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***Instructions***

***This report will be used to ensure a good mix of the diverse BrAPI community is represented on the board. If a vote becomes necessary, the reports will also be used to convey information about each candidate to the voters.***

***Please complete a copy of this report and submit it to the BrAPI Project Coordinator at brapicoordinatorselby@gmail.com***

***All text contained in brackets (<>) and highlighted in YELLOW is instructional and can be deleted***

***Page 2 contains the template with instructions***

***Page 3 contains a GOOD example of a completed report***

***Page 4 contains a BAD example of a completed report***

***Pages 1, 3, and 4 can be deleted before submission***

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**BrAPI Advisory Board Candidate Report**

**Name: *<Candidate Name>***

**Title: *<Candidate Job Title(s)>***

**Organization: *<Relevant organization(s) the candidate is associated with>***

**Section 1 – Motivation**

*<In this section, please briefly describe why you would like to become a member of the BrAPI project advisory board. You might include things like your history with the BrAPI project, the support you can provide to the community, changes you would like to see in how the project is run, or a vision of the future you would like to help create.>*

**Section 2 – Relevant Experience**

*<In this section, please briefly describe your knowledge and experience in* ***AT LEAST ONE*** *of the following topics. Please delete all other, unused headings.*

*The goal of these topics is to maintain a diverse advisory board with experts across this range of subjects. Having overlapping knowledge and experience within the board is great. However, if there are six phenotyping experts and no data management experts, then something has gone wrong.>*

General Breeding Workflow

*<Describe your knowledge and experience with general breeding workflows>*

Phenotyping and Phenomics

*<Describe your knowledge and experience with phenotyping and phenomics>*

Genotyping and Genomics

*<Describe your knowledge and experience with genotyping and genomics>*

Germplasm and Accession Management

*<Describe your knowledge and experience with germplasm and accession management>*

New and Emerging Breeding Technologies

*<Describe your knowledge and experience with new and emerging breeding technologies>*

Computer Programming

*<Describe your knowledge and experience with computer programming>*

Data Management

*<Describe your knowledge and experience with data management>*

Additional Relevant Experience

*<OPTIONAL - Describe any additional knowledge or experience that you feel is relevant but was not mentioned above>*

***<GOOD EXAMPLE – This page can be deleted when finished>***

**BrAPI Advisory Board Candidate Report**

**Name: Dr Good F. Example**

**Title: Professor of Bioinformatics and Project Lead for The Awesome Project (TAP)**

**Organization: University of Gotham**

**Section 1 – Motivation**

I have been a part of the BrAPI community for the past 5 years. In that time, the BrAPI standard has become a vital part of the TAP software over that time. We have been able to standardize much of our data management through APIs and we have been able to contribute some of our tools back to the community by making them BrAPI compatible. As the Project Lead for TAP, the continued success of BrAPI is very important to me, and I believe it can help many other groups in this community. I fore see a future where each important food crop has a global network of data and tools connected through APIs. BrAPI is a crucial part of this vision, but there is still work to be done before the BrAPI project will see its full potential. Specifically, I believe the funding model of the project needs to change. I have some ideas and I hope to work with the project leadership and community to help make that happen. Becoming a member of the advisory board will allow me to give back to the project and ensure its continued success.

**Section 2 – Relevant Experience**

General Breeding Workflow

I have had 20 years of experience working with breeding workflows. 10 years in industry working for the Pow maize program, and 10 more years with TAP. I am intimately familiar with how new lines are developed at Pow as I helped implement the workflow from crossing decisions, to planting, to data analysis.

Germplasm and Accession Management

TAP began as a project for storing germplasm data for gene banks. The scope has expanded somewhat, but it is still what we specialize in. I have had a lot of personal experience helping to design the systems for storing germplasm annotations, and tracking germplasm as our seeds are sent around the world to be tested.

New and Emerging Breeding Technologies

As part of TAP, we have been implementing some simple tools for managing HTP data, sent to us from our partners. We have been working on this over the past 2 years and we have learned many lessons about how to store and transfer this data efficiently. I would like to push the BrAPI community to create a standard for this type of data.

Computer Programming

I am not a software developer, but I am competent in R and Python. In the early days of TAP, I wrote some of the software to manage the germplasm database and our first attempt at an API. I expect much of that code has been replaced by our team of developers, but I do have some experience in the area.

***<BAD EXAMPLE – This page can be deleted when finished>***

**BrAPI Advisory Board Candidate Report**

**Name: Dr Bad J. Example**

**Title: Professor and TAP lead**

**Organization: University of Gotham**

**Section 1 – Motivation**

I work for TAP and we use BrAPI. I want to become a member of the BrAPI Advisory Board so that I can change the spec to fit our needs.

**Section 2 – Relevant Experience**

General Breeding Workflow

I have worked at Dow and TAP and I know the General Breeding Workflow

Germplasm and Accession Management

Germplasm management is very important. The community needs more accession management tools. I used GermManage one time for a project. It was good, but had some bugs and was not BrAPI compatible. Someday, I would like to help a team build a new version of GermManage that fixes these problems.

Computer Programming

I am not a software developer.