

**UCC Library and UCC researchers have made this item openly available.
Please [let us know](#) how this has helped you. Thanks!**

| | |
|------------------------------------|---|
| Title | Things are getting hairy: Enterobacteria bacteriophage vB_PcaM_CBB |
| Author(s) | Buttimer, Colin; Hendrix, Hanne; Oliveira, Hugo; Casey, Aidan; Neve, Horst; McAuliffe, Olivia; Ross, R. Paul; Hill, Colin; Noben, Jean-Paul; O'Mahony, Jim; Lavigne, Rob; Coffey, Aidan |
| Publication date | 2017-01-24 |
| Original citation | Buttimer, C., Hendrix, H., Oliveira, H., Casey, A., Neve, H., McAuliffe, O., Ross, R. P., Hill, C., Noben, J.-P., O'Mahony, J., Lavigne, R. and Coffey, A. (2017) 'Things are getting hairy: Enterobacteria bacteriophage vB_PcaM_CBB', <i>Frontiers In Microbiology</i> , 8, 44 (16pp). doi:10.3389/fmicb.2017.00044 |
| Type of publication | Article (peer-reviewed) |
| Link to publisher's version | http://dx.doi.org/10.3389/fmicb.2017.00044 Access to the full text of the published version may require a subscription. |
| Rights | © 2017, the Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms. https://creativecommons.org/licenses/by/4.0/ |
| Item downloaded from | http://hdl.handle.net/10468/3694 |

Downloaded on 2023-03-21T23:58:39Z

Table S1 - Annotation of Enterobacteria phage vB_PcaM_CBB

| ORF | Predicted product | start | Stop | Length (aa) | Strand | Start Codon |
|------------|--------------------------------|--------------|-------------|------------------------|---------------|------------------------|
| CBB_1 | Hypothetical protein | 20 | 197 | 55 | + | ATG |
| CBB_2 | Hypothetical protein | 1427 | 1615 | 62 | + | ATG |
| CBB_3 | Conserved hypothetical protein | 1800 | 2477 | 225 | + | ATG |
| CBB_4 | Conserved hypothetical protein | 2627 | 2896 | 89 | + | ATG |
| CBB_5 | Conserved hypothetical protein | 3032 | 3316 | 94 | + | ATG |
| CBB_6 | Conserved hypothetical protein | 3352 | 3741 | 129 | + | ATG |
| CBB_7 | Hypothetical protein | 3906 | 3793 | 57 | - | ATG |
| CBB_8 | Hypothetical protein | 3965 | 4117 | 50 | + | ATG |
| CBB_9 | Conserved hypothetical protein | 4165 | 4437 | 90 | + | ATG |
| CBB_10 | Conserved hypothetical protein | 4501 | 4947 | 148 | + | ATG |
| CBB_11 | Conserved hypothetical protein | 5024 | 5479 | 151 | + | ATG |
| CBB_12 | Hypothetical protein | 5560 | 5685 | 41 | + | ATG |
| CBB_13 | Hypothetical protein | 5758 | 5985 | 75 | + | ATG |
| CBB_14 | Conserved hypothetical protein | 6059 | 6481 | 140 | + | ATG |
| CBB_15 | Conserved hypothetical protein | 6663 | 6998 | 111 | + | ATG |
| CBB_16 | Conserved hypothetical protein | 7068 | 7235 | 55 | + | ATG |
| CBB_17 | Conserved hypothetical protein | 7319 | 7498 | 59 | + | ATG |
| CBB_18 | Conserved hypothetical protein | 7989 | 8243 | 123 | + | ATG |
| CBB_19 | Conserved hypothetical protein | 7989 | 8243 | 84 | + | ATG |
| CBB_20 | Hypothetical protein | 8248 | 8406 | 52 | + | ATG |
| CBB_21 | Conserved hypothetical protein | 8696 | 8929 | 77 | + | ATG |
| CBB_22 | Putative membrane protein | 8953 | 9111 | 52 | + | ATG |
| CBB_23 | Conserved hypothetical protein | 9123 | 9326 | 67 | + | ATG |
| CBB_24 | Conserved hypothetical protein | 9326 | 9502 | 58 | + | ATG |
| CBB_25 | Conserved hypothetical protein | 9581 | 9784 | 67 | + | ATG |

| | | | | | | |
|--------|--------------------------------|-------|-------|-----|---|-----|
| CBB_26 | Conserved hypothetical protein | 9814 | 10164 | 116 | + | ATG |
| CBB_27 | Putative membrane protein | 10391 | 10642 | 83 | + | ATG |
| CBB_28 | Hypothetical protein | 10674 | 10832 | 52 | + | ATG |
| CBB_29 | Structural protein | 10841 | 11716 | 291 | + | ATG |
| CBB_30 | Conserved hypothetical protein | 11856 | 12053 | 65 | + | ATG |
| CBB_31 | Conserved hypothetical protein | 12017 | 12142 | 41 | + | ATG |
| CBB_32 | Hypothetical protein | 12132 | 12326 | 64 | + | ATG |
| CBB_33 | Putative membrane protein | 12370 | 12723 | 117 | + | ATG |
| CBB_34 | Hypothetical protein | 12720 | 13109 | 129 | + | ATG |
| CBB_35 | Conserved hypothetical protein | 13181 | 13372 | 63 | + | ATG |
| CBB_36 | Conserved hypothetical protein | 13435 | 13821 | 128 | + | ATG |
| CBB_37 | Conserved hypothetical protein | 13941 | 14183 | 80 | + | ATG |
| CBB_38 | Structural protein | 14240 | 14758 | 172 | + | ATG |
| CBB_39 | Conserved hypothetical protein | 14822 | 15160 | 112 | + | ATG |
| CBB_40 | Hypothetical protein | 15403 | 15750 | 115 | + | ATG |
| CBB_41 | Conserved hypothetical protein | 15841 | 16059 | 72 | + | ATG |
| CBB_42 | Conserved hypothetical protein | 16235 | 16837 | 200 | + | ATG |
| CBB_43 | Conserved hypothetical protein | 17042 | 17374 | 110 | + | ATG |
| CBB_44 | Conserved hypothetical protein | 17584 | 17826 | 80 | + | ATG |
| CBB_45 | Conserved hypothetical protein | 17906 | 18793 | 295 | + | ATG |
| CBB_46 | Conserved hypothetical protein | 18869 | 19207 | 112 | + | ATG |
| CBB_47 | Conserved hypothetical protein | 19411 | 19641 | 76 | + | ATG |
| CBB_48 | Conserved hypothetical protein | 19725 | 20072 | 115 | + | ATG |

| | | | | | | |
|--------|--------------------------------|-------|-------|-----|---|-----|
| CBB_49 | Hypothetical protein | 20272 | 20463 | 63 | + | ATG |
| CBB_50 | Conserved hypothetical protein | 20533 | 20709 | 58 | + | ATG |
| CBB_51 | Conserved hypothetical protein | 21113 | 21382 | 89 | + | ATG |
| CBB_52 | Hypothetical protein | 21452 | 22009 | 185 | + | ATG |
| CBB_53 | Conserved hypothetical protein | 22520 | 23107 | 195 | + | ATG |
| CBB_54 | Conserved hypothetical protein | 23110 | 23721 | 203 | + | ATG |
| CBB_55 | Conserved hypothetical protein | 23696 | 24328 | 210 | + | ATG |
| CBB_56 | Conserved hypothetical protein | 24459 | 25058 | 199 | + | ATG |
| CBB_57 | Conserved hypothetical protein | 25055 | 25576 | 173 | + | ATG |
| CBB_58 | Conserved hypothetical protein | 25537 | 26139 | 200 | + | ATG |
| CBB_59 | Conserved hypothetical protein | 26146 | 26559 | 137 | + | ATG |
| CBB_60 | Conserved hypothetical protein | 26573 | 27016 | 147 | + | ATG |
| CBB_61 | Conserved hypothetical protein | 27096 | 27572 | 158 | + | ATG |
| CBB_62 | Conserved hypothetical protein | 27576 | 27746 | 56 | + | ATG |
| CBB_63 | Conserved hypothetical protein | 27751 | 28359 | 202 | + | ATG |
| CBB_64 | Conserved hypothetical protein | 28360 | 29247 | 295 | + | ATG |
| CBB_65 | Conserved hypothetical protein | 29231 | 29551 | 105 | + | ATG |
| CBB_66 | Conserved hypothetical protein | 29595 | 29993 | 132 | + | ATG |
| CBB_67 | Conserved hypothetical protein | 30018 | 30368 | 116 | + | ATG |
| CBB_68 | Putative membrane protein | 30409 | 30729 | 106 | + | ATG |
| CBB_69 | Conserved hypothetical protein | 30733 | 31506 | 257 | + | TTG |
| CBB_70 | Conserved hypothetical protein | 31506 | 32300 | 264 | + | ATG |
| CBB_71 | Conserved hypothetical protein | 32990 | 33514 | 174 | + | ATG |

| | | | | | | |
|--------|-----------------------------------|-------|-------|-----|---|-----|
| CBB_72 | DNA N-6-adenine-methyltransferase | 33527 | 34069 | 180 | + | ATG |
| CBB_73 | cytidyltransferase | 34091 | 34630 | 179 | + | ATG |
| CBB_74 | Conserved hypothetical protein | 34614 | 34895 | 93 | + | ATG |
| CBB_75 | Conserved hypothetical protein | 34942 | 35490 | 182 | + | ATG |
| CBB_76 | Conserved hypothetical protein | 35528 | 35686 | 52 | + | ATG |
| CBB_77 | Conserved hypothetical protein | 35673 | 36374 | 233 | + | ATG |
| CBB_78 | Putative membrane protein | 36371 | 36574 | 67 | + | ATG |
| CBB_79 | Conserved hypothetical protein | 36555 | 37667 | 370 | + | TTG |
| CBB_80 | Conserved hypothetical protein | 37709 | 38440 | 243 | + | ATG |

| | | | | | | |
|--------|---|-------|-------|-----|---|-----|
| CBB_81 | Conserved hypothetical protein | 38485 | 38784 | 99 | + | ATG |
| CBB_82 | Conserved hypothetical protein | 38781 | 39077 | 98 | + | ATG |
| CBB_83 | RNA ligase 1 and tail fiber attachment catalyst | 39142 | 40290 | 382 | + | ATG |
| CBB_84 | Conserved hypothetical protein | 40325 | 40561 | 78 | + | ATG |
| CBB_85 | Conserved hypothetical protein | 40554 | 40774 | 74 | + | GTG |
| CBB_86 | Conserved hypothetical protein | 40791 | 41015 | 74 | + | ATG |
| CBB_87 | polynucleotide 5'-kinase and 3'-phosphatase | 41003 | 41935 | 310 | + | ATG |
| CBB_88 | Conserved hypothetical protein | 41991 | 42200 | 69 | + | ATG |
| CBB_89 | Putative membrane protein | 42213 | 42380 | 55 | + | ATG |
| CBB_90 | Conserved hypothetical protein | 42370 | 42642 | 90 | + | ATG |
| CBB_91 | Conserved hypothetical protein | 42639 | 42977 | 112 | + | ATG |
| CBB_92 | Putative membrane protein | 42979 | 43206 | 75 | + | ATG |
| CBB_93 | Conserved hypothetical protein | 43187 | 43435 | 82 | + | ATG |
| CBB_94 | Conserved hypothetical protein | 43432 | 43788 | 118 | + | ATG |
| CBB_95 | Conserved hypothetical protein | 43788 | 44033 | 81 | + | ATG |
| CBB_96 | Conserved hypothetical protein | 44077 | 44715 | 212 | + | ATG |

| | | | | | | |
|---------|---|-------|-------|-----|---|-----|
| CBB_97 | putative serine/threonine protein phosphatase | 44715 | 45494 | 259 | + | ATG |
| CBB_98 | Conserved hypothetical protein | 45494 | 45952 | 152 | + | ATG |
| CBB_99 | Conserved hypothetical protein | 45963 | 47201 | 412 | + | ATG |
| CBB_100 | DNA ligase | 47228 | 48643 | 471 | + | ATG |
| CBB_101 | Conserved hypothetical protein | 48640 | 49065 | 141 | + | ATG |
| CBB_102 | metallophosphoesterase | 49043 | 49834 | 263 | + | ATG |
| CBB_103 | Conserved hypothetical protein | 49836 | 50264 | 142 | + | ATG |

| | | | | | | |
|---------|---|-------|-------|-----|---|-----|
| CBB_104 | ATP-dependent Clp protease proteolytic subunit | 50278 | 50970 | 230 | + | ATG |
| CBB_105 | Conserved hypothetical protein | 50987 | 51274 | 95 | + | ATG |
| CBB_106 | Conserved hypothetical protein | 51280 | 51735 | 151 | + | ATG |
| CBB_107 | Conserved hypothetical protein | 51781 | 52335 | 184 | + | ATG |
| CBB_108 | Conserved hypothetical protein | 52320 | 52847 | 175 | + | ATG |
| CBB_109 | Conserved hypothetical protein | 52837 | 53319 | 160 | + | ATG |
| CBB_110 | CMP/dCMP deaminase | 53306 | 53761 | 151 | + | ATG |
| CBB_111 | Putative membrane protein | 53763 | 54032 | 89 | + | ATG |
| CBB_112 | Major tail protein | 54740 | 54084 | 218 | + | ATG |
| CBB_113 | bifunctional nicotinamide mononucleotide adenylyltransferase/ADP-ribose pyrophosphatase | 54982 | 56079 | 365 | + | ATG |
| CBB_114 | Conserved hypothetical protein | 56123 | 56641 | 172 | + | ATG |

| | | | | | | |
|---------|---|-------|-------|-----|---|-----|
| CBB_115 | nicotinamide phosphoribosyltransferase | 56702 | 58189 | 495 | + | ATG |
| CBB_116 | Putative membrane protein | 58232 | 58453 | 73 | + | ATG |
| CBB_117 | Conserved hypothetical protein | 58455 | 59402 | 315 | + | ATG |
| CBB_118 | Structural protein | 59615 | 60061 | 148 | + | ATG |
| CBB_119 | Conserved hypothetical protein | 60073 | 60315 | 80 | + | ATG |
| CBB_120 | putative Sir2-like protein | 60328 | 61119 | 263 | + | ATG |
| CBB_121 | Conserved hypothetical protein | 61135 | 62034 | 299 | + | ATG |
| CBB_122 | Putative membrane protein | 62034 | 62336 | 100 | + | ATG |
| CBB_123 | PhoH family protein | 62407 | 63846 | 479 | + | ATG |
| CBB_124 | Conserved hypothetical protein | 63894 | 64076 | 60 | + | ATG |
| CBB_125 | Conserved hypothetical protein | 64251 | 64943 | 230 | + | ATG |
| CBB_126 | Putative membrane protein | 64940 | 65146 | 68 | + | ATG |
| CBB_127 | Putative membrane protein | 65153 | 65302 | 49 | + | ATG |
| CBB_128 | Conserved hypothetical protein | 65377 | 65922 | 181 | + | ATG |

| | | | | | | |
|---------|--------------------------------|-------|-------|-----|---|-----|
| CBB_129 | Conserved hypothetical protein | 65949 | 66791 | 200 | + | ATG |
| CBB_130 | Conserved hypothetical protein | 66793 | 67407 | 204 | + | ATG |
| CBB_131 | co-chaperonin GroES | 67407 | 67688 | 93 | + | ATG |
| CBB_132 | tyrosyl-tRNA synthetase | 67698 | 6893 | 421 | + | ATG |
| CBB_133 | Putative lipoprotein | 68985 | 69171 | 68 | + | ATG |
| CBB_134 | Conserved hypothetical protein | 69317 | 69958 | 213 | + | ATG |
| CBB_135 | dCMP deaminase | 69948 | 70313 | 121 | + | ATG |
| CBB_136 | Hypothetical protein | 70300 | 70620 | 106 | + | TTG |
| CBB_137 | Hypothetical protein | 70613 | 71239 | 208 | + | ATG |
| CBB_138 | Conserved hypothetical protein | 71229 | 71486 | 85 | + | ATG |
| CBB_139 | Hypothetical protein | 71483 | 71683 | 66 | + | ATG |
| CBB_140 | Conserved hypothetical protein | 71696 | 72247 | 183 | + | ATG |

| | | | | | | |
|---------|--|-------|-------|-----|---|-----|
| | | | | | | |
| CBB_141 | anaerobic NTP reductase large subunit | 72380 | 74217 | 611 | + | ATG |
| CBB_142 | Hypothetical protein | 74304 | 74621 | 105 | + | ATG |
| CBB_143 | Conserved hypothetical protein | 74628 | 75074 | 148 | + | ATG |
| CBB_144 | Structural protein | 75120 | 75884 | 254 | + | ATG |
| | | | | | | |
| CBB_145 | anaerobic ribonucleoside-triphosphate reductase activating protein | 75881 | 76354 | 157 | + | ATG |
| CBB_146 | Conserved hypothetical protein | 76347 | 76523 | 58 | + | ATG |
| CBB_147 | Conserved hypothetical protein | 76602 | 79310 | 902 | + | ATG |
| CBB_148 | Structural protein | 79320 | 82070 | 916 | + | ATG |
| CBB_149 | Structural protein | 82083 | 84833 | 916 | + | ATG |
| CBB_150 | Conserved hypothetical protein | 84966 | 85526 | 186 | + | ATG |
| CBB_151 | Hypothetical protein | 85483 | 85752 | 89 | + | ATG |

| | | | | | | |
|---------|---|-------|-------|-----|---|-----|
| CBB_152 | putative tRNA-His guanylyltransferase | 85749 | 86528 | 259 | + | ATG |
| CBB_153 | Conserved hypothetical protein | 87000 | 87302 | 154 | + | ATG |
| CBB_154 | Conserved hypothetical protein | 87000 | 87302 | 100 | + | ATG |
| CBB_155 | Conserved hypothetical protein | 87310 | 87789 | 159 | + | ATG |
| CBB_156 | Conserved hypothetical protein | 87786 | 88418 | 210 | + | ATG |
| CBB_157 | putative N-4 cytosine-specific methyltransferase | 88427 | 89287 | 286 | + | ATG |
| CBB_158 | Conserved hypothetical protein | 89284 | 89619 | 111 | + | ATG |
| CBB_159 | nucleotidyltransferase | 89628 | 90878 | 416 | + | ATG |
| CBB_160 | Conserved hypothetical protein | 90878 | 91294 | 138 | + | ATG |
| CBB_161 | Conserved hypothetical protein | 91298 | 91801 | 167 | + | ATG |
| CBB_162 | Conserved hypothetical protein | 91791 | 92360 | 189 | + | GTG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_163 | acyl carrier protein | 92332 | 92748 | 138 | + | ATG |
| CBB_164 | Structural protein | 92821 | 93189 | 122 | + | ATG |
| CBB_165 | Structural protein | 93186 | 93500 | 104 | + | ATG |
| CBB_166 | Conserved hypothetical protein | 93574 | 93963 | 129 | + | ATG |
| CBB_167 | Conserved hypothetical protein | 93974 | 94228 | 84 | + | ATG |
| CBB_168 | Conserved hypothetical protein | 94890 | 95255 | 121 | + | ATG |
| CBB_169 | Structural protein | 95287 | 95727 | 146 | + | ATG |
| CBB_170 | Conserved hypothetical protein | 95771 | 96202 | 143 | + | ATG |
| CBB_171 | GTP cyclohydrolase | 96192 | 96695 | 167 | + | GTG |
| CBB_172 | Conserved hypothetical protein | 96676 | 96963 | 95 | + | ATG |
| CBB_173 | thymidine kinase | 96976 | 97545 | 189 | + | ATG |
| CBB_174 | Putative membrane protein | 97599 | 98108 | 169 | + | ATG |
| CBB_175 | Putative membrane protein | 98105 | 98713 | 202 | + | ATG |
| CBB_176 | Conserved hypothetical protein | 98710 | 99069 | 119 | + | ATG |
| CBB_177 | Putative membrane protein | 99071 | 99205 | 44 | + | ATG |
| CBB_178 | Hypothetical protein | 99207 | 99806 | 199 | + | ATG |
| CBB_179 | Hypothetical protein | 99808 | 100128 | 106 | + | ATG |
| CBB_180 | Conserved hypothetical protein | 100131 | 100678 | 182 | + | ATG |
| CBB_181 | RNA ligase | 100759 | 101995 | 418 | + | ATG |

| | | | | | | |
|---------|--|--------|--------|-----|---|-----|
| CBB_182 | Conserved hypothetical protein | 101998 | 102606 | 202 | + | ATG |
| CBB_183 | Structural protein | 102737 | 104251 | 504 | + | ATG |
| CBB_184 | Putative membrane protein | 104304 | 104444 | 46 | + | ATG |
| CBB_185 | Conserved hypothetical protein | 104498 | 104920 | 140 | + | GTG |
| CBB_186 | Conserved hypothetical protein | 104913 | 105488 | 191 | + | ATG |
| CBB_187 | lysozyme | 105603 | 106538 | 311 | + | TTG |
| CBB_188 | sigma 54 modulation protein/ribosomal protein S30EA | 106561 | 106899 | 112 | + | ATG |
| CBB_189 | Conserved hypothetical protein | 106983 | 107384 | 133 | + | ATG |
| CBB_190 | Hypothetical protein | 107371 | 107514 | 47 | + | ATG |
| CBB_191 | Conserved hypothetical protein | 107501 | 107716 | 71 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|-----|---|-----|
| CBB_192 | multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase | 107713 | 108828 | 371 | + | ATG |
| CBB_193 | nudix hydrolase | 108894 | 109316 | 140 | + | ATG |
| CBB_194 | glutaredoxin | 109342 | 109578 | 140 | + | ATG |
| CBB_195 | Conserved hypothetical protein | 109580 | 109993 | 137 | + | ATG |
| CBB_196 | Conserved hypothetical protein | 109996 | 110340 | 114 | + | ATG |
| CBB_197 | Conserved hypothetical protein | 110388 | 110630 | 80 | + | ATG |
| CBB_198 | Conserved hypothetical protein | 110675 | 111175 | 166 | + | ATG |
| CBB_199 | Conserved hypothetical protein | 111202 | 111531 | 109 | + | ATG |
| CBB_200 | Conserved hypothetical protein | 111541 | 111903 | 120 | + | ATG |
| CBB_201 | Neck protein | 111951 | 112736 | 261 | + | ATG |
| CBB_202 | Conserved hypothetical protein | 112774 | 113028 | 84 | + | ATG |

| | | | | | | |
|---------|--|--------|--------|-----|---|-----|
| CBB_203 | putative deoxynucleoside monophosphate kinase | 113067 | 113708 | 213 | + | ATG |
| CBB_204 | tail sheath monomer | 113797 | 116451 | 884 | + | ATG |
| CBB_205 | Structural protein | 116558 | 117247 | 229 | + | ATG |
| CBB_206 | Structural protein | 117331 | 118107 | 258 | + | ATG |
| CBB_207 | Structural protein | 118118 | 119212 | 364 | + | ATG |
| CBB_208 | head completion protein | 119212 | 119670 | 152 | + | ATG |
| CBB_209 | Conserved hypothetical protein | 119672 | 120235 | 187 | + | ATG |
| CBB_210 | Structural protein | 120263 | 120808 | 181 | + | ATG |
| CBB_211 | Structural protein | 120811 | 121371 | 186 | + | ATG |
| CBB_212 | Structural protein | 121384 | 122820 | 478 | + | ATG |
| CBB_213 | Structural protein | 122838 | 123767 | 309 | + | ATG |
| CBB_214 | Structural protein | 123767 | 124177 | 136 | + | ATG |
| CBB_215 | Conserved hypothetical protein | 124181 | 124555 | 124 | + | ATG |
| CBB_216 | ATPase | 124693 | 126036 | 447 | + | ATG |
| CBB_217 | Putative membrane protein | 126078 | 127430 | 450 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|------|---|-----|
| CBB_218 | Conserved hypothetical protein | 127539 | 127775 | 218 | + | ATG |
| CBB_219 | Conserved hypothetical protein | 127777 | 128469 | 230 | + | ATG |
| CBB_220 | Conserved hypothetical protein | 128469 | 128777 | 102 | + | ATG |
| CBB_221 | Conserved hypothetical protein | 128764 | 129351 | 195 | + | ATG |
| CBB_222 | Conserved hypothetical protein | 129358 | 129687 | 109 | + | ATG |
| CBB_223 | thymidylate synthase | 129650 | 130579 | 309 | + | ATG |
| CBB_224 | Structural protein | 132533 | 130611 | 640 | - | ATG |
| CBB_225 | Structural protein | 133259 | 132621 | 212 | - | ATG |
| CBB_226 | Long tail fiber proximal subunit | 138084 | 137934 | 1553 | - | ATG |
| CBB_227 | Structural protein | 138944 | 138084 | 286 | - | ATG |
| CBB_228 | Structural protein | 140166 | 139024 | 380 | - | ATG |
| CBB_229 | Structural protein | 140272 | 140769 | 165 | + | ATG |
| CBB_230 | Structural protein | 140780 | 141388 | 202 | + | ATG |
| CBB_231 | Structural protein | 141399 | 142505 | 368 | + | ATG |
| CBB_232 | MutT/NUDIX hydrolase family protein | 142976 | 142509 | 148 | - | ATG |
| CBB_233 | Tail sheath stabilizer and completion protein | 144323 | 142986 | 445 | - | ATG |
| CBB_234 | Structural protein | 145816 | 144320 | 498 | - | ATG |

| | | | | | | |
|---------|---|--------|--------|------|---|-----|
| CBB_235 | ATP-dependent Clp protease ATP-binding subunit clpA | 144320 | 145816 | 765 | + | ATG |
| CBB_236 | Structural protein | 158274 | 148252 | 3340 | - | ATG |
| CBB_237 | Baseplate wedge | 161820 | 158356 | 1154 | - | ATG |
| CBB_238 | base plate protein | 162285 | 161896 | 129 | - | ATG |
| CBB_239 | baseplate hub subunit and tail lysozyme | 162784 | 162296 | 162 | - | ATG |
| CBB_240 | Baseplate hub subunit and tail lysozyme | 165504 | 162820 | 894 | - | ATG |
| CBB_241 | Structural protein | 167891 | 165504 | 795 | - | ATG |
| CBB_242 | Baseplate wedge protein | 168217 | 167903 | 104 | - | ATG |

| | | | | | | |
|---------|-------------------------------------|--------|--------|-----|---|-----|
| CBB_243 | Structural protein | 169931 | 169071 | 245 | - | ATG |
| CBB_244 | sigma factor for late transcription | 169071 | 169931 | 286 | + | ATG |
| CBB_245 | recombination endonuclease subunit | 169918 | 170949 | 343 | + | ATG |
| CBB_246 | recombination endonuclease subunit | 170962 | 173103 | 713 | + | ATG |
| CBB_247 | Structural protein | 173132 | 173866 | 244 | + | ATG |
| CBB_248 | DNA endonuclease VII | 174344 | 173868 | 158 | - | ATG |
| CBB_249 | Conserved hypothetical protein | 175307 | 175131 | 58 | - | ATG |
| CBB_250 | Structural protein | 176185 | 175328 | 285 | - | ATG |
| CBB_251 | Structural protein | 176250 | 178418 | 722 | + | ATG |
| CBB_252 | portal vertex protein of head | 178435 | 180171 | 578 | + | ATG |
| CBB_253 | Conserved hypothetical protein | 180229 | 180459 | 76 | + | ATG |
| CBB_254 | Structural protein | 181414 | 182043 | 274 | + | ATG |
| CBB_255 | prohead core scaffold and protease | 181414 | 182043 | 209 | + | ATG |
| CBB_256 | Structural protein | 182112 | 183236 | 274 | + | ATG |

| | | | | | | |
|---------|--|--------|--------|------|---|-----|
| CBB_257 | Precursor of major head subunit | 183315 | 184490 | 391 | + | ATG |
| CBB_258 | Conserved hypothetical protein | 184644 | 185060 | 138 | + | ATG |
| CBB_259 | Conserved hypothetical protein | 185089 | 185400 | 103 | + | ATG |
| CBB_260 | Putative tail fiber protein | 185445 | 187064 | 539 | + | ATG |
| CBB_261 | Tail fiber assembly protein | 187057 | 187470 | 137 | + | ATG |
| CBB_262 | Conserved hypothetical protein | 187916 | 190948 | 100 | + | ATG |
| CBB_263 | DNA polymerase | 187916 | 190948 | 1010 | + | ATG |
| CBB_264 | Conserved hypothetical protein | 190964 | 191476 | 170 | + | ATG |
| CBB_265 | Conserved hypothetical protein | 191541 | 192272 | 243 | + | ATG |
| CBB_266 | putative phosphoesterase or phosphohydrolase | 192319 | 192933 | 204 | + | ATG |

| | | | | | | |
|---------|--|--------|--------|-----|---|-----|
| CBB_267 | Conserved hypothetical protein | 192945 | 193154 | 69 | + | ATG |
| CBB_268 | co-chaperonin GroES | 193160 | 193459 | 90 | + | ATG |
| CBB_269 | Structural protein | 193452 | 194171 | 239 | + | ATG |
| CBB_270 | Structural protein | 194219 | 194875 | 218 | - | ATG |
| CBB_271 | Structural protein | 194891 | 195451 | 186 | - | ATG |
| CBB_272 | RNaseH ribonuclease | 195646 | 196632 | 328 | + | ATG |
| CBB_273 | Conserved hypothetical protein | 196632 | 197132 | 166 | + | ATG |
| CBB_274 | terminase DNA packaging enzyme large subunit | 197176 | 197883 | 235 | + | ATG |
| CBB_275 | DNA terminase packaging enzyme large subunit | 197870 | 199519 | 549 | + | ATG |
| CBB_276 | Structural protein | 199556 | 200845 | 429 | + | ATG |
| CBB_277 | ssDNA binding protein | 201073 | 202116 | 347 | + | ATG |
| CBB_278 | RecA-like protein | 202175 | 203305 | 376 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|-----|---|-----|
| CBB_279 | Conserved hypothetical protein | 203307 | 203771 | 154 | + | ATG |
| CBB_280 | putative DNA polymerase III epsilon subunit | 203817 | 204662 | 281 | + | ATG |
| CBB_281 | NA-DNA + DNA-DNA helicase | 204685 | 206169 | 494 | + | ATG |
| CBB_282 | Conserved hypothetical protein | 204685 | 206169 | 145 | + | ATG |
| CBB_283 | Conserved hypothetical protein | 206670 | 207173 | 167 | + | ATG |
| CBB_284 | Conserved hypothetical protein | 207173 | 208018 | 281 | + | ATG |
| CBB_285 | Conserved hypothetical protein | 208005 | 208724 | 239 | + | ATG |
| CBB_286 | Structural protein | 208721 | 209068 | 115 | + | ATG |
| CBB_287 | Putative membrane protein | 209034 | 209684 | 216 | + | ATG |
| CBB_288 | Conserved hypothetical protein | 209668 | 210021 | 117 | - | ATG |
| CBB_289 | Structural protein | 210079 | 211050 | 323 | + | ATG |
| CBB_290 | putative DNA primase | 211113 | 212159 | 348 | + | ATG |
| CBB_291 | DNA primase-helicase | 212167 | 213663 | 498 | + | ATG |
| CBB_292 | Structural protein | 213666 | 213935 | 89 | + | ATG |

| | | | | | | |
|---------|--|--------|--------|-----|---|-----|
| CBB_293 | Conserved hypothetical protein | 213937 | 214095 | 52 | + | ATG |
| CBB_294 | Structural protein | 214097 | 214495 | 132 | + | ATG |
| CBB_295 | Conserved hypothetical protein | 214541 | 215485 | 314 | + | ATG |
| CBB_296 | Conserved hypothetical protein | 215485 | 215703 | 72 | + | ATG |
| CBB_297 | Conserved hypothetical protein | 215700 | 216503 | 267 | + | ATG |
| CBB_298 | Structural protein | 216536 | 217180 | 214 | + | ATG |
| CBB_299 | Structural protein | 217193 | 217528 | 111 | + | ATG |
| CBB_300 | Restriction endonuclease type II-like | 217568 | 218269 | 233 | + | ATG |
| CBB_301 | Conserved hypothetical protein | 218274 | 218825 | 183 | + | ATG |
| CBB_302 | Structural protein | 218854 | 219432 | 192 | + | ATG |
| CBB_303 | ribonucleotide-diphosphate reductase alpha subunit | 219508 | 221838 | 776 | + | ATG |
| CBB_304 | Conserved hypothetical protein | 221881 | 222054 | 257 | + | ATG |
| CBB_305 | ribonucleotide-diphosphate reductase subunit beta | 222664 | 223785 | 373 | + | ATG |
| CBB_306 | Putative membrane protein | 223824 | 224012 | 62 | + | ATG |
| CBB_307 | Conserved hypothetical protein | 224073 | 224306 | 77 | + | ATG |
| CBB_308 | Structural protein | 224318 | 224698 | 126 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_309 | Conserved hypothetical protein | 224698 | 225414 | 238 | + | ATG |
| CBB_310 | Structural protein | 225436 | 226089 | 217 | - | ATG |
| CBB_311 | Putative membrane protein | 226101 | 226811 | 236 | - | ATG |
| CBB_312 | Putative membrane protein | 226944 | 227318 | 124 | + | ATG |
| CBB_313 | dihydrofolate reductase | 227315 | 227833 | 172 | + | ATG |
| CBB_314 | ribonuclease H | 227833 | 228267 | 144 | + | ATG |
| CBB_315 | DNA helicase Dda | 228264 | 229604 | 446 | + | ATG |
| CBB_316 | Structural protein | 229672 | 230217 | 181 | + | ATG |
| CBB_317 | Conserved hypothetical protein | 230236 | 230430 | 64 | + | ATG |

| | | | | | | |
|---------|------------------------------------|--------|--------|-----|---|-----|
| CBB_318 | translation initiation factor IF-3 | 230504 | 231010 | 168 | + | ATG |
| CBB_319 | ATP-dependent Clp protease | 231071 | 231604 | 177 | + | ATG |
| CBB_320 | Structural protein | 231666 | 232199 | 177 | + | ATG |
| CBB_321 | Structural protein | 231189 | 233799 | 536 | + | ATG |
| CBB_322 | Structural protein | 233799 | 236342 | 847 | + | ATG |
| CBB_323 | Putative membrane protein | 236433 | 236717 | 94 | + | ATG |
| CBB_324 | DNA gyrase subunit B | 236813 | 238786 | 657 | + | ATG |

| | | | | | | |
|---------|----------------------------------|--------|--------|-----|---|-----|
| CBB_325 | DNA topoisomerase II | 238837 | 240243 | 468 | + | ATG |
| CBB_326 | Structural protein | 240331 | 243014 | 789 | + | ATG |
| CBB_327 | Conserved hypothetical protein | 242709 | 243014 | 101 | + | ATG |
| CBB_328 | DNA polymerase III alpha subunit | 242974 | 243492 | 172 | + | ATG |
| CBB_329 | Conserved hypothetical protein | 243539 | 243913 | 124 | + | ATG |
| CBB_330 | Conserved hypothetical protein | 243924 | 244244 | 106 | + | ATG |
| CBB_331 | Conserved hypothetical protein | 244288 | 244578 | 96 | + | ATG |
| CBB_332 | sliding clamp loader subunit | 244581 | 245534 | 317 | + | ATG |
| CBB_333 | Conserved hypothetical protein | 245543 | 246163 | 206 | + | ATG |
| CBB_334 | Structural protein | 246221 | 246790 | 189 | + | ATG |
| CBB_335 | Structural protein | 246790 | 247473 | 227 | + | ATG |
| CBB_336 | Conserved hypothetical protein | 247473 | 248267 | 264 | + | ATG |
| CBB_337 | Conserved hypothetical protein | 248404 | 248943 | 179 | + | ATG |
| CBB_338 | Conserved hypothetical protein | 248977 | 249177 | 66 | + | ATG |
| CBB_339 | Conserved hypothetical protein | 249236 | 250432 | 398 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_340 | toxic ion resistance protein | 250525 | 251667 | 380 | + | ATG |
| CBB_341 | Conserved hypothetical protein | 251734 | 252066 | 110 | + | ATG |
| CBB_342 | putative metallopeptidase | 252066 | 252740 | 224 | + | ATG |
| CBB_343 | Putative membrane protein | 252797 | 253894 | 365 | + | ATG |
| CBB_344 | Structural protein | 253891 | 254445 | 184 | + | ATG |
| CBB_345 | Conserved hypothetical protein | 254558 | 254737 | 59 | + | ATG |
| CBB_346 | Putative membrane protein | 254749 | 255096 | 115 | + | ATG |
| CBB_347 | Conserved hypothetical protein | 255145 | 255777 | 210 | + | ATG |
| CBB_348 | Conserved hypothetical protein | 255777 | 256262 | 161 | + | ATG |
| CBB_349 | Conserved hypothetical protein | 256322 | 256046 | 574 | + | ATG |
| CBB_350 | Hypothetical protein | 258785 | 259024 | 79 | + | ATG |
| CBB_351 | Conserved hypothetical protein | 259027 | 259467 | 146 | + | ATG |
| CBB_352 | Conserved hypothetical protein | 259469 | 259672 | 67 | + | ATG |
| CBB_353 | Conserved hypothetical protein | 259672 | 260019 | 115 | + | ATG |
| CBB_354 | Conserved hypothetical protein | 260021 | 260335 | 104 | + | ATG |
| CBB_355 | Hypothetical protein | 260322 | 260672 | 116 | + | ATG |
| CBB_356 | Conserved hypothetical protein | 260659 | 261378 | 239 | + | ATG |
| CBB_357 | Conserved hypothetical protein | 361368 | 261616 | 82 | + | ATG |
| CBB_358 | Conserved hypothetical protein | 361621 | 261815 | 64 | + | ATG |
| CBB_359 | Conserved hypothetical protein | 261832 | 262851 | 339 | + | ATG |
| CBB_360 | Conserved hypothetical protein | 262861 | 263232 | 123 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|-----|---|-----|
| CBB_361 | nicotinamide-nucleotide adenylyltransferase | 263250 | 264299 | 349 | + | ATG |
| CBB_362 | nicotinamide mononucleotide transporter PnuC | 264296 | 265099 | 267 | + | ATG |
| CBB_363 | Hypothetical protein | 365101 | 265212 | 103 | + | ATG |
| CBB_364 | Conserved hypothetical protein | 265432 | 265674 | 80 | + | ATG |
| CBB_365 | Conserved hypothetical protein | 265721 | 265924 | 67 | + | ATG |
| CBB_366 | Conserved hypothetical protein | 265921 | 266358 | 145 | + | ATG |
| CBB_367 | Hypothetical protein | 266355 | 266660 | 101 | + | ATG |
| CBB_368 | Conserved hypothetical protein | 266657 | 266968 | 103 | + | ATG |
| CBB_369 | Conserved hypothetical protein | 266977 | 267321 | 114 | + | ATG |
| CBB_370 | Structural protein | 267305 | 267658 | 117 | + | ATG |
| CBB_371 | Conserved hypothetical protein | 267658 | 268017 | 119 | + | ATG |
| CBB_372 | Conserved hypothetical protein | 268028 | 268333 | 101 | + | ATG |
| CBB_373 | Conserved hypothetical protein | 268330 | 268779 | 149 | + | ATG |
| CBB_374 | Conserved hypothetical protein | 268895 | 269311 | 138 | + | ATG |

| | | | | | | |
|---------|-------------------------------------|--------|--------|-----|---|-----|
| CBB_375 | Conserved hypothetical protein | 269337 | 270125 | 275 | + | ATG |
| CBB_376 | Conserved hypothetical protein | 270125 | 271390 | 421 | + | ATG |
| CBB_377 | Conserved hypothetical protein | 271430 | 272620 | 396 | + | ATG |
| CBB_378 | Conserved hypothetical protein | 272817 | 273290 | 157 | + | ATG |
| CBB_379 | Conserved hypothetical protein | 273314 | 273646 | 110 | + | ATG |
| CBB_380 | putative 5'3'-deoxyribonucleotidase | 273650 | 274237 | 195 | + | ATG |
| CBB_381 | Conserved hypothetical protein | 274231 | 274755 | 184 | + | ATG |
| CBB_382 | Conserved hypothetical protein | 274908 | 275486 | 192 | + | ATG |
| CBB_383 | Conserved hypothetical protein | 276036 | 276362 | 108 | + | ATG |
| CBB_384 | Conserved hypothetical protein | 276721 | 276870 | 49 | + | ATG |
| CBB_385 | Conserved hypothetical protein | 276870 | 277124 | 84 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_386 | Conserved hypothetical protein | 277124 | 277815 | 263 | + | ATG |
| CBB_387 | Conserved hypothetical protein | 277908 | 278285 | 125 | + | GTG |
| CBB_388 | Conserved hypothetical protein | 278242 | 278703 | 153 | + | ATG |
| CBB_389 | Conserved hypothetical protein | 278703 | 278972 | 89 | + | ATG |
| CBB_390 | Conserved hypothetical protein | 278969 | 279484 | 171 | + | ATG |
| CBB_391 | Hypothetical protein | 279438 | 279893 | 151 | + | GTG |
| CBB_392 | peptidyl-tRNA hydrolase | 279874 | 280302 | 142 | + | ATG |
| CBB_393 | Putative membrane protein | 280575 | 280934 | 119 | + | ATG |
| CBB_394 | Conserved hypothetical protein | 280924 | 281157 | 77 | + | ATG |
| CBB_395 | Hypothetical protein | 281139 | 281300 | 53 | + | ATG |
| CBB_396 | Conserved hypothetical protein | 281303 | 281557 | 84 | + | ATG |
| CBB_397 | Conserved hypothetical protein | 281564 | 281926 | 120 | + | ATG |
| CBB_398 | Conserved hypothetical protein | 281910 | 282374 | 154 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| | | | | | | |
| CBB_399 | DNA-cytosine methyltransferase | 282396 | 283256 | 286 | + | ATG |
| CBB_400 | Conserved hypothetical protein | 283249 | 283560 | 103 | + | ATG |
| CBB_401 | Conserved hypothetical protein | 283563 | 283904 | 113 | + | ATG |
| CBB_402 | Conserved hypothetical protein | 283901 | 284605 | 234 | + | ATG |
| CBB_403 | Conserved hypothetical protein | 284616 | 284972 | 118 | + | ATG |
| CBB_404 | Hypothetical protein | 284976 | 285500 | 174 | + | ATG |
| CBB_405 | Conserved hypothetical protein | 285502 | 285699 | 65 | + | ATG |
| CBB_406 | Conserved hypothetical protein | 286108 | 286341 | 77 | + | TTG |
| CBB_407 | Conserved hypothetical protein | 286338 | 286478 | 46 | + | ATG |
| CBB_408 | Conserved hypothetical protein | 286581 | 286904 | 107 | + | TTG |
| CBB_409 | Conserved hypothetical protein | 286950 | 287381 | 143 | + | ATG |
| CBB_410 | Conserved hypothetical protein | 287391 | 287585 | 64 | + | ATG |
| CBB_411 | Conserved hypothetical protein | 287587 | 287937 | 116 | + | ATG |
| CBB_412 | Conserved hypothetical protein | 287948 | 288283 | 111 | + | ATG |
| CBB_413 | Hypothetical protein | 288587 | 288790 | 67 | + | ATG |
| CBB_414 | Hypothetical protein | 288793 | 288909 | 38 | + | ATG |
| CBB_415 | Putative membrane protein | 288912 | 289204 | 97 | + | ATG |
| CBB_416 | Hypothetical protein | 289202 | 289468 | 88 | + | ATG |
| CBB_417 | Conserved hypothetical protein | 289425 | 289715 | 96 | + | ATG |
| CBB_418 | Conserved hypothetical protein | 289786 | 289986 | 66 | + | ATG |
| CBB_419 | Conserved hypothetical protein | 290507 | 290740 | 77 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_420 | HNH | 290851 | 291255 | 134 | + | ATG |
| CBB_421 | Putative membrane protein | 291456 | 291608 | 50 | + | ATG |
| CBB_422 | Conserved hypothetical protein | 291615 | 291815 | 66 | + | ATG |
| CBB_423 | Putative membrane protein | 291815 | 292030 | 71 | + | ATG |
| CBB_424 | Putative membrane protein | 292027 | 292224 | 65 | + | ATG |
| CBB_425 | Conserved hypothetical protein | 292224 | 292664 | 146 | + | ATG |
| CBB_426 | Hypothetical protein | 292771 | 292983 | 70 | + | ATG |
| CBB_427 | Hypothetical protein | 292983 | 293228 | 81 | + | ATG |
| CBB_428 | Hypothetical protein | 293231 | 293458 | 75 | + | ATG |
| CBB_429 | Hypothetical protein | 293458 | 293718 | 86 | + | ATG |
| CBB_430 | Hypothetical protein | 293781 | 293984 | 67 | + | ATG |
| CBB_431 | Conserved hypothetical protein | 293985 | 294785 | 266 | + | ATG |
| CBB_432 | Hypothetical protein | 294787 | 295089 | 100 | + | ATG |
| CBB_433 | Conserved hypothetical protein | 295082 | 295489 | 135 | + | ATG |
| CBB_434 | Hypothetical protein | 295486 | 295713 | 75 | + | ATG |
| CBB_435 | Conserved hypothetical protein | 295860 | 296153 | 97 | + | ATG |
| CBB_436 | Conserved hypothetical protein | 296228 | 296510 | 93 | + | ATG |
| CBB_437 | Conserved hypothetical protein | 296513 | 296710 | 65 | + | ATG |
| CBB_438 | Conserved hypothetical protein | 296694 | 297059 | 121 | + | ATG |
| CBB_439 | Conserved hypothetical protein | 297059 | 297415 | 118 | + | ATG |
| CBB_440 | Conserved hypothetical protein | 297566 | 297799 | 77 | + | ATG |
| CBB_441 | Hypothetical protein | 287796 | 298419 | 207 | + | ATG |
| CBB_442 | Putative membrane protein | 298580 | 298416 | 54 | - | ATG |
| CBB_443 | Putative membrane protein | 298638 | 299012 | 124 | + | ATG |
| CBB_444 | Conserved hypothetical protein | 299204 | 299788 | 194 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_445 | Conserved hypothetical protein | 299807 | 300313 | 168 | + | ATG |
| CBB_446 | Conserved hypothetical protein | 300462 | 300677 | 71 | + | ATG |
| CBB_447 | Conserved hypothetical protein | 300741 | 300983 | 80 | + | ATG |
| CBB_448 | Putative membrane protein | 300996 | 301466 | 156 | + | ATG |
| CBB_449 | Hypothetical protein | 301822 | 301499 | 107 | - | TTG |
| CBB_450 | Conserved hypothetical protein | 301908 | 302054 | 48 | + | ATG |
| CBB_451 | Conserved hypothetical protein | 302871 | 303272 | 133 | + | TTG |
| CBB_452 | Conserved hypothetical protein | 303296 | 303505 | 69 | + | ATG |
| CBB_453 | Conserved hypothetical protein | 303601 | 303825 | 74 | + | ATG |
| CBB_454 | Conserved hypothetical protein | 303825 | 304223 | 132 | + | ATG |
| CBB_455 | Conserved hypothetical protein | 304960 | 305559 | 199 | + | ATG |
| CBB_456 | Conserved hypothetical protein | 305594 | 305947 | 117 | + | GTG |
| CBB_457 | Conserved hypothetical protein | 306246 | 306680 | 144 | + | GTG |
| CBB_458 | Conserved hypothetical protein | 306761 | 307072 | 103 | + | ATG |
| CBB_459 | Conserved hypothetical protein | 307418 | 307648 | 76 | + | ATG |
| CBB_460 | Hypothetical protein | 307810 | 308058 | 82 | + | ATG |
| CBB_461 | Conserved hypothetical protein | 308384 | 308710 | 108 | + | ATG |
| CBB_462 | Conserved hypothetical protein | 308798 | 309034 | 78 | + | ATG |
| CBB_463 | Conserved hypothetical protein | 309027 | 309512 | 161 | + | ATG |
| CBB_464 | Conserved hypothetical protein | 309514 | 309717 | 67 | + | ATG |
| CBB_465 | Hypothetical protein | 309819 | 310202 | 127 | + | ATG |
| CBB_466 | Conserved hypothetical protein | 310195 | 310458 | 87 | + | ATG |
| CBB_467 | Conserved hypothetical protein | 310740 | 310958 | 72 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_468 | Conserved hypothetical protein | 310951 | 311301 | 116 | + | ATG |
| CBB_469 | Conserved hypothetical protein | 311332 | 311727 | 131 | + | ATG |
| CBB_470 | Conserved hypothetical protein | 311949 | 312266 | 105 | + | ATG |
| CBB_471 | Conserved hypothetical protein | 312370 | 312621 | 83 | + | GTG |
| CBB_472 | Conserved hypothetical protein | 312784 | 313227 | 147 | + | ATG |
| CBB_473 | Conserved hypothetical protein | 313316 | 313441 | 41 | + | ATG |
| CBB_474 | Conserved hypothetical protein | 313431 | 313574 | 47 | + | ATG |
| CBB_475 | Conserved hypothetical protein | 313561 | 313809 | 82 | + | ATG |
| CBB_476 | PrIF antitoxin like protein | 313917 | 314393 | 158 | + | ATG |
| CBB_477 | Conserved hypothetical protein | 314383 | 314901 | 172 | + | ATG |
| CBB_478 | Conserved hypothetical protein | 314891 | 315019 | 42 | + | ATG |
| CBB_479 | Putative membrane protein | 315019 | 315333 | 104 | + | ATG |
| CBB_480 | Putative membrane protein | 315333 | 315671 | 112 | + | ATG |
| CBB_481 | Putative lipoprotein | 315671 | 315988 | 105 | + | ATG |
| CBB_482 | Putative membrane protein | 315998 | 316297 | 99 | + | ATG |
| CBB_483 | Conserved hypothetical protein | 316356 | 316493 | 45 | + | AAG |
| CBB_484 | Conserved hypothetical protein | 316468 | 316671 | 67 | + | ATG |
| CBB_485 | Conserved hypothetical protein | 316707 | 317192 | 161 | + | ATG |
| CBB_486 | Hypothetical protein | 317245 | 317511 | 88 | + | ATG |
| CBB_487 | Putative lipoprotein | 317511 | 317957 | 148 | + | ATG |
| CBB_488 | Conserved hypothetical protein | 318005 | 318136 | 43 | + | ATG |
| CBB_489 | Conserved hypothetical protein | 318191 | 318814 | 207 | + | GTG |
| CBB_490 | Conserved hypothetical protein | 318898 | 319257 | 119 | + | ATG |
| CBB_491 | Conserved hypothetical protein | 319369 | 319557 | 62 | + | ATG |
| CBB_492 | Conserved hypothetical protein | 319565 | 319762 | 65 | + | ATG |
| CBB_493 | Hypothetical protein | 319847 | 320068 | 73 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|-----|---|-----|
| CBB_494 | Structural protein | 320745 | 321431 | 228 | + | ATG |
| CBB_495 | S-adenosyl-L-methionine-dependent methyltransferase | 321487 | 322026 | 179 | + | ATG |
| CBB_496 | Structural protein | 323175 | 322042 | 377 | + | ATG |
| CBB_497 | Conserved hypothetical protein | 323350 | 323925 | 191 | + | ATG |
| CBB_498 | Putative membrane protein | 323937 | 324242 | 101 | + | ATG |
| CBB_499 | Putative membrane protein | 324246 | 324728 | 160 | + | ATG |
| CBB_500 | Conserved hypothetical protein | 324788 | 325309 | 173 | + | ATG |
| CBB_501 | Putative membrane protein | 325354 | 325824 | 156 | + | ATG |
| CBB_502 | Putative membrane protein | 325834 | 326283 | 149 | + | ATG |
| CBB_503 | Conserved hypothetical protein | 326355 | 326600 | 81 | + | ATG |
| CBB_504 | Putative membrane protein | 326593 | 327318 | 241 | + | GTG |
| CBB_505 | Conserved hypothetical protein | 327311 | 327430 | 39 | + | ATG |
| CBB_506 | Putative membrane protein | 327433 | 327867 | 144 | + | ATG |
| CBB_507 | Conserved hypothetical protein | 327921 | 328448 | 175 | + | ATG |
| CBB_508 | Conserved hypothetical protein | 328450 | 328773 | 107 | + | ATG |
| CBB_509 | Conserved hypothetical protein | 328773 | 329156 | 125 | + | ATG |
| CBB_510 | Conserved hypothetical protein | 329214 | 329405 | 63 | + | ATG |
| CBB_511 | transcriptional regulator | 330631 | 330861 | 76 | + | ATG |
| CBB_512 | Conserved hypothetical protein | 330858 | 331007 | 49 | + | ATG |

| | | | | | | |
|---------|---|--------|--------|-----|---|-----|
| CBB_513 | subfamily RNA polymerase sigma-70 subunit | 331103 | 332091 | 330 | + | GTG |
| CBB_514 | Conserved hypothetical protein | 332108 | 312818 | 236 | + | ATG |
| CBB_515 | Conserved hypothetical protein | 332827 | 333018 | 63 | + | ATG |
| CBB_516 | Conserved hypothetical protein | 333073 | 334047 | 324 | + | ATG |
| CBB_517 | Hypothetical protein | 334461 | 334634 | 98 | + | ATG |
| CBB_518 | Hypothetical protein | 334461 | 334634 | 57 | + | ATG |
| CBB_519 | endonuclease V N-glycosylase UV repair enzyme | 334700 | 335134 | 144 | + | ATG |
| CBB_520 | Conserved hypothetical protein | 335198 | 335383 | 61 | + | ATG |
| CBB_521 | Conserved hypothetical protein | 335458 | 335853 | 131 | + | ATG |
| CBB_522 | Putative membrane protein | 335850 | 336044 | 64 | + | ATG |
| CBB_523 | Conserved hypothetical protein | 336041 | 336274 | 77 | + | ATG |
| CBB_524 | Conserved hypothetical protein | 336949 | 337752 | 267 | + | ATG |
| CBB_525 | Conserved hypothetical protein | 337822 | 338832 | 336 | + | ATG |
| CBB_526 | Conserved hypothetical protein | 338899 | 339423 | 174 | + | ATG |
| CBB_527 | Conserved hypothetical protein | 339433 | 340227 | 264 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_528 | HNH | 340294 | 340860 | 188 | + | ATG |
| CBB_529 | Putative membrane protein | 340862 | 341182 | 106 | + | ATG |
| CBB_530 | Conserved hypothetical protein | 341299 | 342369 | 356 | + | ATG |
| CBB_531 | Conserved hypothetical protein | 342424 | 342612 | 62 | + | ATG |
| CBB_532 | Conserved hypothetical protein | 342609 | 342866 | 85 | + | ATG |
| CBB_533 | Conserved hypothetical protein | 342863 | 342030 | 55 | + | ATG |
| CBB_534 | Structural protein | 343063 | 343335 | 90 | + | ATG |
| CBB_535 | Conserved hypothetical protein | 343417 | 344337 | 306 | + | ATG |
| CBB_536 | Structural protein | 344368 | 345027 | 219 | + | ATG |
| CBB_537 | Structural protein | 345042 | 345689 | 215 | + | ATG |
| CBB_538 | Conserved hypothetical protein | 345789 | 346571 | 260 | + | ATG |
| CBB_539 | Putative membrane protein | 345789 | 346571 | 107 | + | ATG |
| CBB_540 | Putative membrane protein | 346911 | 347099 | 62 | + | ATG |
| CBB_541 | Putative membrane protein | 347102 | 347263 | 53 | + | TTG |
| CBB_542 | Conserved hypothetical protein | 347277 | 348047 | 256 | + | ATG |
| CBB_543 | Putative membrane protein | 348094 | 348444 | 116 | + | ATG |

| | | | | | | |
|---------|---------------------------|--------|--------|-----|---|-----|
| CBB_544 | Putative membrane protein | 348444 | 348782 | 112 | + | ATG |
| CBB_545 | Putative membrane protein | 348782 | 349132 | 116 | + | ATG |
| CBB_546 | Putative membrane protein | 349199 | 349495 | 98 | + | ATG |
| CBB_547 | Putative lipoprotein | 349547 | 350170 | 207 | + | ATG |
| CBB_548 | Structural protein | 350849 | 350196 | 217 | - | ATG |
| CBB_549 | Structural protein | 351530 | 350859 | 223 | - | ATG |
| CBB_550 | Kelch-like protein | 352396 | 351539 | 285 | - | ATG |
| CBB_551 | Structural protein | 353100 | 352396 | 234 | - | ATG |
| CBB_552 | Structural protein | 353952 | 353119 | 280 | - | ATG |
| CBB_553 | Structural protein | 354701 | 354030 | 223 | - | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_554 | Kelch-like protein | 355464 | 354667 | 265 | - | ATG |
| CBB_555 | Hypothetical protein | 357350 | 357538 | 62 | + | ATG |
| CBB_556 | Conserved hypothetical protein | 357723 | 358400 | 225 | + | ATG |
| CBB_557 | Conserved hypothetical protein | 358550 | 358819 | 89 | + | ATG |
| CBB_558 | Conserved hypothetical protein | 358955 | 359239 | 94 | + | ATG |
| CBB_559 | Conserved hypothetical protein | 359275 | 359664 | 129 | + | ATG |
| CBB_560 | Hypothetical protein | 359889 | 359716 | 57 | - | ATG |
| CBB_561 | Hypothetical protein | 359888 | 360040 | 50 | + | ATG |
| CBB_562 | Conserved hypothetical protein | 360088 | 360360 | 90 | + | ATG |
| CBB_563 | Conserved hypothetical protein | 360424 | 360870 | 148 | + | ATG |
| CBB_564 | Conserved hypothetical protein | 360947 | 361402 | 151 | + | ATG |
| CBB_565 | Hypothetical protein | 361483 | 361608 | 41 | + | ATG |
| CBB_566 | Hypothetical protein | 361681 | 361908 | 75 | + | ATG |
| CBB_567 | Conserved hypothetical protein | 361982 | 362404 | 140 | + | ATG |
| CBB_568 | Conserved hypothetical protein | 362586 | 362921 | 111 | + | ATG |
| CBB_569 | Conserved hypothetical protein | 362991 | 363158 | 55 | + | ATG |
| CBB_570 | Conserved hypothetical protein | 363242 | 363421 | 59 | + | ATG |
| CBB_571 | Conserved hypothetical protein | 363494 | 363865 | 123 | + | ATG |
| CBB_572 | Conserved hypothetical protein | 363912 | 364166 | 84 | + | ATG |
| CBB_573 | Hypothetical protein | 365171 | 365329 | 52 | + | ATG |
| CBB_574 | Conserved hypothetical protein | 364619 | 364852 | 77 | + | ATG |
| CBB_575 | Putative membrane protein | 364876 | 365034 | 52 | + | ATG |
| CBB_576 | Conserved hypothetical protein | 365046 | 365249 | 67 | + | ATG |
| CBB_577 | Conserved hypothetical protein | 365282 | 365425 | 47 | + | ATG |
| CBB_578 | Conserved hypothetical protein | 365504 | 365707 | 67 | + | ATG |

| | | | | | | |
|---------|--------------------------------|--------|--------|-----|---|-----|
| CBB_579 | Conserved hypothetical protein | 365737 | 366087 | 116 | + | ATG |
| CBB_580 | Putative membrane protein | 366314 | 366565 | 83 | + | ATG |
| CBB_581 | Hypothetical protein | 366597 | 366755 | 52 | + | ATG |
| CBB_582 | Structural protein | 366764 | 367639 | 291 | + | ATG |
| CBB_583 | Conserved hypothetical protein | 367779 | 367976 | 65 | + | ATG |
| CBB_584 | Conserved hypothetical protein | 367940 | 368065 | 41 | + | ATG |
| CBB_585 | Hypothetical protein | 368055 | 368249 | 64 | + | ATG |
| CBB_586 | Putative membrane protein | 368293 | 368646 | 117 | + | ATG |
| CBB_587 | Hypothetical protein | 368643 | 369032 | 129 | + | ATG |
| CBB_588 | Conserved hypothetical protein | 369104 | 369295 | 63 | + | ATG |
| CBB_589 | Conserved hypothetical protein | 369358 | 369744 | 128 | + | ATG |
| CBB_590 | Conserved hypothetical protein | 369864 | 370106 | 80 | + | ATG |
| CBB_591 | Conserved hypothetical protein | 370163 | 370681 | 172 | + | ATG |
| CBB_592 | Conserved hypothetical protein | 370745 | 371083 | 112 | + | ATG |
| CBB_593 | Hypothetical protein | 371326 | 371673 | 115 | + | ATG |
| CBB_594 | Conserved hypothetical protein | 371764 | 371982 | 72 | + | ATG |
| CBB_595 | Conserved hypothetical protein | 372158 | 372760 | 200 | + | ATG |
| CBB_596 | Conserved hypothetical protein | 372965 | 373297 | 110 | + | ATG |
| CBB_597 | Conserved hypothetical protein | 373507 | 373749 | 80 | + | ATG |
| CBB_598 | Conserved hypothetical protein | 373829 | 374716 | 295 | + | ATG |
| CBB_599 | Conserved hypothetical protein | 374792 | 375130 | 112 | + | ATG |
| CBB_600 | Conserved hypothetical protein | 375334 | 375564 | 76 | + | ATG |
| CBB_601 | Conserved hypothetical protein | 375648 | 375995 | 115 | + | ATG |

| Stop codon | Molecular weight (KDa) | Blastp result |
|------------|------------------------|--|
| TAG | 6.65 | _ |
| TAA | 7.00 | _ |
| TAA | 25.17 | hypothetical protein GAP32_005 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.13 | hypothetical protein GAP32_006 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 10.83 | hypothetical protein GAP32_008 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.96 | hypothetical protein GAP32_007 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.30 | _ |
| TGA | 5.58 | _ |
| TGA | 10.08 | hypothetical protein GAP32_009 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.80 | hypothetical protein GAP32_010 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.13 | hypothetical protein GAP32_011 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 4.54 | _ |
| TAA | 8.43 | _ |
| TAA | 16.39 | hypothetical protein GAP32_012 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.23 | hypothetical protein [Citrobacter amalonaticus] |
| TAA | 6.68 | hypothetical protein N748_03710 [Legionella pneumophila str. 121004] |
| TAA | 6.51 | hypothetical protein VPBG_00116 [Vibrio phage helene 12B3] |
| TAA | 14.45 | hypothetical protein GAP32_014 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.99 | hypothetical protein GAP32_015 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.88 | _ |
| TAA | 8.56 | hypothetical protein GAP32_017 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.06 | hypothetical protein GAP32_018A [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.51 | hypothetical protein GAP32_019 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.86 | hypothetical protein GAP32_020 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.56 | hypothetical protein GAP32_021 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 13.40 | hypothetical protein GAP32_022 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.44 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 5.87 | _ |
| TAA | 31.54 | hypothetical protein GAP32_025 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.04 | hypothetical protein GAP32_026 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 4.86 | hypothetical protein GAP32_027 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.12 | _ |
| TGA | 13.52 | _ |
| TAA | 14.27 | _ |
| TAA | 7.27 | hypothetical protein GAP32_029 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.27 | hypothetical protein GAP32_030 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.53 | hypothetical protein GAP32_031 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.82 | hypothetical protein GAP32_032 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.64 | hypothetical protein GAP32_033 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.92 | _ |
| TAA | 8.27 | hypothetical protein GAP32_034 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 23.42 | hypothetical protein GAP32_035 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.84 | hypothetical protein GAP32_036 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.16 | hypothetical protein GAP32_037 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 33.78 | hypothetical protein GAP32_039 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.26 | hypothetical protein GAP32_040 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.64 | hypothetical protein GAP32_041 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.49 | hypothetical protein GAP32_042 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 7.18 | _ |
| TAA | 6.43 | hypothetical protein GAP32_044 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.35 | hypothetical protein GAP32_046 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.69 | _ |
| TAA | 23.35 | hypothetical protein GAP32_048 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 23.78 | hypothetical protein GAP32_050 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 25.13 | hypothetical protein GAP32_051 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 23.04 | hypothetical protein GAP32_052 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 20.85 | hypothetical protein GAP32_053 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.71 | hypothetical protein GAP32_054 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 15.94 | hypothetical protein GAP32_055 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.35 | hypothetical protein GAP32_057 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.37 | hypothetical protein GAP32_058 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.48 | hypothetical protein GAP32_059 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.72 | hypothetical protein [Aeromonas allosaccharophila] |
| TAA | 35.49 | hypothetical protein GAP32_060 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.91 | hypothetical protein GAP32_061 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.79 | hypothetical protein GAP32_062 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.41 | hypothetical protein GAP32_063 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.54 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 29.85 | hypothetical protein GAP32_065 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.72 | hypothetical protein GAP32_066 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.26 | hypothetical protein GAP32_067 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 20.59 | DNA N-6-adenine-methyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.43 | cytidyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.90 | hypothetical protein GAP32_070 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.01 | hypothetical protein GAP32_071 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.20 | hypothetical protein GAP32_073 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 27.34 | hypothetical protein GAP32_074 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.65 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 42.67 | hypothetical protein GAP32_076 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 28.09 | hypothetical protein GAP32_077 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TGA | 11.32 | hypothetical protein GAP32_078 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.45 | hypothetical protein GAP32_079 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 44.10 | RNA ligase 1 and tail fiber attachment catalyst [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.27 | hypothetical protein GAP32_081 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.71 | hypothetical protein GAP32_082 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.52 | hypothetical protein GAP32_083 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 35.99 | polynucleotide 5'-kinase and 3'-phosphatase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.71 | GAP32_085 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.47 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.90 | hypothetical protein GAP32_088 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.94 | hypothetical protein GAP32_089 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.47 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.58 | hypothetical protein GAP32_091 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.06 | hypothetical protein GAP32_092 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.78 | hypothetical protein GAP32_093 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.93 | hypothetical protein GAP32_094 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 30.02 | putative serine/threonine protein phosphatase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.25 | hypothetical protein GAP32_097 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 47.48 | hypothetical protein GAP32_098 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 53.23 | DNA ligase [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 16.67 | hypothetical protein GAP32_100 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.56 | metallophosphoesterase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.64 | hypothetical protein GAP32_102 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 25.46 | ATP-dependent Clp protease proteolytic subunit [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.46 | hypothetical protein GAP32_104 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.75 | hypothetical protein GAP32_105 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.46 | hypothetical protein GAP32_106 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 20.60 | hypothetical protein GAP32_107 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.09 | hypothetical protein GAP32_108 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.85 | CMP/dCMP deaminase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.40 | hypothetical protein GAP32_110 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.75 | Ig domain-containing protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 42.17 | bifunctional nicotinamide mononucleotide adenylyltransferase/ADP-ribose pyrophosphatase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.20 | hypothetical protein GAP32_113 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 55.68 | nicotinamide phosphoribosyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.39 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 37.08 | hypothetical protein GAP32_116 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.64 | hypothetical protein GAP32_118 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.60 | hypothetical protein GAP32_118A [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 29.72 | putative Sir2-like protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 34.45 | hypothetical protein GAP32_120 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 11.13 | hypothetical protein GAP32_121 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 53.57 | PhoH family protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.03 | hypothetical protein GAP32_123 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 27.02 | hypothetical protein GAP32_124 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.26 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.62 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.37 | hypothetical protein GAP32_126 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 31.87 | hypothetical protein GAP32_127 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.68 | hypothetical protein GAP32_129 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.26 | co-chaperonin GroES [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 47.60 | tyrosyl-tRNA synthetase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.80 | hypothetical protein GAP32_132 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 25.45 | hypothetical protein GAP32_133 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.72 | dCMP deaminase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.88 | _ |
| TAA | 24.62 | _ |
| TGA | 10.21 | hypothetical protein GAP32_135 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.74 | _ |
| TAA | 21.16 | hypothetical protein GAP32_136 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|--------|--|
| | | |
| TGA | 69.42 | anaerobic NTP reductase large subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.19 | _ |
| TAA | 18.00 | hypothetical protein GAP32_139 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 25.22 | _ |
| | | |
| TGA | 17.91 | anaerobic ribonucleoside-triphosphate reductase activating protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.57 | hypothetical protein GAP32_142 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 98.07 | hypothetical protein GAP32_143 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 98.70 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 100.67 | hypothetical protein GAP32_145 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.00 | hypothetical protein GAP32_146 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.61 | _ |

| | | |
|-----|-------|--|
| TGA | 29.85 | putative tRNA-His guanylyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.59 | hypothetical protein GAP32_148 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.23 | hypothetical protein GAP32_149 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 18.38 | hypothetical protein GAP32_150 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 25.22 | hypothetical protein GAP32_151 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 33.21 | putative N-4 cytosine-specific methyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.97 | hypothetical protein GAP32_153 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 48.92 | hypothetical protein GAP32_154 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.13 | hypothetical protein GAP32_155 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.46 | hypothetical protein GAP32_156 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 21.48 | hypothetical protein GAP32_158 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| | | |
| TAA | 15.80 | acyl carrier protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 14.09 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 11.90 | hypothetical protein GAP32_161 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.24 | hypothetical protein GAP32_162 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.36 | hypothetical protein GAP32_163 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.61 | hypothetical protein GAP32_164 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.18 | hypothetical protein GAP32_165 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.86 | hypothetical protein GAP32_167 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.77 | GTP cyclohydrolase [Terasakiella pusilla] |
| TAA | 11.16 | hypothetical protein GAP32_168 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TGA | 21.41 | thymidine kinase [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 19.78 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 23.04 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.58 | hypothetical protein GAP32_173 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 4.71 | _ |
| TAA | 23.57 | _ |
| TAA | 12.32 | _ |
| TTG | 21.27 | hypothetical protein GAP32_174 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 47.45 | RNA ligase [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 24.17 | hypothetical protein GAP32_355 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 55.82 | hypothetical protein GAP32_176 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.03 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 17.28 | hypothetical protein GAP32_178 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 21.94 | hypothetical protein GAP32_179 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 35.38 | lysozyme [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.88 | sigma 54 modulation protein/ribosomal protein S30EA [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 16.15 | hypothetical protein GAP32_184 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 5.63 | _ |
| TGA | 8.66 | hypothetical protein GAP32_185 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 42.75 | multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.50 | nudix hydrolase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.70 | glutaredoxin [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.18 | hypothetical protein GAP32_189 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.50 | hypothetical protein GAP32_190 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.39 | hypothetical protein GAP32_191 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.85 | hypothetical protein GAP32_192 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.97 | hypothetical protein GAP32_193 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.48 | hypothetical protein GAP32_194 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 29.62 | neck protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.77 | hypothetical protein GAP32_196 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TGA | 24.82 | putative deoxynucleoside monophosphate kinase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 95.91 | tail sheath monomer [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 25.39 | hypothetical protein GAP32_199 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 29.03 | hypothetical protein GAP32_200 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 39.83 | hypothetical protein GAP32_201 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.69 | head completion protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.53 | hypothetical protein GAP32_203 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.95 | hypothetical protein GAP32_204 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.24 | hypothetical protein GAP32_205 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 53.17 | hypothetical protein GAP32_206 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 33.36 | hypothetical protein GAP32_207 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.86 | hypothetical protein GAP32_208 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 14.33 | hypothetical protein GAP32_209 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 50.67 | ATPase [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 51.29 | hypothetical protein GAP32_211 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|--------|---|
| TAA | 8.64 | hypothetical protein GAP32_212 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 26.15 | hypothetical protein GAP32_213 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.58 | hypothetical protein GAP32_214 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.36 | hypothetical protein GAP32_215 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.86 | hypothetical protein GAP32_216 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 35.33 | thymidylate synthase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 68.10 | hypothetical protein GAP32_218 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.19 | hypothetical protein GAP32_219 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 153.27 | long tail fiber proximal subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.02 | hypothetical protein GAP32_221 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 41.68 | hypothetical protein GAP32_222 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.05 | hypothetical protein GAP32_223 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.80 | hypothetical protein GAP32_224 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 40.39 | hypothetical protein GAP32_225 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 17.72 | MutT/NUDIX hydrolase family protein [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 51.35 | tail sheath stabilizer and completion protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 57.00 | hypothetical protein GAP32_228 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|--------|---|
| TAA | 84.34 | ATP-dependent Clp protease ATP-binding subunit clpA [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 379.94 | hypothetical protein GAP32_230 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 131.71 | baseplate wedge [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.83 | base plate protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.49 | baseplate hub subunit and tail lysozyme [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 97.09 | baseplate hub subunit and tail lysozyme [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 88.83 | hypothetical protein GAP32_235 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.23 | hypothetical protein GAP32_236 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 27.69 | hypothetical protein GAP32_237 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 33.56 | sigma factor for late transcription [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 39.92 | recombination endonuclease subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 82.05 | recombination endonuclease subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 27.28 | hypothetical protein [Erwinia phage PhiEaH1] |
| TAA | 18.15 | DNA endonuclease VII [Escherichia phage 121Q] |
| TAA | 6.93 | hypothetical protein GAP32_242 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 32.55 | hypothetical protein GAP32_243 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 78.41 | hypothetical protein GAP32_244 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 65.18 | portal vertex protein of head [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.63 | hypothetical protein GAP32_246 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.25 | hypothetical protein GAP32_247 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.24 | prohead core scaffold and protease [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 42.55 | hypothetical protein GAP32_249 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|--------|--|
| TAA | 42.11 | precursor of major head subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.98 | hypothetical protein GAP32_252 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.02 | hypothetical protein GAP32_253 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 56.65 | putative tail fiber protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.06 | tail fiber assembly protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.31 | hypothetical protein GAP32_256 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 115.94 | DNA polymerase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.32 | hypothetical protein GAP32_258 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 26.74 | hypothetical protein GAP32_259 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.92 | putative phosphoesterase or phosphohydrolase [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 8.22 | hypothetical protein GAP32_261 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.74 | co-chaperonin GroES [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 28.50 | hypothetical protein GAP32_263 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.43 | hypothetical protein GAP32_264 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.23 | hypothetical protein GAP32_265 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 38.17 | RNaseH ribonuclease [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.04 | hypothetical protein GAP32_267 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 27.52 | terminase DNA packaging enzyme large subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 62.89 | DNA terminase packaging enzyme large subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 48.67 | hypothetical protein GAP32_270 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 38.62 | ssDNA binding protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 41.44 | RecA-like protein [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 17.96 | hypothetical protein GAP32_273 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 32.53 | putative DNA polymerase III epsilon subunit [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 56.09 | RNA-DNA + DNA-DNA helicase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.16 | hypothetical protein GAP32_277 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.15 | hypothetical protein GAP32_278 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 32.25 | hypothetical protein GAP32_279 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 28.82 | hypothetical protein GAP32_280 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.30 | hypothetical protein GAP32_281 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 25.11 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.23 | hypothetical protein GAP32_283 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 36.68 | hypothetical protein GAP32_284 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 40.38 | putative DNA primase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 55.75 | DNA primase-helicase [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.37 | hypothetical protein GAP32_287 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 5.60 | hypothetical protein GAP32_288 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.70 | hypothetical protein GAP32_289 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 34.25 | hypothetical protein GAP32_290 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.36 | hypothetical protein GAP32_291 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.22 | hypothetical protein GAP32_292 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.65 | hypothetical protein GAP32_293 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.15 | hypothetical protein GAP32_294 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 26.64 | hypothetical protein GAP32_295 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.26 | hypothetical protein GAP32_296 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.83 | hypothetical protein GAP32_297 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 87.79 | ribonucleotide-diphosphate reductase alpha subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.80 | gp559 [Bacillus phage G] |
| TAA | 43.37 | ribonucleotide-diphosphate reductase subunit beta [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.09 | hypothetical protein GAP32_301 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.14 | hypothetical protein GAP32_302 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.78 | hypothetical protein GAP32_303 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 26.30 | hypothetical protein GAP32_304 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.21 | hypothetical protein GAP32_305 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 26.33 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.97 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.68 | dihydrofolate reductase [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 16.20 | ribonuclease H [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 51.65 | DNA helicase Dda [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.94 | hypothetical protein GAP32_311 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.30 | hypothetical protein GAP32_312 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 18.74 | translation initiation factor IF-3 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.09 | ATP-dependent Clp protease [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.64 | hypothetical protein GAP32_315 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 61.65 | hypothetical protein GAP32_316 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 96.34 | hypothetical protein GAP32_317 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.58 | hypothetical membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 74.42 | DNA gyrase subunit B [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| | | |
| TAA | 53.17 | DNA topoisomerase II [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 87.98 | hypothetical protein GAP32_321 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.84 | hypothetical protein GAP32_322 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 20.57 | DNA polymerase III alpha subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.94 | hypothetical protein GAP32_324 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.70 | hypothetical protein GAP32_325 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.15 | hypothetical protein GAP32_326 [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 36.15 | sliding clamp loader subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.06 | hypothetical protein GAP32_328 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.94 | hypothetical protein GAP32_329 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 25.70 | hypothetical protein GAP32_330 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.76 | hypothetical protein GAP32_331 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.20 | hypothetical protein GAP32_332 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.02 | hypothetical protein GAP32_333 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 45.96 | hypothetical protein GAP32_334 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 42.63 | toxic ion resistance protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.01 | hypothetical protein GAP32_336 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 25.57 | putative metallopeptidase [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 42.11 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.71 | hypothetical protein GAP32_339 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.44 | hypothetical protein GAP32_340 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.26 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 25.48 | hypothetical protein VPBG_00153 [Vibrio phage helene 12B3] |
| TGA | 18.99 | hypothetical protein GAP32_342 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 64.97 | hypothetical protein GAP32_343 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.26 | _ |
| TAA | 17.29 | hypothetical protein GAP32_344 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.74 | hypothetical protein GAP32_345 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.81 | hypothetical protein GAP32_346 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 12.35 | hypothetical protein GAP32_347 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 13.29 | _ |
| TGA | 27.60 | hypothetical protein GAP32_348 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.91 | hypothetical protein GAP32_349 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.65 | hypothetical protein GAP32_350 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 39.69 | hypothetical protein GAP32_351 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.27 | hypothetical protein GAP32_352 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TGA | 40.33 | nicotinamide-nucleotide adenyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.12 | nicotinamide mononucleotide transporter PnuC [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.83 | _ |
| TAA | 9.22 | hypothetical protein GAP32_356 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.38 | hypothetical protein JS09_0194 [Escherichia phage vB_EcoM_JS09] |
| TGA | 17.42 | hypothetical protein GAP32_357 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.61 | _ |
| TAA | 11.70 | hypothetical protein GAP32_358 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.01 | hypothetical protein GAP32_359 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.82 | hypothetical protein RaK2_00182 [Enterobacteria phage vB_KleM-RaK2] |
| TAG | 13.97 | hypothetical protein GAP32_360 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.83 | hypothetical protein GAP32_361 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.30 | hypothetical protein GAP32_362 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.96 | hypothetical protein GAP32_364 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 29.73 | hypothetical protein GAP32_365 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 49.56 | hypothetical protein GAP32_366 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 45.37 | hypothetical protein GAP32_367 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 18.24 | hypothetical protein GAP32_368 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.84 | hypothetical protein GAP32_369 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.98 | putative 5'3'-deoxyribonucleotidase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.05 | hypothetical protein GAP32_371 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.86 | hypothetical protein GAP32_372 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.90 | hypothetical protein GAP32_374 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 5.31 | hypothetical protein GAP32_374A [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.80 | hypothetical protein GAP32_375 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| | | |
| TAA | 30.18 | hypothetical protein GAP32_376 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 15.24 | hypothetical protein GAP32_377 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 17.78 | hypothetical protein GAP32_378 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.60 | hypothetical protein GAP32_379 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.33 | hypothetical protein GAP32_380 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 17.79 | _ |
| | | |
| TAA | 16.92 | peptidyl-tRNA hydrolase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.85 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.75 | hypothetical protein GAP32_385 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.27 | _ |
| TGA | 10.07 | hypothetical protein GAP32_387 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 13.63 | hypothetical protein GAP32_388 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.72 | hypothetical protein GAP32_389 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| | | |
| TAA | 32.94 | DNA-cytosine methyltransferase [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.73 | hypothetical protein GAP32_391 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 13.37 | hypothetical protein GAP32_392 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 27.62 | hypothetical protein GAP32_393 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.28 | hypothetical protein GAP32_394 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.74 | _ |
| TAA | 7.88 | hypothetical protein GAP32_395 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.78 | hypothetical protein GAP32_397 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 5.33 | hypothetical protein GAP32_398 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.32 | hypothetical protein GAP32_399 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.39 | hypothetical protein GAP32_400 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.45 | hypothetical protein GAP32_401 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.34 | hypothetical protein GAP32_402 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.02 | hypothetical protein [Paenibacillus elgii] |
| TGA | 7.68 | _ |
| TAA | 4.50 | _ |
| TGA | 11.07 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.43 | _ |
| TAA | 11.02 | hypothetical protein GAP32_404 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.38 | hypothetical protein AE04_00280 [Enterobacter aerogenes MGH 78] |
| TAA | 8.78 | hypothetical protein GAP32_405 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| | | |
| TAA | 15.88 | hypothetical protein RaK2_00219 [Enterobacteria phage vB_KleM-RaK2] |
| TGA | 5.85 | hypothetical protein GAP32_408 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.92 | hypothetical protein GAP32_409 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.79 | _ |
| TAA | 7.46 | hypothetical protein GAP32_411 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.95 | hypothetical protein GAP32_412 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.96 | _ |
| TAA | 9.06 | _ |
| TAA | 8.91 | _ |
| TAA | 9.76 | _ |
| TAA | 7.37 | _ |
| TAA | 31.18 | hypothetical protein GAP32_415 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 11.17 | _ |
| TGA | 16.01 | hypothetical protein GAP32_416 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.65 | _ |
| TAA | 11.65 | hypothetical protein GAP32_417 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.10 | hypothetical protein GAP32_418 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.77 | hypothetical protein GAP32_419 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 14.35 | hypothetical protein GAP32_420 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.86 | hypothetical protein GAP32_421 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.77 | hypothetical protein GAP32_422 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.95 | _ |
| TAG | 6.21 | _ |
| TAA | 13.92 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.99 | hypothetical protein [Clostridiaceae bacterium mt10] |

| | | |
|-----|-------|--|
| TAA | 19.31 | hypothetical protein GAP32_425 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.28 | hypothetical protein GAP32_426 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.42 | hypothetical protein GAP32_427 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.67 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 12.97 | _ |
| TAA | 5.50 | hypothetical protein GAP32_431 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 15.96 | hypothetical protein GAP32_432 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.15 | hypothetical protein GAP32_433 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.40 | hypothetical protein GAP32_434 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.67 | hypothetical protein GAP32_435 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 22.79 | hypothetical protein GAP32_436 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.68 | hypothetical protein GAP32_437 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.17 | hypothetical protein [Clostridium sp. GD3] |
| TAA | 12.15 | hypothetical protein [Escherichia phage vB_EcoS_FFH1] |
| TAA | 9.02 | hypothetical protein GAP32_439 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.86 | _ |
| TAA | 12.71 | hypothetical protein GAP32_440 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.29 | hypothetical protein GAP32_441 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.18 | hypothetical protein GAP32_442 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.19 | hypothetical protein GAP32_443 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.22 | _ |
| TAG | 10.19 | hypothetical protein GAP32_445 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 8.66 | hypothetical protein GAP32_446 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 14.25 | hypothetical protein GAP32_447 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 15.68 | hypothetical protein GAP32_448 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.42 | hypothetical protein GAP32_451 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.83 | hypothetical protein GAP32_453A [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.05 | hypothetical protein GAP32_454 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 4.56 | hypothetical protein GAP32_455 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.31 | hypothetical protein [Yersinia kristensenii] |
| TAG | 9.26 | hypothetical protein GAP32_456 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 18.14 | hypothetical protein GAP32_457 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 19.72 | hypothetical protein VPFG_00288 [Vibrio phage nt-1] |
| TAA | 5.11 | hypothetical protein GAP32_458 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.86 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.40 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.60 | hypothetical protein GAP32_461 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.85 | hypothetical protein GAP32_462 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 5.33 | hypothetical protein GAP32_462A [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.91 | hypothetical protein GAP32_463 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.55 | hypothetical protein GAP32_464 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.26 | _ |
| TAA | 16.31 | hypothetical protein GAP32_465 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 4.84 | hypothetical protein GAP32_466 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 24.12 | hypothetical protein GAP32_468 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.22 | hypothetical protein GAP32_469 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.20 | hypothetical protein GAP32_470 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 7.44 | hypothetical protein GAP32_471 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.43 | _ |

| | | |
|-----|-------|--|
| TAA | 24.72 | hypothetical protein GAP32_473 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.99 | hypothetical protein GAP32_474 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 40.94 | hypothetical protein GAP32_475 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 21.62 | hypothetical protein GAP32_476 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.57 | hypothetical protein GAP32_477 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.21 | hypothetical protein GAP32_478 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.65 | hypothetical protein GAP32_479 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.63 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.81 | _ |
| TAA | 9.24 | hypothetical protein GAP32_481 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 28.55 | hypothetical protein GAP32_482 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 3.96 | hypothetical protein GAP32_483 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.72 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 20.65 | hypothetical protein GAP32_485 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.01 | hypothetical protein GAP32_486 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 14.78 | hypothetical protein GAP32_487 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.99 | hypothetical protein [Salmonella phage SKML-39] |
| TGA | 8.77 | transcriptional regulator [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.55 | hypothetical protein GAP32_489 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| | | |
| TAA | 37.92 | subfamily RNA polymerase sigma-70 subunit [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 26.63 | hypothetical protein GAP32_492 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.20 | hypothetical protein GAP32_493 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 37.22 | hypothetical protein GAP32_494 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 11.47 | _ |
| TGA | 6.57 | _ |
| | | |
| TAA | 16.95 | endonuclease V N-glycosylase UV repair enzyme [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.99 | hypothetical protein GAP32_499 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 15.54 | hypothetical protein GAP32_500 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.15 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.82 | hypothetical protein GAP32_502 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 31.25 | hypothetical protein GAP32_504 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 39.56 | hypothetical protein GAP32_505 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 19.85 | hypothetical protein GAP32_506 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 30.74 | hypothetical protein GAP32_507 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| | | |
| TAA | 21.78 | HNH endonuclease [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.48 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| | | |
| TAA | 40.50 | hypothetical protein GAP32_510 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 7.21 | hypothetical protein GAP32_511 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 10.40 | hypothetical protein GAP32_512 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.23 | hypothetical protein GAP32_514 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.45 | hypothetical protein GAP32_515 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 35.70 | hypothetical protein GAP32_520 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.75 | hypothetical protein SP19_190 [Salmonella phage 19] |
| TAA | 24.14 | hypothetical protein SP19_190 [Salmonella phage 19] |
| TAG | 29.12 | hypothetical protein GAP32_521 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 12.12 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.10 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.89 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 29.98 | hypothetical protein GAP32_524 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.14 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 13.12 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.29 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.86 | _ |
| TAA | 22.41 | hypothetical protein GAP32_529 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 23.81 | hypothetical protein GAP32_530 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 24.84 | hypothetical protein GAP32_531 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 31.83 | kelch-like protein 17 [Chrysochromulina sp. CCMP291] |
| TAA | 25.38 | _ |
| TAG | 31.25 | _ |
| TAA | 25.40 | hypothetical protein GAP32_002 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|---|
| TAA | 29.91 | _ |
| TAA | 7.00 | _ |
| TAA | 25.17 | hypothetical protein GAP32_005 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 10.13 | hypothetical protein GAP32_006 [Cronobacter phage vB_CsaM_GAP32] |
| TAG | 10.83 | hypothetical protein GAP32_008 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.96 | hypothetical protein GAP32_007 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.30 | _ |
| TGA | 5.58 | _ |
| TAA | 10.08 | hypothetical protein GAP32_009 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 16.80 | hypothetical protein GAP32_010 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 17.13 | hypothetical protein GAP32_011 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 4.54 | _ |
| TAA | 8.43 | _ |
| TAA | 16.39 | hypothetical protein GAP32_012 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.23 | hypothetical protein [Citrobacter amalonaticus] |
| TAA | 6.68 | hypothetical protein Lste_0119 [Legionella steelei] |
| TAA | 6.51 | hypothetical protein VPBG_00116 [Vibrio phage helene 12B3] |
| TAA | 14.45 | hypothetical protein GAP32_014 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.99 | hypothetical protein GAP32_015 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 5.88 | _ |
| TAA | 8.56 | hypothetical protein GAP32_017 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 6.06 | hypothetical protein GAP32_018A [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.51 | hypothetical protein GAP32_019 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 6.86 | hypothetical protein GAP32_020 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 7.56 | hypothetical protein GAP32_021 [Cronobacter phage vB_CsaM_GAP32] |

| | | |
|-----|-------|--|
| TAA | 13.40 | hypothetical protein GAP32_022 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.44 | Putative membrane protein [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 5.87 | _ |
| TAA | 31.54 | hypothetical protein GAP32_025 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.04 | hypothetical protein GAP32_026 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 4.86 | hypothetical protein GAP32_027 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.12 | _ |
| TGA | 13.52 | _ |
| TAA | 14.27 | _ |
| TAG | 7.27 | hypothetical protein GAP32_029 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 14.27 | hypothetical protein GAP32_030 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 9.53 | hypothetical protein GAP32_031 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 18.82 | hypothetical protein GAP32_032 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.64 | hypothetical protein GAP32_033 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.92 | _ |
| TAA | 8.27 | hypothetical protein GAP32_034 [Cronobacter phage vB_CsaM_GAP32] |
| TGA | 23.42 | hypothetical protein GAP32_035 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 12.84 | hypothetical protein GAP32_036 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 9.16 | hypothetical protein GAP32_037 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 33.78 | hypothetical protein GAP32_039 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.26 | hypothetical protein GAP32_040 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 8.64 | hypothetical protein GAP32_041 [Cronobacter phage vB_CsaM_GAP32] |
| TAA | 13.49 | hypothetical protein GAP32_042 [Cronobacter phage vB_CsaM_GAP32] |

| Acession number | E value | MS identification of structural proteins of CBB capsid | Shared Structural proteins of GAP32 | Structural proteins shared with Rak2 | pfam domain hit | E-value |
|------------------------|----------------|---|--|---|------------------------|----------------|
| YP_006987 | 2.00E-88 | | | | | |
| YP_006987 | 6.00E-56 | | | | | |
| YP_006987 | 1.00E-38 | | | | | |
| YP_006987 | 1.00E-83 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 8.00E-56 | | | | | |
| YP_006987 | 5.00E-100 | | | | | |
| YP_006987 | 3.00E-102 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-60 | | | | | |
| WP_04649 | 5.00E-09 | | | | | |
| CAH17234. | 1.00E-10 | | | | | |
| YP_007877 | 9.00E-06 | | | | | |
| YP_006987 | 8.00E-51 | | | | | |
| YP_006987 | 2.00E-52 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-48 | | | | | |
| YP_006987 | 2.00E-15 | | | | | |
| YP_006987 | 7.00E-37 | | | | | |
| YP_006987 | 8.00E-24 | | | | | |
| YP_006987124.1 | 4.00E-39 | | | | | |

| | | | | | | |
|-----------|----------|-----|-----|-----|----------------------|----------|
| YP_006987 | 2.00E-60 | | | | | |
| YP_006987 | 2.00E-29 | | | | | |
| | | | | | | |
| | | | | | PF01145.22 Band_7 | |
| YP_006987 | 1.00E-83 | Yes | Yes | | | 1.00E-27 |
| YP_006987 | 1.00E-29 | | | | | |
| YP_006987 | 8.00E-03 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-18 | | | | | |
| YP_006987 | 7.00E-23 | | | | | |
| YP_006987 | 3.00E-41 | | | | | |
| YP_006987 | 1.00E-96 | Yes | Yes | Yes | | |
| YP_006987 | 1.00E-60 | | | | | |
| | | | | | | |
| YP_006987 | 7.00E-16 | | | | | |
| YP_006987 | 5.00E-88 | | | | | |
| YP_006987 | 5.00E-58 | | | | | |
| YP_006987 | 7.00E-46 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF06067.8 DUF932 | 5.10E-37 |
| YP_006987 | 2.00E-63 | | | | | |
| YP_006987 | 2.00E-28 | | | | | |
| YP_006987 | 1.00E-64 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|--|--|
| | | | | | | |
| YP_006987 | 9.00E-28 | | | | | |
| YP_006987 | 2.00E-37 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-108 | | | | | |
| YP_006987 | 3.00E-19 | | | | | |
| YP_006987 | 1.00E-33 | | | | | |
| YP_006987 | 2.00E-88 | | | | | |
| YP_006987 | 1.00E-53 | | | | | |
| YP_006987 | 5.00E-72 | | | | | |
| YP_006987 | 1.00E-59 | | | | | |
| YP_006987 | 1.00E-81 | | | | | |
| YP_006987 | 1.00E-107 | | | | | |
| YP_006987 | 2.00E-19 | | | | | |
| WP_04206 | 4.00E-30 | | | | | |
| YP_006987 | 0.E+00 | | | | | |
| YP_006987 | 1.00E-54 | | | | | |
| YP_006987 | 3.00E-79 | | | | | |
| YP_006987 | 2.00E-74 | | | | | |
| YP_006987 | 5.00E-25 | | | | | |
| YP_006987 | 1.00E-92 | | | | | |
| YP_006987 | 9.00E-99 | | | | | |
| YP_006987 | 2.00E-87 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|-------------------------------|----------|
| | | | | | PF05869.8 Dam | |
| YP_006987 | 3.00E-125 | | | | | 2.00E-27 |
| | | | | | PF01467.23 CTP_transf_like | |
| YP_006987 | 2.00E-86 | | | | | 8.90E-06 |
| YP_006987 | 2.00E-46 | | | | | |
| YP_006987 | 9.00E-75 | | | | | |
| YP_006987 | 2.00E-04 | | | | | |
| | | | | | PF01966.19 HD | |
| YP_006987 | 6.00E-129 | | | | | 2.30E-04 |
| YP_006987 | 3.00E-20 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 4.00E-169 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|---------------------------|----------|
| YP_006987 | 1.00E-46 | | | | | |
| YP_006987 | 6.00E-50 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF09511.7 RNA_lig_T4_1 | 8.40E-15 |
| YP_006987 | 2.00E-34 | | | | | |
| YP_006987 | 6.00E-29 | | | | | |
| YP_006987 | 2.00E-41 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF13671.3 AAA_33 | 1.70E-16 |
| YP_006987 | 5.00E-29 | | | | | |
| YP_006987 | 8.00E-15 | | | | | |
| YP_006987 | 6.00E-45 | | | | | |
| YP_006987 | 1.00E-69 | | | | | |
| YP_006987 | 6.00E-19 | | | | | |
| YP_006987 | 8.00E-45 | | | | | |
| YP_006987 | 4.00E-65 | | | | | |
| YP_006987 | 3.00E-42 | | | | | |
| YP_006987 | 1.00E-125 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|------------------------------|----------|
| | | | | | PF00149.25 Metallophos | |
| YP_006987 | 0.00E+00 | | | | | 1.70E-15 |
| YP_006987 | 4.00E-92 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| | | | | | PF01068.18 DNA_ligase_A_M | |
| YP_006987 | 0.00E+00 | | | | | 6.20E-20 |
| YP_006987 | 3.00E-72 | | | | | |
| | | | | | PF00149.25 Metallophos | |
| YP_006987 | 1.00E-163 | | | | | 4.20E-11 |
| YP_006987 | 1.00E-67 | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|--|----------------|
| | | | | | PF00574.20 CLP_protease | |
| YP_006987 | 2.00E-153 | Yes | | | | 4.20E-40 |
| YP_006987 | 2.00E-56 | | | | | |
| YP_006987 | 4.00E-90 | | | | | |
| YP_006987 | 9.00E-41 | | | | | |
| YP_006987 | 6.00E-98 | | | | | |
| YP_006987 | 4.00E-60 | | | | | |
| | | | | | PF00383.20 dCMP_cyt_deam_1 | |
| YP_006987 | 5.00E-106 | | | | | 7.00E-24 |
| YP_006987 | 7.00E-37 | | | | | |
| | | | | | PF02368.15 Big_2 | |
| YP_006987 | 2.00E-98 | Yes | Yes | Yes | | 1.90E-20 |
| | | | | | PF00293.25CTP_tr ansf_like, PF00293.25 NUDIX | |
| YP_006987 | 0 | | | | | 4.7E-6, 5.6E-1 |
| YP_006987 | 3.00E-72 | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|---|-------------------------------------|----------------|
| | | | | | PF04095.13 NAPRTase | |
| YP_006987 | 0.00E+00 | | | | | 2.40E-36 |
| YP_006987 | 3.00E-07 | | | | | |
| YP_006987 | 1.00E-74 | | | | | |
| YP_006987 | 7.00E-99 | Yes | Yes | | | |
| YP_006987 | 1.00E-11 | | | | | |
| | | | | | PF02146.14 SIR2 | |
| YP_006987 | 1.00E-158 | | | | | 5.90E-26 |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 8.00E-56 | | | | | |
| | | | | | PF13638.3 PIN_4, PF02562.13 PhoH | |
| YP_006987 | 0 | | | ? | | 2.1E-23, 1.2E- |
| YP_006987 | 4.00E-16 | | | | | |
| YP_006987 | 5.00E-137 | | | | | |
| YP_006987 | 9.00E-17 | | | | | |
| YP_006987 | 3.00E-21 | | | | | |
| YP_006987 | 1.00E-107 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|---|-------------------|
| YP_006987 | 7.00E-54 | | | | | |
| YP_006987 | 7.00E-135 | | | | | |
| YP_006987 | 1.00E-55 | | | | PF00166.18 Cpn10 | 1.60E-12 |
| YP_006987 | 0.00E+00 | | | | PF00579.22 tRNA-synt_1b, PF01479.22 S4 | 1.4E-64, 2.60E-64 |
| YP_006987 | 4.00E-40 | | | | | |
| YP_006987 | 5.00E-129 | | | | | |
| YP_006987 | 4.00E-75 | | | | PF00383.20 dCMP_cyt_deam_1 | 2.40E-06 |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-16 | | | | | |
| | | | | | | |
| YP_006987 | 7.00E-115 | | | | PF13521.3 AAA_28 | 5.20E-20 |

| | | | | | | |
|-----------|----------|-----|-----|--|----------------------|-----------|
| | | | | | PF13597.3 NRDD | |
| YP_006987 | 0 | | | | | 2.50E-160 |
| | | | | | | |
| YP_006987 | 1.00E-61 | | | | | |
| | | Yes | | | | |
| | | | | | PF13353.3 Fer4_12 | |
| YP_006987 | 1.00E-98 | | | | | 2.10E-50 |
| YP_006987 | 3.00E-24 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 0.00E+00 | | Yes | | | |
| YP_006987 | 0.00E+00 | | Yes | | | |
| YP_006987 | 1.00E-99 | | | | | |
| | | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|---------------------------|----------|
| | | | | | PF04446.9 Thg1 | |
| YP_006987 | 6.00E-175 | | | | | 1.60E-31 |
| YP_006987 | 2.00E-77 | | | | | |
| YP_006987 | 8.00E-63 | | | | PF14216.3 DUF4326 | 6.80E-18 |
| YP_006987 | 1.00E-71 | | | | | |
| YP_006987 | 2.00E-51 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF01555.15 N6_N4_Mtase | 1.90E-34 |
| YP_006987 | 2.00E-40 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF10127.6 Nuc- transf | 3.80E-18 |
| YP_006987 | 2.00E-71 | | | | | |
| YP_006987 | 3.00E-65 | | | | | |
| YP_006987 | 8.00E-120 | | | | | |

| | | | | | | |
|-----------|-----------|-----|--|-----|-------------------------|----------|
| | | | | | PF00550.22 PP-binding | |
| YP_006987 | 3.00E-12 | | | | | 4.40E-09 |
| YP_006987 | 7.00E-63 | | | Yes | | |
| YP_006987 | 2.00E-52 | | | Yes | | |
| YP_006987 | 1.00E-73 | | | | | |
| YP_006987 | 5.00E-32 | | | | | |
| YP_006987 | 2.00E-32 | | | | | |
| YP_006987 | 2.00E-95 | Yes | | | | |
| YP_006987 | 1.00E-57 | | | | | |
| WP_02887 | 1.00E-47 | | | | PF08719.8 DUF1768 | 8.40E-52 |
| YP_006987 | 8.00E-08 | | | | | |
| | | | | | PF00265.15 TK | |
| YP_006987 | 3.00E-120 | | | | | 1.70E-52 |
| YP_006987 | 2.00E-93 | | | | | |
| YP_006987 | 1.00E-103 | | | | | |
| YP_006987 | 3.00E-80 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-73 | | | | | |
| YP_006987 | 0 | | | | PF09414.7 RNA_ligase | 1.60E-15 |

| | | | | | | |
|-----------|----------|-----|--|--|---|----------------|
| YP_006987 | 7.00E-44 | | | | | |
| | | | | | PF11443.5 DUF2828, PF11443.5 DUF2828 | |
| YP_006987 | 0 | Yes | | | | 6.7E-10, 9.9E- |
| YP_006987 | 8.00E-17 | | | | | |
| YP_006987 | 2.00E-89 | | | | | |
| YP_006987 | 9.00E-76 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 8.00E-64 | | | | PF02482.16 Ribosomal_S30AE | 3.10E-13 |
| YP_006987 | 2.00E-52 | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-26 | | | | | |

| | | | | | | |
|-----------|----------|-----|--|-----|--|----------------|
| | | | | | PF01743.17 PolyA_pol, PF12627.4 PolyA_pol_RNAbd | |
| YP_006987 | 0.00E+00 | | | | | 2.60E-17, 3.50 |
| | | | | | PF00293.25 NUDIX | |
| YP_006987 | 2.00E-93 | | | | | 7.60E-15 |
| | | | | | PF00462.21 Glutaredoxin | |
| YP_006987 | 1.00E-45 | | | | | 7.70E-11 |
| YP_006987 | 7.00E-84 | | | | PF09424.7 YqeY | 4.50E-06 |
| YP_006987 | 2.00E-66 | | | | | |
| YP_006987 | 1.00E-48 | | | | | |
| | | | | | PF01661.18 Macro | |
| YP_006987 | 4.00E-95 | | | | | 8.90E-08 |
| YP_006987 | 6.00E-59 | | | | | |
| YP_006987 | 4.00E-70 | | | | | |
| YP_006987 | 0.00E+00 | Yes | | Yes | | |
| YP_006987 | 4.00E-24 | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|--|----------------|
| YP_006987 | 2.00E-113 | | | | | |
| | | | | | PF04984.11 Phage_sheath_1 | |
| YP_006987 | 0.00E+00 | | Yes | Yes | | 1.40E-27 |
| YP_006987 | 3.00E-167 | Yes | Yes | Yes | | |
| YP_006987 | 0.00E+00 | | Yes | Yes | | |
| YP_006987 | 0 | Yes | | | | |
| | | | | | PF08722.8 Tn7_Tnp_TnsA_N | |
| YP_006987 | 2.00E-103 | | | | | 6.40E-07 |
| YP_006987 | 1.00E-103 | | | | | |
| YP_006987 | 1.00E-126 | Yes | Yes | Yes | | |
| YP_006987 | 1.00E-83 | | Yes | Yes | | |
| YP_006987 | 0.00E+00 | | Yes | Yes | | |
| YP_006987 | 6.00E-177 | Yes | | Yes | | |
| YP_006987 | 1.00E-65 | Yes | | Yes | | |
| YP_006987 | 6.00E-76 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| | | | | | PF13203.3 DUF2201_N, PF13203.3 DUF2201_N, PF09967.6 DUF2201 | |
| YP_006987 | 0.00E+00 | | | | | 2.4E-5, 1.9E-2 |

| | | | | | | |
|-----------|-----------|-----|-----|-----|-------------------------------|-----------|
| YP_006987 | 8.00E-38 | | | | | |
| YP_006987 | 1.00E-146 | | | | | |
| YP_006987 | 2.00E-61 | | | | | |
| YP_006987 | 9.00E-131 | | | | | |
| YP_006987 | 4.00E-45 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF00303.16 Thymidylat_synt | 5.50E-104 |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| YP_006987 | 1.00E-133 | Yes | Yes | | PF14301.3 DUF4376 | 7.20E-12 |
| YP_006987 | 0.00E+00 | Yes | Yes | | | |
| YP_006987 | 5.00E-163 | Yes | Yes | Yes | | |
| YP_006987 | 0.00E+00 | Yes | Yes | | | |
| YP_006987 | 5.00E-98 | | Yes | Yes | | |
| YP_006987 | 6.00E-141 | Yes | Yes | | | |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| YP_006987 | 2.00E-107 | | | | PF00293.25 NUDIX | 4.50E-14 |
| YP_006987 | 0.00E+00 | Yes | Yes | | PF16724.2 T4- gp15_tss | 2.40E-07 |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|---|----------------|
| | | | | | PF00004.26 AAA, PF07724.11 AAA_2, PF10431.6 ClpB_D2-small, PF02861.17 Clp_N | |
| YP_006987 | 0.00E+00 | | | | | 3.30E-15, 2E-3 |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| | | | | | PF04965.11 GPW_gp25 | |
| YP_006987 | 3.00E-83 | | Yes | Yes | | 3.60E-10 |
| | | | | | PF00959.16 Phage_lysozyme | |
| YP_006987 | 8.00E-100 | | | | | 3.40E-08 |
| | | | | | PF00959.16 Phage_lysozyme | |
| YP_006987 | 0.00E+00 | Yes | Yes | | | 9.30E-09 |
| YP_006987 | 0.00E+00 | Yes | | Yes | | |
| | | | | | PF11246.5 Phage_gp53 | |
| YP_006987 | 7.00E-62 | Yes | | | | 7.50E-05 |

| | | | | | | |
|-----------|-----------|-----|-----|-----|-----------------------------|----------|
| YP_006987 | 6.00E-174 | Yes | Yes | Yes | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF00149.25 Metallophos | 1.70E-04 |
| YP_006987 | 0.00E+00 | | | | PF13476.3 AAA_23 | 1.10E-11 |
| YP_009010 | 4.00E-23 | Yes | | | | |
| YP_009102 | 3.00E-64 | | | | | |
| YP_006987 | 2.00E-24 | | | | | |
| YP_006987 | 1.00E-178 | | | Yes | | |
| YP_006987 | 0.00E+00 | Yes | Yes | | | |
| YP_006987 | 0.00E+00 | | Yes | Yes | PF07230.8 Peptidase_S80 | 2.00E-36 |
| YP_006987 | 2.00E-33 | | | | | |
| YP_006987 | 7.00E-120 | Yes | | Yes | | |
| YP_006987 | 4.00E-142 | | Yes | Yes | PF03420.10 Peptidase_S77 | 4.00E-21 |
| YP_006987 | 0.00E+00 | Yes | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|--|----------------|
| | | | | | PF07068.8 Gp23, PF07068.8 Gp23 | |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | 9.60E-11, 7.6E |
| YP_006987 | 2.00E-92 | | | | | |
| | | | | | PF10544.6 T5orf172 | |
| YP_006987 | 3.00E-70 | | | | | 1.50E-09 |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| YP_006987 | 4.00E-72 | | | | | |
| YP_006987 | 8.00E-63 | | | | | |
| | | | | | PF03104.16 DNA_pol_B_exo1, PF00136.18 DNA_pol_B, PF00136.18 DNA_pol_B | |
| YP_006987 | 0.00E+00 | | | | | 9.60E-20, 1.90 |
| YP_006987 | 3.00E-31 | | | | | |
| YP_006987 | 4.00E-175 | | | | | |
| | | | | | PF00149.25 Metallophos | |
| YP_006987 | 7.00E-139 | | | | | 1.70E-04 |

| | | | | | | |
|-----------|-----------|-----|-----|-----|----------------------------|----------|
| YP_006987 | 1.00E-25 | | | | | |
| | | | | | PF00166.18 Cpn10 | |
| YP_006987 | 3.00E-58 | | | | | 4.70E-17 |
| YP_006987 | 2.00E-141 | | | Yes | | |
| YP_006987 | 1.00E-121 | Yes | Yes | Yes | | |
| YP_006987 | 3.00E-124 | Yes | Yes | Yes | | |
| | | | | | PF02739.13 5_3_exonuc_N | |
| YP_006987 | 0.00E+00 | | | | | 7.50E-17 |
| YP_006987 | 1.00E-99 | | | | | |
| YP_006987 | 6.00E-93 | | | | | |
| | | | | | PF03237.12 Terminase_6 | |
| YP_006987 | 0.00E+00 | | | | | 3.50E-23 |
| YP_006987 | 0.00E+00 | Yes | | | | |
| | | | | | | |
| YP_006987 | 0.00E+00 | | | ? | | |
| | | | | | PF00154.18 RecA | |
| YP_006987 | 0.00E+00 | | | | | 9.90E-15 |

| | | | | | | |
|-----------|-----------|-----|-----|--|--|--------------------|
| YP_006987 | 9.00E-98 | | | | | |
| | | | | | PF00929.21RNase_T, PF12843.4 QSregVF_b | |
| YP_006987 | 0.00E+00 | | | | | 1.10E-19, 1.50E-19 |
| | | | | | PF00271.28 Helicase_C, PF04851.12 ResIII | |
| YP_006987 | 0.00E+00 | | | | | 6.30E-7, 7.10E-7 |
| YP_006987 | 8.00E-79 | | | | | |
| YP_006987 | 5.00E-116 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 9.00E-170 | | | | | |
| YP_006987 | 1.00E-63 | Yes | | | | |
| YP_006987 | 1.00E-154 | | | | | |
| YP_006987 | 5.00E-78 | | | | | |
| YP_006987 | 0.00E+00 | | Yes | | | |
| YP_006987 | 0.00E+00 | | | | | |
| | | | | | PF03796.12 DnaB_C | |
| YP_006987 | 0.00E+00 | | | | | 2.80E-15 |
| YP_006987 | 4.00E-51 | Yes | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|--|----------------|
| YP_006987 | 1.00E-18 | | | | | |
| YP_006987 | 2.00E-85 | Yes | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 4.00E-38 | | | | | |
| YP_006987 | 5.00E-169 | | | | | |
| YP_006987 | 5.00E-137 | Yes | Yes | Yes | | |
| YP_006987 | 1.00E-68 | Yes | | | | |
| YP_006987 | 2.00E-165 | | | | PF12705.4 PDDEXK_1 | 2.10E-04 |
| YP_006987 | 6.00E-112 | | | | | |
| YP_006987 | 3.00E-123 | | Yes | Yes | | |
| YP_006987 | 0.00E+00 | | | | PF03477.13 ATP- cone, PF00317.18 Ribonuc_red_lgN, PF02867.12 Ribonuc_red_lgC | 8.50E-13, 2.40 |
| YP_009015 | 4.00E-07 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF00268.18 Ribonuc_red_sm | 1.10E-48 |
| YP_006987 | 1.00E-17 | | | | | |
| YP_006987 | 4.00E-41 | | | | | |
| YP_006987 | 5.00E-85 | | | Yes | | |

| | | | | | | |
|-----------|-----------|--|-----|-----|---|----------------|
| | | | | | PF01503.14 PRA-PH | |
| YP_006987 | 2.00E-133 | | | | | 5.60E-09 |
| YP_006987 | 2.00E-136 | | | Yes | | |
| YP_006987 | 5.00E-158 | | | | | |
| YP_006987 | 4.00E-46 | | | | | |
| | | | | | PF00186.16 DHFR_1 | |
| YP_006987 | 2.00E-94 | | | | | 5.60E-38 |
| | | | | | PF00075.21 RNase_H | |
| YP_006987 | 9.00E-93 | | | | | 1.20E-37 |
| | | | | | PF13604.3 AAA_30, PF13538.3 UvrD_C_2 | |
| YP_006987 | 0 | | | | | 1.40E-21, 1.70 |
| YP_006987 | 2.00E-100 | | Yes | Yes | | |
| YP_006987 | 1.00E-34 | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|--|----------------|
| | | | | | PF05198.13 IF3_N, PF00707.19 IF3_C | |
| YP_006987 | 2.00E-105 | | | | | 3.80E-19, 5.80 |
| | | | | | PF02617.14 ClpS | |
| YP_006987 | 9.00E-98 | | | | | 1.10E-13 |
| | | | | | PF13619.3 KTSC | |
| YP_006987 | 1.00E-122 | Yes | Yes | | | 1.60E-14 |
| YP_006987 | 0.00E+00 | | Yes | | | |
| YP_006987 | 0.00E+00 | Yes | Yes | Yes | | |
| YP_006987 | 5.00E-52 | | | | | |
| | | | | | PF02518.23 HATPase_c, PF00204.22 PF01751.19 DNA_gyraseB, Toprim | |
| YP_006987 | 0.00E+00 | | | | | 3.10E-10, 2.50 |

| | | | | | | |
|-----------|-----------|-----|-----|-----|------------------------------|----------|
| | | | | | PF00521.17 DNA_topoisolV | |
| YP_006987 | 0.00E+00 | | | | | 1.90E-65 |
| YP_006987 | 0.00E+00 | | Yes | Yes | | |
| YP_006987 | 6.00E-60 | | | | | |
| | | | | | PF07733.9 DNA_pol3_alpha | |
| YP_006987 | 2.00E-114 | | | | | 5.70E-08 |
| YP_006987 | 2.00E-83 | | | | | |
| YP_006987 | 4.00E-66 | | | | | |
| YP_006987 | 2.00E-50 | | | | | |
| | | | | | PF13177.3 DNA_pol3_delta2 | |
| YP_006987 | 0.00E+00 | | | | | 6.80E-14 |
| YP_006987 | 6.00E-140 | | | | | |
| YP_006987 | 2.00E-124 | Yes | | | | |
| YP_006987 | 1.00E-151 | | Yes | | | |
| YP_006987 | 1.00E-180 | | | | | |
| YP_006987 | 2.00E-54 | | | | | |
| YP_006987 | 3.00E-33 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |

| | | | | | | |
|-----------|-----------|--|-----|-----|----------------|----------|
| YP_006987 | 0.00E+00 | | | | PF05816.8 Tela | 5.30E-52 |
| YP_006987 | 5.00E-48 | | | | | |
| YP_006987 | 2.00E-118 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 6.00E-107 | | Yes | Yes | | |
| YP_006987 | 2.00E-16 | | | | | |
| YP_006987 | 1.00E-61 | | | | | |
| YP_007877 | 2.00E-48 | | | | | |
| YP_006987 | 3.00E-102 | | | | | |
| YP_006987 | 5.00E-132 | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-28 | | | | | |
| YP_006987 | 6.00E-35 | | | | | |
| YP_006987 | 5.00E-63 | | | | | |
| YP_006987 | 5.00E-63 | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-133 | | | | | |
| YP_006987 | 1.00E-41 | | | | | |
| YP_006987 | 3.00E-23 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| YP_006987 | 1.00E-78 | | | | | |

| | | | | | | |
|-----------|----------|--|--|-----|---|----------------|
| | | | | | PF01467.23 CTP_transf_like, PF13521.3 AAA_28 | |
| YP_006987 | 0.00E+00 | | | | | 0.00014, 2.6E- |
| | | | | | PF04973.9 NMN_transporter | |
| YP_006987 | 0.00E+00 | | | | | 7.50E-38 |
| | | | | | | |
| YP_006987 | 2.00E-43 | | | | | |
| YP_009037 | 6.00E-03 | | | | | |
| YP_006987 | 2.00E-81 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-66 | | | | | |
| YP_006987 | 7.00E-60 | | | | | |
| YP_007007 | 9.00E-30 | | | Yes | | |
| YP_006987 | 4.00E-59 | | | | | |
| YP_006987 | 8.00E-33 | | | | | |
| YP_006987 | 7.00E-92 | | | | | |
| YP_006987 | 3.00E-43 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|----------------------|----------|
| | | | | | PF14243.3 DUF4343 | |
| YP_006987 | 0.00E+00 | | | | | 1.80E-23 |
| YP_006987 | 0.00E+00 | | | | | |
| | | | | | PF00004.26 AAA | |
| YP_006987 | 0.00E+00 | | | | | 4.20E-06 |
| YP_006987 | 4.00E-98 | | | | | |
| YP_006987 | 1.00E-46 | | | | | |
| | | | | | PF06941.9 NT5C | |
| YP_006987 | 3.00E-128 | | | | | 7.70E-13 |
| YP_006987 | 1.00E-104 | | | | | |
| YP_006987 | 5.00E-118 | | | | | |
| YP_006987 | 5.00E-59 | | | | | |
| YP_006987 | 7.00E-26 | | | | | |
| YP_006987 | 1.00E-48 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|----------------------|----------|
| | | | | | PF14243.3 DUF4343 | |
| YP_006987 | 2.00E-124 | | | | | 4.50E-26 |
| YP_006987 | 1.00E-46 | | | | | |
| YP_006987 | 9.00E-95 | | | | | |
| YP_006987 | 7.00E-44 | | | | | |
| YP_006987 | 6.00E-59 | | | | | |
| | | | | | | |
| | | | | | PF01981.13 PTH2 | |
| YP_006987 | 1.00E-85 | | | | | 1.50E-11 |
| YP_006987 | 5.00E-64 | | | | | |
| YP_006987 | 9.00E-39 | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-46 | | | | | |
| YP_006987 | 1.00E-40 | | | | | |
| YP_006987 | 2.00E-72 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|---|----------------|
| | | | | | PF00145.14 DNA_methylase, PF00145.14 DNA_methylase | |
| YP_006987 | 0.00E+00 | | | | | 5.3E-25, 1.30E |
| YP_006987 | 2.00E-49 | | | | | |
| YP_006987 | 8.00E-60 | | | | | |
| YP_006987 | 1.00E-110 | | | | | |
| YP_006987 | 7.00E-71 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-38 | | | | | |
| YP_006987 | 2.00E-48 | | | | | |
| YP_006987 | 4.00E-24 | | | | | |
| YP_006987 | 7.00E-67 | | | | | |
| YP_006987 | 3.00E-61 | | | | | |
| YP_006987 | 2.00E-25 | | | | | |
| YP_006987 | 1.00E-70 | | | | | |
| WP_01049 | 6.00E-21 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-39 | | | | | |
| | | | | | | |
| YP_006987 | 3.00E-38 | | | | | |
| KDF37778. | 2.00E-09 | | | | | |
| YP_006987 | 4.00E-35 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|--|----------------|
| | | | | | PF13392.3 HNH_3, PF10955.5 DUF2757 | |
| YP_007007 | 2.00E-49 | | | | | 5.1E-7, 3.0E-5 |
| YP_006987 | 1.00E-22 | | | | | |
| YP_006987 | 2.00E-26 | | | | | |
| | | | | | | |
| YP_006987 | 8.00E-04 | | | | | |
| YP_006987 | 3.00E-56 | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-179 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-89 | | | | | |
| | | | | | | |
| YP_006987 | 2.00E-60 | | | | | |
| YP_006987 | 2.00E-33 | | | | | |
| YP_006987 | 4.00E-37 | | | | | |
| YP_006987 | 2.00E-82 | | | | | |
| YP_006987 | 2.00E-78 | | | | | |
| YP_006987 | 1.00E-38 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 5.00E-22 | | | | | |
| WP_05566 | 1.00E-04 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|----------------------|----------|
| YP_006987 | 7.00E-69 | | | | | |
| YP_006987 | 2.00E-44 | | | | | |
| YP_006987 | 2.00E-34 | | | | | |
| YP_006987 | 6.00E-77 | | | | | |
| | | | | | | |
| YP_006987 | 5.00E-20 | | | | | |
| YP_006987 | 2.00E-69 | | | | | |
| YP_006987 | 9.00E-34 | | | | | |
| YP_006987 | 6.00E-43 | | | | | |
| YP_006987 | 6.00E-56 | | | | | |
| YP_006987 | 2.00E-107 | | | | | |
| | | | | | PF07087.8 DUF1353 | |
| YP_006987 | 2.00E-75 | | | | | 6.60E-26 |
| WP_05062 | 5.00E-04 | | | | | |
| YP_009031 | 3.00E-12 | | | | | |
| YP_006987 | 3.00E-22 | | | | | |
| | | | | | | |
| YP_006987 | 3.00E-70 | | | | | |
| YP_006987 | 9.00E-39 | | | | | |
| YP_006987 | 2.00E-112 | | | | | |
| YP_006987 | 1.00E-38 | | | | | |
| | | | | | | |
| YP_006987 | 5.00E-50 | | | | | |
| YP_006987 | 2.00E-38 | | | | | |

| | | | | | | |
|-----------|----------|--|--|--|-----------------------------|----------|
| YP_006987 | 7.00E-31 | | | | | |
| YP_006987 | 3.00E-59 | | | | | |
| YP_006987 | 5.00E-65 | | | | | |
| YP_006987 | 2.00E-46 | | | | | |
| YP_006987 | 4.00E-48 | | | | | |
| YP_006987 | 1.00E-12 | | | | | |
| WP_05029 | 2.00E-05 | | | | | |
| YP_006987 | 1.00E-47 | | | | | |
| YP_006987 | 4.00E-20 | | | | PF15937.2 PrIF_antitoxin | 2.30E-10 |
| YP_008125 | 6.00E-08 | | | | | |
| YP_006987 | 5.00E-22 | | | | | |
| YP_006987 | 1.00E-33 | | | | | |
| YP_006987 | 2.00E-51 | | | | | |
| YP_006987 | 2.00E-42 | | | | | |
| YP_006987 | 4.00E-36 | | | | | |
| YP_006987 | 8.00E-03 | | | | | |
| YP_006987 | 1.00E-23 | | | | | |
| YP_006987 | 5.00E-55 | | | | | |
| | | | | | | |
| YP_006987 | 3.00E-22 | | | | | |
| YP_006987 | 2.00E-15 | | | | | |
| YP_006987 | 2.00E-40 | | | | | |
| YP_006987 | 4.00E-63 | | | | | |
| YP_006987 | 8.00E-19 | | | | | |
| YP_006987 | 1.00E-04 | | | | | |
| | | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|-----|---------------------|----------|
| YP_006987 | 1.00E-72 | Yes | | Yes | | |
| YP_006987 | 3.00E-97 | | | | | |
| YP_006987 | 0.00E+00 | Yes | Yes | | | |
| YP_006987 | 6.00E-116 | | | | | |
| YP_006987 | 2.00E-48 | | | | | |
| YP_006987 | 6.00E-70 | | | | | |
| YP_006987 | 3.00E-94 | | | | | |
| YP_006987 | 1.00E-48 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-36 | | | | | |
| YP_006987 | 5.00E-115 | | | | | |
| YP_006987 | 3.00E-13 | | | | | |
| YP_006987 | 4.00E-32 | | | | | |
| YP_006987 | 7.00E-58 | | | | | |
| YP_006987 | 8.00E-30 | | | | | |
| YP_006987 | 5.00E-80 | | | | | |
| YP_007236 | 3.00E-11 | | | | | |
| | | | | | PF13744.3 HTH_37 | |
| YP_006987 | 2.00E-29 | | | | | 5.10E-18 |
| YP_006987 | 3.00E-23 | | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|--------------------------|----------|
| | | | | | PF04542.11 Sigma70_r2 | |
| YP_006987 | 0.00E+00 | | | | | 5.90E-05 |
| YP_006987 | 7.00E-139 | | | | | |
| YP_006987 | 7.00E-33 | | | | | |
| YP_006987 | 0.00E+00 | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | PF03013.11 Pyr_excise | |
| YP_006987 | 2.00E-87 | | | | | 4.90E-40 |
| YP_006987 | 7.00E-24 | | | | | |
| YP_006987 | 6.00E-25 | | | | | |
| YP_006987 | 9.00E-03 | | | | | |
| YP_006987 | 3.00E-39 | | | | | |
| YP_006987 | 1.00E-64 | | | | | |
| YP_006987 | 1.00E-138 | | | | | |
| YP_006987 | 3.00E-49 | | | | | |
| YP_006987 | 2.00E-108 | | | | | |

| | | | | | | |
|------------|-----------|-----|-----|--|----------------|----------|
| | | | | | PF01844.20 HNH | |
| YP_006987 | 2.00E-79 | | | | | 8.70E-07 |
| YP_006987 | 2.00E-42 | | | | | |
| | | | | | PF00004.26 AAA | |
| YP_006987 | 0.00E+00 | | | | | 3.10E-13 |
| YP_006987 | 6.00E-27 | | | | | |
| YP_006987 | 6.00E-44 | | | | | |
| YP_006987 | 1.00E-23 | | | | | |
| YP_006987 | 3.00E-49 | | Yes | | | |
| YP_006987 | 6.00E-119 | | | | | |
| AKJ74681.1 | 6.00E-14 | Yes | | | | |
| AKJ74681.1 | 2.00E-20 | Yes | | | | |
| YP_006987 | 6.00E-180 | | | | | |
| YP_006987 | 1.00E-15 | | | | | |
| YP_006987 | 6.00E-09 | | | | | |
| YP_006987 | 1.00E-03 | | | | | |
| YP_006987 | 6.00E-96 | | | | | |
| YP_006987 | 3.00E-18 | | | | | |

| | | | | | | |
|-----------|-----------|-----|-----|--|---|----------------|
| YP_006987 | 3.00E-21 | | | | | |
| YP_006987 | 5.00E-07 | | | | | |
| | | | | | | |
| YP_006987 | 5.00E-122 | | | | PF06693.8 DUF1190 | 2.90E-36 |
| YP_006987 | 3.00E-98 | Yes | Yes | | PF13385.3 Laminin_G_3 | 1.50E-12 |
| YP_006987 | 1.00E-80 | Yes | Yes | | | |
| | | | | | PF13415.3 Kelch_3, PF13964.3 Kelch_6 | |
| KOO35119 | 6.00E-13 | | | | | 1.50E-5, 3.70E |
| | | | | | PF13385.3 Laminin_G_3 | |
| | | Yes | | | | 6.80E-14 |
| | | | | | PF01344.22 Kelch_1 | |
| | | Yes | | | | 5.20E-06 |
| YP_006987 | 2.00E-18 | Yes | | | | |

| | | | | | | |
|-----------|-----------|--|--|--|--|------------------|
| | | | | | PF01344.22 Kelch_1, PF13964.3 Kelch_6 | |
| | | | | | | 1.20E-7, 1.40E-7 |
| YP_006987 | 2.00E-88 | | | | | |
| YP_006987 | 6.00E-56 | | | | | |
| YP_006987 | 1.00E-38 | | | | | |
| YP_006987 | 1.00E-83 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 8.00E-56 | | | | | |
| YP_006987 | 5.00E-100 | | | | | |
| YP_006987 | 3.00E-102 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-60 | | | | | |
| WP_04649 | 5.00E-09 | | | | | |
| KTD71834. | 9.00E-11 | | | | | |
| YP_007877 | 9.00E-06 | | | | | |
| YP_006987 | 8.00E-51 | | | | | |
| YP_006987 | 2.00E-52 | | | | | |
| | | | | | | |
| YP_006987 | 4.00E-48 | | | | | |
| YP_006987 | 2.00E-15 | | | | | |
| YP_006987 | 8.00E-37 | | | | | |
| YP_006987 | 2.00E-14 | | | | | |
| YP_006987 | 4.00E-39 | | | | | |

| | | | | | | |
|-----------|----------|--|-----|--|----------------------|----------|
| YP_006987 | 2.00E-60 | | | | | |
| YP_006987 | 2.00E-29 | | | | | |
| | | | | | | |
| | | | | | PF01145.22 Band_7 | |
| WP_01326 | 1.00E-83 | | Yes | | | 1.00E-27 |
| YP_006987 | 1.00E-29 | | | | | |
| YP_006987 | 8.00E-03 | | | | | |
| | | | | | | |
| | | | | | | |
| YP_006987 | 1.00E-18 | | | | | |
| YP_006987 | 7.00E-23 | | | | | |
| YP_006987 | 3.00E-41 | | | | | |
| YP_006987 | 1.00E-96 | | | | | |
| YP_006987 | 1.00E-60 | | | | | |
| | | | | | | |
| YP_006987 | 7.00E-16 | | | | | |
| YP_006987 | 5.00E-88 | | | | | |
| YP_006987 | 5.00E-58 | | | | | |
| YP_006987 | 8.00E-46 | | | | | |
| YP_006987 | 0.00E+00 | | | | PF06067.8 DUF932 | 5.10E-37 |
| YP_006987 | 3.00E-63 | | | | | |
| YP_006987 | 2.00E-28 | | | | | |
| YP_006987 | 1.00E-64 | | | | | |

| HHpred | E-value | Interproscan (Protein family, Domains and repeats) | No. of Transmembrane domains (TMHMM) |
|--------|---------|--|--------------------------------------|
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | -- |
| | | | 1 |
| | | | -- |
| | | | -- |
| | | | -- |

| | | | |
|---|----------|---|---|
| | | | - |
| | | | 2 |
| | | | |
| PH stomatin; archaea, trimer, coiled- coil, flotillin, SPFH, membrane fusion, trafficking, transmembrane, membrane protein; 3.20A {Pyrococcus horikoshii} | 4.70E-28 | Stomatin family (IPR001972), Band 7 domain (IPR001107) | 1 |
| | | | - |
| | | | - |
| | | | 1 |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | Protein of unknown function DUF932 (IPR026325) | - |
| | | | - |
| | | | - |
| | | | - |

| | | | |
|--|--|---|---|
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | - | - |
| | | | - |
| | | - | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | 2 |
| | | | - |
| | | | - |
| | | | - |
| | | | - |

| | | | |
|---|----------|--|---|
| Modification methylase TAQI; DNA, DNA methyltransferase, target base partner, 5-methylpyr 2(1H)-ONE, base flipping; HET: 5PY 6MA NEA; 1.61A {Thermus aquaticus} | 0.31 | DNA N-6-adenine-methyltransferase (IPR008593), | - |
| Nicotinate (nicotinamide) nucleotide adenyltran; NAD, nucleotidyltransferase, pyridine nucleotide biosynthesis transferase; HET: NXX; 1.70A {Bacillus anthracis} | 6.00E-29 | Cytidyltransferase-like domain (IPR004821), Rossmann-like alpha/beta/alpha sandwich fold (IPR014729) | - |
| | | | - |
| | | | - |
| | | | - |
| Bifunctional RELA/SPOT; HD domain, alpha beta 2-layer sandwich, helix bundle, mangan PPG2':3'P, (P)PPGPP, PPGPP; HET: GDP GPX; 2.10A {Streptococcus dysgalactiae subsp} | 1.60E-51 | HD domain (IPR006674) | - |
| | | | 2 |
| | | | - |
| | | | - |

| | | | |
|---|----------|--|---|
| | | | - |
| | | | - |
| RNA ligase, T4 RNA ligase 1; nucleotidyl transferase, ATP-binding; HET: APC; 2.21A {Bacteriophage T4} | 1.10E-83 | RNA ligase T4 Rnl1, N-terminal (IPR019039) | - |
| | | | - |
| | | | - |
| | | | - |
| PNKP1; RNA repair, kinase, phosphatase, methyltransferase, ligase, binding; 3.30A {Capnocytophaga gingivalis} | 2.30E-35 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), HAD-like domain (IPR023214) | - |
| | | | - |
| | | | 2 |
| | | | - |
| | | | - |
| | | | 2 |
| | | | - |
| | | | - |
| | | | - |
| | | | - |

| | | | |
|--|-----------------|--|----------|
| <p>Serine/threonine protein phosphatase; bacteriophage lambda, Ser/Thr protein phosphatase, ppase, manganese, sulfate, viral protein; 2.15A {Enterobacteria phage lambda}</p> | <p>1.40E-32</p> | <p>Metallo-dependent phosphatase-like (IPR029052) Calcineurin-like phosphoesterase domain, apaH type (IPR004843)</p> | <p>—</p> |
| | | | <p>—</p> |
| | | | <p>—</p> |
| <p>Thermostable DNA ligase; protein-nucleotide complex, cell cycle, cell division, DNA damage, DNA, recombination, DNA repair, DNA replication; HET: AMP; 1.8A {Pyrococcus furiosus}</p> | <p>4.70E-78</p> | <p>DNA ligase, ATP-dependent, central (IPR012310), Nucleic acid-binding, OB-fold (IPR012340)</p> | <p>—</p> |
| | | | <p>—</p> |
| <p>Phosphohydrolase; glycerophosphodiesterase, metallohydrolase, phosphatase, metal ION; 1.90A {Enterobacter aerogenes}</p> | <p>6.90E-24</p> | <p>Metallo-dependent phosphatase-like (IPR029052) Calcineurin-like phosphoesterase domain, apaH type (IPR004843)</p> | <p>—</p> |
| | | | <p>—</p> |

| | | | |
|---|----------|--|---|
| Putative ATP-dependent CLP protease proteolytic S; mitochondrial CLPP, CLP/HSP 100, ATP-dependent protease, HYD; HET: FME; 2.10A {Homo sapiens} | 7.00E-42 | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| Deoxycytidylate deaminase; DCMP deaminase, cytidine deaminase, deoxycytidylate deaminas TIM5, hydrolase; HET: DCM DU; 2.60A {Cyanophage s-tim5} | 4.70E-36 | Deoxycytidylate deaminase-related (IPR015517), Deoxycytidylate deaminase (IPR016473), Cytidine deaminase-like (IPR016193), Cytidine and deoxycytidylate deaminases, zinc-binding (IPR002125) | — |
| | | | 1 |
| Major tail protein V; bacteriophage lambda, phage tail, GPV, IG-like domain, viral; NMR {Enterobacteria phage lambda} | 1.10E-19 | Invasin/intimin cell-adhesion fragments (IPR008964), Bacterial Ig-like, group 2 (IPR003343) | — |
| | | Rossmann-like alpha/beta/alpha sandwich fold (IPR014729), Cytidyltransferase-like domain (IPR004821), NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086) | — |
| | | | — |

| | | | |
|--|-----------|---|---|
| Nicotinamide-nucleotide adenylyltransferase; two individual domains, hydrolase; HET: AMP; 2.30A {Francisella tularensis} | 9.50E-54 | Nicotinate phosphoribosyltransferase family (IPR007229), Nicotinamide phosphoribosyl transferase (IPR016471), Quinolinate phosphoribosyl transferase, C-terminal (IPR002638), | — |
| | | | 2 |
| | | | — |
| | | — | — |
| | | | — |
| Nicotinamide phosphoribosyltransferase; transferase-transferase inhibitor complex; HET: 20P; 1.50A {Homo sapiens} | 9.00E-113 | Sirtuin family (IPR003000), DHS-like NAD/FAD-binding domain (IPR029035), Sirtuin family, catalytic core domain (IPR026590), Sirtuin family (IPR003000), Sirtuin family, catalytic core small domain (IPR026591) Sirtuin family, catalytic core small domain (IPR026591) | — |
| | | NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086) | — |
| | | | 1 |
| Silent information regulator 2; protein-ligand complex, gene regulation; HET: APR; 1.47A {Archaeoglobus fulgidus} | 1.30E-62 | PIN domain-like (IPR029060), PIN domain (IPR002716), P-loop containing nucleoside triphosphate hydrolase (IPR027417), PhoH-like protein (IPR003714) | — |
| | | | — |
| | | | — |
| | | | 2 |
| | | | 1 |
| | | | — |

| | | | |
|---|-----------|--|--|
| | | | |
| CMP/hydroxymethyl CMP hydrolase; CMP N-glycosidase; HET: C5P; 1.55A {Streptomyces rimofaciens} | 4.00E-18 | | |
| Groes protein; chaperone; HET: ADP; 2.81A {Escherichia coli} | 1.50E-38 | GroES chaperonin family (IPR020818), GroES- like (IPR011032), | |
| Tyrosyl-tRNA synthetase; complex with L-tyrosine, rossmann fold, ligase; HET: BIF TYR; 2.65A {Escherichia coli} | 2.00E-101 | Aminoacyl-tRNA synthetase, class Ic (IPR002305) Tyrosine-tRNA ligase (IPR002307), Tyrosine- tRNA ligase, bacterial-type (IPR024088), Tyrosine-tRNA ligase, bacterial-type, type 1 (IPR024107), Rossmann-like alpha/beta/alpha sandwich fold (IPR014729), RNA-binding S4 domain (IPR002942) | |
| | | | |
| | | | |
| DCMP deaminase, deoxycytidylate deaminase; hydrolase; HET: DDN; 2.20A {Enterobacteria phage T4} | 8.20E-27 | | |
| | | | |
| | | | |
| | | | |
| DTMP kinase, thymidylate kinase; nucleotide biosynthesis, ATP- binding, nucleotide- binding, poxvirus, transferase; HET: TYD POP; 2.4A {Vaccinia virus copenhagen} | 9.60E-19 | P-loop containing nucleoside triphosphate hydrolase (IPR027417) | |

| | | | |
|---|----------|--|---|
| THG1-like uncharacterized protein; polymerase PALM-like catalytic domain, transferase, GTP and binding; HET: ATP; 2.36A {Bacillus thuringiensis} | 1.30E-83 | tRNAHis guanylyltransferase Thg1 (IPR007537) | — |
| | | | — |
| | | Protein of unknown function DUF4326 (IPR025475) | — |
| | | | — |
| | | | — |
| Protein (N-4 cytosine-specific methyltransferase PVU II); type II DNA- (cytosine N4) methyltransferase, amino methylation, selenomethionine; HET: SAH; 2.80A {Proteus vulgaris} | 1.40E-45 | Restriction/modification DNA-methylase (IPR001091), S-adenosyl-L-methionine-dependent methyltransferase (IPR029063), DNA methylase N-4/N-6 (IPR002941) | — |
| | | | — |
| | | Nucleotidyltransferase, predicted (IPR018775) | — |
| | | | — |
| | | | — |
| | | | — |

| | | | |
|--|----------|--|---|
| Acyl carrier protein; structural genomics, riken structural genomics/proteomic s in RSGI, NPPSFA; 1.50A {Thermus thermophilus} | 1.20E-15 | Acyl carrier protein (ACP) (IPR003231), Acyl carrier protein-like (IPR009081) | — |
| | | | 1 |
| | | | 1 |
| | | | — |
| | | | — |
| | | | — |
| | | Ferritin-like superfamily (IPR009078) | — |
| | | | — |
| | | | — |
| Thymidine kinase; transferase, type II, transferase; HET: TTP; 1.83A {Homo sapiens} | 2.40E-38 | | — |
| | | | 1 |
| | | | 1 |
| | | | 2 |
| | | | — |
| | | | — |
| Naegleria gruberi RNA ligase; RNA repair, adenylyltransferase; HET: AMP; 1.69A {Naegleria gruberi} | 7.00E-68 | RNA ligase, DRB0094 (IPR012646), RNA ligase domain, REL/Rln2 (IPR021122), | — |

| | | | |
|--|------------------|---|---|
| | | | — |
| RO sixty-related protein, RSR; alpha helical repeats, VON willebrand factor A domain, beta- RNA binding protein; 1.89A {Deinococcus radiodurans} | 5.80E-35 | Domain of unknown function DUF2828 (IPR024553), Domain of unknown function DUF2828 (IPR024553), von Willebrand factor, type A (IPR002035) | — |
| | | | 1 |
| | | | — |
| | | | — |
| Oxygen-regulated invasion protein ORGB, endolysin; type III secretion system, protein transport; 2.00A {Salmonella typhimurium}, P60_TTH, cell WALL-binding endopeptidase-related protein; hydrolase; HET: NAG NDG; 1.75A {Thermus thermophilus} | 3.8E-30, 3.6e-09 | LysM domain (IPR018392), Lysozyme domain (IPR023347) | 1 |
| | | Ribosomal protein S30Ae/sigma 54 modulation protein (IPR003489), | — |
| | | | — |
| | | | — |

| | | | |
|---|----------|--|---|
| TRNA CCA-adding enzyme; tRNA nucleotidyltransferase, translation, transferase; HET: ATP; 3.00A {Geobacillus stearothermophilus} | 7.60E-70 | Poly A polymerase, head domain (IPR002646), tRNA nucleotidyltransferase/poly(A) polymerase, RNA and SrmB- binding domain (IPR032828) | _ |
| NDX1; nudix protein, diadenosine polyphosphate, AP6A, thermus THER HB8, hydrolase, riken structural genomics/proteomics initia RSGI; 1.70A {Thermus thermophilus} | 5.70E-25 | NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086), NUDIX hydrolase (IPR020476) | _ |
| Glutaredoxin 3; GSH, oxidoreductase; HET: CSU GSH; 1.58A {Alkaliphilus oremlandii} | 3.20E-21 | Glutaredoxin (IPR002109), Thioredoxin-like fold (IPR012336) | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| Glutamyl-tRNA(Gln) amidotransferase subunit E; ligase, ligase/RNA complex; 3.15A {Methanothermobacter thermautotrophicus} | 2.60E-39 | Macro domain (IPR002589) | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |

| | | | |
|--|----------|--|---|
| | | P-loop containing nucleoside triphosphate hydrolase (IPR027417) | — |
| Conserved hypothetical protein protein BT1257; structural genomics, PSI, PROT structure initiative; HET: MSE; 1.25A {Bacteroides thetaiotaomicron} | 1.50E-40 | Tail sheath protein (IPR007067) | — |
| | | | — |
| | | | — |
| | | | — |
| Sheath; pyocin, bacteriocin, sheath, structural protein; 3.50A {Pseudomonas aeruginosa} | 1.10E-53 | Restriction endonuclease, FokI, C-terminal/endonuclease I, core (IPR011578), TnsA endonuclease, N-terminal (IPR014833) | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593) | — |
| Transposon TN7 transposition protein TNSA; protein-protein complex, mixed alpha-beta, DNA binding prote; 1.85A {Escherichia coli} | 6.10E-26 | Putative metallopeptidase domain (IPR025154), Putative metallopeptidase domain (IPR025154), VWA-like domain (IPR018698), von Willebrand factor, type A (IPR002035) | 1 |

| | | | |
|--|----------|--|--|
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| Microneme protein 2; A/I domain, cell adhesion, hydrolase; 2.05A {Toxoplasma gondii} | 2.60E-10 | Thymidylate synthase (IPR000398), Thymidylate synthase/dCMP hydroxymethylase domain (IPR023451) | |
| | | | |
| | | Domain of unknown function DUF4376 (IPR025484) | |
| | | Parallel beta-helix repeat (IPR006626) | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| ORF135, CTP pyrophosphohydrolase; NMR {Escherichia coli} | 6.90E-23 | NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086) | |
| Tail connector protein GP15; bacteriophage T4, phage tail terminator protein, viral; 2.70A {Enterobacteria phage T4} | 3.20E-71 | Myoviridae tail sheath stabiliser (IPR031997) | |
| | | | |

| | | | |
|---|-----------|---|---|
| CLPA protein; AAA+, N-terminal domain, CLPS, crystal, binding mechanism, hydrolase; HET: ADP; 2.25A {Escherichia coli} SCOP | 8.00E-101 | ClpA/B family (IPR001270), Clp, N-terminal (IPR004176), P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593), Clp ATPase, C-terminal (IPR019489) | — |
| | | | — |
| | | | — |
| Tail lysozyme; GP25-like fold, initiation of sheath polymerization, baseplate component, T4 GP18, T4 GP53, T4 GP6, hydrolase; 2.47A {Enterobacteria phage T4} | 1.50E-31 | GpW/Gp25/anti-adaptor protein IraD (IPR007048) | — |
| Lysozyme; direct methods, lanthidine binding sites, hydrolase; 1.04A {Enterobacteria phage P22} | 1.80E-41 | Glycoside hydrolase, family 24 (IPR002196), T4-type lysozyme (IPR001165), Lysozyme-like domain (IPR023346), Lysozyme domain (IPR023347) | — |
| beta-barrel, OB-fold, beta-helix, type VI secretion system C spike, secreted outside of the cell, toxin; HET: TAM; 3.32A {Pseudomonas aeruginosa} | 1.70E-36 | Glycoside hydrolase, family 24 (IPR002196), Gp5 N-terminal (IPR006531), Lysozyme-like domain (IPR023346), Lysozyme domain (IPR023347) | — |
| | | | — |
| Tail protein X, GPX; LYSM, phage tail, viral protein; NMR {Enterobacteria phage P2} | 0.019 | Baseplate wedge protein gp53, bacteriophage T4 (IPR022607) | — |

| | | | |
|---|-----------|--|---|
| | | | - |
| | | | - |
| Exonuclease, putative; adenosine triphosphate, bacterial proteins, DNA breaks, DOUB stranded, DNA repair, DNA repair enzymes; HET: ADP; 2.61A {Thermotoga maritima} | 9.70E-41 | Metallo-dependent phosphatase-like (IPR029052), Calcineurin-like phosphoesterase domain, IpxH type (IPR024654) | - |
| DNA double-strand break repair RAD50 ATPase; DNA repair, ABC transporter ATPase domain-like; HET: DNA ADP; 2.70A {Methanocaldococcus jannaschii} | 3.40E-35 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| Portal protein GP20; viral protein; 3.63A {Enterobacteria phage T4} | 6.00E-129 | Structural protein of head Gp20 (IPR010823) | - |
| | | | - |
| | | | - |
| | | Peptidase U9, T4 prohead protease (IPR005082) | - |
| | | | - |

| | | | |
|--|-----------|---|---|
| Head vertex protein GP24; bacteriophage T4, capsid protein, bacteriophage, virus, HK97, MAD, viral protein; 2.90A {Enterobacteria phage T4} | 8.00E-108 | Capsid protein, T4-like bacteriophage (IPR010762) | - |
| | | | - |
| Structure-specific endonuclease subunit SLX1; DNA repair, GIY-YIG, homologous recombination, HYD; 1.78A {Candida glabrata} | 3.30E-05 | Bacteriophage T5, Orf172 DNA-binding (IPR018306) | - |
| | | | - |
| | | | - |
| | | | - |
| DNA polymerase, GP43; difluorotoluene nucleoside; HET: DNA DOC DGT; 1.73A {Enterobacteria phage RB69} | 4.00E-130 | DNA-directed DNA polymerase, family B (IPR006172), DNA-directed DNA polymerase, family B, multifunctional domain (IPR006134), DNA polymerase, palm domain (IPR023211) | - |
| | | | - |
| | | | - |
| Hypothetical protein AQ_1665; structural genomics, protein structure initiative midwest center for structural genomics, PSI, MCSG, unknown; 2.40A {Aquifex aeolicus} | 1.40E-26 | Metallo-dependent phosphatase-like (IPR029052), Calcineurin-like phosphoesterase domain, apaH type (IPR004843) | - |

| | | | |
|---|----------|--|---|
| | | Putative regulatory protein, FmdB, Zinc ribbon domain (IPR013429) | — |
| Groes protein; chaperone; HET: ADP; 2.81A {Escherichia coli} | 1.50E-41 | GroES chaperonin family (IPR020818), GroES-like (IPR011032) | — |
| | | | — |
| | | | — |
| | | | — |
| Ribonuclease H, RNase H; BPT4 RNase H, 5'-3' exonuclease, hydrolase, endonuclease; 1.50A {Enterobacteria phage T4} | 1.40E-57 | PIN domain-like (IPR029060), 5'-3' exonuclease, alpha-helical arch, N-terminal (IPR020046) | — |
| | | | — |
| | | | — |
| Terminase, DNA packaging protein GP17; large terminase, alternative initiation, ATP-binding, DNA-binding, hydrolase, nuclease; HET: DNA; 2.80A {Bacteriophage T4} | 2.60E-50 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), Terminase, large subunit (IPR004921) | — |
| | | | — |
| | | Bacteriophage T4, Gp32, single-stranded DNA-binding (IPR012339), Nucleic acid-binding, OB-fold (IPR012340) | — |
| | | DNA recombination and repair protein RecA (IPR013765), P-loop containing nucleoside triphosphate hydrolase (IPR027417), DNA recombination and repair protein RecA, monomer-monomer interface (IPR020587) | — |

| | | | |
|---|----------|--|---|
| | | | — |
| DNA polymerase III epsilon subunit; DNA polymerase proofreading domain, transferase; HET: DNA U5P; 1.60A {Escherichia coli} | 1.60E-30 | Putative quorum-sensing-regulated virulence factor (IPR024530), Ribonuclease H-like domain (IPR012337), Exonuclease, RNase T/DNA polymerase III (IPR013520) | — |
| DAR protein, ATP-dependent DNA helicase UVSW; ATP-dependant helicase, T4-bacteriophage, recombination, hydrolase; 2.70A {Enterobacteria phage T4} | 8.30E-61 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), Helicase superfamily 1/2, ATP-binding domain (IPR014001), Helicase/UvrB, N-terminal (IPR006935), Helicase, C-terminal (IPR001650) | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | S-adenosyl-L-methionine-dependent methyltransferase (IPR029063) | — |
| | | | 1 |
| | | | — |
| | | | — |
| | | | — |
| Replicative DNA helicase; RECA-type helicase, ATP binding, D binding, replication; HET: ADP; 3.30A {Aquifex aeolicus} | 8.80E-58 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), P-loop containing nucleoside triphosphate hydrolase (IPR027417) | — |
| | | | — |

| | | | |
|--|-----------|--|---|
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| Exodeoxyribonuclease 8; exonuclease, recombination, hydrolase; 2.80A {Escherichia coli} | 2.50E-17 | Restriction endonuclease type II-like (IPR011335) | |
| | | | |
| | | | |
| Ribonucleoside-diphosphate reductase 1 subunit alpha; oxidoreductase, DNA replication, allosteric enzyme, nucleotide-binding; HET: NIY; 2.10A {Escherichia coli} | 1.00E-187 | ATP-cone domain (IPR005144), Ribonucleotide reductase large subunit, C-terminal (IPR000788), Ribonucleotide reductase, class I, alpha subunit (IPR013346), Ribonucleotide reductase R1 subunit, N-terminal (IPR008926), Ribonucleotide reductase large subunit, N-terminal (IPR013509) | |
| | | | |
| Ribonucleotide reductase R2; radical protein, DI iron, oxidoreductase; 1.42A {Escherichia coli} | 3.90E-89 | Ribonucleotide reductase small subunit (IPR000358), Ferritin-like superfamily (IPR009078) Ribonucleotide reductase-related (IPR012348) | |
| | | | 1 |
| | | | |
| | | | |

| | | | |
|--|----------|---|---|
| Putative NTP pyrophosphohydrolase; structural genomics, joint center for structural genomics, J protein structure initiative; 1.78A {Exiguobacterium sibiricum 255-15} | 1.30E-42 | Phosphoribosyl-ATP pyrophosphohydrolase-like (IPR021130), NTP pyrophosphohydrolase-like domain (IPR023292), | — |
| | | | 2 |
| | | | 1 |
| | | | 2 |
| Dihydrofolate reductase; DHFR, NADP, oxidoreductase; 2.00A {Geobacillus stearothermophilus} | 2.70E-39 | Dihydrofolate reductase (IPR012259), Dihydrofolate reductase-like domain (IPR024072) Dihydrofolate reductase domain (IPR001796) | — |
| Ribonuclease HI, RNase HI; hydrolase, endoribonuclease; 2.00A {Shewanella oneidensis} | 6.20E-36 | Ribonuclease H-like domain (IPR012337) Ribonuclease H domain (IPR002156) | — |
| ATP-dependent DNA helicase DDA; RECA-like domain, SH3 domain, PIN-tower interface, coupling hydrolysis to DNA unwinding, ssDNA; 3.30A {Enterobacteria phage T4} | 1.30E-45 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), UvrD-like helicase C-terminal domain | — |
| | | | — |
| | | | — |

| | | | |
|--|-----------|--|---|
| Protein (translation initiation factor IF3); gene regulation; NMR {Escherichia coli} | 3.70E-30 | Translation initiation factor 3, N-terminal (IPR019814), Translation initiation factor 3, C-terminal (IPR019815) | - |
| ATP-dependent CLP protease adaptor protein CLPS; adaptor, protein-peptide complex, peptide binding protein; 1.15A {Caulobacter vibrioides} | 1.60E-31 | Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like (IPR014719) Adaptor protein ClpS, core (IPR003769) | - |
| Uncharacterized protein; chicago center for functional annotation, structural genomic biology, midwest center for structural genomics, MCSG; HET: MSE; 1.73A {Yersinia pestis} | 3.50E-28 | KTSC domain (IPR025309) | - |
| | | | - |
| | | | - |
| | | | 1 |
| Topoisomerase IV subunit B, DNA topoisomerase 4 S chimera; DNA unwinding, supercoiling, isomerase-DNA complex; HET: DNA; 3.70A {Streptococcus pneumoniae} | 1.00E-154 | | - |

| | | | |
|--|----------|---|---|
| Putative acetylornithine deacetylase; ATP-dependent amine/thiol ligase family, ATP-dependent amine ligase, enzyme-carrier protein complex; HET: ADP GLU; 1.80A {Sulfolobus tokodaii} | 1.20E-06 | Protein of unknown function DUF4343 (IPR025643) | — |
| | | | — |
| CLPA protein; AAA+, N-terminal domain, CLPS, crystal, binding mechanism, hydrolase; HET: ADP; 2.25A {Escherichia coli} | 9.00E-22 | | — |
| | | | — |
| | | | — |
| 5'(3')-deoxyribonucleotidase, cytosolic type; protein conformation, sequence homology, HA hydrolase, dephosphorylation; 1.08A {Homo sapiens} | 1.50E-20 | HAD-like domain (IPR023214), 5'(3')-deoxyribonucleotidase (IPR010708) | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |

| | | | |
|--|----------|--|---|
| Putative acetylornithine deacetylase; ATP-dependent amine/thiol ligase family, ATP-dependent amine ligase, enzyme-carrier protein complex; HET: ADP GLU; 1.80A {Sulfolobus tokodaii} | 2.30E-13 | Protein of unknown function DUF4343 (IPR02 | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| Hypothetical protein TA0108; structural genomics, Conserved hypothetical protein protein, PSI, PR structure initiative; HET: SO4; 1.95A {Thermoplasma acidophilum} | 2.00E-44 | Peptidyl-tRNA hydrolase II domain (IPR023476), Peptidyl-tRNA hydrolase, PTH2 (IPR002833) | _ |
| | | | 1 |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |

| | | | |
|---|----------|---|---|
| Modification methylase HHA1; base flipping, restriction system, transferase-DNA complex; HET: 5CM 2PR SAH EPE CIT; 1.7A {Haemophilus haemolyticus} | 1.30E-64 | S-adenosyl-L-methionine-dependent methyltransferase (IPR029063), C-5 cytosine methyltransferase (IPR001525) | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | _ |
| | | | 2 |
| | | | _ |
| | | | _ |
| | | | _ |
| | | Heat shock protein DnaJ, cysteine-rich domain (IPR001305) | _ |

| | | | |
|---|----------|---|---|
| HNH homing endonuclease; HNH catalytic motif, helix-turn-helix DNA binding domain, PR complex, DNA binding protein-DNA complex; 2.92A {Bacillus phage SPO1} | 5.90E-20 | HNH nuclease (IPR003615), Uncharacterised protein family YabK (IPR020115) | - |
| | | | 1 |
| | | | - |
| | | | 2 |
| | | | 2 |
| | | Acyl-CoA N-acyltransferase (IPR016181) | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | 1 |
| | | | 1 |
| | | | - |

| | | | |
|---|----------|--|---|
| | | | - |
| | | S-adenosyl-L-methionine-dependent methyltransferase (IPR029063) | - |
| | | | - |
| | | | - |
| | | | 1 |
| | | | 1 |
| | | | - |
| | | | 3 |
| | | | 4 |
| | | | - |
| | | | 1 |
| | | | - |
| | | | 2 |
| | | | - |
| | | | - |
| | | | - |
| BLDD, putative DNA-binding protein; the DNA-binding domain of BLDD; 1.81A {Streptomyces coelicolor} | 3.90E-18 | Lambda repressor-like, DNA-binding domain (IPR010982), Cro/C1-type helix-turn-helix domain (IPR001387) | - |
| | | | - |

| | | | |
|--|----------|---|---|
| Sigma-70, RNA polymerase sigma factor RPOD; switch region, squaramide, transcription-inhibitor complex; HET: 4C6; 3.57A {Escherichia coli} | 2.30E-48 | RNA polymerase sigma factor, region 2 (IPR013325), RNA polymerase sigma-70 like domain (IPR014284), RNA polymerase sigma-70 region 2 (IPR007627), RNA polymerase sigma factor, region 3/4 (IPR013324) | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| Endonuclease V; 1.45A {Enterobacteria phage T4} | 1.80E-72 | T4 endonuclease V (IPR024796) | - |
| | | | - |
| | | | - |
| | | | 2 |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |

| | | | |
|---|----------|---|---|
| HNH endonuclease; structural genomics, PSI-biology, protein structure initiati northeast structural genomics consortium (NESG); 2.60A {Geobacter metallireducens} | 3.80E-14 | HNH endonuclease (IPR002711), HNH nuclease (IPR003615) | - |
| | | | 3 |
| 26S protease regulatory subunit 8 homolog; hydrolase, AAA-ATPase, ATP- analog, classification; 7.70A {Saccharomyces cerevisiae} | 7.30E-28 | P-loop containing nucleoside triphosphate hydrolase (IPR027417), P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593), ATPase, AAA-type, core (IPR003959) | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | - |
| | | | 3 |
| | | | 2 |
| | | | 1 |
| | | | - |
| | | | 3 |

| | | | |
|--|----------|--|---|
| | | | 3 |
| | | | 3 |
| | | - | 1 |
| - | | Biofilm formation YgiB (IPR009576) | 1 |
| - | | Concanavalin A-like lectin/glucanase domain (IPR013320) | - |
| | | | - |
| Kelch-like protein 3; signaling protein-transferase complex, KLHL3, ubiquitin, ADA protein, protein-binding, kelch repeat; HET: 12P; 1.56A {Homo sapiens} | 1.20E-43 | Kelch-type beta propeller (IPR015915) | - |
| SAP-like pentraxin; physiological doubly-stacked heptamer, pentraxin fold, cyclic heptamer, invertebrate lectin, sugar binding protein; 2.30A {Limulus polyphemus} | 8.30E-07 | Concanavalin A-like lectin/glucanase domain (IPR013320) | - |
| Kelch-like ECH-associated protein 1; beta-propeller, kelch repeat motif, protein binding; HET: MSE; 1.35A {Homo sapiens} | 1.20E-40 | Kelch-type beta propeller (IPR015915), Kelch repeat type 1 (IPR006652) | - |
| | | | - |

| | | | |
|--|----------|--|---|
| Kelch-like ECH-associated protein 1; beta-propeller, kelch repeat motif, protein binding; HET: MSE; 1.35A {Homo sapiens} | 3.20E-40 | Kelch-type beta propeller (IPR015915), Kelch repeat type 1 (IPR006652) | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | — |
| | | | 1 |
| | | | — |
| | | | — |
| | | | — |

