

## Competition Guidelines - Spring 2011

### **1. Completeness of the annotation**

*a) A fully synthesized annotation includes all fields with required/optional information and a record of the supporting evidence*

- i) All annotations must at the very least include a GO term, evidence term, reference and a brief description of the evidence in the notes field and may require other components to be considered complete.
- ii) A brief description of the evidence means that the annotator must record the figure, table, etc that provides the evidence for the annotation (ie "Figure 2"). It is strongly encouraged that curators add additional information about the experiment/figure/table, in particular for ISS and related evidence codes.
- iii) Some annotations may also include a qualifier term as optional information.
  - `Contributes_to` is only used with molecular function terms, never with biological process terms. (If it is annotated as being involved in a process, it is assumed it contributes to it.)
  - `Colocalizes_with` is only used with cellular component terms, but never with the IPI evidence code.
  - `NOT` is only appropriate if there is an annotation for this term already on the gene product page that you find evidence to the contrary for or if the gene products is specifically recorded in the literature to have a specific molecular function/biological process/cellular component and you find evidence to the contrary.
- iv) The use of certain evidence codes will require the team to enter additional data into the with/from field as optional information.
  - IPI, IGI, ISS, ISA, ISO, ISM must have the with/from field filled in with the database and accession number of the object of similarity/partner. (ie UniProtKB:P01023)
  - No annotations will be accepted using the evidence codes EXP:Inferred from Experiment, TAS: Traceable Author Statement, NAS:Non-traceable Author Statement, IC:Inferred by Curator or ND:No Biological Data Available.
- vi) All information must be properly formatted for an annotation to be complete and any annotation must be clearly and fully defended in case of a challenge. The team responsible for creating the annotation will be given an opportunity to defend the annotation during the challenge period.
- vii) No annotations to binding terms will be accepted (ie. Protein binding, ATP binding, etc)
- viii) Annotations from a high throughput method/paper will only be awarded points for the first annotation. Annotators are free to add the other annotations from the high throughput paper, but they will not count towards your team's score (nor will they count for challenge points). Whether a paper is a high throughput paper will be decided by the judges and their decision is final. As a guide, greater than 15 proteins annotated with the same GO term are likely to be considered high throughput data.

ix) Full points (5 points per annotation) will be awarded if the annotation is judged as complete and accurate and is successfully defended if challenged.

*b) An incomplete annotation includes any annotation that is missing one or more required/optional fields of information or any information is incorrectly formatted.*

- i) Missing or incomplete information refers to both required or optional information.
- ii) This will primarily be judged by peer review during the competition by the use of challenges. The judges will decide how many points will be awarded to each team (1-5 points for a total of 5 points per annotation).
- iii) If unchallenged throughout the competition, an annotation missing a required/optional field will be awarded zero points at the final review.
- iv) If unchallenged throughout the competition, an annotation that has a field that is incorrectly formatted will only be awarded 2 points.
- v) Judges will have the final decision on completeness.

## **2. Accuracy of the annotation**

*a) All content included in the annotation must be unambiguously accurate.*

- i) This includes ensuring the GO term selected is the most appropriate for the evidence cited, the evidence term is appropriate for the methods used, the reference chosen must include the actual data (not a reference to another paper or the abstract), the experiment described provides the evidence for the chosen GO term, the appropriate partner(s) is(are) included in the with/from field (if necessary).
- ii) The annotation must be added to the correct gene product page.
- iii) If only a part of a figure (ie "Figure 2b") is the evidence for the annotation, this must be correctly identified.
- iv) Some annotations may also include a qualifier term. (see above - 1.iii)
- v) The use of certain evidence codes will require the team to enter additional data into the with/from field. (see above - 1.iv)
- vi) The reference must be a peer-reviewed scientific paper and be in the format PMID:12345678. No annotations will be accepted if reference is a review article, book, news article, conference paper, or blog or other non-reviewed source.
- vii) No annotations will be accepted to any binding term (ie ATP binding, protein binding, etc)
- viii) If an annotation is challenged on the basis of accuracy, the team responsible for creating the annotation will be given the opportunity to defend the annotation during the challenge period. The accuracy of the annotation must be sufficiently justified upon a challenge.

*b) There are one or more errors in the content of the annotation.*

- i) This might include selection of a GO term, evidence code or description that is provided in the notes field is not appropriate for the experimental evidence, etc.
- ii) If challenged, judges will assign points based on the challenger's reason for challenging, the suggested correction and the rebuttal by the team responsible for the original annotation. (see below - 3. and 4.)

iii) If unchallenged, zero points will be awarded for an inaccurate annotation at the final review.

iv) Expert curators/judges will review the annotations and will have the final decision on accuracy.

### **3. Defense of a challenge of an annotation constructed by your team**

#### *a) Successful defense of your annotation.*

i) Your team is able to present and defend the description of the evidence and logic for all components of the annotation and ***NO*** changes are made to the annotation as a result.

ii) Full points remain with your team for this annotation.

#### *b) Lose the defense of your annotation.*

i) Your team can retain a portion of the points for an annotation if the challenging team identifies a problematic annotation, but does not suggest the most appropriate correction. The number of points awarded to the challenging team will depend on the severity of the problem(s) with the annotation and what problem(s) are identified by the challengers.

ii) Your team will lose all points for an annotation, which are then awarded to the challenging team, if the judges agree with the challenge ***and*** challenger's suggested correction(s).

iii) Expert curators/judges will have the final decision on challenges.

### **4. Challenge of an annotation contributed by another team**

#### *a) Successful challenge of an opponent's annotation*

i) The challenge can be on any annotation contributed during the competition by another team. To be awarded any points, your team must identify a problematic annotation.

ii) If a team is caught arbitrarily entering non-substantive challenges, the team will be penalized. The judges will decide the severity of the infraction and will determine the penalty.

iii) Your team can steal a portion of the points for an annotation made by another team if you correctly identify a part of the annotation that is inaccurate or incomplete (as deemed by the expert curators/judges in cases of dispute). The number of points awarded to your team will depend on the severity of the problem(s) with the annotation, what problem(s) your team has identified, and the accuracy or completion of correction proposed.

iv) To be awarded all of the points for a challenge, your team must present a valid challenge ***and*** propose a complete/accurate correction.

v) Expert curators/judges will review the annotations/challenges and will have the final decision on allotment of points.

#### *b) Lose the challenge of an opponent's annotation*

i) There is no penalty for challenging and losing a challenge (where no correction is required to the original annotation).

- ii) If a team is caught arbitrarily entering non-substantive challenges, your team will be penalized. The judges will decide the severity of the infraction and will determine the penalty.
- iii) If your challenge to an annotation, is inaccurate or incomplete (as deemed by the expert curators/judges in cases of dispute), the other team will lose a portion of their points and your team will be awarded a portion of the points for the annotation. The number of points awarded to your team will depend on the severity of the problem(s) with the annotation and what problem(s) your team has identified.
- iv) To be awarded full points for the annotation (and to cause the other team to lose these points from their total score), you must rightly challenge a problematic annotation ***and*** suggest the complete/accurate correction.
- v) Expert curators/judges will review the annotations/challenges and will have the final decision on allotment of points.

## **5) Identification of an ontology development site**

### *a) Successful identification of a term lacking in GO*

- i) If your team correctly identifies a term that is needed in GO, you will be awarded bonus points that will be added to your team score at the end of the competition.
- ii) Expert curators/judges will review the terminology proposed and will have the final decision on allotment of points. For example, 1 point for suggestion of a new 'regulation term', up to 5 points for complex ontology request.