

AA1

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Allow researchers to annotate one other's work

Annotation of Crystallographic Structures (Annotating) - Microsoft Internet Explorer

Address: <http://data.a.itee.uq.edu.au/mjh/3molAnnotated/index.php?model=models/2AN3.pdb>

dart dataset acquisition accessibility & annotation e-research technologies

Annotating crystallographic structures

THE UNIVERSITY OF QUEENSLAND

Search Journals: ACS, RCSB/PDB, CCDC. Local models: select Model URL: Load (Find Models)

Viewing models/2AN3.pdb

Annotations at selection:

- [Wat2 confirmation \(by rovalds\)](#)
- [Position of Wat2 \(by michael\)](#)

PDF RSS

Locate selection

Show bounding box

Show cartoons

Show using [RCSB Protein Databank](#): default view

Spin the model

Zoom: 100%

The crystal structure of hPNMT complexed with cis-(1R,2S)-AT confirms this.

DEMO



Looks impressive, but...



Behind the scenes

- Not using the data's URL
- `//SAH//2002.0//number:421,moveto//1//-425//-90//-8`
- Communicating with the sidebar
- Modified Jmol
- Browser Security



Browser Security

- Javascript and Java heavily affected
 - Nothing across domains
 - Nothing across frames
 - So how can we pull information from several hosts?
 - Journal Databases, Annotea, FOAF profiles...
- Standalone applications vs Browser



Future Work



Modernize Annotea

- Catch up to current use patterns
 - Blogs, trackback, feeds, re-use...?
 - The CMM daily notebooks
 - Identity & FOAF
 - Usable URLs



- Integrate into Vannotea