Table X. DMSP lyase sequences used in this study as BLAST queries for retrieving homologs in the Organic Lake metagenomes. (%ID) is the minimum amino acid sequence identity threshold applied to matches to that DMSP lyase to be considered homologous.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene (% ID) | Organism | accession | reference |
| *ddd*D (60) | *Marinomonas* sp.MWYL1 | ABR72937.1 | Todd *et al*., 2007 |
|  | *Pseudomonas* sp.J465 | ACY01992.1 | Curson *et al.*, 2010 |
|  | *Psychrobacter* sp.J466 | ACY02894.1 | Curson *et al*., 2010 |
|  | *Halomonas* sp. HTNK1 | ACV84065.1 | Todd *et al*., 2010 |
| *ddd*L (45) | *Sulfitobacter* sp. EE36 | ADK55772.1 |  |
|  | *Rhodobacter sphaeroides* 2.4.1 | ABA77574.1 |  |
| *ddd*P (45) | *Roseovarius nubinhibens* ISM | EAP77700.1 |  |
| *ddd*Q | Ruegeria pomeroyi DSS-3 | AAV94883.1 |  |
|  | Roseovarius nubinhibens ISM | EAP76001.1,  EAP76002.1 |  |
|  | marine metagenome | GOS\_7860946 |  |
|  | marine metagenome | GOS\_2632696 |  |
|  | marine metagenome | GOS\_2469775 |  |
| *ddd*W | *Ruegeria pomeroyi* DSS-3 | AAV93771.1 |  |
| *ddd*Y | *Alcaligenes faecalis* | ADT64689.1 |  |