDS | VC-22 | 46763 | 45804 | -2 | - | 960 | FIG00351404: hypothetical protein |
| fig|6666666.692457.peg.60 | CDS | VC-22 | 50703 | 46798 | -3 | - | 3906 | IcmF-related protein |
| fig|6666666.692457.peg.61 | CDS | VC-22 | 52129 | 50738 | -1 | - | 1392 | FIG00350534: hypothetical protein |
| fig|6666666.692457.peg.62 | CDS | VC-22 | 53122 | 52130 | -1 | - | 993 | Uncharacterized protein ImpH/VasB |
| fig|6666666.692457.peg.63 | CDS | VC-22 | 54894 | 53086 | -3 | - | 1809 | Protein ImpG/VasA |
| fig|6666666.692457.peg.64 | CDS | VC-22 | 55385 | 54912 | -2 | - | 474 | Uncharacterized protein ImpF |
| fig|6666666.692457.peg.65 | CDS | VC-22 | 55952 | 55449 | -2 | - | 504 | Putative cytoplasmic protein USSDB7A |
| fig|6666666.692457.peg.66 | CDS | VC-22 | 57480 | 55999 | -3 | - | 1482 | Uncharacterized protein ImpC |
| fig|6666666.692457.peg.67 | CDS | VC-22 | 57982 | 57473 | -1 | - | 510 | Uncharacterized protein ImpB |
| fig|6666666.692457.peg.68 | CDS | VC-22 | 58662 | 58012 | -3 | - | 651 | FIG00350028: hypothetical protein |
| fig|6666666.692457.peg.69 | CDS | VC-22 | 59028 | 61700 | 3 | + | 2673 | ClpB protein |
| fig|6666666.692457.peg.70 | CDS | VC-22 | 61720 | 62823 | 1 | + | 1104 | Uncharacterized protein ImpA |
| fig|6666666.692457.peg.71 | CDS | VC-22 | 62830 | 64194 | 1 | + | 1365 | Uncharacterized protein ImpJ/VasE |
| fig|6666666.692457.peg.72 | CDS | VC-22 | 64209 | 65009 | 3 | + | 801 | Probable transmembrane protein |
| fig|6666666.692457.peg.73 | CDS | VC-22 | 65021 | 65617 | 2 | + | 597 | hypothetical protein |
| fig|6666666.692457.peg.74 | CDS | VC-22 | 65671 | 66597 | 1 | + | 927 | Probable transmembrane protein |
| fig|6666666.692457.peg.75 | CDS | VC-22 | 67175 | 66864 | -2 | - | 312 | FIG00350053: hypothetical protein |