**Supplementary Table S4.** Genes encoding protein relating to antibiotics production, plant growth promoting, enzyme production and bioremediation of *Streptomyces spinosus* SBTS01T

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  |  |  |
| **product** | **Span (nt)** | **Score** | **Percent similarity** | **Closest Match** |
| **Antibiotic production** |  |  |  |  |
| Isopenicillin N synthase family oxygenase | 304163-305188 | 1,827 | 99.7% | *Streptomyces* sp. jing01 |
| Isopenicillin N synthase family oxygenase | 39922-40221 | 535 | 99.0% | *Streptomyces* sp. jing01 |
| Isopenicillin N synthase family oxygenase | 40336-40884 | 946 | 99.4% | *Streptomyces* sp. jing01 |
| [Tetracenomycin](https://www.jbc.org/article/S0021-9258(20)73069-3/pdf)  family type II polyketide cyclase | 10733-11062 | 575 | 100.0% | *Streptomyces* sp. jing01 |
| [Tetracenomycin](https://www.jbc.org/article/S0021-9258(20)73069-3/pdf)  family type II polyketide cyclase | 233784-234113 | 569 | 100.0% | *Streptomyces* sp. jing01 |
| Enterotoxin | 52827-53948 | 1,673 | 87.3% | *Streptomyces longwoodensis* |
| **Drought tolerance** |  |  |  |  |
| Indole-3-glycerol phosphate synthase | 304526-305335 | 1,313 | 100.0% | *Streptomyces* sp. jing01 |
| L-ectoine synthase | 93957-94361 | 718 | 99.3% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Ectoine dioxygenase | 94368-95261 | 1,516 | 97.0% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Glycine betaine/  L-proline transporter *pro*P | 84958-86349 | 2,328 | 99.8% | *Streptomyces* sp. jing01 |
| Glycine betaine/  L-proline ABC transporter ATP-binding protein | 48790-49980 | 1,990 | 99.5% | *Streptomyces* sp. jing01 |
| Proline dehydrogenase | 234130-235056 | 1,549 | 99.4% | *Streptomyces* sp. jing01 |
| Sodium:solute symporter | 252230-253690 | 2,440 | 100.0% | *Streptomyces* sp. jing01 |
| Chloride channel protein | 53910-55706 | 2,406 | 81.3% | *Streptomyces* sp. P3 |
| Ionic transporter *y4h*A | 203388-204488 | 1,786 | 100.0% | *Streptomyces* sp. jing01 |
| Potassium channel family protein | 338642-339772 | 1,671 | 91.8% | *Streptomyces* sp. DSM 40868 |
| **Stress response** |  |  |  |  |
| Calcium homeostasis/redox stress adaptation protein | 54561-55136 | 980 | 100.0% | *Streptomyces* sp. jing01 |
| Asp23/Gls24 family envelope stress response protein | 55221-55691 | 771 | 100.0% | *Streptomyces* sp. jing01 |
| Chemical-damaging agent resistance protein C | 397654-398229 | 969 | 97.9% | *Streptomyces incarnatus* |
| Cold shock protein | 40990-41193 | 383 | 100.0% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Cold shock protein | 63769-63972 | 383 | 100.0% | *Streptomyces* sp. CB01373 |
| Cold shock protein | 86675-86878 | 385 | 98.5% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Cold shock protein | 239827-240030 | 380 | 100.0% | *Streptomyces* sp. Act143 |
| Cold shock protein | 268544-268747 | 381 | 100.0% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Cold shock protein | 380867-381070 | 380 | 100.0% | *Streptomyces* sp. Act143 |
| Putative heat shock protein | 155170-155595 | 706 | 97.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Heat shock protein | 221248-221712 | 753 | 97.4% | *Streptomyces* sp. NRRL B-3648 |
| Hsp70 family protein | 120078-121838 | 2,885 | 95.9% | *Streptomyces globosus* |
| HSP90 family protein | 163644-165482 | 3,138 | 99.8% | *Streptomyces* sp. jing01 |
| HSP90 family protein | 11297-114544 | 3,037 | 96.3% | *Streptomyces* sp. RLA2-12 |
| 10 kDa chaperonin | 221966-222274 | 507 | 100.0% | *Streptomyces luteoverticillatus* |
| 60 kDa chaperonin | 222393-224021 | 2,669 | 100.0% | *Streptomyces* sp. jing01 |
| Chaperone protein *Dna*J | 55120-56256 | 1,995 | 100.0% | *Streptomyces antibioticus* |
| Chaperone protein *Dna*K | 620121-622007 | 3,133 | 99.7% | *Streptomyces* sp. jing01 |
| Chaperone protein *Clp*B | 213655-216252 | 4,214 | 97.7% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Chaperone protein *Dna*J | 221718-222887 | 2,029 | 99.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Chaperone protein *Dna*K | 223580-225424 | 3,040 | 98.5% | *Streptomyces* sp. Z022 |
| 60 kDa chaperonin | 378945-380567 | 2,628 | 100.0% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Chaperone protein *Htp*G | 150011-151921 | 3,203 | 97.3% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Universal stress protein | 114454-114933 | 806 | 100.0% | *Streptomyces* sp. jing01 |
| Universal stress protein | 32371-33261 | 1,457 | 98.0% | *Streptomyces* sp. jing01 |
| Universal stress protein | 131930-132832 | 1,524 | 99.7% | *Streptomyces* sp. jing01 |
| Universal stress protein | 268421-269287 | 1,451 | 99.7% | *Streptomyces* sp. jing01 |
| Universal stress protein | 148647-149600 | 1,269 | 85.1% | *Streptomyces* sp. SID161 |
| Universal stress protein | 13103-13978 | 1,216 | 81.5% | *Streptomyces* sp. AS58 |
| Universal stress protein | 127292-128167 | 1,333 | 90.0% | *Streptomyces* sp. jing01 |
| Universal stress protein | 134686-135564 | 1,429 | 93.1% | *Streptomyces* sp. jing01 |
| Stress-inducible protein | 147716-148621 | 1,413 | 91.0% | *Streptomyces* sp. AS58 |
| Stress-inducible protein | 7727-8641 | 1,171 | 80.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Stress-inducible protein | 8668-9573 | 1,325 | 87.0% | *Streptomyces* sp. AS58 |
| Stress-inducible protein | 12325-12768 | 679 | 90.5% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| **Lipase** |  |  |  |  |
| Lipase | 53987-54796 | 1,309 | 93.7% | *Streptomyces* sp. NRRL B-3648 |
| Putative esterase/lipase | 400622-401353 | 1,210 | 96.7% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| **Protease** |  |  |  |  |
| Extracellular small neutral protease | 134407-135096 | 1,121 | 95.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| M6 family metalloprotease domain-containing protein | 121883-124240 | 4,210 | 99.9% | *Streptomyces* sp. jing01 |
| M48 family metalloprotease | 161778-163475 | 2,128 | 97.8% | *Streptomyces* sp. jing01 |
| M56 family metallopeptidase | 163512-164459 | 1,587 | 99.7% | *Streptomyces* sp. jing01 |
| |  |  | | --- | --- | | Neutral  metalloproteinase |  | | 79641-80723 | 1,831 | 96.9% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Zinc metalloprotease | 6449-7615 | 1,624 | 85.4% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Putative M48-family peptidase | 346425-347318 | 1,364 | 95.6% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Peptidase M48 domain-containing protein | 111947-114901 | 2,257 | 49.5% | *Streptomyces lydicus* |
| Peptidase M48 domain-containing protein | 18466-19548 | 1,782 | 96.7% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Peptidase S1 | 6423-7601 | 1,865 | 91.1% | *Streptomyces bungoensis* |
| Peptidase C56 PfpI | 62915-63481 | 928 | 95.7% | *Streptomyces* sp. 1-11 |
| Putative prolyl aminopeptidase | 236610-237911 | 2,211 | 96.3% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Protease HtpX homolog | 223072-223992 | 1,510 | 100.0% | *Streptomyces* sp. jing01 |
| Site-2 protease family protein | 56514-57815 | 2,230 | 99.5% | *Streptomyces* sp. jing01 |
| Site-2 protease family protein | 153096-153896 | 1,389 | 98.9% | *Streptomyces* sp. jing01 |
| MarP family serine protease | 244416-245600 | 1,960 | 100.0% | *Streptomyces* sp. jing01 |
| Insulinase family protein | 6304-7683 | 2,354 | 100.0% | *Streptomyces* sp. jing01 |
| Tricorn protease homolog | 59255-62524 | 5,459 | 96.3% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Hydrogenase maturation protease | 14079-14582 | 647 | 81.6% | *Streptomyces monashensis* |
| **Chitinase** |  |  |  |  |
| Chitinase | 71713-73521 | 3,157 | 99.5% | *Streptomyces* sp. jing01 |
| Chitinase | 100296-101339 | 1,823 | 99.4% | *Streptomyces* sp. jing01 |
| Chitinase | 207611-209329 | 2,957 | 100.0% | *Streptomyces* sp. jing01 |
| Chitinase | 339161-340984 | 3,271 | 99.8% | *Streptomyces* sp. jing01 |
| **Polysaccharide degradation** |  |  |  |  |
| Maltose alpha-D-glucosyltransferase | 304861-305262 | 695 | 99.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Alpha-amylase | 196608-197984 | 2,353 | 98.4% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Secreted cellulose binding protein | 99453-100541 | 1,895 | 95.9% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Glycoside hydrolase family 18 protein | 55721-56953 | 2,204 | 99.3% | *Streptomyces* sp. jing01 |
| Cellulose-binding protein | 39025-39702 | 1,129 | 91.1% | *Streptomyces* sp. FBKL.4005 |
| Polysaccharide deacetylase family protein | 57784-58467 | 1,174 | 100.0% | *Streptomyces* sp. jing01 |
| Glycohydrolase | 30743-31750 | 1,682 | 93.7% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| **Xylanase** |  |  |  |  |
| Endo-1,4-beta-xylanase | 58537-59232 | 1,259 | 100.0% | *Streptomyces* sp. jing01 |
| Beta-xylanase | 59546-60631 | 1,903 | 98.9% | *Streptomyces* sp. jing01 |
| Beta-xylanase | 731010-732449 | 2,413 | 94.4% | *Streptomyces longwoodensis* |
| **Phosphatase** |  |  |  |  |
| Putative alkaline phosphatase | 116972-118612 | 2,838 | 96.5% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Ppx/GppA family phosphatase | 291082-292089 | 1,724 | 100.0% | *Streptomyces* sp. jing01 |
| Histidine phosphatase family protein | 203657-204253 | 1,049 | 99.5% | *Streptomyces* sp. jing01 |
| Phosphatase | 249605-250402 | 1,376 | 99.6% | *Streptomyces* sp. jing01 |
| HAD family phosphatase | 1049-1906 | 1,458 | 100.0% | *Streptomyces* sp. jing01 |
| Phosphatase | 30862-31644 | 1,339 | 99.6% | *Streptomyces* sp. jing01 |
| Phosphatase | 395419-396021 | 987 | 93.4% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Exopolyphosphatase | 12170-13102 | 1,525 | 97.4% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Inorganic pyrophosphatase | 67420-67911 | 875 | 100.0% | *Streptomyces cyaneogriseus* |
| **Isomerase** |  |  |  |  |
| Sugar isomerase | 227819-228979 | 1,969 | 96.9% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Xylose isomerase | 157492-158658 | 2,024 | 99.7% | *Streptomyces* sp. jing01 |
| **Xenobiotic degradation** |  |  |  |  |
| Aldehyde dehydrogenase family protein | 45698-47218 | 2,608 | 99.6% | *Streptomyces* sp. jing01 |
| Alpha/beta hydrolase | 130174-131022 | 1,475 | 98.9% | *Streptomyces* sp. jing01 |
| Alpha/beta hydrolase | 99827-100744 | 1,499 | 91.5% | *Streptomyces corchorusii* |
| Alpha/beta hydrolase | 27849-28712 | 1,498 | 100.0% | *Streptomyces* sp. jing01 |
| Aspartyl beta-hydroxylase | 739734-740558 | 1,413 | 100.0% | *Streptomyces* sp. jing01 |
| 2-nitropropane dioxygenase | 123769-124800 | 1,214 | 70.8% | *Streptomyces cattleya* (strain ATCC 35852) |
| Haloacid dehalogenase type II | 26763-27488 | 1,236 | 100.0% | *Streptomyces* sp. jing01 |
| **Ion detoxification** |  |  |  |  |
| Selenium-binding protein | 47983-49413 | 2,580 | 98.7% | *Streptomyces* sp. jing01 |
| Selenium-binding protein | 47983-49413 | 2,580 | 98.7% | *Streptomyces* sp. jing01 |
| Alpha/beta fold hydrolase | 50584-51291 | 1,213 | 94.0% | *Streptomyces* sp. SID161 |
| Tellurium resistance protein | 31898-32473 | 956 | 98.4% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| *Ter*D family protein | 55249-55827 | 1,001 | 100.0% | *Streptomyces* sp. jing01 |
| **Arsenate reduction** |  |  |  |  |
| Mycoredoxin | 154584-154826 | 448 | 100.0% | *Streptomyces* sp. jing01 |
| **Antioxidant** |  |  |  |  |
| Glutathione peroxidase | 247153-247659 | 863 | 98.8% | *Streptomyces* sp. jing01 |
| Glutathione-independent formaldehyde dehydrogenase | 284419-285597 | 2,005 | 99.5% | *Streptomyces* sp. jing01 |
| Lactoylglutathione lyase | 60689-61135 | 740 | Ident.: 95.3% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Glutathione peroxidase | 247153-247659 | 855 | 98.2% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| **Others** |  |  |  |  |
| Squalene-hopene cyclase | 9402-11432 | 3,594 | 97.6% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Squalene-hopene cyclase | 9402-11432 | 3,594 | 97.6% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Gamma-glutamyl transferase | 279589-281409 | 3,137 | 97.0% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Gamma-glutamyltranspeptidase | 298790-300592 | 2,984 | 97.8% | *Streptomyces hygroscopicus* subsp*. jinggangensis* (strain 5008) |
| Luciferase-type oxidoreductase, BA3436 family | 60232-61284 | 1,742 | 95.1% | *Streptomyces* sp. Ag109\_O5-10 |