Title: Science in the open /or/ How I learned to stop worrying and love my blog

Date: Sep 12, 2008 11:00 AM

URL: http://pirsa.org/08090038

Abstract: The idea behind the \'Open Science Movement\' is that by making data, results, and protocols freely available to the research community for use and re-use a step change in the efficiency of carrying out science can be achieved. In this talk I will discuss the experience of my research group in pursuing \'Open Notebook Science\' in which we make our laboratory notebooks freely available on the web as experiments are recorded. This involves both the development and use of new tools to make the recording process practical and useful and the cultural challenges of convincing other scientists that this is a worthwhile, and not completely foolhardy, approach.

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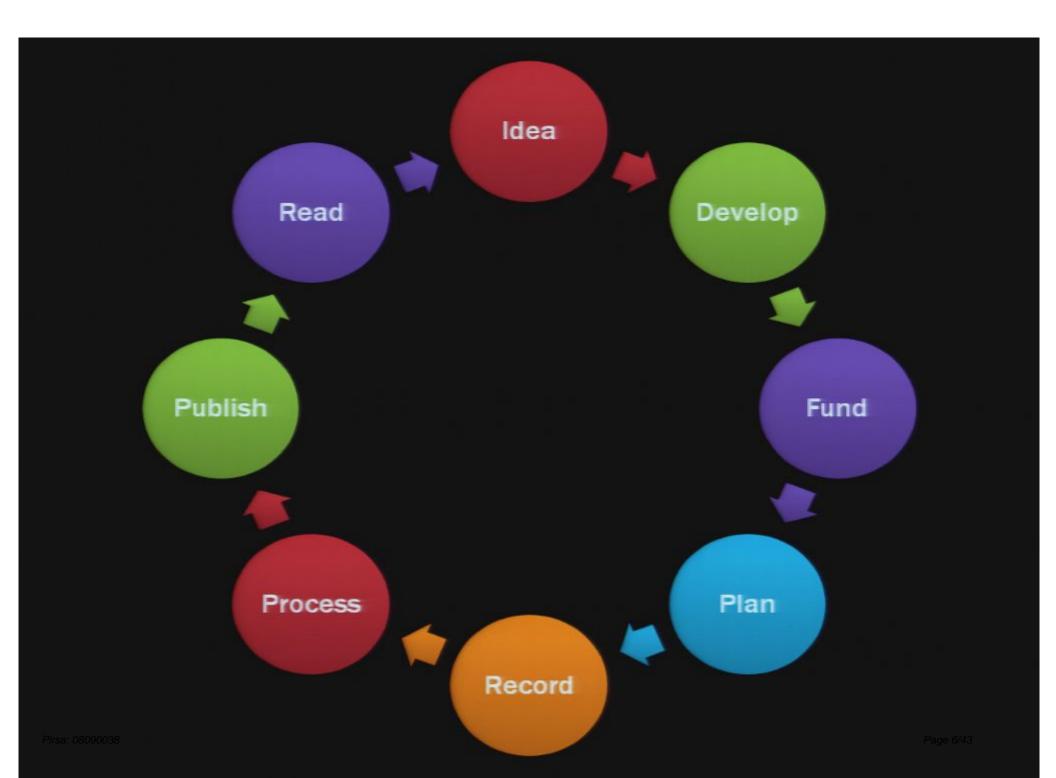


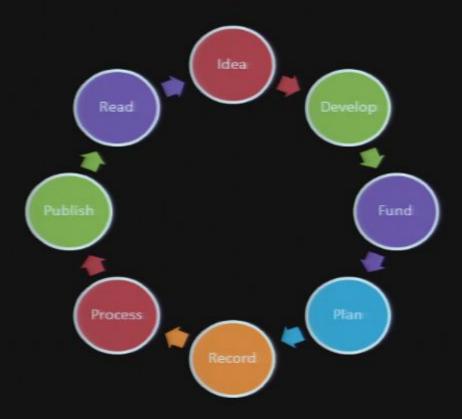


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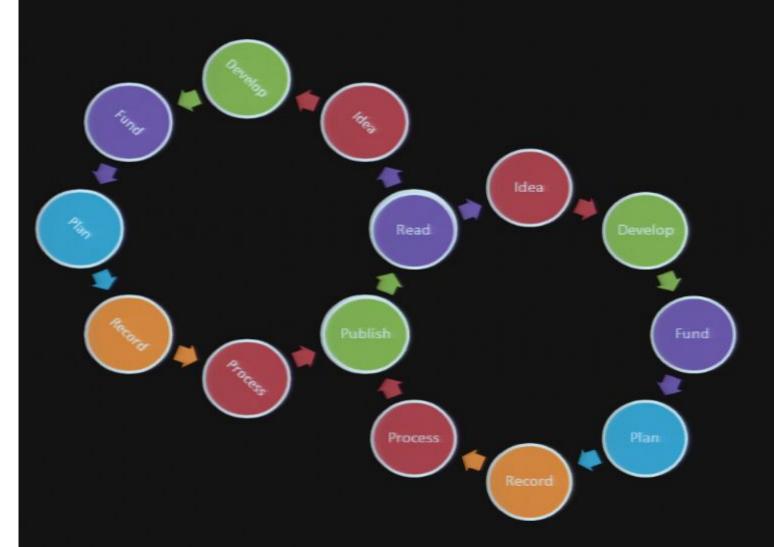


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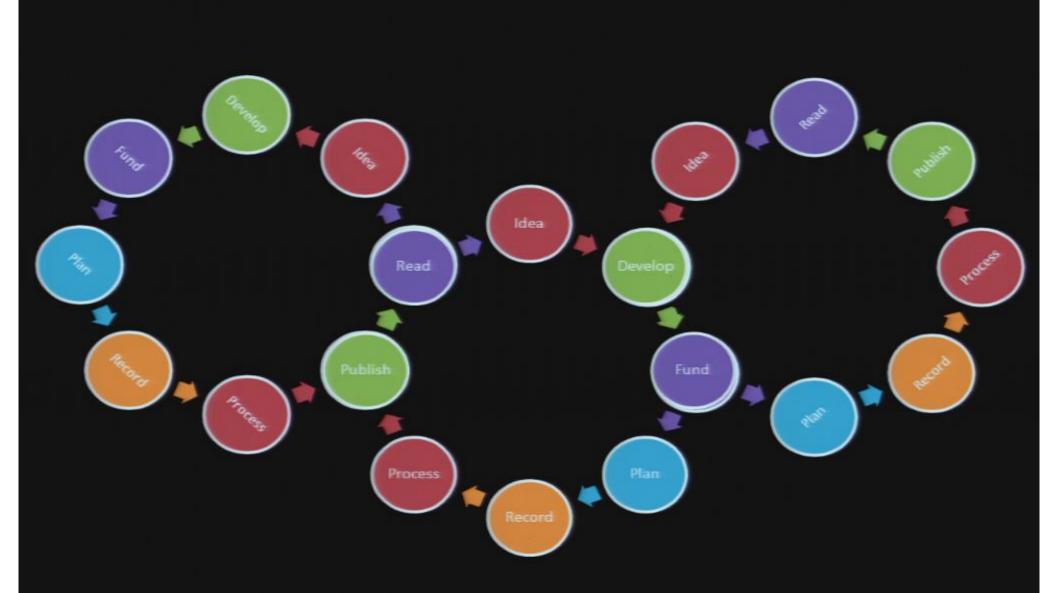




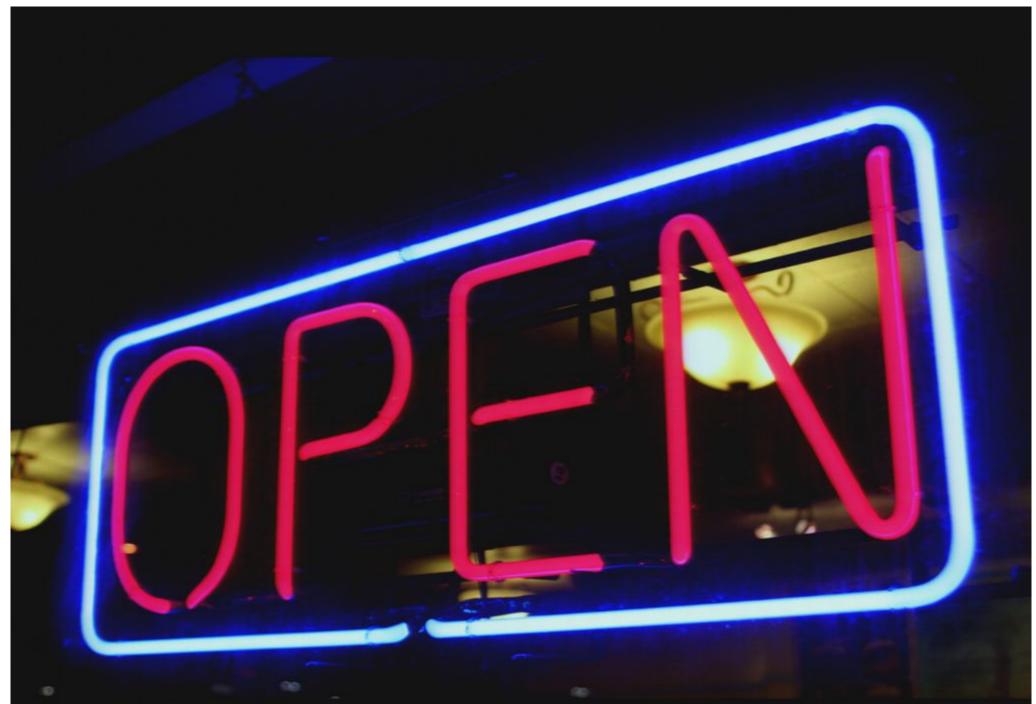
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Sortase Cloning

Weighing of dried samples

4th September 2008 49 09:05

Instrument: Mettler_4_place_balance

Project: usefulchem_solubility

Post Type: Weighing

The following samples were weighed on a balance tared to zero with a holder in place, i.e. the weight reported is the weight of the sample and the container or tube it is held in.

Sample	Recorded weight (g)
Dried solution of boc-Gly in methanol	1.2063
Dried solution of gly-Ome from methanol	1.0730
Dried solution of vanillin from methanol	1.0799
Dried solution of glucose from methanol	1.0535
Dried solution ofmannitol from methanol	1.0534
Dried solution of NaCl from methanol	1.0513
Dried solution of boc-Gly from ethanol	1.1757
Dried solution of gly-OMe from ethanol	1.0546
Dried solution of vanillin from ethanol	1.1232
Dried solution of glucuse from ethanol	1.0532
Dried solution of mannitol from ethanol	1.0491
Oned solution of NaCl from ethanol	1.0597
Dried solution of boc-Gly from THF	1.1722
Dried solution of gly-Ome from THF	1.0547
Dried solution of vanillin from THF	1.1673
Dried solution of glucose from THF	1.0500
Dried solution of mannitol from THF	1.0492
Dried solution of NaCl in THE	1.0530

David Neylon | Edit Post | Procedure | Comments (2)

Weighing of empty tubes

765 September 2008 / 5 09:57

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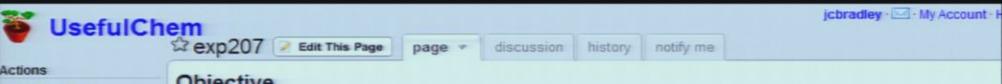
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sitemeter 4.4

Objective

To establish a method of measuring the solubility of some compounds in organic solvents.

Procedure

Solid is added to 1.5 mL Eppendorf tubes containing 500 uL of solvent until saturated after 30 s of vortexing. The tubes are then centrifuged for 60 s then 200 uL of clear solution is transferred to pre-weighed 1.5 mL Eppendorf tubes. The tubes with the clear solution are then evaporated down in a SpeedVac for 2 h and re-weighed to obtain the amount of dissolved solid.

Results

The list of compounds, solvents and measurements is on workbook 207-WB1 # The pics are tagged as EXP207 on Flickr ₽.

Discussion

This technique was adequate to measure solubilities of the following compounds:

boc-glycine in methanol (4.40 M) and THF (3.45 M)

glycine methyl ester in methanol (1.32 M)

vanillin in methanol (4.19 M) ethanol (2.50 M) THF (3.89 M)

The solubility of boc-glycine in ethanol was measured at 3.57 M but because it appeared as a gel it should be put back on the speedvac to see if a powder can be obtained.

All other compounds measured to less than 5 mg and should be redone using much more solvent to get an accurate measurement



salubility of bac-Glycine in the

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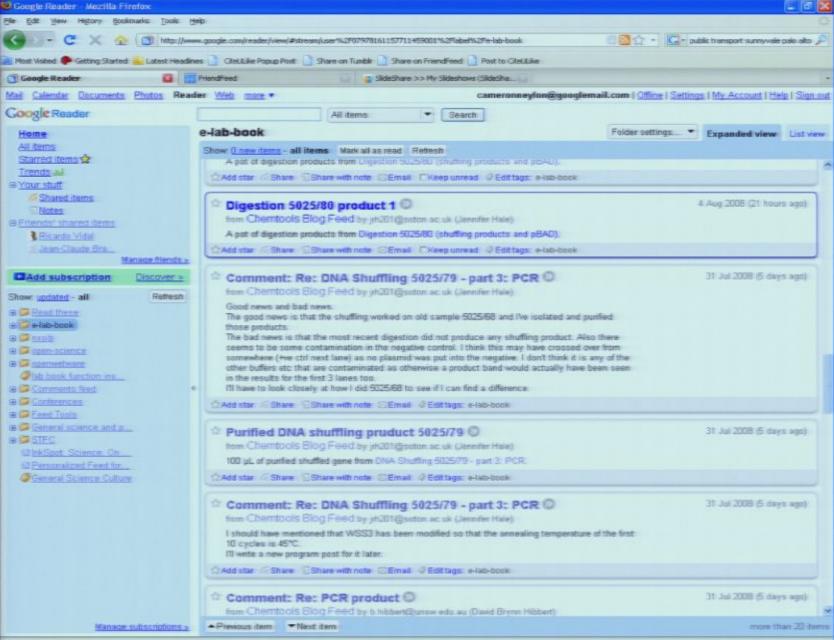
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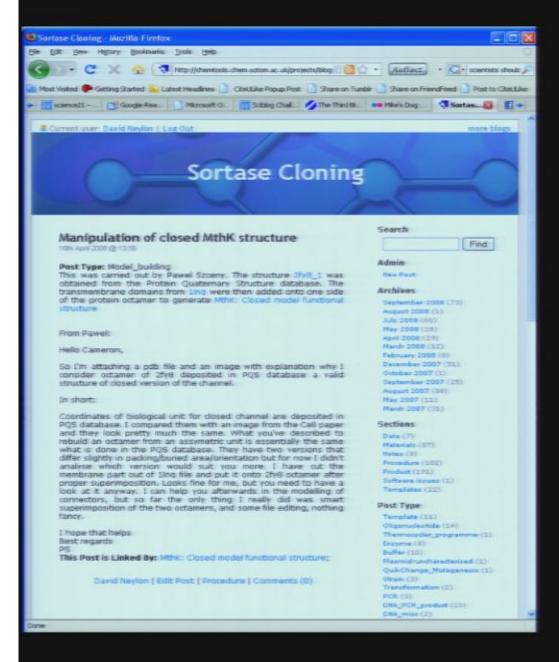
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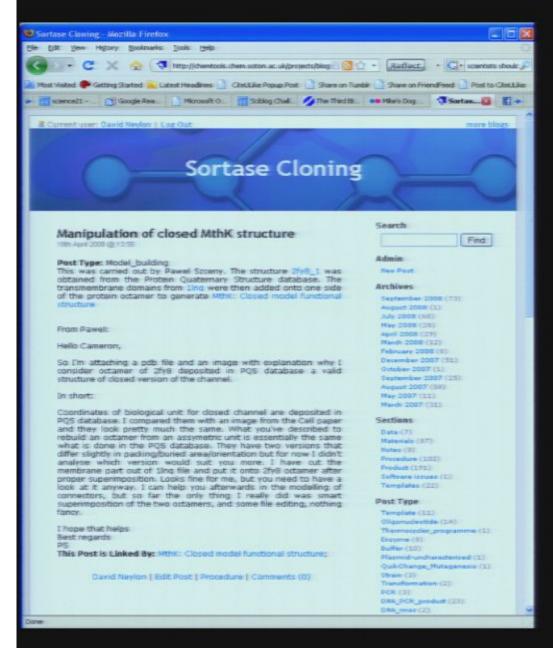
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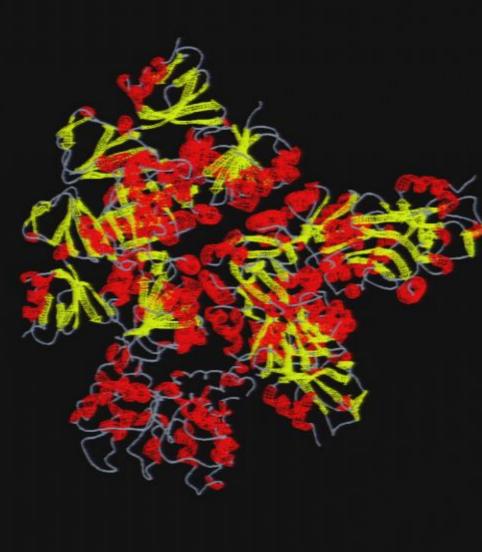
- I'm trying to build a model of the calcium gated potassium channel MthK using the PDB files 1Inq and 2fy8. MthK has a gating domain (rck domain) and a transmembrane domain and works as a tetramer of full length proteins with a tetramer of just rck domain. So I can build the ligand bound (open conformation) from 1Inq by removing residues 19-98 from chains A, B, C, and D. The closed conformation is harder. 2fy8 has the rck domain in the closed conformation but the deposited structure is the asymmetric unit and not the biological unit. What I need to do is build the rck octamer in the closed conformation and then to put that back on top of the transmembrane domain tetramer. Swiss pdb viewer which isn't really cutting the mustard. If anyone can help us by building the models that would be brilliant. Our aim is to determine the structure of these molecules in solution (with detergent) by small angle scattering so good models to compare with data are crucial. Authorship on papers a given can't offer any money You (edit | delete)
- How fast that needs to be done? I think I can help, but I can start in the middle of the next week. Pawel Szczesny

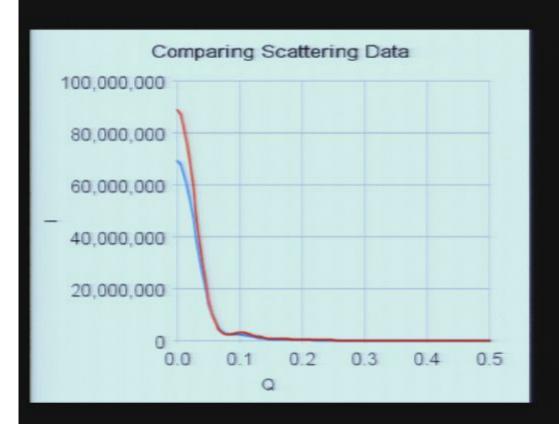
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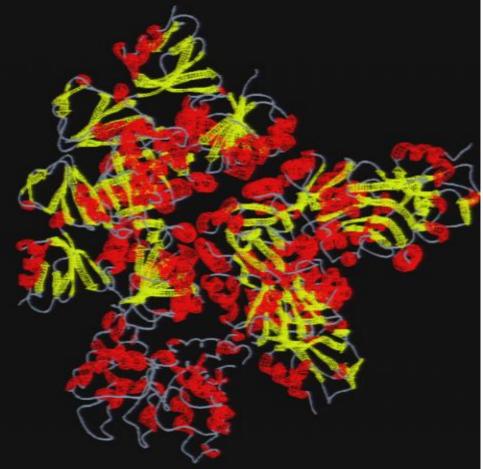
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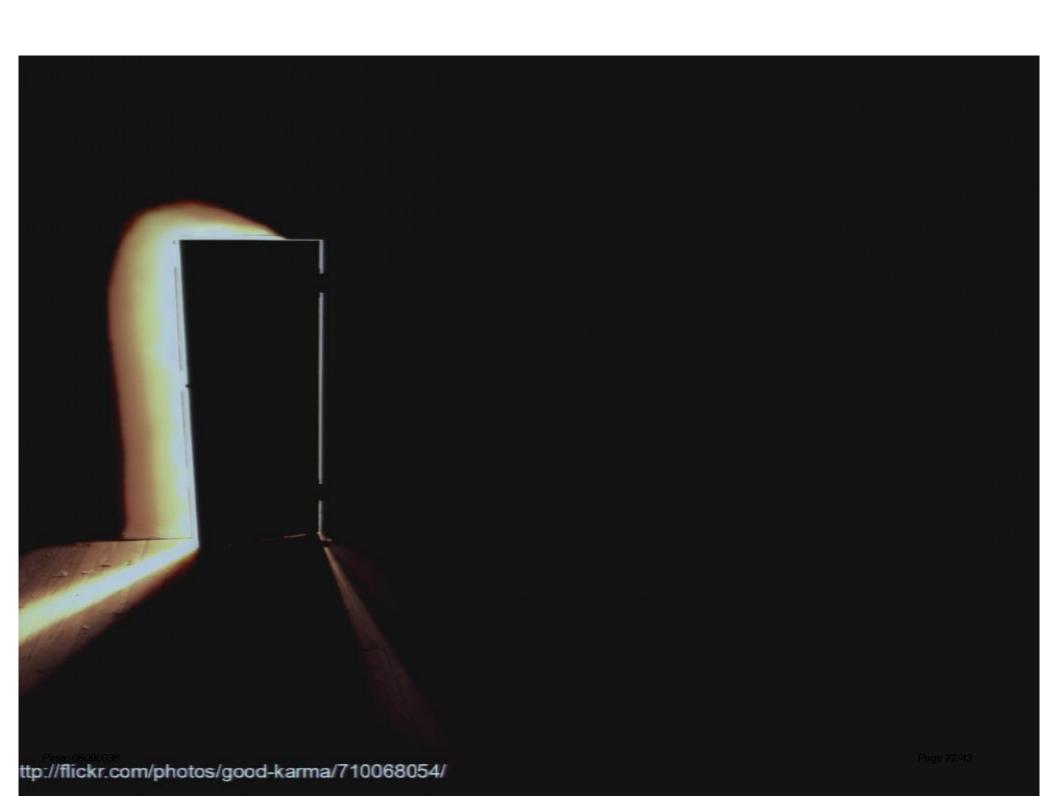




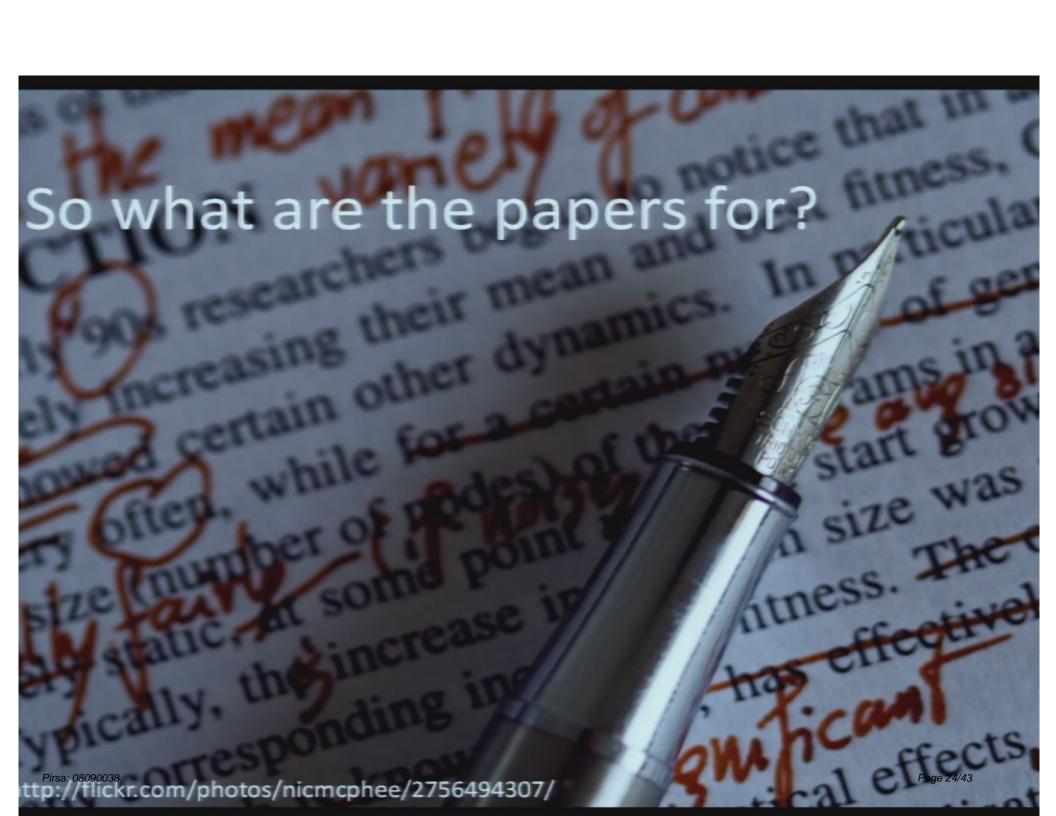












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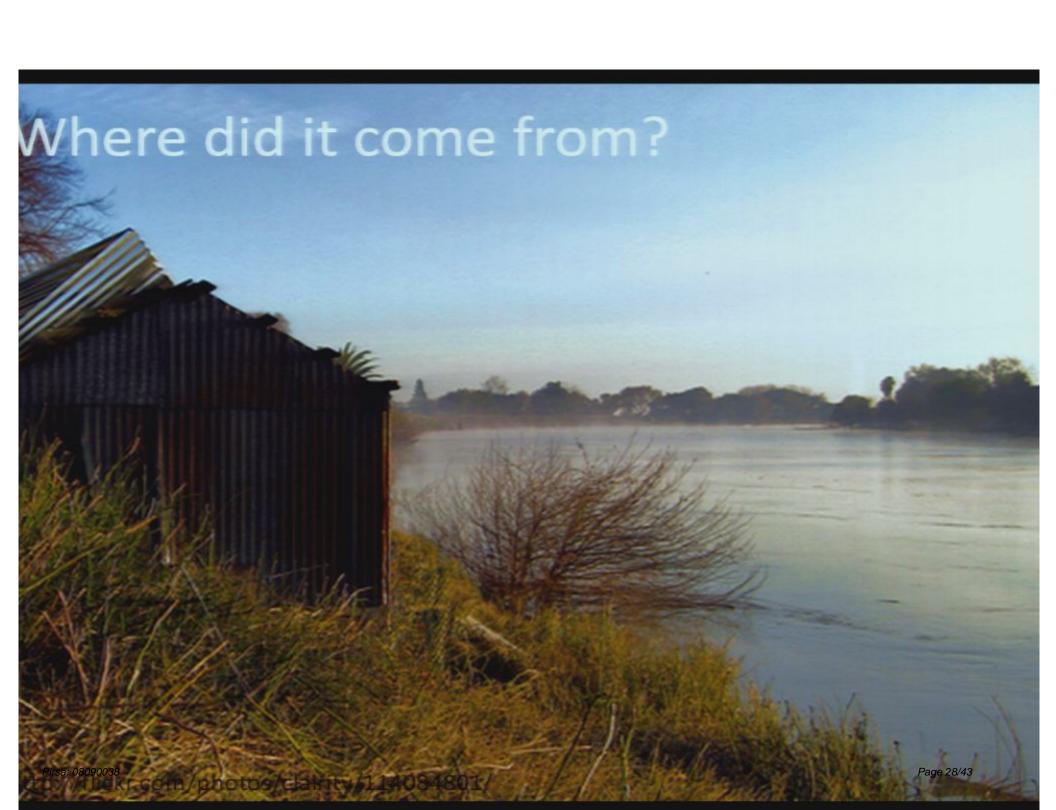
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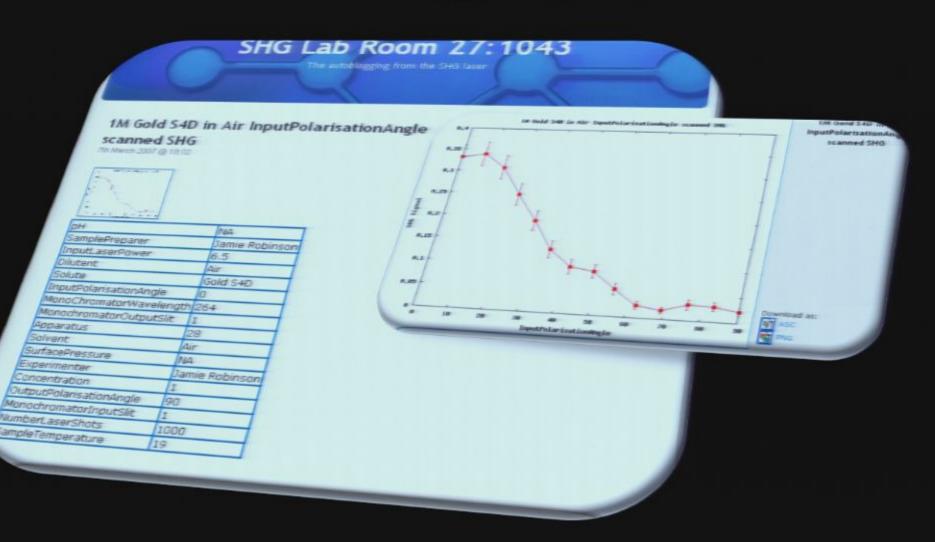
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Automatic Blogging by Machines



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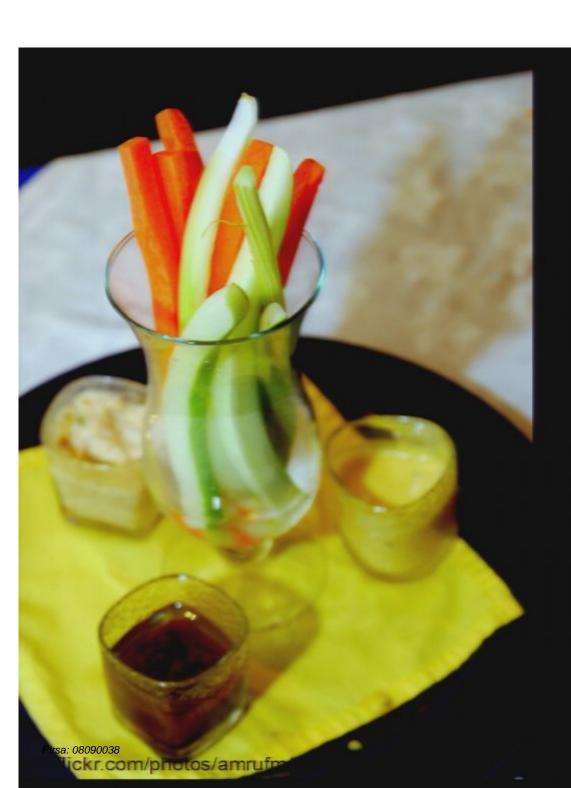
- Fit the existing workflow
- Outperform
- 100% reliable
- One killer feature
- Prepopulate



- 1. Fit the existing workflow
- Compelling first time user experience
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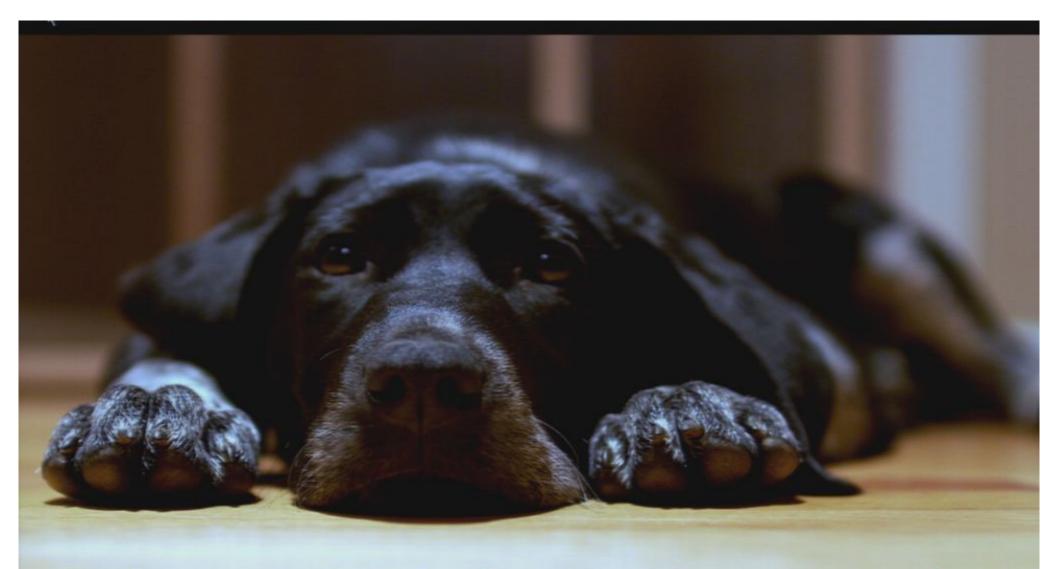
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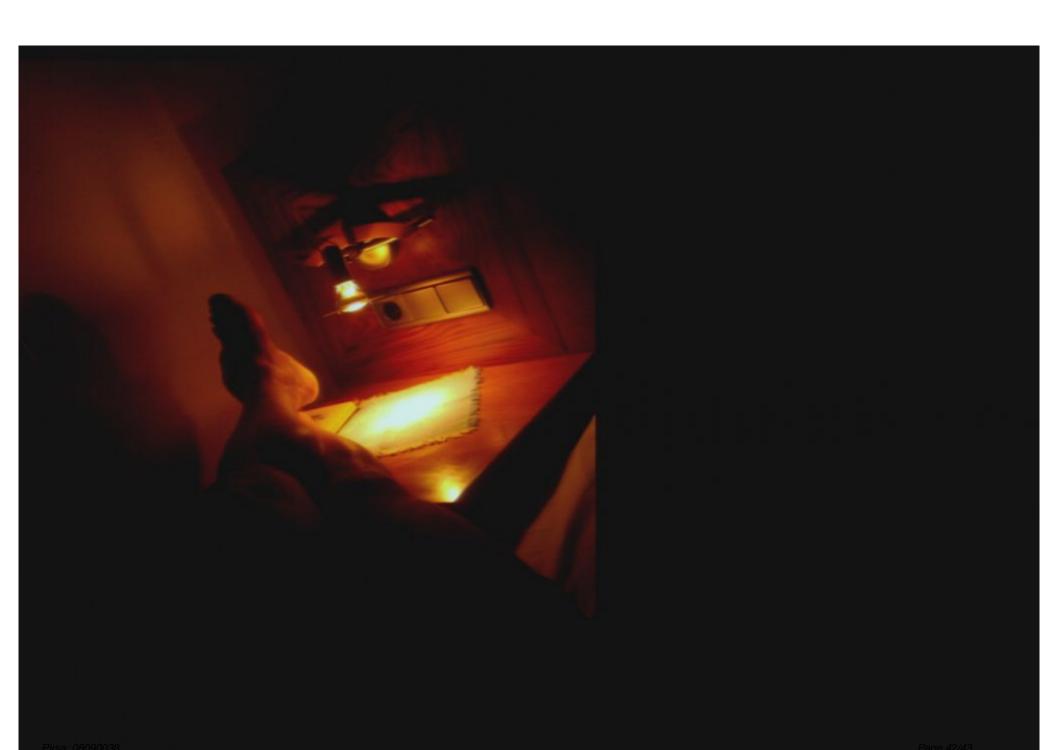
"..open data is free...as in a puppy"
Anna Gold, Cal Poly



Motivation?

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