

Click on any column header to sort the table by that header.
Click on any query_id number to view the query fasta sequence

| query_species | query_id | norm_lpi | query_description | bestmatch_id |
|------------------------------|--|----------|---|---------------------------------|
| Pseudomonas_fluorescens_Pf-5 | gi 70728378 ref YP_258127.1 | 0.507 | hypothetical protein | gi 223935564 ref ZP_03627480.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70728379 ref YP_258128.1 | 0.508 | acid phosphatase, putative | gi 88809729 ref ZP_01125236.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70728434 ref YP_258183.1 | 0.507 | hypothetical protein | gi 94971174 ref YP_593222.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70728595 ref YP_258344.1 | 0.463 | glycosyl hydrolase family protein | gi 219848302 ref YP_002462735.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70728939 ref YP_262179.1 | 0.463 | O antigen biosynthesis abequosyltransferase | gi 149200119 ref ZP_01877143.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70728941 ref YP_262555.1 | 0.508 | hypothetical protein | gi 196255486 ref ZP_03154024.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729409 ref YP_259147.1 | 0.432 | glycosyl transferase, group 2 family protein | gi 192812792 ref ZP_03041459.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729410 ref YP_259148.1 | 0.433 | SanC, putative | gi 7407127 gb AAF61921.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729497 ref YP_259235.1 | 0.417 | acetyltransferase, putative | gi 169628675 ref YP_001702324.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729501 ref YP_259239.1 | 0.001 | pentapeptide repeat- containing protein | gi 167043641 gb ABZ08334.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729509 ref YP_259247.1 | 0.432 | fumarate hydratase | gi 94986425 ref YP_605789.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729548 ref YP_259286.1 | 0.432 | hypothetical protein | gi 118445222 ref YP_891192.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729550 ref YP_259288.1 | 0.432 | hypothetical protein | gi 218848150 ref YP_002454739.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729602 ref YP_259341.1 | 0.432 | oxidoreductase, FAD-binding, putative | gi 75758450 ref ZP_00738572.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729790 ref YP_259529.1 | 0.432 | hypothetical protein | gi 146299898 ref YP_001194489.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729792 ref YP_259531.1 | 0.433 | tautomerase, putative | gi 29833710 ref NP_828344.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70729869 ref YP_259608.1 | 0.463 | heat shock protein HtpX | gi 46446535 ref YP_007900.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730137 ref YP_259876.1 | 0.463 | hypothetical protein | gi 149196640 ref ZP_01873694.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730175 ref YP_259914.1 | 0.432 | hypothetical protein | gi 168699894 ref ZP_02732171.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730224 ref YP_259963.1 | 0.432 | ThiJ/PfpI family protein | gi 75760741 ref ZP_00740763.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730237 ref YP_259976.1 | 0.001 | hypothetical protein | gi 220064490 gb EED42599.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730332 ref YP_260071.1 | 0.432 | type I restriction- modification system, M | gi 182626301 ref ZP_02954057.1 |

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| Pseudomonas_fluorescens_Pf-5 | gi 70730383 ref YP_260124.1 | 0.001 | enoyl-CoA hydratase | gi 11498293 ref NP_069519.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730696 ref YP_260437.1 | 0.432 | hypothetical protein | gi 29348163 ref NP_811666.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730823 ref YP_260564.1 | 0.417 | hypothetical protein | gi 54024341 ref YP_118583.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70730990 ref YP_260731.1 | 0.432 | hypothetical protein | gi 168705140 ref ZP_02737417.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731105 ref YP_260846.1 | 0.001 | prophage LambdaSo, tail assembly protein I | gi 46402106 ref YP_006600.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731107 ref YP_260848.1 | 0.001 | phage protein | gi 209552444 ref YP_002284359.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731134 ref YP_260875.1 | 0.001 | phage D3 protein | gi 9635667 ref NP_061575.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731147 ref YP_260888.1 | 0.001 | hypothetical protein | gi 56692938 ref YP_164283.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731387 ref YP_261128.1 | 0.507 | DNA-binding protein | gi 94971537 ref YP_593585.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731402 ref YP_261143.1 | 0.432 | AraC family transcriptional regulator | gi 87307459 ref ZP_01089603.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731576 ref YP_261317.1 | 0.508 | RuIA protein, putative | gi 87303597 ref ZP_01086376.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731993 ref YP_261735.1 | 0.432 | oxidoreductase, zinc-binding | gi 192807879 ref ZP_03036556.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70731995 ref YP_261737.1 | 0.001 | coenzyme F420-reducing hydrogenase, beta | gi 15678369 ref NP_275484.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732339 ref YP_262095.1 | 0.432 | acetyltransferase | gi 56965079 ref YP_176811.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732495 ref YP_262258.1 | 0.432 | 5prime-nucleotidase | gi 4586218 emb CAB40970.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732512 ref YP_262275.1 | 0.432 | hypothetical protein | gi 89097766 ref ZP_01170654.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732775 ref YP_262538.1 | 0.432 | ethanolamine utilization protein EutH | gi 224477848 ref YP_002635454.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732776 ref YP_262539.1 | 0.463 | reactivating factor for ethanolamine ammonia | gi 51893200 ref YP_075891.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732849 ref YP_262616.1 | 0.508 | hypothetical protein | gi 196258280 ref ZP_03156815.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70732850 ref YP_262617.1 | 0.507 | hypothetical protein | gi 163813639 ref ZP_02205137.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733042 ref YP_262815.1 | 0.463 | hypothetical protein | gi 45656771 ref YP_000857.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733106 ref YP_262879.1 | 0.433 | hypothetical protein | gi 197783205 ref YP_002205975.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733767 ref YP_257407.1 | 0.433 | pyoverdine synthetase | gi 197757764 ref YP_002181032.1 |

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| Pseudomonas_fluorescens_Pf-5 | gi 70733768 ref YP_257408.1 | 0.433 | fatty acid desaturase family proteiin | gi 197757765 ref YP_002181033.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733773 ref YP_257413.1 | 0.463 | hypothetical protein | gi 183219544 ref YP_001837540.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733822 ref YP_257462.1 | 0.508 | TPR domain-containing protein | gi 172035397 ref YP_001801898.1 |
| Pseudomonas_fluorescens_Pf-5 | gi 70733889 ref YP_257529.1 | 0.001 | chorismate mutase | gi 220065128 gb EED42958.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77456390 ref YP_345895.1 | 0.504 | adenylsulfate kinase | gi 88809888 ref ZP_01125394.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77456557 ref YP_346062.1 | 0.410 | hypothetical protein | gi 111223391 ref YP_714185.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77456736 ref YP_346241.1 | 0.460 | hypothetical protein | gi 159898209 ref YP_001544456.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77456931 ref YP_346436.1 | 0.412 | luciferase-like | gi 72162329 ref YP_289986.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457270 ref YP_346775.1 | 0.416 | amino acid permease-associated region | gi 29828162 ref NP_822796.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457365 ref YP_346870.1 | 0.002 | hypothetical protein | gi 126010857 ref YP_001039825.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457366 ref YP_346871.1 | 0.002 | Phage baseplate assembly protein V | gi 167832354 ref YP_001686745.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457367 ref YP_346872.1 | 0.002 | hypothetical protein | gi 167832355 ref YP_001686746.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457368 ref YP_346873.1 | 0.002 | baseplate J-like protein | gi 167832356 ref YP_001686747.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457372 ref YP_346877.1 | 0.002 | Phage tail sheath protein FI-like | gi 167832365 ref YP_001686756.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457373 ref YP_346878.1 | 0.002 | hypothetical protein | gi 167832366 ref YP_001686757.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457374 ref YP_346879.1 | 0.002 | hypothetical protein | gi 167832367 ref YP_001686758.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457376 ref YP_346881.1 | 0.002 | hypothetical protein | gi 167832369 ref YP_001686760.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457377 ref YP_346882.1 | 0.002 | Phage tail X | gi 126010875 ref YP_001039844.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457378 ref YP_346883.1 | 0.002 | Phage protein D-like | gi 167832370 ref YP_001686761.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457741 ref YP_347246.1 | 0.504 | DegT/DnrJ/EryC1/StrS aminotransferase | gi 81298867 ref YP_399075.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77457977 ref YP_347482.1 | 0.429 | hypothetical protein | gi 23100817 ref NP_694284.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458068 ref YP_347573.1 | 0.416 | Terpene synthase, metal-binding | gi 34098708 sp Q9F1V8.1 YGLK_STRC |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458097 ref YP_347602.1 | 0.429 | hypothetical protein | gi 116624557 ref YP_826713.1 |

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| Pseudomonas_fluorescens_Pf0_1 | gi 77458168 ref YP_347673.1 | 0.000 | hypothetical protein | gi 91773700 ref YP_566392.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458268 ref YP_347773.1 | 0.429 | hypothetical protein | gi 157692529 ref YP_001486991.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458310 ref YP_347815.1 | 0.573 | FAD dependent oxidoreductase | gi 158335020 ref YP_001516192.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458318 ref YP_347823.1 | 0.429 | hypothetical protein | gi 88804440 ref ZP_01119960.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458400 ref YP_347905.1 | 0.504 | ferredoxin | gi 94970138 ref YP_592186.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458401 ref YP_347906.1 | 0.504 | hypothetical protein | gi 163813394 ref ZP_02204952.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458402 ref YP_347907.1 | 0.504 | hypothetical protein | gi 163813393 ref ZP_02204951.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458465 ref YP_347970.1 | 0.002 | hypothetical protein | gi 32394546 gb AAM93971.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458476 ref YP_347981.1 | 0.504 | two component LuxR family transcriptional | gi 94969472 ref YP_591520.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458479 ref YP_347984.1 | 0.075 | zinc-containing alcohol dehydrogenase | gi 223517410 gb EEF25260.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458568 ref YP_348073.1 | 0.429 | oxidoreductase, molybdopterin binding | gi 192809857 ref ZP_03038531.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458570 ref YP_348075.1 | 0.460 | amino acid permease-associated region | gi 17229011 ref NP_485559.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458583 ref YP_348088.1 | 0.460 | Na ⁺ /malate symporter | gi 34763814 ref ZP_00144725.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458653 ref YP_348159.1 | 0.428 | hypothetical protein | gi 78189920 ref YP_380258.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458664 ref YP_348170.1 | 0.504 | hypothetical protein | gi 223940019 ref ZP_03631884.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458678 ref YP_348184.1 | 0.460 | transcriptional regulator | gi 37521395 ref NP_924772.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458686 ref YP_348192.1 | 0.504 | Alpha/beta hydrolase fold | gi 94970129 ref YP_592177.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458851 ref YP_348357.1 | 0.020 | hypothetical protein | gi 156304179 ref XP_001617504.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458940 ref YP_348446.1 | 0.075 | hypothetical protein | gi 223524366 gb EEF27466.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458978 ref YP_348484.1 | 0.075 | Short-chain dehydrogenase/reductase SDR | gi 223523704 gb EEF27152.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458985 ref YP_348491.1 | 0.416 | AraC family transcriptional regulator | gi 197776016 ref YP_002198897.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77458992 ref YP_348498.1 | 0.429 | NADP oxidoreductase, coenzyme F420-dependent | gi 86143485 ref ZP_01061870.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459043 ref YP_348549.1 | 0.429 | glycosyl transferase WecB/TagA/CpsF | gi 212693048 ref ZP_03301176.1 |

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| Pseudomonas_fluorescens_Pf0_1 | gi 77459088 ref YP_348594.1 | 0.428 | esterase/lipase /thioesterase | gi 94971985 ref YP_594025.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459272 ref YP_348779.1 | 0.429 | hypothetical protein | gi 189459512 ref ZP_03008297.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459283 ref YP_348790.1 | 0.002 | transcription regulator | gi 220065503 gb EED43193.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459284 ref YP_348791.1 | 0.002 | plasmid stabilization system protein | gi 220065504 gb EED43194.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459354 ref YP_348861.1 | 0.002 | hypothetical protein | gi 220064970 gb EED42862.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459356 ref YP_348863.1 | 0.504 | anti-sigma-factor antagonist (STAS) | gi 94969442 ref YP_591490.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459587 ref YP_349094.1 | 0.429 | GCN5-related N-acetyltransferase | gi 89096757 ref ZP_01169649.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459683 ref YP_349190.1 | 0.416 | tyrosinase | gi 146446762 gb ABQ41256.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459692 ref YP_349199.1 | 0.075 | Short-chain dehydrogenase/reductase SDR | gi 223514354 gb EEF24407.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459729 ref YP_349236.1 | 0.020 | peptidylprolyl isomerase, FKBP-type | gi 156346349 ref XP_001621515.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459841 ref YP_349348.1 | 0.002 | hypothetical protein | gi 220062562 gb EED41646.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459850 ref YP_349357.1 | 0.410 | hypothetical protein | gi 5669597 gb AAD46393.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459859 ref YP_349366.1 | 0.429 | major facilitator transporter | gi 75764489 ref ZP_00743972.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77459986 ref YP_349493.1 | 0.504 | metallothionein, putative | gi 209525334 ref ZP_03273875.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460012 ref YP_349519.1 | 0.075 | hypothetical protein | gi 223519650 gb EEF25931.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460027 ref YP_349534.1 | 0.429 | hypothetical protein | gi 218128925 ref ZP_03457729.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460131 ref YP_349638.1 | 0.460 | LysR family transcriptional regulator | gi 37522120 ref NP_925497.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460264 ref YP_349771.1 | 0.429 | glycosyl transferase family protein | gi 15895615 ref NP_348964.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460267 ref YP_349774.1 | 0.429 | DegT/DnrJ/EryC1/StrS aminotransferase | gi 149276433 ref ZP_01882577.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460283 ref YP_349790.1 | 0.429 | DegT/DnrJ/EryC1/StrS aminotransferase | gi 116625988 ref YP_828144.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460284 ref YP_349791.1 | 0.429 | GCN5-related N-acetyltransferase | gi 116625987 ref YP_828143.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460285 ref YP_349792.1 | 0.429 | hypothetical protein | gi 116625986 ref YP_828142.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460286 ref YP_349793.1 | 0.429 | ABC transporter-like | gi 116625985 ref YP_828141.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460288 ref YP_349795.1 | 0.429 | glycosyl transferase | gi 116625984 ref YP_828140.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77460290 ref YP_349797.1 | 0.429 | glycosyltransferase-like protein | gi 116625982 ref YP_828138.1 |

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| Pseudomonas_fluorescens_Pf0_1 | gi 77460984 ref YP_350491.1 | 0.075 | hypothetical protein | gi 223514139 gb EEF24359.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461121 ref YP_350628.1 | 0.460 | hypothetical protein | gi 62464776 ref YP_220397.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461151 ref YP_350658.1 | 0.429 | hypothetical protein | gi 121535484 ref ZP_01667293.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461152 ref YP_350659.1 | 0.429 | hypothetical protein | gi 83589330 ref YP_429339.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461263 ref YP_350770.1 | 0.428 | isochorismatase hydrolase | gi 87308408 ref ZP_01090549.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461373 ref YP_350880.1 | 0.412 | histidine triad (HIT) protein | gi 72162310 ref YP_289967.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461415 ref YP_350922.1 | 0.002 | hypothetical protein | gi 41057293 ref NP_958191.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461507 ref YP_351014.1 | 0.113 | hypothetical protein | gi 74207933 dbj BAE29091.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461732 ref YP_351239.1 | 0.460 | methyltransferase | gi 124024633 ref YP_001018940.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461733 ref YP_351240.1 | 0.460 | hypothetical protein | gi 124024632 ref YP_001018939.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461734 ref YP_351241.1 | 0.460 | glutamine amidotransferase class-I | gi 124024631 ref YP_001018938.1 |
| Pseudomonas_fluorescens_Pf0_1 | gi 77461735 ref YP_351242.1 | 0.460 | nucleotidyl transferase | gi 124024630 ref YP_001018937.1 |
| Pseudomonas_putida_F1 | gi 148546151 ref YP_001266253.1 | 0.446 | hypothetical protein | gi 225516616 ref ZP_03763585.1 |
| Pseudomonas_putida_F1 | gi 148546152 ref YP_001266254.1 | 0.415 | glyoxalase/bleomycin resistance | gi 149279805 ref ZP_01885932.1 |
| Pseudomonas_putida_F1 | gi 148546159 ref YP_001266261.1 | 0.416 | rubredoxin-type Fe(Cys) ₄ protein | gi 9845225 gb AAG00801.1 |
| Pseudomonas_putida_F1 | gi 148546598 ref YP_001266700.1 | 0.415 | cupin 2 domain-containing protein | gi 87306927 ref ZP_01089073.1 |
| Pseudomonas_putida_F1 | gi 148546724 ref YP_001266826.1 | 0.416 | FkbM family methyltransferase | gi 187932909 ref YP_001886521.1 |
| Pseudomonas_putida_F1 | gi 148546725 ref YP_001266827.1 | 0.415 | NAD-dependent epimerase/dehydratase | gi 193213102 ref YP_001999055.1 |
| Pseudomonas_putida_F1 | gi 148547079 ref YP_001267181.1 | 0.103 | LysR family transcriptional regulator | gi 223517669 gb EEF25329.1 |
| Pseudomonas_putida_F1 | gi 148547117 ref YP_001267219.1 | 0.103 | hypothetical protein | gi 223501853 gb EEF22545.1 |
| Pseudomonas_putida_F1 | gi 148547207 ref YP_001267309.1 | 0.446 | DSBA oxidoreductase | gi 75812802 ref YP_320419.1 |
| Pseudomonas_putida_F1 | gi 148547362 ref YP_001267464.1 | 0.416 | acylamide amidohydrolase | gi 31339994 sp Q9RQ17.1 AMIE_BACS |
| Pseudomonas_putida_F1 | gi 148547667 ref YP_001267769.1 | 0.489 | hypothetical protein | gi 67922784 ref ZP_00516284.1 |
| Pseudomonas_putida_F1 | gi 148548089 ref YP_001268191.1 | 0.402 | glyoxalase/bleomycin resistance | gi 927237 gb AAB07755.1 |

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| Pseudomonas_putida_F1 | gi 148548283 ref YP_001268385.1 | 0.103 | hydroxymethylglutaryl-CoA reductase, | gi 223517785 gb EEF25361.1 |
| Pseudomonas_putida_F1 | gi 148548601 ref YP_001268703.1 | 0.001 | hypothetical protein | gi 209552483 ref YP_002284398.1 |
| Pseudomonas_putida_F1 | gi 148548604 ref YP_001268706.1 | 0.001 | hypothetical protein | gi 209552480 ref YP_002284395.1 |
| Pseudomonas_putida_F1 | gi 148548629 ref YP_001268731.1 | 0.001 | hypothetical protein | gi 56692932 ref YP_164269.1 |
| Pseudomonas_putida_F1 | gi 148549297 ref YP_001269399.1 | 0.446 | hypothetical protein | gi 37521837 ref NP_925214.1 |
| Pseudomonas_putida_F1 | gi 148549307 ref YP_001269409.1 | 0.001 | hypothetical protein | gi 209552440 ref YP_002284355.1 |
| Pseudomonas_putida_F1 | gi 148549308 ref YP_001269410.1 | 0.001 | hypothetical protein | gi 9635614 ref NP_061518.1 |
| Pseudomonas_putida_F1 | gi 148549328 ref YP_001269430.1 | 0.001 | hypothetical protein | gi 9635673 ref NP_061583.1 |
| Pseudomonas_putida_F1 | gi 148549823 ref YP_001269925.1 | 0.597 | hypothetical protein | gi 162454431 ref YP_001616798.1 |
| Pseudomonas_putida_F1 | gi 148550216 ref YP_001270318.1 | 0.001 | thymidylate synthase-like protein | gi 45686030 ref YP_003793.1 |
| Pseudomonas_putida_F1 | gi 148550235 ref YP_001270337.1 | 0.489 | hypothetical protein | gi 172034841 ref YP_001798618.1 |
| Pseudomonas_putida_F1 | gi 148550237 ref YP_001270339.1 | 0.402 | hypothetical protein | gi 58003974 gb AAW62375.1 |
| Pseudomonas_putida_F1 | gi 148550482 ref YP_001270584.1 | 0.010 | dihydrodipicolinate synthetase | gi 39968277 ref XP_365529.1 |
| Pseudomonas_putida_GB_1 | gi 167031214 ref YP_001666445.1 | 0.001 | hypothetical protein | gi 220065870 gb EED43435.1 |
| Pseudomonas_putida_GB_1 | gi 167031544 ref YP_001666775.1 | 0.492 | DNA mismatch endonuclease Vsr | gi 94968157 ref YP_590205.1 |
| Pseudomonas_putida_GB_1 | gi 167031698 ref YP_001666929.1 | 0.492 | phage transcriptional regulator, AlpA | gi 88809196 ref ZP_01124705.1 |
| Pseudomonas_putida_GB_1 | gi 167032382 ref YP_001667613.1 | 0.418 | hemolytic protein HlpA-like protein | gi 160881620 ref YP_001560588.1 |
| Pseudomonas_putida_GB_1 | gi 167032384 ref YP_001667615.1 | 0.418 | glycosyl transferase group 1 | gi 160881621 ref YP_001560589.1 |
| Pseudomonas_putida_GB_1 | gi 167032397 ref YP_001667628.1 | 0.449 | glycosyl transferase group 1 | gi 172056841 ref YP_001813301.1 |
| Pseudomonas_putida_GB_1 | gi 167032628 ref YP_001667859.1 | 0.418 | radical SAM domain-containing protein | gi 125625197 ref YP_001033680.1 |
| Pseudomonas_putida_GB_1 | gi 167032743 ref YP_001667974.1 | 0.002 | hypothetical protein | gi 9635584 ref NP_061567.1 |
| Pseudomonas_putida_GB_1 | gi 167032750 ref YP_001667981.1 | 0.002 | hypothetical protein | gi 56692925 ref YP_164325.1 |
| Pseudomonas_putida_GB_1 | gi 167032751 ref YP_001667982.1 | 0.002 | glycoside hydrolase family protein | gi 56692926 ref YP_164326.1 |
| Pseudomonas_putida_GB_1 | gi 167032753 ref YP_001667984.1 | 0.002 | terminase small subunit | gi 30387380 ref NP_848209.1 |
| Pseudomonas_putida_GB_1 | gi 167032754 ref YP_001667985.1 | 0.002 | putative phage terminase, large subunit | gi 89152423 ref YP_512256.1 |

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| Pseudomonas_putida_GB_1 | gi 167032756 ref YP_001667987.1 | 0.002 | putative tail protein | gi 89152428 ref YP_512261.1 |
| Pseudomonas_putida_GB_1 | gi 167032759 ref YP_001667990.1 | 0.002 | hypothetical protein | gi 89152431 ref YP_512264.1 |
| Pseudomonas_putida_GB_1 | gi 167032760 ref YP_001667991.1 | 0.002 | hypothetical protein | gi 89152432 ref YP_512265.1 |
| Pseudomonas_putida_GB_1 | gi 167032764 ref YP_001667995.1 | 0.002 | hypothetical protein | gi 89152437 ref YP_512270.1 |
| Pseudomonas_putida_GB_1 | gi 167032765 ref YP_001667996.1 | 0.002 | hypothetical protein | gi 30387393 ref NP_848222.1 |
| Pseudomonas_putida_GB_1 | gi 167033031 ref YP_001668262.1 | 0.080 | cyclase family protein | gi 223515261 gb EEF24643.1 |
| Pseudomonas_putida_GB_1 | gi 167033224 ref YP_001668455.1 | 0.120 | cytochrome c class I | gi 82408001 pdb 2B4Z A |
| Pseudomonas_putida_GB_1 | gi 167033413 ref YP_001668644.1 | 0.080 | hypothetical protein | gi 223509238 gb EEF23365.1 |
| Pseudomonas_putida_GB_1 | gi 167033967 ref YP_001669198.1 | 0.080 | LysR family transcriptional regulator | gi 223503533 gb EEF22697.1 |
| Pseudomonas_putida_GB_1 | gi 167033988 ref YP_001669219.1 | 0.001 | response regulator receiver protein | gi 220065877 gb EED43440.1 |
| Pseudomonas_putida_GB_1 | gi 167034045 ref YP_001669276.1 | 0.403 | AraC family transcriptional regulator | gi 31794261 ref NP_856754.1 |
| Pseudomonas_putida_GB_1 | gi 167034172 ref YP_001669403.1 | 0.403 | ABC transporter related | gi 225020900 ref ZP_03710092.1 |
| Pseudomonas_putida_GB_1 | gi 167034253 ref YP_001669484.1 | 0.080 | phosphonate ABC transporter, ATPase subunit | gi 223513991 gb EEF24325.1 |
| Pseudomonas_putida_GB_1 | gi 167034288 ref YP_001669519.1 | 0.418 | hypothetical protein | gi 126645387 ref ZP_01717931.1 |
| Pseudomonas_putida_GB_1 | gi 167034384 ref YP_001669615.1 | 0.002 | lysozyme | gi 209552446 ref YP_002284361.1 |
| Pseudomonas_putida_GB_1 | gi 167034451 ref YP_001669682.1 | 0.002 | ERF family protein | gi 9635643 ref NP_061548.1 |
| Pseudomonas_putida_GB_1 | gi 167034452 ref YP_001669683.1 | 0.002 | exonuclease, phage-type | gi 9635642 ref NP_061547.1 |
| Pseudomonas_putida_GB_1 | gi 167034803 ref YP_001670034.1 | 0.418 | ABC transporter related | gi 86141425 ref ZP_01059971.1 |
| Pseudomonas_putida_GB_1 | gi 167035155 ref YP_001670386.1 | 0.403 | hypothetical protein | gi 154507564 ref ZP_02043206.1 |
| Pseudomonas_putida_GB_1 | gi 167035159 ref YP_001670390.1 | 0.418 | hypothetical protein | gi 189347733 ref YP_001944262.1 |
| Pseudomonas_putida_GB_1 | gi 167035755 ref YP_001670986.1 | 0.449 | hypothetical protein | gi 91200749 emb CAJ73801.1 |
| Pseudomonas_putida_GB_1 | gi 167035790 ref YP_001671021.1 | 0.418 | hypothetical protein | gi 47565553 ref ZP_00236594.1 |
| Pseudomonas_putida_GB_1 | gi 167036405 ref YP_001671636.1 | 0.403 | hypothetical protein | gi 108803996 ref YP_643933.1 |
| Pseudomonas_putida_KT2440 | gi 26987376 ref NP_742801.1 | 0.490 | hypothetical protein | gi 196246298 ref ZP_03145018.1 |
| Pseudomonas_putida_KT2440 | gi 26987463 ref NP_742888.1 | 0.417 | hypothetical protein | gi 167769567 ref ZP_02441620.1 |

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| Pseudomonas_putida_KT2440 | gi 26987467 ref NP_742892.1 | 0.000 | phosphatidylserine synthase, putative | gi 91772800 ref YP_565492.1 |
| Pseudomonas_putida_KT2440 | gi 26988280 ref NP_743705.1 | 0.002 | hypothetical protein | gi 33323569 gb AAQ07539.1 AF50340 |
| Pseudomonas_putida_KT2440 | gi 26988294 ref NP_743719.1 | 0.002 | phage terminase, small subunit, putative | gi 9635587 ref NP_061497.1 |
| Pseudomonas_putida_KT2440 | gi 26988314 ref NP_743739.1 | 0.447 | hypothetical protein | gi 183220609 ref YP_001838605.1 |
| Pseudomonas_putida_KT2440 | gi 26988522 ref NP_743947.1 | 0.490 | aldolase/synthase, putative | gi 209527034 ref ZP_03275550.1 |
| Pseudomonas_putida_KT2440 | gi 26988674 ref NP_744099.1 | 0.417 | hypothetical protein | gi 83591114 ref YP_431123.1 |
| Pseudomonas_putida_KT2440 | gi 26988681 ref NP_744106.1 | 0.408 | hypothetical protein | gi 29828325 ref NP_822959.1 |
| Pseudomonas_putida_KT2440 | gi 26988682 ref NP_744107.1 | 0.408 | cytochrome P450 family protein | gi 134099170 ref YP_001104831.1 |
| Pseudomonas_putida_KT2440 | gi 26988990 ref NP_744415.1 | 0.002 | DNA-directed RNA polymerase, bacteriophage and | gi 194100470 ref YP_002003315.1 |
| Pseudomonas_putida_KT2440 | gi 26988992 ref NP_744417.1 | 0.002 | phage endodeoxyribonuclease I | gi 9634009 ref NP_052083.1 |
| Pseudomonas_putida_KT2440 | gi 26988994 ref NP_744419.1 | 0.002 | DNA primase/helicase | gi 83308132 emb CAJ29365.1 |
| Pseudomonas_putida_KT2440 | gi 26988997 ref NP_744422.1 | 0.002 | DNA polymerase | gi 68299732 ref YP_249581.1 |
| Pseudomonas_putida_KT2440 | gi 26989746 ref NP_745171.1 | 0.002 | hypothetical protein | gi 17313260 ref NP_490640.1 |
| Pseudomonas_putida_KT2440 | gi 26989831 ref NP_745256.1 | 0.130 | hypothetical protein | gi 37700485 gb AAR00252.1 |
| Pseudomonas_putida_KT2440 | gi 26989834 ref NP_745259.1 | 0.001 | ISPpu13, transposase Orf3 | gi 220065770 gb EED43368.1 |
| Pseudomonas_putida_KT2440 | gi 26990480 ref NP_745905.1 | 0.001 | sarcosine oxidase, putative | gi 220065806 gb EED43392.1 |
| Pseudomonas_putida_KT2440 | gi 26990481 ref NP_745906.1 | 0.447 | rarD protein | gi 159898185 ref YP_001544432.1 |
| Pseudomonas_putida_KT2440 | gi 26990486 ref NP_745911.1 | 0.490 | oxygen-independent coproporphyrinogen III | gi 86608370 ref YP_477132.1 |
| Pseudomonas_putida_KT2440 | gi 26990491 ref NP_745916.1 | 0.416 | aminotransferase | gi 87306715 ref ZP_01088862.1 |
| Pseudomonas_putida_KT2440 | gi 26990493 ref NP_745918.1 | 0.447 | non-ribosomal peptide synthetase, putative | gi 75911029 ref YP_325325.1 |
| Pseudomonas_putida_KT2440 | gi 26990559 ref NP_745984.1 | 0.002 | endolysin | gi 9635623 ref NP_061527.1 |
| Pseudomonas_putida_KT2440 | gi 26990582 ref NP_746007.1 | 0.002 | hypothetical protein | gi 17975167 ref NP_536362.1 |
| Pseudomonas_putida_KT2440 | gi 26990584 ref NP_746009.1 | 0.002 | HK97 family phage portal protein | gi 17975165 ref NP_536360.1 |
| Pseudomonas_putida_KT2440 | gi 26990600 ref NP_746025.1 | 0.002 | regulatory protein Cro, putative | gi 9635583 ref NP_061566.1 |
| Pseudomonas_putida_KT2440 | gi 26990911 ref NP_746336.1 | 0.447 | non-ribosomal siderophore peptide synthetase | gi 186686725 ref YP_001869919.1 |

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|---------------------------|--|-------|---|----------------------------------|
| Pseudomonas_putida_KT2440 | gi 26991134 ref NP_746559.1 | 0.490 | hypothetical protein | gi 88712338 ref ZP_01106425.1 |
| Pseudomonas_putida_W619 | gi 170719867 ref YP_001747555.1 | 0.492 | hypothetical protein | gi 113478055 ref YP_724116.1 |
| Pseudomonas_putida_W619 | gi 170719869 ref YP_001747557.1 | 0.449 | DNA mismatch endonuclease Vsr | gi 225079463 ref YP_002673228.1 |
| Pseudomonas_putida_W619 | gi 170719983 ref YP_001747671.1 | 0.403 | chitin-binding domain-containing protein | gi 111219625 ref YP_710419.1 |
| Pseudomonas_putida_W619 | gi 170720048 ref YP_001747736.1 | 0.001 | GtrA family protein | gi 9910695 sp Q9T1D7.1 GTRA_BPSF |
| Pseudomonas_putida_W619 | gi 170720049 ref YP_001747737.1 | 0.001 | ribonuclease III | gi 9635491 ref NP_059582.1 |
| Pseudomonas_putida_W619 | gi 170720445 ref YP_001748133.1 | 0.401 | molybdopterin oxidoreductase | gi 169629524 ref YP_001703173.1 |
| Pseudomonas_putida_W619 | gi 170720508 ref YP_001748196.1 | 0.002 | hypothetical protein | gi 148912822 ref YP_001293401.1 |
| Pseudomonas_putida_W619 | gi 170720544 ref YP_001748232.1 | 0.401 | hypothetical protein | gi 111026145 ref YP_708428.1 |
| Pseudomonas_putida_W619 | gi 170720573 ref YP_001748261.1 | 0.419 | ABC transporter related | gi 45250001 gb AAS55714.1 |
| Pseudomonas_putida_W619 | gi 170720879 ref YP_001748567.1 | 0.001 | hypothetical protein | gi 220063005 gb EED41874.1 |
| Pseudomonas_putida_W619 | gi 170720882 ref YP_001748570.1 | 0.001 | LysR family transcriptional regulator | gi 220063849 gb EED42255.1 |
| Pseudomonas_putida_W619 | gi 170720883 ref YP_001748571.1 | 0.401 | major facilitator transporter | gi 41350172 gb AAS00434.1 |
| Pseudomonas_putida_W619 | gi 170720884 ref YP_001748572.1 | 0.419 | alpha/beta hydrolase fold | gi 89893616 ref YP_517103.1 |
| Pseudomonas_putida_W619 | gi 170721010 ref YP_001748698.1 | 0.419 | putative esterase | gi 75759843 ref ZP_00739918.1 |
| Pseudomonas_putida_W619 | gi 170721185 ref YP_001748873.1 | 0.449 | putative esterase/lipase | gi 186682680 ref YP_001865876.1 |
| Pseudomonas_putida_W619 | gi 170721187 ref YP_001748875.1 | 0.449 | esterase/lipase-like protein | gi 159896864 ref YP_001543111.1 |
| Pseudomonas_putida_W619 | gi 170721199 ref YP_001748887.1 | 0.403 | alpha/beta hydrolase fold | gi 197783422 ref YP_002206190.1 |
| Pseudomonas_putida_W619 | gi 170721215 ref YP_001748903.1 | 0.401 | aldo/keto reductase | gi 152964936 ref YP_001360720.1 |
| Pseudomonas_putida_W619 | gi 170721242 ref YP_001748930.1 | 0.419 | hypothetical protein | gi 42779910 ref NP_977157.1 |
| Pseudomonas_putida_W619 | gi 170721460 ref YP_001749148.1 | 0.403 | adenine-specific DNA methylase containing a | gi 108804625 ref YP_644562.1 |
| Pseudomonas_putida_W619 | gi 170721461 ref YP_001749149.1 | 0.403 | AAA ATPase | gi 108804624 ref YP_644561.1 |
| Pseudomonas_putida_W619 | gi 170721523 ref YP_001749211.1 | 0.419 | diguanylate cyclase/phosphodiesterase | gi 65319824 ref ZP_00392783.1 |
| Pseudomonas_putida_W619 | gi 170721656 ref YP_001749344.1 | 0.048 | ribonuclease T2 | gi 223547939 gb EEF49431.1 |

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| Pseudomonas_putida_W619 | gi 170721795 ref YP_001749483.1 | 0.001 | hypothetical protein | gi 220065601 gb EED43259.1 |
| Pseudomonas_putida_W619 | gi 170721858 ref YP_001749546.1 | 0.401 | Acyl-CoA synthetase (AMP-forming)/AMP-acid | gi 86279135 gb ABC88668.1 |
| Pseudomonas_putida_W619 | gi 170722075 ref YP_001749763.1 | 0.418 | sulfatase | gi 60682678 ref YP_212822.1 |
| Pseudomonas_putida_W619 | gi 170722160 ref YP_001749848.1 | 0.492 | hypothetical protein | gi 196257446 ref ZP_03155982.1 |
| Pseudomonas_putida_W619 | gi 170722188 ref YP_001749876.1 | 0.418 | hypothetical protein | gi 189346575 ref YP_001943104.1 |
| Pseudomonas_putida_W619 | gi 170722286 ref YP_001749974.1 | 0.401 | major facilitator transporter | gi 220910997 ref YP_002486306.1 |
| Pseudomonas_putida_W619 | gi 170722402 ref YP_001750090.1 | 0.492 | diguanylate cyclase with GAF sensor | gi 220905724 ref YP_002481035.1 |
| Pseudomonas_putida_W619 | gi 170722487 ref YP_001750175.1 | 0.134 | major facilitator transporter | gi 215498639 gb EEC08133.1 |
| Pseudomonas_putida_W619 | gi 170722515 ref YP_001750203.1 | 0.449 | short-chain dehydrogenase/reductase SDR | gi 225519544 ref ZP_03766468.1 |
| Pseudomonas_putida_W619 | gi 170722522 ref YP_001750210.1 | 0.419 | hypothetical protein | gi 154484130 ref ZP_02026578.1 |
| Pseudomonas_putida_W619 | gi 170722910 ref YP_001750598.1 | 0.403 | hypothetical protein | gi 86742612 ref YP_483012.1 |
| Pseudomonas_putida_W619 | gi 170722914 ref YP_001750602.1 | 0.419 | hypothetical protein | gi 188588864 ref YP_001920188.1 |
| Pseudomonas_putida_W619 | gi 170722915 ref YP_001750603.1 | 0.418 | phytanoyl-CoA dioxygenase | gi 149276450 ref ZP_01882594.1 |
| Pseudomonas_putida_W619 | gi 170723080 ref YP_001750768.1 | 0.002 | putative lipoprotein | gi 9635625 ref NP_061529.1 |
| Pseudomonas_putida_W619 | gi 170723081 ref YP_001750769.1 | 0.002 | hypothetical protein | gi 209552447 ref YP_002284362.1 |
| Pseudomonas_putida_W619 | gi 170723119 ref YP_001750807.1 | 0.002 | hypothetical protein | gi 148912815 ref YP_001293394.1 |
| Pseudomonas_putida_W619 | gi 170723127 ref YP_001750815.1 | 0.002 | carbon storage regulator, CsrA | gi 56692917 ref YP_164288.1 |
| Pseudomonas_putida_W619 | gi 170723130 ref YP_001750818.1 | 0.002 | hypothetical protein | gi 209552451 ref YP_002284366.1 |
| Pseudomonas_putida_W619 | gi 170723394 ref YP_001751082.1 | 0.403 | cold-shock DNA-binding domain-containing | gi 197769249 ref YP_002192259.1 |