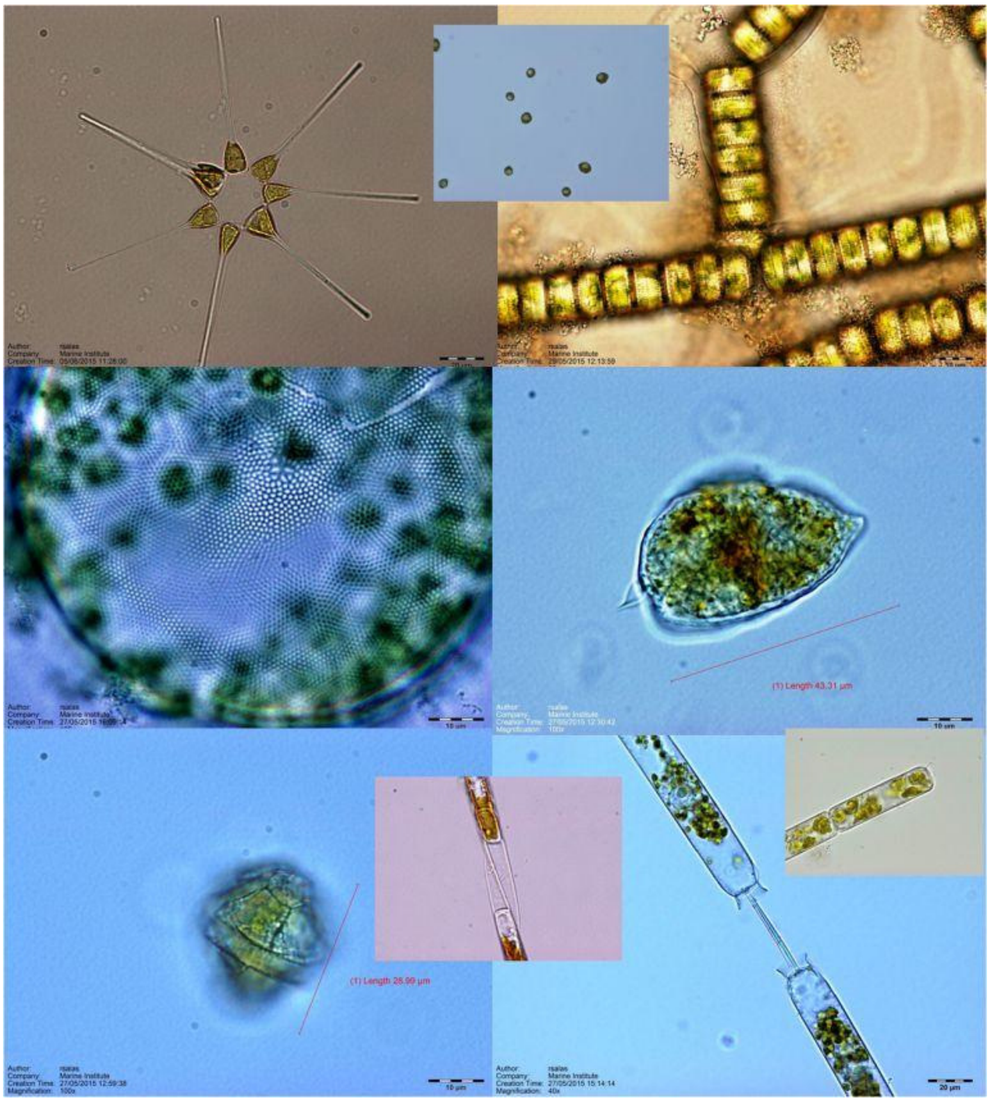
BEQUALM Phytoplankton proficiency test in the abundance and composition of marine microalgae 2015 report.

PHY-ICN-15-MI1 VR 1.0



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1. Summary of results

- 89 analysts from 39 laboratories took part in this intercomparison exercise. 84 analysts returned sample results and 81 completed the online Hab quiz.

- There were 68 participants from laboratories across Europe, 18 from South America, 2 in Australia and 1 in Asia.

- There were nine species of interest in this intercomparison exercise. These were: *Scrippsiella trochoidea* (Stein) Loeblich III, *Prorocentrum micans* Ehrenberg, *Pseudo-nitzschia australis* Frenguelli, *Lingulodinium polyedrum* (F.Stein) J.D.Dodge, *Paralia sulcata* (Ehrenberg) Cleve, *Dytilum brightwellii* (T.West) Grunow, *Guinardia delicatula* (Cleve) Hasle, *Coscinodiscus granii* Gough and *Asterionellopsis glacialis* (Castracane) Round.

- The cell counts of the species *Asterionellopsis glacialis* and *Paralia sulcata* which did not preserve well in the samples were finally not used for statistical purposes.

- The average and confidence limit for each test item was calculated using the robust algorithm in annex C of ISO13528 which takes into account the heterogeneity of the samples and the between samples standard deviation from the homogeneity and stability test. ISO 13528 is only valid for quantitative data. We have used the consensus values from the participants.

- All measurands passed the F-test but not all passed ISO13528.The homogeneity test according to ISO 13528 was passed for 3 of the measurands (*S.trochoidea, P. micans , L. polyedrum*) and failed 4 (*P.australis, D.brightwellii G.delicatula* and *C.granii*). The stability test passed 6 of the 7 measurands but failed *C.granii.*

- The consensus values new Standard deviation (STD) was used for all measurands regardless of the Pass/Fail flags from the homogeneity test.

- The assigned value uncertainties across all measurands for the test are negligible but the comparison with the homogeneity test suggests significant differences for some of the measurands. The relative STD for the measurands seems to be independent of the cell concentration and the frequency distribution is not normal across all measurands.

- Z-scores show a small number of action signals across all measurands. 4 red flags and 18 yellow flags from 588 flags is evidence of good performance overall. 4 analysts did not pass the full test. Below 80% of all scores. There is evidence of poor reproducibility between samples and also evidence of analyst results bias due to the volume of sample analysed.

- The Ocean teacher online HAB quiz results suggests a high rate of proficiency. 77% of analysts achieved a score over 90% (Proficient). Another 21% of analysts above 80% and 2% need improvement.

- There was a reasonably good consensus among analysts on species identification on questions Q1-Q4. However, analysts found it difficult to give an answer to genus level Even though answers were not used for the final mark.

- There were no real problems with numerical questions (Q5-Q11). 98.72% answered within the model answer given. ±1 cell tolerance was allowed in some answers. There are small differences caused by interpretation of what a viable cell is; Q5 an empty theca was counted. In Q11 opinion was divided: a cell only half visible on one side of the image gave a 70:30 counted in:out ratio. There is consensus among analysts on approach to enumeration, but small differences can mean large differences overall in sample cell counts.

- Questions 12 to 16 were 'short answer' type questions using videos for the identification of species. Some spelling mistakes and not following instructions properly meant some analysts lost marks here. Q16 caused technical problems to some analysts. Q16 also turned out to be the most difficult question in the quiz: identified correctly by 60% only. 30% identified incorrectly, 10% was not able to answer it.

- The questions Q17-18 on the taxonomical characters of *Pseudo-nitzschia* found that only 81% knows the difference between valve view and girdle view of these species when shown in an image. 7-8% confuses the stria and the interstria in *Pseudo-nitzschia*.

- The questions Q19-20 on the taxonomical characters of *Protoperidinium* showed that there are no problems with kofoidean tabulation of armoured dinoflagellates with mostly near perfect scores. All *Protoperidinium* marks were over 90%.

- Q21 to Q27 on *Protoperidinium* species identification were answered well. In Q21 *P.depressum* was easy to identify because of its distinctive large size. Q22 *P.conicum* differs from *P.leonis* on typical 'V' shape and spines, they can be confused as both are ortho-hexa. Q23 *P.divergens* caused most problems. This is confused with *P.crassipes* (13%) as both are meta-quadra, but diverging horns and horns in *P.crassipes* differ. Q24 *P.leonis* as above. Q25 & 27 are very distinctive if unusual *Protoperidinium* species. Q26 *P.pentagonum* another ortho-hexa like *P.leonis* and *P.conicum* but with a really wide sulcal area between horns.

2. Introduction

The Phytoplankton Bequalm intercomparison study in 2015 was designed to test the ability of analysts to identify and enumerate correctly marine phytoplankton species in lugol's preserved water samples. As in previous years, samples have been spiked using laboratory cultures. There were nine species of interest in this intercomparison exercise. These were: *Scrippsiella trochoidea* (Stein) Loeblich III, *Prorocentrum micans* Ehrenberg, *Pseudo-nitzschia australis* Frenguelli, *Lingulodinium polyedrum* (F.Stein) J.D.Dodge, *Paralia sulcata* (Ehrenberg) Cleve, *Dytilum brightwellii* (T.West) Grunow, *Guinardia delicatula* (Cleve) Hasle, *Coscinodiscus granii* Gough and *Asterionellopsis glacialis* (Castracane) Round.

Collaboration between the Marine Institute in Ireland and the IOC UNESCO Centre for Science and Communication of Harmful algae in Denmark on the Bequalm intercomparison exercise commenced in 2011. This collaboration involves the use of algal cultures from the Scandinavian Culture Collection of Algae and Protozoa in Copenhagen, cultures isolated from field samples and from the Marine Institute culture collection. This collaboration also includes the elaboration of a marine phytoplankton taxonomy quiz using an online platform called 'Ocean Teacher'. This online HAB quiz was designed by Jacob Larsen (IOC) and Rafael Salas (MI).

This year, 89 analysts from 49 laboratories took part in this intercomparison exercise. 84 analysts returned sample results and 81 completed the online Hab quiz. There were 68 participants from laboratories across Europe, 18 from South America, 2 in Australia and 1 in Asia. The list of participating laboratories can be found in Annex V and a breakdown of participation from each country in figure 1 below.

This intercomparison exercise has been coded in accordance with defined protocols in the Marine Institute, for the purposes of quality traceability and auditing. The code assigned to the current study is PHY-ICN-15-MI1. PHY standing for phytoplankton, ICN for intercomparison, 15 refers to the year 2015, MI refers to the Marine Institute and 1 is a sequential number of intercomparisons for the year. So, 1 indicates the first intercomparison for the year 2015.

Also, as part of this intercomparison exercise, a training workshop is held annually to discuss the results of the intercomparison exercise and to provide training in some areas of interest on phytoplankton taxonomy to the participants. This workshop has been held in various places over the years and it has taken the format of a 3 days training workshop with at least 2 days dedicated to lectures on algal groups in rooms equipped with microscopes and using live cultures (see workshop agenda: Annex IV).

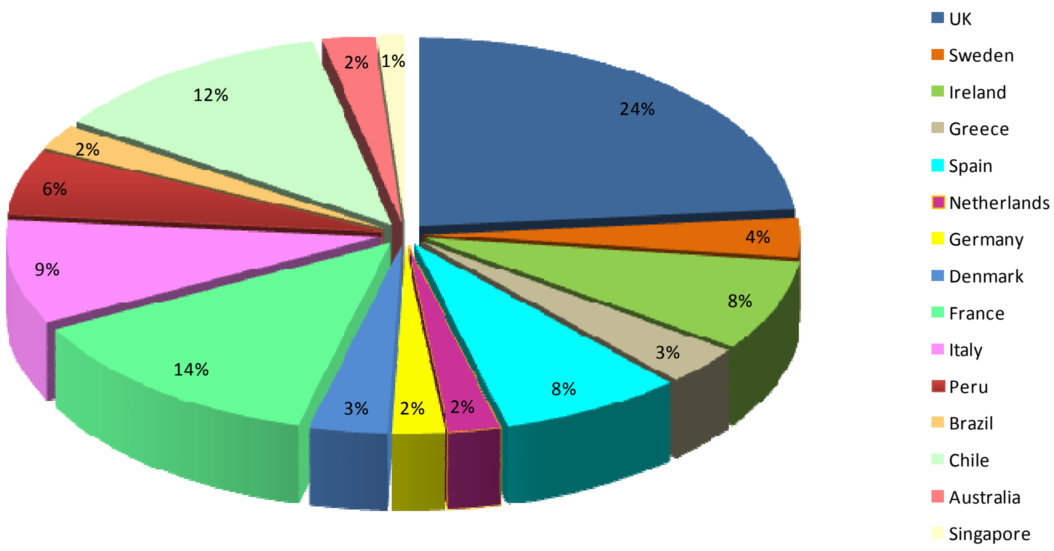

Figure 1: Breakdown participation per country of the Phytoplankton intercomparison exercise Bequalm 2015

This workshop has become an important forum for scientists working on phytoplankton monitoring programmes from around the world to convene and be able to discuss taxonomical matters related to monitoring, new advances and finds, taxonomical nomenclature changes, looking at samples from different geographical areas and listen to relevant stories from other laboratories about issues with harmful algal events in their regions of relevant ecological importance.

3. Materials and Methods

3.1 Sample preparation, homogenization and spiking

All samples were prepared following this protocol: The seawater used in this experiment was natural field water collected at Ballyvaughan pier, Galway bay, Ireland, filtered through 47mm GF/C Whatmann filters (Whatmann™, Kent, UK), autoclaved (Systec V100, Wettenberg , Germany) and preserved using Lugol's iodine solution (Clin-tech, Dublin, Ireland). The centrifuge tubes were made up to the required volume with sterile filtered seawater containing neutral lugol's iodine. This was carried out using 25ml serological pipettes (Sardstedt, Nümbrech, Germany) and the volume weighted in a calibrated balance (ME414S Sartorius, AG Gottingen, Germany). The density of seawater was considered for this purpose to be 1.025g/ml. The final volume of each sample was 45 ml approximately before spiking the samples.

A stock solution for each of the nine species was prepared using 50ml glass screw top bottles (Duran®, Mainz, Germany). Then, a working stock containing the nine species to the required cell concentration was prepared using a measured aliquot from each stock solution into a 2l Schott glass bottle. Then, each working stock was inverted 100 times to homogenate the samples and 5ml aliquots were pipetted out after each 100 times inversion using a calibrated 5ml pipette (Gilson, Middleton, USA) with 1-10ml pipette tips (Eppendorf, Cambridge, UK). The 5ml aliquots were dispensed into the 50ml centrifuge tubes (Sardstedt, Nümbrech, Germany) containing 45ml.

Samples were capped and labeled. Parafilm was used around the neck of the centrifuge tube to avoid water loss through evaporation or leaking, placed in padded envelopes and couriered via TNT or DHL couriers for a one day delivery across the world, in order for all the laboratories to have approximately the same arrival time.

3.2 Culture material, treatments and replicates.

The laboratory cultures used in this exercise were collected in Galway bay, Bantry bay and Carlingford Lough during the months of February and May 2015. All the cultures were isolated using the micro-pipette technique as unialgal cultures. Most species were identified through light microscopy techniques using an inverted microscope Olympus IX-51 except for *Pseudo-nitzschia australis* which was confirmed to species level using qPCR species specific gene probes.

A total of 500 samples were produced for the enumeration and identification study. Each participant was sent a set of four samples, three for analysis and one spare sample that is a total of 356 samples to 39 laboratories. Another 15 samples were sent to an expert laboratory to carry out the homogeneity and stability test. The data generated by this laboratory was used to test the homogeneity and stability of the samples. A minimum of 10 samples (50ml volume) were necessary for the homogeneity test and a minimum of 3 samples for the stability test. Samples had to be divided in two portions of 25ml each.

A time delay between the homogeneity test and the stability test is required. ISO 13528 indicates that this delay should be similar to that experienced by the participants in the test. As analysts have a month to return results from sample receipt, it was decided that this time delayed should be of one month as well.

3.3 Cell concentrations

Preliminary cell counts from the original stock solutions were made to establish the cell concentration of each species and this was carried out using a glass Sedgewick-Rafter cell counting chamber (Pyser-SGI, Kent, UK) to ascertain an approximation of the cell concentration of each species in the samples.

Generally cell concentrations were low to medium and ranging from concentrations of 2000 cells/Litre for *C.granii*, 4000 cells/L for *P.australis*, 5000 cells/L for *D.brightwellii,* 7500cells/L for *L.polyedrum,* 10000 cells/L for *G.delicatula* and 15000 cells/L for *P.micans* and 30000 cells/L for *Scrippsiella.*

3.4 Sample randomization

All samples were allocated randomly to the participants using Minitab® Statistical Software Vr16.0 randomization tool.

3.5 Forms and instructions

A set of instructions and forms required were sent via e-mail to all the analysts to complete the exercise including their unique identifiable laboratory and analyst code. Form 1 (Annex I) to confirm the receipt of materials; number and condition of samples and correct sample code. Form 2 (Annex II) in an Excel spreadsheet format to input species composition and calculate abundance for each species. Form 2 was used for the identification and enumeration part of the exercise. All analysts were asked to read and follow the instructions (Annex III) before commencing the test.

At the end of the exercise and with the publication of this report, analysts will be issued with a statement of performance certificate (See Annex VI) which is tailored specifically for each test. This is an important document for auditing purposes and ongoing competency.

3.6 Statistical analysis

Statistical analysis was carried out using PROlab Plus version 2.14, dedicated software for the statistical analysis of intercalibration and proficiency testing exercises from Quodata, Minitab® Statistical Software Vr16.0 and Microsoft office Excel 2007.

We followed the standard ISO normative 13528 which describes the statistical methods to be used in proficiency testing by interlaboratory comparisons. Here, we use this standard to determine and assess the homogeneity and stability of the samples, what to do with outliers, determining assigned values and calculating their standard uncertainty. Comparing these values with their standard uncertainty and calculating the performance statistics for the test through graphical representation and the combination of performance scores.

The statistical analysis of the data and final scores generated from this exercise has been carried out using the consensus values from the participants. The main difference with previous years is that by using ISO13528, the consensus values from the participants must undergo several transformations before they can be used to generate Z-scores.

The main transformation is the use of iteration to arrive at robust averages and standard deviations for each test item. This process allows for outliers and missing values to be dealt with, and it also allows for the heterogeneity of the samples to be taken into consideration when calculating these values.

3.7 Bequalm online HAB quiz

The online HAB quiz was organized and set up by Jacob Larsen (IOC UNESCO, Centre for Science and Communication on Harmful Algae, Denmark) and Rafael Salas (Marine Institute, Ireland). The exercise was prepared in the web platform 'Ocean teacher'. The Ocean teacher training facility is run by the IODE (International Oceanographic Data and information Exchange) office based in Oostende, Belgium. The IODE and IOC organize some collaborative activities among them, the IOC training courses on toxic algae and the Bequalm online HAB quiz. The online quiz uses the open source software Moodle Vr2.0 (https://moodle.org).

First time participants had to register in the following web address: http://classroom.oceanteacher.org/ before allowed to access the quiz content, while analysts already registered from previous years, could go directly to the login page. Once registered, participants could login into the site and using a password, able to access the quiz. Twelve weeks were given to analysts to register, complete and submit the online quiz. The course itself was found under the courses tab in the main menu page. Analysts could link to the Harmful Algal Bloom programme BEQUALM 2015 and quiz content from here.

The test itself consisted of 27 questions (see Annex XVI). There were different question types used in this quiz; Eassy type Q1-4, Numerical Q5-11, Short answer videos Q12-16, Matching Q17-20 and Multiple choice Q21-27. In essay type questions analysts can write their answers and any comments in the box provided, matching questions have dropdown menus including an array of answers which analysts must choose from, numerical questions need numerical values as answers and in short answer type questions analysts must match the correct answer given by the organizers in terms of the correct identification and also must be grammatically sound. All questions have equal value and the quiz have a maximum grade of 100% for a perfect score.

The online quiz can only be submitted once. After that, no changes can be made. However, analysts can login and out as many times as they wish throughout the period of time allocated and changes to the quiz can be saved and accessed at a later stage, so the quiz doesn't have to be completed in one sitting.

4. Results

4.1 Homogeneity and stability study

The procedure for a homogeneity and stability test is recorded in annex b (pg 60) of ISO13528. The assessment criteria for suitability, is also explained here. See Annex VII to see all the results from the homogeneity and stability test for each measurand.

The calculations have been carried out using ProLab Plus version 2.14 and the reports for homogeneity and stability are given separately for each measurand. The top of the report gives you information on the measurand, mean and analytical standard deviation for the homogeneity analysis and the homogeneity and stability mean comparison in the stability analysis. The reports also show the target standard deviation for each measurand which in this case was calculated manually using the consensus results of the participants and taking into consideration the heterogeneity of the samples as will be explained later.

The middle part of the report gives you the results of the different tests. ProLab Plus calculates whether the data has passed the criteria for the F-test, ISO13528 and the harmonized protocol. The bottom part of the report is the actual graphical representation of the sample results as box plots. The homogeneity test shows the 10 samples analysed for this test and calculates the heterogeneity standard deviation (SD between samples) and the analytical standard deviation (SD within samples). The stability test graph show the 10 samples of the homogeneity test plus the 3 samples of the stability test, thirteen in total and compare their mean values. This is done for each measurand.

ISO13528	F-test	Homogeneity test ISO 13528	Homogeneity Harmonized protocol	Stability test 13528	Stability harmonized protocol
Scrippsiella trochoidea	Pass	Pass	Pass	Pass	Pass
Prorocentrum micans	Pass	Pass	Pass	Pass	Pass
Pseudo-nitzschia australis	Pass	Fail	Fail	Pass	Pass
Lingulodinium polyedrum	Pass	Pass	Fail	Pass	Pass
Dytilum brightwellii	Pass	Fail	Pass	Pass	Pass
Coscinodiscus granii	Pass	Fail	Fail	Fail	Pass
Guinardia delicatula	Pass	Fail	Fail	Pass	Pass

Table 1: Homogeneity and stability pass/fail test

Table 1 above shows the pass/fail flag for each measurand. All measurands passed the F-test but not all passed ISO13528 or the Harmonised protocol. The homogeneity test according to ISO 13528 was passed for 3 of the measurands (S.trochoidea, P. micans , L. polyedrum) and failed 4 (P.australis, D.brightwellii G.delicatula and C.granii). The stability test passed 6 of the 7 measurands but failed C.granii. All measurands passed the stability test according to the harmonized protocol.

According to ISO13528, if the homogeneity test fails, the heterogeneity standard deviation has to be taken into account when calculating the standard deviation for the measurand. The consensus values new heterogeneity standard deviation (STD) was used for all measurands regardless of the Pass/Fail on the homogeneity test.

4.2 Outliers and missing values

Outliers in the data have been addressed by using the robust analysis as set out in Annex C algorithm A + S of ISO 13528. The robust estimates for this exercise have been derived by iterative calculation, that is, by convergence of the modified data (Annex IX) for each measurand.

In relation to missing values, the standard proposes that participants must report 0.59 n replicate measurements, so in the case of three replicates, at least two replicate results from each measurand must be obtained from each participant for the data to be included in the statistical calculations. If this rule is not fulfilled results from these participants won't be included in the calculation of statistics that affect other laboratories but they may be used for the calculation of their own.

4.3 Analysts' Data

The results of the participants were collated using Excel spreadsheets. 84 analysts from 49 laboratories returned results for this exercise. There were nine measurands in the samples: *Scrippsiella trochoidea* (Stein) Loeblich III, *Prorocentrum micans* Ehrenberg, *Pseudo-nitzschia australis* Frenguelli, *Lingulodinium polyedrum* (F.Stein) J.D.Dodge, *Paralia sulcata* (Ehrenberg) Cleve, *Dytilum brightwellii* (T.West) Grunow, *Guinardia delicatula* (Cleve) Hasle, *Coscinodiscus granii* Gough and *Asterionellopsis glacialis* (Castracane) Round.

The table of results from all participants can be found in Annex VIII at the end of this report. The average of the participant replicate results for each measurand were used to calculate the robust averages and standard deviations first by iteration, which then were used to calculate the confidence limits for the Z-scores (See Annex X).

For the purpose of this exercise we have used the consensus standard deviation from the participants and we have calculated the new standard deviation for each test item by adding the between samples standard deviation from the homogeneity test according to the formula below (A) from ISO13528.

$$\sigma_{r1} = \sqrt{\sigma_r^2 + s_s^2}$$

(A)

Where;

σ_{r1} =the new SD for the homogeneity test

σ_r =between samples Standard deviation and

Ss= the robust standard deviation for the test

Table 2 below show the results which are used to generate the confidence limits of this test for each measurand. These values are calculated using the robust analysis using algorithm A +S from annex C of the standard ISO13528. The calculations are generated by iteration and can be found for each measurand in this report in annex IX.

Species	Scrippsiella trochoidea	Prorocentrum micans	Pseudo-nitzschia australis	Lingulodinium polyedrum	Dytilum brightwellii	Coscinodiscus granii	Guinardia delicatula
SD	7146	2914	735	1229	981	209	1826
new SD	7208	2940	1161	1284	1105	252	2035

Table 2: Standard deviations for each measurand based on consensus values (SD) and consensus values plus the between sample standard deviation (new SD) calculated using Excel.

The new standard deviation (new SD) will be used to set the 2 and 3 sigma limits of the robust averages for each test item.

4.4 Assigned value and its standard uncertainty

The assigned values (robust mean and standard deviation) for a test material is calculated as explained before using algorithm A in annex C from the consensus values of the participants (Annex IX). The standard uncertainty of the assigned value can then be calculated using the equation (B) below;

$$u_X = 1{,}25 \times s^* / \sqrt{p}$$

B)

Where;

u_x= Standard uncertainty of the assigned value,

s^*= robust standard deviation for the test

p= number of analysts

	Scrippsiella	P.micans	P. asutralis	L.polyedrum	D.brightwellii	C.granii	G.delicatula	
Robust mean x*	18102	12770	2494	6440	2473	1640	5173	
Robust Stdev s*	7146	2914	735	1229	981	209	1826	
Standard Ux	975	397	100	169	134	29	249	
n=	84	84	84	83	84	84	84	
if Ux < 0.3xSTdev	2144	874	221	369	294	63	548	
then Ux is negligible	neg	neg	neg	neg	neg	neg	neg	
The equation is satisfied in all cases								

Table 3: Assigned values and standard uncertainties for the test.

If *Ux* is less than 0.3 times the standard deviation for the test, then this uncertainty is negligible for the test material. In our case, all our test materials satisfy the equation (Table 3).

4.5 Comparison of the assigned value

When the consensus values from the participants are used to calculate the standard uncertainty of the assigned values, the values can then be compared against a reference value from an expert laboratory. As we don't have a reference value as such, we used the homogeneity test results to compare these values against the values calculated by the participants using equation (C) below:

$$\sqrt{\frac{(1,25s^*)^2}{p} + u_X{}^2}$$

C)

Where;

u_x= Standard uncertainty of the assigned value,

s^*= robust standard deviation for the test

p= number of analysts

	Scrippsiella	P.micans	P. asutralis	L.polyedrum	D.brightwellii	C.granii	G.delicatula
Robust mean x*	18102	12770	2494	6440	2473	1640	5173
Robust Stdev s*	7146	2914	735	1229	981	209	1826
Standard Ux	975	397	100	169	134	29	249
n=	84	84	84	83	84	84	84
if Ux < 0.3xSTdev	2144	874	221	369	294	63	548
then Ux is negligible	neg	neg	neg	neg	neg	neg	neg
The equation is satisfied in all cases							
Cumulative distribution function cut off points for normal distribution							
*x *-1.5s**	7383	8399	1392	4597	1002	1327	2434
*x *+1.5s**	28821	17141	3597	8284	3945	1954	7912
Homogeneity test	Scrippsiella	P.micans	P. asutralis	L.polyedrum	D.brightwellii	C.granii	G.delicatula
Reference value mean	32133	15726	3980	7524	5342	1804	10038
Reference value stdev	1246	614	1150	709	632	253	1240
	Comparison with assigned value						
	Scrippsiella	P.micans	P. asutralis	L.polyedrum	D.brightwellii	C.granii	G.delicatula
*x *-X*	14031	2956	1486	1084	2869	164	4865
Uncertainty of diff.	1378	562	142	238	189	40	352
2* Uncertainty of diff.	2757	1124	284	477	378	81	704
If diff. Is more than twice its Uncertainty then rule is not satisfied							

Table 4: Comparison of the assigned value.

ISO13528 says that if the difference between the consensus values and the reference values (homogeneity test values in our case) is more than twice its uncertainty, then possible reasons need to be sought regarding bias. In our comparison, none of the cell counts satisfy the equation (Table 4).

4.6 Calculation of performance statistics

The performance statistics for the exercise have been calculated using ProLab Plus software version 2.14. The summary table of all the Z-scores can be found in Annex X of this report. The summary of laboratory means and statistical parameters (Annex XI) show the results by measurand and analyst of all the results for the test including the Z-scores and outliers, the statistical method used for the data (Q Huber), means and standard deviations, measures of repeatability and reproducibility for each measurand, number of participants and other relevant information on the test. The graphical summary for each measurand by analyst can be found in Annex XII of this report.

4.6.1 Z-scores

The z-scores derived using the robust averages and standard deviations can be found in annex X. Any results in blue are within the specification of the test (2SD). The yellow triangles indicate warning signals and red triangles indicate action signals.

There were eighteen warning (yellow) and four action (red) signals. The four red signals correspond to analysts 11 and 8 for *L.polyedrum* cell counts and analysts 6 and 75 for *C.granii* cell counts. The warning signals correspond to analyst 22 for *C.granii* cell counts, analysts 20, 33, 45, 68 and 79 on *S.trochoidea* counts, analyst 42 on *P.australis* counts, analysts 20, 26, 32, 4, 53, 6 and 67 on *L.polyedrum* cell counts, analysts 8, 54 and 32 on *P.micans* counts and analyst 60 on *G.delicatula* counts.

Overall, all analysts passed the test except for four analysts which failed two counts out of seven each and are below the 80% of results necessary to pass the test. Analysts 20 and 32 have two warning signals each and analysts 6 and 8 have one action and one warning signal each. This has to be seen within the contest of performance over several rounds, while improvement is necessary it is also important to remark that these four analysts were participating in the scheme for the first time.

4.7 Combined performance scores

Mandel's h and k statistic present measures for graphically surveying the consistency of the data for all measurands in the test (Annex XIII). Mandel's h statistics determines the differences between the mean values of all the laboratories and measurand combinations and it may point out at particular patterns for specific laboratories. In this graph, laboratories may have positive or negative values. Laboratories with large all-positive values or all-negative values for all measurands may indicate laboratory bias.
The k statistics only produce positive results, zero is the baseline and it looks at repeatability precision between measurands. Generally analysts with larger values tend to have poorer repeatability precision between replicates than the consensus mean values.

4.7.1 Relative Laboratory Performance (RLP) and Rescaled Sum of Z-scores (RSZ)

The chart of RLP against RSZ (Annex XIV) for all measurands combined shows systematic laboratory bias. Laboratories dotted within the green colored area in the graph are within the consensus values shown by the analysts. Those outside it are showing a systematic bias towards over or under-estimating their counts in the samples, suggesting some kind of methodology bias.

4.7.2 Plots of repeatability standard deviation

The plots of repeatability standard deviations are used to identify analysts whose average and standard deviations are unusual from the consensus. They assume that the data is normally distributed and the null hypothesis is that there are no differences between the analyst means and standard deviations using the van Nuland circle technique (Annex XV) for each measurand. The graphs show poor repeatability for the

Scrippsiella cell counts. There is good correlation however in all the other measurand counts for most analysts.

4.8 Qualitative data

Table 5 below shows what species did analysts identified in the samples. Analysts were asked to give their answers to species level but for the purpose of the exercise and final marks, it was only necessary an answer to genus level. However, by allowing the participants to identify the measurands to species level we obtain more information on decision making by analysts on identification and whether there are particular patterns of thinking or teaching between laboratories in different geographical areas.

The dinoflagellates were identified correctly by most analysts. *L.polyedrum* (96%) was the only organism not identified by an analyst and mis-identified as *Protoceratium reticulatum* by two others. *Prorocentrum (99%)* and *Scrippsiella (96%)* were identified correctly by most analysts. 3 analysts identified *Pentapharsodinium* instead of *Scrippsiella* and these results are given as correct here. There are not real differences between *Scrippsiella, Pentapharsodiniun* and *Ensiculifera* genera at the light microscopy level and therefore it is impossible to tell them apart unless scanning electron microscopy or other tools are used to identify these closely related species. The reason most analysts used *Scrippsiella* here is that it is the better known of the three genera. *Prorocentrum* was identified correctly to genus by all analysts although one analyst did incorrectly identify the wrong species.

The diatoms were also identified fine by the analysts. Perhaps the hardest to identify to genus was *Coscinodiscus (96%)* which was identified as *Actynocyclus* by 2 analysts. *Ditylum (100%)* returned perfect scores to species level, The synonym R*hizosolenia* was used by 5 analyst on the identification of *Guinardia,* 87% to species level and *Pseudo-nitzschia (100%)* was correctly identified by all to genus level. Most analysts 67% did not go further with their identification and left it as *P.seriata* complex but those that did, reckoned it was either *P.australis (14%)* or *P.seriata (14%).* The right answer was *P.australis* based on rdna sequence data and qPCR species specific probes assay, but both these two species are quite similar, so analysts were really close to the correct species identification of the species based only in light microscopy observation.

Species id	Number	%	Species id	Number	%
Scrippsiella trochoidea	43	51	Prorocentrum micans	83	99
Scrippsiella sp.	38	45	Prorocentrum lima	1	1
Pentapharsodinium sp.	1	1			
Pentapharsodinium daleii	2	2			
Species id	**Number**	**%**	**Species id**	**Number**	**%**
P.seriata complex	56	67	L.polyedrum	81	96
P.australis	12	14	P.reticulatum	2	2
P.seriata	12	14	Not identified	1	1
P.pungens	3	4			
P.multiseries	1	1			
Species id	**Number**	**%**	**Species id**	**Number**	**%**
C.granii	80	95	D.brightwellii	84	100
C.wailesii	1	1			
Actynocyclus sp.	2	2			
C. Concinnus	1	1			
			Species id	**Number**	**%**
			G.delicatula	68	81
			Guinardia sp.	11	13
			Rhizosolenia delicatula	5	6

Table 5: Qualitative data by measurand

4.9 Ocean Teacher online HAB quiz

The online HAB quiz consisted of 27 questions; annex XVI shows the questions and right answers for the online HAB quiz and annex XVII show the final grades. 81 of the 89 analysts submitted this quiz but not all the analysts responded to all the questions. Questions 1 to 4 were essay type questions and no marks were given for these as there is no right answer to them. These questions were 4 sets of 3 images per set per question. Each image showed an organism regularly found in water samples and we asked analysts to identify to genus level only based on the image. Each image had a scale bar for each photograph to aid the identification. Here, we were looking for some sort of consensus answers based on not enough information. Tables 6 show the actual response given to questions 1 to 4 by analysts the count of analysts that gave that particular answer and the frequency as a percentage of that answer.

Q1	Actual response	Count	Frequency (%)
1.1	Helicostomella	47	57.3
	Tintinnid	10	12.2
	Parundella	7	8.5
	Parafavella/favella	5	6.1
	Rhabdonella	3	3.7
	Amphora/amphorella	3	3.7
	Rhizosolenia	2	2.4
	Dinobryon	2	2.4
	Ciliate	1	1.2
	Salpingella	1	1.2
	Xystonella	1	1.2
		82	**100.0**
1.2	Navicula/Lyrella/Fallacia	68	89.5
	Amphora	3	3.9
	Diploneis	3	3.9
	Delphineis	1	1.3
	Bacillariales	1	1.3
		76	**100.0**
1.3	Guinardia	60	75.0
	Leptocylindrus	12	15.0
	Pseudo-guinardia	4	5.0
	Cerataulina	2	2.5
	dactiliosolen	2	2.5
		80	**100.0**
Q2	**Actual response**	**Count**	**Frequency (%)**
2.1	Alexandrium	65	82.3
	Gonyaulax	5	6.3
	Heterocapsa	2	2.5
	Lingulodinium	2	2.5
	Peridinium	1	1.3
	Gymnodinium	1	1.3
	Protoperidinium	1	1.3
	Scrippsiella	1	1.3
	Dino thecate	1	1.3
		79	**100**
2.2	Navicula	78	97.5
	Bacillariales	1	1.3
	Mastogloia	1	1.3
		80	100
2.3	Gonyaulax	2	66.7
	Protoperidinium	1	33.3
		3	**100**

Q3	Actual response	Count	Frequency (%)
3.1	Protoperidinium	**80**	**80**
			100
3.2	Detonula	62	77.5
	Lauderia	10	12.5
	Thalassiosira	6	7.5
	Melosira	1	1.3
	Lithodesmium	1	1.3
		80	**100**
3.3	Protoperidinium	78	98.7
	Gonyaulax	1	1.3
		79	**100**
Q4	**Actual response**	**Count**	**Frequency (%)**
4.1	Rhabdonema	45	55.6
	Striatella	24	29.6
	Fragillaria	10	12.3
	Fragillariopsis	1	1.2
	Tabellaria	1	1.2
		81	**100**
4.2	Navicula	34	43.6
	Pinnularia	12	15.4
	Entomoneis	6	7.7
	Trachyneis	6	7.7
	Plagiotropis	6	7.7
	Nitzschia	3	3.8
	Amphora	3	3.8
	Diploneis	3	3.8
	Amphiprora	2	2.6
	Tropidoneis	1	1.3
	Scoliotropis	1	1.3
	Thalassiosira	1	1.3
		78	**100**
4.3	Tintinnopsis	46	56.8
	Tintinnid	15	18.5
	Favella	8	9.9
	Parafavella	2	2.5
	Acanthostomella	2	2.5
	Syracosphaera	1	1.2
	Stenosomella	1	1.2
	Epiplocylis	1	1.2
	Coxliella	1	1.2
	ciliate	1	1.2
	Rhizosolenia	1	1.2
	Undella	1	1.2
	Epiplocilys	1	1.2
		81	**100**

Table 6: Questions 1-4 answers

Questions 5 to 11 (Table 7) were all numerical questions. Analysts were presented with images of different organisms and they were asked to count the number of cells depicted in the images. A model response was built into the answer by the organizers and expected the consensus answer to be similar. A tolerance of + or – 1 cell was also built in around the model response for some of the questions. Only 8 answers in total on the 7 questions were answered outside the specified parameters.

Q5	Model response	Actual response	Partial credit	Count	Frequency
	2 (2..2)	2	100.00%	76	93.83%
	[Did not match any answer]	1	0.00%	3	3.70%
	[Did not match any answer]	3	0.00%	2	2.47%
	[No response]		0.00%	0	0.00%
Q6	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	26 (25..27)	25	100.00%	4	4.94%
	26 (25..27)	26	100.00%	76	93.83%
	[Did not match any answer]	16	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q7	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	8 (7..9)	7	100.00%	1	1.23%
	8 (7..9)	8	100.00%	80	98.77%
	[Did not match any answer]		0.00%	0	0.00%
	[No response]		0.00%	0	0.00%
Q8	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	5 (5..5)	5	100.00%	79	97.53%
	[Did not match any answer]	4	0.00%	1	1.23%
	[Did not match any answer]	6	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q9	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	29 (28..30)	29	100.00%	81	100.00%
	[Did not match any answer]		0.00%	0	0.00%
	[No response]		0.00%	0	0.00%
Q10	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	4 (4..4)	4	100.00%	81	100.00%
	[Did not match any answer]		0.00%	0	0.00%
	[No response]		0.00%	0	0.00%
Q11	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	9 (8..10)	8,5	100.00%	1	1.23%
	9 (8..10)	8	100.00%	25	30.86%
	9 (8..10)	9	100.00%	55	67.90%
	[Did not match any answer]		0.00%	0	0.00%
	[No response]		0.00%	0	0.00%

Table 7: QuestionS 5-11 model response table.

Q12	Model response	Actual response	Partial credit	Count	Frequency
	Dinophysis	Dinophysis	100.00%	75	92.59%
	[Did not match any answer]	Dinophysis acuta	0.00%	3	3.70%
	Dinophysis	DInophysis	100.00%	1	1.23%
	[Did not match any answer]	Amylax	0.00%	1	1.23%
	[Did not match any answer]	Dinopjysis	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q13	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	Gyrodinium	Gyrodinium	100.00%	77	95.06%
	[Did not match any answer]	Gyrodinium spirale	0.00%	2	2.47%
	[Did not match any answer]	Gymnodinium	0.00%	1	1.23%
	[Did not match any answer]	Eutreptia	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q14	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	Bacillaria	Bacillaria	100.00%	71	87.65%
	[Did not match any answer]	Pseudo-nitzschia	0.00%	3	3.70%
	[Did not match any answer]	Bacillaria paxillifer	0.00%	2	2.47%
	[Did not match any answer]	Bacillaria.	0.00%	1	1.23%
	[Did not match any answer]	Baccilaria	0.00%	1	1.23%
	[Did not match any answer]	Pseudonitzschia	0.00%	1	1.23%
	[Did not match any answer]	Fragilaria	0.00%	1	1.23%
	[Did not match any answer]	Bacteriastrum	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q15	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	Heterosigma	Heterosigma	100.00%	70	86.42%
	[Did not match any answer]	Heterosigma akas	0.00%	2	2.47%
	[Did not match any answer]	Karenia	0.00%	2	2.47%
	[Did not match any answer]	Gymnodinium	0.00%	1	1.23%
	[Did not match any answer]	Rhodomonas	0.00%	1	1.23%
	[Did not match any answer]	Dinophyceae athe	0.00%	1	1.23%
	[Did not match any answer]	Amphidinium	0.00%	1	1.23%
	[Did not match any answer]	Lepidodinium	0.00%	1	1.23%
	[Did not match any answer]	Olisthodiscus	0.00%	1	1.23%
	[Did not match any answer]	Karlodinium	0.00%	1	1.23%
	[No response]		0.00%	0	0.00%
Q16	**Model response**	**Actual response**	**Partial credit**	**Count**	**Frequency**
	Oblea	Oblea	100.00%	27	33.33%
	Diplopsalis	Diplopsalis	100.00%	20	24.69%
	[Did not match any answer]	Protoperidinium	0.00%	13	16.05%
	[Did not match any answer]	Alexandrium	0.00%	12	14.81%
	[Did not match any answer]	Technical problem	0.00%	5	6.15%
	[Did not match any answer]	Alexandrium oster	0.00%	1	1.23%
	[Did not match any answer]	Herdmania	0.00%	1	1.23%
	[Did not match any answer]	Gonyaulax	0.00%	1	1.23%
	[No response]	[No response]	0.00%	1	1.23%

Table 8. Model responses to numerical questions 12-16

Questions 12-16 were short answer type questions and participants were ask to write the genus name of the organism featured in the video clip. In Q12, the video feature a cell of *Dinophysis acuta.* 1 analyst did not identify correctly and 2 others made grammar mistakes and were deducted marks for that reason. The rest answered correctly, although 2 analysts identified to species level which was not what was asked of them. This is important as in this type of questions the answer given by the participant has to fully match the answer built into the software by the organizers.

In Q13, the model answer was *Gyrodinium,* 2 analysts did not identify correctly the organism and 2 went to species level, although the answer was given as correct. In Q14, the model answer was *Bacillaria,* 6 analysts did not identify correctly, 2 went to species level and 1 analyst made a grammar mistake. In Q15, the model answer was *Heterosigma,* 9 analysts did not identify correctly and one went to species level. In Q16, the model answer was *Oblea/Diplopsalis/Diplopsalopsis/Diplopelta* and *Boreadinium* , 28 analysts identify incorrectly this organism even though 5 possible correct answers were given in the model response and 5 analysts had technical problems viewing this particular video.

Question 17 to 20 are matching type questions, Q17 and 18 on *Pseudo-nitzschia* terminology. Table 9 & 10 shows the model responses and actual answers by the participants to these questions. In Q17 (table 9), participants were shown 4 images of the chain diatom forming *Pseudo-nitzschia* and they were asked to tell us which images showed the chains in girdle view and which in valve view. Only 81% gave correct answers to figure 4, the only image showing the species in valve view. In Q18 (table 10), participants were asked to name the different taxonomic features of *Pseudo-nitzschia* valves. Most answers were above the 90% correct mark. The highest error rate was found on the answers to stria and interstria. 7-8% of participants mixed these two answers.

Questions 19 and 20 were terminology matching questions on armoured dinoflagellates. Q19 show a schematic drawing of a peridinioid dinoflagellate typical plate pattern and participants were asked to name the plates series (table 11). The results show that participants have no problems with the kofoidean tabulation of armoured dinoflagellates. In Q20 (table 12), participants were asked to identify the typical descriptive features of Protoperidinium species by naming the shapes of the 1 apical plate and the second anterior intercalary plate where most participants score above the 90% mark.

Q17	Part of question	Model response	Actual response	Partial credit	Count	Frequency
	313	Fig. 1: girdle view or valve view: girdle view	girdle view	25.00%	75	92.59%
	313	Fig. 1: girdle view or valve view: valve view	valve view	0.00%	5	6.17%
	313	[No response]	[No response]	0.00%	1	1.23%
	314	Fig. 2: girdle view or valve view: girdle view	girdle view	25.00%	71	87.65%
	314	Fig. 2: girdle view or valve view: valve view	valve view	0.00%	9	11.11%
	314	[No response]	[No response]	0.00%	1	1.23%
	315	Fig. 3. girdle view or valve view: girdle view	girdle view	25.00%	72	88.89%
	315	Fig. 3. girdle view or valve view: valve view	valve view	0.00%	8	9.88%
	315	[No response]	[No response]	0.00%	1	1.23%
	316	Fig. 4. girdle view or valve view: girdle view	girdle view	0.00%	15	18.52%
	316	Fig. 4. girdle view or valve view: valve view	valve view	25.00%	65	80.25%
	316	[No response]	[No response]	0.00%	1	1.23%

Table 9. Model answers for question 17 on the genus *Pseudo-nitzschia*.

Q18	Part of question	Model response	Actual response	Partial credit	Count	Frequency
	297	Arrow 1 points to: Interstria	Interstria	16.67%	74	91.36%
	297	Arrow 1 points to: Fibula		0.00%	0	0.00%
	297	Arrow 1 points to: Raphe slit		0.00%	0	0.00%
	297	Arrow 1 points to: Stria	Stria	0.00%	6	7.41%
	297	Arrow 1 points to: Poroid		0.00%	0	0.00%
	297	Arrow 1 points to: Central interspace		0.00%	0	0.00%
	297	[No response]	[No response]	0.00%	1	1.23%
	298	Arrow / arrow head 2 points to: Interstria	Interstria	0.00%	2	2.47%
	298	Arrow / arrow head 2 points to: Fibula	Fibula	16.67%	74	91.36%
	298	Arrow / arrow head 2 points to: Raphe slit	Raphe slit	0.00%	2	2.47%
	298	Arrow / arrow head 2 points to: Stria		0.00%	0	0.00%
	298	Arrow / arrow head 2 points to: Poroid		0.00%	0	0.00%
	298	Arrow / arrow head 2 points to: Central interspace	Central interspace	0.00%	2	2.47%
	298	[No response]	[No response]	0.00%	1	1.23%
	299	Arrow / arrow head 3 points to: Interstria		0.00%	0	0.00%
	299	Arrow / arrow head 3 points to: Fibula	Fibula	0.00%	4	4.94%
	299	Arrow / arrow head 3 points to: Raphe slit	Raphe slit	16.67%	73	90.12%
	299	Arrow / arrow head 3 points to: Stria		0.00%	0	0.00%
	299	Arrow / arrow head 3 points to: Poroid	Poroid	0.00%	1	1.23%
	299	Arrow / arrow head 3 points to: Central interspace	Central interspace	0.00%	2	2.47%
	299	[No response]	[No response]	0.00%	1	1.23%
	300	Arrow / arrow head 4 points to: Interstria	Interstria	0.00%	5	6.17%
	300	Arrow / arrow head 4 points to: Fibula	Fibula	0.00%	1	1.23%
	300	Arrow / arrow head 4 points to: Raphe slit	Raphe slit	0.00%	1	1.23%
	300	Arrow / arrow head 4 points to: Stria	Stria	16.67%	73	90.12%
	300	Arrow / arrow head 4 points to: Poroid		0.00%	0	0.00%
	300	Arrow / arrow head 4 points to: Central interspace		0.00%	0	0.00%
	300	[No response]	[No response]	0.00%	1	1.23%
	301	Arrow 5 points to: Interstria		0.00%	0	0.00%
	301	Arrow 5 points to: Fibula		0.00%	0	0.00%
	301	Arrow 5 points to: Raphe slit	Raphe slit	0.00%	1	1.23%
	301	Arrow 5 points to: Stria	Stria	0.00%	1	1.23%
	301	Arrow 5 points to: Poroid	Poroid	16.67%	78	96.30%
	301	Arrow 5 points to: Central interspace		0.00%	0	0.00%
	301	[No response]	[No response]	0.00%	1	1.23%
	302	Arrow head 6 points to: Interstria		0.00%	0	0.00%
	302	Arrow head 6 points to: Fibula	Fibula	0.00%	1	1.23%
	302	Arrow head 6 points to: Raphe slit	Raphe slit	0.00%	3	3.70%
	302	Arrow head 6 points to: Stria		0.00%	0	0.00%
	302	Arrow head 6 points to: Poroid		0.00%	0	0.00%
	302	Arrow head 6 points to: Central interspace	Central interspace	16.67%	76	93.83%
	302	[No response]	[No response]	0.00%	1	1.23%

Table 10. Model responses for question 18 on the genus *Pseudo-nitzschia*.

Q19	Part of question	Model response	Actual response	Partial credit	Count	Frequency
	292	The plates marked 1'-4' indicate: The apical plates	The apical plates	20.00%	77	95.06%
	292	The plates marked 1'-4' indicate: The anterior intercalary plates	The anterior intercalary plates	0.00%	1	1.23%
	292	The plates marked 1'-4' indicate: The precingular plates		0.00%	0	0.00%
	292	The plates marked 1'-4' indicate: The postcingular plates	The postcingular plates	0.00%	2	2.47%
	292	The plates marked 1'-4' indicate: The antapical plates		0.00%	0	0.00%
	292	[No response]	[No response]	0.00%	1	1.23%
	293	The plates marked 1a-3a indicate: The apical plates	The apical plates	0.00%	1	1.23%
	293	The plates marked 1a-3a indicate: The anterior intercalary plates	The anterior intercalary plates	20.00%	78	96.30%
	293	The plates marked 1a-3a indicate: The precingular plates		0.00%	0	0.00%
	293	The plates marked 1a-3a indicate: The postcingular plates		0.00%	0	0.00%
	293	The plates marked 1a-3a indicate: The antapical plates	The antapical plates	0.00%	1	1.23%
	293	[No response]	[No response]	0.00%	1	1.23%
	294	The plates marked 1"-7" indicate: The apical plates	The apical plates	0.00%	1	1.23%
	294	The plates marked 1"-7" indicate: The anterior intercalary plates		0.00%	0	0.00%
	294	The plates marked 1"-7" indicate: The precingular plates	The precingular plates	20.00%	79	97.53%
	294	The plates marked 1"-7" indicate: The postcingular plates		0.00%	0	0.00%
	294	The plates marked 1"-7" indicate: The antapical plates		0.00%	0	0.00%
	294	[No response]	[No response]	0.00%	1	1.23%
	295	The plates marked 1'"-5'" indicate: The apical plates		0.00%	0	0.00%
	295	The plates marked 1'"-5'" indicate: The anterior intercalary plates	The anterior intercalary plates	0.00%	1	1.23%
	295	The plates marked 1'"-5'" indicate: The precingular plates		0.00%	0	0.00%
	295	The plates marked 1'"-5'" indicate: The postcingular plates	The postcingular plates	20.00%	78	96.30%
	295	The plates marked 1'"-5'" indicate: The antapical plates	The antapical plates	0.00%	1	1.23%
	295	[No response]	[No response]	0.00%	1	1.23%
	296	The plates marked 1""-2"" indicate: The apical plates	The apical plates	0.00%	2	2.47%
	296	The plates marked 1""-2"" indicate: The anterior intercalary plates		0.00%	0	0.00%
	296	The plates marked 1""-2"" indicate: The precingular plates	The precingular plates	0.00%	1	1.23%
	296	The plates marked 1""-2"" indicate: The postcingular plates		0.00%	0	0.00%
	296	The plates marked 1""-2"" indicate: The antapical plates	The antapical plates	20.00%	77	95.06%
	296	[No response]	[No response]	0.00%	1	1.23%

Table 11. Model answers for question 19 on *Protoperidinium*

Q20	Part of question	Model response	Actual response	Partial credit	Count	Frequency
	303	Fig.1 shows: 1' ortho configuration	1' ortho configuration	16.67%	79	97.53%
	303	Fig.1 shows: 1' meta configuration		0.00%	0	0.00%
	303	Fig.1 shows: 1' para configuration	1' para configuration	0.00%	1	1.23%
	303	Fig.1 shows: 2a quadra configuration		0.00%	0	0.00%
	303	Fig.1 shows: 2a hexa configuration		0.00%	0	0.00%
	303	Fig.1 shows: 2a penta configuration		0.00%	0	0.00%
	303	[No response]	[No response]	0.00%	1	1.23%
	304	Fig..2 shows: 1' ortho configuration		0.00%	0	0.00%
	304	Fig..2 shows: 1' meta configuration	1' meta configuration	16.67%	78	96.30%
	304	Fig..2 shows: 1' para configuration	1' para configuration	0.00%	1	1.23%
	304	Fig..2 shows: 2a quadra configuration		0.00%	0	0.00%
	304	Fig..2 shows: 2a hexa configuration	2a hexa configuration	0.00%	1	1.23%
	304	Fig..2 shows: 2a penta configuration		0.00%	0	0.00%
	304	[No response]	[No response]	0.00%	1	1.23%
	305	Fig.3 shows: 1' ortho configuration	1' ortho configuration	0.00%	1	1.23%
	305	Fig.3 shows: 1' meta configuration	1' meta configuration	0.00%	1	1.23%
	305	Fig.3 shows: 1' para configuration	1' para configuration	16.67%	78	96.30%
	305	Fig.3 shows: 2a quadra configuration		0.00%	0	0.00%
	305	Fig.3 shows: 2a hexa configuration		0.00%	0	0.00%
	305	Fig.3 shows: 2a penta configuration		0.00%	0	0.00%
	305	[No response]	[No response]	0.00%	1	1.23%
	306	Fig.4 shows: 1' ortho configuration		0.00%	0	0.00%
	306	Fig.4 shows: 1' meta configuration		0.00%	0	0.00%
	306	Fig.4 shows: 1' para configuration		0.00%	0	0.00%
	306	Fig.4 shows: 2a quadra configuration	2a quadra configuration	16.67%	75	92.59%
	306	Fig.4 shows: 2a hexa configuration	2a hexa configuration	0.00%	3	3.70%
	306	Fig.4 shows: 2a penta configuration	2a penta configuration	0.00%	2	2.47%
	306	[No response]	[No response]	0.00%	1	1.23%
	307	Fig.5 shows: 1' ortho configuration		0.00%	0	0.00%
	307	Fig.5 shows: 1' meta configuration		0.00%	0	0.00%
	307	Fig.5 shows: 1' para configuration		0.00%	0	0.00%
	307	Fig.5 shows: 2a quadra configuration	2a quadra configuration	0.00%	2	2.47%
	307	Fig.5 shows: 2a hexa configuration	2a hexa configuration	16.67%	75	92.59%
	307	Fig.5 shows: 2a penta configuration	2a penta configuration	0.00%	3	3.70%
	307	[No response]	[No response]	0.00%	1	1.23%
	308	Fig.6 shows: 1' ortho configuration		0.00%	0	0.00%
	308	Fig.6 shows: 1' meta configuration	1' meta configuration	0.00%	1	1.23%
	308	Fig.6 shows: 1' para configuration		0.00%	0	0.00%
	308	Fig.6 shows: 2a quadra configuration	2a quadra configuration	0.00%	1	1.23%
	308	Fig.6 shows: 2a hexa configuration	2a hexa configuration	0.00%	3	3.70%
	308	Fig.6 shows: 2a penta configuration	2a penta configuration	16.67%	75	92.59%
	308	[No response]	[No response]	0.00%	1	1.23%

Table 12. Model answers for question 20 on *Protoperidinium*

Questions 21 to 27 are multiple choice type questions on the identification of *Protoperidinium* species. Each question showed several light microscopy and calcofluor images of *Protoperidinium* species and participants were asked to choose from a drop-down list of choices the correct one. Table 13 shows the model answer for each question and the count and frequency of answers.

Q21	Model response	Partial credit	Count	Frequency
	Protoperidinium depressum	100.00%	76	93.83%
	Protoperidinium claudicans	0.00%	2	2.47%
	Protoperidinium divergens	0.00%	1	1.23%
	Protoperidinium crassipes	0.00%	1	1.23%
	Protoperidinium conicum	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	Protoperidinium pentagonum	0.00%	0	0.00%
	Protoperidinium leonis	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q24	Model response	Partial credit	Count	Frequency
	Protoperidinium leonis	100.00%	75	92.59%
	Protoperidinium conicum	0.00%	2	2.47%
	Protoperidinium pentagonum	0.00%	2	2.47%
	Protoperidinium claudicans	0.00%	1	1.23%
	Protoperidinium divergens	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium crassipes	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	Protoperidinium depressum	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q22	Model response	Partial credit	Count	Frequency
	Protoperidinium conicum	100.00%	73	90.12%
	Protoperidinium crassipes	0.00%	3	3.70%
	Protoperidinium depressum	0.00%	2	2.47%
	Protoperidinium pentagonum	0.00%	1	1.23%
	Protoperidinium leonis	0.00%	1	1.23%
	Protoperidinium divergens	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	Protoperidinium claudicans	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q25	Model response	Partial credit	Count	Frequency
	Protoperidinium minutum	100.00%	80	98.77%
	Protoperidinium leonis	0.00%	0	0.00%
	Protoperidinium depressum	0.00%	0	0.00%
	Protoperidinium conicum	0.00%	0	0.00%
	Protoperidinium divergens	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium crassipes	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	Protoperidinium pentagonum	0.00%	0	0.00%
	Protoperidinium claudicans	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q23	Model response	Partial credit	Count	Frequency
	Protoperidinium divergens	100.00%	68	83.95%
	Protoperidinium crassipes	0.00%	10	12.35%
	Protoperidinium pentagonum	0.00%	1	1.23%
	Protoperidinium claudicans	0.00%	1	1.23%
	Protoperidinium conicum	0.00%	0	0.00%
	Protoperidinium leonis	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium depressum	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q26	Model response	Partial credit	Count	Frequency
	Protoperidinium pentagonum	100.00%	74	91.36%
	Protoperidinium conicum	0.00%	2	2.47%
	Protoperidinium pellucidum	0.00%	2	2.47%
	Protoperidinium leonis	0.00%	1	1.23%
	Protoperidinium divergens	0.00%	1	1.23%
	Protoperidinium depressum	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium thorianum	0.00%	0	0.00%
	Protoperidinium crassipes	0.00%	0	0.00%
	Protoperidinium claudicans	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Q27	Model response	Partial credit	Count	Frequency
	Protoperidinium thorianum	100.00%	79	97.53%
	Protoperidinium claudicans	0.00%	1	1.23%
	Protoperidinium leonis	0.00%	0	0.00%
	Protoperidinium depressum	0.00%	0	0.00%
	Protoperidinium conicum	0.00%	0	0.00%
	Protoperidinium divergens	0.00%	0	0.00%
	Protoperidinium minutum	0.00%	0	0.00%
	Protoperidinium crassipes	0.00%	0	0.00%
	Protoperidinium pellucidum	0.00%	0	0.00%
	Protoperidinium pentagonum	0.00%	0	0.00%
	[No response]	0.00%	1	1.23%

Table 13. Model answers for questions 21-27 on *Protoperidinium*

In Q21 *P.depressum* was easy to identify because of its large size and very distinctive shape. In Q22 *P.conicum* differs from *P.leonis* on typical 'V' shape suture and spines which is seen in the image. Both can be confused as they are ortho-hexa shape. In Q23, *P.divergens* caused most problems. It was confused with *P.crassipes* by 13% of the participants. Both have a meta-quadra arrangement, but *P.divergens* diverging horns and horns from *P.crassipes* differ in shape and size. In Q24, the answer was *P.leonis* and the same comments apply as in question 22. In Q25 & Q27 these are very distinctive species if also highly unusual shapes to actually belong to the *Protoperidinium* genus. Yet it is this distinctiveness that make them easier to be identified, perfect scores by all here. In Q26, *P.pentagonum* another ortho-hexa *Protoperidinium* like *P.leonis* and *P.conicum* but with a very wide sulcal area between horns and that typical pentagonal shape as it sname indicates.

Q#	Question type	Question name	Attempts	Facility index
5	Numerical	Enumerate 1 BEQ15	81	93.83%
6	Numerical	Enumeration 2 BEQ2015	81	98.77%
7	Numerical	Enumeration 3 BEQ15	81	100.00%
8	Numerical	Enumeration 4 BEQ15	81	97.53%
9	Numerical	Enumeration 5 BEQ15	81	100.00%
10	Numerical	Enumeration 6 BEQ15	81	100.00%
11	Numerical	Enumeration 7 BEQ15	81	100.00%
12	Short answer	Identification video 2 BEQ15	81	97.53%
13	Short answer	Identification video1 BEQ15	81	97.53%
14	Short answer	Identification video3 BEQ15	81	91.36%
15	Short answer	Identification video4 BEQ15	81	88.89%
16	Short answer	Identification video5 BEQ15	81	61.73%
17	Matching	Pseudo-nitzschia chains	81	87.35%
18	Matching	Pseudo-nitzschia terminology,2015	81	92.18%
19	Matching	Peridinioid terminology,2015	81	96.05%
20	Matching	Protoperidinium identification 1	81	94.65%
21	Multiple choice	Protoperidinium 1	81	93.83%
22	Multiple choice	Protoperidinium 2	81	90.12%
23	Multiple choice	Protoperidinium 3	81	83.95%
24	Multiple choice	Protoperidinium 4	81	92.59%
25	Multiple choice	Protoperidinium 5	81	98.77%
26	Multiple choice	Protoperidinium 6	81	91.36%
27	Multiple choice	Protoperidinium 7	81	97.53%

Table 14: Statistics by question type

Table 14 shows the statistics of percentage of correct answers by question and question type. Generally, scores are high for most questions. Questions 16 with 61.73% of correct answers appear to have been the most difficult one for analysts, followed by question 23 on the genus *Protoperidinium* identification (83.95%), but most questions are above the 90% mark with perfect scores for questions 9, 10 and 11.

5. Discussion

The present format of this intercomparison exercise is in operation since 2011 and appears to be a successful working model. This test is divided into two clearly defined sections; an online HAB quiz test set up in a remote platform accessed via the web and the analysis of marine algae in lugol's preserved water samples for abundance and composition. These samples are generally spiked with algal cultures, which allows for a better control of the spiked material in terms of their cell concentration and their identity.

The identification and enumeration exercise has been prepared in a similar fashion to previous years but a number of changes have taken place since 2013 in relation to the use of statistics. This time, we are following the statistical methods laid out in ISO13528 to calculate the performance statistics for the test. Also, some of the forms used to fill the test results have been revamped. The enumeration and identification logsheet (See Annex II), which in previous years have been set up as a Word document for analysts to enter their results and calculations, now is set up as an Excel spreadsheet.

The Excel spreadsheet contains an embedded reduced marine phytoplankton species list which is linked to the identification logsheet table and appears as a dropdown menu list, where analysts must choose the right entries for each sample. The advantages of using these forms set up in this way to include the analysts' results are various but primarily, the results are always readable, numerical transcription errors are avoided and no interpretation of the results are needed as it avoids identifications like e.g. unidentified armoured dinoflagellate, centric diatom, naked dinoflagellates, etc. There are also some disadvantages, as the reduced list can be construed to be an aid to the identification of the species and a deviation to the method.

The results of the exercise have been processed similarly to previous years particularly in relation to using the consensus values of all the analysts to form the basis of the final Z-scores. However, there are definite and important changes to the way we arrive at these averages and confidence interval values.

The new way of calculating these values using the robust averages and standard deviations from ISO 13528 is a definitive departure from previous years. ISO 13528 is the standard used for statistical methods in proficiency testing by interlaboratory comparisons. It describes sound statistical methods and recommendations of their use which can be applied to demonstrate unacceptable levels of laboratory bias. It gives the statistical guidelines for the interpretation of tests and it is to be used as the reference document in future exercises. This standard is only applicable to quantitative data only.

Since 2014, we are using the statistical software programme ProLab Plus version 2.14 to calculate the descriptive statistics for the test and the performance characteristics including the graphical representation of all the results.

<u>Homogeneity and stability test</u>

A homogeneity and stability test carried out by an expert laboratory was calculated using ProLab Plus (Annex VII) and summarized in table 1. This shows that not all items passed the homogeneity and stability test criteria. The standards ISO 17043 and 13528 give some solutions to this problem.

ISO 17043 in note 3 says: "In some cases, materials that are not sufficiently homogeneous or stable are the best available; in such cases, they can still be useful as proficiency test items, provided that the uncertainties of the assigned values or the evaluation of results take due account of this".

We have calculated the standard uncertainty of the assigned values (table 3) from the consensus values by the participants and we have found that in all the test items used in this round the standard uncertainty is negligible.

Also, ISO13528 indicates that when the consensus values form the participants are used, the assigned value can be compared with a reference value in order to ascertain that there is no bias in the method. We have used the data generated in the homogeneity test by an expert laboratory (table 4) as reference data for comparison purposes and we found that the differences between the consensus values and the reference values by the expert laboratory are more than twice its uncertainty for all the test items.

This suggests some level of bias in the measurement method either by the participants, by the expert laboratory or both. This is not critical but it demonstrates that certified reference materials will be essential to investigate further where this bias lies. Also a repeatability study would be necessary to investigate how much of this variation is due to the analysts and how much is due to the analytical method.

ISO 17043 gives another option when the materials are not sufficiently homogeneous or stable which is to include the between sample standard deviation from the homogeneity test values to the assigned standard deviation calculated from the consensus values for each test item. This is usually sufficient to take into account the heterogeneity of the samples.

In this test, although not all the test items have failed the homogeneity test we have decided to include the between sample standard deviation from the homogeneity test to all the measurands (see table 2). It must be noted that the calculations have been done both with and without adding the in between sample standard deviation to the test items (not shown in this report) and that the differences are not really significant to the final results. In any case, the addition of the in between sample SD effect is to widen the confidence limits for each test item allowing more participants to be within the set limits.

Calculation of performance statistics

The consensus values from the participants (Annex VIII) were used to calculate the performance statistics for the test. These values take into account the heterogeneity of the samples (between sample SD) from the homogeneity test and the assigned values for the test materials used in this round were calculated using the robust algorithm A in annex C of ISO13528 which are derived by an iterative calculation using the new modified averages and standard deviations until the process converges (Annex IX). This method deals with outliers in the dataset and missing values.

These assigned values for each measurand were then used to calculate the Z-scores (Annex X). Laboratory bias assumes a normal distribution of the data across zero and any results outside the warning signal (2SD) or action signal (3SD) would suggest an out of specification result. The results show that Z-scores are generally within the specification of the test for most analysts with a number of warning and action signals. A warning signal is a result between 2 and 3SD of zero and an action signal is a result outside 3SD. Two warning signals in consecutive intercomparisons give rise to an action signal. An action signal signifies that an investigation of the causes by the laboratory should be carried out.

There are a number of warning and action signals arising from this intercomparison which can be found in the table of Z-scores in annex X. Generally, the performance is good for most analysts with perfect scores in all measurands. In this exercise, we had a complete total of 18 Warning signals, 4 Action signals and 1 non-identifications from 588 results which suggests a good overall agreement for all measurands and laboratories.

Combined performance scores

It is common in any rounds of a proficiency testing exercise to obtain results from several test items or measurands, in our case each species found in the samples is a test item or measurand. As this is generally the case during monitoring work, the individual scores for each measurand is analysed individually but also can be used to calculate combined effects for a particular laboratory or analysts such as correlation between results for different measurands. Graphical methods for this include histograms, bar plots and repeatability standard deviations plots.

Mandel's h and k statistics in annex XIII present measures for graphically surveying the consistency of the data and specific patterns of laboratory performance. The h plot represents all measurand-sample combination possible and reveals that a small number of analysts have consistently over or underestimated the cell counts which indicate a common source of laboratory bias. It is up to individual laboratories to investigate the causes which may cause these anomalies.

The k plot can be interpreted as repeatability precision measures. Again, this graph represents all the measurand-sample combinations possible. Large values here indicate poor repeatability precision. Several large values indicate poor repeatability precision for some or all of the measurands.

The chart of RLP against RSZ (Annex XIV) for all measurands combined indicates systematic laboratory bias. RSZ is based on the standardized sum of all the z-scores for each analyst and it can be interpreted as a single Z-score: that is an evaluation across all samples and measurands. If the RSZ value is within the tolerance limits (2SD), there are no significant systematic deviations of the measurement values for that analyst compared to the rest. The RLP is the mean length of all the Z-scores for each analyst and is derived from the sum of the squared mean length of all the Z-scores. Deviations in RLP are accepted as long as the mean deviations for the analysts don't exceed 1.5 times the average deviations of all laboratories. This is the top of the green area of the rectangle. Laboratories dotted within the green colored area in the graph are within the consensus values shown by the majority of analysts. Those outside it are showing a systematic bias towards over or under-estimating most of their counts in the samples, suggesting some kind of methodology bias.

The plot of repeatability standard deviations shown in annex XV uses a modified approach to the circle technique of van Nuland. This plot uses the average and standard deviation of each laboratory/analyst and plots one against the other. Because of this modified approach, the critical region drawn doesn't have the shape of a circle anymore. This critical region corresponds to a significance level of 5% for the inner layer, 1% and 0.1% for the most outer layer. This plot determines which laboratories/analysts are having unusual averages and standard deviations. Plots of repeatability standard deviation assume that there is no difference between laboratories means +SD.

Qualitative data

The scope of ISO13528 does not include qualitative results, but the correct identification of the organisms in the samples is still a very important part of the exercise, as correct/incorrect/not-identified flags will be given for this.

The data received from the analysts (Table 5) shows that analysts are highly skilled in the identification of marine phytoplankton and the results suggest that there is consensus among analysts on most of the species identified in the samples with near perfect scores for all identifications.

The diatom cultures used in this year's intercomparison were grown using orbital shakers to improve the strength of their silica frustules but we did not find any particular improvement of the organisms used. *P.australis* for example grew better without movement while others like *C.granii* grew quite nicely on the orbital shakers. *D.brightwellii* did too but at the end did not preserve that well in the samples and individual cells broke down in halves which we found last year with *Rhizosolenia*. Other chain formers like *A.glacialis* or *G.delicatula* also broke apart upon preservation.

This would indicate that while orbital shakers or rotational apparatus may enhance a number of cultures during growth, we didn't appreciate any significant strengthening of the silica structures of diatoms which did break down upon lugol's preservation and homogenization.

Originally, nine species have been spiked in the samples. The organisms *P.sulcata* and *A.glacialis* could not finally be included in the statistical analysis and final scores as we had encountered problems upon spiking of the samples. *P.sulcata* clumped together and chains were stuck to each other within a kind of mucilage substance and therefore did not allow for proper mixing causing large differences between samples. The problem with *A.glacialis* was different, this diatom which is found in spiraling chains broke down into individual cells upon homogenization and their shape changed upon preservation causing difficulty in identification. Therefore, it was decided that these two species would not be included in data analysis for the test.

While problems were also encountered with other species in the samples like *D.brightwellii* which tended to breakdown upon preservation and homogenization, the results were used for the test and it was one of the species where all participants scored well. Only one analyst failed to identify *L.polyedrum* in the samples. That was the only non-identification in the whole test. The identification of the organisms was given to species level for all species and a small number of mis-identifications occur; 2 analysts identified *Actynociclus* instead of *C.granii* and 2 others identified *P.reticulatum* instead of *L.polyedrum*.

The identification of *Pseudo-nitzschia* was carried out mainly to genus level. 67% of analysts decided to identify to genus level only as 'seriata group' while those identifying to species level were divided between *P.seriata* and *P.australis* 14% each. *P.pungens* and *P.multiseries* were the other choices.
The flags for correct identifications are based on a correct genus answer rather than on species taxon as discussed in the instructions (see annex III). However, for the purpose of the intercomparison we asked

analysts to identify to species level to give us a better insight on the analysts and laboratories approach to identification and while this is not used for final marks, the information is still valuable for discussion among the participants. It also gives the coordinators of the scheme invaluable data towards species selection in future exercises.

It has been observed from the data received that there is a level of conferring between colleagues working in the same laboratory which becomes obvious when analyzing the results. This sometimes means that one incorrect identification runs throughout all the analysts from the same laboratory. The advice to analysts here is always do your own work and do not confer with others for the purpose of the exercise.

Online HAB quiz

The online HAB quiz has proven very successful and original problems with the software have been ironed out as much as possible. There are still a small number of concerns, specifically with 'short answer' type questions and shuffling within questions and answers. Also, there are problems with analysts not reading or understanding what is required of them and some spelling mistakes which ultimately mean losing marks. Nevertheless, the HAB online quiz is otherwise a good addition to the exercise and this online facility helps greatly the administration and reporting of results.

Descriptive Statistics: code

Variable	Grade/100.0	Total Count	N	N*	CumN	Percent	CumPct
code	43.5	1	1	0	1	1.2346	1.235
	62.0	1	1	0	2	1.2346	2.469
	65.9	1	1	0	3	1.2346	3.704
	80.1	1	1	0	4	1.2346	4.938
	80.8	1	1	0	5	1.2346	6.173
	82.6	2	2	0	7	2.4691	8.642
	84.3	1	1	0	8	1.2346	9.877
	86.2	1	1	0	9	1.2346	11.111
	86.6	1	1	0	10	1.2346	12.346
	87.0	1	1	0	11	1.2346	13.580
	87.7	1	1	0	12	1.2346	14.815
	89.1	4	4	0	16	4.9383	19.753
	89.5	1	1	0	17	1.2346	20.988
	89.6	1	1	0	18	1.2346	22.222
	89.9	1	1	0	19	1.2346	23.457
	91.3	8	8	0	27	9.8765	33.333
	92.8	1	1	0	28	1.2346	34.568
	93.3	1	1	0	29	1.2346	35.802
	93.5	4	4	0	33	4.9383	40.741
	94.2	2	2	0	35	2.4691	43.210
	95.7	15	15	0	50	18.5185	61.728
	97.8	4	4	0	54	4.9383	66.667
	98.6	2	2	0	56	2.4691	69.136
	99.3	1	1	0	57	1.2346	70.370
	100.0	24	24	0	81	29.6296	100.000

Table 15 HAB online quiz cummulative percentage of total scores

This year the overall grade was 93.28% across all analysts with 77% of analysts scoring over 90% mark and another 20% scoring over 80% which is a good showing with a small number of analysts (3%) in need of improvement (table 15).

Questions 1 to 4 which did not carry any final marks were phytoplankton image sets and we were interested in the consensus answer by the analysts. Here, there is no right answer to these questions because the information supplied with the images is not enough to identify with certainty. However, sometimes we are asked to give opinions based in images sent to us, so we wanted to know if there was good consensus among participants on these phytoplankton images regardless of whether the answers were right or wrong. The responses suggest that there is a good general consensus among analysts in all sets supplied.

In question 1, most analysts agreed on 'tintinnid' for the first image, although different analysts used different 'tintinnid' names for their answer, 57% agreed on the name *Helicostomella sp.,* 89% of analyst agreed on *navicula* for the second image and 75% on *Guinardia* for the third image of the first set (Annex XVI). In question 2, analysts agreed on *Alexandrium* (81%) and *Navicula* (97%) for the first two images but there was divided opinion on the third one between *Gonnyaulax* (66%) and *Protoperidinium* (33%), so no consensus here.

In question 3, analysts agreed on all the images in the set: *Protoperidinium* (100%), *Detonula* (78%) and *Protoperidinium* (98%). In question 4, the images proved difficult with 56% of analysts choosing *Rhabdonema* , 30% *Striatella* and 12% *Fragillaria* for the first image. 44% *Navicula* for the second image plus an array of other benthic diatom names and for the third image, 76% of analysts went for some kind of 'tintinnid'.

We can conclude that there was good consensus generally for all images of dinoflagellates, planktonic diatoms and even ciliates except for the benthic diatom images which were harder to consensuate to genus level, although everyone agreed on 'benthic diatoms'.

There was good overall consensus between participants on the numerical questions (Q5 to Q11). Most analysts responded within the parameters of the model response and tolerance applied, but there were a small number of inconsistent answers. Only 8 answers from a total of 567 on the 7 questions were answered outside the specification parameters which suggest that we all have a similar approach on the enumeration of phytoplankton cells with small variations due to differences in interpretation of what a viable cell is. The biggest problem wasn't caused by the amount of cells to be counted in the images, but rather by interpreting which cells should be counted, that is why in question 5 whose image showed only 2 cells of the dinoflagellate *P.micans* and two empty thecae caused great problems to participants with five responses outside the model response, that is 5 out 8 of all the responses that were wrong , happened in this particular question. Some analysts interpreted that the empty theca could be counted and others that one of the 2 cells to be counted didn't qualify for counting as it didn't' contain enough intra-cellular material. Small variations in cell counts can mean large variations over a whole sample and it is something to be aware of.

Questions 12 to 16 were short video clips showing different species in movement. Analysts were able to identify the species well based on these videos, although the worst answered question of the whole quiz was 16 which was the most difficult one of the set of videos.

The taxonomic terminology questions on *pseudo-nitzschia* and *Protoperidinium* (Q17 to 20) were answered well with high scores all around. However, analysts had difficulties differentiating between *pseudo-nitzschia* in valve or girdle view.

The set of questions Q21 to Q27 on *Protoperidinium* didn't create difficulties generally but there was confusion between *P.leonis* and *P.conicum* and *P.pentagonum* which analysts should be aware of in the one instance and *P.divergens* and *P.crassipes* as well.

ANNEX I: Form 1 return slip and checklist

United Nations Educational, Scientific and Cultural Organization

Intergovernmental Oceanographic Commission

Marine Institute
Foras na Mara

BEQUALM

NMBAQC SCHEME

Bequalm Intercomparison PHY-ICN-15-MI1
FORM 1: RETURN SLIP AND CHECKLIST

Please ensure to complete the table below upon receipt of samples, then fax to + 353 91 387201 or scan and e-mail to rafael.salas@marine.ie			
Analyst Name:			
Laboratory Name:			
Analyst Code Assigned :			
Contact Tel. No. / e-mail			
CHECKLIST OF ITEMS RECEIVED (Please circle the relevant answer)			
Please enter Sample numbers received ____________________		YES	NO
Set of Instructions		YES	NO
Enumeration and identification result log sheet **(Form 2)**		YES	NO

I confirm that I have received the items, as detailed above.

(If any of the above items are missing, please contact Rafael.salas@marine.ie)

SIGNED: ____

DATE: __________________________

ANNEX II: Form 2 Enumeration and identification results log sheet

Bequalm 2015 Phytoplankton Intercomparison Exercise

Analyst Name:	
Laboratory Code:	
Analyst Code :	

Settlement date:			
Volume Chamber (ml)			
Analysis date:			
Sample No:			

Organism	Cell count	Cell count	Cell count	Multiplication factor			Number cells/L	Number cells/L	Number cells/L	Average
										#DIV/0!
										#DIV/0!
										#DIV/0!
										#DIV/0!
										#DIV/0!
										#DIV/0!
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Comments:

Form 2: Results logsheet

Marine Institute-IOC- BEQUALM-NMBAQC Phytoplankton Proficiency Test

PHY-ICN-15-MI1 Vr1.0

Instructions

Please note that these instructions are designed strictly for use in this Intercomparison only.

ANNEX III

1. Introduction

The Marine Institute, Galway, Ireland, has conducted a phytoplankton enumeration and identification ring trial, under the auspices of BEQUALM-NMBAQC annually since 2005. In 2011, the IOC Science and Communication Centre on Harmful Algae and the Marine Institute initiated collaboration on the design and organization of this exercise which continues under the Marine Institute- IOC -BEQUALM-NMBAQC banner.

Information about this intercomparison exercise can be obtained in the NMBAQC website (www.nmbaqcs.org) under scheme components and Phytoplankton, you'll find information on the current timetable schedule for the exercise, the list of participants, previous reports and the workshop agenda from the previous exercises to give you an idea of the range of activities within this intercomparison exercise. There is also information on all the other Bequalm-NMBAQC schemes. Also, in the IOC website; http://hab.ioc-unesco.org there is information about the exercise under Activities and training courses. Registration to the exercise is through the Marine institute. You need to contact our administrator Fiona Bradley at fiona.bradley@marine.ie to register.

The purpose of this exercise is to compare the performance of laboratories engaged in national official/non-official phytoplankton monitoring programmes, water framework directive, marine strategy framework directive and other laboratories (environmental agencies, consultancies, private companies) working in the area of marine phytoplankton analysis.

The Marine Institute is accredited to the ISO 17025 standard for toxic marine phytoplankton identification and enumeration since 2005 and recognises that regular quality control assessments are crucial to ensure a high quality output of phytoplankton data.

This interlaboratory comparison exercise is conducted to determine the performance of individual laboratories on the composition and abundance of marine microalgae in preserved marine samples and to monitor the laboratories continuing performance.

Participants are asked to carry out microscopic analysis on three marine water samples spiked with cultured material and preserved with neutral lugol's iodine and return results on the composition of the samples to the highest possible taxon and the average abundance in cells per litre for each species in each sample. Each analyst will receive an envelope containing four samples (3 +1 spare) 50ml volume in plastic sterilin tubes.

Please adhere to the following instructions strictly. Please note that these instructions are specific to this ring test only.

2. Preliminary checks, deadlines and use of forms

Upon receipt of the samples, every analyst must make sure that they have received everything listed in the Return Slip and checklist form (Form 1). Make sure that all the samples are intact and sealed properly and check that you have received the enumeration and identification results log sheet (Form 2) as an Excel workbook. Please complete form 1: Return slip and checklist form and send it by fax to (+353 91 387201) or scan, pdf and send it via e-mail to rafael.salas@marine.ie . If you send the form via e-mail, please title the file as Form 1 followed by the exercise code and your full name **i.e. Form 1: BEQ15 Rafael Salas** A receipt of fax/e-mail is necessary for the Marine Institute to validate the test process for each analyst.

Once samples have been receipt, analysts have four weeks to complete the exercise and return the results to Rafael Salas, Marine Institute, Phytoplankton laboratory, Rinville, Oranmore, Co. Galway, Ireland by e-mail (rafael.salas@marine.ie), fax as above or post. If you decide to post your results, make sure first to make a copy of them and then send the originals to the address above. The enumeration and identification results log sheet (Form 2) **must be received** in the Marine Institute by **Friday, July 3rd 2015**.

Please note: Results received after this date will not be included in the final report. Also, if you are posting your results make sure to make a copy for your records before sending the originals. Just in case they never arrive.

An Excel workbook named 'Enumeration and identification logsheet' for you to input your results should be used to write in your results. In this form, first fill in your name, analyst and laboratory code at the top of the form. Fill in all the information relevant to the analysis of your samples like settlement date, settlement chamber volume used in mls, analysis date and sample number in the corresponding cells. Under the column 'organism' a drop down menu will appear with a list of possible species names. You must choose from this list your answers. The list of species is a reduced list and is designed to have more entries than species are in the samples, you must choose which ones you think have been spiked in the samples and provide a count.

If is not in the list, is not in the sample. The number of rows under the name 'organism' is fourteen but this is arbitrary. It doesn't mean you need to enter fourteen names or that there are fourteen species in the samples. The number of species spiked in the samples is a fixed number but you must decide that yourselves.

In the comments box, you can write information about the test method you used if deviates from the Utermöhl test method and how you performed your calculations if you think is necessary.

Finally, if you send your form back via e-mail, please re-name in the same way as Form 1 above.

3. Test method

The Utermöhl cell counting method (Utermöhl 1931, 1958) is the standard quantitative and qualitative test method used in the Marine Institute phytoplankton national monitoring programme in Ireland. We use 25ml volume sedimentation chambers and we are accredited under the ISO 17025 quality standard.

We advise the use of 25ml sedimentation chambers for the purpose of this intercomparison exercise if these are available. If not, other sub-sample volumes and/or chambers may be used.

If a different method is used, please state all this information in your results.

4. Equipment

The following are the equipment requirements to complete this exercise:

Sedimentation chambers (25ml volume if possible).

ANNEX III

Inverted Microscope: This should be equipped with long distance working lenses up to 40 x objective or higher and condenser of Numerical Aperture (NA) of 0.3 or similar and capable

for bright field microscopy. Other types of reflected or transmitted light capabilities may be helpful depending on the type of organisms in the samples and can be used if required.

Tally counters

5. Sedimentation chambers and sample preparation

Sedimentation chambers consist of a clear plastic cylinder, a metal plate, a glass disposable cover-slip base plate and a glass cover plate (Fig 1). Three sedimentation chambers are required.

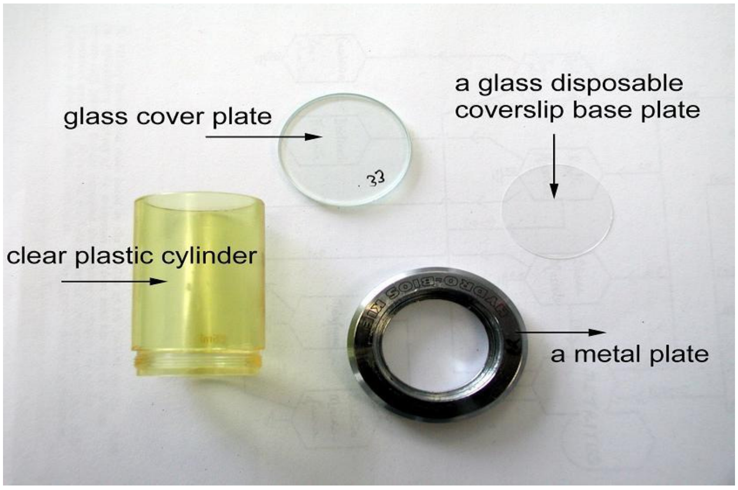


Fig 1: Sedimentation counting chamber

5.1 All sedimentation chambers should be cleaned before start

5.2 Place a new not used disposable cover slip base plate inside a cleaned metal plate.

5.3 Screw the plastic cylinder into the metal plate. Extra care should be taken when setting up chambers. Disposable cover slip base plates are fragile and break easily causing cuts and grazes.

5.4 **Important:** Once the chamber is set up, it should be tested for the possibility of leaks by filling the completed chamber with sterile filtered seawater and allowing it to rest for a few minutes. If no leakage occurs, pour out the water, dry out completely and proceed with the next step.

5.5 To set up a sample for analysis or sub-sample. Firmly invert the sample 100 times to ensure that the contents are homogenised properly.

5.5.1 Pour the sample into the counting chamber. Samples must be adapted to room temperature beforehand to reduce the risk of air bubbles in the chambers due to temperature changes.

5.5.2 There should be enough sample volume in each sample to fill a 25ml sedimentation chamber. Top up the sedimentation chamber and cover with a glass cover plate to complete the vacuum and avoid air pockets.

5.5.3 Label the sedimentation chamber with the sample number from the sterilin tube.

5.6 Use a horizontal surface to place chambers protected from vibration and strong sunlight.

5.6 Allow the sample to settle for a minimum of twelve hours.

5.7 Set the chamber on the inverted microscope and analyse.

5.8 Enumeration and identification results for each sample are to be entered in the Excel workbook **Form 2 enumeration and identification results log sheet.**

5.9 If using a different method to the Utermöhl test method, please send the Standard Operating Procedure for your method with your results. Explain briefly how it works and how samples are homogenized, set up, analysed, counted and how you calculate the final concentration.

6. <u>Counting strategy</u>

Each analyst should carry out a whole chamber cell count (WC) of all the species identified in the samples where possible. Other counting strategies can also be used where the cell density in the sample for a particular organism is high. Show your calculations if using a field of view or transect count.

7. <u>Samples</u>

Analysts will have to analyse three samples to complete this test.

The set consist of four samples. Three must be analysed and one is a spare in case of leakages or breaks. These are made up in sterile filtered Seawater and spiked with culture material of one or more organisms. Participants are asked to carry out a whole chamber count (where possible ; see 6.) on each organism and sample.

The cultures come from the Marine Institute Phytoplankton culture collection, and the IOC Science and communication centre for Harmful Algae culture collection in Denmark. All the materials have been preserved using neutral lugol's iodine and then homogenized following the IOC Manual on Harmful Marine Algae technique of 100 times sample inversion to extract sub-samples.

Each analyst must **count and identify all phytoplankton species** found in the three samples.

It is very important to spend some time becoming familiar with the samples and how the cells appear on the base plate before any count is carried out. The reason for this is that cultured cells could be undergoing division or fusion and look different to the known standard vegetative cell type. See figure 1.

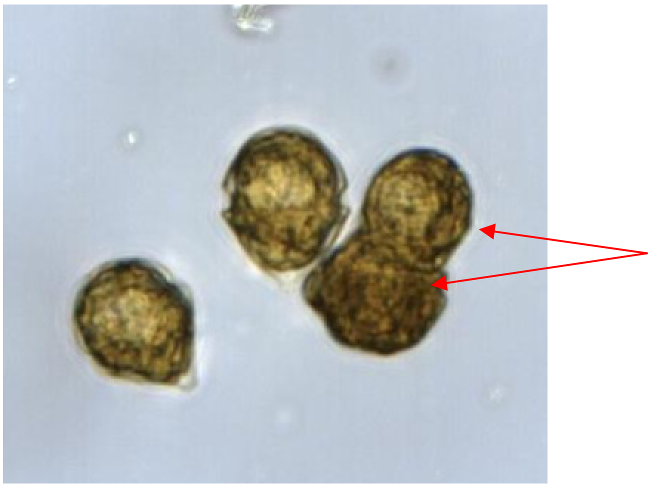


Figure 1: Two Cells fusing

Also note that cells' emptied thecae of dinoflagellates may appear in the samples (see figure 2), or silica frustules in diatoms.

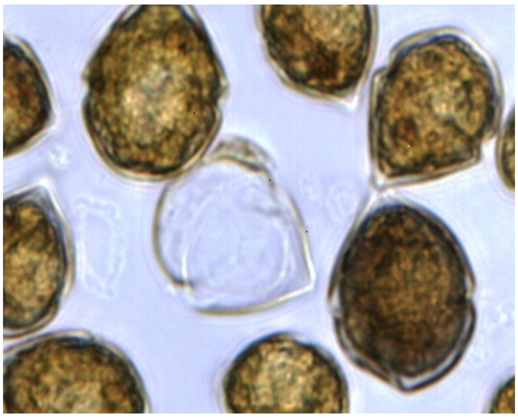
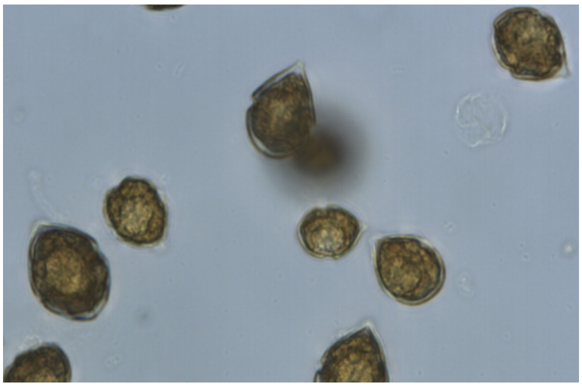


Figure 2: Empty theca

Cells may also vary in size, some cells will appear smaller than others, this is normal in culture conditions (see figure 3). Sometimes Plasmolysis may occur and the cells appear naked and rounded (see figure 4). Aberration of cell morphology can occur also in culture conditions and upon preservation of samples with lugol's iodine.



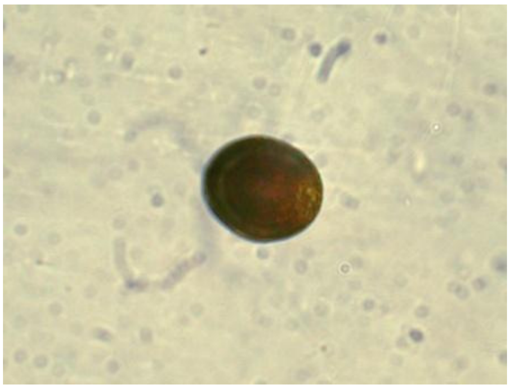
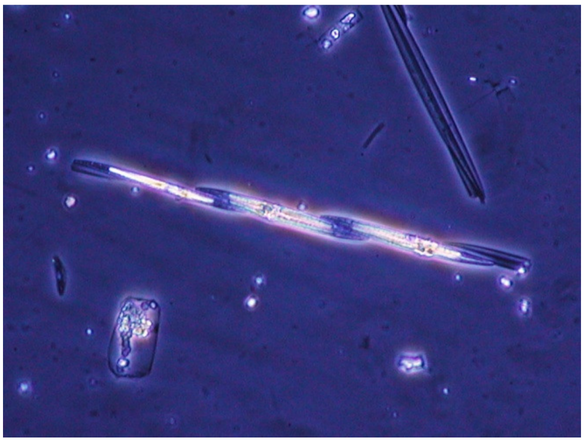


Figure 3: Big versus small cells

Figure 4: Plasmolised cell

ANNEX III

When counting cell chains, only count fully intact and divided cells, counting half cells should be avoided (fig.5).



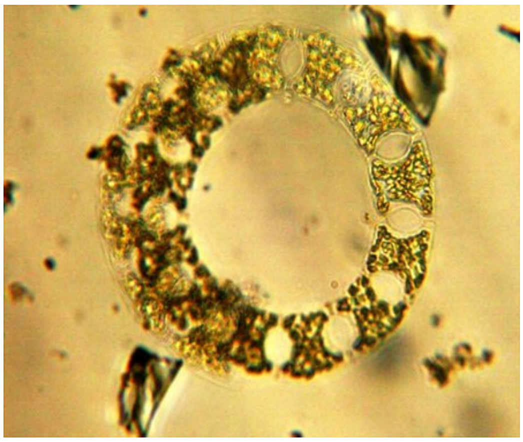


Figure 5 Figure 6

Sometimes cells may not be in the same focus plane (fig.6) but you still need to count them.

The following rules should be applied for cell counting and identifying in this exercise:

a) Any cells that are dividing or fusing, no matter how advance the stage of division or fusion is should be counted as one cell.

b) Empty theca/ silica frustules should not be counted.

c) Cells should be counted regardless of size, different sizes doesn't necessarily mean different species

d) Plasmolised cells should not be counted

e) Aberrant forms should be counted

f) When counting cell chains, do not count half or broken cells which are part of the chain

g) Identify to the highest taxonomic level possible all species in the samples

h) Participants should name phytoplankton species according to the current literature and scientific name for that species. Where species have been named using a synonym to the current name and if this synonym is still valid or recognized the answer will be accepted as correct.

These rules are only applicable to this intercomparison exercise.

8. Conversion calculations of cell counts

The number of cells found should be converted to cells per litre.
Please show the calculation step in Form 2: enumeration and identification results log sheet.

9. Online HABs quiz

A HAB taxonomic quiz will be developed in the web platform 'Ocean teacher' and it should be ready by the end of June 2015. All participants will need access to the internet to complete this part of the exercise. More information on when participants will be able to access this exercise will be sent to you by e-mail later on.

In order to access the exercise you need to go to the webpage http://classroom.oceanteacher.org/ and login. Analysts which took part in the exercise in any of the last four years will already have a username and password which is still active, those using this facility for the first time need to register first.

When you go to the page http://classroom.oceanteacher.org/ in the top right hand corner of this page, you'll see a link to login. Press login and in the next page if you already have registered in the previous four years (2011-2014), enter your username and password to access the course, if you forgot your password press the forgotten password link. If this is your first time using this system, then go to create new account and register your details. Once you register your details we will be able to activate your account. Participants should be able to self-enrol to this exercise, so once you are registered and logged in you must supply an enrolment key to access the exercise. This key is **Beq2015**. We will tell you the exact date the exercise is opened.

So, how do you do access the course?, Once you are all logged in, in the main page scroll down to the bottom and under interdisciplinary courses, click courses, on the next page and under categories click Harmful Algal Bloom (HAB). The Harmful algal bloom programme

Bequalm 2015 link will appear, click on it, enter your key (**Beq2015**) and start your quiz. Make sure you enter the right course.

Analysts will have several months to complete the exercise once it opens (dates to be decided). Only one attempt to the exercise is allowed and once the exercise is submitted analysts won't have access to it, only to review. So, make sure you review all your answers before submitting. There are a number questions and a maximum grade of 100% for a perfect score. All questions have the same score.

There are different types of questions (true/false, numerical, matching, multiple choice short answer). Please note that if you are asked for a number as the answer do not use text, use a numerical value. Also, in questions where you are asked to write the answer, please make sure that the grammar is correct. Incorrect grammar will give an incorrect answer. Please review your work carefully before submitting.

10. Points to remember

1. **All results must be the analysts' own work. Conferring with other analysts is not allowed.**

2. The Excel worksheet Form 2: Enumeration and identification results log sheet must be received by the Marine Institute, Phytoplankton unit by **Friday July 3rd 2015**.

ANNEX IV: Workshop agenda

Agenda Bequalm Phytoplankton Intercomparison workshop

Danhostel, Hillerød, Denmark, 8-12 Nov 2015.

	Morning 9.00-12.00	**Afternoon 13.30-17.00**
Sunday 8 Nov		Arrival to Danhostel at 16.00
Monday, 9 Nov	Intercomparison exercise results Enumeration and identification exercise results, Rafael Salas. Ocean teacher online HABs quiz exercise results, Rafael Salas	Presentations by the participants
Tuesday, 10 Nov	Lecture and microscope demonstration Update on *Pseudo-nitzschia*, Nina Lundholm	Field samples from participants, Nina Lundholm, Rafael Salas, Jacob Larsen
Wednesday 11 Nov	Lecture and microscope demonstration Planktonic *Prorocentrum* species Jacob Larsen	Lecture and microscope demonstration *Protoperidnium*, Jacob Larsen
Thursday 12 Nov	10 am, departure	

ANNEX V: Participating Laboratories

	Company Name		Company Name
1	Marine Scotland Marine Laboratory	21	IFREMER
2	Cefas	22	Istituto Zooprofilattico Sperimentale delle Venezie
3	Scottish Assocation for Marine Science (SAMS)	23	ARPA Puglia
4	Aquagestión S.A.	24	Jacobs UK Ltd
5	Microalgal Services	25	APEM Limited
6	Isle of Man Government Laboratory	26	LABORATORIOS ACUÍCOLAS S.A.
7	IMARES	27	Instituto de Fomento Pesquero
8	Agri Food and Biosciences Institute (AFBI)	28	Instituto Federal de Santa Catarina IFSC
9	DHI Water and Environment (S) Pte Ltd	29	ARPAM (Agenzia Regionale per la Protezione Ambientale delle Marche)
10	Alfred Wegener Institut	30	Scottish Environment Protection Agency
11	Sydney Water	31	MEA-nl
12	ARPA FVG	32	Orbicon A/S
13	Fondazione Centro Ricerche Marine	33	Laboratorio de Control de Calidad de los Recursos Pesqueros
14	Instituto del Mar del Peru - IMARPE	34	Sir Alister Hardy Foundation for Ocean Science (SAHFOS)
15	Laboratorios de Control de la Calidad Ambiental	35	DOE (NI) Environment and Marine Group Laboratory
16	OCEANSNELL	36	SMHI / Swedish Meteorological and Hydrological Institute
17	IRTA	37	Marine Institute Galway
18	CBBA	38	Marine Institute Bantry
19	Aristotle University of Thessaloniki	39	Complete laboratory Solutions (CLS)
20	ARPAC-Agenzia Regionale Protezione Ambientale Campania		

ANNEX VI: Statement of performance certificate

Marine Institute
Foras na Mara

BEQUALM

NMBAQC SCHEME

UNESCO
United Nations Educational, Scientific and Cultural Organization

Intergovernmental Oceanographic Commission

Biological Effects Quality Assurance in Monitoring Programmes / National Marine Biological Analytical Quality Control Scheme / Marine Institute

STATEMENT OF PERFORMANCE

Phytoplankton Component of Community Analysis

Year 2015

Participant details:
Name of organisation:
Country:
Participant:
Year of joining:
Years of participation:

Statement Issued: XX/XX/2015
Statement Number: MI-BQM-15-001

Summary of results:

Component Name	Subcontracted	Results Z-score (+/- 2 Sigma limits)		identification
Phytoplankton abundance and composition PHY-ICN-15-MI1	Marine Institute	*Scrippsiella trochoidea*		
		Prorocentrum micans		
		Lingulodinium polyedrum		
		Pseudo-nitzschia australis		
		Ditylum brightwellii		
		Coscinodiscus granii		
		Guinardia delicatula		
Overall Result Taxonomic quiz (Pass Mark 70%, over 90% proficient)				
Phytoplankton Taxonomy quiz PHY-ICN-14-MI1	IOC Science and communication Centre on Harmful algae			

n/a: component not applicable to the participant; n/p: Participant not participating in this component;
n/r: no data received from participant
The list shows the results for all components in which the laboratory participated. See over for details.

Notes:

Details certified by:

Rafael Gallardo Salas

Joe Silke
Section manager

Rafael Gallardo Salas
Scientific Technical Officer

ANNEX VI

Description of Scheme components and associated performance standards

In the table overleaf, for those components on which a standard has been set, 'Proficient', 'Good', and ' "Pass" flags indicate that the participants results met or exceeded the standards set by the Bequalm Phytoplankton scheme; 'Participated' flag indicates that the candidate participated in the exercise but did not reach these standards. The Scheme standards are under continuous review.

Component	Annual exercises	Purpose	Description	Standard
Phytoplankton Enumeration Exercise	1	To assess the performance of participants using the Utermöhl cell counting technique on the analysis of prepared sample/s of Seawater preserved in Lugol's iodine spiked using biological or synthetic materials.	Prepared marine water sample/s distributed to participants for abundance and composition of marine phytoplankton species	Participants are required to enumerate the test/s material/s and give a result to within ±2SD or sigma limits of the robust average/s. The robust average/s is/are the mean calculated from the consensus values by the participants following the assessment criteria as set out in ISO13528, Annex c robust analysis: Algorithm A. Participants are also required to identify the organisms found in the samples correctly to the required taxon. Flags will be given as correct, incorrect or not identified
Phytoplankton Oceanteacher online HAB quiz	1	To assess the accuracy of identification of a wide range of Marine phytoplankton organisms.	This is a proficiency test in the identification of marine phytoplankton The exercise tests the participant's ability to identify organisms from photographs and/or illustrations supplied.	The pass mark for the identification exercise is 70%. Results above 90% are deemed proficient, results above 80% are deemed good, results above 70% are deemed acceptable, and results below 70% are reported as "Participated". There are no standards for phytoplankton identification. These exercises are unique and made from scratch.

ANNEX VII: Homogeneity and stability test using ProLab plus

Scrippsiella trochoidea homogeneity test

BEQ2015

Survey of homogeneity test results

Sample: water3 Date: 29/09/2015
Measurand: Scrippsiella

Mean:	32133
Analytical standard deviation:	1246
Heterogeneity standard deviation s(samples):	946
Target standard deviation:	7208 (Manual)

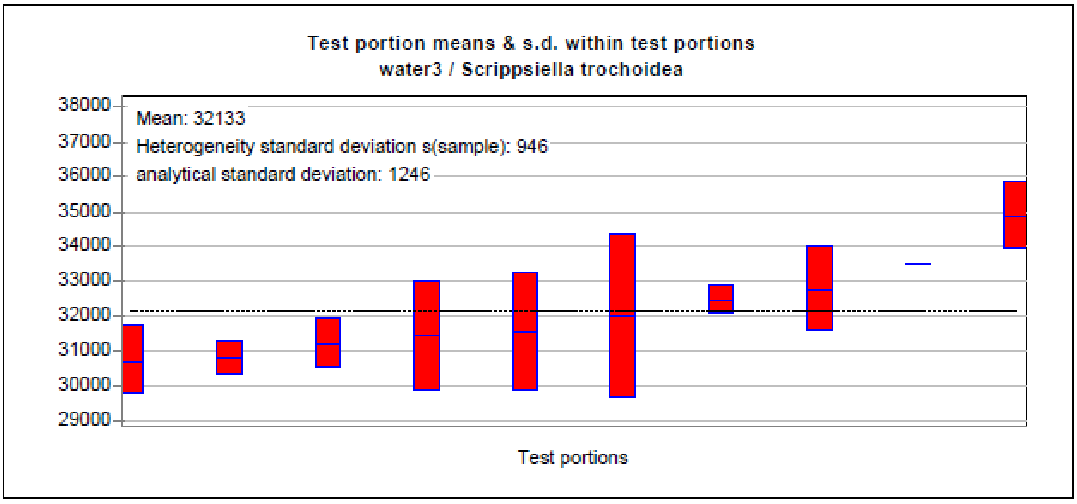
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Scrippsiella trochoidea w as analyzed 2 times. The mean across all 10 test portions is 32133, the standard deviation w ithin test portions s (analytical) (=analytical precision) is 1246, and the standard deviation betw een test portions s(sample) is 946.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is less than 30% of the target s.d. 7208 (Manual), therefore the sample can be considered adequately homogeneous according to ISO 13528.

Harmonized Protocol: test on significant heterogeneity
The analytical precision of the method does not exceed 50% of the target s.d. 7208 (Manual). Therefore the evaluation according to the Harmonized Protocol can be carried out for this sample: The heterogeneity standard deviation is less than 30% of the target s.d., therefore the sample can be considered homogeneous.



ANNEX VII: *Scrippsiella trochoidea* stability test

BEQ2015

Survey of stability test results

Sample: water3 Date: 29/09/2015
Measurand: Scrippsiella

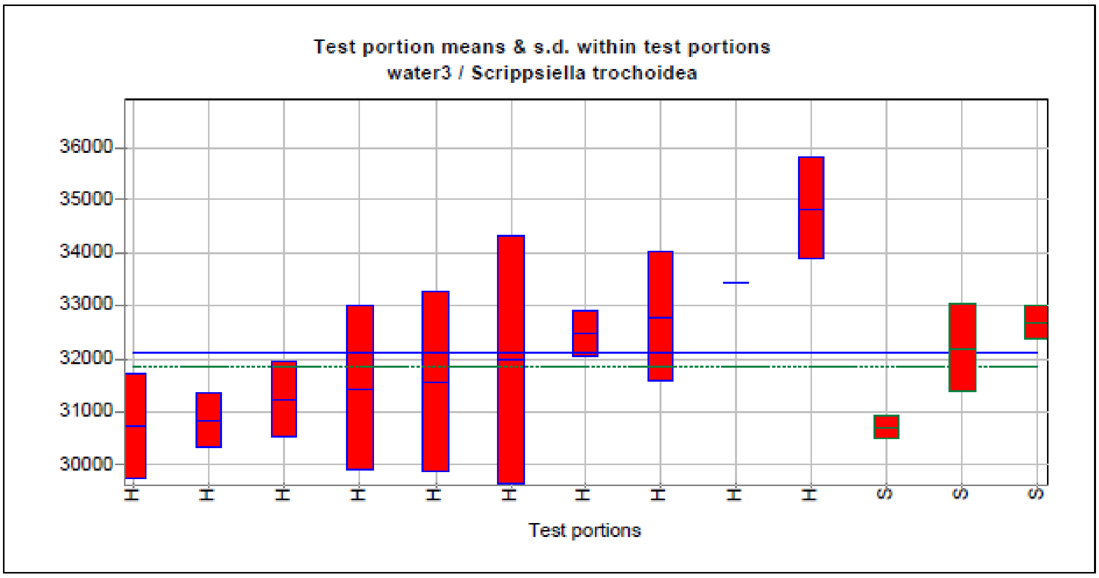
Mean of homogeneity:	32133
Mean of stability:	31863
Target standard deviation:	7208 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Scrippsiella trochoidea has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 32133, the mean value across all test portions of the stability analysis equals 31863.
Therefore, the mean value of the stability analysis lies 0.8 % below the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 7208, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Coscinodiscus granii* homogeneity test

BEQ2015

Survey of homogeneity test results

Sample:	**water3**	Date:	29/09/2015
Measurand:	**Coscinodiscu**		

Mean:	1804
Analytical standard deviation:	298
Heterogeneity standard deviation s(samples):	141
Target standard deviation:	252 (Manual)

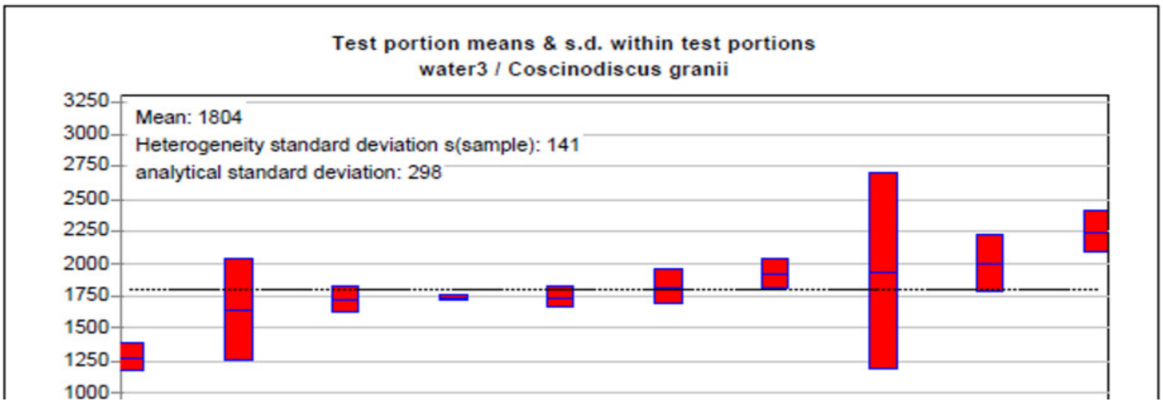
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Coscinodiscus granii w as analyzed 2 times. The mean across all 10 test portions is 1804, the standard deviation w ithin test portions s(analytical) (=analytical precision) is 298, and the standard deviation betw een test portions s(sample) is 141.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is greater than 30% of the target s.d. 252 (Manual), therefore the sample should be considered heterogeneous.

Harmonized Protocol: test on significant heterogeneity
For the specified target standard deviation 252 (Manual), the analytical precision of the method does not fulfil the requirements of the Harmonized Protocol (s(analytical) > 50% of the target standard deviation), and it may not be possible to determine the heterogeneity of the samples. Accordingly, an adequate homogeneity test is not possible.



ANNEX VII: *Coscinodiscus granii* stability test

BEQ2015

Survey of stability test results

Sample: water3 Date: 29/09/2015
Measurand: Coscinodiscu

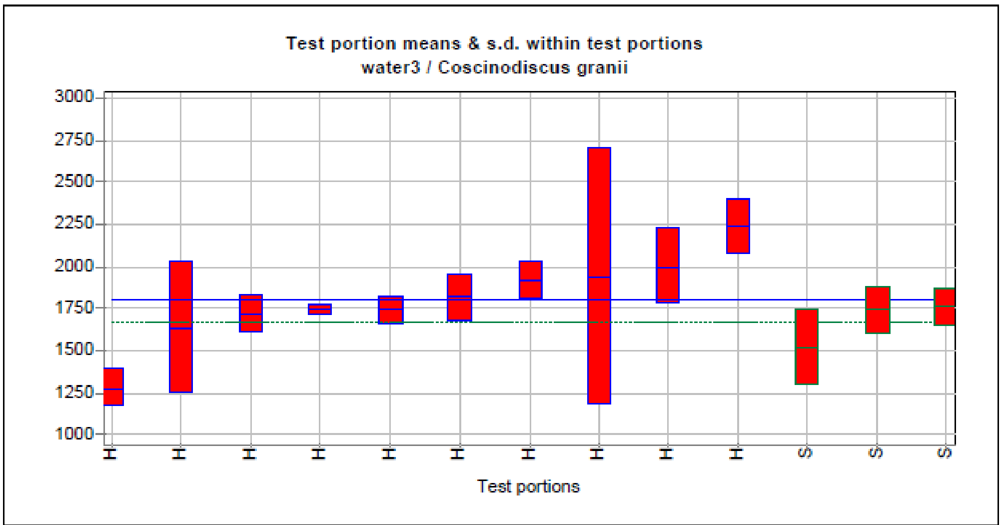
Mean of homogeneity:	1804
Mean of stability:	1673
Target standard deviation:	252 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Coscinodiscus granii has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 1804, the mean value across all test portions of the stability analysis equals 1673.
Therefore, the mean value of the stability analysis lies 7.2 % below the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 252, the sample may not be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Pseudo-nitzschia australis* homogeneity test

BEQ2015

Survey of homogeneity test results

Sample: water3 — Date: 29/09/2015

Measurand: Pseudo-

Mean:	3980
Analytical standard deviation:	1015
Heterogeneity standard deviation s(samples):	898
Target standard deviation:	1161 (Manual)

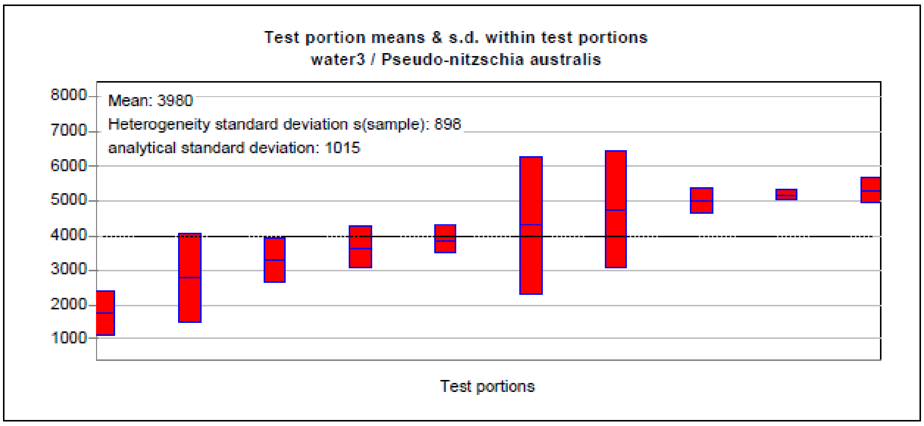
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Pseudo-nitzschia australis w as analyzed 2 times. The mean across all 10 test portions is 3980, the standard deviation w ithin test portions s(analytical) (=analytical precision) is 1015, and the standard deviation betw een test portions s(sample) is 898.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is greater than 30% of the target s.d. 1161 (Manual), therefore the sample should be considered heterogeneous.

Harmonized Protocol: test on significant heterogeneity
For the specified target standard deviation 1161 (Manual), the analytical precision of the method does not fulfil the requirements of the Harmonized Protocol (s(analytical) > 50% of the target standard deviation), and it may not be possible to determine the heterogeneity of the samples. Accordingly, an adequate homogeneity test is not possible.



ANNEX VII: *Pseudo-nitzschia australis* stability test

Survey of stability test results

Sample: water3 | Date: 29/09/2015

Measurand: Pseudo-

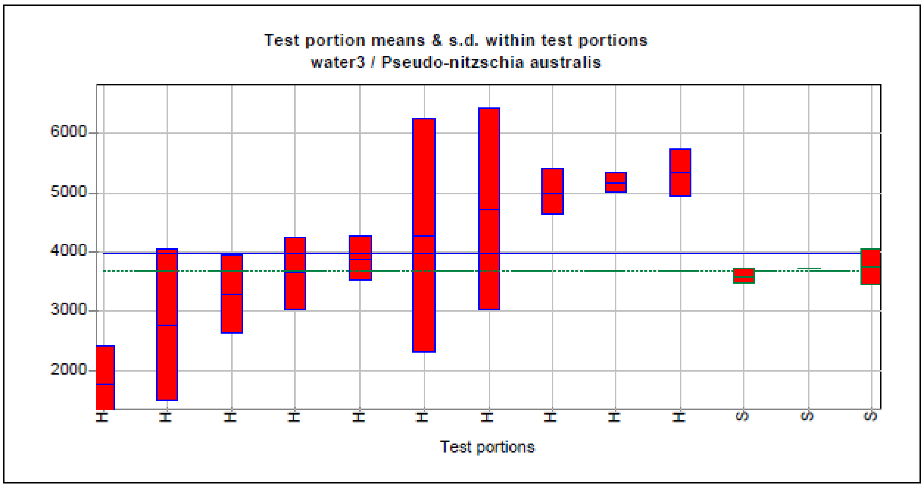
Mean of homogeneity:	3980
Mean of stability:	3680
Target standard deviation:	1161 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Pseudo-nitzschia australis has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 3980, the mean value across all test portions of the stability analysis equals 3680.
Therefore, the mean value of the stability analysis lies 7.5 % below the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 1161, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Ditylum brightwellii* homogeneity test

Survey of homogeneity test results

Sample: water3 Date: 29/09/2015
Measurand: Dytilum

Mean:	5342
Analytical standard deviation:	528
Heterogeneity standard deviation s(samples):	510
Target standard deviation:	1105 (Manual)

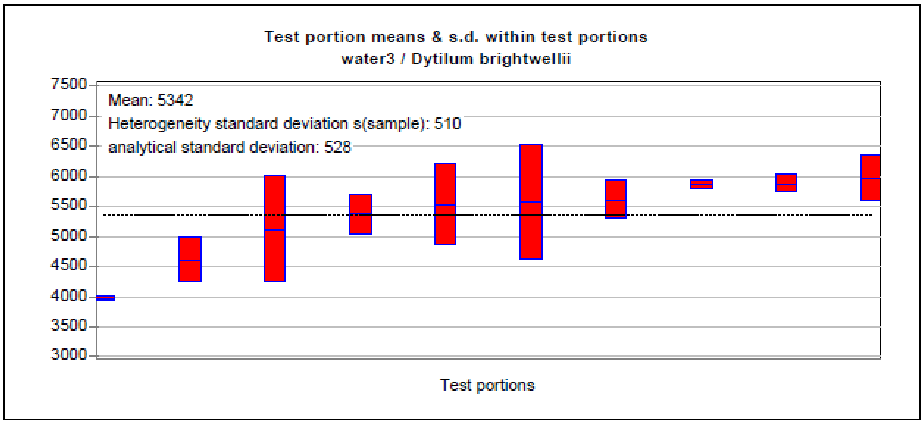
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Dytilum brightw ellii w as analyzed 2 times. The mean across all 10 test portions is 5342, the standard deviation w ithin test portions s (analytical) (=analytical precision) is 528, and the standard deviation betw een test portions s(sample) is 510.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is greater than 30% of the target s.d. 1105 (Manual), therefore the sample should be considered heterogeneous.

Harmonized Protocol: test on significant heterogeneity
The analytical precision of the method does not exceed 50% of the target s.d. 1105 (Manual). Therefore the evaluation according to the Harmonized Protocol can be carried out for this sample: Even though the heterogeneity standard deviation is greater than 30% of the target s.d., this is not statistically significantly the case, and the sample can thus be considered homogeneous.



ANNEX VII: *Ditylum brightwellii* stability test

BEQ2015

Survey of stability test results

Sample: water3 | Date: 29/09/2015

Measurand: Dytilum

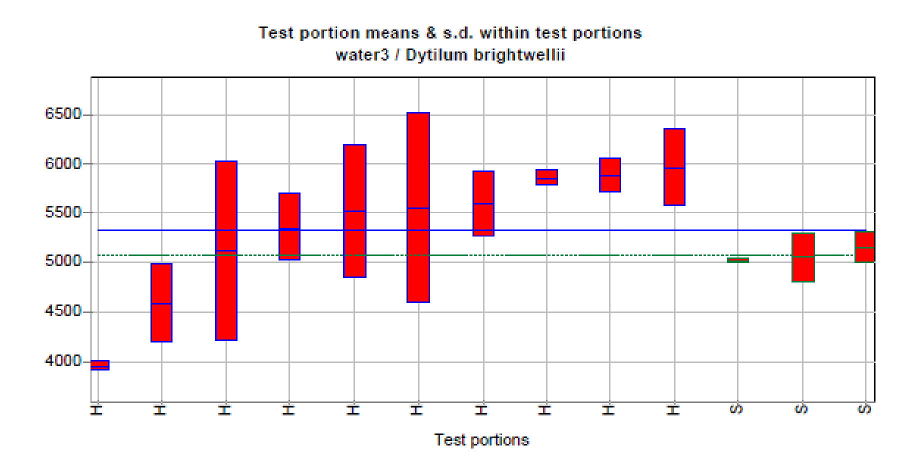
Mean of homogeneity:	5342
Mean of stability:	5080
Target standard deviation:	1105 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Dytilum brightw ellii has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 5342, the mean value across all test portions of the stability analysis equals 5080.
Therefore, the mean value of the stability analysis lies 4.9 % below the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 1105, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Guinardia delicatula* homogeneity test

BEQ2015

Survey of homogeneity test results

Sample: water3 Date: 29/09/2015
Measurand: Guinardia

Mean:	10038
Analytical standard deviation:	1210
Heterogeneity standard deviation s(samples):	897
Target standard deviation:	2035 (Manual)

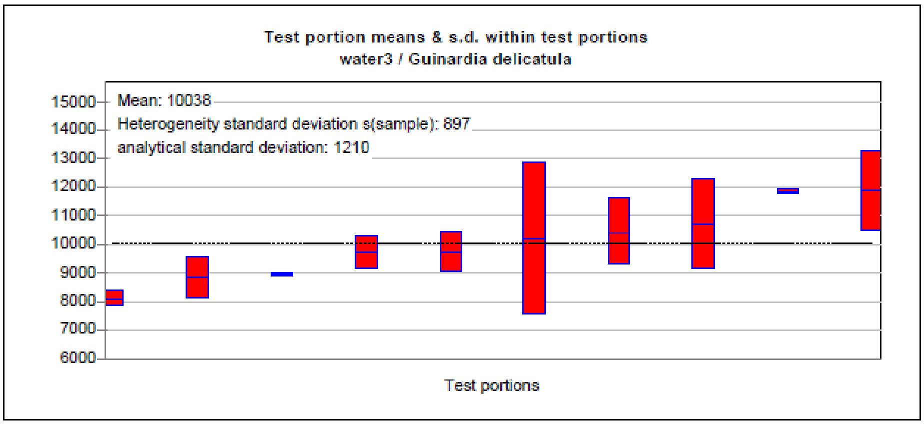
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Guinardia delicatula w as analyzed 2 times. The mean across all 10 test portions is 10038, the standard deviation w ithin test portions s (analytical) (=analytical precision) is 1210, and the standard deviation betw een test portions s(sample) is 897.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is greater than 30% of the target s.d. 2035 (Manual), therefore the sample should be considered heterogeneous.

Harmonized Protocol: test on significant heterogeneity
For the specified target standard deviation 2035 (Manual), the analytical precision of the method does not fulfil the requirements of the Harmonized Protocol (s(analytical) > 50% of the target standard deviation), and it may not be possible to determine the heterogeneity of the samples. Accordingly, an adequate homogeneity test is not possible.



ANNEX VII: *Guinardia delicatula* stability test

BEQ2015

Survey of stability test results

Sample: water3 Date: 29/09/2015
Measurand: Guinardia

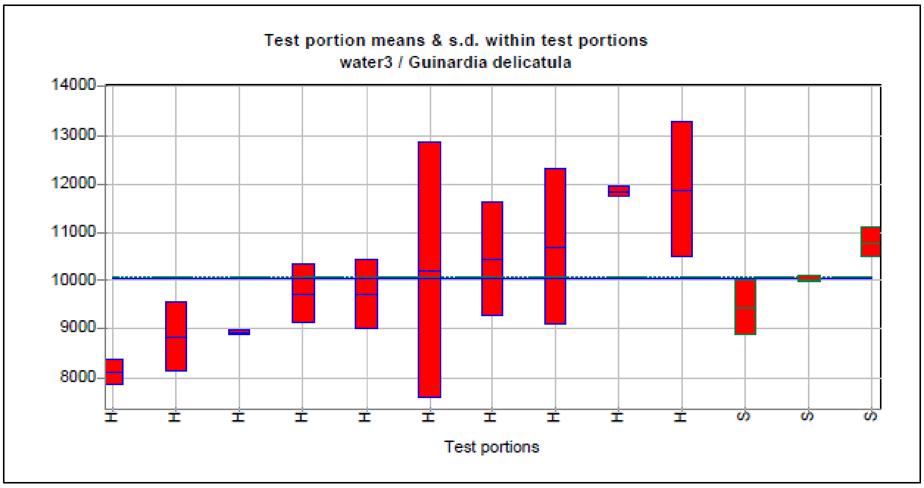
Mean of homogeneity:	10038
Mean of stability:	10080
Target standard deviation:	2035 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Guinardia delicatula has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 10038, the mean value across all test portions of the stability analysis equals 10080.
Therefore, the mean value of the stability analysis lies 0.4 % above the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 2035, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Lingulodinium polyedrum* homogeneity test

BEQ2015

Survey of homogeneity test results

Sample: water3 | Date: 29/09/2015

Measurand: Lingulodinium

Mean:	7524
Analytical standard deviation:	854
Heterogeneity standard deviation s(samples):	371
Target standard deviation:	1284 (Manual)

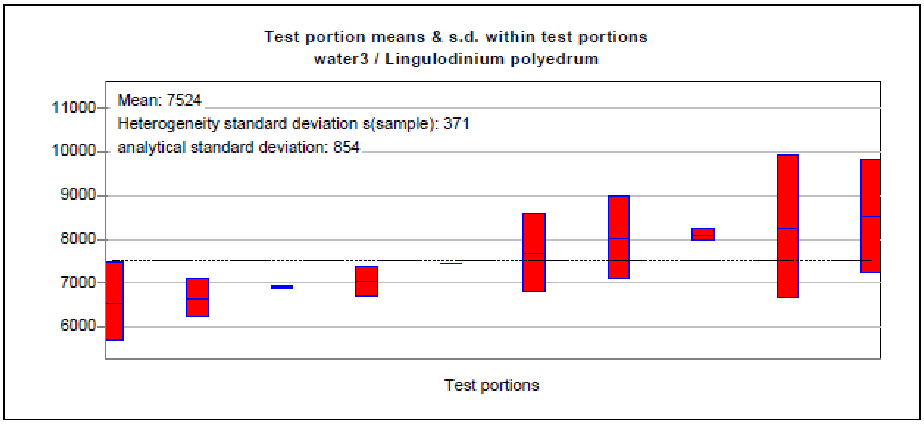
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Lingulodinium polyedrum w as analyzed 2 times. The mean across all 10 test portions is 7524, the standard deviation w ithin test portions s(analytical) (=analytical precision) is 854, and the standard deviation betw een test portions s(sample) is 371.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is less than 30% of the target s.d. 1284 (Manual), therefore the sample can be considered adequately homogeneous according to ISO 13528.

Harmonized Protocol: test on significant heterogeneity
For the specified target standard deviation 1284 (Manual), the analytical precision of the method does not fulfil the requirements of the Harmonized Protocol (s(analytical) > 50% of the target standard deviation), and it may not be possible to determine the heterogeneity of the samples. Accordingly, an adequate homogeneity test is not possible.



ANNEX VII: *Lingulodinium polyedrum* stability test

BEQ2015

Survey of stability test results

Sample: water3 Date: 29/09/2015
Measurand: Lingulodinium

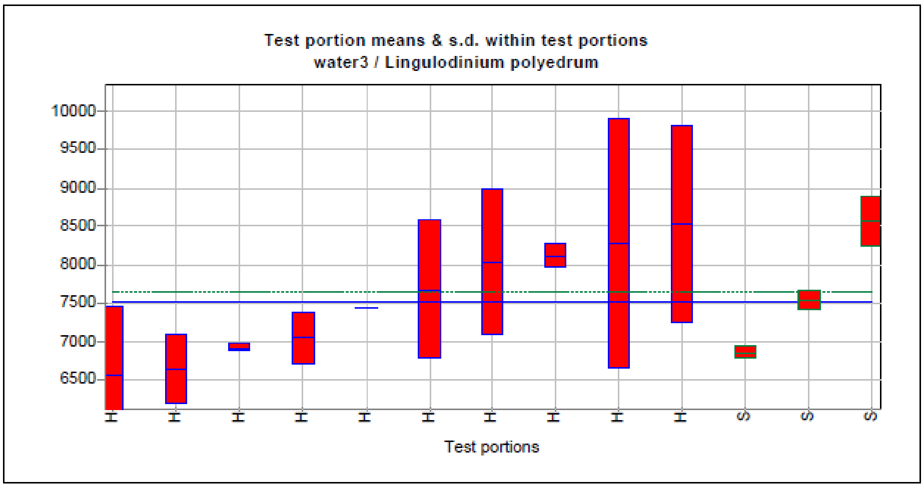
Mean of homogeneity:	7524
Mean of stability:	7653
Target standard deviation:	1284 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Lingulodinium polyedrum has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 7524, the mean value across all test portions of the stability analysis equals 7653.
Therefore, the mean value of the stability analysis lies 1.7 % above the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 1284, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VII: *Prorocentrum micans* homogeneity test

BEQ2015

Survey of homogeneity test results

Sample: water3 Date: 29/09/2015
Measurand: Prorocentrum

Mean:	15726
Analytical standard deviation:	673
Heterogeneity standard deviation s(samples):	389
Target standard deviation:	2940 (Manual)

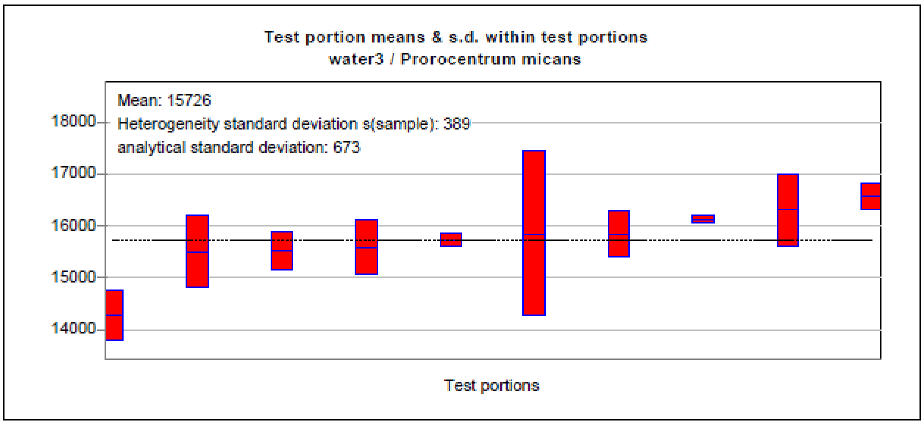
Results of homogeneity analysis (with statistical background)

For the homogeneity test, 10 of the test portions of sample w ater3 w ere randomly selected, and the measurand Prorocentrum micans w as analyzed 2 times. The mean across all 10 test portions is 15726, the standard deviation w ithin test portions s(analytical) (=analytical precision) is 673, and the standard deviation betw een test portions s(sample) is 389.

F-Test: statistical test on significant heterogeneity
According to the F-test, the heterogeneity standard deviation is not significantly different from 0 (significance level 5%), therefore the sample can be considered sufficiently homogeneous according to this criterion.

ISO 13528: Check for sufficient homogeneity
According to ISO 13528, the heterogeneity standard deviation s(sample) betw een the test portions of the sample should not exceed 30 % of the target standard deviation.
The heterogeneity standard deviation is less than 30% of the target s.d. 2940 (Manual), therefore the sample can be considered adequately homogeneous according to ISO 13528.

Harmonized Protocol: test on significant heterogeneity
The analytical precision of the method does not exceed 50% of the target s.d. 2940 (Manual). Therefore the evaluation according to the Harmonized Protocol can be carried out for this sample: The heterogeneity standard deviation is less than 30% of the target s.d., therefore the sample can be considered homogeneous.



ANNEX VII: *Prorocentrum micans* stability test

BEQ2015

Survey of stability test results

Sample: water3   Date: 29/09/2015
Measurand: Prorocentrum

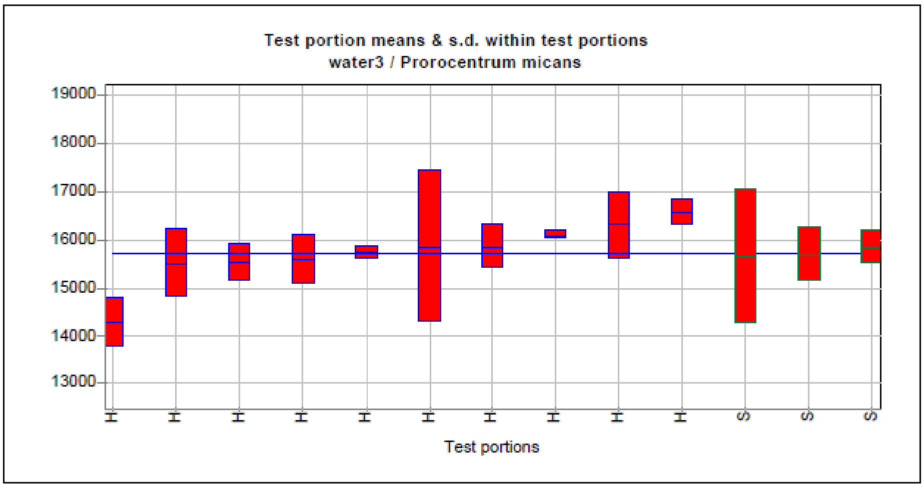
Mean of homogeneity:	15726
Mean of stability:	15720
Target standard deviation:	2940 (Manual)

Results of Stability Test

For the test of stability, 3 of the test portions of sample w ater3 have been selected randomly and the measurand Prorocentrum micans has been analysed 2 times.
The mean value across all test portions of the homogeneity analysis equals 15726, the mean value across all test portions of the stability analysis equals 15720.
Therefore, the mean value of the stability analysis lies 0.0 % below the mean value of the homogeneity analysis.

According to ISO 13528, the absolute difference betw een the mean values of the homogeneity analysis and the stability analysis should not exceed 30 % of the target standard deviation.
Therefore, given the target standard deviation of 2940, the sample may be considered as adequately stable according to ISO 13528.

According to the Harmonized Protocol it is checked w hether the mean values of the homogeneity analysis and the stability analysis differ significantly (level of signficance 5%).
The difference of the mean values is not statistically significant. Therefore - according to the Harmonized Protocol - the sample can be considered adequately stable.



ANNEX VIII: Analysts results

Analyst Code	Scrippsiella sp. (cells/L)			Analyst Code	P.micans (cells/L)			Analyst Code	Pseudo-nitzschia australis (cells/L)		
	sample 1	sample 2	sample 3		sample 1	sample 2	sample 3		sample 1	sample 2	sample 3
12	16200	19000	18200	12	12400	8440	8120	12	1440	2440	1240
88	10200	8920	8960	88	7080	17600	14440	88	1720	2680	3000
64	18200	13840	11680	64	10560	8360	12640	64	1760	3280	1320
19	12880	14840	13000	19	7320	6880	12160	19	2680	3440	2720
42	10800	9720	13760	42	10440	14200	20520	42	9520	5760	2160
62	18040	19240	18480	62	13320	10080	11640	62	2160	1880	1760
80	13360	20200	12000	80	12480	14000	13480	80	2120	2920	2040
5	17320	20520	21400	5	9720	10760	14720	5	2560	2200	2640
41	15400	17040	22160	41	13600	13080	21080	41	2640	4160	3120
60	20550	16900	16200	60	9950	8450	12550	60	2100	1450	1600
89	30640	30240	30560	89	18360	17240	19600	89	2760	2080	3000
75	13400	10800	18400	75	13200	16200	15600	75	3600	2400	2800
49	13465	19758	22394	49	13838	15947	16145	49	2909	2997	2976
81	22520	24520	18040	81	9400	13160	9520	81	200	760	640
68	33148	32217	39022	68	7360	8800	8820	68	3280	2360	2520
10	35360	24400	20920	10	11200	10880	17160	10	2400	2840	2440
6	8690	17653	5290	6	8690	12357	3527	6	5214	7061	1763
61	21440	17080	16000	61	9280	13520	13240	61	1400	2120	2440
23	18760	16400	16520	23	12000	15760	13600	23	3000	2440	2720
11	11240	6280	6640	11	13440	10480	9280	11	1360	1680	1160
86	15920	19000	15560	86	9720	9920	16200	86	3200	1280	1360
17	38040	30600	27680	17	16480	12560	16080	17	760	1720	600
16	10800	10560	8640	16	10520	10280	8640	16	920	120	1440
3	20560	19320	17680	3	13160	10320	18960	3	1160	960	2080
24	10200	11800	15500	24	12700	11500	13500	24	2100	2700	2200
72	12535	14490	18819	72	16371	10400	20655	72	3000	3560	3440
2	23358	24274	21526	2	15114	14198	15343	2	2760	2880	3040
14	22712	22304	23528	14	14552	11832	15368	14	2360	2480	2400
26	19480	14960	15400	26	6840	7520	7120	26	1400	1600	880
21	22044	22870	18479	21	15175	16305	15740	21	4044	3565	1478
18	22392	18436	21610	18	16435	16522	15870	18	2478	3739	5000
38	18479	24523	36436	38	12131	11261	15392	38	2217	3000	957
50	17640	18480	14960	50	12080	11040	14160	50	2080	2080	2400
44	15360	21960	18360	44	9080	10240	9880	44	2560	1560	1080
48	19840	15200	13240	48	18040	11440	13120	48	3200	2280	1000
32	8560	3440	9680	32	6480	4800	4480	32	1600	1120	640
13	22520	16640	22880	13	10480	14720	14240	13	2840	2880	2120
39	22400	17120	18320	39	11800	13200	16720	39	2920	2800	2520
54	12012	11127	10049	54	6776	6969	6661	54	2695	2271	2271
30	9615	12462	10077	30	10962	8385	18308	30	3038	1154	2885
58	6538	5038	4385	58	14577	11577	8269	58	1769	2538	1077
87	14885	17577	17577	87	9346	9577	11692	87	4846	3769	2192
59	23920	33920	29600	59	16640	13440	11160	59	2480	1840	2520
31	22900	24700	30600	31	11000	13000	11500	31	4500	700	3000
70	19000	28300	31000	70	13500	11600	12400	70	2500	2000	2600
22	21300	27900	27800	22	17600	17000	11500	22	4500	3500	2400
79	41600	38200	31600	79	15200	18000	16500	79	2600	700	700
45	34200	37900	31700	45	13600	14700	11700	45	2400	2200	2700
47	21800	23700	26900	47	11400	17700	17500	47	2600	2600	1600
33	29900	32600	36300	33	15800	11700	11500	33	2300	2000	2500
29	11100	8800	10600	29	10500	11200	13700	29	1400	1900	1400
37	31700	31900	31600	37	11100	12000	16500	37	1900	2100	3000
53	30200	26200	26100	53	12300	14900	13400	53	3500	4200	3300
20	45600	40800	31000	20	17600	18500	16200	20	1100	4100	3000
28	22700	24800	3050	28	9750	15350	7900	28	1350	1500	1550
35	23800	20900	23380	35	14280	11620	14400	35	2360	2680	2000
25	10960	19300	20700	25	7520	13700	6200	25	1560	2600	1300
7	17520	13120	8160	7	10760	8640	3520	7	2960	1760	880
52	8840	8300	6460	52	14480	16660	17000	52	5440	2040	3740
82	8640	10240	9320	82	8640	12320	20160	82	2480	2080	2480
71	22114	21463	26992	71	18536	18536	14309	71	2440	3200	3280
40	14000	12520	17440	40	9640	14880	15480	40	1080	1800	1480
43	14600	29320	27120	43	6960	12600	15840	43	840	3240	4520
4	7560	8080	9080	4	8160	8560	9560	4	2160	1760	2280
15	15600	14950	18768	15	15450	12100	17493	15	2450	4550	3009
55	16550	14000	13200	55	11250	12350	16650	55	3000	2950	2800
36	22542	15092	16150	36	8976	10682	15250	36	2601	2107	5100
8	11324	22474	28012	8	19072	17847	23840	8	3120	4160	2600
63	21800	23840	20960	63	17440	17560	15040	63	3520	2760	2920
76	11560	15840	23880	76	12560	11200	17120	76	2680	2320	2680
51	13000	5800	8480	51	9880	11880	11840	51	3240	1840	3560
77	24040	23920	26040	77	15120	15200	14400	77	3080	2800	3200
84	7920	9680	9360	84	6400	10400	10120	84	3040	2560	3000
56	14760	20640	16560	56	9040	11520	15040	56	2120	2400	2920
78	22900	19600	27200	78	8600	14100	15000	78	1700	4400	800
65	22150	13950	10000	65	12150	9900	18000	65	1900	2000	3150
83	13480	14840	9640	83	14960	11400	15280	83	2320	3080	3120
69	12250	8400	10900	69	10800	4450	13150	69	1800	1700	3350
1	20800	18450	22300	1	17500	16500	17050	1	4650	2400	3250
27	20120	19360	27840	27	9800	20960	22160	27	2800	3600	4200
85	7760	9360	9840	85	7760	9040	10920	85	4360	3800	3680
9	16150	12850	10700	9	13800	8750	14350	9	3050	2500	2500
67	13680	11320	14000	67	8640	6320	8120	67	1880	2600	2080
66	21300	18400	12600	66	9400	18500	14900	66	2900	4200	2800

ANNEX VIII Analysts results

Analyst Code	Lingulodinium polyedrum (cells/L)			Analyst Code	paralia sulcata (cells/L)			Analyst Code	Dytilum Brightwellii (cells/L)		
	sample 1	sample 2	sample 3		sample 1	sample 2	sample 3		sample 1	sample 2	sample 3
12	4200	5320	5560	12	5400	15880	14080	12	1400	1760	720
88	6000	6720	6040	88	1880	9800	11640	88	1520	3120	2280
64	6360	6760	5440	64	4720	12760	11720	64	2680	2600	1120
19	7360	6120	5480	19	15720	13320	22560	19	3400	4000	3760
42	7640	3440	6280	42	33280	30960	8840	42	3200	5360	2600
62	5560	7240	5920	62	19760	22480	25760	62	3480	4320	2680
80	5800	7000	7320	80	14720	20840	9680	80	2880	3400	2800
5	6880	6760	7560	5	12480	9920	14600	5	4200	3480	4440
41	5760	7440	7360	41	13840	7440	8880	41	5080	5440	3200
60	6200	6500	7450	60	5850	15400	10200	60	2650	2600	1650
89	7920	7880	7760	89	11320	19440	25960	89	4080	3120	3400
75	7800	6600	6800	75	11600	8400	19200	75	2600	1800	1800
49	7161	7696	6361	49	14472	12802	9895	49	3059	3367	2864
81	4320	6240	7440	81	6520	18640	11680	81	960	680	560
68	5280	5600	9120	68	8320	6840	10720	68	2680	2840	2680
10	8400	8320	6840	10	14680	19480	23560	10	1240	3040	2360
6	1738	5296	1763	6	132088	31775	NR	6	1738	1765	NR
61	7120	7920	6280	61	13600	21360	9160	61	1120	3880	3160
23	5400	6040	6480	23	19720	12040	22560	23	1640	1240	1040
11	1280	2200	1560	11	NR	NR	NR	11	0	1360	5320
86	3080	3920	6400	86	NR	NR	NR	86	2960	120	80
17	6960	6720	8560	17	0	12240	15440	17	0	1320	200
16	5560	4480	6720	16	NR	NR	NR	16	120	40	1680
3	7240	5640	8160	3	12520	6960	6800	3	3120	2680	1920
24	6800	4000	6300	24	3800	11500	32600	24	3200	2700	2600
72	6520	4840	7800	72	8440	14560	10680	72	3280	2880	3760
2	6412	6870	8244	2	11200	12400	11720	2	2600	2800	3040
14	6720	7000	5200	14	22800	8680	12880	14	2960	2800	3400
26	3640	2960	3120	26	7120	10680	9600	26	1320	1480	720
21	8479	7218	7087	21	16827	10653	18870	21	5000	2870	478
18	8174	7131	7479	18	11783	16218	20653	18	2435	3261	2957
38	5696	6826	8783	38	15001	12827	17305	38	2826	2565	1130
50	5000	8320	6280	50	13520	14080	9720	50	2040	2640	3200
44	2480	4960	4040	44	5640	11600	4160	44	2400	2040	2160
48	7040	7400	6120	48	4480	16840	29440	48	3840	3120	2800
32	2400	2560	4720	32	11200	12960	4560	32	400	640	560
13	6400	4560	4800	13	14400	6200	6280	13	2240	1120	920
39	7560	6120	5640	39	11640	9320	11320	39	3040	3080	1560
54	7700	7623	8278	54	4813	4312	10164	54	3157	2657	3427
30	7038	5769	7615	30	6500	8846	19654	30	3731	1346	3192
58	5846	5885	3385	58	8808	19692	9692	58	3808	5385	2923
87	7654	6654	7923	87	8692	12423	17885	87	3654	2615	5346
59	5360	8680	7280	59	8040	30800	7920	59	480	280	1440
31	5500	5300	7600	31	7300	27700	2500	31	4500	0	2600
70	6400	7500	7900	70	6500	4200	15300	70	2100	600	2500
22	7000	8800	8100	22	17700	19700	8800	22	2800	1200	500
79	7000	8700	6200	79	16900	21600	8100	79	3400	0	100
45	6700	6600	7000	45	12300	13000	15700	45	2000	1000	2500
47	5700	6800	8000	47	10400	18900	15700	47	2300	1100	1700
33	3600	5900	7900	33	18700	11800	16300	33	400	1300	1100
29	3000	4400	5700	29	5300	7600	8400	29	1400	1600	1100
37	5900	6800	6600	37	15000	13900	12000	37	2100	2800	800
53	9900	9100	8400	53	14900	15200	12900	53	1200	2600	2900
20	9900	9600	7700	20	2700	9900	12100	20	100	1300	1100
28	6550	8200	3550	28	11950	16800	7800	28	NR	200	1100
35	5200	5320	5720	35	8980	4040	11000	35	2540	2940	1260
25	NR	NR	NR	25	NR	NR	NR	25	2520	3800	900
7	7120	5360	4000	7	11280	16160	7120	7	3040	2520	1920
52	6460	5440	5780	52	3400	5780	7820	52	4080	2720	3120
82	4720	5200	5920	82	16960	12160	13760	82	3360	1600	2320
71	6880	7240	6640	71	21680	23040	10680	71	920	1200	2720
40	6400	6360	6440	40	15080	16600	14880	40	1040	1480	2480
43	3080	5600	7600	43	22240	33480	19040	43	1480	3760	4040
4	2480	2600	3880	4	9840	8720	10880	4	2320	2480	2680
15	6300	5900	8109	15	28000	5050	4284	15	1950	3100	3570
55	6900	5800	7500	55	10450	22750	10000	55	3550	3650	2700
36	7140	6419	7750	36	2091	1519	2600	36	1479	1470	3950
8	9536	11237	10728	8	18960	15800	15920	8	3280	3720	2120
63	9160	7720	8080	63	22200	17320	12880	63	5400	2960	2560
76	6000	4840	5320	76	8920	6040	24320	76	2000	1440	1880
51	7400	6600	7840	51	18160	10400	16440	51	3520	3920	3720
77	6800	6720	6920	77	12080	22560	12320	77	2680	2040	2640
84	3880	5080	3960	84	8040	12000	10120	84	1880	3040	2760
56	7400	7320	8160	56	24040	9360	18240	56	1640	1680	2080
78	8300	7700	7500	78	3400	18200	7000	78	1900	4800	5000
65	7300	5100	4450	65	15200	25400	8450	65	1800	1800	3050
83	6560	5760	6680	83	30000	5280	11080	83	4160	3280	3760
69	6550	5400	7000	69	11400	4350	19400	69	3350	1200	4150
1	8450	7600	8950	1	5900	20300	25600	1	2300	2850	2850
27	5840	8320	9680	27	13280	13360	9720	27	2840	3000	2640
85	5160	4280	4960	85	27400	20600	26120	85	3400	2280	2560
9	5900	4650	4750	9	23950	14250	15550	9	4100	3700	3650
67	3560	3920	3520	67	8560	3000	17000	67	1200	3160	2840
66	4800	6900	4800	66	2100	3800	21200	66	3200	3800	4400

ANNEX VIII Analysts results

Analyst Code	Coscinodiscus granii(cells/L)			Analyst Code	Guinardia delicatula (cells/L)			Analyst Code	Asterionellopsis gracialis (cells/L)		
	sample 1	sample 2	sample 3		sample 1	sample 2	sample 3		sample 1	sample 2	sample 3
12	1520	1120	1400	12	3200	3920	5160	12	NR	NR	NR
88	1120	1560	1440	88	3440	9200	7440	88	NR	NR	NR
64	1800	1600	1880	64	4400	4200	6640	64	NR	NR	NR
19	1840	1480	1360	19	2760	5200	6840	19	600	160	0
42	2400	2320	1440	42	5920	5280	5480	42	120	0	0
62	2000	1200	1360	62	7200	6440	3960	62	0	120	1520
80	2040	1520	1840	80	5760	6360	6880	80	0	0	120
5	1680	2120	1480	5	4800	5880	8400	5	NR	NR	NR
41	1600	1480	1600	41	6920	6600	9720	41	NR	NR	NR
60	2250	1650	1250	60	7050	14900	8800	60	NR	NR	NR
89	1520	1680	2240	89	6960	7000	9200	89	0	160	120
75	2200	2400	3200	75	4000	9200	7800	75	NR	NR	NR
49	1790	1739	1488	49	6042	7770	8407	49	0	148	2939
81	1800	1720	1480	81	2200	5360	3800	81	NR	NR	NR
68	1280	960	1320	68	5760	6480	6880	68	NR	NR	NR
10	1920	1880	1520	10	2000	4120	8840	10	NR	NR	NR
6	5214	1765	3527	6	8690	1765	3527	6	NR	NR	NR
61	2320	1800	1720	61	1800	7600	8080	61	80	40	0
23	1640	1600	1560	23	3240	5920	5120	23	NR	NR	NR
11	1160	1800	1320	11	1480	880	2480	11	NR	NR	NR
86	1440	2280	2000	86	2440	1720	3200	86	NR	NR	NR
17	1720	1720	1600	17	4480	1600	3440	17	360	0	0
16	1520	1400	1560	16	1720	3280	1960	16	NR	NR	NR
3	1360	1040	1600	3	4720	3280	8120	3	NR	NR	NR
24	1400	1400	1900	24	3800	4000	2800	24	NR	NR	NR
72	1880	1000	1720	72	3920	4560	7640	72	NR	NR	NR
2	1760	1720	1520	2	4800	4520	4640	2	NR	NR	NR
14	1760	1920	1680	14	2520	3920	4520	14	NR	NR	NR
26	1440	1360	1320	26	2800	2680	3200	26	NR	NR	NR
21	1826	1391	1391	21	4435	5392	6565	21	174	130	87
18	1913	2044	1652	18	5826	6305	5826	18	87	43	0
38	1478	2000	1522	38	4522	1391	5870	38	217	2391	609
50	1520	1440	1480	50	3440	3880	6840	50	280	0	0
44	1560	1440	1280	44	4240	1920	4000	44	NR	NR	NR
48	1720	1680	1800	48	6000	4200	4680	48	NR	NR	NR
32	1520	1680	1120	32	1520	1280	1440	32	NR	NR	NR
13	1960	1560	1760	13	2360	4920	3600	13	40	120	200
39	1640	1400	1600	39	5960	6320	7920	39	NR	NR	NR
54	1964	1579	1540	54	5852	5583	6699	54	NR	NR	NR
30	1115	1308	1692	30	7500	3962	8962	30	0	808	0
58	885	1808	1000	58	5808	4808	1615	58	462	77	0
87	1423	1923	1885	87	6462	4269	3038	87	0	38	0
59	1640	1760	1120	59	3160	3240	3120	59	NR	NR	NR
31	1600	1100	2400	31	3900	5000	3400	31	200	0	0
70	1200	1400	2100	70	4700	1600	2700	70	NR	NR	NR
22	2400	2100	2200	22	7500	9700	1900	22	NR	NR	NR
79	2300	1800	1800	79	4200	7300	7700	79	NR	NR	NR
45	1600	2000	1300	45	5800	7200	5600	45	100	300	0
47	1500	2000	1900	47	4300	9500	4300	47	200	900	1400
33	1400	1100	1900	33	4900	3200	2300	33	500	0	0
29	1000	1700	900	29	1900	2100	1400	29	NR	NR	NR
37	1400	1300	1600	37	4400	4800	6600	37	0	0	900
53	1400	1200	1600	53	4200	7500	7100	53	NR	NR	NR
20	2500	2300	1600	20	1000	3200	2300	20	NR	NR	NR
28	1200	1450	1350	28	1500	4100	250	28	NR	NR	400
35	1800	1920	1700	35	6180	4480	6720	35	NR	NR	NR
25	1480	1600	1600	25	4320	7600	4600	25	NR	NR	NR
7	1880	1280	1320	7	4160	3440	1680	7	NR	NR	NR
52	2040	1120	1680	52	8840	6120	9180	52	NR	NR	NR
82	2320	1360	1600	82	2880	6800	8000	82	NR	NR	NR
71	1360	2040	1880	71	6080	5480	3520	71	NR	NR	NR
40	1360	1680	1720	40	1360	5560	4800	40	NR	NR	NR
43	800	1360	1880	43	3200	3680	5400	43	NR	NR	NR
4	1880	1680	1760	4	5800	4880	4400	4	NR	NR	NR
15	1800	1200	1632	15	7150	5500	8313	15	NR	NR	NR
55	1200	1700	1050	55	2300	5000	7050	55	50	50	250
36	1275	1617	2450	36	3264	2744	5200	36	NR	NR	NR
8	1520	1840	1520	8	9400	7640	9080	8	360	160	640
63	1880	1520	1760	63	9160	8960	9560	63	520	720	320
76	1280	1360	1520	76	7680	4680	4960	76	280	440	240
51	1600	1640	1880	51	11080	8680	6720	51	1280	560	320
77	1600	1640	1680	77	7920	6600	6920	77	NR	NR	NR
84	1880	1920	1480	84	4480	4200	4040	84	NR	NR	NR
56	1960	1560	1640	56	4480	2880	9280	56	80	1320	120
78	1300	1700	1600	78	5100	7900	6000	78	NR	NR	NR
65	1800	2200	1350	65	3700	3800	9600	65	NR	NR	NR
83	1360	1800	1480	83	10120	4760	8240	83	NR	NR	NR
69	1750	2050	2500	69	3750	2500	8950	69	NR	NR	NR
1	1600	1750	2700	1	5600	11450	9400	1	NR	NR	NR
27	1400	1560	1960	27	5280	10080	12320	27	NR	NR	NR
85	1720	1800	1400	85	3240	2800	3360	85	280	0	0
9	2050	1450	1650	9	3200	3050	4850	9	NR	NR	NR
67	1200	1200	1280	67	2520	4760	6520	67	NR	NR	NR
66	2500	1500	1400	66	3300	8200	7000	66	500	200	100

Annex IX: Robust mean and Standard deviation calculation according to algorithm A annex C ISO13528

Scrippsiella iteration

ANALYST CODE	Average	X-X*	X*i	it2	it3	it4	it5
58	5320	12296	6731	7344	7379	7383	7383
32	7227	10390	7227	7344	7379	7383	7383
52	7867	9750	7867	7867	7867	7867	7867
11	8053	9563	8053	8053	8053	8053	8053
4	8240	9377	8240	8240	8240	8240	8240
84	8987	8630	8987	8987	8987	8987	8987
85	8987	8630	8987	8987	8987	8987	8987
51	9093	8523	9093	9093	9093	9093	9093
88	9360	8257	9360	9360	9360	9360	9360
82	9400	8217	9400	9400	9400	9400	9400
16	10000	7617	10000	10000	10000	10000	10000
29	10167	7450	10167	10167	10167	10167	10167
69	10517	7100	10517	10517	10517	10517	10517
6	10544	7072	10544	10544	10544	10544	10544
30	10718	6899	10718	10718	10718	10718	10718
54	11063	6554	11063	11063	11063	11063	11063
42	11427	6190	11427	11427	11427	11427	11427
24	12500	5117	12500	12500	12500	12500	12500
83	12653	4963	12653	12653	12653	12653	12653
7	12933	4683	12933	12933	12933	12933	12933
67	13000	4617	13000	13000	13000	13000	13000
9	13233	4383	13233	13233	13233	13233	13233
19	13573	4043	13573	13573	13573	13573	13573
75	14200	3417	14200	14200	14200	14200	14200
64	14573	3043	14573	14573	14573	14573	14573
55	14583	3033	14583	14583	14583	14583	14583
40	14653	2963	14653	14653	14653	14653	14653
80	15187	2430	15187	15187	15187	15187	15187
72	15281	2335	15281	15281	15281	15281	15281
65	15367	2250	15367	15367	15367	15367	15367
48	16093	1523	16093	16093	16093	16093	16093
15	16439	1177	16439	16439	16439	16439	16439
26	16613	1003	16613	16613	16613	16613	16613
87	16680	937	16680	16680	16680	16680	16680
86	16827	790	16827	16827	16827	16827	16827
28	16850	767	16850	16850	16850	16850	16850
25	16987	630	16987	16987	16987	16987	16987
50	17027	590	17027	17027	17027	17027	17027
76	17093	523	17093	17093	17093	17093	17093
23	17227	390	17227	17227	17227	17227	17227
56	17320	297	17320	17320	17320	17320	17320
66	17433	183	17433	17433	17433	17433	17433
12	17800	183	17800	17800	17800	17800	17800
60	17883	267	17883	17883	17883	17883	17883
36	17928	311	17928	17928	17928	17928	17928
61	18173	557	18173	18173	18173	18173	18173
41	18200	583	18200	18200	18200	18200	18200
49	18539	922	18539	18539	18539	18539	18539
44	18560	943	18560	18560	18560	18560	18560
62	18587	970	18587	18587	18587	18587	18587
3	19187	1570	19187	19187	19187	19187	19187
39	19280	1663	19280	19280	19280	19280	19280
5	19747	2130	19747	19747	19747	19747	19747
1	20517	2900	20517	20517	20517	20517	20517
8	20603	2987	20603	20603	20603	20603	20603
13	20680	3063	20680	20680	20680	20680	20680
18	20813	3196	20812	20812	20812	20812	20812
21	21131	3514	21131	21131	21131	21131	21131
81	21693	4077	21693	21693	21693	21693	21693
63	22200	4583	22200	22200	22200	22200	22200
27	22440	4823	22440	22440	22440	22440	22440
35	22693	5077	22693	22693	22693	22693	22693
14	22848	5231	22848	22848	22848	22848	22848
2	23053	5436	23053	23053	23053	23053	23053
78	23233	5617	23233	23233	23233	23233	23233
71	23523	5906	23523	23523	23523	23523	23523
43	23680	6063	23680	23680	23680	23680	23680
47	24133	6517	24133	24133	24133	24133	24133
77	24667	7050	24667	24667	24667	24667	24667
22	25667	8050	25667	25667	25667	25667	25667
31	26067	8450	26067	26067	26067	26067	26067
70	26100	8483	26100	26100	26100	26100	26100
38	26479	8863	26479	26479	26479	26479	26479
10	26893	9277	26893	26893	26893	26893	26893
53	27500	9883	27500	27500	27500	27500	27500
59	29147	11530	28502	28502	28502	28502	28502
89	30480	12863	28502	28502	28502	28502	28502
37	31733	14117	28502	28502	28502	28502	28502
17	32107	14490	28502	28502	28502	28502	28502
33	32933	15317	28502	28502	28502	28502	28502
45	34600	16983	28502	28502	28502	28502	28502
68	34796	17179	28502	28502	28502	28502	28502
79	37133	19517	28502	28502	28502	28502	28502
20	39133	21517	28502	28502	28502	28502	28502
Average X	18617		18092	18101	18101	18102	18102
SD S	7432		6318	6303	6302	6301	6301
robust average X^*	17617	new X^*	18092	18101	18101	18102	18102
robust stdev S^*	7257	new S^*	7165	7148	7146	7146	7146
$\delta = 1.5S^*$	10885		10747	10721	10719	10719	10719
$X^* - \delta$	6731		7344	7379	7383	7383	7383
$X^* + \delta$	28502		28839	28822	28820	28820	28820
no of analysts P	84		84	84	84	84	84
Between Samples SD	946	From homogeneity test					
new stdev for Scripps	7208						

Annex IX: *Prorocentrum micans* iteration

ANALYST CODE	Averag	X-X*	X*i	it2	it3	it4
32	5253	7807	8833	8541	8440	8440
54	6802	6258	8833	8541	8440	8440
26	7160	5900	8833	8541	8440	8440
7	7640	5420	8833	8541	8440	8440
67	7693	5367	8833	8541	8440	8440
6	8191	4869	8833	8541	8440	8440
68	8327	4733	8833	8541	8440	8440
4	8760	4300	8833	8541	8440	8440
19	8787	4273	8833	8541	8440	8440
84	8973	4087	8973	8973	8973	8973
25	9140	3920	9140	9140	9140	9140
85	9240	3820	9240	9240	9240	9240
69	9467	3593	9467	9467	9467	9467
12	9653	3407	9653	9653	9653	9653
44	9733	3327	9733	9733	9733	9733
16	9813	3247	9813	9813	9813	9813
87	10205	2855	10205	10205	10205	10205
60	10317	2743	10317	10317	10317	10317
64	10520	2540	10520	10520	10520	10520
81	10693	2367	10693	10693	10693	10693
28	11000	2060	11000	11000	11000	11000
11	11067	1993	11067	11067	11067	11067
51	11200	1860	11200	11200	11200	11200
58	11474	1586	11474	11474	11474	11474
36	11636	1424	11636	11636	11636	11636
62	11680	1380	11680	11680	11680	11680
5	11733	1327	11733	11733	11733	11733
29	11800	1260	11800	11800	11800	11800
43	11800	1260	11800	11800	11800	11800
31	11833	1227	11833	11833	11833	11833
56	11867	1193	11867	11867	11867	11867
86	11947	1113	11947	11947	11947	11947
61	12013	1047	12013	12013	12013	12013
9	12300	760	12300	12300	12300	12300
50	12427	633	12427	12427	12427	12427
70	12500	560	12500	12500	12500	12500
30	12552	508	12552	12552	12552	12552
24	12567	493	12567	12567	12567	12567
78	12567	493	12567	12567	12567	12567
38	12928	132	12928	12928	12928	12928
33	13000	60	13000	13000	13000	13000
88	13040	20	13040	13040	13040	13040
10	13080	20	13080	13080	13080	13080
13	13147	87	13147	13147	13147	13147
37	13200	140	13200	13200	13200	13200
80	13320	260	13320	13320	13320	13320
45	13333	273	13333	13333	13333	13333
40	13333	273	13333	13333	13333	13333
65	13350	290	13350	13350	13350	13350
55	13417	357	13417	13417	13417	13417
35	13433	373	13433	13433	13433	13433
53	13533	473	13533	13533	13533	13533
76	13627	567	13627	13627	13627	13627
82	13707	647	13707	13707	13707	13707
59	13747	687	13747	13747	13747	13747
23	13787	727	13787	13787	13787	13787
83	13880	820	13880	13880	13880	13880
39	13907	847	13907	13907	13907	13907
14	13917	857	13917	13917	13917	13917
3	14147	1087	14147	14147	14147	14147
48	14200	1140	14200	14200	14200	14200
66	14267	1207	14267	14267	14267	14267
2	14885	1825	14885	14885	14885	14885
77	14907	1847	14907	14907	14907	14907
75	15000	1940	15000	15000	15000	15000
15	15014	1954	15014	15014	15014	15014
17	15040	1980	15040	15040	15040	15040
42	15053	1993	15053	15053	15053	15053
49	15310	2250	15310	15310	15310	15310
22	15367	2307	15367	15367	15367	15367
47	15533	2473	15533	15533	15533	15533
21	15740	2680	15740	15740	15740	15740
72	15809	2749	15809	15809	15809	15809
41	15920	2860	15920	15920	15920	15920
52	16047	2987	16047	16047	16047	16047
18	16276	3216	16276	16276	16276	16276
79	16567	3507	16567	16567	16567	16567
63	16680	3620	16680	16680	16680	16680
1	17017	3957	17017	17017	17017	17017
71	17127	4067	17127	17101	17101	17101
20	17433	4373	17287	17101	17101	17101
27	17640	4580	17287	17101	17101	17101
89	18400	5340	17287	17101	17101	17101
8	20253	7193	17287	17101	17101	17101
Average *X*	12746		12821	12780	12770	12770
SD *S*	2875		2516	2551	2570	2570
robust average *X**	13060	new *X**	12821	12780	12770	12770
robust stdev *S**	2818	new *S**	2853	2893	2914	2914
δ= 1.5*S**	4227		4280	4340	4371	4371
X*- δ	8833		8541	8440	8398	8398
X*+ δ	17287		17101	17120	17141	17141
no of analysts *P*	84		84	84	84	84
Between Samples SD	389	From homogeneity test				

Annex IX: *P. australis* iteration

ANALYST CODE	Averag	X-X*	X*i	it2
81	533	1917	1393	1393
16	827	1623	1393	1393
17	1027	1423	1393	1393
32	1120	1330	1393	1393
26	1293	1157	1393	1393
79	1333	1117	1393	1393
11	1400	1050	1400	1400
3	1400	1050	1400	1400
40	1453	997	1453	1453
28	1467	983	1467	1467
29	1567	883	1567	1567
12	1707	743	1707	1707
60	1717	733	1717	1717
44	1733	717	1733	1733
58	1795	655	1795	1795
25	1820	630	1820	1820
7	1867	583	1867	1867
62	1933	517	1933	1933
86	1947	503	1947	1947
61	1987	463	1987	1987
38	2058	392	2058	2058
4	2067	383	2067	2067
64	2120	330	2120	2120
48	2160	290	2160	2160
50	2187	263	2187	2187
67	2187	263	2187	2187
47	2267	183	2267	2267
33	2267	183	2267	2267
59	2280	170	2280	2280
69	2283	167	2283	2283
78	2300	150	2300	2300
24	2333	117	2333	2333
37	2333	117	2333	2333
35	2347	103	2347	2347
82	2347	103	2347	2347
65	2350	100	2350	2350
30	2359	91	2359	2359
80	2360	90	2360	2360
70	2367	83	2367	2367
54	2412	38	2412	2412
14	2413	37	2413	2413
45	2433	17	2433	2433
88	2467	17	2467	2467
5	2467	17	2467	2467
56	2480	30	2480	2480
10	2560	110	2560	2560
76	2560	110	2560	2560
89	2613	163	2613	2613
13	2613	163	2613	2613
9	2683	233	2683	2683
68	2720	270	2720	2720
23	2720	270	2720	2720
31	2733	283	2733	2733
20	2733	283	2733	2733
39	2747	297	2747	2747
83	2840	390	2840	2840
43	2867	417	2867	2867
84	2867	417	2867	2867
51	2880	430	2880	2880
2	2893	443	2893	2893
55	2917	467	2917	2917
75	2933	483	2933	2933
19	2947	497	2947	2947
49	2961	511	2961	2961
71	2973	523	2973	2973
77	3027	577	3027	3027
21	3029	579	3029	3029
63	3067	617	3067	3067
36	3269	819	3269	3269
8	3293	843	3293	3293
66	3300	850	3300	3300
41	3307	857	3307	3307
72	3333	883	3333	3333
15	3336	886	3336	3336
1	3433	983	3433	3433
22	3467	1017	3467	3467
27	3533	1083	3507	3507
87	3602	1152	3507	3507
53	3667	1217	3507	3507
18	3739	1289	3507	3507
52	3740	1290	3507	3507
85	3947	1497	3507	3507
6	4679	2229	3507	3507
42	5813	3363	3507	3507
Average *X*	2523		2494	2494
SD *S*	832		648	648
robust average *X**	2450	new *X**	2494	2494
robust stdev *S**	704	new *S**	735	735
δ= 1.5*S**	1057		1103	1103
X*- δ	1393		1391	1391
X*+ δ	3507		3597	3597
no of analysts *P*	84		84	84
Between Samples SD	898	From homogeneity test		
new stdev for PAUS	1161			

Annex IX: *Lingulodinium polyedrum* iteration

ANALYST CODE	Average	X-X*	X*i	it2
11	1680	4760	4608	4608
6	2932	3508	4608	4608
4	2987	3453	4608	4608
32	3227	3213	4608	4608
26	3240	3200	4608	4608
67	3667	2773	4608	4608
44	3827	2613	4608	4608
84	4307	2133	4608	4608
29	4367	2073	4608	4608
86	4467	1973	4608	4608
85	4800	1640	4800	4800
12	5027	1413	5027	5027
58	5039	1401	5039	5039
9	5100	1340	5100	5100
13	5253	1187	5253	5253
82	5280	1160	5280	5280
76	5387	1053	5387	5387
35	5413	1027	5413	5413
43	5427	1013	5427	5427
7	5493	947	5493	5493
66	5500	940	5500	5500
16	5587	853	5587	5587
65	5617	823	5617	5617
24	5700	740	5700	5700
42	5787	653	5787	5787
33	5800	640	5800	5800
52	5893	547	5893	5893
23	5973	467	5973	5973
81	6000	440	6000	6000
28	6100	340	6100	6100
31	6133	307	6133	6133
64	6187	253	6187	6187
62	6240	200	6240	6240
88	6253	187	6253	6253
14	6307	133	6307	6307
69	6317	123	6317	6317
19	6320	120	6320	6320
83	6333	107	6333	6333
72	6387	53	6387	6387
40	6400	40	6400	6400
37	6433	7	6433	6433
39	6440	0	6440	6440
50	6533	93	6533	6533
68	6667	227	6667	6667
80	6707	267	6707	6707
60	6717	277	6717	6717
55	6733	293	6733	6733
45	6767	327	6767	6767
15	6770	330	6770	6770
30	6807	367	6807	6807
77	6813	373	6813	6813
47	6833	393	6833	6833
41	6853	413	6853	6853
48	6853	413	6853	6853
71	6920	480	6920	6920
3	7013	573	7013	7013
5	7067	627	7067	7067
75	7067	627	7067	7067
49	7073	633	7073	7073
38	7102	662	7102	7102
36	7103	663	7103	7103
61	7107	667	7107	7107
59	7107	667	7107	7107
2	7175	735	7175	7175
70	7267	827	7267	7267
51	7280	840	7280	7280
79	7300	860	7300	7300
87	7410	970	7410	7410
17	7413	973	7413	7413
21	7595	1155	7595	7595
18	7595	1155	7595	7595
56	7627	1187	7627	7627
78	7833	1393	7833	7833
89	7853	1413	7853	7853
10	7853	1413	7853	7853
54	7867	1427	7867	7867
27	7947	1507	7947	7947
22	7967	1527	7967	7967
63	8320	1880	8272	8272
1	8333	1893	8272	8272
20	9067	2627	8272	8272
53	9133	2693	8272	8272
8	10500	4060	8272	8272
25	not id	not id	not id	not id
Average *X*	6320		6409	6409
SD *S*	1471		1084	1084
robust average *X**	6440	new *X**	6440	6440
robust stdev *S**	1221	new *S**	1229	1229
δ= 1.5*S**	1832		1844	1844
X*- δ	4608		4596	4596
X*+ δ	8272		8284	8284
no of analysts *P*	83		83	83
Between Samples SD		371	From homogeneity t	
new stdev for L.polyedrum		1284		

Annex IX: *Ditylum brightwellii* iteration

ANALYST COD	Averag	X-X*	X*i	it2
17	507	1967	1068	1068
32	533	1940	1068	1068
16	613	1860	1068	1068
28	650	1823	1068	1068
81	733	1740	1068	1068
59	733	1740	1068	1068
20	833	1640	1068	1068
33	933	1540	1068	1068
86	1053	1420	1068	1068
79	1167	1307	1167	1167
26	1173	1300	1173	1173
12	1293	1180	1293	1293
23	1307	1167	1307	1307
29	1367	1107	1367	1367
13	1427	1047	1427	1427
22	1500	973	1500	1500
71	1613	860	1613	1613
40	1667	807	1667	1667
47	1700	773	1700	1700
70	1733	740	1733	1733
6	1752	722	1752	1752
76	1773	700	1773	1773
56	1800	673	1800	1800
45	1833	640	1833	1833
37	1900	573	1900	1900
75	2067	407	2067	2067
64	2133	340	2133	2133
38	2174	300	2174	2174
44	2200	273	2200	2200
10	2213	260	2213	2213
65	2217	257	2217	2217
11	2227	247	2227	2227
53	2233	240	2233	2233
35	2247	227	2247	2247
36	2300	174	2300	2300
60	2300	173	2300	2300
88	2307	167	2307	2307
31	2367	107	2367	2367
67	2400	73	2400	2400
25	2407	67	2407	2407
82	2427	47	2427	2427
77	2453	20	2453	2453
7	2493	20	2493	2493
4	2493	20	2493	2493
39	2560	87	2560	2560
84	2560	87	2560	2560
3	2573	100	2573	2573
50	2627	153	2627	2627
1	2667	193	2667	2667
61	2720	247	2720	2720
68	2733	260	2733	2733
85	2747	273	2747	2747
30	2756	283	2756	2756
21	2783	309	2783	2783
2	2813	340	2813	2813
27	2827	353	2827	2827
24	2833	360	2833	2833
15	2873	400	2873	2873
18	2884	411	2884	2884
69	2900	427	2900	2900
80	3027	553	3027	3027
8	3040	567	3040	3040
14	3053	580	3053	3053
54	3080	607	3080	3080
43	3093	620	3093	3093
49	3097	623	3097	3097
48	3253	780	3253	3253
55	3300	827	3300	3300
72	3307	833	3307	3307
52	3307	833	3307	3307
62	3493	1020	3493	3493
89	3533	1060	3533	3533
63	3640	1167	3640	3640
19	3720	1247	3720	3720
42	3720	1247	3720	3720
51	3720	1247	3720	3720
83	3733	1260	3733	3733
66	3800	1327	3800	3800
9	3817	1343	3817	3817
87	3872	1398	3872	3872
78	3900	1427	3878	3878
58	4039	1565	3878	3878
5	4040	1567	3878	3878
41	4573	2100	3878	3878
Average *X*	2432		2455	2455
SD *S*	952		865	865
robust average *X**	2473	new *X**	2473	2473
robust stdev *S**	937	new *S**	981	981
δ= 1.5*S**	1405		1471	1471
X*- δ	1068		1002	1002
X*+ δ	3878		3944	3944
no of analysts *P*	84		84	84
Between Samples SD		510	From homogeneity test	
new stdev for D.brightwellii		1105		

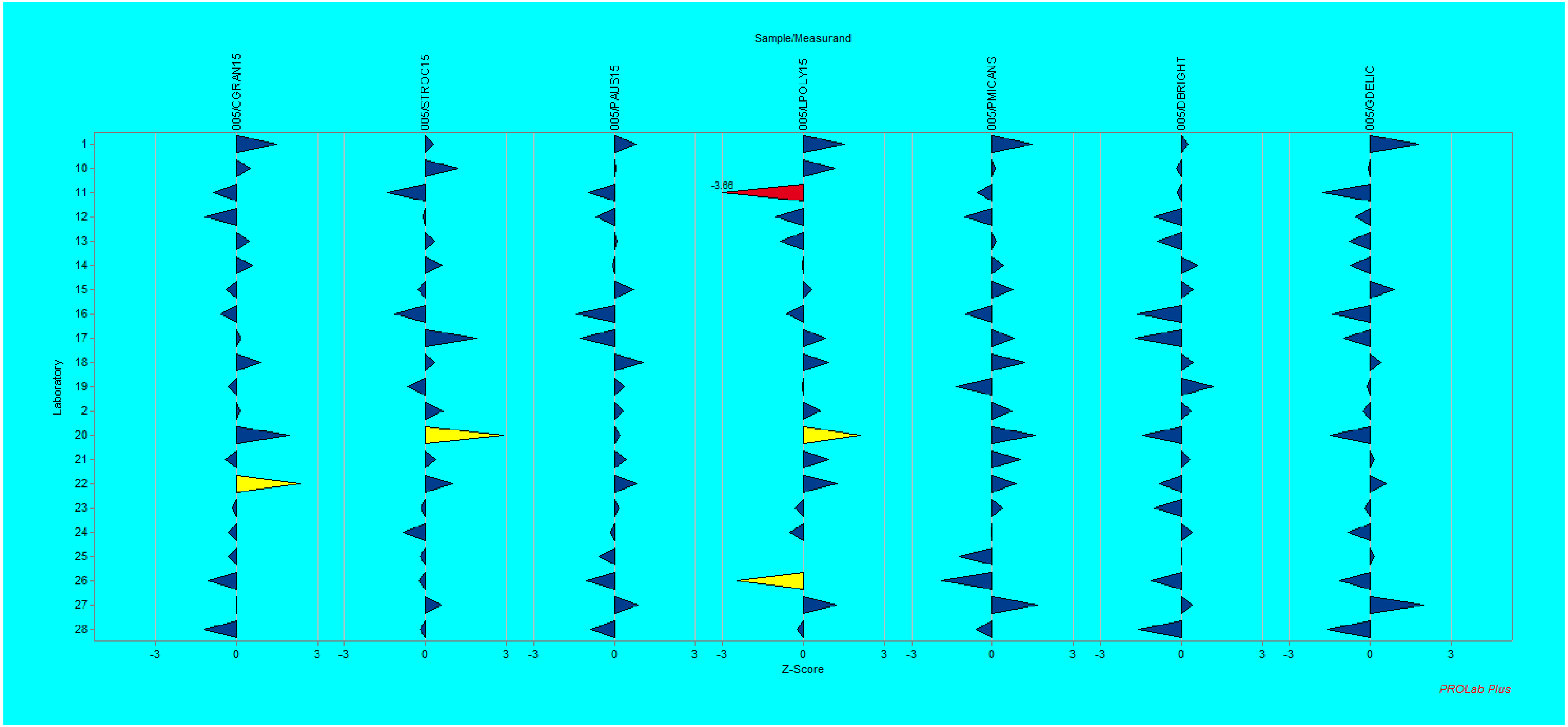
Annex IX: *Coscinodiscus granii* iteration

ANALYST COD	Averag	X-X*	X*i	it2
68	1187	453	1343	1343
29	1200	440	1343	1343
67	1227	413	1343	1343
58	1231	409	1343	1343
55	1317	323	1343	1343
3	1333	307	1343	1343
28	1333	307	1343	1343
12	1347	293	1347	1347
43	1347	293	1347	1347
30	1372	268	1347	1347
88	1373	267	1373	1373
26	1373	267	1373	1373
76	1387	253	1387	1387
53	1400	240	1400	1400
11	1427	213	1427	1427
44	1427	213	1427	1427
37	1433	207	1433	1433
32	1440	200	1440	1440
33	1467	173	1467	1467
50	1480	160	1480	1480
16	1493	147	1493	1493
7	1493	147	1493	1493
59	1507	133	1507	1507
62	1520	120	1520	1520
72	1533	107	1533	1533
78	1533	107	1533	1533
21	1536	104	1536	1536
15	1544	96	1544	1544
39	1547	93	1547	1547
83	1547	93	1547	1547
19	1560	80	1560	1560
41	1560	80	1560	1560
25	1560	80	1560	1560
24	1567	73	1567	1567
70	1567	73	1567	1567
40	1587	53	1587	1587
23	1600	40	1600	1600
52	1613	27	1613	1613
8	1627	13	1627	1627
45	1633	7	1633	1633
77	1640	0	1640	1640
27	1640	0	1640	1640
85	1640	0	1640	1640
81	1667	27	1667	1667
2	1667	27	1667	1667
38	1667	27	1667	1667
49	1672	32	1672	1672
17	1680	40	1680	1680
54	1694	54	1694	1694
31	1700	60	1700	1700
51	1707	67	1707	1707
60	1717	77	1717	1717
9	1717	77	1717	1717
63	1720	80	1720	1720
56	1720	80	1720	1720
48	1733	93	1733	1733
87	1744	104	1744	1744
64	1760	120	1760	1760
5	1760	120	1760	1760
13	1760	120	1760	1760
82	1760	120	1760	1760
71	1760	120	1760	1760
84	1760	120	1760	1760
10	1773	133	1773	1773
4	1773	133	1773	1773
36	1781	141	1781	1781
65	1783	143	1783	1783
14	1787	147	1787	1787
80	1800	160	1800	1800
47	1800	160	1800	1800
66	1800	160	1800	1800
35	1807	167	1807	1807
89	1813	173	1813	1813
18	1870	230	1870	1870
86	1907	267	1907	1907
61	1947	307	1937	1937
79	1967	327	1937	1937
1	2017	377	1937	1937
42	2053	413	1937	1937
69	2100	460	1937	1937
20	2133	493	1937	1937
22	2233	593	1937	1937
75	2600	960	1937	1937
6	3502	1862	1937	1937
Average *X*	1664		1633	1633
SD *S*	312		185	185
robust average *X**	1640	new *X**	1640	1640
robust stdev *S**	198	new *S**	209	209
δ= 1.5*S**	297		314	314
X*- δ	1343		1326	1326
X*+ δ	1937		1954	1954
no of analysts *P*	84		84	84
Between Samples SD		141	From homogeneity test	
new stdev for C.granii		252		

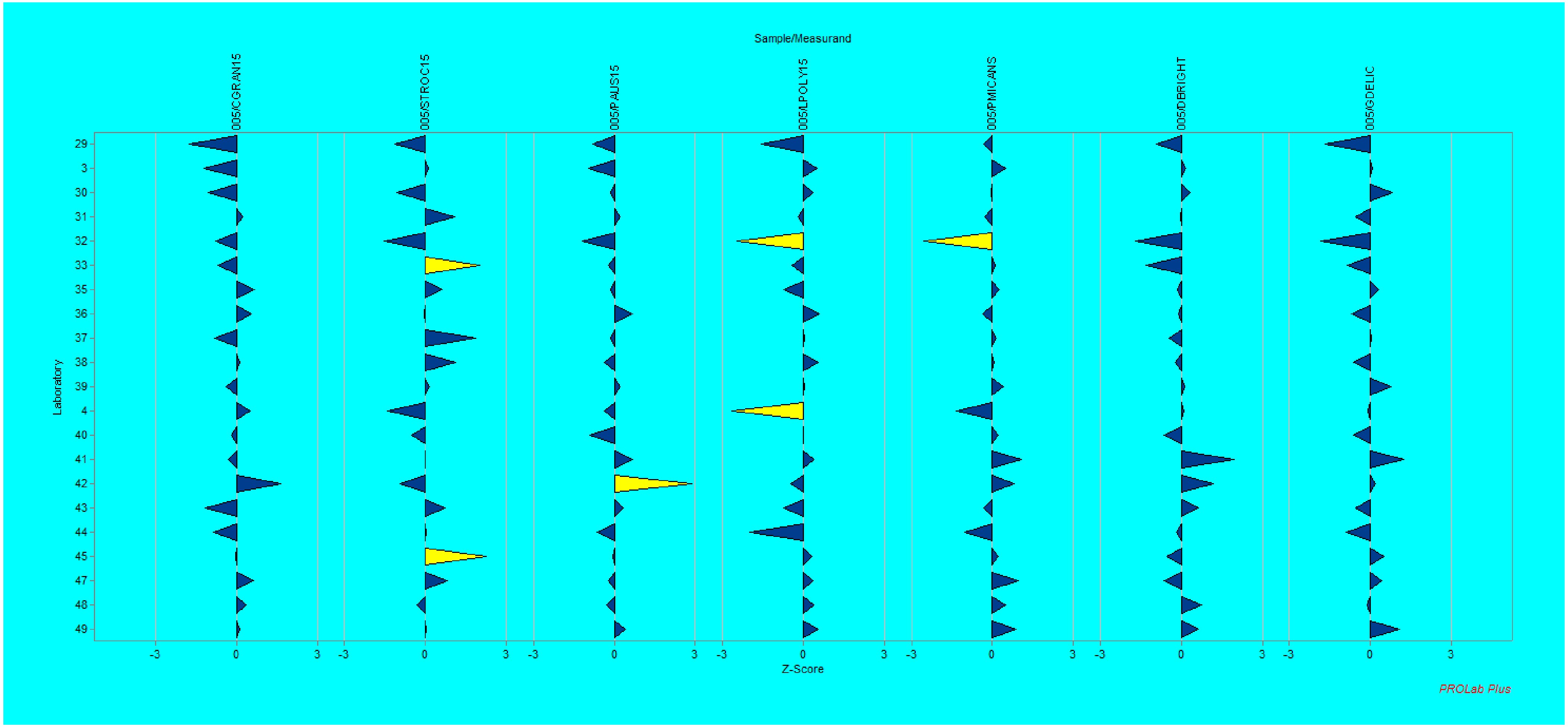
Annex IX: *Guinardia delicatula* iteration

ANALYST COD	Averag	X-X*	X*i	it2
32	1413	3760	2511	2511
11	1613	3560	2511	2511
29	1800	3373	2511	2511
28	1950	3223	2511	2511
20	2167	3007	2511	2511
16	2320	2853	2511	2511
86	2453	2720	2511	2511
26	2893	2280	2893	2893
70	3000	2173	3000	3000
7	3093	2080	3093	3093
85	3133	2040	3133	3133
17	3173	2000	3173	3173
59	3173	2000	3173	3173
44	3387	1787	3387	3387
33	3467	1707	3467	3467
24	3533	1640	3533	3533
13	3627	1547	3627	3627
14	3653	1520	3653	3653
9	3700	1473	3700	3700
36	3736	1437	3736	3736
81	3787	1387	3787	3787
40	3907	1267	3907	3907
38	3928	1246	3928	3928
58	4077	1096	4077	4077
12	4093	1080	4093	4093
43	4093	1080	4093	4093
31	4100	1073	4100	4100
84	4240	933	4240	4240
87	4590	584	4590	4590
67	4600	573	4600	4600
2	4653	520	4653	4653
6	4661	513	4661	4661
50	4720	453	4720	4720
23	4760	413	4760	4760
55	4783	390	4783	4783
19	4933	240	4933	4933
48	4960	213	4960	4960
10	4987	187	4987	4987
71	5027	147	5027	5027
4	5027	147	5027	5027
69	5067	107	5067	5067
64	5080	93	5080	5080
37	5267	93	5267	5267
3	5373	200	5373	5373
72	5373	200	5373	5373
21	5464	291	5464	5464
25	5507	333	5507	5507
56	5547	373	5547	5547
42	5560	387	5560	5560
65	5700	527	5700	5700
76	5773	600	5773	5773
35	5793	620	5793	5793
61	5827	653	5827	5827
62	5867	693	5867	5867
82	5893	720	5893	5893
18	5986	812	5986	5986
47	6033	860	6033	6033
54	6045	871	6045	6045
66	6167	993	6167	6167
45	6200	1027	6200	6200
53	6267	1093	6267	6267
80	6333	1160	6333	6333
78	6333	1160	6333	6333
5	6360	1187	6360	6360
22	6367	1193	6367	6367
68	6373	1200	6373	6373
79	6400	1227	6400	6400
88	6693	1520	6693	6693
39	6733	1560	6733	6733
30	6808	1635	6808	6808
15	6988	1814	6988	6988
75	7000	1827	7000	7000
77	7147	1973	7147	7147
49	7406	2233	7406	7406
83	7707	2533	7707	7707
89	7720	2547	7720	7720
41	7747	2573	7747	7747
52	8047	2873	7835	7835
8	8707	3533	7835	7835
1	8817	3643	7835	7835
51	8827	3653	7835	7835
63	9227	4053	7835	7835
27	9227	4053	7835	7835
60	10250	5077	7835	7835
Average X	5241		5188	5188
SD S	1885		1610	1610
robust average X^*	5173	new X^*	5173	5173
robust stdev S^*	1775	new S^*	1826	1826
$\delta = 1.5S^*$	2662		2739	2739
$X^* - \delta$	2511		2434	2434
$X^* + \delta$	7835		7913	7913
no of analysts P	84		84	84
Between Samples SD		897	From homogeneity test	
new stdev for G.delicatula		2035		

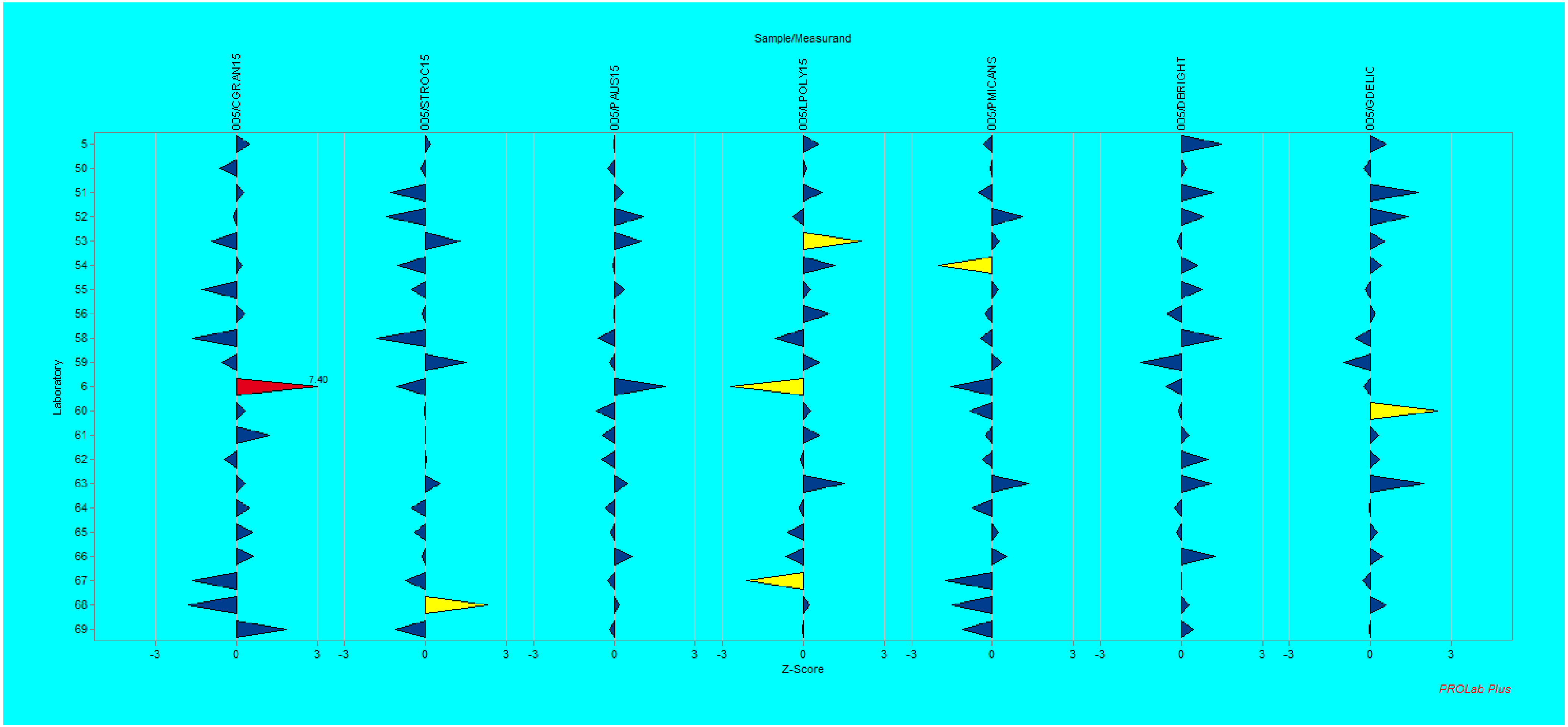
ANNEX X: Summary of Z-scores for all measurands



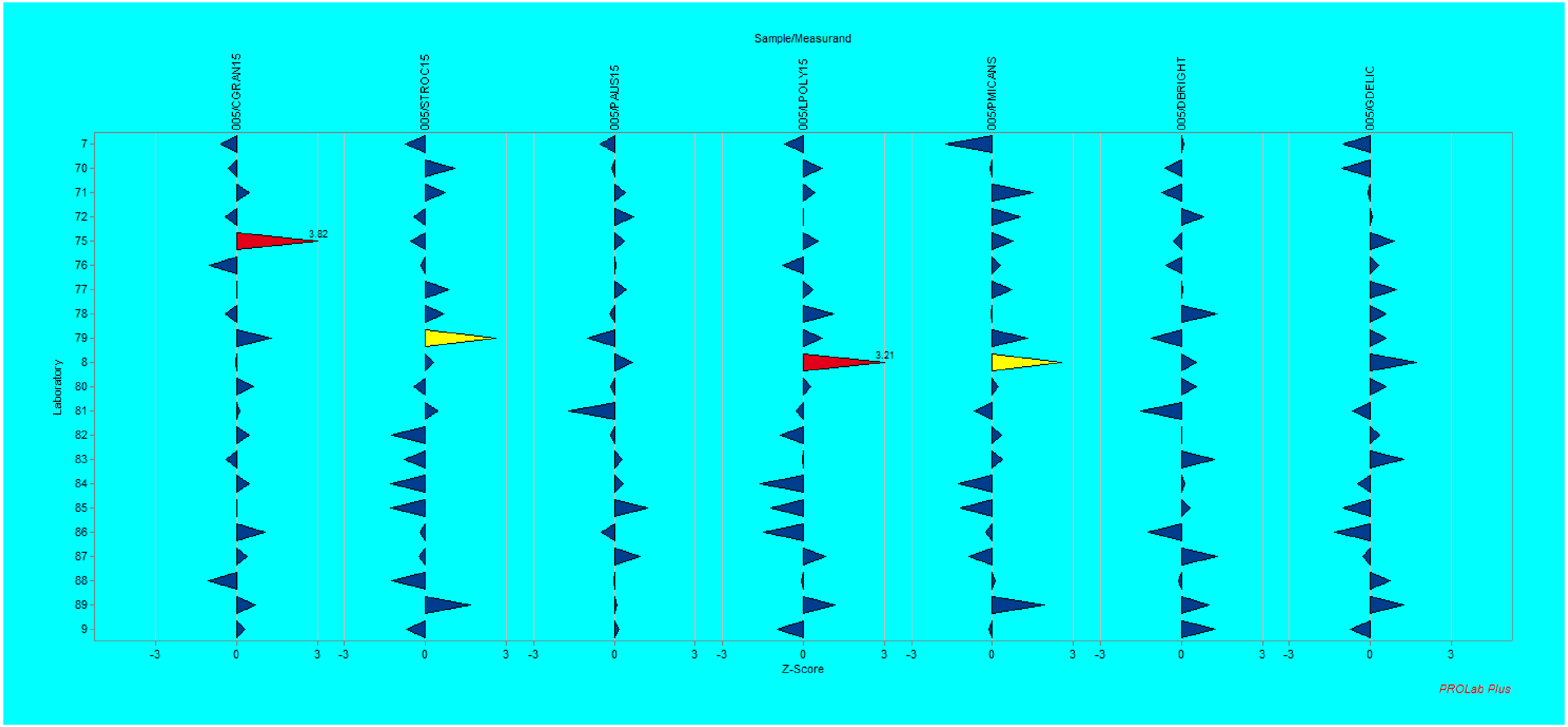
ANNEX X: Summary of Z-scores for all measurands



ANNEX X: Summary of Z-scores for all measurands



ANNEX X: Summary of Z-scores for all measurands



ANNEX XI: Summary of laboratory means

	Coscinodiscus	Z	Scrippsiella	Z	Pseudo-nitzschia	Z	Lingulodinium	Z	Prorocentrum	Z	Dytilum	Z	Guinardia	Z
	granii	score	trochoidea	score	australis	score	polyedrum	score	micans	score	brightwelli	score	delicatula	score
analyst code	cells/Litre		cells/Litre		cells/Litre		cells/Litre		cells/Litre		cells/Litre		cells/Litre	
1	2017	1.51	20517	0.31	3433	0.8	8333	1.52	17017	1.46	2667	0.23	8817	1.77
2	1667	0.12	23053	0.66	2893	0.34	7175	0.62	14885	0.73	2813	0.36	4653	-0.27
3	1333	-1.2	19187	0.12	1400	-0.95	7013	0.5	14147	0.48	2573	0.14	5373	0.08
4	1773	0.54	8240	-1.39	2067	-0.37	2987	-2.64	8760	-1.35	2493	0.07	5027	-0.09
5	1760	0.49	19747	0.2	2467	-0.03	7067	0.54	11733	-0.34	4040	1.47	6360	0.57
6	3502	7.4	10544	-1.08	4679	1.88	2932	-2.68	8191	-1.55	1752	-0.6	4661	-0.27
7	1493	-0.57	12933	-0.74	1867	-0.54	5493	-0.69	7640	-1.73	2493	0.07	3093	-1.04
8	1627	-0.04	20603	0.32	3293	0.68	10500	3.21	20253	2.56	3040	0.57	8707	1.72
9	1717	0.32	13233	-0.7	2683	0.16	5100	-0.99	12300	-0.15	3817	1.27	3700	-0.74
10	1773	0.54	26893	1.19	2560	0.05	7853	1.15	13080	0.12	2213	-0.18	4987	-0.11
11	1427	-0.83	8053	-1.42	1400	-0.95	1680	-3.66	11067	-0.57	2227	-0.17	1613	-1.77
12	1347	-1.15	17800	-0.07	1707	-0.68	5027	-1.05	9653	-1.05	1293	-1.01	4093	-0.55
13	1760	0.49	20680	0.33	2613	0.1	5253	-0.87	13147	0.14	1427	-0.89	3627	-0.78
14	1787	0.59	22848	0.63	2413	-0.07	6307	-0.05	13917	0.4	3053	0.58	3653	-0.76
15	1544	-0.37	16439	-0.26	3336	0.72	6770	0.31	15014	0.77	2873	0.42	6988	0.88
16	1493	-0.57	10000	-1.15	827	-1.44	5587	-0.61	9813	-0.99	613	-1.63	2320	-1.42
17	1680	0.17	32107	1.92	1027	-1.27	7413	0.81	15040	0.78	507	-1.73	3173	-1
18	1870	0.92	20813	0.35	3739	1.07	7595	0.95	16276	1.2	2884	0.43	5986	0.38
19	1560	-0.3	13573	-0.65	2947	0.39	6320	-0.04	8787	-1.34	3720	1.18	4933	-0.13
20	2133	1.97	39133	2.89	2733	0.2	9067	2.1	17433	1.6	833	-1.43	2167	-1.49
21	1536	-0.4	21131	0.39	3029	0.46	7595	0.95	15740	1.02	2783	0.33	5464	0.13
22	2233	2.37	25667	1.02	3467	0.83	7967	1.24	15367	0.89	1500	-0.83	6367	0.57
23	1600	-0.15	17227	-0.15	2720	0.19	5973	-0.31	13787	0.36	1307	-1	4760	-0.22
24	1567	-0.28	12500	-0.8	2333	-0.14	5700	-0.53	12567	-0.06	2833	0.38	3533	-0.82
25	1560	-0.3	16987	-0.18	1820	-0.59	< 0		9140	-1.22	2407	-0.01	5507	0.15
26	1373	-1.05	16613	-0.23	1293	-1.04	3240	-2.44	7160	-1.9	1173	-1.12	2893	-1.14
27	1640	0.01	22440	0.58	3533	0.89	7947	1.22	17640	1.67	2827	0.37	9227	1.98
28	1333	-1.2	16850	-0.2	1467	-0.89	6100	-0.21	11000	-0.59	650	-1.6	1950	-1.6
29	1200	-1.73	10167	-1.13	1567	-0.8	4367	-1.56	11800	-0.32	1367	-0.95	1800	-1.67
30	1372	-1.05	10718	-1.05	2359	-0.12	6807	0.34	12552	-0.06	2756	0.31	6808	0.79

ANNEX XI

analyst code	Coscinodiscus granii cells/Litre	Z score	Scrippsiella trochoidea cells/Litre	Z score	Pseudo-nitzschia australis cells/Litre	Z score	Lingulodinium polyedrum cells/Litre	Z score	Prorocentrum micans cells/Litre	Z score	Dytilum brightwelli cells/Litre	Z score	Guinardia delicatula cells/Litre	Z score
31	1700	0.25	26067	1.08	2733	0.2	6133	-0.19	11833	-0.31	2367	-0.04	4100	-0.54
32	1440	-0.78	7227	-1.54	1120	-1.19	3227	-2.45	5253	-2.55	533	-1.7	1413	-1.86
33	1467	-0.67	32933	2.03	2267	-0.2	5800	-0.45	13000	0.09	933	-1.34	3467	-0.86
35	1807	0.67	22693	0.61	2347	-0.13	5413	-0.75	13433	0.24	2247	-0.15	5793	0.29
36	1781	0.57	17928	-0.05	3269	0.66	7103	0.57	11636	-0.37	2300	-0.1	3736	-0.72
37	1433	-0.81	31733	1.86	2333	-0.14	6433	0.04	13200	0.16	1900	-0.47	5267	0.03
38	1667	0.12	26479	1.14	2058	-0.38	7102	0.57	12928	0.06	2174	-0.22	3928	-0.63
39	1547	-0.36	19280	0.14	2747	0.21	6440	0.05	13907	0.4	2560	0.13	6733	0.75
40	1587	-0.2	14653	-0.51	1453	-0.9	6400	0.02	13333	0.2	1667	-0.68	3907	-0.64
41	1560	-0.3	18200	-0.01	3307	0.7	6853	0.37	15920	1.08	4573	1.95	7747	1.25
42	2053	1.65	11427	-0.95	5813	2.85	5787	-0.46	15053	0.79	3720	1.18	5560	0.17
43	1347	-1.15	23680	0.75	2867	0.32	5427	-0.74	11800	-0.32	3093	0.61	4093	-0.55
44	1427	-0.83	18560	0.04	1733	-0.66	3827	-1.99	9733	-1.02	2200	-0.19	3387	-0.89
45	1633	-0.01	34600	2.26	2433	-0.06	6767	0.3	13333	0.2	1833	-0.53	6200	0.49
47	1800	0.65	24133	0.81	2267	-0.2	6833	0.36	15533	0.95	1700	-0.65	6033	0.41
48	1733	0.38	16093	-0.31	2160	-0.29	6853	0.37	14200	0.5	3253	0.76	4960	-0.12
49	1672	0.14	18539	0.03	2961	0.4	7073	0.54	15310	0.87	3097	0.62	7406	1.08
50	1480	-0.62	17027	-0.18	2187	-0.27	6533	0.12	12427	-0.11	2627	0.19	4720	-0.24
51	1707	0.28	9093	-1.28	2880	0.33	7280	0.7	11200	-0.52	3720	1.18	8827	1.78
52	1613	-0.09	7867	-1.45	3740	1.07	5893	-0.38	16047	1.13	3307	0.81	8047	1.4
53	1400	-0.94	27500	1.28	3667	1.01	9133	2.15	13533	0.27	2233	-0.16	6267	0.52
54	1694	0.23	11063	-1	2412	-0.07	7867	1.16	6802	-2.02	3080	0.6	6045	0.41
55	1317	-1.27	14583	-0.51	2917	0.36	6733	0.28	13417	0.23	3300	0.8	4783	-0.21
56	1720	0.33	17320	-0.14	2480	-0.02	7627	0.97	11867	-0.3	1800	-0.56	5547	0.17
58	1231	-1.61	5320	-1.8	1795	-0.61	5039	-1.04	11474	-0.43	4039	1.47	4077	-0.56
59	1507	-0.52	29147	1.51	2280	-0.19	7107	0.57	13747	0.34	733	-1.52	3173	-1
60	1717	0.32	17883	-0.06	1717	-0.67	6717	0.27	10317	-0.82	2300	-0.1	10250	2.48
61	1947	1.23	18173	-0.02	1987	-0.44	7107	0.57	12013	-0.25	2720	0.28	5827	0.3
62	1520	-0.46	18587	0.04	1933	-0.49	6240	-0.11	11680	-0.36	3493	0.98	5867	0.32

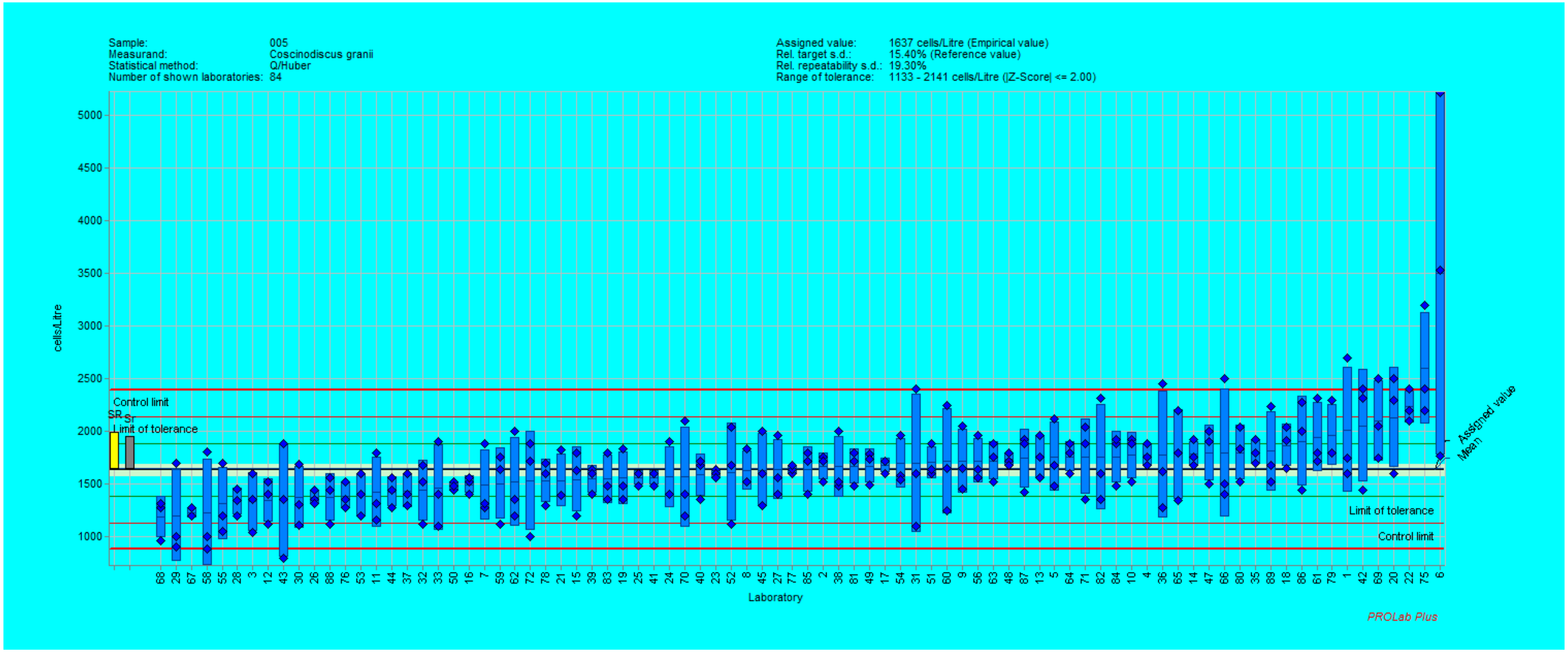
ANNEX XI

analyst code	Coscinodiscus granii cells/Litre	Z score	Scrippsiella trochoidea cells/Litre	Z score	Pseudo-nitzschia australis cells/Litre	Z score	Lingulodinium polyedrum cells/Litre	Z score	Prorocentrum micans cells/Litre	Z score	Dytilum brightwelli cells/Litre	Z score	Guinardia delicatula cells/Litre	Z score
63	1720	0.33	22200	0.54	3067	0.49	8320	1.51	16680	1.34	3640	1.11	9227	1.98
64	1760	0.49	14573	-0.52	2120	-0.33	6187	-0.15	10520	-0.75	2133	-0.25	5080	-0.06
65	1783	0.58	15367	-0.41	2350	-0.13	5617	-0.59	13350	0.21	2217	-0.18	5700	0.24
66	1800	0.65	17433	-0.12	3300	0.69	5500	-0.68	14267	0.52	3800	1.25	6167	0.47
67	1227	-1.63	13000	-0.73	2187	-0.27	3667	-2.11	7693	-1.72	2400	-0.01	4600	-0.3
68	1187	-1.79	34796	2.29	2720	0.19	6667	0.23	8327	-1.5	2733	0.29	6373	0.57
69	2100	1.84	10517	-1.08	2283	-0.19	6317	-0.05	9467	-1.11	2900	0.44	5067	-0.07
70	1567	-0.28	26100	1.08	2367	-0.11	7267	0.69	12500	-0.08	1733	-0.62	3000	-1.08
71	1760	0.49	23523	0.73	2973	0.41	6920	0.42	17127	1.49	1613	-0.72	5027	-0.09
72	1533	-0.41	15281	-0.42	3333	0.72	6387	0.01	15809	1.04	3307	0.81	5373	0.08
75	2600	3.82	14200	-0.57	2933	0.37	7067	0.54	15000	0.77	2067	-0.31	7000	0.88
76	1387	-0.99	17093	-0.17	2560	0.05	5387	-0.77	13627	0.3	1773	-0.58	5773	0.28
77	1640	0.01	24667	0.88	3027	0.45	6813	0.34	14907	0.74	2453	0.04	7147	0.95
78	1533	-0.41	23233	0.69	2300	-0.17	7833	1.14	12567	-0.06	3900	1.34	6333	0.55
79	1967	1.31	37133	2.61	1333	-1	7300	0.72	16567	1.3	1167	-1.13	6400	0.59
80	1800	0.65	15187	-0.43	2360	-0.12	6707	0.26	13320	0.2	3027	0.55	6333	0.55
81	1667	0.12	21693	0.47	533	-1.69	6000	-0.29	10693	-0.7	733	-1.52	3787	-0.7
82	1760	0.49	9400	-1.23	2347	-0.13	5280	-0.85	13707	0.33	2427	0.01	5893	0.34
83	1547	-0.36	12653	-0.78	2840	0.29	6333	-0.03	13880	0.39	3733	1.19	7707	1.23
84	1760	0.49	8987	-1.29	2867	0.32	4307	-1.61	8973	-1.28	2560	0.13	4240	-0.48
85	1640	0.01	8987	-1.29	3947	1.25	4800	-1.23	9240	-1.19	2747	0.3	3133	-1.02
86	1907	1.07	16827	-0.2	1947	-0.48	4467	-1.49	11947	-0.27	1053	-1.23	2453	-1.35
87	1744	0.42	16680	-0.22	3602	0.95	7410	0.81	10205	-0.86	3872	1.32	4590	-0.3
88	1373	-1.05	9360	-1.24	2467	-0.03	6253	-0.1	13040	0.1	2307	-0.1	6693	0.73
89	1813	0.7	30480	1.69	2613	0.1	7853	1.15	18400	1.93	3533	1.01	7720	1.23

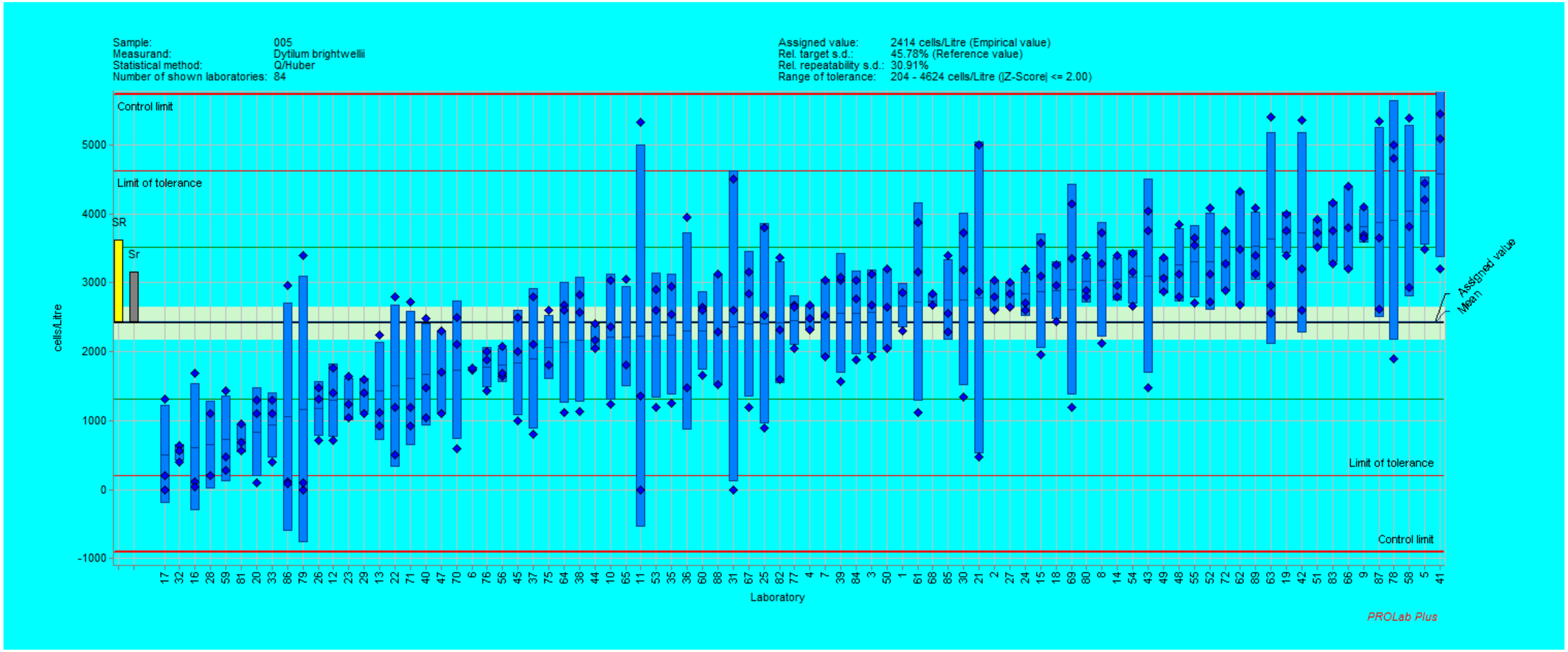
ANNEX XI

	Coscinodiscus granii cells/Litre	Z score	Scrippsiella trochoidea cells/Litre	Z score	Pseudo-nitzschia australis cells/Litre	Z score	Lingulodinium polyedrum cells/Litre	Z score	Prorocentrum micans cells/Litre	Z score	Dytilum brightwelli cells/Litre	Z score	Guinardia delicatula cells/Litre	Z score
Statistical method	Q/Huber		Q/Huber		Q/Huber		Q/Huber		Q/Huber		Q/Huber		Q/Huber	
Assessment	|Z|<=2.00		|Z|<=2.00		|Z|<=2.00		|Z|<=2.00		|Z|<=2.00		|Z|<=2.00		|Z|<=2.00	
No. of laboratories that submitted results	84		84		84		84		84		84		84	
No. of participants (according to design)	84		84		84		84		84		84		84	
No. of laboratories with quantitative values	84		84		84		83		84		84		84	
Arithmetical mean	1644		18538		2491		6277		12729		2433		5196	
Median	1625		17609		2500		6550		12580		2600		4800	
Assigned value	1637		18294		2499		6376		12738		2414		5207	
Mean	1637		18294		2499		6376		12738		2414		5207	
Reference value	1640		18102		2494		6440		12770		2473		5173	
Target s.d.	252		7208		1161		1284		2940		1105		2035	
Reproducibility s.d.	353		7901		933		1599		3819		1205		2443	
Repeatability s.d.	316		3096		611		1149		2499		746		1764	
Rel. target s.d.	15.40 %		39.40 %		46.45 %		20.14 %		23.08 %		45.78 %		39.08 %	
Rel. reproducibility s.d.	21.57 %		43.19 %		37.31 %		25.08 %		29.98 %		49.91 %		46.91 %	
Rel. repeatability s.d.	19.30 %		16.92 %		24.44 %		18.03 %		19.62 %		30.91 %		33.87 %	
Reference s.d.	252		7208		1161		1284		2940		1105		2035	
Limit of reproducibility, R (2.80 X sR)	989		22124		2611		4478		10693		3373		6839	
Limit of repeatability, r (2.80 X sr)	885		8668		1710		3218		6998		2089		4939	
Rel. limit of reproducibility	60.40 %		120.94 %		104.48 %		70.24 %		83.95 %		139.74 %		131.35 %	
Rel. limit of repeatability	54.04 %		47.38 %		68.42 %		50.47 %		54.93 %		86.55 %		94.84 %	
HORRAT	23.45		86.29		75.39		37.63		47.87		73.91		70.84	
Absolute classical Horwitz s.d.	11		84		15		34		61		15		29	
Relative classical Horwitz s.d.	0.66 %		0.46 %		0.62 %		0.54 %		0.48 %		0.62 %		0.55 %	
Lower limit of tolerance	1133		3878		177		3808		6858		204		1137	
Upper limit of tolerance	2141		32710		4821		8944		18618		4624		9277	
Standard error	26		817		86		142		352		113		215	
Lower confidence limit	1584		16660		2327		6091		12034		2187		4776	
Upper confidence limit	1689		19927		2671		6660		13442		2641		5638	
Type F outliers	0		0		0		0		0		0		0	
No. of laboratories	84		84		84		83		84		84		84	
Number of laboratories with replicates outside of tolerance limits	31		11		7		21		17		15		15	
Number of laboratories with mean outside of tolerance limits	3		5		1		9		3		0		1	
No. of measurement values and states	84		84		84		84		84		84		84	
No. of measurement values	252		252		252		249		252		250		252	
No. of measurement values without outliers	252		252		252		249		252		250		252	

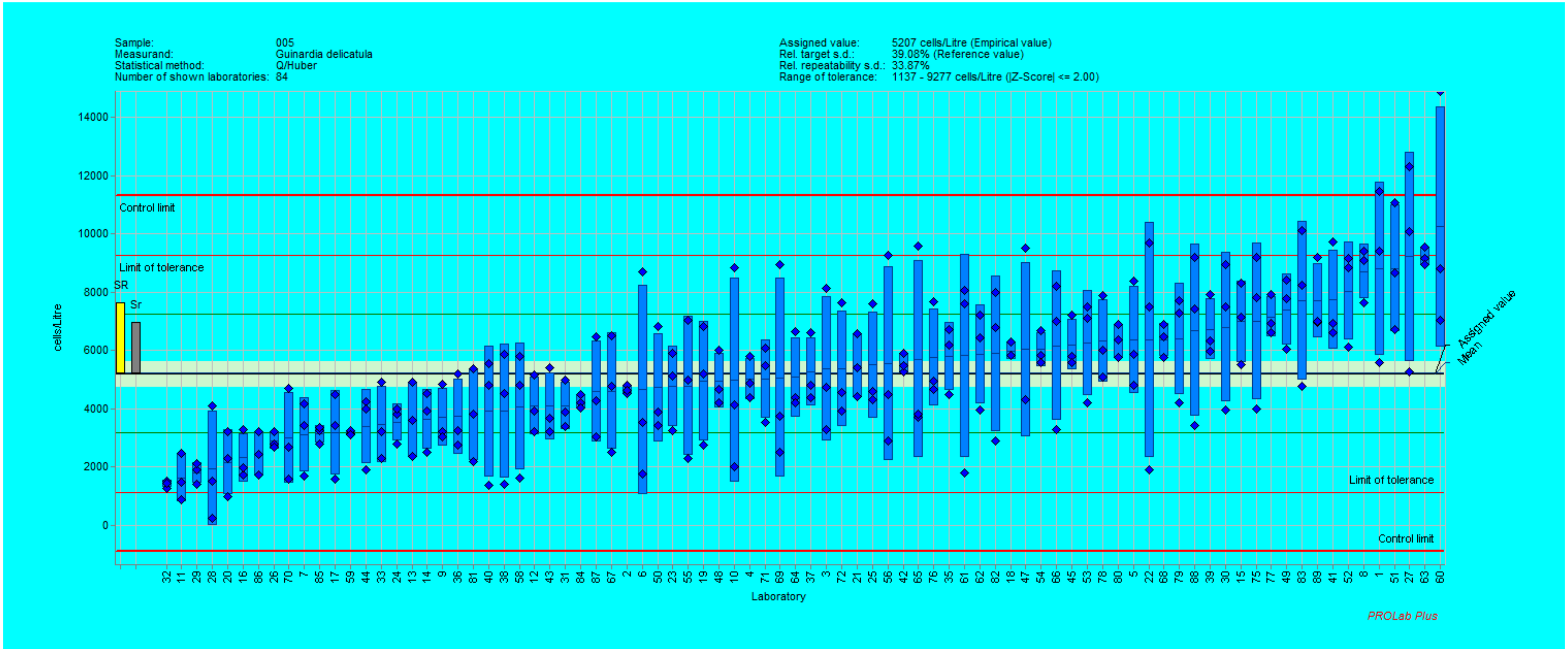
ANNEX XII: Graphical summary of results cells/L by analysts



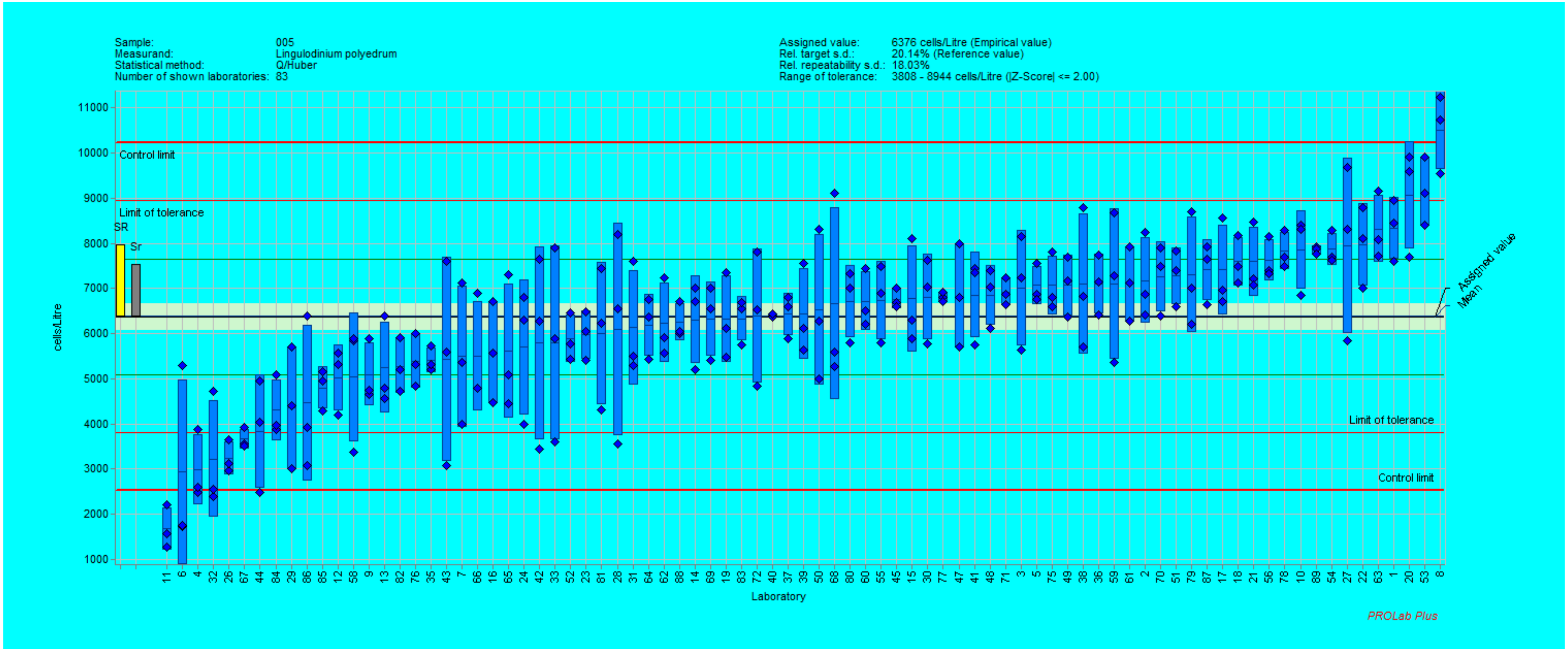
ANNEX XII Graphical summary of results cells/L by analysts



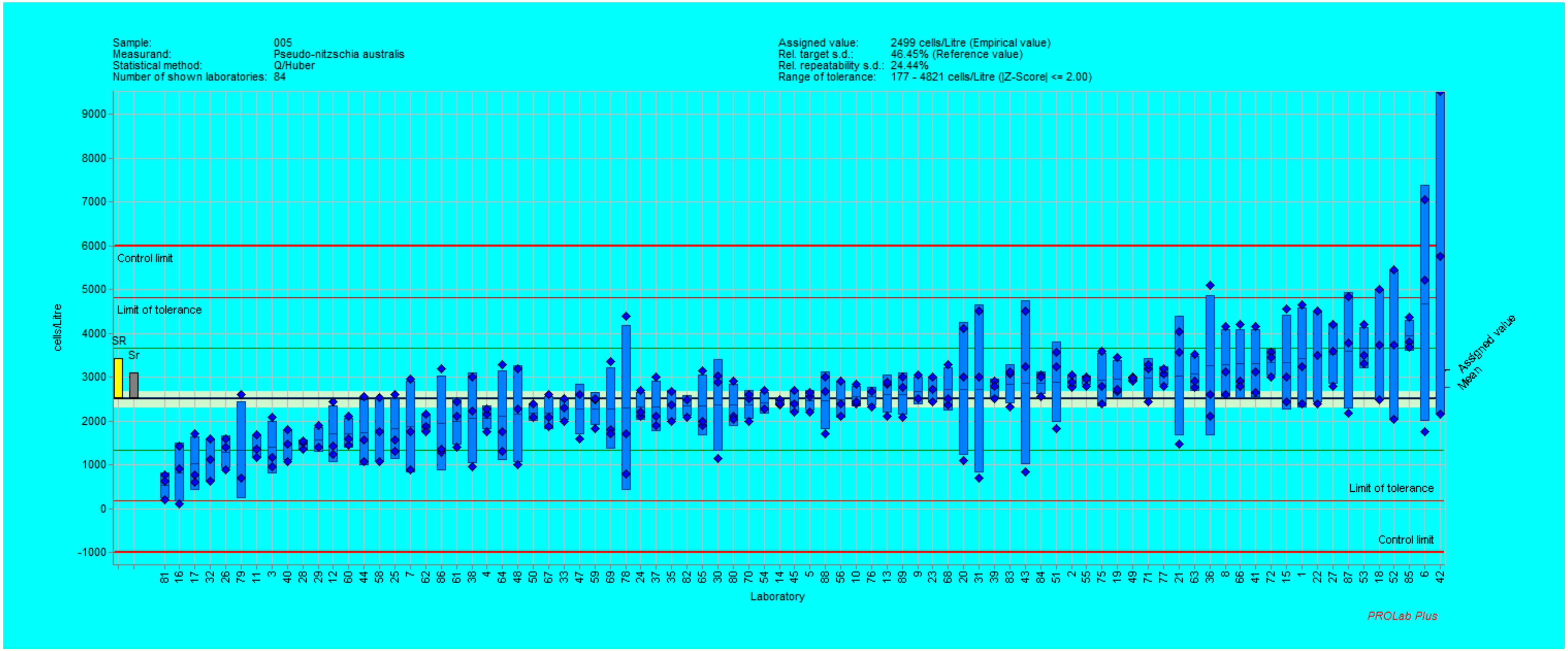
ANNEX XII Graphical summary of results cells/L by analysts



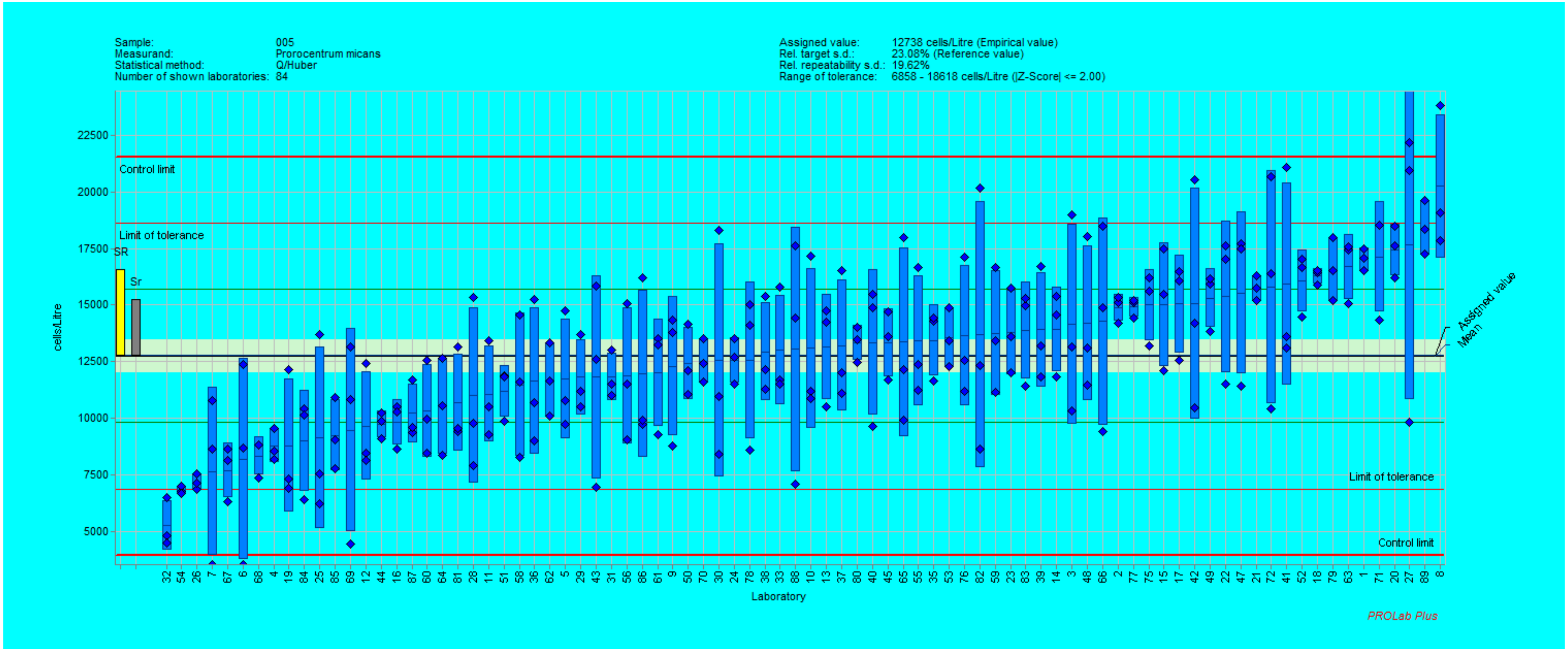
ANNEX XII Graphical summary of results cells/L by analysts



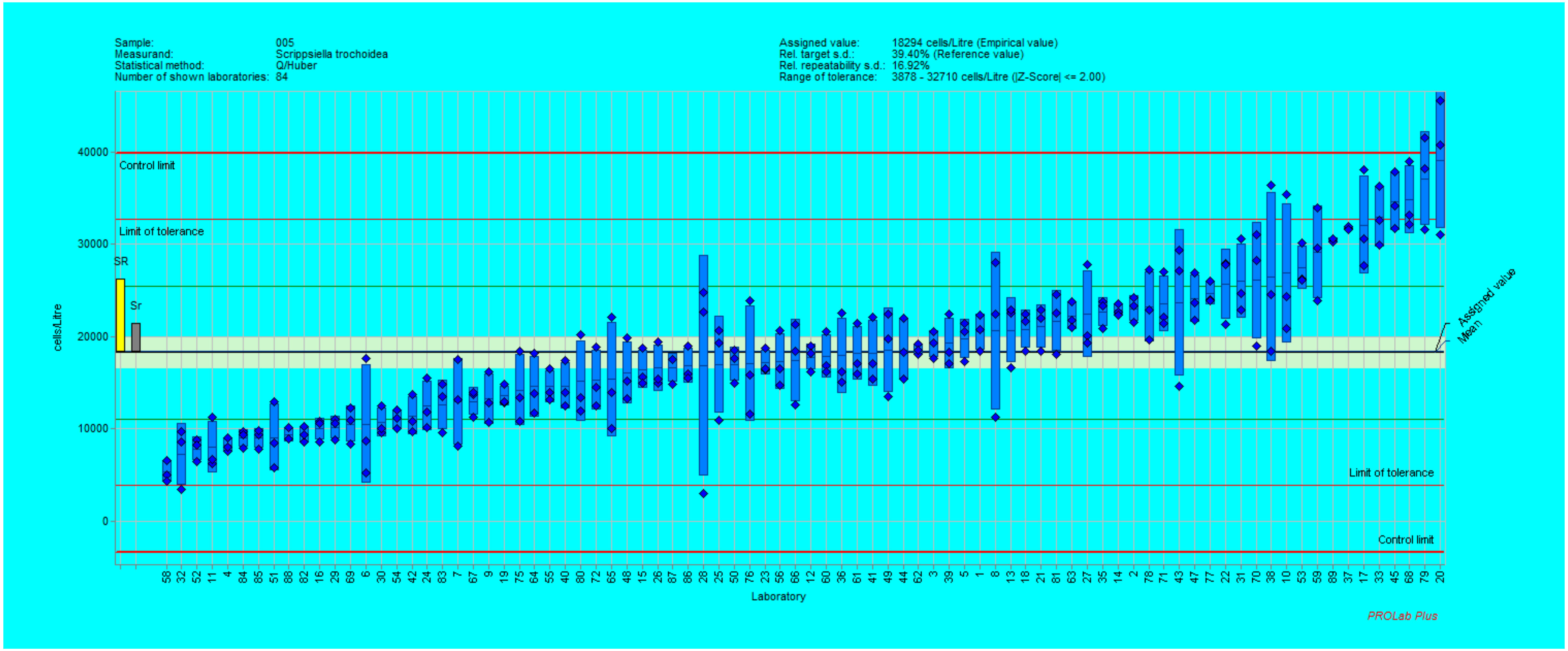
ANNEX XII Graphical summary of results cells/L by analysts



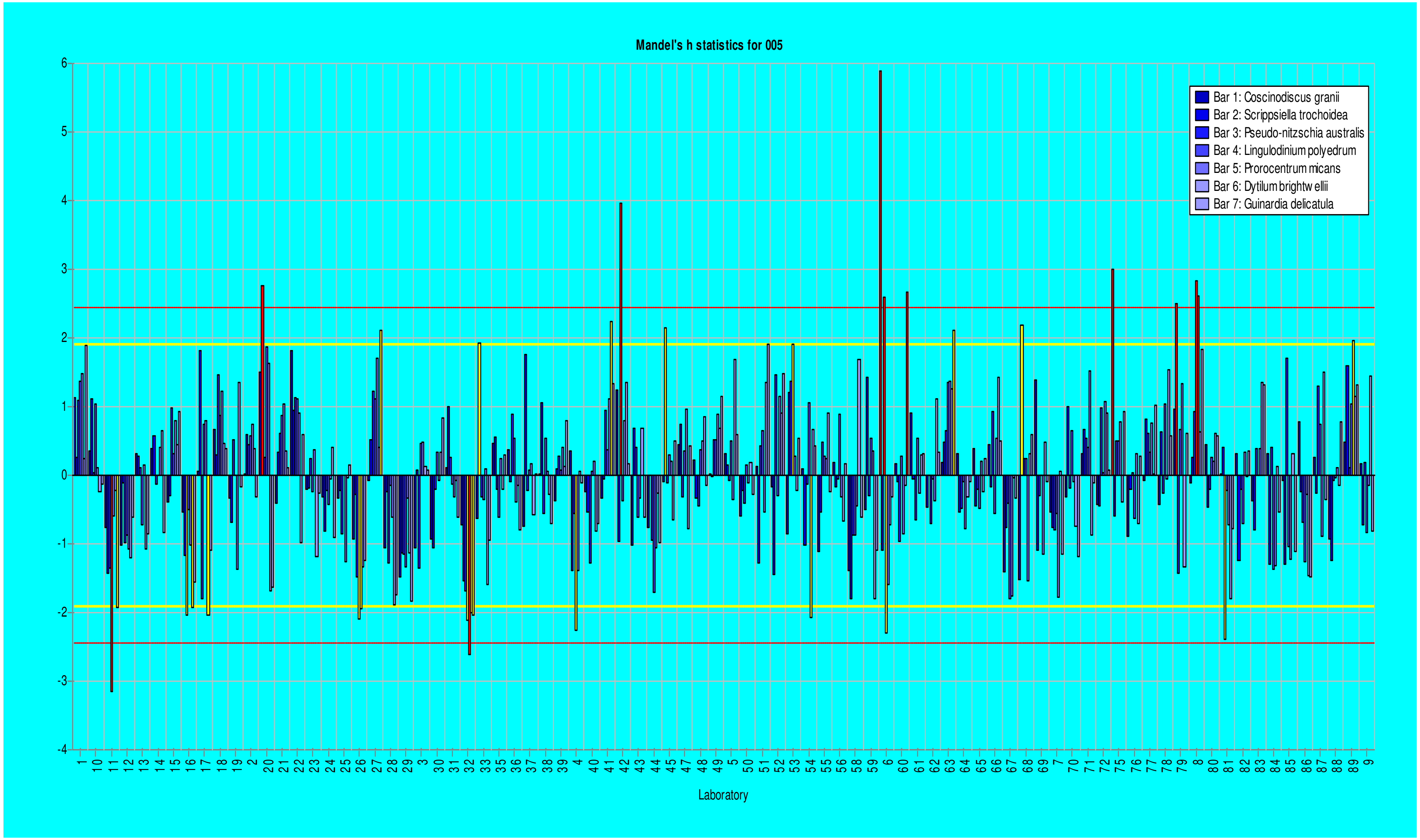
ANNEX XII Graphical summary of results cells/L by analysts



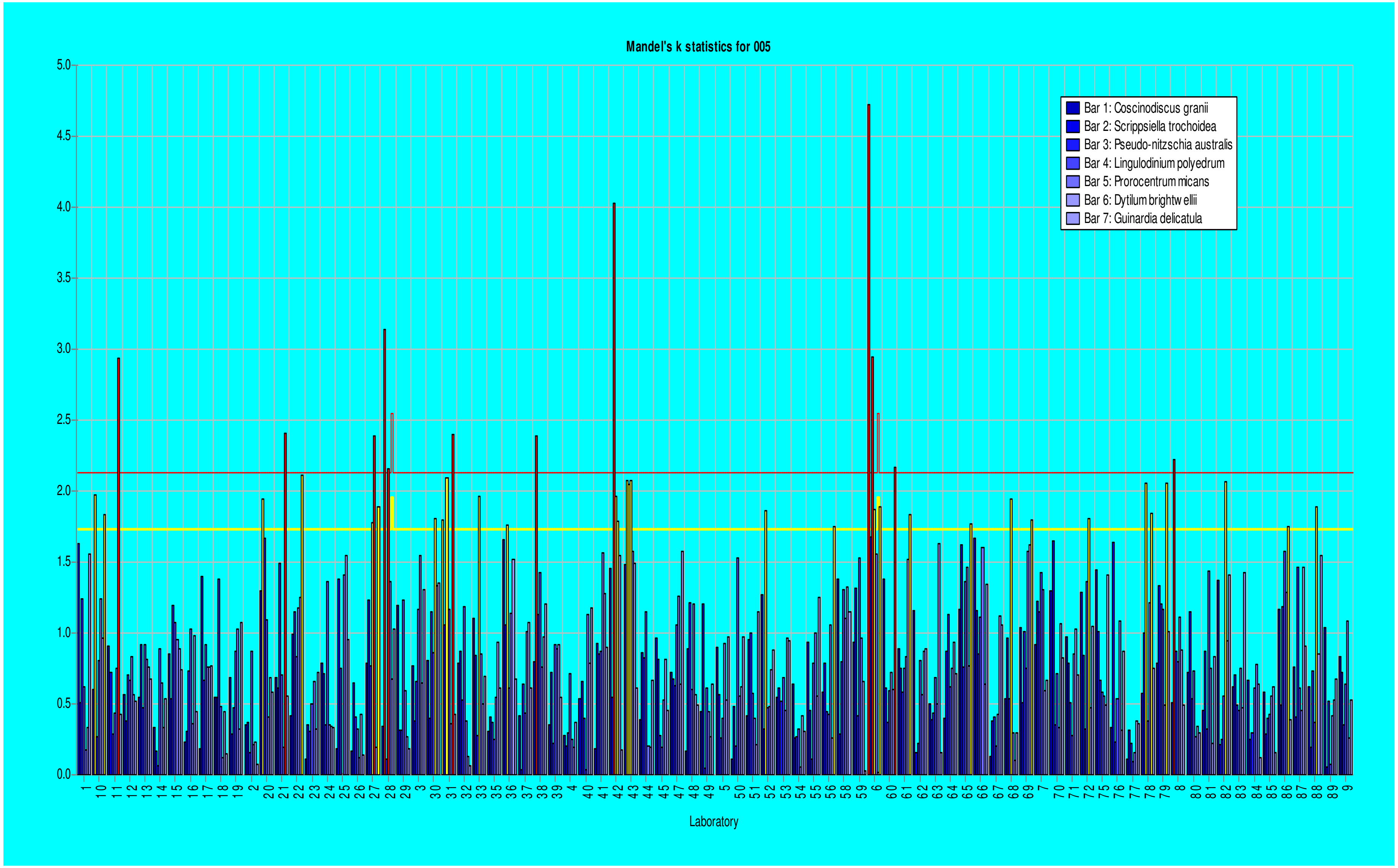
ANNEX XII Graphical summary of results cells/L by analysts



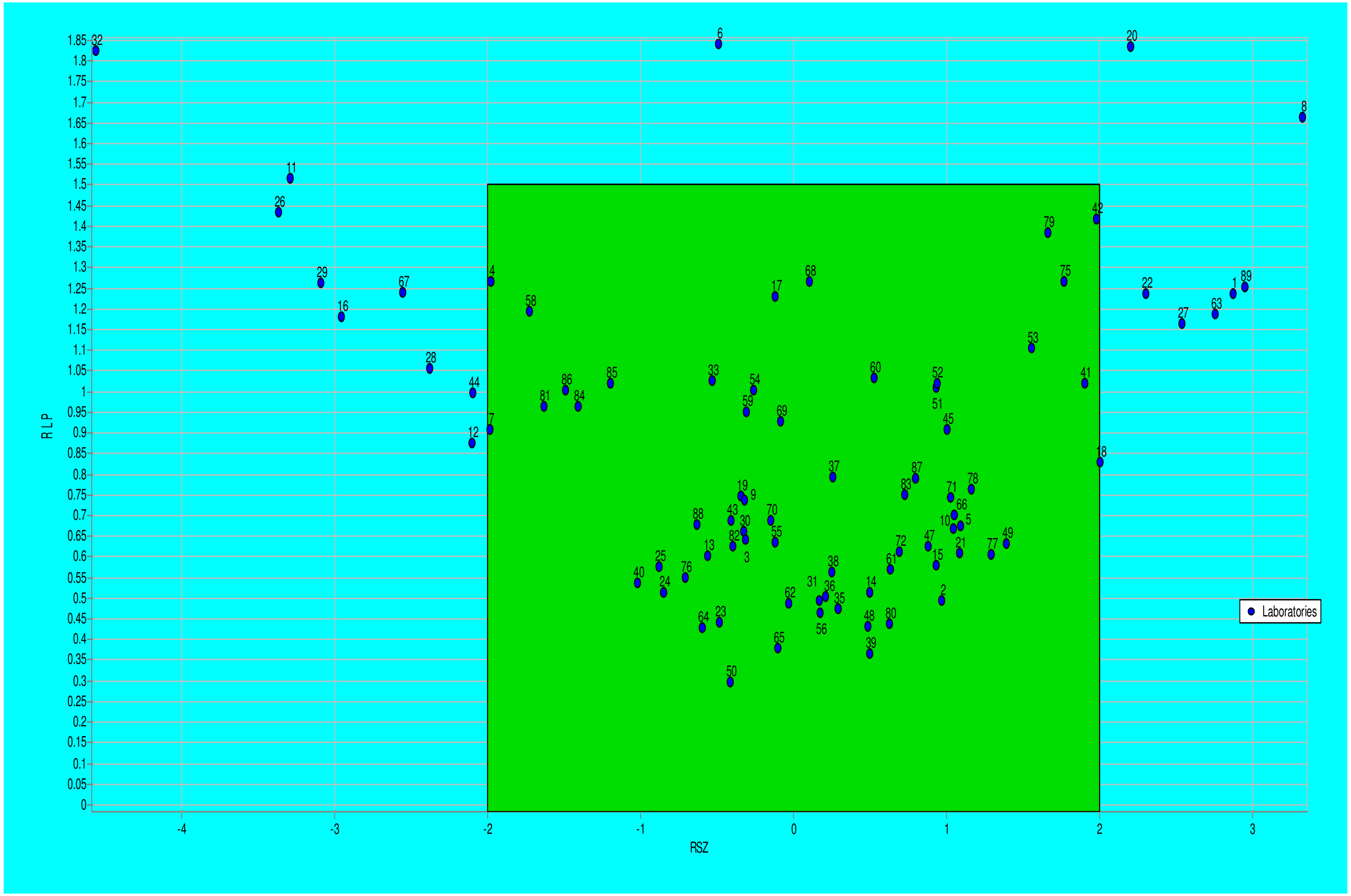
ANNEX XIII: Mandel's h and k statistics



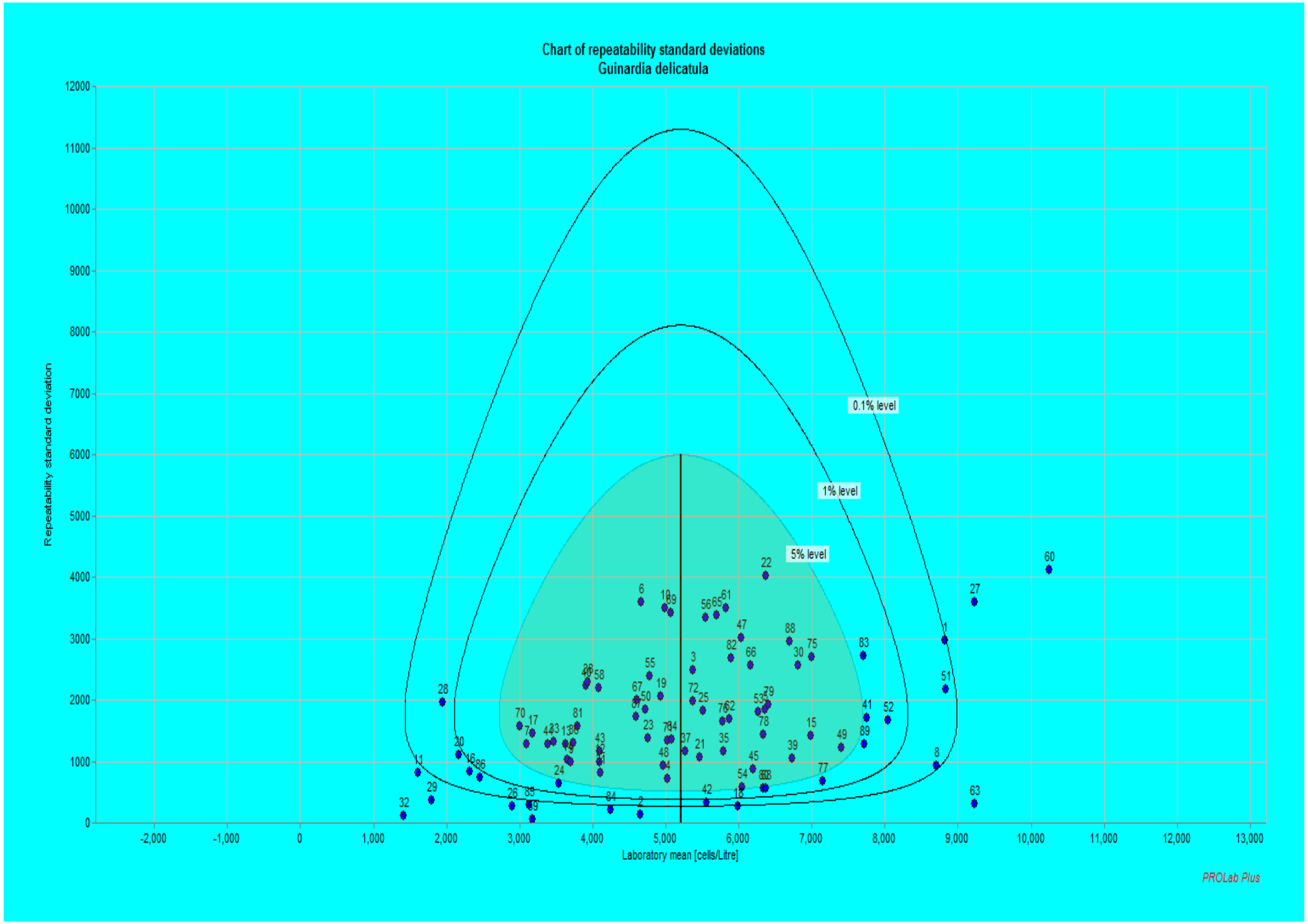
ANNEX XIII Mandel's h and k statistics



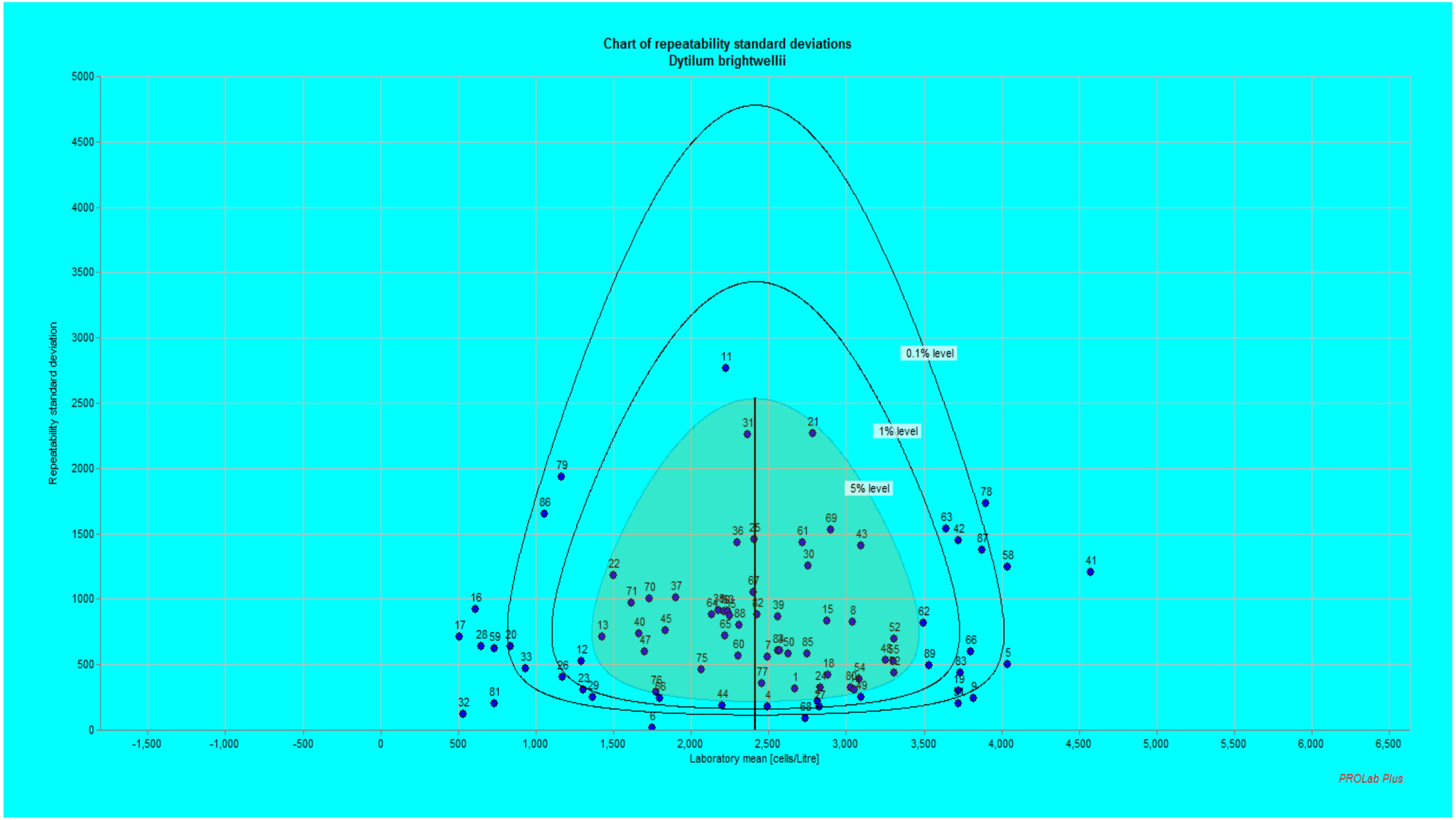
ANNEX XIV: RLP and RSZ for all measurands Bequalm 2015



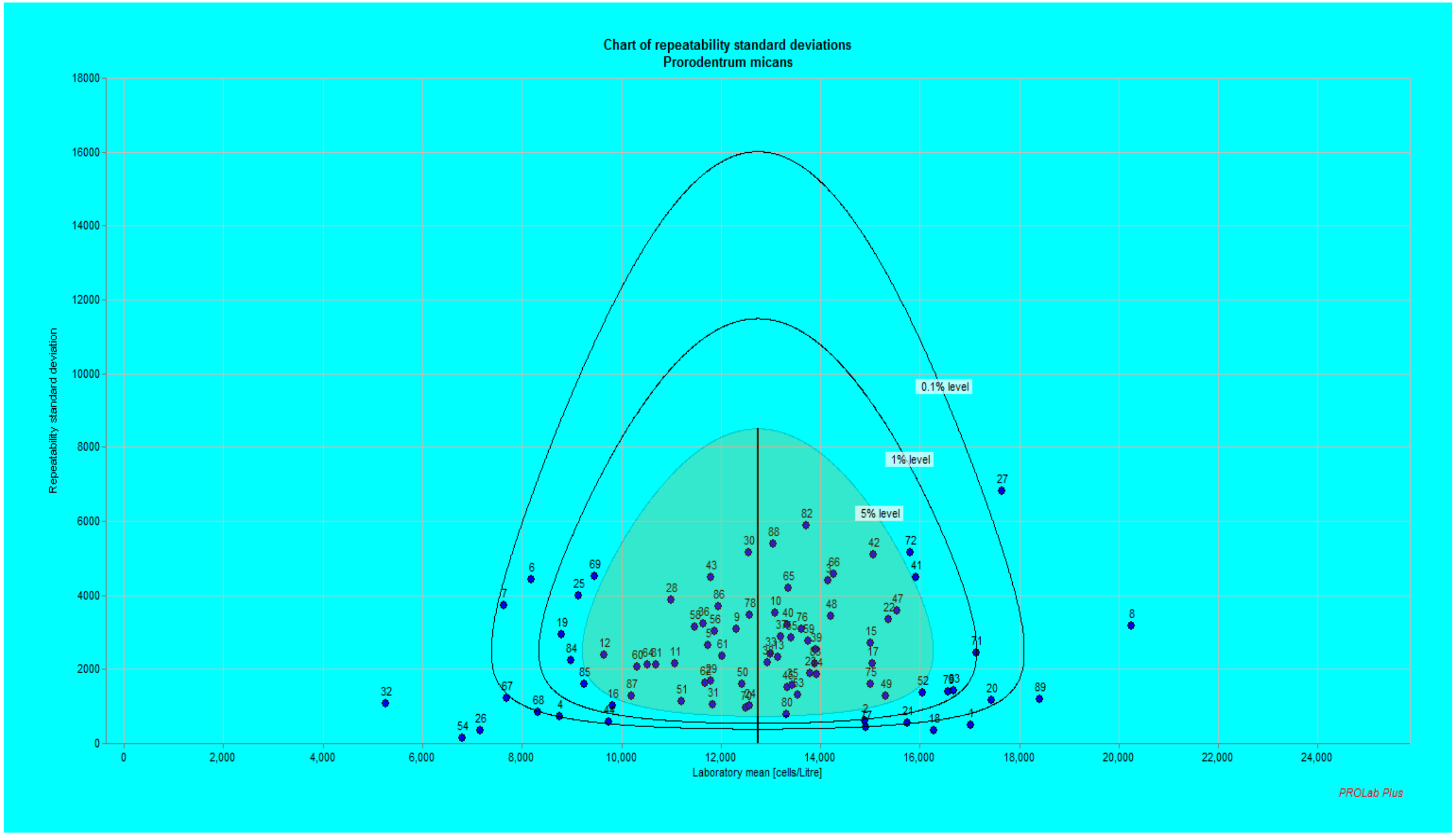
ANNEX XV: Chart of repeatability standard deviations



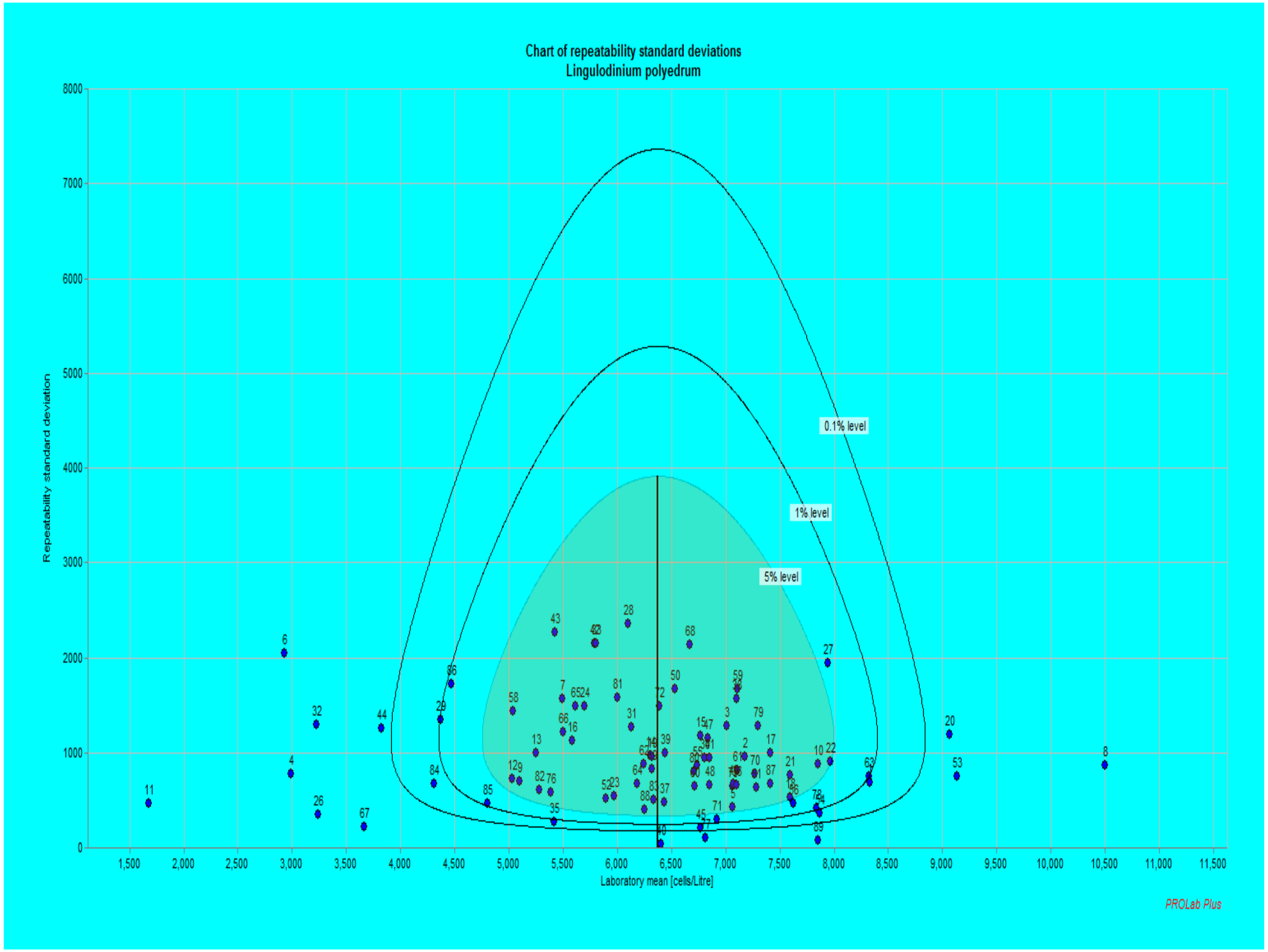
ANNEX XV: Chart of repeatability standard deviations



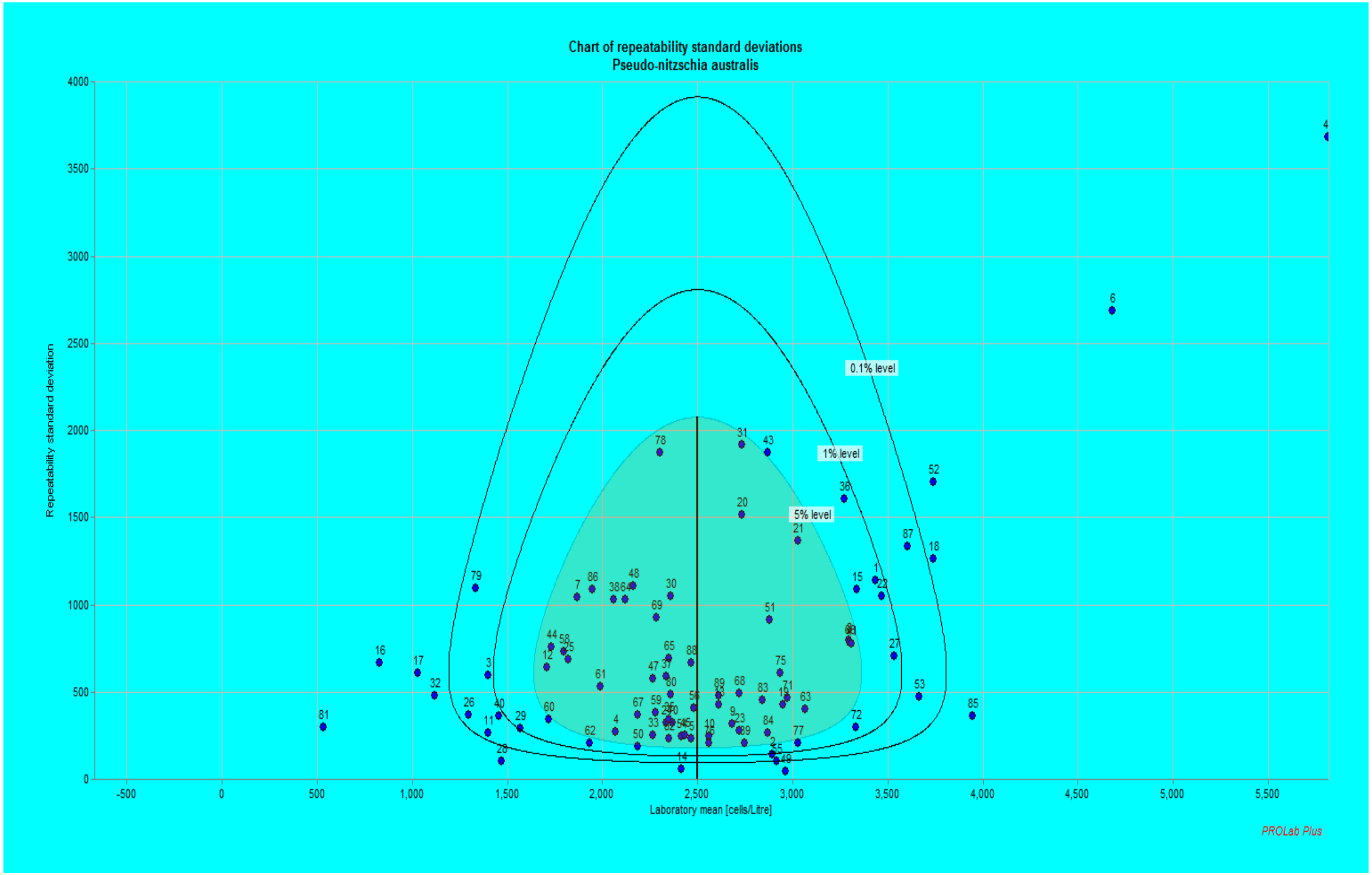
ANNEX XV: Chart of repeatability standard deviations



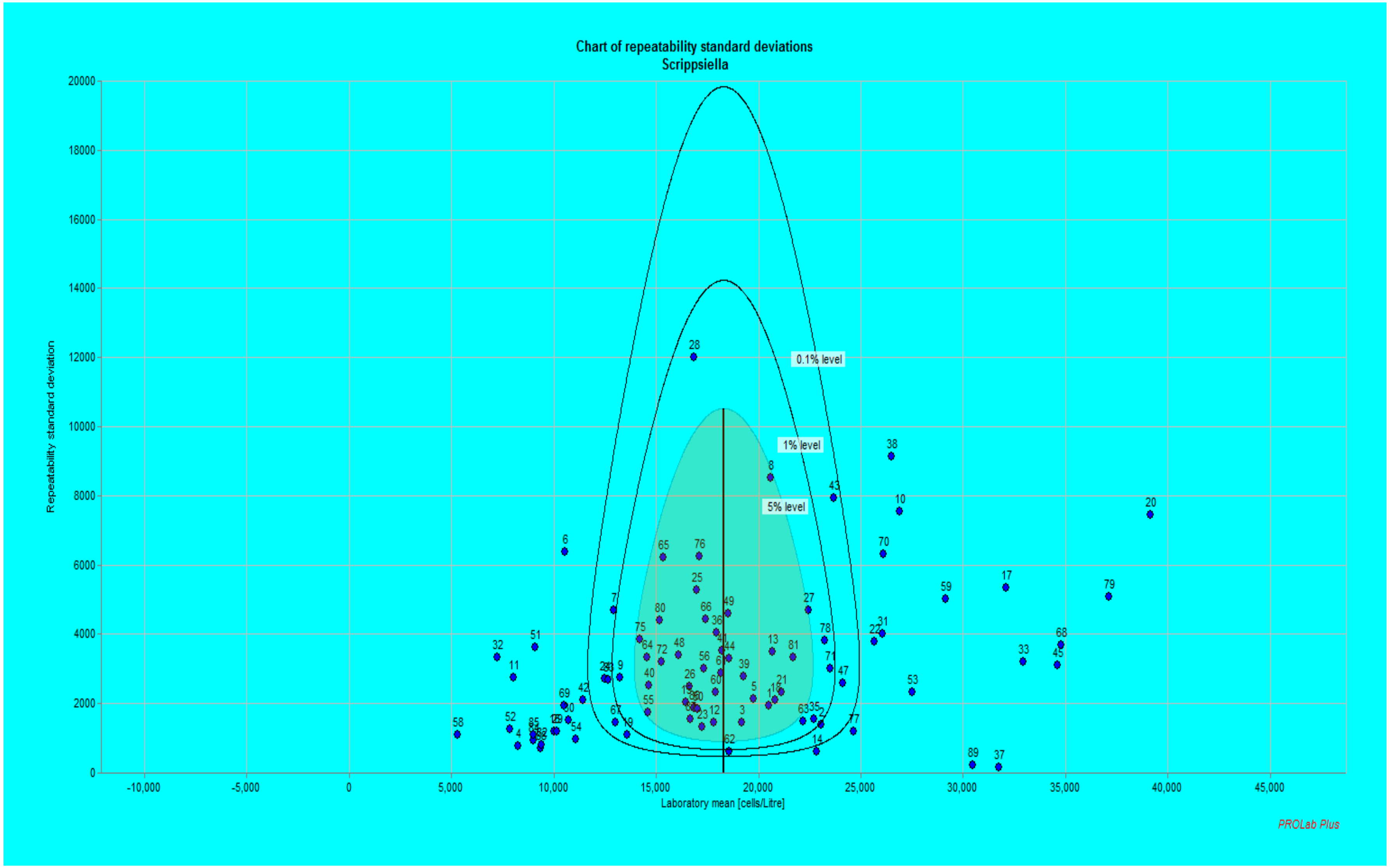
ANNEX XV: Chart of repeatability standard deviations



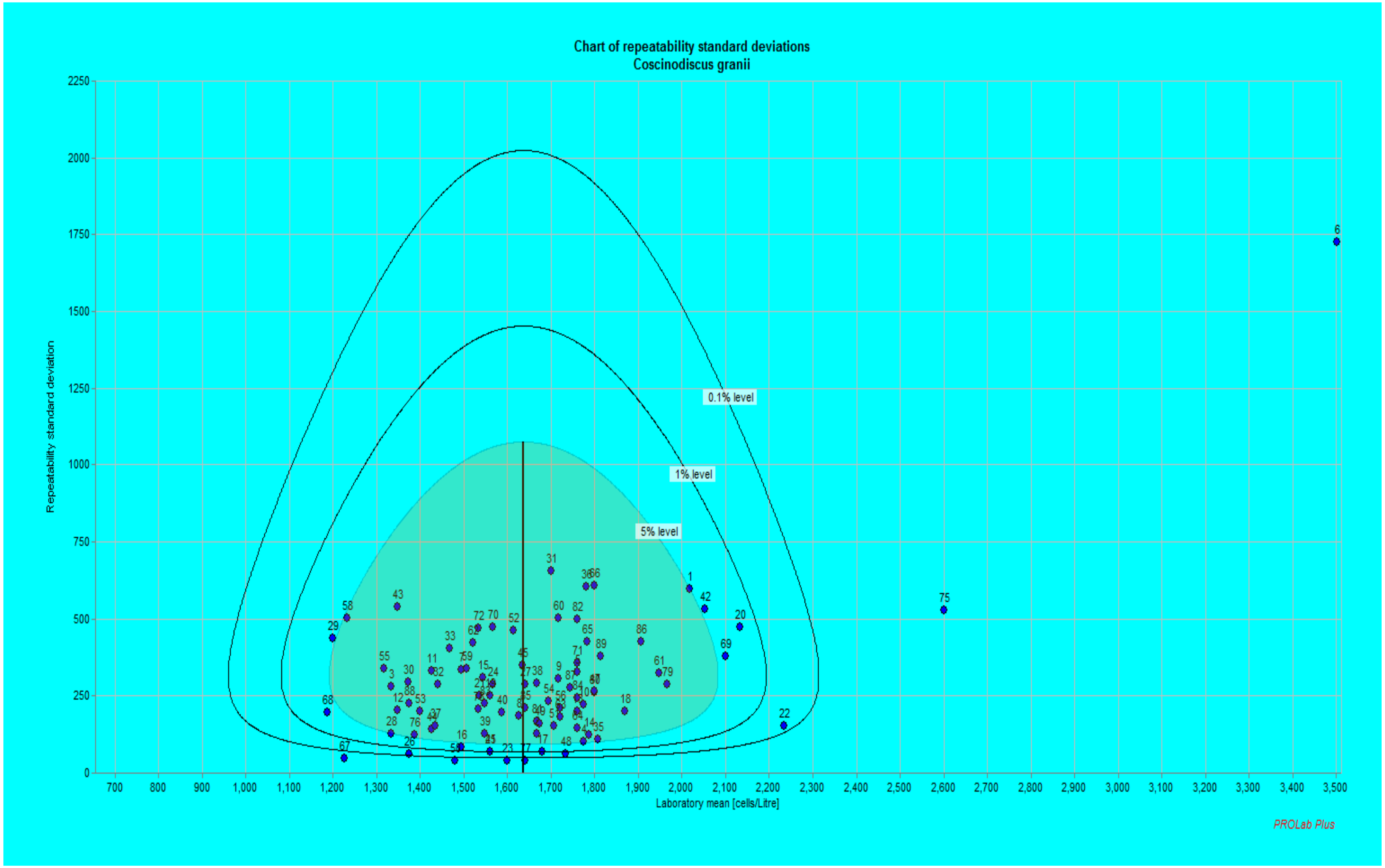
ANNEX XV: Chart of repeatability standard deviations



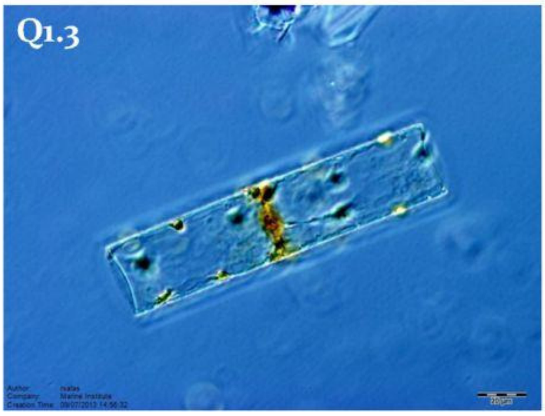
ANNEX XV: Chart of repeatability standard deviations

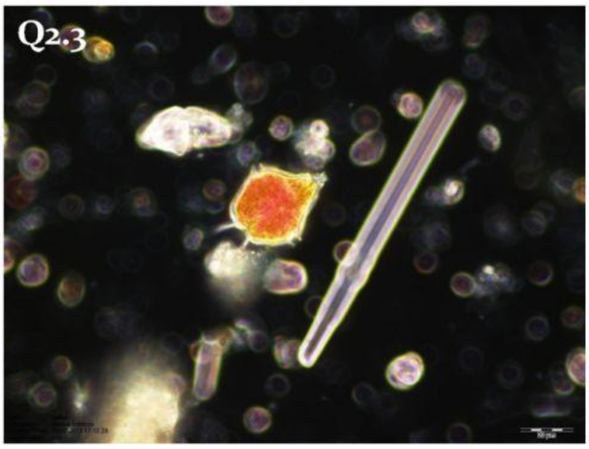


ANNEX XV: Chart of repeatability standard deviations

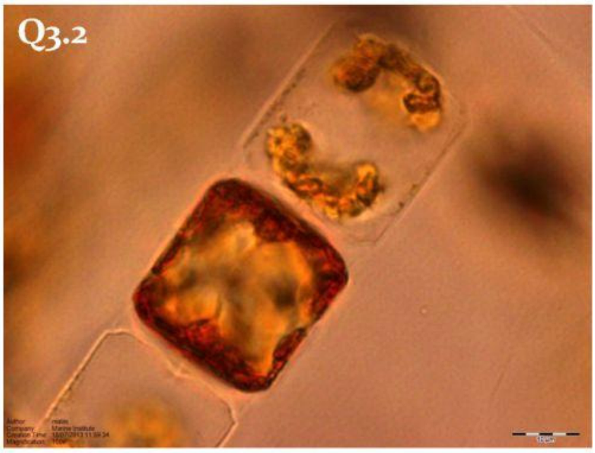


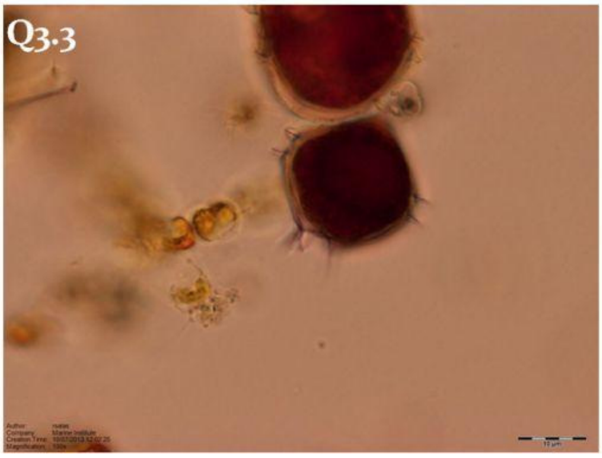
ANNEX XVI: Ocean Teacher HAB Quiz

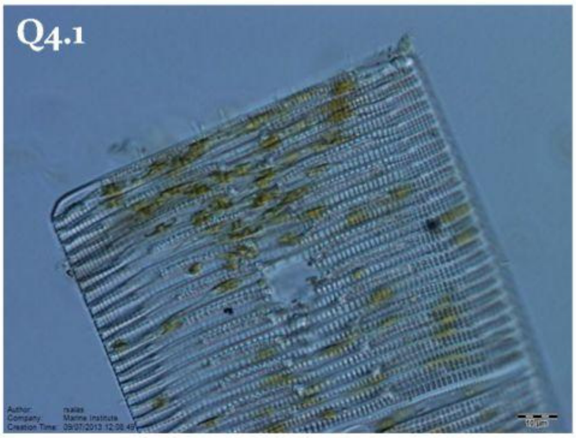


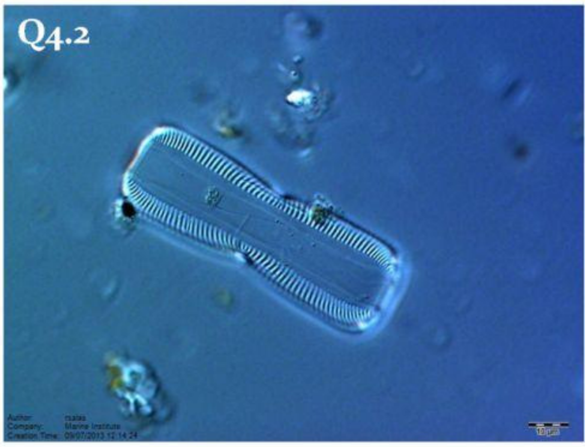


ANNEX XVI: Ocean Teacher HAB Quiz



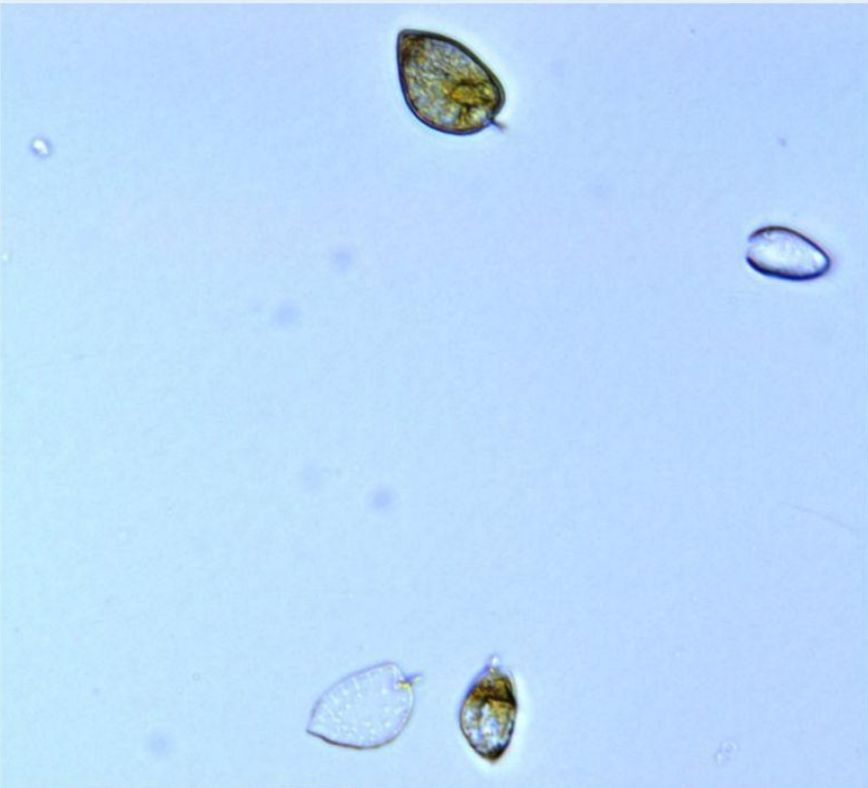






Question 5
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Enumerate the phytoplankton cells in this image: (Please use a numeral as the answer).



Answer: 2

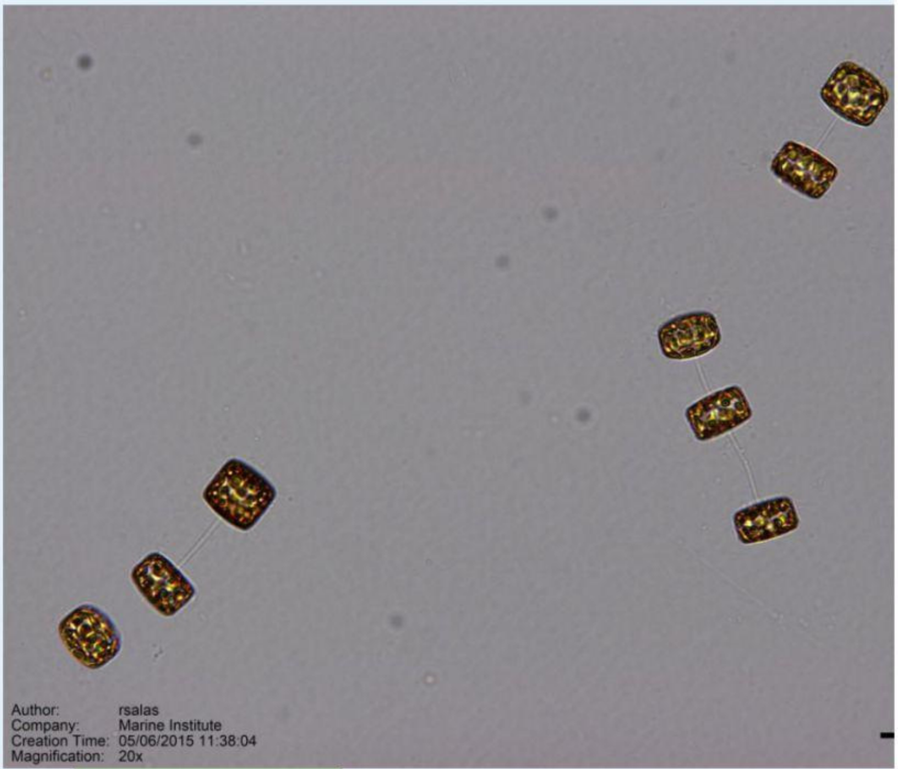
Question 6
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Enumerate the phytoplankton cells in the following images: (Please use a numeral as the answer)

Answer: 26

Question 7
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

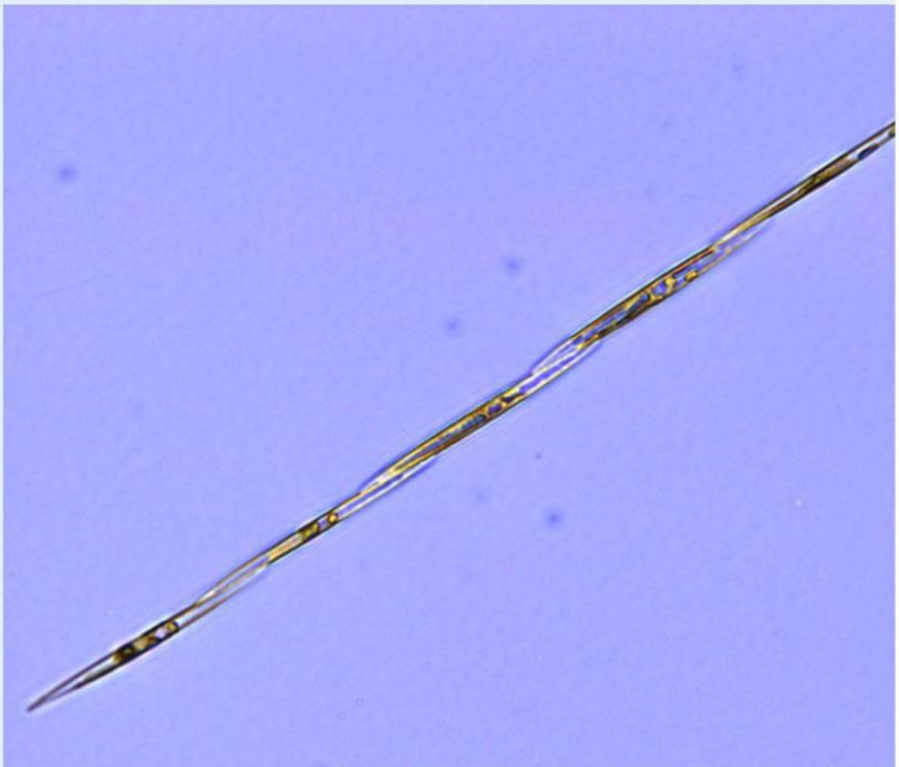
Enumerate the phytoplankton cells shown in the image: (Please use a numeral as the answer)



Answer: 8

Question 8
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Enumerate the following phytoplankton cells in the image: (Please use a numeral as the answer).



Answer: 5

ANNEX XVI: Ocean Teacher HAB Quiz

Question 9

Correct

Mark 1.0 out of 1.0

Flag question

Edit question

Enumerate the Phytoplankton cells shown in this image: (Please use a numeral as the answer).

Answer: 29 ✓

Question 10

Correct

Mark 1.0 out of 1.0

Flag question

Edit question

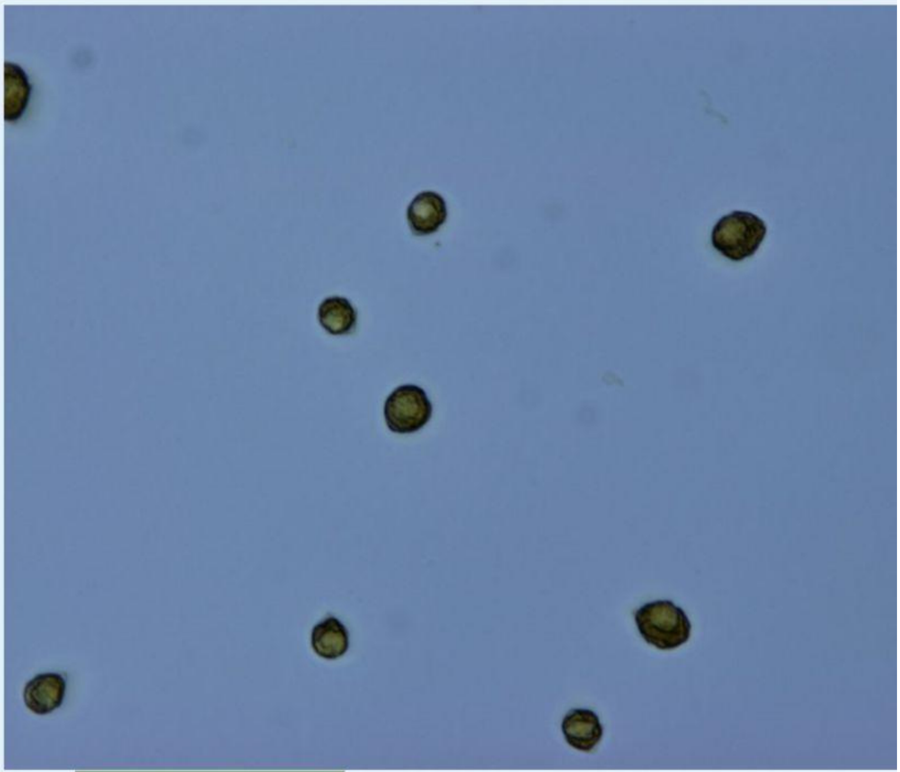
Enumerate the Phytoplankton cells shown in this image: (Please use a numeral as the answer).

Answer: 4 ✓

ANNEX XVI: Ocean Teacher HAB Quiz

Question 11
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Enumerate the Phytoplankton cells shown in this image. (Please use a numeral as the answer).



Answer: 8 ✓

Question 12
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identify to genus level the phytoplankton featured in this video. Do not write species name or 'sp.' or 'spp.' on answer. Capitalise first letter of genus name.

Answer: Dinophysis ✓

The correct answer is: Dinophysis

ANNEX XVI: Ocean Teacher HAB Quiz

Question 13
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identify the species in the following video to genus level only. Do not write species name or sp. or spp. Capitalise genus first letter.

Answer: Gyrodinium

The correct answer is: Gyrodinium

Question 14
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identify the organism featured in this video to genus level only. Capitalise first letter of genus name.

Answer: Bacillaria

The correct answer is: Bacillaria

ANNEX XVI: Ocean Teacher HAB Quiz

Question 15
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identify the following species featured in this video to genus level. Capitalise first letter of genus name.

size: 12-15um

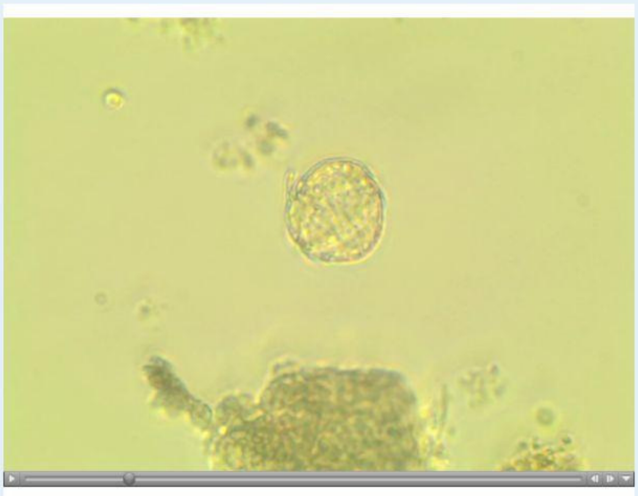
Answer: Heterosigma

The correct answer is: Heterosigma

Question 16
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identify the following species featured in this video to genus level only. Capitalise first letter of genus.

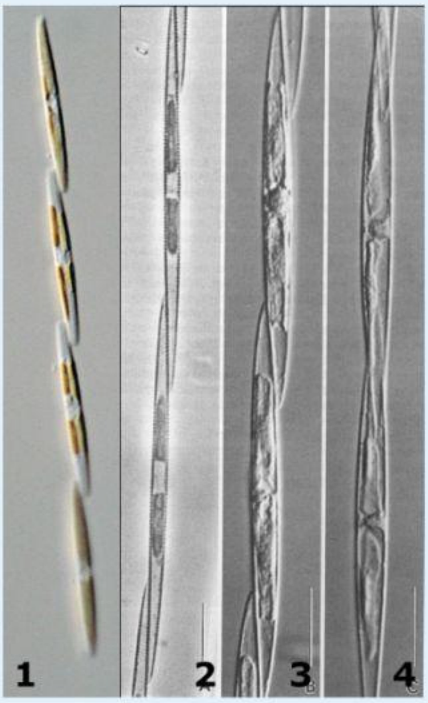
Size:20-30um



Answer: Diplopsalis

The correct answer is: Diplopsalis

Question 17
Correct
Mark 1.0 out of 1.0
Flag question
Edit question



The photos show 4 different chains of Pseudo-nitzschia spp. Indicate whether they are seen in valve view or girdle view.

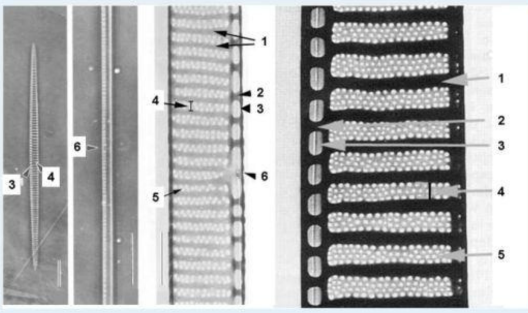
Fig. 2: girdle view or valve view	girdle view
Fig. 1: girdle view or valve view	girdle view
Fig. 4. girdle view or valve view	valve view
Fig. 3. girdle view or valve view	girdle view

Your answer is correct.

The correct answer is: Fig. 2: girdle view or valve view – girdle view, Fig. 1: girdle view or valve view – girdle view, Fig. 4. girdle view or valve view – valve view, Fig. 3. girdle view or valve view – girdle view

Question 18
Correct
Mark 1.0 out of 1.0

Name the features indicated by the arrows



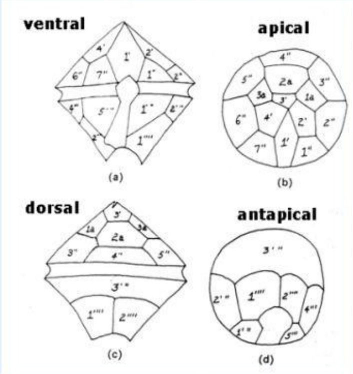
Arrow 1 points to	Interstria
Arrow / arrow head 4 points to	Stria
Arrow / arrow head 3 points to	Raphe slit
Arrow 5 points to	Poroid
Arrow / arrow head 2 points to	Fibula
Arrow head 6 points to	Central interspace

Your answer is correct

The correct answer is: Arrow 1 points to – Interstria, Arrow / arrow head 4 points to – Stria, Arrow / arrow head 3 points to – Raphe slit, Arrow 5 points to – Poroid, Arrow / arrow head 2 points to – Fibula, Arrow head 6 points to – Central interspace

Question 19
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

The illustrations show schematic drawings in ventral, dorsal, apical, and antapical views of the main series of plates in a peridinioid dinoflagellate. Assign the right names to the plate series.



The plates marked 1"-7" indicate	The precingular plates ✓
The plates marked 1'-4' indicate	The apical plates ✓
The plates marked 1""-2"" indicate	The antapical plates ✓
The plates marked 1'"-5'" indicate	The postcingular plates ✓
The plates marked 1a-3a indicate	The anterior intercalary plates ✓

Your answer is correct

smile

The correct answer is: The plates marked 1"-7" indicate – The precingular plates, The plates marked 1'-4' indicate – The apical plates, The plates marked 1""-2"" indicate – The antapical plates, The plates marked 1'"-5'" indicate – The postcingular plates, The plates marked 1a-3a indicate – The anterior intercalary plates

Question 20
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

Identification of species of Protoperidinium usually requires careful examination of the first apical plate (1') and the second anterior intercalary plate (2a). The different images show different types of plate configuration; name these configurations.

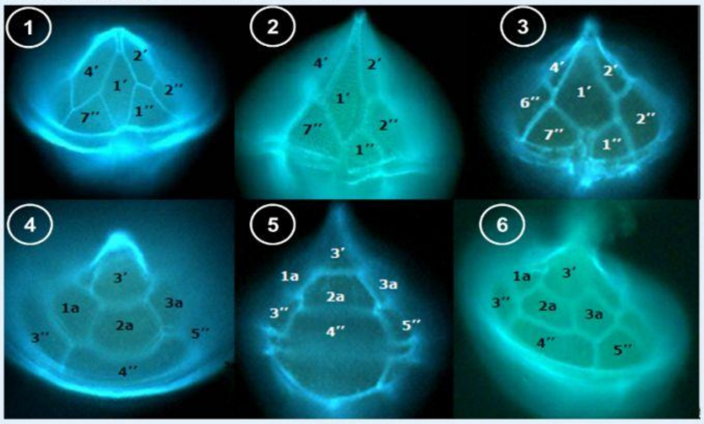
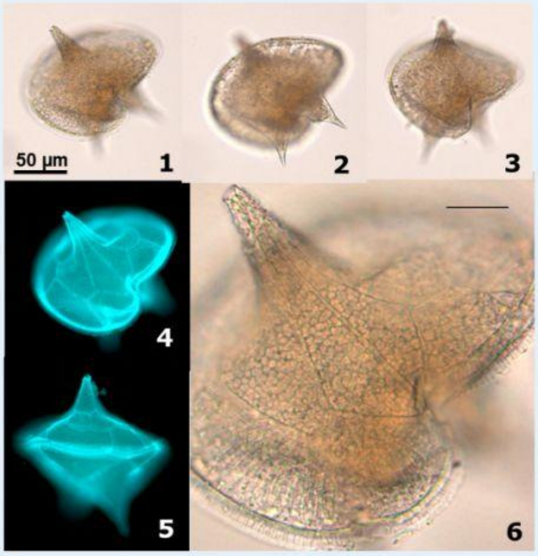


Fig.6 shows	2a penta configuration ✓
Fig.4 shows	2a quadra configuration ✓
Fig..2 shows	1' meta configuration ✓
Fig.1 shows	1' ortho configuration ✓
Fig.5 shows	2a hexa configuration ✓
Fig.3 shows	1' para configuration ✓

Your answer is correct.

The correct answer is: Fig.6 shows – 2a penta configuration, Fig.4 shows – 2a quadra configuration, Fig..2 shows – 1' meta configuration, Fig.1 shows – 1' ortho configuration, Fig.5 shows – 2a hexa configuration, Fig.3 shows – 1' para configuration

Question 21
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

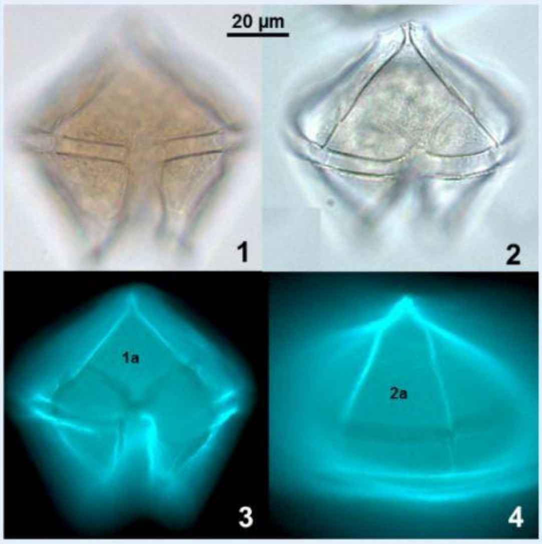


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium minutum
- b. Protoperidinium thorianum
- c. Protoperidinium divergens
- d. Protoperidinium leonis
- e. Protoperidinium crassipes
- f. Protoperidinium depressum ✓ correct
- g. Protoperidinium pentagonum
- h. Protoperidinium pellucidum
- i. Protoperidinium claudicans
- j. Protoperidinium conicum

Your answer is correct.
The correct answer is: Protoperidinium depressum

Question 22
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

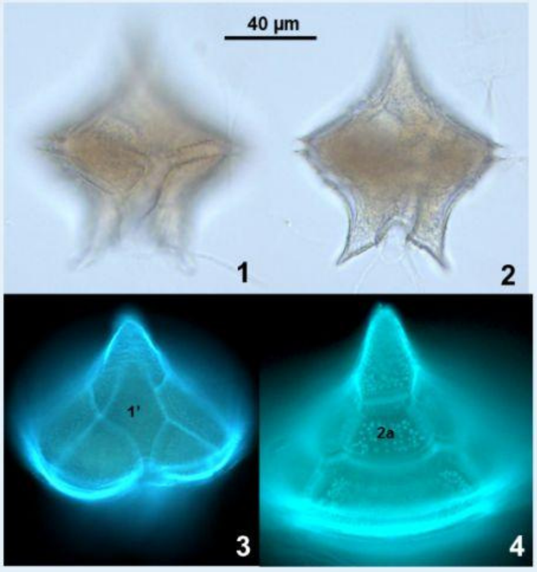


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium pentagonum
- b. Protoperidinium thorianum
- c. Protoperidinium minutum
- d. Protoperidinium claudicans
- e. Protoperidinium crassipes
- f. Protoperidinium leonis
- g. Protoperidinium depressum
- h. Protoperidinium divergens
- i. Protoperidinium pellucidum
- j. Protoperidinium conicum ✓ correct

Your answer is correct.
The correct answer is: Protoperidinium conicum

Question 23
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

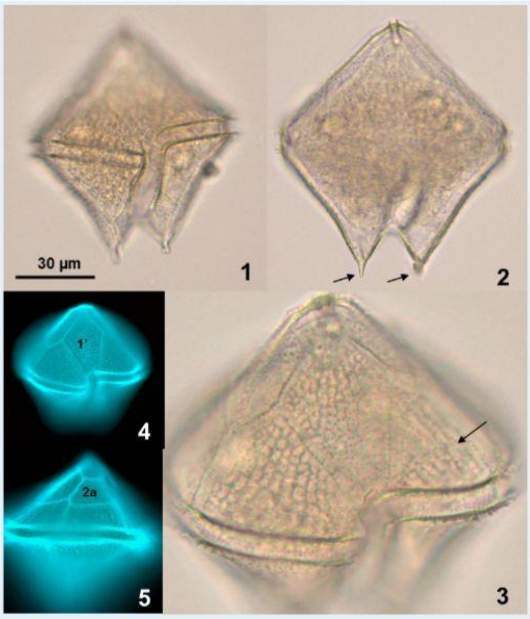


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium divergens ✓ correct
- b. Protoperidinium claudicans
- c. Protoperidinium leonis
- d. Protoperidinium conicum
- e. Protoperidinium pellucidum
- f. Protoperidinium minutum
- g. Protoperidinium depressum
- h. Protoperidinium thorianum
- i. Protoperidinium crassipes
- j. Protoperidinium pentagonum

Your answer is correct.
The correct answer is: Protoperidinium divergens

Question 24
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

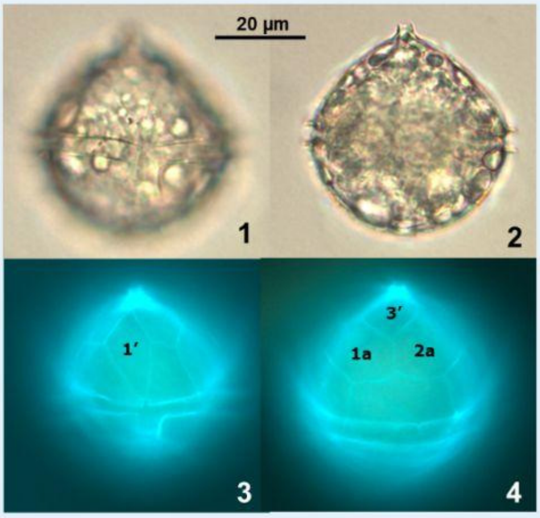


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium crassipes
- b. Protoperidinium conicum
- c. Protoperidinium divergens
- d. Protoperidinium claudicans
- e. Protoperidinium minutum
- f. Protoperidinium pellucidum
- g. Protoperidinium depressum
- h. Protoperidinium pentagonum
- i. Protoperidinium thorianum
- j. Protoperidinium leonis ✓ correct

Your answer is correct.
The correct answer is: Protoperidinium leonis

Question 25
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

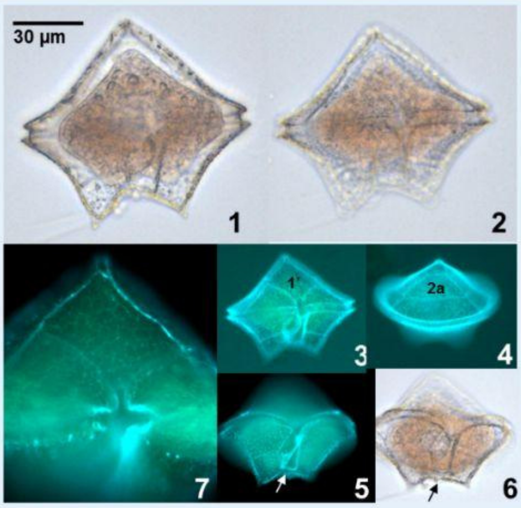


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium depressum
- b. Protoperidinium thorianum
- c. Protoperidinium crassipes
- d. Protoperidinium divergens
- e. Protoperidinium leonis
- f. Protoperidinium claudicans
- g. Protoperidinium pellucidum
- h. Protoperidinium conicum
- i. Protoperidinium minutum ✓ correct
- j. Protoperidinium pentagonum

Your answer is correct.
The correct answer is: Protoperidinium minutum

Question 26
Correct
Mark 1.0 out of 1.0
Flag question
Edit question

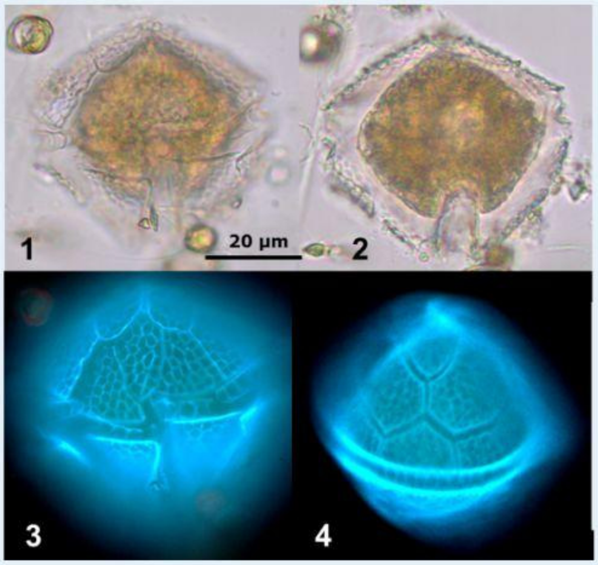


Identify the species illustrated using the list of names

Select one:
- a. Protoperidinium crassipes
- b. Protoperidinium claudicans
- c. Protoperidinium minutum
- d. Protoperidinium divergens
- e. Protoperidinium pellucidum
- f. Protoperidinium conicum
- g. Protoperidinium depressum
- h. Protoperidinium pentagonum ✓ correct
- i. Protoperidinium thorianum
- j. Protoperidinium leonis

Your answer is correct.
The correct answer is: Protoperidinium pentagonum

Question 27
Correct
Mark 1.0 out of 1.0
Flag question
Edit question



Identify the species illustrated using the list of names

Select one:

- a. Protoperidinium depressum
- b. Protoperidinium crassipes
- c. Protoperidinium thorianum ✓ correct
- d. Protoperidinium minutum
- e. Protoperidinium leonis
- f. Protoperidinium claudicans
- g. Protoperidinium pellucidum
- h. Protoperidinium divergens
- i. Protoperidinium conicum
- j. Protoperidinium pentagonum

Your answer is correct.
The correct answer is: Protoperidinium thorianum

ANNEX XVII: HABs Oceanteacher quiz results

Analyst code	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Final Grade
64	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
41	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
89	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
80	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
61	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
5	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
85	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
65	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
88	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
1	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
10	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
50	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
76	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
2	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
84	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
6	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
14	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
38	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
72	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
49	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
54	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
21	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
18	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
31	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
73	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	83.7	100	100	100	100	100	100	100	99.3
28	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	100	100	100	100	100	100	100	100	100	98.6
15	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	100	100	100	100	100	100	100	98.6
86	100	100	100	100	100	100	100	100	100	100	100	100	51.2	100	100	100	100	100	100	100	100	100	100	97.8
30	100	100	100	100	100	100	100	100	100	100	100	100	51.2	100	100	100	100	100	100	100	100	100	100	97.8
36	100	100	100	100	100	100	100	100	100	100	100	100	51.2	100	100	100	100	100	100	100	100	100	100	97.8

ANNEX XVII: HABs Oceanteacher quiz results

Analyst code	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Final Grade
55	100	100	100	100	100	100	100	100	100	100	100	100	51.2	100	100	100	100	100	100	100	100	100	100	97.8
42	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
23	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	95.7
77	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	95.7
53	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
75	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
37	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
13	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	95.7
45	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
22	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
43	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	100	95.7
70	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
47	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
58	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	95.7
87	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	95.7
79	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	95.7
48	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	100	100	100	100	0	100	100	100	100	94.2
44	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	100	100	100	100	0	100	100	100	100	94.2
32	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	51.2	100	100	100	100	100	100	100	93.5
35	100	100	100	100	100	100	100	100	100	100	100	0	51.2	100	100	100	100	100	100	100	100	100	100	93.5
3	100	100	100	100	100	100	100	100	100	100	100	0	51.2	100	100	100	100	100	100	100	100	100	100	93.5
29	100	100	100	100	100	100	100	100	100	100	100	0	51.2	100	100	100	100	100	100	100	100	100	100	93.5
20	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	81.4	100	100	100	0	100	100	100	100	93.3
74	100	100	100	100	100	100	100	100	100	100	100	100	100	67.4	100	67.4	100	0	100	100	100	100	100	92.8
19	100	100	100	100	100	100	100	100	100	0	100	0	100	100	100	100	100	100	100	100	100	100	100	91.3
69	100	100	100	100	100	100	100	100	100	0	100	0	100	100	100	100	100	100	100	100	100	100	100	91.3
60	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	0	100	100	100	100	91.3
27	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	0	100	91.3
51	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	91.3
56	100	100	100	100	100	100	100	100	100	0	100	0	100	100	100	100	100	100	100	100	100	100	100	91.3

ANNEX XVII: HABs Oceanteacher quiz results

Analyst code	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Final Grade
62	0	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	100	100	100	100	91.3
24	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	0	100	100	100	91.3
83	100	100	100	0	100	100	100	100	100	100	100	100	100	67.4	100	100	0	100	100	100	100	100	100	89.9
26	100	100	100	100	100	100	100	100	100	100	0	0	100	100	60.5	100	100	100	100	100	100	100	100	89.6
52	100	100	100	100	100	100	100	100	100	100	0	100	76.7	32.6	100	51.2	100	100	100	100	100	100	100	89.5
40	0	100	100	100	100	100	100	100	100	100	100	0	51.2	100	100	100	100	100	100	100	100	100	100	89.1
78	100	100	100	100	100	100	100	100	100	100	0	0	51.2	100	100	100	100	100	100	100	100	100	100	89.1
33	100	100	100	100	100	100	100	100	100	100	100	0	51.2	100	100	100	100	100	0	100	100	100	100	89.1
8	0	100	100	100	100	100	100	100	0	100	100	100	51.2	67.4	100	100	100	100	100	100	100	100	100	87.7
16	100	100	100	100	100	100	100	0	100	100	100	100	100	100	0	100	100	100	0	100	100	100	100	87
59	100	100	100	100	100	100	100	100	100	0	100	-	76.7	51.2	100	67.4	100	100	100	100	100	100	100	86.6
68	100	100	100	100	100	100	100	100	100	100	0	0	100	100	100	83.7	100	100	100	100	100	0	100	86.2
11	0	100	100	100	100	100	100	100	100	100	100	0	100	100	39.5	100	100	100	0	100	100	100	100	84.3
12	100	100	100	100	100	100	100	100	100	100	0	0	100	100	100	100	100	0	100	0	100	100	100	82.6
39	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	0	100	0	100	0	100	82.6
81	100	100	100	100	100	100	100	0	100	0	0	100	25.6	67.4	100	67.4	100	100	100	100	100	100	100	80.8
17	0	100	100	100	100	100	100	100	100	100	100	0	25.6	16.3	100	100	100	100	0	100	100	100	100	80.1
4	100	0	100	100	100	100	100	100	0	100	0	0	51.2	100	100	67.4	100	0	100	100	100	0	0	65.9
66	100	100	100	100	100	100	100	100	100	0	100	0	25.6	32.6	100	67.4	0	0	0	0	100	0	100	62
67	100	100	100	100	100	100	100	100	100	100	0	0	-	-	-	-	-	-	-	-	-	-	-	43.5
Overall	93.8	98.8	100.0	97.5	100.0	100.0	100.0	97.5	97.5	91.3	88.8	63.3	89.2	93.3	97.2	95.9	94.9	91.1	84.8	93.7	100.0	93.7	98.7	93.3