

Annotation handbook and user guide to “Dataset from a human-in-the-loop approach to identify functionally important protein residues from literature”

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1 Annotation handbook

1.1 Entity types

Below are the entity types that were fixed at a corpus size of 30 publications. Some examples are given in Table 1.

Bond interaction

Any type of covalent or non-covalent bond or interaction. This covers, for example, hydrogen bonds, salt bridges, stacking of aromatic amino acid side chains and nucleic acids as $\pi-\pi$ stacking, electrostatic, hydrophobic, hydrophilic interactions and van der Waals interactions. These interactions are usually created by specific residues at a specific position in the protein of interest. This also covers covalent bonds that have been created between the primary protein of interest and a "chemical" as part of a reaction mechanism. Excluded are disulfide bridges as they fall under "ptm" and artificially introduced bonds from cross-linking experiments.

Chemical

This covers any chemical compound that is found in the publication and is not a protein. Most commonly this refers to small molecules/ drugs/compounds and fragments thereof, co-factors/ligands/metals and other molecules interacting with the primary protein that are not a protein themselves. This also includes short peptides and peptide fragments that may have been used instead of the corresponding full-length protein. Amino and nucleic acids are also included if they represent a substrate or product of a reaction carried out by the primary protein rather than a specific residue in a sequence. Unspecific references such as "moiety" or "group" are excluded.

Complex assembly

A higher order, often heterogeneous, assembly or complex is covered by this entity type. The primary protein of interest serves as the main component in such a complex and interacts with another component, e.g. another "protein" or "chemical", and this interaction can be measured, even if only transiently. This is different from the entity type "oligomeric state" as distinct oligomeric states of the primary protein can be combined to higher order complexes.

Evidence

Any measured quantity or experimental output that provides support for any conclusion drawn is annotated as "evidence".

Experimental method

This covers any procedure/experiment/method employed to produce the "evidence" that supports the conclusions drawn.

Gene

This refers to a specific gene/operon/open reading frame mentioned in the publication and is often used as a synonym for the gene product, i.e. the protein of interest.

Mutant

This represents a sequence-edited version of the primary protein or a related protein for comparison. The changes covered are point mutations of a specific residue in a specific sequence position and deletion/insertion mutants where whole sections/domains have been removed or added to a protein. We also include domain swaps between proteins to create chimeras. However, alterations such as expression tags, fluorescence labeling or adding other reporter tags are included in "experimental method".

Oligomeric state

The "oligomeric state" is only concerned with the polypeptide and no other components like those covered by "chemical". As mentioned above, this is different from "complex assembly" as some proteins require a distinct oligomeric state, i.e. require multiple copies of the same polypeptide, to be in their active form or even stable. As such, smaller oligomers serve as building blocks that can be assembled into higher order complexes.

Protein

The primary protein of interest or related proteins (homologues/orthologues/paralogues from other "species") used for additional analysis and comparison are annotated as "protein". Not included are proteins that are mentioned in the "Methods" section, e.g. restriction enzymes when creating an expression construct or those used as part of the protein purification process.

Protein state

Properties of a protein are captured by the "protein state". This covers anything regarding its functional state, whether it carries a "ptm", if it is bound to/void of/in complex with something, e.g. a component annotated as "chemical". Also included are whether the protein is in its full-length native state or a variant/mutant or whether particular residues or a motif are conserved between related proteins.

Protein type

Proteins are classed into different families/groups/classes based on their location in a cell or organism, or their function, or the process they are involved in. Terms capturing this are annotated as "protein type" refers to a family/group/class of proteins. So a particular protein discussed in a publication is one example of the proteins covered by a whole family.

PTM

Post-translational modifications, "ptm", cover any modification applied to a protein after creation of the main polypeptide chain. This covers modifications such as the formation of disulfide bridges, glycosylation, methylation, acetylation, ubiquitination, (auto)proteolytic cleavage and many more. These modifications rely on the creation/breakage of a covalent peptide bond. This excludes any covalent changes as part of a reaction mechanism, e.g. a covalent intermediate state which is covered by "bond interaction", and artificially introduced changes as part of an experiment.

Residue name

This refers to a specific amino acid in the primary protein (a related protein for comparison) or a nucleic acid in an interaction partner such as DNA/RNA without giving a sequence position. This is distinct from an amino or nucleic acid serving as a "chemical" in a reaction mechanism of a protein.

Residue number

If only the position in a sequence is given but the name of the residue, which can be either from a protein (primary or interaction partner or related), a peptide or a DNA/RNA, is not available then such a term is annotated as "residue number".

Residue name number

Residues in a sequence are uniquely identified by their name and position and therefore are annotated as "residue name number". This applies to the primary protein of interest, interacting proteins or peptides and DNA/RNA ("chemical"). For proteins and peptides the residues in question are amino acids and for DNA/RNA they are nucleic acids.

Residue range

A "residue range" refers to a stretch of amino acid or nucleic acid residues, usually with a starting and ending position, or the number of residues spanning a particular stretch in a sequence. In cases where "residue name number" defines the start and end of the range, preference is given to "residue range".

Site

Any site of interest in the primary protein or in an interaction partner such as another protein or DNA/RNA is annotated "site". This can be a binding site for a ligand, cofactor or metal, a protein-protein interaction point, specific residues involved in a mechanism.

Species

This entity type refers to specific species/strain the primary protein or a related protein originates from. However, this excludes species given in the "Methods" section.

Structure element

Secondary structure elements are used to create more complex structural arrangements and division of a polypeptide into domains. Such structural features are annotated as "structure element" in the primary protein as well as in any interaction partners such as other proteins, peptides or DNA/RNA. Also, for large complexes and molecular machines, a large number of very different polypeptides can be involved, each serving as

a subunit of a larger assembly and therefore representing a "structure element" to a larger "complex assembly".

Taxonomy domain

This entity type captures organisms on a higher hierarchical level compared to "species". Often a taxonomy term is used to refer to a specific organism ignoring the "species". For example, "yeast" is generally assumed to refer to "Saccharomyces cerevisiae" and in our case the former was annotated as "taxonomy domain" and the latter as "species". The exception is the word "human" which always refers to "Homo sapiens" and therefore is included in "species".

1.2 Document sections

We restricted the manual annotation to the sections "Introduction", "Results", "Discussion", and "Conclusion" as well as tables and the captions for figures and tables. The named entities of interest were mainly found in the "Results" section and to a lesser extend in "Introduction", "Discussion", and "Conclusion", but almost no information could be gained from the "Methods" and the "References" and therefore these were excluded in the manual annotation. Also, any supplemental material was excluded as such contributions are usually in non-standardised formats which were not supported by the annotation tool. In the case of the iterative annotation with a semi-automated approach, annotations automatically added by the predictor to "Methods" and "References" were removed before using the data for the next round of training.

1.3 Subspan annotation

In a number of publications we found authors used hand-crafted abbreviations. Such short-hands were split and annotated with separate entity types. Some examples are given below. "Hyp64IDA" represents a post-translational modification ("ptm") for span fragment "Hyp64" and a "protein" for "IDA". Similarly, "H3K9me3" is also a post-translational modification "ptm" for the partial span "K9me3" whereas "H3" refers to a "protein type". "SceCD" refers to the entity type "species" as "Sce" stands for "Saccharomyces cerevisiae" and "CD" stands for "central domain" or "CD" covered by entity type "structure element". "Arg409HAESA" refers to the specific "residue name number" "Arg409" in "protein" "HAESA". And finally, some spans found for example "residue name number" like "Thr1OH" were only partially annotated, here "Thr1", as we were not interested in the specific group or atom in the residue that was involved in an interaction.

1.4 Exclusion of non-specific spans

For the entity type "chemical" we also decided to limit annotations to specific chemical names and would ignore terms such as "moiety" or "group", if they referred to a part of a larger molecule. Also, more generally, any molecule that was not a protein was annotated as "chemical". This could be nucleic acids, a peptide, some cofactor or ligand or some other small molecule or fragment interacting with the primary protein of interest.

1.5 Usage of ontologies and controlled vocabularies

TeamTat allows linking entity types to ontologies and controlled vocabularies by defining a prefix, which can then be expanded with a reference to specific ID to ground a term. Although, we did not apply grounding in our project, we decided to define the prefix for a number of ontologies that are relevant for proteins and their structures: GO [1], [2], MESH [3], CHEBI [4], PR [5], SO [6], GENE [7] and DUMMY. DUMMY represents a placeholder for terms that were not found in any of the other ontologies or at the time of writing the authors were not aware of an ontology to hold these terms. Initially, annotators were also tasked in retrieving specific ontology IDs for each term. However, the time commitment for this task was not sustainable and therefore grounding for a specific ID was not applied after the initial set of annotations had been created. Instead, using ontology prefixes accelerated the annotation process. If a prefix for an ontology was set in TeamTat, an annotation could be automatically applied to all identical text spans in a publication when annotating manually.

2 TeamTat User Guide

TeamTat <https://www.teamtat.org/about> is an open access, browser-based text annotation tool. In this user guide we describe how one can set up the tool for one's own project, how annotations can be added to a document, and how these annotations can be retrieved for downstream processes. To summarize the two different ways to operate TeamTat, as a project manager or annotator, we provide an overview for each of the participation options to emphasize the differences. Figure 1 displays the view an annotator will have when working on an annotation project and Figure 2 shows the more complex setup used by a project manager.

2.1 Setting up TeamTat for an annotation project

2.1.1 Starting a new project

A new project is started from TeamTat's landing page, which is given in Figure 3. If one has never used TeamTat before, then the first step is to click on "Click here to Start" at the very top, right-hand corner of the homepage. One is then asked to confirm to not be a robot in a pop-up window. After ticking the box and clicking on "Continue" one receives a unique "User" link, see Figure 4. This link represents one's unique access to the TeamTat tool and allows for the creation/management of annotation projects. As is stated in the image, the link can be shared with others, if multiple people are involved in managing a project. It is worth noting here that there is a difference between a "User" who manages a project and one who only annotates the text. The former has full access to all levels of the project, whereas the latter is restricted to only the publications they have been assigned to. Before continuing, one also needs to understand that if the project manager is also involved in annotating documents, then they should have a separate "User" link for annotation work alongside the project manager link. Care should be taken to bookmark this unique user link to be able to easily return to one's projects.

To start a new project, one clicks on the button labelled "New Project", see Figure 5. Enter a descriptive project name. A project description can be given, but is not necessary. Generally, when using the unique user link, when clicking on "Project" at the top of the page one is presented with all the projects one is involved in. An example of such a project list is given in Figure 6.

2.1.2 Adding publications

TeamTat is fully integrated with PubMed and PubMedCentral, so publications can easily be added to a project by providing a list of IDs. For PubMed IDs (PMIDs) title and abstract will be retrieved for a given article, whereas for PubMedCentral IDs (PMCsIDs), if a publication is open access, retrieval will cover the full-text including tables and figures and their captions. On the "Documents" tab of the created project one clicks on the "Add Documents" button, which will lead to a new window with upload and retrieval options Figure 7 and Figure 8. Please note that supplying an excessively long list of PMIDs or PMCsIDs will fail and may even incapacitate the hosting server at NCBI. We recommend to keep the upload to ten publications at a time. Once all documents have been added to a project, one can navigate between them in a list via the "Documents" tab Figure 9. The numerical part of a PMCID/PMID is used to create a unique document identifier in the table. Additionally, publication title and number of annotations for each document are shown in columns "Title" and "Annotation", respectively. Columns "Done", "Curatable" and "Last Update" help monitoring when a publication is ready for downstream processes. There is an option to add documents by uploading from a local computer as

text or PDF files. However, for our project, we did not use this option and cannot comment on how well this works.

2.1.3 Adding team members

Annotators can be added to a project by re-using their name from a previous project or by adding them new. In order to keep things as anonymous as possible we decided to add all annotators by giving them non-identifiable names. Also, each annotator was given a personalized link to access the documents in the project and only the project manager knew which name and link corresponded to which annotator. Click on the button "Add Anonymous Annotator", add a non-identifiable name, bookmark the link and forward the link in an email to the annotator it is destined for. Setting a password is an option, but is not required for running a project. Once all team members have been given their personalized links, the project manager can assign documents. Please note again, if the project manager is also involved in the annotation process then they need to be given an annotator link as well. Also, please be aware that a project manager cannot have their manager link and annotator link open at the same time, even in separate browser windows, as annotations will always be created under the user ID that was last active. So if a project manager was using their manager link last and then wants to do annotation work they will have to switch links in order to have a consistent annotator for a document. Figure 10 shows a list of all members of an annotation project.

2.1.4 Assigning publications to annotators

The tab "Assignments" allows the project manager to assign documents to individual annotators. This can be done manually by clicking on the circle in the document-annotator matrix or by using the "Random Assign" button, which will randomly assign publications to annotators, depending on a ratio specified by the project manager. Figure 11 shows the document-annotator matrix for a project aiming for double annotation of each document.

2.1.5 Defining entity types

The project manager is also required to define and add entity types to a project. Using the tab "Types" this can be set up. Here, the project manager first clicks on the button "New Entity Type" to be prompted with a form which asks for "Name" and "Prefix" for the new entity type. As was explained in the main text of our publication, the "Prefix" enables linking of an entity type to an ontology or controlled vocabulary. Colors can be chosen for the different entity types. The colors can be personalized by each team member, including the annotators, and only applies to each individual link. In case an annotator may be colorblind this will allow them to choose a set of colors they are able to differentiate. Figure 12 gives the input form to create a new entity type and Figure 13 shows an example list of defined entity types.

2.1.6 Opening/Closing an annotation round

An annotation round is opened/closed for all annotators and their assigned documents by clicking on the button "Start Round" (see Figure 14). The project manager has to choose between two options. Using the "Individual Round", as was done for our project, means that the different annotators work independently and cannot see the annotation results of each other while annotating. Once an annotation round has been closed annotations are exchanged so annotators can see each other's work. For the "Collaborative Round" annotators can see each other's annotations and can therefore work together when resolving annotation disagreements. While an annotation round is open, the project manager can see how many annotations for each entity type have been found by the annotators and how many unique text spans they represent. Once all documents have had their status set by the annotators an annotation round can be closed. Closing a round will automatically set TeamTat to calculate inter annotator agreement for each document. Figure 15 gives a shortened list of annotations found for different entity types. An example of calculated inter-annotator agreement can be found in Figure 16.

2.2 Using TeamTat when annotating

As mentioned above, the annotator view in TeamTat has limited options available which are only focused on the annotation process and not the project management. Once a project manager has assigned all the documents to the annotators and has opened an annotation round, an annotator can access the documents through their personalized link. Figure 17 displays an example of a document list an annotator finds in their project. By clicking on the document identifier one can select and open a document to work on (see Figure 18).

2.2.1 Creating an annotation

There are multiple ways how an annotator can create an annotation. Below are examples for how one may want to annotate a text span with an entity type. Importantly, TeamTat does not have an "undo" function. If annotations are created/removed in error then they have to be manually removed/added to remedy the mistake. Also, it is good practice to reload the browser page to ensure that the autosave function of the tool has indeed carried all changes over to the document.

A combination of versions 2-4 has proven to be the most time efficient and user friendly way to annotate a text. Version 5 is a very good way when resolving annotation conflicts and cleaning and consolidating annotations.

Version 1 (Figure 19)

1. select entity type from drop-down menu
2. mark text span

Version 2 (Figure 20)

1. mark text span
2. click on text span
3. edit text span in pop-up window/delete annotation
4. click on "Update" button

Version 3 (Figure 21)

1. click on magnifying glass next to an item in the list/tab "Annotations" 8
2. text will move to focus on selected entity
3. the entity of interest is high-lighted by a red underline
4. edit text span in the pop-up window/delete annotation
5. click on "Update" button

Version 4 (Figure 22)

Annotating the same text span throughout an entire publication requires multiple clicks for each instance. However, by linking an annotation to an ontology using the "Prefix" one can annotate all instances of the same text span by following the instructions below. Note, never use "Update all mentions with the same concept ID" unless there is a fine-grained selection/hierarchy of ontologies in place. If "Concept ID" is not set, then using the "Update all mentions with the same concept ID" option will corrupt annotations.

1. either click on marked text span or select from list and click on magnifying glass
2. edit text span in the pop-up window
3. click on "Annotate each instance of this mention text"
4. if needed also set "Case sensitive match"
5. "Match whole word only" is set by default

Version 5 (Figure 23 and Figure 24)

1. highlight text span, sentence or paragraph containing annotations
2. edit existing annotations from list in pop-up window
3. do not click on "+Create New Annotation"

Note, this will create a new annotation for the entire highlighted text, which one does not want to create, but at the same time also brings any existing annotation into a new pop-up window as a list. One can then work their way through all entries in the list, if necessary. In particular, for removing annotations this is a very convenient way to reduce the number of clicks.

2.2.2 Flagging documents ready for curation

Each document has two sliders at the top that allow an annotator to set the status of the document as "Curatable" and "Done" which will be reflected in the document list for annotator and project manager (see Figure 25). These flags tell the project manager when the different documents are ready and they can close an annotation round.

2.3 Curating annotations

After closing an annotation round in our project, the curation and consolidation of annotations was left to the project manager with the lead biocurator serving as a proof-reader. Inter-annotator agreement was calculated at this stage, as was already

mentioned above, and all the annotations of the different annotators were combined into their respective documents. Figure 26 shows how the text will be displayed with all the annotations combined. The project manager was then required to go through all the annotations to either accept them, as they were in full agreement between the two annotators, apply the necessary fixes to produce an agreement or add annotations, if they were missing. In order to keep track of changes and be able to calculate inter-annotator agreement during the different curation rounds, the project manager used the personalized annotator links. Figure 27 gives an idea of how the different versions to annotate text described above can be used to work through the list of annotations. The side panel that holds a list of all the annotations in the text also indicates which require attention by the curator. We also found that the "Skip" button stayed active once it had been clicked and resulted in annotations worked on afterwards were also skipped.

2.4 Downloading annotated documents

Once the annotation project has reached desired maturity, the documents can be downloaded in a variety of ways. Individual documents can be downloaded by selecting a document from the the list in the "Documents" tab, clicking on it and then using the "Download" button at the top choosing between BioC XML or JSON as format. Using the "Version" button at the top of the document one is able to download a specific version of the document, depending on the annotation rounds carried out (see Figure 28). Only the project manager is able to download all documents in a project at once. This can be accomplished by using the "Download" button on the project overview page (see Figure 29). After selecting the version of the project one wants to download, a compressed folder of all the documents with their annotations in BioC XML is created. The "BioCXML" version contains the publication cut into paragraphs and set within XML tags <passage>. Each paragraph has its corresponding annotations included within the tags. Individual annotations are surrounded by the tag <annotation id="xxxx"> which also includes a unique, non-changeable ID for the annotation. The text span covered by the annotation as well as the entire text of the paragraph is enclosed within the tags <text>. Offsets based on character counts allow to determine the start and end of an annotation and where it is located in the document. The "PubAnnotatorJSON" version contains a JSON dictionary with keys "sourceid", "sourcedb", "project", "target", "text" and "denotations". The plain text as a single string is found under "text". The annotations are collected as a list of dictionaries under "denotations". The individual dictionaries contain the following keys "span", "obj", "id". The key "span" itself contains a dictionary with keys "begin" and "end" giving the the start and end position of the text span with respect to the character offset for the text not considering individual paragraphs. The key "obj" contains a string crafted from the entity type name, the set "Prefix" to link to an ontology, the annotator and a time stamp. The key "id" refers to a unique, non-changable ID for the annotation. The annotated text span itself is not included. The document and text and the found annotations are not directly linked.

References

- [1] Ashburner et al., Gene ontology: tool for the unification of biology, *Nat Genet*, 25, 25-9, 2000, <https://doi.org/10.1038/75556>
- [2] The Gene Ontology Consortium, The Gene Ontology knowledgebase in 2023, *Genetics*, 224, 2023, <https://doi.org/10.1093/genetics/iyad031>
- [3] Rogers FB, Medical subject headings, *Bull Med Libr Assoc*, 51, 114–6, 1963
- [4] Hastings J, Owen G, et al., ChEBI in 2016: Improved services and an expanding collection of metabolites, *Nucleic Acids Res*, 2016
- [5] Natale DA, Arighi CN, et al., Protein Ontology (PRO): enhancing and scaling up the representation of protein entities, *Nucleic Acids Res*, 45, D339- D346, 2017
- [6] Eilbeck K., Lewis S.E. et al, The Sequence Ontology: A tool for the unification of genome annotations, *Genome Biology*, 6, R44, 2005
- [7] Maglott D., Ostell J., et al., Entrez Gene: gene-centered information at NCBI, *Nucleic Acids Research*, 39, D52–D57, 2011, <https://doi.org/10.1093/nar/gkq1237>

List of publications to annotate Other annotators in the team "Types" of annotations to find, entities and relations

The screenshot shows the TeamTat interface for an annotator. At the top, there's a navigation bar with 'TeamTat' and links for 'Home', 'Projects', 'Tutorial', and 'About'. A button 'Show my access URL (annotator0)' is also present. Below the navigation, the URL 'Projects / group_annotation_for_autoannotator' is shown. A yellow box labeled 'Preparing' indicates the status. The main content area displays 'group_annotation_for_autoannotator' with a warning message: '10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator'. There are three tabs: 'Documents (0/10)', 'Members (7)', and 'Types'. A callout box points to the 'Documents' tab with the text 'Click on "Doc ID" to start annotating'. Below this, a table lists 10 documents assigned for annotation. The first document, '4887326', is highlighted with a red box.

Doc ID	Title	Annotation	Done	Curatable	Last Update	⋮
4887326	Structural insights into the regulatory mechanism of the Pseu...	0	<input type="checkbox"/>	N	about 1 hour ago	
4852598	Structural basis for Mep2 ammonium transceptor activation b...	0	<input type="checkbox"/>	N	about 1 hour ago	
4850288	Crystal Structure and Activity Studies of the C11 Cysteine Pe...	0	<input type="checkbox"/>	N	about 1 hour ago	
4850273	Molecular Dissection of Xyloglucan Recognition in a Promine...	0	<input type="checkbox"/>	N	about 1 hour ago	
4848090	Mechanistic insight into a peptide hormone signaling complex...	0	<input type="checkbox"/>	N	about 1 hour ago	

Figure 1: Annotator view for TeamTat

Download as BioCXML in zip folder Train/Apply AI tool Annotation round control Project version Access URL, here for project manager

List of publications to annotate Team members Assignment matrix Entity types definition Annotation statistics

The screenshot shows the TeamTat interface from the perspective of a project manager. At the top, there's a navigation bar with 'TeamTat' and links for 'Home', 'Projects', 'Tutorial', and 'About'. A user profile 'melanie' is shown. Below the navigation, the URL 'Projects / group_annotation_for_autoannotator' is shown. A yellow box labeled 'Version #3' indicates the project version. The main content area displays 'group_annotation_for_autoannotator' with a warning message: '10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator'. There are several buttons: 'Download', 'AI Tool', 'End Round' (highlighted in blue), 'Assignments (20)', 'Types', 'AI Tool', and 'Statistics'. A callout box points to the 'Reviewing' status in the 'AI Tool' section. Below these buttons, a table shows 'Entity types definition' and 'Annotation statistics'. The first row of the table is highlighted with a red box.

Doc ID	Title	Annotation	Done	Curatable	Review	Last Update	⋮
4887326	Structural insights into the regulatory mechanism of the ...	3130	0 / 2	2 / 2		14 days ago	
4852598	Structural basis for Mep2 ammonium transceptor activa...	5982	0 / 2	2 / 2		14 days ago	
4850288	Crystal Structure and Activity Studies of the C11 Cystein...	1857	0 / 2	2 / 2		14 days ago	
4850273	Molecular Dissection of Xyloglucan Recognition in a Pro...	5565	0 / 2	2 / 2		14 days ago	
4848090	Mechanistic insight into a peptide hormone signaling complex...	4877	0 / 2	2 / 2		16 days ago	

Figure 2: Project manager view for TeamTat

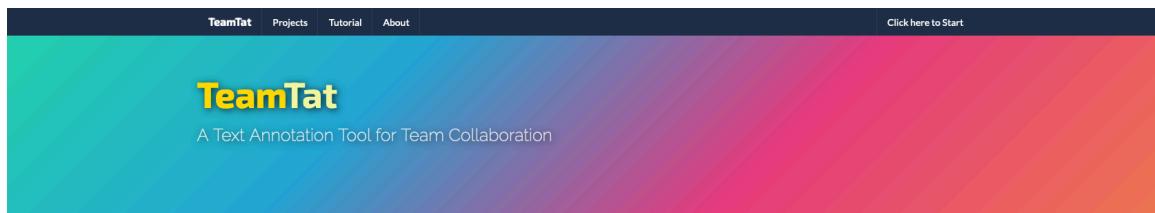


Figure 3: Arriving on TeamTat's homepage

You can change your nickname Change nickname

Please save the URL below. You can re-use or share this session using the URL. (This message does not show to others)

<https://www.teamtat.org/sessions/2f94dfba-1316-4497-9278-b0f6d5e4957f>

Enter an email address to send the URL ✉️ Send the URL above

* We do not collect or store your email address here.

Figure 4: Receiving unique user link

Projects

No Project. Try Sample Projects
You can use sample projects by clicking the green button below.



- Gene-Disease project (sample): 2 annotators, 3 documents with 602 annotations before a round
- PMC-article (sample): 2 annotators, 2 documents with 868 annotations at round #1

[New Project](#) [Try Sample Projects](#)

Figure 5: Creating a new project

Click on the project name

Number of publications to annotate

Name	Manager	Articles	Annotators	Round	Status	⋮
group_annotation_for_autoannotator	ME melaniev	10	6	0	Preparing	⚙️

* Click setting icons (⚙️) for more options.

New Project Try Sample Projects

Figure 6: List of projects one is part of

Projects / my.test.project

my_test_project Version #0 Preparing

Download AI Tool Start Round ⚙️

Documents (0) Members (1) Assignments (0) Types AI Tool Statistics

Total 0 documents Doc ID or Title

This project is empty. Please upload documents by clicking the Add Documents button below.

Add Documents

Figure 7: Input form to add documents to a project

Add Documents

Upload Multiple BioC / text / PDF Documents or DRAG & DROP FILES IN THIS BOX

⚠ Supporting text or PDF files are an experimental feature. The layout of a document may not be reserved.

OR

PMID(s) or PMCID(s)

- PMC4841544
- PMC4848761
- PMC4887326
- PMC4850273
- PMC4810460

Upload Documents **Copy & Paste IDs from a File**

< Back

Figure 8: Adding publications by providing a list of PMCsIDs

my_test_project

Version #0

Preparing

⚠ You need to assign annotators first before starting a round.

Download

AI Tool

Start Round

00

Documents (28)

Members (1)

Assignments (0)

Types

AI Tool

Statistics

Total 28 documents

Doc ID or Title



Doc ID	Title	Annotation	Done	Curatable	Last Update	⚙
4968113	Structural diversity in a human antibody germline library	0	0/0	0/0	3 minutes ago	⚙
4937325	Structure elucidation of the Pribnow box consensus promoter ...	0	0/0	0/0	3 minutes ago	⚙
4919469	Investigation of the Interaction between Cdc42 and Its Effect...	0	0/0	0/0	3 minutes ago	⚙
4918766	Mechanism of extracellular ion exchange and binding-site occl...	0	0/0	0/0	3 minutes ago	⚙
4918759	Structures of human ADAR2 bound to dsRNA reveal base-flip...	0	0/0	0/0	3 minutes ago	⚙
4887326	Structural insights into the regulatory mechanism of the Pseu...	0	0/0	0/0	3 minutes ago	⚙

Figure 9: Example of a document list for a project

TeamTat Home Projects Tutorial About melaniev

Projects / group_annotation_for_autoannotator Version #3

10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator

[Download](#) [AI Tool](#) [End Round](#) [Not all documents are marked as done](#)

Documents (10) Members (8) Assignments (20) Types AI Tool Statistics

Total 8 members

Name *	Access URL	Role
ME melaniev	melaniev@ebi.ac.uk	Project Manager
AN annotator0	b750aa15ee9f	Annotator
AN annotator1	3885f0c7df0b	Annotator
AN annotator2	a6e3ad4c5b6f	Annotator
AN annotator3	805a1ced19ff	Annotator
AN annotator4	2902804a84f9	Annotator
AN annotator5	7aa3cd28fb3e	Annotator
AN annotator6	6ce96618dae2	Annotator

Please enter a user's email [Add Existing Annotator](#)

If the annotator does not exist, a new account will be created automatically.

OR

Please enter a nickname [Add Anonymous Annotator](#)

You can make anonymous accounts for annotators. You can get session URLs for created users.

Copyright © 2019 TeamTat, Contact us: Rezarta.Islamaj@nih.gov, dongseop@mju.ac.kr, Zhiyong.Lu@nih.gov | Site Map
Rezarta Islamaj, Dongseop Kwon, Sun Kim, Zhiyong Lu, TeamTat: a collaborative text annotation tool, Nucleic Acids Research, 2020, gkaa333, https://doi.org/10.1093/nar/gkaa333

Figure 10: List of team members in an annotation project

⚠ You cannot change assignments after a round begins

Save Upload Random Assign Clear All

• By clicking a circle in a cell, you can assign or unassign a document to an annotator.

Doc ID	Title	AN	#						
4784909	The Structural Basis of Coenzyme A Recycling in a Bacterial O...	●	○	●	○	○	○	○	2
4786784	An extended U2AF65–RNA-binding domain recognizes the 3' ...	○	●	●	○	○	○	○	2
4792962	A unified mechanism for proteolysis and autocatalytic activati...	○	○	●	●	○	○	○	2
4832331	Structural insights into the Escherichia coli lysine decarboxyla...	○	○	●	○	●	○	○	2
4833862	The dynamic organization of fungal acetyl-CoA carboxylase	○	○	○	○	○	●	●	2
4848090	Mechanistic insight into a peptide hormone signaling complex ...	●	○	○	○	○	●	○	2
4850273	Molecular Dissection of Xyloglucan Recognition in a Prominen...	○	●	●	○	○	○	○	2
4850288	Crystal Structure and Activity Studies of the C11 Cysteine Pe...	○	○	●	●	○	○	○	2
4852598	Structural basis for Mep2 ammonium transceptor activation b...	○	○	●	○	●	○	○	2
4887326	Structural insights into the regulatory mechanism of the Pseu...	○	○	●	○	○	○	●	2
10 documents		2	2	8	2	2	2	2	20

• By clicking a circle in a cell, you can assign or unassign a document to an annotator.

Figure 11: Document-annotator matrix for a project aiming for double annotation of each document

Projects / group_annotation_for_autoannotator / Entity Types / new

New Entity Type

Name

Please enter a concept name, e.g. Gene. Alphanumeric characters and '-' are only allowed

Prefix

-- none --

Color

#D8D4C8

Sample colors

#CCFFFF	#CCFFCC	#FFFF99	#FFCCCC	#66CCFF	#99FF66	#FFCC00	#CCFF66	#FF66FF	#FF9999	#99CC00	#00CC99	#00CCFF
#9966FF	#CCCC00	#FF9933										

Back

Save

Figure 12: Input form to create a new entity type

TeamTat Home Projects Tutorial About

melaniev

Projects / group_annotation_for_autoannotator / Entity Types

group_annotation_for_autoannotator Version #3

10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator

Download AI Tool End Round Not all documents are marked as done

Documents (10) Members (8) Assignments (20) Types AI Tool Statistics

Entity Types (36) Relation Types (28)

Name	Color	Sample	Prefix	
protein	Pick Color	sample annotated text in a sentence	PR:	Edit Delete
ptm	Pick Color	sample annotated text in a sentence	MESH:	Edit Delete
residue_name	Pick Color	sample annotated text in a sentence	SO:	Edit Delete
residue_number	Pick Color	sample annotated text in a sentence	DUMMY:	Edit Delete
residue_name_number	Pick Color	sample annotated text in a sentence	DUMMY:	Edit Delete
species	Pick Color	sample annotated text in a sentence	MESH:	Edit Delete

Figure 13: Example list of different entity types

Download AI Tool Start Round Generate Final Merge

Documents (29) Members (3) A

Total 29 documents

Doc ID Title

Individual Round
Each annotator performs the task individually. The result of the previous round will be duplicated for each annotator.

Collaborative Round
All assigned annotators share the result of the previous round and perform the task together.

Figure 14: Opening/closing of an annotation round

The screenshot shows the TeamTat web application interface. At the top, there is a navigation bar with links for 'TeamTat', 'Home', 'Projects', 'Tutorial', and 'About'. On the right side of the top bar, there is a user profile icon labeled 'melaniev'. Below the navigation bar, the page title 'Projects' is displayed. Under the 'Projects' title, there is a card for a project named 'clean_condence_initial10'. The card includes a lock icon, the project name, a yellow button labeled 'Version #0', and a teal button labeled 'Finished'. A message box below the card says '⚠ You need to assign annotators first before starting a round.' There are three buttons at the bottom of this message box: 'Download', 'AI Tool', and 'Start Round'. To the right of these buttons is a gear icon. Below this section, there is a horizontal navigation bar with tabs: 'Documents (10)', 'Members (1)', 'Assignments (0)', 'Types', 'AI Tool', and 'Statistics'. The 'Statistics' tab is currently selected and highlighted in blue. At the bottom of the page, there is a summary table titled 'Number of Annotations per Entity Types'.

Total 10 documents

Version 0 ▾

Number of Annotations per Entity Types

Entity Type	Total	Uniq. Mentions	Uniq. IDs	No-ID Mentions	Avg.	Avg. Uniq. Mentions	Avg. Uniq. IDs	Avg. No-ID Mentions
taxonomy_domain	314	47	1	0	31.4	4.7	0.1	0.0
location	166	47	1	0	16.6	4.7	0.1	0.0
complex_assembly	305	93	1	0	30.5	9.3	0.1	0.0
protein_state	1093	303	1	0	109.3	30.3	0.1	0.0
chemical	1029	262	1	0	102.9	26.2	0.1	0.0

Figure 15: Example of annotations for different entity types and their raw counts

Doc ID	#	FA	CA	TA	PA	DA	SN	FA (%)	CA (%)	TA (%)	PA (%)	DA (%)	SN (%)
4784909	1126	1102	4	0	1	7	12	97.87	0.36	0.0	0.09	0.62	1.07
4786784	1961	1909	9	0	7	12	24	97.35	0.46	0.0	0.36	0.61	1.22
4792962	1806	1771	0	0	7	7	21	98.06	0.0	0.0	0.39	0.39	1.16
4832331	997	985	2	0	1	0	9	98.8	0.2	0.0	0.1	0.0	0.9
4833862	1432	1387	3	0	6	18	18	96.86	0.21	0.0	0.42	1.26	1.26
4848090	1360	1329	0	0	2	8	21	97.72	0.0	0.0	0.15	0.59	1.54
4850273	1492	1335	10	0	2	65	80	89.48	0.67	0.0	0.13	4.36	5.36
4850288	928	916	0	0	2	4	6	98.71	0.0	0.0	0.22	0.43	0.65
4852598	1679	1405	10	4	18	189	53	83.68	0.6	0.24	1.07	11.26	3.16
4887326	1297	1273	2	1	2	15	4	98.15	0.15	0.08	0.15	1.16	0.31
Total	14078	13412	40	5	48	325	248	95.27	0.28	0.04	0.34	2.31	1.76

- FA - Full Agree: same type, concept ID and text span
- CA - Concept Agree: same concept ID and text span, but different types
- TA - Type Agree: same type and text span, but different concept IDs
- PA - Partial Agree: same type and concept ID for overlapping text
- DA - Disagree: different types, concept IDs or text spans
- SN - Single: text annotated by only some of annotators

Figure 16: Example of calculated inter-annotator agreement

TeamTat Home Projects Tutorial About Show my access URL (annotator0)

Projects / group_annotation_for_autoannotator Version #0 Preparing

10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator

Documents (0/10) Members (7) Types

Total 10 documents assigned

Doc ID	Title	Annotation	Done	Curatable	Last Update	⋮
4887326	Structural insights into the regulatory mechanism of the Pseu...	0	<input type="checkbox"/>	N	about 1 hour ago	⋮
4852598	Structural basis for Mep2 ammonium transceptor activation b...	0	<input type="checkbox"/>	N	about 1 hour ago	⋮
4850288	Crystal Structure and Activity Studies of the C11 Cysteine Pe...	0	<input type="checkbox"/>	N	about 1 hour ago	⋮
4850273	Molecular Dissection of Xyloglucan Recognition in a Promine...	0	<input type="checkbox"/>	N	about 1 hour ago	⋮
4848090	Mechanistic insight into a peptide hormone signaling complex...	0	<input type="checkbox"/>	N	about 1 hour ago	⋮

Figure 17: Example of a document list for an annotator

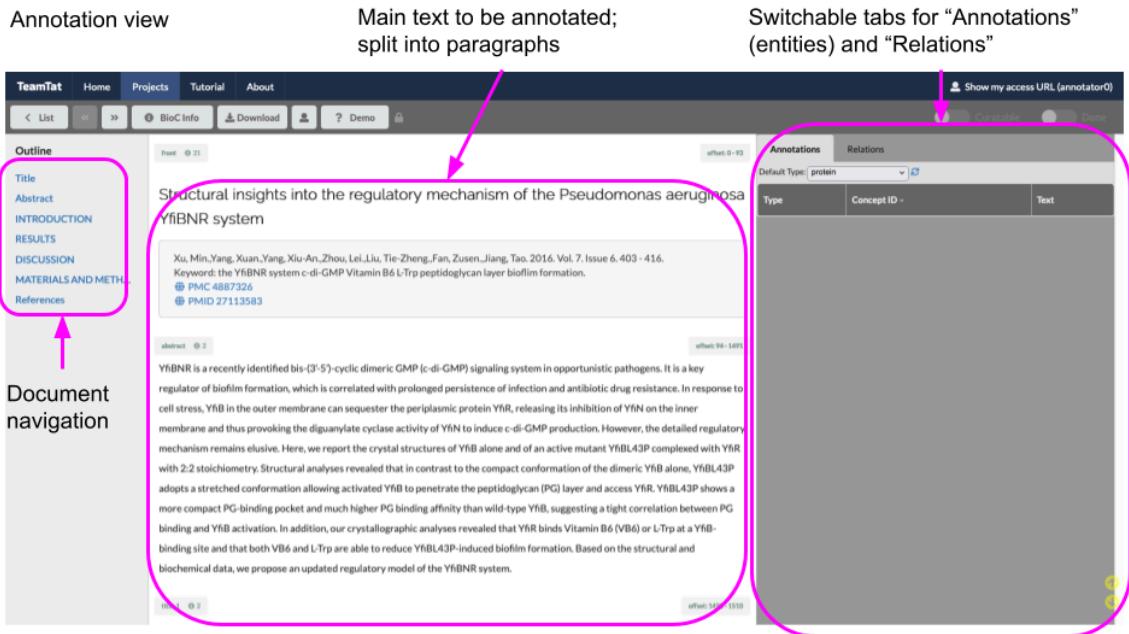


Figure 18: View when opening a document for annotation

Annotating an entity

This screenshot illustrates the first step in creating a new annotation. It shows the 'Annotations' tab of the BioC Annotation interface. A pink box highlights the 'Default Type' dropdown menu, which is set to 'location'. To the right of the dropdown is a 'Concept ID' input field and a 'Text' input field. Below these fields is a table with three rows: 'location' (with a green circular icon), 'indigestible complex' (with a blue circular icon), and 'chemical' (with a red circular icon). A pink arrow points from the 'Default Type' dropdown to the 'Default Type' label above it.

Figure 19: Creating a new annotation, version 1

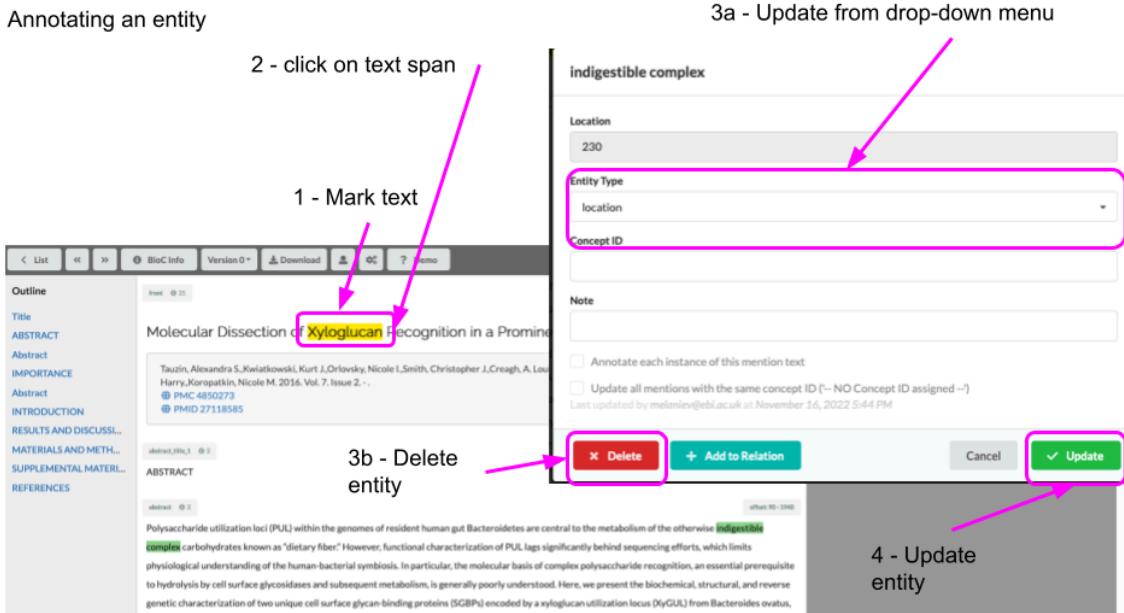


Figure 20: Creating a new annotation, version 2

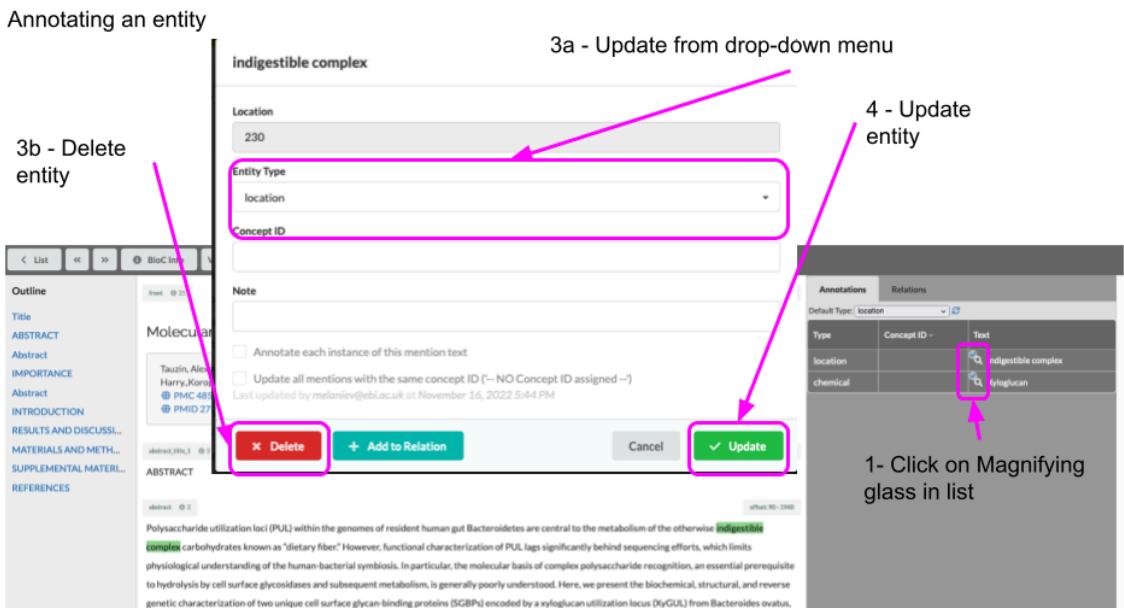


Figure 21: Creating a new annotation, version 3

Annotate each instance of this mention text

Case sensitive match
 Match whole word only

Update all mentions with the same concept ID ('CHEBI:')

Last updated by melaniev@ebi.ac.uk at March 15, 2023 11:33 AM

Figure 22: Creating a new annotation, version 4

paragraph ② offset: 7653 - 7864

We obtained two crystal forms of YfIB (residues 34–168, lacking the signal peptide from residues 1–26 and periplasmic residues 27–33), crystal forms I and II, belonging to space groups P21 and P41, respectively.

Figure 23: Selecting text with multiple annotations

We obtained two crystal forms of YfIB (residues 34–168, lacking the signal peptide from residues 1–26 and periplasmic residues 27–33), crystal forms I and I...

24 annotation(s) exist(s) in this range.

<input type="checkbox"/>	Type	Concept ID	Text	Offset	Annotator	Updated at
<input type="checkbox"/>	result_outc...	DUMMY:	Q obtained	7656	annotator5	2023-03-02
<input type="checkbox"/>	result_outc...	DUMMY:	Q obtained	7656	annotator0	2023-03-02
<input type="checkbox"/>	evidence	DUMMY:	Q crystal forms	7669	annotator5	2023-03-02
<input type="checkbox"/>	evidence	DUMMY:	Q crystal forms	7669	annotator0	2023-03-02
<input type="checkbox"/>	protein	PR:	Q YfIB	7686	annotator5	2023-03-02
<input type="checkbox"/>	protein	PR:	Q YfIB	7686	annotator0	2023-03-02
<input type="checkbox"/>	protein	PR:	Q YfIB	7686	annotator0	2023-03-02
<input type="checkbox"/>	residue_ra...	DUMMY:	Q 34–168	7701	annotator5	2023-03-02
<input type="checkbox"/>	residue_ra...	DUMMY:	Q 34–168	7701	annotator5	2023-03-02
<input type="checkbox"/>	residue_ra...	DUMMY:	Q 34–168	7701	annotator0	2023-03-02
<input type="checkbox"/>	protein_sta...	DUMMY:	Q lacking	7709	annotator5	2023-03-02

X Delete **+ Add to Relation** **+ Create New Annotation** **Close**

Figure 24: Updating multiple annotations at the same time

The screenshot shows the TeamTat annotation interface. At the top, there's a navigation bar with links for TeamTat, Home, Projects, Tutorial, About, and a 'Show my access URL (annotator)' button. Below the navigation is a toolbar with icons for List, BioC Info, Download, and Demo. On the left, there's an 'Outline' sidebar with sections like Title, Abstract, INTRODUCTION, RESULTS, DISCUSSION, MATERIALS AND METHODS, and References. The main content area displays a document titled 'Structural insights into the regulatory mechanism of the *Pseudomonas aeruginosa* YfBNR system'. It includes author information (Xu, Min., Yang, Xuan., Yang, Xiu-An., Zhou, Lei., Liu, Tie-Zheng., Fan, Zusen., Jiang, Tao. 2016. Vol. 7, Issue 6. 403 - 416.), a keyword (YfBNR system c-di-GMP Vitamin B6 L-Trp peptidoglycan layer biofilm formation.), and PMID (PMID 27113583). To the right, there are two tabs: 'Annotations' and 'Relations'. Under 'Annotations', there's a table with columns for Type, Concept ID, and Text. Entries include species (MESH: Pseudomonas aeruginosa), complex_as... (GO: YfBNR), chemical (CHEBI: bis-(3'-5')-cyclic dimeric), and function (GO: signaling system). There are also 'Curable' and 'Done' status sliders at the top right.

Figure 25: Example showing sliders to set document status

Example of annotated publication - after consolidation and merging

The diagram illustrates the outcomes of annotation consolidation and merging. It shows a paragraph of text with various annotations highlighted in green and purple boxes. A green bracket labeled 'Full annotator agreement' covers the first few sentences. A purple bracket labeled 'Single annotator' covers a section where only one annotator made an annotation. A red bracket labeled 'Annotator disagreement' covers a section where two annotators had different annotations. Arrows point from these labels to the respective sections in the text.

Full annotator agreement

The final region in **Mep2** that shows large differences compared with the **bacterial transporters** is the **CTR** in **Mep2**, the **CTR** has moved away and makes relatively few contacts with the **main body** of the **transporter**, generating a **more elongated** protein (Figs 1 and 4). By contrast, in the **structures of bacterial proteins**, the **CTR** is **docked tightly** onto the **N-terminal half** of the **transporters** (corresponding to **TM1-5**), resulting in a more **compact structure**. This is illustrated by the positions of the five **universally conserved** residues within the **CTR**, that is, **Arg415(370)**, **Glu421(376)**, **Gly424(379)**, **Asp426(381)** and **Tyr435(390)** in **CaMep2(Amt-1)** (Fig. 2). These residues include those of the **ExxGxD' motif**, which when mutated generate **inactive transporters**. In **Amt-1** and other **bacterial ammonium transporters**, these **CTR** residues interact with residues within the **N-terminal half** of the protein. On one side, the **Tyr390 hydroxyl** in **Amt-1** is **hydrogen bonded** with the **side chain** of the **conserved His185** at the **C-terminal end of loop ICL3**. At the **other end of ICL3**, the **backbone carbonyl groups** of **Gly172** and **Lys173** are **hydrogen bonded** to the **side chain** of **Arg370**. Similar interactions were also modelled in the **active, non-phosphorylated plant Amt-1;1 structure** (for example, **Y467-H499** and **D458-K71**). The result of these interactions is that the **CTR** 'hugs' the **N-terminal half** of the **transporters** (Fig. 4). Also noteworthy is **Asp381**, the **side chain** of which **interacts strongly** with the **positive dipole** on the **N-terminal end of TM2**. This interaction in the **centre of the protein** may be particularly important to stabilize the **open conformations** of **ammonium transporters**. In the **Mep2 structures**, **none** of the **interactions** mentioned above are present.

Single annotator

Annotator disagreement

Figure 26: Example text showing the different outcomes when annotations of two annotators are combined after closing an annotation round

Example of annotated publication - after consolidation and merging

The screenshot shows a comparison of annotations for the entity "Mep2 ammonium transceptors".

Left Panel (Top): Shows the "Annotate Entity Type" interface. The entity type is set to "protein_type". A red box highlights the "Update" button, which is also highlighted with a pink box.

Left Panel (Bottom): Shows the annotation table with one row:

Type	Concept ID	Text	Other	Annotator	Updated at
protein_type	MESH	transporter phosphorylation and dephosphorylation	0.00%	User 1	2023-01-01
protein_type	MESH	transporter	0.00%	User 1	2023-01-01

Right Panel (Top): Shows a list of annotations from a single annotator ("User 1") with a pink border:

- kinase
- ammonium transporters
- AMTs
- AMT transporter

Right Panel (Bottom): Shows a list of annotations from multiple annotators with a green border:

- transporter phosphorylation and dephosphorylation
- transporter
- Mep2 ammonium transceptors
- ammonium transceptors
- AMT proteins
- Amts
- channel
- Mep2 ammonium transceptor
- Mep2 proteins
- transporters
- transporters
- ammonium transporters

Bottom Left: Text spans with single annotation; check, whether you agree or disagree

Bottom Middle: Text spans with conflicting annotation; need more careful thinking and checking

Bottom Right: Text spans with double annotator agreement

Figure 27: Different ways to curate annotations

List	«	»	BioC Info	Version 3 ▾	Download	User	Settings	Demo
----------------------	-------------------	-------------------	---------------------------	-----------------------------	--------------------------	----------------------	--------------------------	----------------------

Figure 28: Selecting download of a single document

group_annotation_for_autoannotator Version #3

10 initial publications to be annotated in triplicates to extract residue level information; annotations will be used to train an auto-annotator

Download AI Tool End Round ⚠ Not all documents are marked as done

Version 0 Version 1 Version 2 Version 3

Members (8) Assignments (20) Types AI Tool Statistics

Doc ID or Title 🔍

Doc ID	Title	Annotation	Done	Curatable	Review	Last Update	Actions

Figure 29: Downloading all documents of a project

Entity type	Example
bond interaction	H-bond, hydrogen bond network, hydrophobic interaction, salt bridge
chemical	NADH, ATP, Zn ²⁺ , RNA, acetyl CoA
complex assembly	Tdp2-DNA, BRCA2:RAD51, TTD-PHD-H3K9me3, UHRF1-DNMT1
evidence	KD, structure, root-mean-square deviation, chromatogram, electron density
experimental method	size exclusion chromatography, mass spectrometry analysis, sequence alignment, analytical ultracentrifugation, single-residue mutation
gene	ectC, Synpcc7942 2462, At2g21370, YOR006c, nep1, nadA, nadR
mutant	YfiBL43P, H7A, MC58-Δ1843, ΔNadR, mep1-3Δ, 449-485Δ
oligomeric state	monomer, dimer, trimer, monomeric, dimeric, heterodimer
protein	YfiB, YfiR, YfiN, HAESA, SERK1, SNF1, BRCA1
protein state	phosphorylated, non-catalytic, highly conserved, full-length, biodegradative, apo, ppGpp-free
protein type	cyclase, lipase, hydrolase, kinase, phosphatase
ptm	glycosylation, phosphorylation, methylation, acetylation, disulfide bridges, propeptide cleavage, K9me3, Diph699, pThr160
residue name	alanine, proline, tyrosine, Glu, Lys, His, adenosine, A, guanosine, G
residue number	123
residue name number	Ala123, A123, X1, X2, U11, mAsp272, hAsp262, glutamate at 474, G-1
residue range	34-52, D21-K26, Arg120 until Ser122, Gln5 to Ser122, 15 residues, three amino acids
site	hydrophobic cleft, HAP binding site, Trp binding pocket, haem binding region, FXF-motif-binding site, active site

species	<i>E. coli</i> , <i>Pseudomonas aeruginosa</i> , <i>Sphingopyxis alaskensis</i> , <i>S. alaskensis</i> , Sa
structure element	beta-sheets, cupin barrel, α -helices, metal-binding motif, antiparallel β -strands
taxonomy domain	Bacteria, nitrifying archaeon, eukaryotic, Xenopus, murin, mam malian

Table 1: Entity types with examples.