

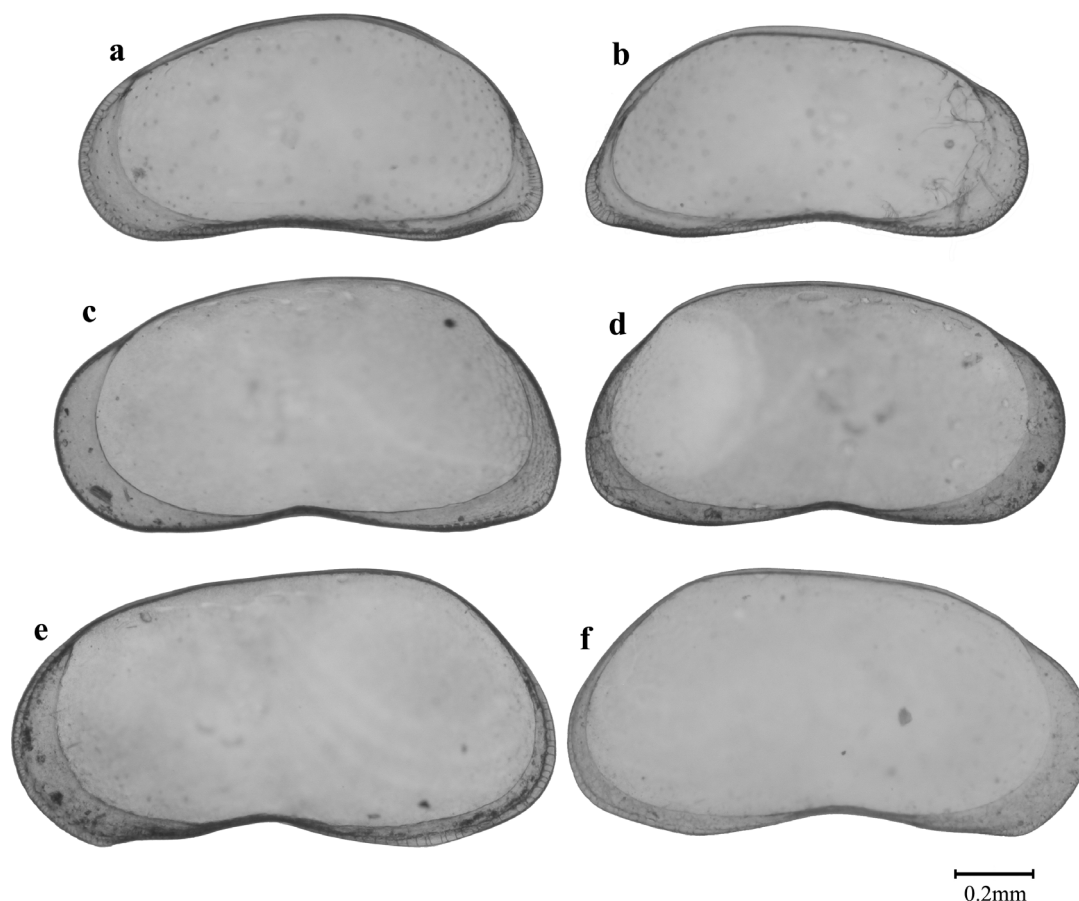
**Comparison of *Fabaeformiscandona caudata* (Kaufmann) and
Fabaeformiscandona lozeki (Absolon) from the sublittoral of Lake Mondsee**

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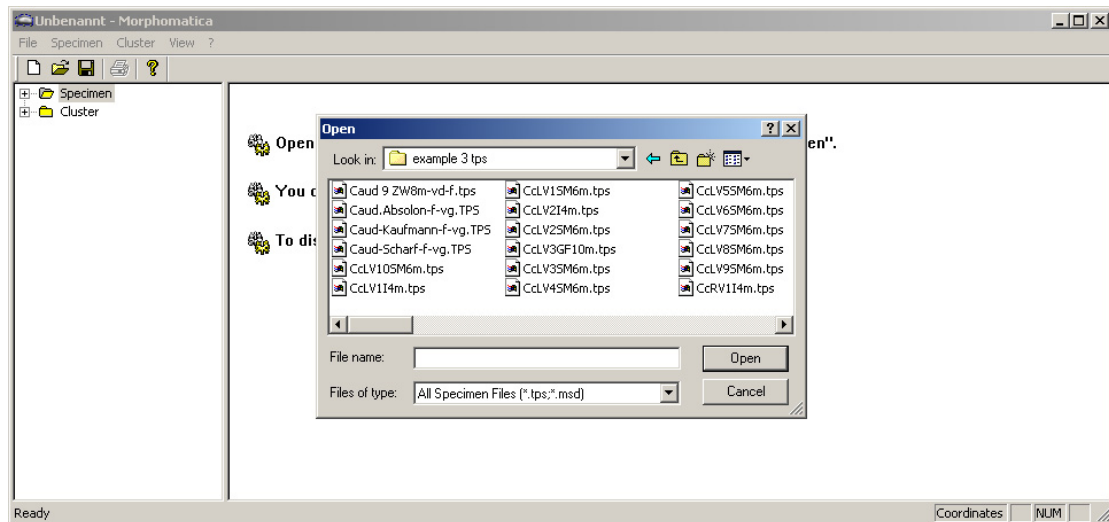


Fabaeformiscandona caudata: left valve (a), right valve (b); *Fabaeformiscandona lozeki*: female left valve (c), right valve (d), male left valve (e), right valve (f).

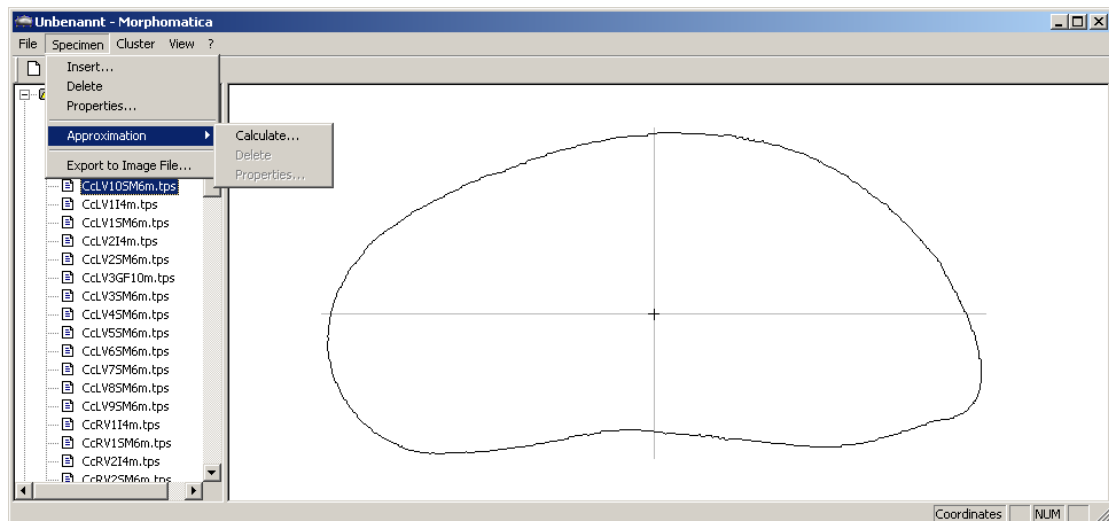
Above, you see microphotographs representing typical specimen of the two species.

The pictures are transformed to a bitmap in a program such as Adobe Photoshop, to enable digitalizing with tps.dig. Collect the specimen you want to compare in one folder, this is not obligatory, but will help keep things organised.

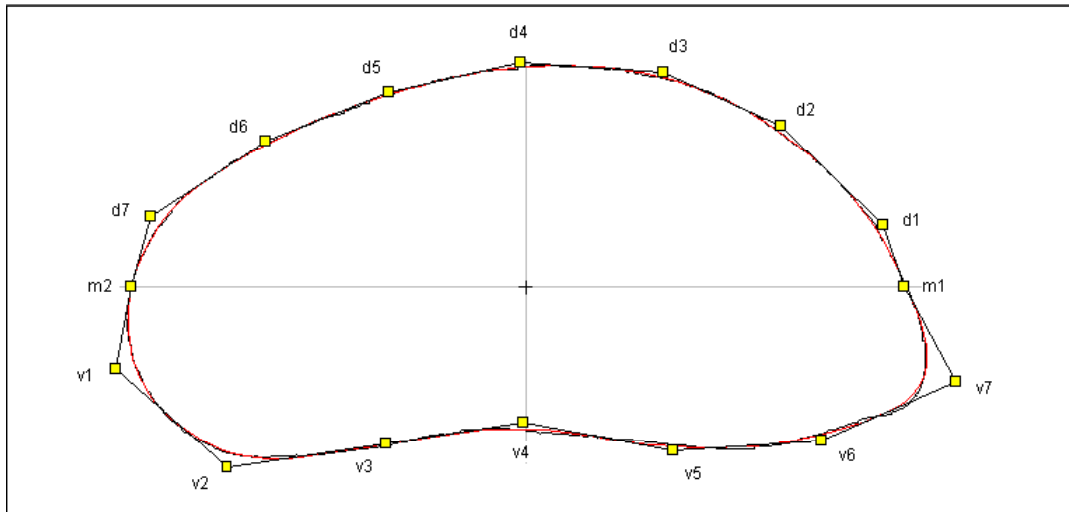
Open MORPHOMATICA, click on *Specimen* in the menubar and choose *Insert*. A dialog field opens where the samples that you want to compare are selected.



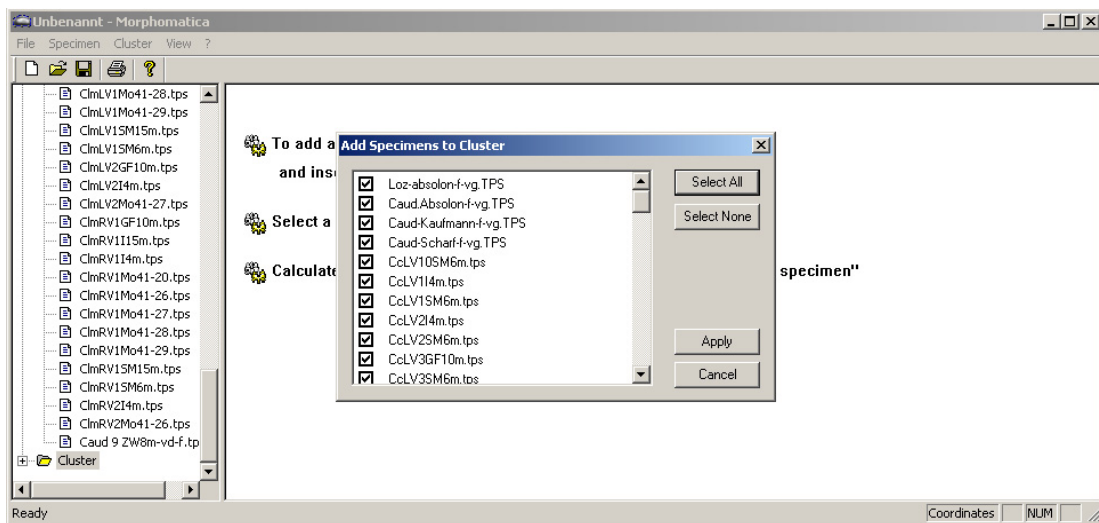
To see the fit of the calculated outline select *Approximation* under *Specimen* in the menubar.



It might be useful to change the number of control points to get a better resemblance between the calculated and the real shape.

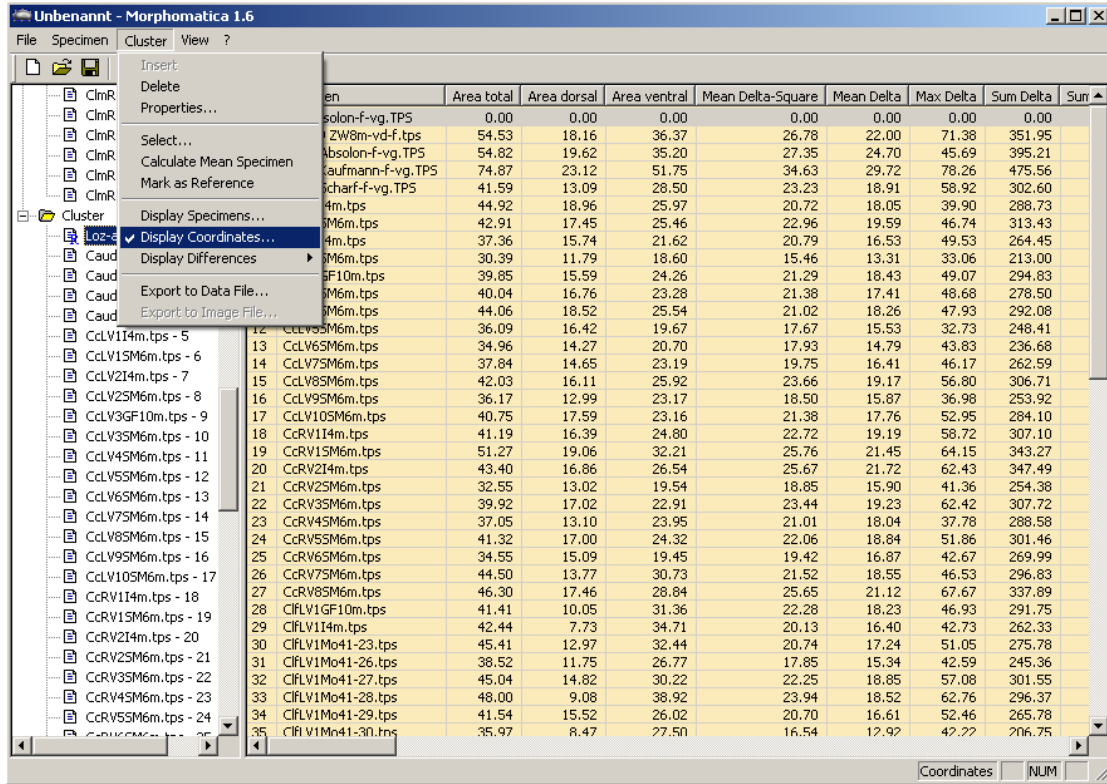


Mark the Cluster folder, select the specimen you want to compare and click *Apply*.

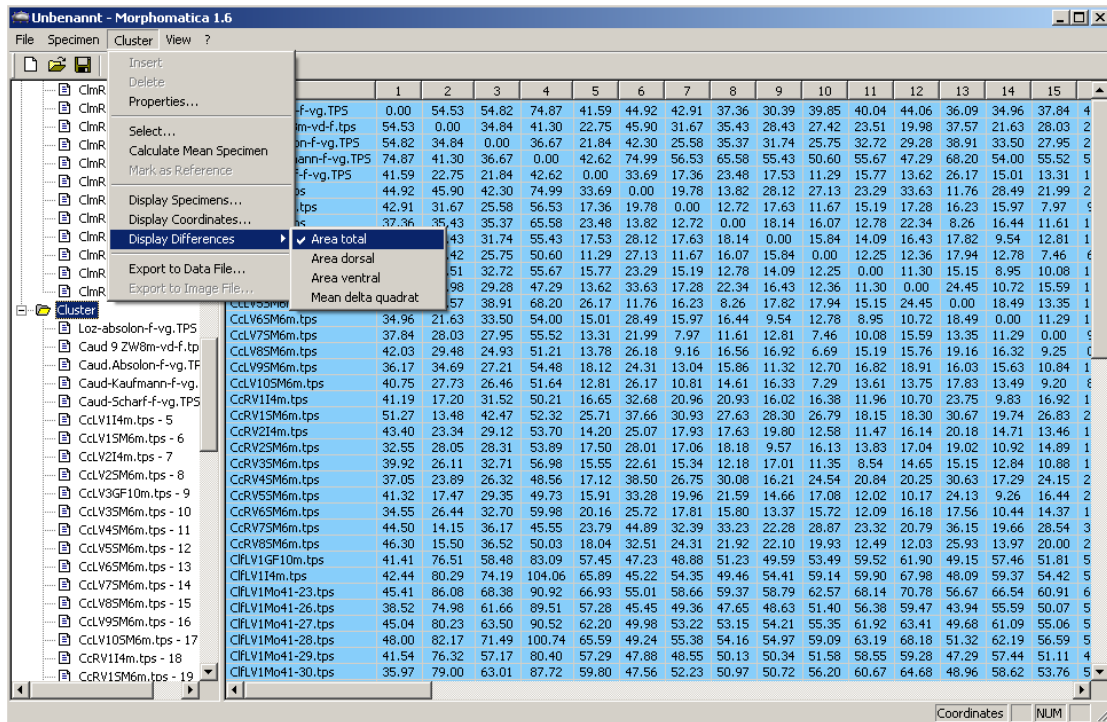


Set the control points to the value that you determined earlier (usually 8 control points on each half of the valve give a good result).

To see the coordinates of the vectors and the differences between the control points, mark one valve as reference and select *Display Coordinates*.



To export the pairwise area deviation of the whole outline select *Display Differences – Area total*.



The resulting sheet is a classical matrix that can easily be exported to Excel. Right click the sheet and choose *Copy Sheet*, open a new Excel table and paste the sheet into the field A3. Into field A1 write a title, copy the names of the specimen and paste it with *Paste Special – Transform* into field B2. Save the Excel file.

Example 1(010708)	Loz-absolon-f.vg.TPS	Caud 9 ZW8m-vd.f.tps	Caud-Absolon-f.vg.TPS	Caud-Kaufmann-f.vg.TPS	Caud-Scharf-f.vg.TPS	CcLV114m.tps	CcLV1SM6m.tps	CcLV214m.tps	CcLV2SM6m.tps	CcLV3GF10m.tps	CcLV3SM6m.tps	CcLV4SM6m.tps	CcLV5SM6m.tps
Loz-absolon-f.vg.TPS	0	54.53	54.82	74.87	41.59	44.92	42.91	37.36	30.39	39.85	40.04	44.06	31.87
Caud 9 ZW8m-vd.f.tps	54.53	0	34.84	41.3	22.75	45.9	31.67	35.43	28.43	27.42	23.51	19.88	31.87
Caud-Absolon-f.vg.TPS	54.82	34.84	0	36.67	21.84	42.3	25.58	35.37	31.74	25.75	32.72	29.28	34.84
Caud-Kaufmann-f.vg.TPS	74.87	41.3	36.67	0	42.62	74.99	56.53	65.58	55.43	50.6	55.67	47.29	41.3
Caud-Scharf-f.vg.TPS	41.59	22.75	21.84	42.62	0	33.69	17.36	23.48	17.53	11.29	15.77	13.62	21.84
CcLV114m.tps	44.92	45.9	42.3	74.99	33.69	0	19.78	13.82	28.12	27.13	23.29	33.63	11.29
CcLV1SM6m.tps	42.91	31.67	25.58	56.53	17.36	19.78	0	12.72	17.63	11.67	15.19	17.28	11.29
CcLV214m.tps	37.36	35.43	35.37	65.58	23.48	13.82	12.72	0	18.14	16.07	12.78	22.34	11.29
CcLV2SM6m.tps	30.39	28.43	31.74	55.43	17.53	28.12	17.63	18.14	0	15.84	14.09	16.43	11.29
CcLV3GF10m.tps	39.85	27.42	25.75	50.6	11.29	27.13	11.67	16.07	15.84	0	12.25	12.36	11.29
CcLV3SM6m.tps	40.04	23.51	32.72	55.67	15.77	23.29	15.19	12.78	14.09	12.25	0	12.25	11.29
CcLV4SM6m.tps	44.06	19.88	29.28	47.29	13.62	33.63	17.28	22.34	16.43	12.36	12.25	0	11.29
CcLV5SM6m.tps	31.87	31.87	34.84	41.3	22.75	45.9	31.67	35.43	28.43	27.42	23.51	19.88	0

Start Primer, select *Open* and choose your Excel table; in the pop up dialog field click *Similarities*, on the second surface, *Dissimilarities*, check that the right number of lines is imported, if not most likely a labelling mistake occurred. If everything is correct, click OK. The matrix is displayed.

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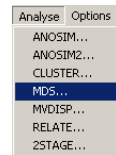
Under the header *Edit* choose *Factors*, a list of the specimen is displayed, click *Factors* and select *Add*.

Factor	Species	Sex
el	Loz-absolon-f.vg.TPS	sex
fa	Caud 9 ZW8m-vd.f.tps	sex
ca	Caud-Absolon-f.vg.TPS	sex
ck	Caud-Kaufmann-f.vg.TPS	sex
cs	Caud-Scharf-f.vg.TPS	sex
c	CcLV10SM6m.tps	sex
c	CcLV114m.tps	sex
c	CcLV1SM6m.tps	sex
c	CcLV214m.tps	sex
c	CcLV2SM6m.tps	sex
c	CcLV3GF10m.tps	sex
c	CcLV3SM6m.tps	sex
c	CcLV4SM6m.tps	sex
c	CcLV5SM6m.tps	sex

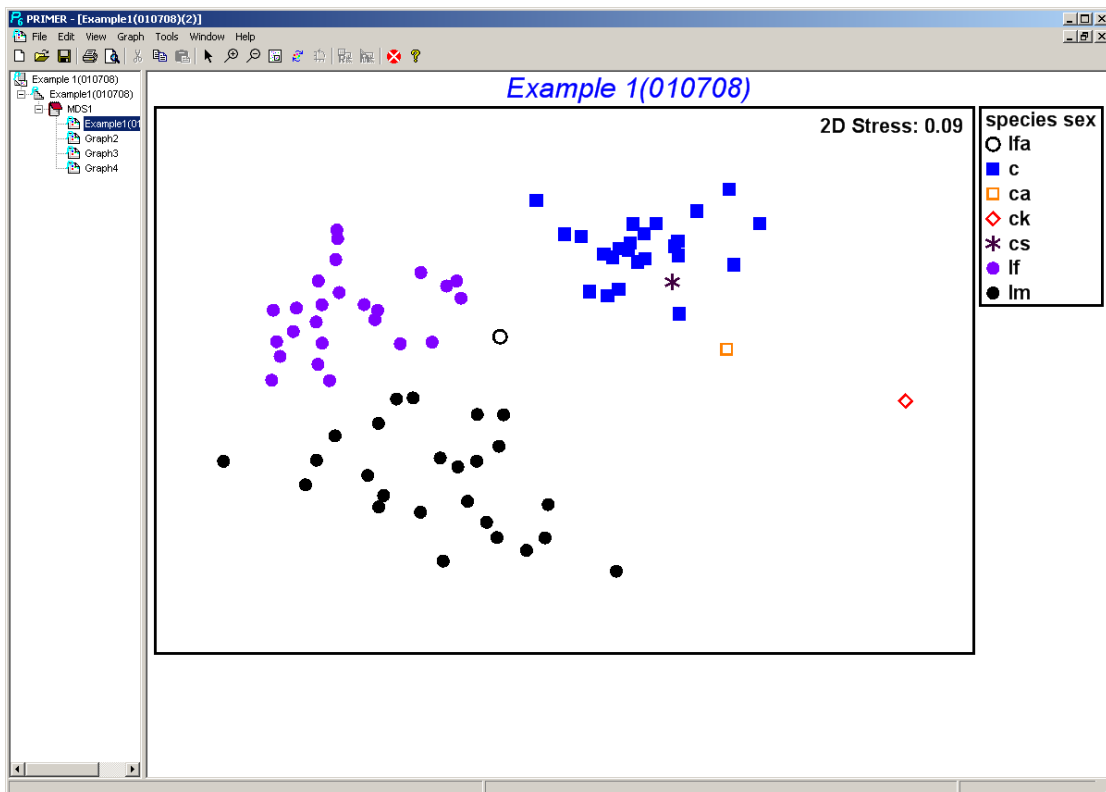
You are now asked to give a name for the factor you are about to make, the name for the factor is important if you give the samples several factors (e.g. species and sex/species, sex plus individual identifier/species, sex plus origin, etc.).

The same factors are used for the statistical methods, such as Anosim or Cluster. It is possible to produce the factor lists in Excel and copy/paste them into Primer (paste only works with the menu or the keys and not the right mouse button); this is helpful since it might speed up the process of labelling. In the Factors menu you can also define a plot key plus you can move the given factors up and down, which makes the legend easier to interpret.

To produce a MDS plot of your matrix click on *Analyse* and select *MDS*.



The program asks for the number of restarts and starts calculating. The more restarts you have the more reliable the results are, but the longer the calculation takes, ten restarts are usually sufficient. The MDS will be displayed in a new window, go to *Graph* and select *Properties*. Choose the factor and whether you want labels and/or factors displayed. The graph can be rotated in order to give the best display of the data.



ca	<i>F. caudata</i> det. A. Absolon (Absolon 1973)
ck	<i>F. caudata</i> det. A. Kaufmann (Kaufmann 1900)
cs	<i>F. caudata</i> , det. B. Scharf (Scharf and Keyser 1993)
c	<i>F. caudata</i> , lake Mondsee (det. D. Danielopol)
lf	<i>F. lozeki</i> female, lake Mondsee (det. D. Danielopol)
lm	<i>F. lozeki</i> male, lake Mondsee (det. D. Danielopol)
lfa	<i>F. lozeki</i> female, det A. Absolon (Absolon 1973)

Further calculations such as Cluster or ANOSIM can be performed using “Primer” as well.

References

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- Kaufmann, A. 1900. Cyprididen und Darwinuliden aus der Schweiz. Rev. Suisse Zool., 8: 209-423.
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Zeitschrift/Journal: [Berichte des Institutes für Geologie und Paläontologie der Karl-Franzens-Universität Graz](#)

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