

SUPPLEMENTAL MATERIAL

Transcriptional studies on *Streptomyces clavuligerus oppA2*-deleted mutant: N-acetylglycyl-clavaminic acid is an extracellular intermediate of clavulanic acid biosynthesis (AEM01301-17)

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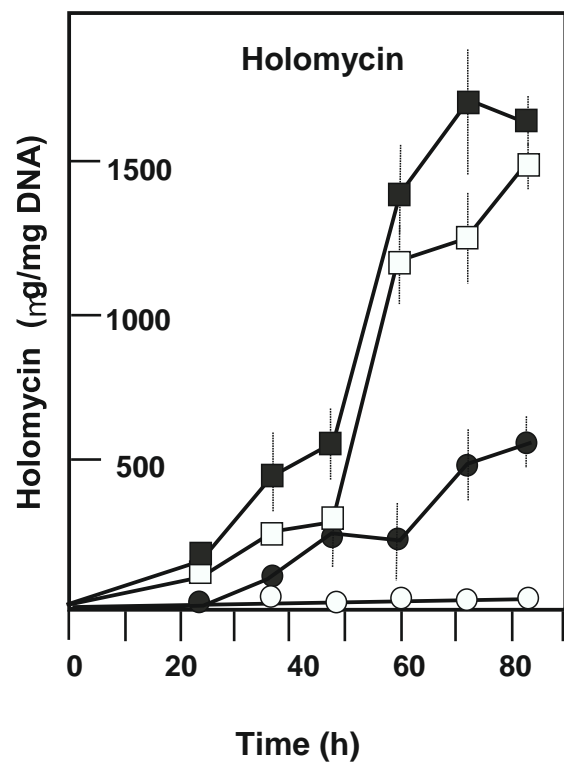


Fig. S1. Holomycin production by the strains used in this work.

The strains used are *S. clavuligerus* ATCC 27064 (white circles), *S. clavuligerus* $\Delta oppA2$ pSCL⁺ (black circles), *S. clavuligerus* pSCL4⁻ (white squares), *S. clavuligerus* $\Delta oppA2$ pSCL4⁻ (black squares).

Supplementary Table 1. Genes differentially transcribed between *S. clavuligerus* Δ oppA2::aac and *S. clavuligerus* ATCC 27064 using a filter of BHcorrected p-value<0.05 and values of $M_c > 2$ or $M_c < -2$, for at least one of the sampling times. The genes shown in Table 1 are not included in this Table.

| Gene | Product | M_c | | | BH-corrected p value | | | Fold change | | |
|--|---|--------|--------|-------|----------------------|----------------------|----------------------|-------------|--------|------|
| | | 22.5 h | 46.5 h | 60 h | 22.5 h | 46.5 h | 60 h | 22.5 h | 46.5 h | 60 h |
| Regulators | | | | | | | | | | |
| SCLAV_1409 | Regulatory protein | -0.77 | -2.34 | 0.06 | 5.88E ⁻⁰¹ | 7.42E ⁻⁰³ | 9.74E ⁻⁰¹ | 1.70 | 5.05 | 1.04 |
| SCLAV_1660 | RNA polymerase ECF-subfamily sigma factor | 1.30 | 2.13 | 2.96 | 2.34E ⁻⁰² | 3.39E ⁻⁰⁴ | 4.86E ⁻⁰⁶ | 2.47 | 4.37 | 7.76 |
| SCLAV_2428 | Regulator | -2.17 | -1.92 | -2.46 | 1.23E ⁻⁰² | 1.84E ⁻⁰² | 5.67E ⁻⁰³ | 4.49 | 3.80 | 5.51 |
| SCLAV_2712 | Regulatory protein | 0.87 | 2.11 | 0.99 | 3.37E ⁻⁰¹ | 3.27E ⁻⁰³ | 2.01E ⁻⁰¹ | 1.83 | 4.32 | 1.99 |
| SCLAV_3047 | Predicted transcriptional regulator | -2.35 | -1.81 | -0.74 | 3.67E ⁻⁰³ | 1.96E ⁻⁰² | 4.76E ⁻⁰¹ | 5.08 | 3.51 | 1.67 |
| SCLAV_3269 | Putative two-component system response regulator | 0.43 | 2.17 | 0.39 | 7.96E ⁻⁰¹ | 7.10E ⁻⁰³ | 7.72E ⁻⁰¹ | 1.35 | 4.51 | 1.31 |
| SCLAV_3358 | Response regulator | 2.49 | -0.04 | 0.32 | 1.76E ⁻⁰² | 9.82E ⁻⁰¹ | 8.70E ⁻⁰¹ | 5.64 | 1.03 | 1.25 |
| SCLAV_5223 | Regulatory protein | -1.21 | -2.12 | -1.21 | 7.48E ⁻⁰² | 1.37E ⁻⁰³ | 5.62E ⁻⁰² | 2.31 | 4.33 | 2.31 |
| SCLAV_p0788 | Pleiotropic regulatory protein DegT | -2.23 | -3.16 | -0.91 | 1.31E ⁻⁰¹ | 1.28E ⁻⁰² | 6.38E ⁻⁰¹ | 4.68 | 8.91 | 1.88 |
| SCLAV_p0948 | AraC family transcription regulator | 2.23 | 0.30 | 0.17 | 1.58E ⁻⁰⁴ | 6.34E ⁻⁰¹ | 8.74E ⁻⁰¹ | 4.70 | 1.23 | 1.12 |
| Proteins with diverse functions | | | | | | | | | | |
| SCLAV_0038 | Phage tail region protein | -0.40 | -2.12 | -1.42 | 8.39E ⁻⁰¹ | 1.29E ⁻⁰² | 1.31E ⁻⁰¹ | 1.32 | 4.36 | 2.67 |
| SCLAV_0075 | Chitinase | 2.80 | 0.38 | 0.20 | 1.50E ⁻⁰³ | 7.28E ⁻⁰¹ | 9.12E ⁻⁰¹ | 6.97 | 1.30 | 1.15 |
| SCLAV_0194 | Hydroxylase | 0.44 | 2.31 | 0.47 | 8.39E ⁻⁰¹ | 1.26E ⁻⁰² | 7.70E ⁻⁰¹ | 1.35 | 4.96 | 1.39 |
| SCLAV_0208 | 2- α -KG-dependent ethylene/succinate-forming enzyme | 0.32 | 2.28 | -0.20 | 8.81E ⁻⁰¹ | 9.41E ⁻⁰³ | 9.14E ⁻⁰¹ | 1.25 | 4.85 | 1.15 |
| SCLAV_0235 | Lipoprotein | 2.14 | 1.31 | 0.35 | 3.00E ⁻⁰⁴ | 1.55E ⁻⁰² | 6.82E ⁻⁰¹ | 4.41 | 2.48 | 1.28 |
| SCLAV_0335 | Thioredoxin-like protein | 0.46 | 2.02 | 0.37 | 8.23E ⁻⁰¹ | 2.83E ⁻⁰² | 8.33E ⁻⁰¹ | 1.38 | 4.05 | 1.29 |
| SCLAV_0345 | Hydrogenase accessory protein | 0.62 | 2.15 | -0.32 | 6.43E ⁻⁰¹ | 5.08E ⁻⁰³ | 8.14E ⁻⁰¹ | 1.53 | 4.43 | 1.25 |
| SCLAV_0422 | NADH:flavin oxidoreductase | 1.33 | 2.07 | 0.68 | 2.80E ⁻⁰¹ | 2.80E ⁻⁰² | 6.38E ⁻⁰¹ | 2.52 | 4.20 | 1.61 |
| SCLAV_0424 | Putative NADPH:quinone reductase | 0.42 | 2.10 | -0.02 | 8.38E ⁻⁰¹ | 1.78E ⁻⁰² | 9.94E ⁻⁰¹ | 1.34 | 4.29 | 1.01 |

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|------------|---|-------|-------|-------|----------------------|----------------------|----------------------|------|-------|------|
| SCLAV_0529 | NLP/P60-family protein | 1.12 | -0.02 | 3.25 | 1.53E ⁻⁰¹ | 9.82E ⁻⁰¹ | 2.52E ⁻⁰⁵ | 2.17 | 1.02 | 9.48 |
| SCLAV_0822 | rRNA methyltransferase | 0.42 | 2.18 | 0.97 | 8.16E ⁻⁰¹ | 9.17E ⁻⁰³ | 3.33E ⁻⁰¹ | 1.34 | 4.54 | 1.95 |
| SCLAV_0909 | Gluconokinase | 0.79 | 2.22 | 0.46 | 6.91E ⁻⁰¹ | 3.12E ⁻⁰² | 8.08E ⁻⁰¹ | 1.72 | 4.67 | 1.38 |
| SCLAV_0939 | Integral membrane protein | 2.13 | 0.60 | 0.72 | 4.42E ⁻⁰² | 6.00E ⁻⁰¹ | 6.18E ⁻⁰¹ | 4.39 | 1.52 | 1.65 |
| SCLAV_1012 | DUF320 domain-containing protein | -1.61 | -3.29 | -0.75 | 3.26E ⁻⁰¹ | 9.21E ⁻⁰³ | 7.40E ⁻⁰¹ | 3.05 | 9.75 | 1.69 |
| SCLAV_1032 | Transglycosylase associated protein | 0.79 | 2.11 | 1.36 | 6.80E ⁻⁰¹ | 3.50E ⁻⁰² | 2.55E ⁻⁰¹ | 1.72 | 4.32 | 2.56 |
| SCLAV_1431 | Glutamine synthetase 2 | 0.91 | 3.44 | 0.42 | 7.33E ⁻⁰¹ | 1.07E ⁻⁰² | 8.74E ⁻⁰¹ | 1.88 | 10.84 | 1.34 |
| SCLAV_1561 | Integral membrane protein | 0.23 | 2.40 | 0.51 | 9.40E ⁻⁰¹ | 2.21E ⁻⁰² | 7.85E ⁻⁰¹ | 1.17 | 5.29 | 1.43 |
| SCLAV_1871 | Cof-like hydrolase | 0.66 | 2.73 | 0.42 | 7.54E ⁻⁰¹ | 9.63E ⁻⁰³ | 8.30E ⁻⁰¹ | 1.58 | 6.63 | 1.34 |
| SCLAV_1916 | Ricin B lectin | 0.02 | -1.70 | -2.33 | 9.94E ⁻⁰¹ | 7.21E ⁻⁰² | 2.18E ⁻⁰² | 1.02 | 3.26 | 5.01 |
| SCLAV_2123 | Nucleotide phosphorylase | 0.00 | 2.26 | -0.33 | 1.00E+00 | 3.32E ⁻⁰² | 8.77E ⁻⁰¹ | 1.00 | 4.80 | 1.26 |
| SCLAV_2337 | Estradiol dioxygenase class III protein subunit B | 0.81 | 2.03 | 0.45 | 3.96E ⁻⁰¹ | 4.47E ⁻⁰³ | 6.82E ⁻⁰¹ | 1.76 | 4.08 | 1.36 |
| SCLAV_2577 | Putative phage integrase | 0.54 | 2.16 | 0.21 | 6.91E ⁻⁰¹ | 4.03E ⁻⁰³ | 8.86E ⁻⁰¹ | 1.45 | 4.47 | 1.16 |
| SCLAV_2964 | Putative acyl-CoA dehydrogenase | -0.07 | -0.61 | -2.66 | 9.83E ⁻⁰¹ | 6.33E ⁻⁰¹ | 1.55E ⁻⁰² | 1.05 | 1.52 | 6.31 |
| SCLAV_2965 | Phenylacetic acid degradation NADH oxidoreductase | -0.59 | 0.09 | -3.10 | 7.48E ⁻⁰¹ | 9.53E ⁻⁰¹ | 3.04E ⁻⁰³ | 1.50 | 1.06 | 8.57 |
| SCLAV_2966 | Phenylacetic acid degradation protein | 0.24 | 1.16 | -2.79 | 9.45E ⁻⁰¹ | 3.44E ⁻⁰¹ | 2.30E ⁻⁰² | 1.18 | 2.23 | 6.92 |
| SCLAV_2967 | Phenylacetic acid degradation protein | 0.03 | 1.05 | -2.38 | 9.93E ⁻⁰¹ | 3.64E ⁻⁰¹ | 3.84E ⁻⁰² | 1.02 | 2.07 | 5.22 |
| SCLAV_2968 | Phenylacetic acid degradation protein | 0.53 | 2.56 | -2.13 | 8.54E ⁻⁰¹ | 3.14E ⁻⁰² | 1.03E ⁻⁰¹ | 1.44 | 5.90 | 4.38 |
| SCLAV_2973 | Dehydrogenase | -0.44 | -0.05 | -2.56 | 8.59E ⁻⁰¹ | 9.76E ⁻⁰¹ | 1.72E ⁻⁰² | 1.35 | 1.03 | 5.92 |
| SCLAV_2977 | Putative branched-chain α keto acid DH E1 α subunit | 0.00 | -0.07 | -2.80 | 1.00E+00 | 9.70E ⁻⁰¹ | 2.48E ⁻⁰² | 1.00 | 1.05 | 6.96 |
| SCLAV_2978 | Branched-chain α keto acid DH E1 α subunit | -0.06 | -0.17 | -2.73 | 9.87E ⁻⁰¹ | 9.30E ⁻⁰¹ | 2.35E ⁻⁰² | 1.04 | 1.13 | 6.65 |
| SCLAV_2979 | Putative dihydrolipoamide acyltransferase | -0.16 | -0.20 | -2.58 | 9.51E ⁻⁰¹ | 8.75E ⁻⁰¹ | 4.98E ⁻⁰³ | 1.11 | 1.15 | 5.96 |
| SCLAV_3019 | Sensor protein | 1.21 | 2.09 | 1.77 | 4.02E ⁻⁰¹ | 3.67E ⁻⁰² | 1.10E ⁻⁰¹ | 2.31 | 4.25 | 3.42 |
| SCLAV_3359 | Sensor protein | 2.18 | 0.29 | 0.27 | 2.10E ⁻⁰⁵ | 5.54E ⁻⁰¹ | 6.99E ⁻⁰¹ | 4.53 | 1.23 | 1.21 |
| SCLAV_3535 | Monooxygenase FAD-binding protein | 2.43 | 0.97 | 0.11 | 3.63E ⁻⁰⁴ | 1.09E ⁻⁰¹ | 9.39E ⁻⁰¹ | 5.39 | 1.96 | 1.08 |
| SCLAV_3825 | Purine nucleoside phosphorylase | 0.46 | 2.28 | 0.90 | 8.20E ⁻⁰¹ | 1.24E ⁻⁰² | 4.47E ⁻⁰¹ | 1.37 | 4.85 | 1.87 |
| SCLAV_3888 | Glycosyl transferase, group 1 | 0.44 | 2.22 | 0.47 | 8.66E ⁻⁰¹ | 3.61E ⁻⁰² | 8.12E ⁻⁰¹ | 1.36 | 4.65 | 1.39 |

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|-------------|--|-------|-------|-------|----------------------|----------------------|----------------------|-------|-------|------|
| SCLAV_3892 | DUF946 domain-containing protein | -3.66 | -3.88 | -2.63 | 3.76E ⁻⁰⁴ | 2.50E ⁻⁰⁴ | 8.40E ⁻⁰³ | 12.63 | 14.72 | 6.20 |
| SCLAV_4039 | Putative reductase | -1.07 | -2.67 | 0.69 | 3.86E ⁻⁰¹ | 3.96E ⁻⁰³ | 5.92E ⁻⁰¹ | 2.09 | 6.38 | 1.62 |
| SCLAV_4072 | CBS domain protein | -1.76 | -2.47 | -1.91 | 7.22E ⁻⁰² | 6.29E ⁻⁰³ | 3.48E ⁻⁰² | 3.38 | 5.56 | 3.77 |
| SCLAV_4084 | Putative integral membrane protein | -0.37 | -2.55 | -0.51 | 7.82E ⁻⁰¹ | 2.73E ⁻⁰⁴ | 5.71E ⁻⁰¹ | 1.29 | 5.85 | 1.42 |
| SCLAV_4085 | Lipoprotein | -0.15 | -2.12 | -0.07 | 9.16E ⁻⁰¹ | 2.39E ⁻⁰⁴ | 9.52E ⁻⁰¹ | 1.11 | 4.35 | 1.05 |
| SCLAV_4108 | Putative polyprenyl diphosphate synthase | -1.40 | -2.45 | 0.28 | 3.03E ⁻⁰¹ | 1.81E ⁻⁰² | 8.98E ⁻⁰¹ | 2.64 | 5.45 | 1.21 |
| SCLAV_4381 | FG-GAP repeat protein | 4.14 | -0.10 | 0.18 | 2.95E ⁻⁰⁴ | 9.54E ⁻⁰¹ | 9.42E ⁻⁰¹ | 17.67 | 1.07 | 1.13 |
| SCLAV_4965 | O-methyltransferase family protein | 0.62 | 2.57 | 0.46 | 6.06E ⁻⁰¹ | 8.52E ⁻⁰⁴ | 6.82E ⁻⁰¹ | 1.54 | 5.93 | 1.37 |
| SCLAV_4967 | Putative sugar acetyltransferase | 0.52 | 2.41 | 0.13 | 7.80E ⁻⁰¹ | 7.87E ⁻⁰³ | 9.50E ⁻⁰¹ | 1.43 | 5.32 | 1.10 |
| SCLAV_5311 | Radical SAM domain protein | -2.05 | -1.53 | -0.86 | 2.40E ⁻⁰³ | 1.84E ⁻⁰² | 2.65E ⁻⁰¹ | 4.15 | 2.89 | 1.81 |
| SCLAV_5317 | Glycosyl transferase, family 2 | -2.03 | -1.95 | -1.35 | 1.83E ⁻⁰³ | 3.37E ⁻⁰³ | 3.98E ⁻⁰² | 4.10 | 3.86 | 2.55 |
| SCLAV_5318 | Putative oxidoreductase | -2.90 | -2.42 | -2.34 | 4.13E ⁻⁰³ | 1.33E ⁻⁰² | 2.14E ⁻⁰² | 7.45 | 5.36 | 5.06 |
| SCLAV_5396 | GCN5-related N-acetyltransferase | 0.28 | 2.69 | 0.12 | 9.04E ⁻⁰¹ | 2.93E ⁻⁰³ | 9.52E ⁻⁰¹ | 1.21 | 6.43 | 1.09 |
| SCLAV_5448 | Rare lipoprotein A | 0.26 | -0.08 | -2.13 | 9.25E ⁻⁰¹ | 9.61E ⁻⁰¹ | 4.15E ⁻⁰² | 1.20 | 1.06 | 4.37 |
| SCLAV_5505 | Phenylacetate-CoA ligase | 0.12 | 0.19 | -2.31 | 9.66E ⁻⁰¹ | 9.00E ⁻⁰¹ | 1.58E ⁻⁰² | 1.09 | 1.14 | 4.95 |
| SCLAV_5641 | Cytochrome P450 | 0.36 | 2.06 | 0.18 | 8.88E ⁻⁰¹ | 3.91E ⁻⁰² | 9.40E ⁻⁰¹ | 1.28 | 4.16 | 1.13 |
| SCLAV_nr015 | nocoRNAC: SIDD_value 3.5, Term_Confidence 93 | -0.18 | -2.02 | -1.17 | 8.99E ⁻⁰¹ | 8.89E ⁻⁰⁴ | 4.42E ⁻⁰² | 1.14 | 4.05 | 2.25 |
| SCLAV_nr066 | nocoRNAC: SIDD_value 4.0, Term_Confidence 91 | -2.01 | -2.05 | -2.70 | 3.34E ⁻⁰² | 1.82E ⁻⁰² | 4.98E ⁻⁰³ | 4.01 | 4.15 | 6.52 |
| SCLAV_nr129 | nocoRNAC: SIDD_value 1.8, Term_Confidence 70 | 3.07 | -0.07 | -0.08 | 1.27E ⁻⁰³ | 9.63E ⁻⁰¹ | 9.72E ⁻⁰¹ | 8.40 | 1.05 | 1.05 |
| SCLAV_p0107 | Transposase | 0.34 | 2.19 | 0.44 | 8.69E ⁻⁰¹ | 1.02E ⁻⁰² | 7.62E ⁻⁰¹ | 1.27 | 4.57 | 1.36 |
| SCLAV_p0109 | Putative glycosyltransferase | -0.26 | -2.44 | 0.82 | 9.18E ⁻⁰¹ | 9.39E ⁻⁰³ | 5.13E ⁻⁰¹ | 1.20 | 5.43 | 1.77 |
| SCLAV_p0140 | Glycosyltransferase-like protein | 0.38 | 2.23 | 0.10 | 8.07E ⁻⁰¹ | 2.93E ⁻⁰³ | 9.51E ⁻⁰¹ | 1.30 | 4.68 | 1.07 |
| SCLAV_p0346 | NUDIX hydrolase | 2.70 | -0.07 | 0.52 | 8.34E ⁻⁰⁴ | 9.58E ⁻⁰¹ | 6.65E ⁻⁰¹ | 6.52 | 1.05 | 1.44 |
| SCLAV_p0347 | Transposase | 2.39 | 0.05 | 0.08 | 9.85E ⁻⁰⁶ | 9.40E ⁻⁰¹ | 9.26E ⁻⁰¹ | 5.26 | 1.04 | 1.06 |
| SCLAV_p0475 | SNARE associated protein | 0.20 | 2.21 | 0.75 | 9.50E ⁻⁰¹ | 3.01E ⁻⁰² | 6.29E ⁻⁰¹ | 1.15 | 4.62 | 1.68 |
| SCLAV_p0540 | Cutinase domain-containing protein | -0.14 | -3.33 | -1.45 | 9.71E ⁻⁰¹ | 9.21E ⁻⁰³ | 3.50E ⁻⁰¹ | 1.10 | 10.09 | 2.73 |
| SCLAV_p0560 | Multimeric flavodoxin WrbA | 2.73 | 0.85 | -0.18 | 7.22E ⁻⁰⁴ | 2.70E ⁻⁰¹ | 9.12E ⁻⁰¹ | 6.63 | 1.81 | 1.13 |

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|--|---|-------|-------|-------|----------------------|----------------------|----------------------|-------|-------|------|
| SCLAV_p0573 | Cytochrome P450 | 0.11 | -2.91 | -0.14 | 9.67E ⁻⁰¹ | 1.82E ⁻⁰³ | 9.46E ⁻⁰¹ | 1.08 | 7.53 | 1.10 |
| SCLAV_p0787 | Putative ribose 5-phosphate isomerase | -2.25 | -3.37 | -1.10 | 4.42E ⁻⁰² | 2.02E ⁻⁰³ | 4.01E ⁻⁰¹ | 4.76 | 10.36 | 2.15 |
| SCLAV_p0789 | Fe-S oxidoreductase | -1.45 | -2.07 | -0.91 | 1.66E ⁻⁰¹ | 1.84E ⁻⁰² | 4.30E ⁻⁰¹ | 2.74 | 4.20 | 1.87 |
| SCLAV_p0790 | Phosphorylase | -1.67 | -2.79 | -0.84 | 5.21E ⁻⁰² | 1.06E ⁻⁰³ | 4.05E ⁻⁰¹ | 3.18 | 6.94 | 1.79 |
| SCLAV_p0794 | Putative PP-dependent aminotransferase | -0.14 | -2.56 | -0.38 | 9.12E ⁻⁰¹ | 4.26E ⁻⁰⁶ | 5.53E ⁻⁰¹ | 1.10 | 5.91 | 1.30 |
| SCLAV_p0797 | Favin-dependent oxidoreductase | -0.84 | -2.74 | 0.28 | 3.53E ⁻⁰¹ | 2.50E ⁻⁰⁴ | 8.23E ⁻⁰¹ | 1.79 | 6.69 | 1.21 |
| SCLAV_p0798 | Class II aldolase, N-terminal domain-containing protein | -0.63 | -3.26 | 0.23 | 5.79E ⁻⁰¹ | 5.41E ⁻⁰⁵ | 8.63E ⁻⁰¹ | 1.54 | 9.55 | 1.17 |
| SCLAV_p0799 | Protein kinase | -0.58 | -3.79 | -0.17 | 7.29E ⁻⁰¹ | 8.48E ⁻⁰⁵ | 9.27E ⁻⁰¹ | 1.49 | 13.84 | 1.13 |
| SCLAV_p0855 | Glyoxalase/bleomycin resistance protein/dioxygenase | -3.87 | -2.26 | -0.85 | 2.05E ⁻⁰² | 1.39E ⁻⁰¹ | 7.53E ⁻⁰¹ | 14.60 | 4.80 | 1.80 |
| SCLAV_p1035 | DUF1326 domain-containing protein | 0.85 | 2.18 | 0.20 | 6.42E ⁻⁰¹ | 3.03E ⁻⁰² | 9.28E ⁻⁰¹ | 1.81 | 4.53 | 1.15 |
| SCLAV_p1197 | Phage tail protein | -2.71 | -4.22 | -2.80 | 7.76E ⁻⁰² | 3.43E ⁻⁰³ | 5.02E ⁻⁰² | 6.54 | 18.62 | 6.98 |
| SCLAV_p1198 | Tail sheath protein | -2.81 | -4.49 | -2.89 | 5.93E ⁻⁰² | 1.88E ⁻⁰³ | 3.93E ⁻⁰² | 7.02 | 22.44 | 7.41 |
| SCLAV_p1200 | Hydrolytic protein | -2.62 | -4.44 | -2.71 | 8.56E ⁻⁰² | 1.76E ⁻⁰³ | 4.89E ⁻⁰² | 6.15 | 21.78 | 6.54 |
| SCLAV_p1254 | Co F420-dependent N5 N10-methylene THMR | 0.55 | 2.04 | 0.54 | 6.80E ⁻⁰¹ | 6.02E ⁻⁰³ | 6.12E ⁻⁰¹ | 1.47 | 4.12 | 1.45 |
| SCLAV_p1537 | Putative subunit of transposase | 0.55 | 2.15 | 0.44 | 7.24E ⁻⁰¹ | 7.99E ⁻⁰³ | 7.40E ⁻⁰¹ | 1.46 | 4.45 | 1.36 |
| SCLAV_t012 | tRNA-Met | 0.56 | 1.32 | 2.85 | 3.75E ⁻⁰¹ | 5.62E ⁻⁰³ | 6.56E ⁻⁰⁷ | 1.47 | 2.49 | 7.23 |
| Secondary metabolite cluster proteins | | | | | | | | | | |
| SCLAV_0159 | Germacradienol/germacrene D synthase | -0.14 | -2.14 | 1.16 | 9.46E ⁻⁰¹ | 4.12E ⁻⁰³ | 1.44E ⁻⁰¹ | 1.10 | 4.41 | 2.23 |
| SCLAV_0476 | Hypothetical protein | -1.54 | -2.00 | -2.41 | 2.38E ⁻⁰¹ | 4.95E ⁻⁰² | 2.52E ⁻⁰² | 2.91 | 4.00 | 5.31 |
| SCLAV_2457 | Putative kinase | -0.66 | -2.80 | -1.68 | 4.72E ⁻⁰¹ | 8.48E ⁻⁰⁵ | 9.17E ⁻⁰³ | 1.58 | 6.99 | 3.20 |
| SCLAV_2459 | Hypothetical protein | -0.57 | -2.68 | -1.33 | 5.53E ⁻⁰¹ | 8.48E ⁻⁰⁵ | 3.16E ⁻⁰² | 1.49 | 6.41 | 2.51 |
| SCLAV_2461 | DUF574 domain-containing protein | -0.46 | -2.20 | -0.97 | 6.41E ⁻⁰¹ | 2.73E ⁻⁰⁴ | 9.85E ⁻⁰² | 1.37 | 4.60 | 1.96 |
| SCLAV_2462 | Hypothetical protein | -0.59 | -2.35 | -0.75 | 6.55E ⁻⁰¹ | 2.33E ⁻⁰³ | 4.29E ⁻⁰¹ | 1.51 | 5.11 | 1.68 |
| SCLAV_2463 | NUDIX hydrolase | -0.92 | -2.46 | -1.40 | 3.59E ⁻⁰¹ | 1.93E ⁻⁰³ | 7.69E ⁻⁰² | 1.90 | 5.51 | 2.64 |
| SCLAV_2925 | Clavamate synthase 1 | 0.07 | 2.03 | -0.01 | 9.82E ⁻⁰¹ | 3.76E ⁻⁰² | 9.96E ⁻⁰¹ | 1.05 | 4.10 | 1.01 |
| SCLAV_4181 | Biotin carboxylase | -0.11 | -0.05 | -2.23 | 9.62E ⁻⁰¹ | 9.70E ⁻⁰¹ | 6.62E ⁻⁰³ | 1.08 | 1.03 | 4.68 |
| SCLAV_4200 | N-δ (α-aminoadipyl-L-cysteinyl-D-valine) synthetase | 0.57 | 0.11 | -2.81 | 7.39E ⁻⁰¹ | 9.38E ⁻⁰¹ | 3.85E ⁻⁰³ | 1.48 | 1.08 | 7.03 |

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|-------------|--|-------|-------|-------|----------------------|----------------------|----------------------|------|-------|------|
| SCLAV_4201 | L-lysine-epsilon aminotransferase | 0.28 | 0.42 | -2.56 | 9.25E ⁻⁰¹ | 7.65E ⁻⁰¹ | 1.74E ⁻⁰² | 1.21 | 1.34 | 5.89 |
| SCLAV_4205 | 3'-hydroxymethylcephem-O-carbamoyltransferase | 0.37 | 0.22 | -2.45 | 8.49E ⁻⁰¹ | 8.63E ⁻⁰¹ | 5.67E ⁻⁰³ | 1.29 | 1.16 | 5.46 |
| SCLAV_4206 | Deacetoxycephalosporin C hydroxylase | 0.63 | 0.83 | -2.43 | 7.92E ⁻⁰¹ | 5.10E ⁻⁰¹ | 3.80E ⁻⁰² | 1.55 | 1.78 | 5.39 |
| SCLAV_4207 | Hypothetical protein | 0.57 | 0.66 | -2.88 | 8.19E ⁻⁰¹ | 6.20E ⁻⁰¹ | 1.38E ⁻⁰² | 1.49 | 1.59 | 7.38 |
| SCLAV_4208 | Cephalosporin hydroxylase Cmcl | 0.59 | 0.61 | -2.23 | 7.84E ⁻⁰¹ | 6.17E ⁻⁰¹ | 3.57E ⁻⁰² | 1.51 | 1.52 | 4.69 |
| SCLAV_4210 | Isopenicillin N epimerase | 0.60 | 0.55 | -2.63 | 8.14E ⁻⁰¹ | 7.09E ⁻⁰¹ | 2.91E ⁻⁰² | 1.52 | 1.47 | 6.20 |
| SCLAV_4387 | Mg ²⁺ or Mn ²⁺ -dependent protein phosphatase, prpM4 | -2.28 | -2.34 | -1.98 | 4.90E ⁻⁰² | 2.51E ⁻⁰² | 7.90E ⁻⁰² | 4.86 | 5.06 | 3.94 |
| SCLAV_4755 | Hypothetical protein | -1.12 | -2.70 | -0.19 | 4.14E ⁻⁰¹ | 7.04E ⁻⁰³ | 9.28E ⁻⁰¹ | 2.18 | 6.49 | 1.14 |
| SCLAV_4756 | Polyprenyl synthetase | -0.88 | -2.46 | -0.02 | 5.75E ⁻⁰¹ | 9.85E ⁻⁰³ | 9.94E ⁻⁰¹ | 1.84 | 5.50 | 1.01 |
| SCLAV_4757 | Hypothetical protein | -0.47 | -2.53 | 0.33 | 8.27E ⁻⁰¹ | 9.58E ⁻⁰³ | 8.60E ⁻⁰¹ | 1.39 | 5.79 | 1.26 |
| SCLAV_5143 | Hypothetical protein | 0.57 | 2.22 | 0.63 | 7.38E ⁻⁰¹ | 1.02E ⁻⁰² | 6.26E ⁻⁰¹ | 1.49 | 4.67 | 1.55 |
| SCLAV_5341 | Hypothetical protein | 0.84 | 2.28 | 0.41 | 5.36E ⁻⁰¹ | 9.13E ⁻⁰³ | 7.86E ⁻⁰¹ | 1.79 | 4.87 | 1.33 |
| SCLAV_5616 | ATP/GTP-binding protein | 3.20 | 0.49 | 0.49 | 2.22E ⁻⁰³ | 7.06E ⁻⁰¹ | 7.83E ⁻⁰¹ | 9.21 | 1.40 | 1.41 |
| SCLAV_p0574 | Pentalene synthase | 0.11 | -2.21 | -0.58 | 9.63E ⁻⁰¹ | 9.52E ⁻⁰³ | 6.57E ⁻⁰¹ | 1.08 | 4.62 | 1.49 |
| SCLAV_p1079 | Putative transcriptional regulator | 0.21 | 2.05 | 0.45 | 9.14E ⁻⁰¹ | 4.47E ⁻⁰³ | 6.82E ⁻⁰¹ | 1.16 | 4.14 | 1.37 |
| SCLAV_p1112 | Staurosporine biosynthesis 4-ketoreductase StaK | 0.76 | 2.07 | 0.42 | 5.88E ⁻⁰¹ | 1.33E ⁻⁰² | 7.74E ⁻⁰¹ | 1.70 | 4.20 | 1.34 |
| SCLAV_p1187 | Hypothetical protein | -1.28 | -2.59 | -1.50 | 1.75E ⁻⁰¹ | 2.02E ⁻⁰³ | 7.25E ⁻⁰² | 2.43 | 6.00 | 2.83 |
| SCLAV_p1190 | GPW/gp25 family protein | -1.34 | -2.97 | -1.98 | 2.38E ⁻⁰¹ | 2.02E ⁻⁰³ | 3.50E ⁻⁰² | 2.53 | 7.82 | 3.95 |
| SCLAV_p1191 | Rhs element Vgr protein | -1.05 | -2.58 | -2.37 | 4.06E ⁻⁰¹ | 4.47E ⁻⁰³ | 9.79E ⁻⁰³ | 2.07 | 5.99 | 5.15 |
| SCLAV_p1192 | Peptidoglycan-binding LysM | -1.72 | -3.33 | -1.91 | 1.48E ⁻⁰¹ | 2.02E ⁻⁰³ | 7.67E ⁻⁰² | 3.31 | 10.03 | 3.75 |
| SCLAV_p1193 | Phage tail protein | -1.78 | -3.46 | -2.30 | 1.92E ⁻⁰¹ | 3.48E ⁻⁰³ | 5.09E ⁻⁰² | 3.44 | 11.04 | 4.93 |
| SCLAV_p1194 | PAT1 domain-containing protein | -0.65 | -2.73 | -1.39 | 8.04E ⁻⁰¹ | 2.13E ⁻⁰² | 3.50E ⁻⁰¹ | 1.57 | 6.65 | 2.61 |
| SCLAV_p1225 | Valine decarboxylase | -0.56 | -2.31 | -0.64 | 7.48E ⁻⁰¹ | 9.17E ⁻⁰³ | 6.16E ⁻⁰¹ | 1.47 | 4.96 | 1.56 |
| SCLAV_p1263 | Putative amine oxidoreductase | 0.43 | 2.79 | 0.01 | 5.85E ⁻⁰¹ | 2.93E ⁻⁰⁶ | 9.91E ⁻⁰¹ | 1.35 | 6.91 | 1.01 |
| SCLAV_p1264 | AMP-dependent synthetase and ligase | 0.25 | 2.65 | 0.13 | 7.75E ⁻⁰¹ | 1.96E ⁻⁰⁶ | 8.78E ⁻⁰¹ | 1.19 | 6.27 | 1.09 |
| SCLAV_p1265 | Cyclopropane-fatty-acyl-phospholipid synthase | 0.03 | 2.84 | -0.38 | 9.91E ⁻⁰¹ | 1.45E ⁻⁰³ | 7.93E ⁻⁰¹ | 1.02 | 7.14 | 1.30 |
| SCLAV_p1266 | Putative acyl-acyl desaturase | 0.08 | 2.72 | -0.21 | 9.71E ⁻⁰¹ | 4.25E ⁻⁰⁴ | 8.84E ⁻⁰¹ | 1.06 | 6.59 | 1.16 |

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|----------------------------------|------------------------------------|-------|-------|-------|----------------------|----------------------|----------------------|------|-------|-------|
| SCLAV_p1268 | Hypothetical protein | -0.10 | 2.41 | -0.83 | 9.71E ⁻⁰¹ | 6.50E ⁻⁰³ | 4.62E ⁻⁰¹ | 1.07 | 5.31 | 1.78 |
| SCLAV_p1269 | Acyltransferase | 0.16 | 2.44 | -0.02 | 9.31E ⁻⁰¹ | 4.82E ⁻⁰⁴ | 9.87E ⁻⁰¹ | 1.11 | 5.44 | 1.02 |
| SCLAV_p1309 | Thioesterase II | 0.04 | 2.31 | 0.04 | 9.77E ⁻⁰¹ | 6.96E ⁻⁰⁵ | 9.70E ⁻⁰¹ | 1.03 | 4.96 | 1.03 |
| SCLAV_p1363 | Monoxygenase FAD-binding protein | 0.53 | 2.42 | -0.10 | 7.29E ⁻⁰¹ | 3.18E ⁻⁰³ | 9.58E ⁻⁰¹ | 1.45 | 5.33 | 1.07 |
| SCLAV_p1373 | Hypothetical protein | 0.65 | 2.02 | 0.26 | 7.38E ⁻⁰¹ | 3.33E ⁻⁰² | 8.96E ⁻⁰¹ | 1.56 | 4.06 | 1.20 |
| SCLAV_p1428 | Prenyltransferase/squalene oxidase | -2.05 | -1.53 | -1.24 | 4.19E ⁻⁰² | 8.99E ⁻⁰² | 2.49E ⁻⁰¹ | 4.15 | 2.88 | 2.37 |
| SCLAV_p1432 | Hypothetical protein | 0.29 | 2.77 | 0.57 | 9.23E ⁻⁰¹ | 1.03E ⁻⁰² | 7.57E ⁻⁰¹ | 1.23 | 6.80 | 1.49 |
| SCLAV_p1471 | Hypothetical protein | 0.23 | 2.30 | 0.04 | 9.31E ⁻⁰¹ | 1.41E ⁻⁰² | 9.85E ⁻⁰¹ | 1.17 | 4.94 | 1.03 |
| Hypothetical Proteins (1) | | | | | | | | | | |
| SCLAV_0035 | Hypothetical protein | -0.17 | -2.43 | -2.10 | 9.42E ⁻⁰¹ | 3.85E ⁻⁰³ | 1.21E ⁻⁰² | 1.13 | 5.39 | 4.27 |
| SCLAV_0195 | Hypothetical protein | 0.27 | 2.53 | 0.62 | 9.17E ⁻⁰¹ | 8.45E ⁻⁰³ | 6.74E ⁻⁰¹ | 1.20 | 5.79 | 1.54 |
| SCLAV_0527 | Hypothetical protein | 2.04 | 3.07 | 4.60 | 1.02E ⁻⁰² | 2.73E ⁻⁰⁴ | 9.31E ⁻⁰⁷ | 4.12 | 8.38 | 24.28 |
| SCLAV_0528 | Hypothetical protein | 0.77 | -0.04 | 3.08 | 3.35E ⁻⁰¹ | 9.64E ⁻⁰¹ | 9.95E ⁻⁰⁶ | 1.70 | 1.03 | 8.47 |
| SCLAV_1658 | Hypothetical protein | 2.63 | 1.90 | 1.00 | 8.64E ⁻⁰³ | 2.83E ⁻⁰² | 3.57E ⁻⁰¹ | 6.17 | 3.72 | 2.01 |
| SCLAV_1664 | Hypothetical protein | 1.06 | 1.96 | 3.01 | 2.14E ⁻⁰² | 8.48E ⁻⁰⁵ | 1.47E ⁻⁰⁷ | 2.09 | 3.89 | 8.05 |
| SCLAV_1665 | Hypothetical protein | 0.26 | 0.58 | 2.07 | 8.45E ⁻⁰¹ | 3.07E ⁻⁰¹ | 3.02E ⁻⁰³ | 1.19 | 1.49 | 4.20 |
| SCLAV_1819 | Hypothetical protein | 0.58 | 2.35 | 0.89 | 8.25E ⁻⁰¹ | 3.97E ⁻⁰² | 6.08E ⁻⁰¹ | 1.49 | 5.11 | 1.85 |
| SCLAV_1971 | Hypothetical protein | -2.06 | -1.46 | 1.42 | 4.28E ⁻⁰² | 1.06E ⁻⁰¹ | 1.73E ⁻⁰¹ | 4.16 | 2.75 | 2.67 |
| SCLAV_2477 | Hypothetical protein | 0.40 | 3.46 | 0.44 | 8.80E ⁻⁰¹ | 4.37E ⁻⁰³ | 8.25E ⁻⁰¹ | 1.32 | 10.97 | 1.36 |
| SCLAV_2496 | Hypothetical protein | 0.74 | 2.40 | 0.43 | 6.30E ⁻⁰¹ | 7.87E ⁻⁰³ | 7.83E ⁻⁰¹ | 1.67 | 5.27 | 1.34 |
| SCLAV_2500 | Hypothetical protein | 0.80 | 2.81 | 0.87 | 6.51E ⁻⁰¹ | 5.51E ⁻⁰³ | 5.13E ⁻⁰¹ | 1.74 | 7.00 | 1.83 |
| SCLAV_2956 | Hypothetical protein | 2.53 | 1.70 | 0.71 | 1.62E ⁻⁰⁴ | 6.38E ⁻⁰³ | 3.33E ⁻⁰¹ | 5.77 | 3.26 | 1.64 |
| SCLAV_2957 | Hypothetical protein | 2.46 | 1.69 | 0.67 | 5.25E ⁻⁰⁴ | 1.07E ⁻⁰² | 4.33E ⁻⁰¹ | 5.48 | 3.23 | 1.59 |
| SCLAV_3072 | Hypothetical protein | 0.34 | 2.26 | -0.05 | 8.66E ⁻⁰¹ | 9.21E ⁻⁰³ | 9.77E ⁻⁰¹ | 1.27 | 4.80 | 1.04 |
| SCLAV_3217 | Hypothetical protein | -0.03 | 2.05 | 0.71 | 9.92E ⁻⁰¹ | 7.25E ⁻⁰³ | 4.65E ⁻⁰¹ | 1.02 | 4.13 | 1.64 |
| SCLAV_3317 | Hypothetical protein | 0.39 | -2.32 | 0.30 | 8.53E ⁻⁰¹ | 1.02E ⁻⁰² | 8.66E ⁻⁰¹ | 1.31 | 5.00 | 1.23 |
| SCLAV_3356 | Hypothetical protein | 2.10 | 0.93 | 0.86 | 3.90E ⁻⁰² | 3.34E ⁻⁰¹ | 4.97E ⁻⁰¹ | 4.29 | 1.91 | 1.81 |

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|-------------|----------------------|-------|-------|-------|----------------------|----------------------|----------------------|-------|-------|------|
| SCLAV_3357 | Hypothetical protein | 2.67 | 0.56 | 0.47 | 1.22E ⁻⁰² | 6.53E ⁻⁰¹ | 7.96E ⁻⁰¹ | 6.36 | 1.47 | 1.38 |
| SCLAV_3367 | Hypothetical protein | 0.14 | 2.11 | 0.07 | 9.54E ⁻⁰¹ | 9.44E ⁻⁰³ | 9.68E ⁻⁰¹ | 1.10 | 4.31 | 1.05 |
| SCLAV_3457 | Hypothetical protein | 2.66 | 1.32 | 0.73 | 5.24E ⁻⁰⁴ | 5.89E ⁻⁰² | 4.31E ⁻⁰¹ | 6.30 | 2.49 | 1.66 |
| SCLAV_3478 | Hypothetical protein | -1.44 | -2.37 | -1.64 | 6.67E ⁻⁰² | 1.81E ⁻⁰³ | 2.51E ⁻⁰² | 2.71 | 5.17 | 3.11 |
| SCLAV_3510 | Hypothetical protein | -1.65 | -3.67 | -2.34 | 2.63E ⁻⁰¹ | 2.76E ⁻⁰³ | 5.40E ⁻⁰² | 3.14 | 12.72 | 5.06 |
| SCLAV_3562 | Hypothetical protein | 5.86 | 3.83 | 3.20 | 8.66E ⁻⁰⁴ | 2.10E ⁻⁰² | 7.03E ⁻⁰² | 57.92 | 14.25 | 9.21 |
| SCLAV_3846 | Hypothetical protein | -0.76 | -3.41 | -2.40 | 5.80E ⁻⁰¹ | 2.21E ⁻⁰⁴ | 6.20E ⁻⁰³ | 1.69 | 10.65 | 5.29 |
| SCLAV_3859 | Hypothetical protein | 0.97 | 3.22 | 0.23 | 5.16E ⁻⁰¹ | 1.76E ⁻⁰³ | 9.11E ⁻⁰¹ | 1.96 | 9.33 | 1.17 |
| SCLAV_3874 | Hypothetical protein | 0.10 | 0.24 | 2.53 | 9.76E ⁻⁰¹ | 8.86E ⁻⁰¹ | 2.25E ⁻⁰² | 1.07 | 1.18 | 5.78 |
| SCLAV_3894 | Hypothetical protein | 2.89 | 2.64 | 1.08 | 6.59E ⁻⁰³ | 1.02E ⁻⁰² | 4.09E ⁻⁰¹ | 7.41 | 6.25 | 2.12 |
| SCLAV_3996 | Hypothetical protein | 0.25 | -3.00 | -0.07 | 9.42E ⁻⁰¹ | 1.12E ⁻⁰² | 9.82E ⁻⁰¹ | 1.19 | 8.01 | 1.05 |
| SCLAV_4311 | Hypothetical protein | 0.21 | 2.93 | 2.11 | 9.25E ⁻⁰¹ | 8.89E ⁻⁰⁴ | 1.24E ⁻⁰² | 1.16 | 7.65 | 4.32 |
| SCLAV_4378 | Hypothetical protein | 4.55 | 0.64 | 0.37 | 1.86E ⁻⁰⁴ | 6.28E ⁻⁰¹ | 8.64E ⁻⁰¹ | 23.41 | 1.56 | 1.30 |
| SCLAV_4379 | Hypothetical protein | 4.08 | 0.07 | 0.04 | 5.86E ⁻⁰⁴ | 9.67E ⁻⁰¹ | 9.88E ⁻⁰¹ | 16.96 | 1.05 | 1.03 |
| SCLAV_4380 | Hypothetical protein | 4.46 | 0.63 | 0.55 | 5.70E ⁻⁰⁴ | 7.09E ⁻⁰¹ | 8.03E ⁻⁰¹ | 22.00 | 1.54 | 1.46 |
| SCLAV_5061 | Hypothetical protein | -0.22 | 2.08 | 0.40 | 9.21E ⁻⁰¹ | 1.02E ⁻⁰² | 7.77E ⁻⁰¹ | 1.17 | 4.24 | 1.32 |
| SCLAV_5161 | Hypothetical protein | 2.87 | 1.34 | 0.55 | 1.84E ⁻⁰⁴ | 4.78E ⁻⁰² | 5.84E ⁻⁰¹ | 7.30 | 2.54 | 1.46 |
| SCLAV_5313 | Hypothetical protein | -2.03 | -1.61 | -1.25 | 4.07E ⁻⁰³ | 1.82E ⁻⁰² | 8.74E ⁻⁰² | 4.09 | 3.05 | 2.38 |
| SCLAV_5319 | Hypothetical protein | -3.22 | -2.35 | -2.90 | 1.43E ⁻⁰² | 5.45E ⁻⁰² | 2.45E ⁻⁰² | 9.31 | 5.08 | 7.48 |
| SCLAV_5383 | Hypothetical protein | 0.30 | 2.06 | 0.22 | 8.79E ⁻⁰¹ | 9.86E ⁻⁰³ | 8.93E ⁻⁰¹ | 1.23 | 4.16 | 1.17 |
| SCLAV_p0086 | Hypothetical protein | 1.40 | 2.14 | 1.33 | 3.18E ⁻⁰¹ | 3.93E ⁻⁰² | 2.99E ⁻⁰¹ | 2.65 | 4.41 | 2.51 |
| SCLAV_p0120 | Hypothetical protein | 0.41 | 2.21 | 0.17 | 8.04E ⁻⁰¹ | 4.89E ⁻⁰³ | 9.20E ⁻⁰¹ | 1.33 | 4.62 | 1.12 |
| SCLAV_p0174 | Hypothetical protein | 0.16 | 2.27 | 0.05 | 9.55E ⁻⁰¹ | 2.03E ⁻⁰² | 9.83E ⁻⁰¹ | 1.12 | 4.81 | 1.04 |
| SCLAV_p0179 | Hypothetical protein | 0.50 | 2.00 | 1.26 | 8.28E ⁻⁰¹ | 4.64E ⁻⁰² | 3.14E ⁻⁰¹ | 1.42 | 4.00 | 2.39 |
| SCLAV_p0249 | Hypothetical protein | 0.90 | 2.09 | 1.35 | 6.46E ⁻⁰¹ | 4.80E ⁻⁰² | 3.02E ⁻⁰¹ | 1.86 | 4.27 | 2.54 |
| SCLAV_p0251 | Hypothetical protein | 0.87 | 2.61 | 0.64 | 6.02E ⁻⁰¹ | 9.17E ⁻⁰³ | 6.79E ⁻⁰¹ | 1.83 | 6.10 | 1.56 |
| SCLAV_p0314 | Hypothetical protein | 1.33 | 1.45 | 2.15 | 3.02E ⁻⁰¹ | 1.28E ⁻⁰¹ | 3.49E ⁻⁰² | 2.51 | 2.74 | 4.44 |

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|-------------|----------------------|-------|-------|-------|----------------------|----------------------|----------------------|------|-------|------|
| SCLAV_p0350 | Hypothetical protein | 2.58 | 0.51 | -0.20 | 4.61E ⁻⁰² | 7.40E ⁻⁰¹ | 9.44E ⁻⁰¹ | 5.96 | 1.43 | 1.15 |
| SCLAV_p0398 | Hypothetical protein | -1.24 | -2.12 | 0.16 | 2.13E ⁻⁰¹ | 9.58E ⁻⁰³ | 9.28E ⁻⁰¹ | 2.36 | 4.35 | 1.12 |
| SCLAV_p0465 | Hypothetical protein | -0.16 | -2.00 | -0.27 | 9.54E ⁻⁰¹ | 2.58E ⁻⁰² | 8.86E ⁻⁰¹ | 1.12 | 4.01 | 1.20 |
| SCLAV_p0603 | Hypothetical protein | -0.95 | -2.89 | -1.76 | 7.20E ⁻⁰¹ | 2.96E ⁻⁰² | 2.67E ⁻⁰¹ | 1.93 | 7.40 | 3.40 |
| SCLAV_p0604 | Hypothetical protein | -1.07 | -3.09 | -1.92 | 5.47E ⁻⁰¹ | 6.73E ⁻⁰³ | 1.07E ⁻⁰¹ | 2.10 | 8.52 | 3.79 |
| SCLAV_p0605 | Hypothetical protein | -1.64 | -3.42 | -1.39 | 2.34E ⁻⁰¹ | 3.37E ⁻⁰³ | 2.96E ⁻⁰¹ | 3.13 | 10.71 | 2.62 |
| SCLAV_p0606 | Hypothetical protein | -1.51 | -3.05 | -1.61 | 1.63E ⁻⁰¹ | 1.82E ⁻⁰³ | 1.03E ⁻⁰¹ | 2.85 | 8.30 | 3.06 |
| SCLAV_p0717 | Hypothetical protein | 2.24 | 1.41 | -0.12 | 6.43E ⁻⁰⁴ | 2.07E ⁻⁰² | 9.28E ⁻⁰¹ | 4.71 | 2.66 | 1.09 |
| SCLAV_p0752 | Hypothetical protein | 2.34 | 0.49 | 0.58 | 5.12E ⁻⁰⁵ | 4.01E ⁻⁰¹ | 3.49E ⁻⁰¹ | 5.05 | 1.40 | 1.50 |
| SCLAV_p0756 | Hypothetical protein | 3.12 | 0.57 | 0.32 | 2.12E ⁻⁰⁵ | 3.93E ⁻⁰¹ | 7.67E ⁻⁰¹ | 8.70 | 1.48 | 1.25 |
| SCLAV_p0792 | Hypothetical protein | -0.90 | -2.08 | -0.60 | 2.20E ⁻⁰¹ | 1.37E ⁻⁰³ | 4.38E ⁻⁰¹ | 1.87 | 4.23 | 1.52 |
| SCLAV_p0800 | Hypothetical protein | -1.02 | -4.71 | -1.40 | 7.04E ⁻⁰¹ | 1.72E ⁻⁰³ | 4.40E ⁻⁰¹ | 2.02 | 26.19 | 2.64 |
| SCLAV_p0840 | Hypothetical protein | 2.21 | 1.15 | 0.03 | 1.18E ⁻⁰² | 1.57E ⁻⁰¹ | 9.90E ⁻⁰¹ | 4.63 | 2.23 | 1.02 |
| SCLAV_p1004 | Hypothetical protein | 0.81 | 2.54 | 0.46 | 6.17E ⁻⁰¹ | 8.05E ⁻⁰³ | 7.79E ⁻⁰¹ | 1.75 | 5.82 | 1.38 |
| SCLAV_p1068 | Hypothetical protein | 0.53 | 3.18 | 0.51 | 8.07E ⁻⁰¹ | 2.28E ⁻⁰³ | 7.67E ⁻⁰¹ | 1.44 | 9.06 | 1.42 |
| SCLAV_p1086 | Hypothetical protein | 3.00 | 1.59 | 1.08 | 4.71E ⁻⁰³ | 1.10E ⁻⁰¹ | 4.13E ⁻⁰¹ | 7.98 | 3.00 | 2.11 |
| SCLAV_p1087 | Hypothetical protein | 2.88 | 1.55 | 0.50 | 2.35E ⁻⁰⁴ | 4.24E ⁻⁰² | 6.54E ⁻⁰¹ | 7.39 | 2.93 | 1.41 |
| SCLAV_p1104 | Hypothetical protein | 0.56 | 2.35 | 0.51 | 7.34E ⁻⁰¹ | 6.49E ⁻⁰³ | 7.05E ⁻⁰¹ | 1.48 | 5.10 | 1.42 |
| SCLAV_p1204 | Hypothetical protein | -1.39 | -2.91 | -2.31 | 4.03E ⁻⁰¹ | 8.86E ⁻⁰³ | 3.99E ⁻⁰² | 2.62 | 7.53 | 4.96 |
| SCLAV_p1315 | Hypothetical protein | 1.25 | 2.22 | 0.20 | 2.97E ⁻⁰¹ | 1.52E ⁻⁰² | 9.22E ⁻⁰¹ | 2.37 | 4.65 | 1.15 |
| SCLAV_p1377 | Hypothetical protein | 0.94 | 2.19 | 0.79 | 4.45E ⁻⁰¹ | 9.97E ⁻⁰³ | 4.86E ⁻⁰¹ | 1.92 | 4.56 | 1.73 |
| SCLAV_p1512 | Hypothetical protein | 0.75 | 2.03 | 0.52 | 6.82E ⁻⁰¹ | 3.36E ⁻⁰² | 7.56E ⁻⁰¹ | 1.68 | 4.08 | 1.43 |
| SCLAV_p1514 | Hypothetical protein | 0.27 | 2.31 | 1.05 | 9.15E ⁻⁰¹ | 1.22E ⁻⁰² | 3.62E ⁻⁰¹ | 1.21 | 4.95 | 2.06 |
| SCLAV_p1523 | Hypothetical protein | 0.59 | 2.29 | -0.13 | 7.18E ⁻⁰¹ | 7.87E ⁻⁰³ | 9.49E ⁻⁰¹ | 1.51 | 4.91 | 1.09 |
| SCLAV_p1532 | Hypothetical protein | 0.15 | 2.41 | 0.03 | 9.57E ⁻⁰¹ | 1.04E ⁻⁰² | 9.89E ⁻⁰¹ | 1.11 | 5.32 | 1.02 |
| SCLAV_p1559 | Hypothetical protein | 0.41 | 2.46 | 1.01 | 8.70E ⁻⁰¹ | 1.55E ⁻⁰² | 4.51E ⁻⁰¹ | 1.32 | 5.49 | 2.01 |

- (1) This hypothetical proteins are not located in secondary metabolites gene clusters.
- (2) The transcription values in *S. clavuligerus* ATCC 27064 are taken as 1.0. Notice that the values shaded in gray corresponds to down-expressed genes at the indicated times.

