**Supplementary information for**

The role of ABC proteins in seaweed chemical defense mechanism

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**Table S1.** Statistical analysis of CC morphometry.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Data summary** | | | | | | |
|  | **Samples** | | | | | |
|  | | **Control** | **200** | **1000** | **Total** |  |
| N | | 43 | 43 | 43 | 129 |  |
| SigmaX | | 593.93 | 550.52 | 330.97 | 1475.42 |  |
| Mean | | 13.8123 | 12.8028 | 7.697 | 11.4374 |  |
| SigmaX2 | | 9009.7827 | 7798.4116 | 3208.8895 | 20017.0838 |  |
| Variance | | 19.1959 | 17.8624 | 15.7481 | 24.5482 |  |
| Standard deviation | | 4.3813 | 4.2264 | 3.9684 | 4.9546 |  |
| Standard error | | 0.6681 | 0.6445 | 0.6052 | 0.4362 |  |
|  | |  |  |  |  |  |
| **ANOVA Summary** | | |  |  |  |  |
| Source | | **SS** | **df** | **MS** | **F** | **P** |
| Treatment | | 924.2992 | 2 | 462.1496 | 24.32 | < 0.0001 |
| Error | | 1596.5442 | 84 | 19.0065 |  |  |
| Ss/BI | | 621.3243 | 42 |  |  |  |
| Total | | 3142.1677 | 128 |  |  |  |
|  | |  |  |  |  |  |
| **Tukey HSD Test** | | |  |  |  |  |
| HSD[0.05] | | 2.24 |  |  |  |  |
| HSD[0.01] | | 2.82 |  |  |  |  |
| Control vs 200 | | No significant |  |  |  |  |
| Control vs 1000 | | P < 0.01 |  |  |  |  |
| 200 vs 1000 | | P < 0.01 |  |  |  |  |

**Table S2.** Statistical analysis of elatol quantification in trichoblasts.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Data summary** | | | | | |
| **Samples** | | | | | |
|  | **Control** | **200** | **1000** | **Total** |  |
| N | 3.0 | 3.0 | 3.0 | 9.0 |  |
| SigmaX | 0.864354 | 0.928288 | 0.452705 | 2.245347 |  |
| Mean | 0.288118 | 0.309429 | 0.150902 | 0.249483 |  |
| SigmaX2 | 0.256286 | 0.292713 | 0.069368 | 0.618367 |  |
| Variance | 0.003625 | 0.002736 | 0.000527 | 0.007274 |  |
| Standard deviation | 0.06021 | 0.052311 | 0.022598 | 0.085287 |  |
| Standard error | 0.034762 | 0.030202 | 0.013255 | 0.028429 |  |
|  |  |  |  |  |  |
| **ANOVA Summary** | |  |  |  |  |
| Source | **SS** | **df** | **MS** | **F** | **P** |
| Treatment | 0.44414 | 2 | 0.022207 | 10.57 | 0.025316 |
| Error | 0.0084 | 4 | 0.0021 |  |  |
| Ss/BI | 0.0054 | 2 |  |  |  |
| Total | 0.058191 | 8 |  |  |  |
|  |  |  |  |  |  |
| **Tukey SD** | |  |  |  |  |
| HSD[0.05] | 0.13 |  |  |  |  |
| HSD[0.01] | 0.21 |  |  |  |  |
| Control vs 200 | No significant |  |  |  |  |
| Control vs 1000 | P < 0.01 |  |  |  |  |
| 200 vs 1000 | P < 0.01 |  |  |  |  |

**Table S3.** Statistical analysis of fouling coverage over algae thalli.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Data summary** | | | | | | |
|  | **Samples** | | | | | |
|  | | **Control** | **200** | **1000** | **Total** |  |
| N | | 10 | 10 | 10 | 30 |  |
| SigmaX | | 53.28 | 805.95 | 924.74 | 1783.97 |  |
| Mean | | 5.328 | 80.595 | 92.474 | 59.4657 |  |
| SigmaX2 | | 740.291 | 65619.1729 | 86527.3648 | 152886.828 |  |
| Variance | | 50.7128 | 73.737 | 112.5509 | 1613.8574 |  |
| Standard deviation | | 7.1213 | 8.587 | 10.609 | 40.1728 |  |
| Standard error | | 2.252 | 2.7155 | 3.3549 | 7.3345 |  |
|  | |  |  |  |  |  |
| **ANOVA Summary** | | |  |  |  |  |
| Source | | **SS** | **df** | **MS** | **F** | **P** |
| Treatment | | 44668.8575 | 2 | 22334.4287 | 234.28 | P < 0.0001 |
| Error | | 1715.9623 | 18 | 95.3312 |  |  |
| Ss/BI | | 417.0435 | 9 |  |  |  |
| Total | | 46801.8633 | 29 |  |  |  |
|  | |  |  |  |  |  |
| **Tukey HSD Test** | | |  |  |  |  |
| HSD[0.05] | | 11.17 |  |  |  |  |
| HSD[0.01] | | 14.53 |  |  |  |  |
| Control vs 200 | | P < 0.01 |  |  |  |  |
| Control vs 1000 | | P < 0.01 |  |  |  |  |
| 200 vs 1000 | | No significant |  |  |  |  |

**Table S4.** Statistical analysis of ABC gene expression.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Time** | **logFC** | **p-value** |
| ABCB | 24 h | 10.155 | 2.10-4 |
| ABCB | 48 h | 10.202 | 8.10-7 |
| ABCB | 72h | 1.751 | 1.0 |
| ABCD | 24 h | 10.981 | 8.10-7 |
| ABCD | 48 h | 6.018 | 1.8.10-3 |
| ABCD | 72h | 2.171 | 1.0 |
| ABCF | 24 h | 9.931 | 4.10-4 |
| ABCF | 48 h | 3.988 | 1.0 |
| ABCF | 72h | 3.893 | 1.0 |
| ABCG1 | 24 h | 9.418 | 6.10-4 |
| ABCG1 | 48 h | 6.997 | 4.10-2 |
| ABCG1 | 72h | 3.893 | 1.0 |
| ABCG2 | 24 h | 9.896 | 3.10-4 |
| ABCG2 | 48 h | 4.186 | 1.0 |
| ABCG2 | 72h | -0.162 | 1.0 |
| ABCG3 | 24 h | 10.061 | 5.10-5 |
| ABCG3 | 48 h | 5.214 | 0.2 |
| ABCG3 | 72h | 1.013 | 1.0 |

The functional annotation and classification of candidate genes into ABC protein subfamilies was confirmed through SmartBLAST (<https://blast.ncbi.nlm.nih.gov/smartblast/>), which searches the query against the nr protein database with an optimized version of BLAST targeted to find closely related sequences. SmartBLAST also simultaneously searches the landmark dataset (http://bit.ly/2aOVhPO) with BLASTP and performs a multiple sequence alignment on the six sequences (the query plus up to five matched subject sequences) using the COBALT multiple sequence alignment tool. The cDNA sequences were previously translated into protein sequences by using the Expasy translate tool (<https://web.expasy.org/translate/>) and standard genetic code.

**Table S5.** Best hits for *L. dendroidea* gene annotated as ABCB protein (LdABCB) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [ABC transporter B family protein [*Dictyostelium discoideum* AX4]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_629136) | 1048 | 1501 | 97% | 0.0 | 43.54% | [XP\_629136.1](https://www.ncbi.nlm.nih.gov/protein/XP_629136.1?report=genbank&log$=prottop&blast_rank=1&RID=BNAMFF4F011) |
| [ABC transporter B family member 4 isoform X1 [Glycine max]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_003518599) | 976 | 976 | 97% | 0.0 | 42.73% | [XP\_003518599.1](https://www.ncbi.nlm.nih.gov/protein/XP_003518599.1?report=genbank&log$=prottop&blast_rank=2&RID=BNAMFF4F011) |
| [ATP-dependent translocase ABCB1 [*Mus musculus*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_035205) | 945 | 1738 | 97% | 0.0 | 40.38% | [NP\_035205.1](https://www.ncbi.nlm.nih.gov/protein/NP_035205.1?report=genbank&log$=prottop&blast_rank=3&RID=BNAMFF4F011) |
| [ATP binding cassette subfamily B4 [*Arabidopsis thaliana*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_001323911) | 943 | 1376 | 96% | 0.0 | 41.91% | [NP\_001323911.1](https://www.ncbi.nlm.nih.gov/protein/NP_001323911.1?report=genbank&log$=prottop&blast_rank=4&RID=BNAMFF4F011) |
| [multidrug resistance protein 1 [Danio rerio]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_001922717) | 942 | 942 | 99% | 0.0 | 40.12% | [XP\_001922717.3](https://www.ncbi.nlm.nih.gov/protein/XP_001922717.3?report=genbank&log$=prottop&blast_rank=5&RID=BNAMFF4F011) |

**Table S6.** Best hits for *L. dendroidea* gene annotated as ABCD protein (LdABCD) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [peroxisomal ABC transporter 1 [*Arabidopsis thaliana*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_001328232) | 724 | 724 | 93% | 0.0 | 35.51% | [NP\_001328232.1](https://www.ncbi.nlm.nih.gov/protein/NP_001328232.1?report=genbank&log$=prottop&blast_rank=1&RID=BPM6183A011) |
| [ABC transporter D family member 1-like isoform X2 [Glycine max]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_014631244) | 721 | 721 | 94% | 0.0 | 35.79% | [XP\_014631244.1](https://www.ncbi.nlm.nih.gov/protein/XP_014631244.1?report=genbank&log$=prottop&blast_rank=2&RID=BPM6183A011) |
| [ATP-binding cassette sub-family D member 1 [*Homo sapiens*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_000024) | 312 | 540 | 84% | 3e-90 | 30.92% | [NP\_000024.2](https://www.ncbi.nlm.nih.gov/protein/NP_000024.2?report=genbank&log$=prottop&blast_rank=3&RID=BPM6183A011) |
| [Peroxisomal Membrane Protein related [*Caenorhabditis elegans*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_001293680) | 307 | 531 | 89% | 1e-88 | 30.25% | [NP\_001293680.1](https://www.ncbi.nlm.nih.gov/protein/NP_001293680.1?report=genbank&log$=prottop&blast_rank=4&RID=BPM6183A011) |
| [ATP-binding cassette sub-family D member 1 isoform X1 [*Danio rerio*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_005166771) | 306 | 306 | 43% | 8e-88 | 29.97% | [XP\_005166771.1](https://www.ncbi.nlm.nih.gov/protein/XP_005166771.1?report=genbank&log$=prottop&blast_rank=5&RID=BPM6183A011) |

**Table S7.** Best hits for *L. dendroidea* gene annotated as ABCF protein (LdABCF) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [ATP-binding cassette protein subfamily F, member 2, putative [*Leishmania donovani*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_003860258) | 219 | 219 | 91% | 8e-62 | 28.47% | [XP\_003860258.1](https://www.ncbi.nlm.nih.gov/protein/XP_003860258.1?report=genbank&log$=prottop&blast_rank=1&RID=BPS1KZES011) |
| [putative AAA family ATPase Gcn20 [*Schizosaccharomyces pombe*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_595837) | 217 | 217 | 90% | 3e-60 | 29.72% | [NP\_595837.1](https://www.ncbi.nlm.nih.gov/protein/NP_595837.1?report=genbank&log$=prottop&blast_rank=2&RID=BPS1KZES011) |
| [uncharacterized protein Dmel\_CG9281, isoform D [*Drosophila melanogaster*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_001285284) | 211 | 211 | 88% | 7e-59 | 29.62% | [NP\_001285284.1](https://www.ncbi.nlm.nih.gov/protein/NP_001285284.1?report=genbank&log$=prottop&blast_rank=3&RID=BPS1KZES011) |
| [ATP-binding cassette family ATPase ARB1 [*Saccharomyces cerevisiae* S288C]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_010953) | 207 | 207 | 94% | 2e-57 | 28.23% | [NP\_010953.1](https://www.ncbi.nlm.nih.gov/protein/NP_010953.1?report=genbank&log$=prottop&blast_rank=4&RID=BPS1KZES011) |
| [ABC transporter-related protein [*Dictyostelium discoideum* AX4]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_637946) | 206 | 206 | 87% | 1e-56 | 31.53% | [XP\_637946.1](https://www.ncbi.nlm.nih.gov/protein/XP_637946.1?report=genbank&log$=prottop&blast_rank=5&RID=BPS1KZES011) |

**Table S8.** Best hits for *L. dendroidea* gene annotated as ABCG protein (**LdABCG1**) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [ATP-binding cassette sub-family G member 4 [*Mus musculus*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_620405) | 290 | 290 | 84% | 5e-88 | 33.52% | [NP\_620405.3](https://www.ncbi.nlm.nih.gov/protein/NP_620405.3?report=genbank&log$=prottop&blast_rank=1&RID=BPP8CNX2011) |
| [ABC-2 type transporter family protein [*Arabidopsis thaliana*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_175734) | 282 | 282 | 82% | 1e-85 | 33.78% | [NP\_175734.1](https://www.ncbi.nlm.nih.gov/protein/NP_175734.1?report=genbank&log$=prottop&blast_rank=2&RID=BPP8CNX2011) |
| [ATP-binding cassette sub-family G member 4 isoform X1 [*Homo sapiens*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_011541254) | 275 | 275 | 85% | 2e-83 | 32.40% | [XP\_011541254.1](https://www.ncbi.nlm.nih.gov/protein/XP_011541254.1?report=genbank&log$=prottop&blast_rank=3&RID=BPP8CNX2011) |
| [ABC transporter domain-containing protein [*Caenorhabditis elegans*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_001367851) | 274 | 274 | 86% | 9e-82 | 32.46% | [NP\_001367851.1](https://www.ncbi.nlm.nih.gov/protein/NP_001367851.1?report=genbank&log$=prottop&blast_rank=4&RID=BPP8CNX2011) |
| [ABC transporter G family member 10 [Glycine max]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_003539614) | 272 | 272 | 83% | 1e-81 | 33.84% | [XP\_003539614.1](https://www.ncbi.nlm.nih.gov/protein/XP_003539614.1?report=genbank&log$=prottop&blast_rank=5&RID=BPP8CNX2011) |

**Table S9.** Best hits for *L. dendroidea* gene annotated as ABCG protein (**LdABCG2**) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [white [*Drosophila melanogaster*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_476787) | 193 | 193 | 36% | 9e-50 | 27.60% | [NP\_476787.1](https://www.ncbi.nlm.nih.gov/protein/NP_476787.1?report=genbank&log$=prottop&blast_rank=1&RID=BPPYYRVF011) |
| [ABC-2 type transporter family protein [*Arabidopsis thaliana*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_191069) | 191 | 191 | 33% | 6e-49 | 28.92% | [NP\_191069.2](https://www.ncbi.nlm.nih.gov/protein/NP_191069.2?report=genbank&log$=prottop&blast_rank=2&RID=BPPYYRVF011) |
| [ATP-binding cassette sub-family G member 2 isoform X1 [*Danio rerio*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_009292498) | 187 | 187 | 37% | 5e-48 | 26.71% | [XP\_009292498.3](https://www.ncbi.nlm.nih.gov/protein/XP_009292498.3?report=genbank&log$=prottop&blast_rank=3&RID=BPPYYRVF011) |
| [ABC transporter G family protein [*Dictyostelium discoideum* AX4]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_646231) | 179 | 179 | 34% | 1e-45 | 27.88% | [XP\_646231.1](https://www.ncbi.nlm.nih.gov/protein/XP_646231.1?report=genbank&log$=prottop&blast_rank=4&RID=BPPYYRVF011) |
| [ABC transporter G family member 20 [Glycine max]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_003553533) | 179 | 179 | 32% | 7e-45 | 28.34% | [XP\_003553533.1](https://www.ncbi.nlm.nih.gov/protein/XP_003553533.1?report=genbank&log$=prottop&blast_rank=5&RID=BPPYYRVF011) |

**Table S10.** Best hits for *L. dendroidea* gene annotated as ABCG protein (**LdABCG3**) through SmartBLAST.

| **Description** | **Max score** | **Total score** | **Query cover** | **E value** | **Identity** | **Accession** |
| --- | --- | --- | --- | --- | --- | --- |
| [pleiotropic drug resistance 1 [*Arabidopsis thaliana*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_566543) | 543 | 702 | 91% | 4e-168 | 31.19% | [NP\_566543.1](https://www.ncbi.nlm.nih.gov/protein/NP_566543.1?report=genbank&log$=prottop&blast_rank=1&RID=BPRFD1XF011) |
| [pleiotropic drug resistance protein 1 [*Glycine max*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_003546230) | 521 | 521 | 90% | 6e-160 | 29.79% | [XP\_003546230.1](https://www.ncbi.nlm.nih.gov/protein/XP_003546230.1?report=genbank&log$=prottop&blast_rank=2&RID=BPRFD1XF011) |
| [ATP-binding cassette sub-family G member 2 isoform X1 [*Danio rerio*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_021325521) | 192 | 343 | 76% | 6e-50 | 29.37% | [XP\_021325521.1](https://www.ncbi.nlm.nih.gov/protein/XP_021325521.1?report=genbank&log$=prottop&blast_rank=3&RID=BPRFD1XF011) |
| [ATP-binding cassette sub-family G member 1 isoform 6 [*Homo sapiens*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_NP_997511) | 188 | 188 | 39% | 2e-48 | 29.55% | [NP\_997511.1](https://www.ncbi.nlm.nih.gov/protein/NP_997511.1?report=genbank&log$=prottop&blast_rank=4&RID=BPRFD1XF011) |
| [ATP-binding cassette sub-family G member 3 isoform X2 [*Mus musculus*]](https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi#alnHdr_XP_017176394) | 162 | 162 | 39% | 1e-39 | 27.96% | [XP\_017176394.1](https://www.ncbi.nlm.nih.gov/protein/XP_017176394.1?report=genbank&log$=prottop&blast_rank=5&RID=BPRFD1XF011) |

**Table S11. Results of the incubation assay about the effect of CSA on area of the CC.**

|  |  |
| --- | --- |
| **Treatment** | **CC area (μm2)** |
| Control | 8.18 |
| Control | 9.06 |
| Control | 9.29 |
| Control | 16.18 |
| Control | 13.26 |
| Control | 10.48 |
| Control | 13.02 |
| Control | 11.41 |
| Control | 9.17 |
| Control | 14.12 |
| Control | 15.7 |
| Control | 15.64 |
| Control | 15.74 |
| Control | 18.81 |
| Control | 17.05 |
| Control | 19.08 |
| Control | 23.8 |
| Control | 19.25 |
| Control | 10.59 |
| Control | 13.6 |
| Control | 12.59 |
| Control | 9.68 |
| Control | 10.4 |
| Control | 14.31 |
| Control | 16.89 |
| Control | 22.32 |
| Control | 10.44 |
| Control | 13.63 |
| Control | 10.17 |
| Control | 13.25 |
| Control | 9.55 |
| Control | 12.45 |
| Control | 11.56 |
| Control | 10.59 |
| Control | 8.69 |
| Control | 12.72 |
| Control | 9.92 |
| Control | 16.16 |
| Control | 10.63 |
| Control | 8.64 |
| Control | 19.08 |
| Control | 22.21 |
| Control | 24.62 |
| CSA 200 ng/mL | 15.49 |
| CSA 200 ng/mL | 18.94 |
| CSA 200 ng/mL | 20.23 |
| CSA 200 ng/mL | 19.69 |
| CSA 200 ng/mL | 16.92 |
| CSA 200 ng/mL | 11.83 |
| CSA 200 ng/mL | 14.79 |
| CSA 200 ng/mL | 8.23 |
| CSA 200 ng/mL | 7.15 |
| CSA 200 ng/mL | 9.06 |
| CSA 200 ng/mL | 10.92 |
| CSA 200 ng/mL | 14.82 |
| CSA 200 ng/mL | 8.15 |
| CSA 200 ng/mL | 5.37 |
| CSA 200 ng/mL | 15.43 |
| CSA 200 ng/mL | 17.6 |
| CSA 200 ng/mL | 17.05 |
| CSA 200 ng/mL | 7.09 |
| CSA 200 ng/mL | 9.38 |
| CSA 200 ng/mL | 8.79 |
| CSA 200 ng/mL | 10.48 |
| CSA 200 ng/mL | 15.13 |
| CSA 200 ng/mL | 7.06 |
| CSA 200 ng/mL | 11.53 |
| CSA 200 ng/mL | 16.6 |
| CSA 200 ng/mL | 17.81 |
| CSA 200 ng/mL | 15.77 |
| CSA 200 ng/mL | 9.69 |
| CSA 200 ng/mL | 19.27 |
| CSA 200 ng/mL | 10.31 |
| CSA 200 ng/mL | 9.43 |
| CSA 200 ng/mL | 11.52 |
| CSA 200 ng/mL | 10.27 |
| CSA 200 ng/mL | 8.94 |
| CSA 200 ng/mL | 18.47 |
| CSA 200 ng/mL | 9.94 |
| CSA 200 ng/mL | 19.81 |
| CSA 200 ng/mL | 14.76 |
| CSA 200 ng/mL | 15.32 |
| CSA 200 ng/mL | 9.18 |
| CSA 200 ng/mL | 8.38 |
| CSA 200 ng/mL | 11.06 |
| CSA 200 ng/mL | 12.86 |
| CSA 1000 ng/mL | 12.64 |
| CSA 1000 ng/mL | 5.49 |
| CSA 1000 ng/mL | 9.13 |
| CSA 1000 ng/mL | 3.88 |
| CSA 1000 ng/mL | 6.86 |
| CSA 1000 ng/mL | 9.33 |
| CSA 1000 ng/mL | 4.1 |
| CSA 1000 ng/mL | 16.2 |
| CSA 1000 ng/mL | 3.69 |
| CSA 1000 ng/mL | 7.69 |
| CSA 1000 ng/mL | 11.55 |
| CSA 1000 ng/mL | 10.83 |
| CSA 1000 ng/mL | 9.56 |
| CSA 1000 ng/mL | 13.79 |
| CSA 1000 ng/mL | 14.48 |
| CSA 1000 ng/mL | 9.91 |
| CSA 1000 ng/mL | 6.55 |
| CSA 1000 ng/mL | 13.65 |
| CSA 1000 ng/mL | 8.3 |
| CSA 1000 ng/mL | 11.62 |
| CSA 1000 ng/mL | 12.85 |
| CSA 1000 ng/mL | 10.15 |
| CSA 1000 ng/mL | 4.47 |
| CSA 1000 ng/mL | 3.26 |
| CSA 1000 ng/mL | 7.03 |
| CSA 1000 ng/mL | 2.31 |
| CSA 1000 ng/mL | 3.78 |
| CSA 1000 ng/mL | 4.62 |
| CSA 1000 ng/mL | 3.43 |
| CSA 1000 ng/mL | 5.27 |
| CSA 1000 ng/mL | 9.08 |
| CSA 1000 ng/mL | 6.73 |
| CSA 1000 ng/mL | 7.35 |
| CSA 1000 ng/mL | 3.75 |
| CSA 1000 ng/mL | 2.23 |
| CSA 1000 ng/mL | 12.34 |
| CSA 1000 ng/mL | 9.17 |
| CSA 1000 ng/mL | 4.72 |
| CSA 1000 ng/mL | 6.03 |
| CSA 1000 ng/mL | 2.51 |
| CSA 1000 ng/mL | 14.41 |
| CSA 1000 ng/mL | 1.82 |
| CSA 1000 ng/mL | 4.41 |

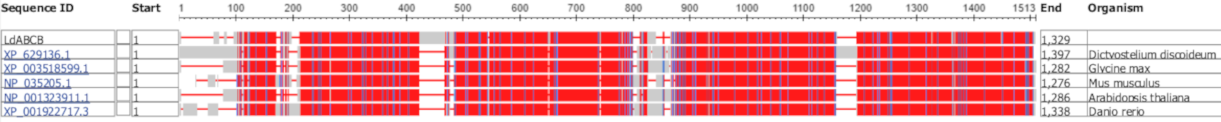
**Table S12. Results of the incubation assay about the effect of CSA on elatol content.**

|  |  |
| --- | --- |
| Treatment | Elatol concentration |
| Control | 0.335025383591322 |
| Control | 0.309105269620527 |
| Control | 0.220222887700245 |
| CSA 200 ng/mL | 0.365705077776143 |
| CSA 200 ng/mL | 0.300298062687688 |
| CSA 200 ng/mL | 0.262285249165043 |
| CSA 1000 ng/mL | 0.138372276327124 |
| CSA 1000 ng/mL | 0.136933988893402 |
| CSA 1000 ng/mL | 0.177398648102593 |

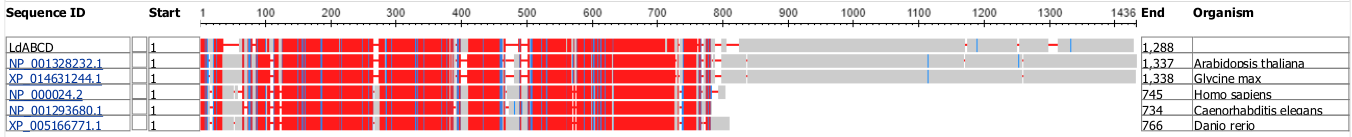
**Table S13. Results of the incubation assay about the indirect effect of CSA on fouling.**

|  |  |
| --- | --- |
| Treatment | Fouled area (%) |
| Control | 0.67 |
| Control | 7.78 |
| Control | 24.48 |
| Control | 1.32 |
| Control | 5.94 |
| Control | 2.70 |
| Control | 4.48 |
| Control | 3.48 |
| Control | 0.67 |
| Control | 1.76 |
| CSA 200 ng/mL | 72.48 |
| CSA 200 ng/mL | 100.0 |
| CSA 200 ng/mL | 71.67 |
| CSA 200 ng/mL | 85.67 |
| CSA 200 ng/mL | 79.78 |
| CSA 200 ng/mL | 75.00 |
| CSA 200 ng/mL | 85.33 |
| CSA 200 ng/mL | 79.33 |
| CSA 200 ng/mL | 83.33 |
| CSA 200 ng/mL | 73.36 |
| CSA 1000 ng/mL | 81.33 |
| CSA 1000 ng/mL | 66.78 |
| CSA 1000 ng/mL | 100.00 |
| CSA 1000 ng/mL | 100.00 |
| CSA 1000 ng/mL | 93.67 |
| CSA 1000 ng/mL | 96.48 |
| CSA 1000 ng/mL | 100.00 |
| CSA 1000 ng/mL | 96.67 |
| CSA 1000 ng/mL | 97.33 |
| CSA 1000 ng/mL | 92.48 |

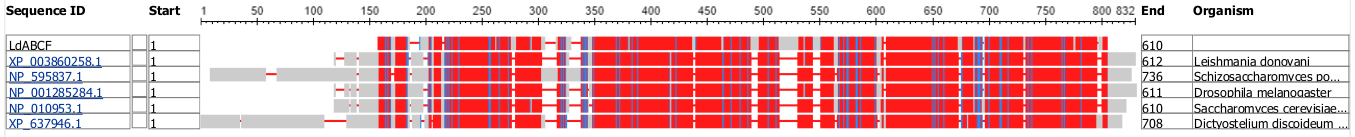
**Figure S1.** Multiple alignment of LdABCB (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.



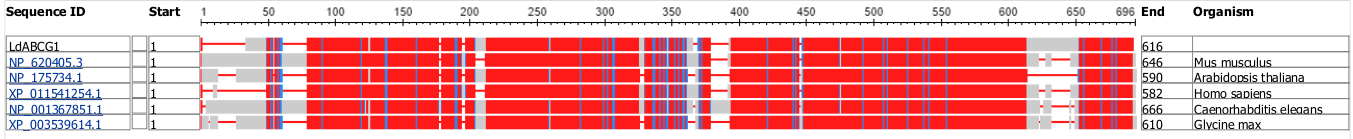
**Figure S2.** Multiple alignment of LdABCD (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.

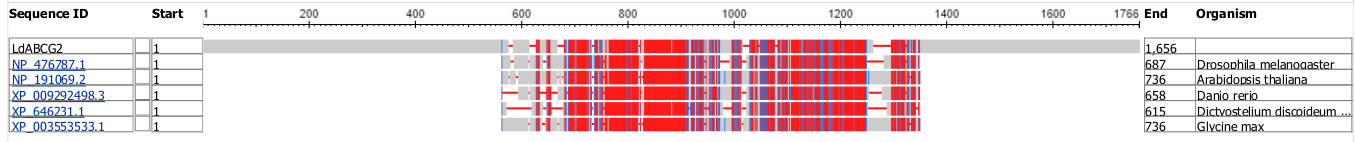


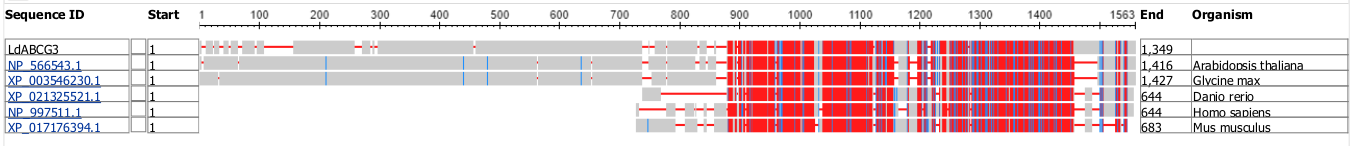
**Figure S3.** Multiple alignment of LdABCF (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.



**Figure S4.** Multiple alignment of LdABCG1 (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.



** Figure S5.** Multiple alignment of LdABCG2 (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.

** Fig S6**. Multiple alignment of LdABCG3 (translated sequence) and five best hit protein sequences (SmartBLAST). Alignment columns with gaps are colored grey. The red color indicates highly conserved columns and blue indicates less conserved ones.