|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Taxa Group** | **mean µg C cell-1** | **Total Cpm, Initial samples** | **Biomass IR total, µg C c-1 d-1** | **Mean CR, ml c-1 d-1** |
| CenDiaLg | 1.15 | 459 | 2.93 | 43.28 |
| CenDiaSm | 0.04 | 1603 | 0.95 | 23.95 |
| ChlLg | 2.59 | 12 | 0.00 | 2.35 |
| ChlSm | 0.04 | 230 | 0.01 | 4.38 |
| ChnDiaLg | 2.06 | 9 | 0.07 | 12.27 |
| ChnDiaSm | 0.06 | 0 | 0.00 | 0.00 |
| CilLg | 5.24 | 119 | 4.08 | 42.30 |
| CilSm | 0.13 | 204 | 0.30 | 31.67 |
| CyanoLg | 0.58 | 66 | -0.25 | 2.81 |
| CyanoSm | 0.13 | 14 | 0.00 | 7.01 |
| DinoLg | 0.55 | 5 | 0.01 | 6.31 |
| FlagLg | 1.10 | 23 | 0.25 | 6.52 |
| FlagSm | 0.08 | 5189 | 0.19 | 8.70 |
| PenDiaLg | 1.45 | 31 | 0.15 | 21.12 |
| PenDiaSm | 0.05 | 268 | 0.02 | 8.67 |
| UnidLg | 4.06 | 25 | -0.08 | -5.25 |
| UnidSm | 0.07 | 1356 | 0.05 | 2.21 |

you can get thrown off by the large, uncommon cells, because they can contribute a lot to biomass ingestion but because of the low numbers the reliability of the data will be low and the replication error will be high.