

Table S1. The top 10 similar sequences obtained by BLAST sequence alignment.

| Describe | Species | Score | Similarity | E value |
|---|--|--------------|-------------------|-----------------------|
| Predicted protein | <i>P. tricornutum</i> CCAP 1055/1 | 481 | 100% | 2.00E ⁻¹⁷¹ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Oceanibium sediminis</i> | 248 | 100% | 1.00E ⁻⁷⁹ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Marinobacter</i> sp. PJ-16 | 232 | 98% | 3.00E ⁻⁷³ |
| short-chain dehydrogenase | <i>Marinobacter</i> sp. B9-2 | 231 | 98% | 6.00E ⁻⁷³ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Marinobacter</i> sp. NP-4 (2019) | 229 | 98% | 7.00E ⁻⁷² |
| SDR family NAD(P)-dependent oxidoreductase | <i>Persicimonas caeni</i> | 228 | 98% | 2.00E ⁻⁷¹ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Persicimonas caeni</i> | 228 | 98% | 2.00E ⁻⁷¹ |
| TPA: SDR family NAD(P)-dependent oxidoreductase | <i>Marinobacter</i> sp. nov. | 227 | 98% | 5.00E ⁻⁷¹ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Marinobacter</i> sp. ELB17 | 226 | 98% | 1.00E ⁻⁷⁰ |
| SDR family NAD(P)-dependent oxidoreductase | <i>Marinobacter</i> sp. BSs20148 | 226 | 98% | 1.00E ⁻⁷⁰ |