

Preparing your samples for the synchrotron (and practical advice for the experiment)

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Caveat Emptor

The tips, experiences and opinions presented are those from the user side after many remote data sessions involving many investigators. They do not necessarily represent the views of the user support at the synchrotron, are frequently being revised, and may change with time, more practice and better sleep. They are in addition to and not replacing those tips available on the user guides at SSRL. The tips and experience may be obvious or new, hopefully they will be useful!

If you have any tips to add they would be most welcome.

Do you have a sample?

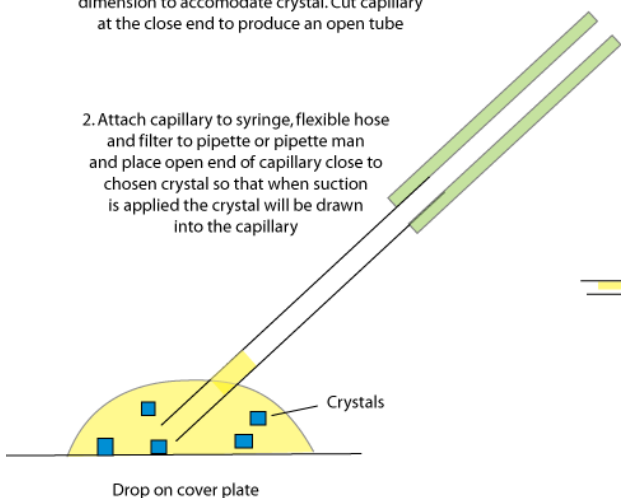
- Is it a crystal?
- Is it a protein crystal?
 - Joe Luft's talk – Chemical and biochemical means
 - Other techniques:
 - Plink test
 - If it plinks it was salt
 - If it doesn't, it was protein
 - X-ray it
 - Find a friendly crystallographer
 - Room temperature first

Can you mount it?

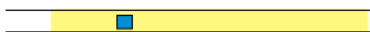
- If you have a friendly crystallographer try capillary mounting and X-ray it.
 - If it's cryocooled and it doesn't diffract you do not know if it's the cryocooling or the crystal. Eliminate one first.

1. Select crystal and capillary of appropriate dimension to accommodate crystal. Cut capillary at the close end to produce an open tube

2. Attach capillary to syringe, flexible hose and filter to pipette or pipette man and place open end of capillary close to chosen crystal so that when suction is applied the crystal will be drawn into the capillary



3. Draw the crystal into the capillary along with the fluid surrounding the crystal. Remove the flexible hose and fix the capillary on a microscope slide with modelling clay so that the crystal can be observed.



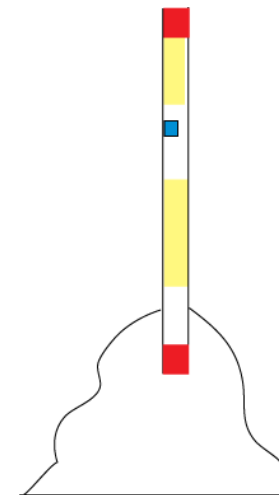
4. Using a smaller capillary or hollow optical fibre draw of the fluid from one side of the crystal leaving a plug of fluid at one end of the capillary.

5. Draw off fluid from the other side of the crystal to leave the crystal adhered to the capillary surface by a thin film of fluid with two plugs of fluid at either end of the capillary. The capillary can then be cut to an appropriate length (see 7).

Note, too much liquid and the crystal will move during data collection, the data will be useless. Too little liquid and the crystal may dry out or drop from the surface of the capillary when it is placed in a vertical position or rotated.



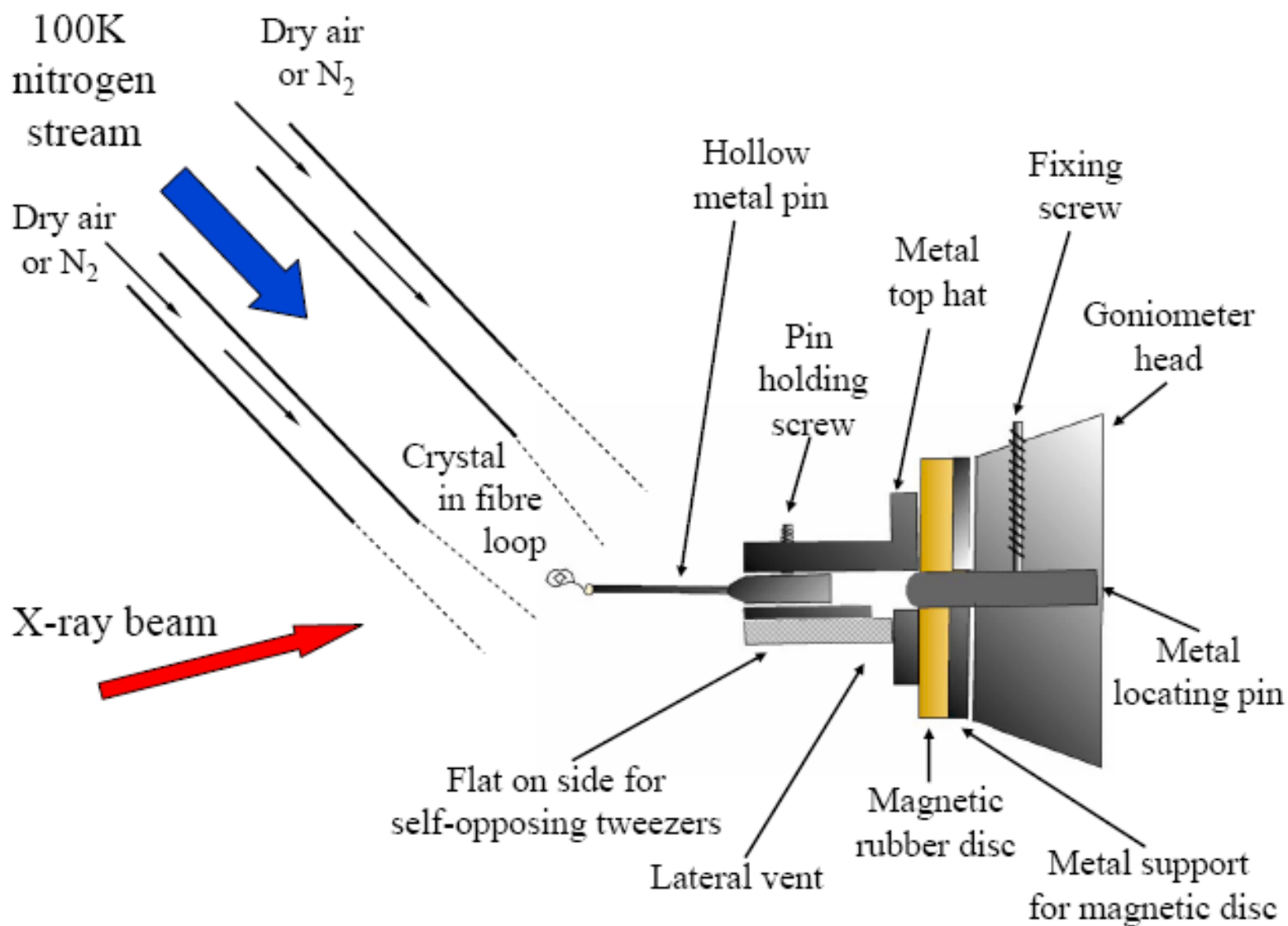
6. The capillary is sealed using wax or epoxy. Care must be taken to ensure that hot wax does not contact the solution or crystal. It is useful to use a thin film of nail varnish to cover the ends of the capillary ensuring it remains vapor tight. Additionally, a useful tip is to place two sharpie marks above and below the crystal position.



7. The mounted crystal is placed in modelling clay which can be attached directly to the goniometer head. Note, it is useful to determine translation range of the goniometer and spacing available for the sample to ensure that the capillary size and position of the crystal is appropriate for data collection.

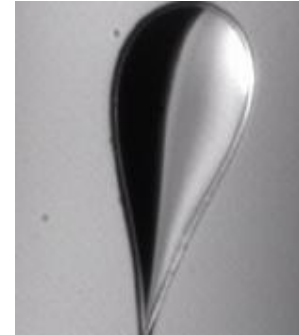
Can you cryocool it?

- Why cool?
 - Reducing radiation damage.
 - Other advantages.
- How the crystal is kept cool, the cryostream.
- How to cryocool.
 - The cryobuffer
 - What cryocooling does
 - Where it can go wrong
 - Methods of cryocooling
 - Getting the crystal
 - Flash cool
 - Optimizing the cryoprotectant
 - Practical methods



Cryocooling – How?

- Cool the crystal fast enough so that amorphous ice rather than crystalline ice is formed (vitrification).
- To vitrify water cooling has to occur in 10^{-8} s.
- Cryoprotectants extend this time to 1-2 s.
- A cryobuffer is the buffer the crystal is grown in with the cryoprotectant added.
- The cryoprotectant replaces water, it does not dilute the solutions.
- Visually clear is usually a good indication of a good cryoprotectant condition.
- Collect data below 130 K, preferably as low as possible but never above 140K.



Good cryobuffer



Bad cryobuffer

Table 2

List of Hampton Screen I and II conditions and the percentage of cryoprotectant necessary for effective cryoprotection determined by X-ray data.

EG = ethylene glycol; PG = propylene glycol (1,2-propanediol). Percentages in parentheses represent unsuccessful trials and are the percentage of cryoprotectant when the observed phenomenon took place. Six conditions listed in the text and indicated in bold in the table were experimentally determined with glycerol and Hampton Screen I. These agreed with the values of German & Mitchell (1996). For the other 44 glycerol conditions and solutions of Hampton Screen I, the values of German & Mitchell (1996) are quoted.

(a) Hampton Screen I

#	Salt	Buffer	Precipitant	Glycerol	PEG 400	EG	PG
1	0.02 M Calcium Chloride	0.1 M Na Acetate pH 4.6	30% w/v MPD	None	None	None	None
2	None	None	0.4 M K/Na Tartrate	35% w/v	30% w/v	30% v/v	25% v/v
3	None	None	0.4 M Ammonium Phosphate	35% w/v	35% w/v	35% v/v	30% v/v
4	None	0.1 M Tris HCl pH 8.5	2.0 M Ammonium Sulfate	25% w/v	15% w/v	25% v/v	20% v/v
5	0.2 M Na Citrate	0.1 M Na HEPES pH 7.5	30% w/v MPD	None	None	None	None
6	0.2 M Magnesium Chloride	0.1 M Tris HCl pH 8.5	30% w/v PEG 4000	20% w/v	10% w/v	10% v/v	5% v/v
7	None	0.1 M Na Cacodylate pH 6.5	1.4 M Na Acetate	30% w/v	20% w/v	20% v/v	15% v/v
8	0.2 M Na Citrate	0.1 M Na Cacodylate pH 6.5	30% w/v Isopropanol	30% w/v	20% w/v	20% v/v	20% v/v
9	0.2 M Ammonium Acetate	0.1 M Na Citrate pH 5.6	30% w/v PEG 4000	15% w/v	5% w/v	10% v/v	5% v/v
10	0.2 M Ammonium Acetate	0.1 M Na Acetate pH 4.6	30% w/v PEG 4000	15% w/v	10% w/v	10% v/v	5% v/v
11	None	0.1 M Na Citrate pH 5.6	1.0 M Ammonium Phosphate	30% w/v	30% w/v	20% v/v	20% v/v
12	0.2 M Magnesium Chloride	0.1 M Na HEPES pH 7.5	30% w/v Isopropanol	10% w/v	25% w/v	20% v/v	10% v/v
13	0.2 M Na Citrate	0.1 M Tris HCl pH 8.5	30% w/v PEG 400	None	None	None	None
14	0.2 M Calcium Chloride	0.1 M Na HEPES pH 7.5	28% w/v PEG 400	5% v/v	5% w/v	10% v/v	5% v/v
15	0.2 M Ammonium Sulfate	0.1 M Na Cacodylate pH 6.5	30% w/v PEG 8000	15% w/v	10% w/v	10% v/v	5% v/v
16	None	0.1 M Na HEPES pH 7.5	1.5 M Lithium Sulfate	25% w/v	15% w/v	20% v/v	10% v/v
17	0.2 M Lithium Sulfate	0.1 M Tris HCl pH 8.5	30% w/v PEG 4000	15% w/v	5% w/v	5% v/v	5% v/v
18	0.2 M Magnesium Acetate	0.1 M Na Cacodylate pH 6.5	20% w/v PEG 8000	20% w/v	15% w/v	20% v/v	10% v/v
19	0.2 M Ammonium Acetate	0.1 M Tris HCl pH 8.5	30% w/v Isopropanol	20% w/v	25% w/v	25% v/v	20% v/v
20	0.2 M Ammonium Sulfate	0.1 M Na Acetate pH 4.6	25% w/v PEG 4000	20% w/v	15% w/v	15% v/v	10% v/v
21	0.2 M Magnesium Acetate	0.1 M Na Cacodylate pH 6.5	30% w/v MPD	None	None	None	None
22	0.2 M Na Acetate	0.1 M Tris HCl pH 8.5	30% w/v PEG 4000	15% w/v	10% w/v	10% v/v	5% v/v
23	0.2 M Magnesium Chloride	0.1 M Na HEPES pH 7.5	30% w/v PEG 400	None	None	None	None
24	0.2 M Calcium Chloride	0.1 M Na Acetate pH 4.6	20% w/v Isopropanol	30% w/v	30% w/v	30% v/v	20% v/v
25	None	0.1 M Imidazole pH 6.5	1.0 M Na Acetate	30% w/v	25% w/v	25% v/v	20% v/v
26	0.2 M Ammonium Acetate	0.1 M Na Citrate pH 5.6	30% w/v MPD	None	None	None	None
27	0.2 M Na Citrate	0.1 M Na HEPES pH 7.5	20% w/v Isopropanol	30% w/v	25% w/v	25% v/v	20% v/v
28	0.2 M Na Acetate	0.1 M Na Cacodylate pH 6.5	30% w/v PEG 8000	15% w/v	5% w/v	10% v/v	5% v/v
29	None	0.1 M Na HEPES pH 7.5	0.8 M Potassium Na Tartrate	35% w/v	30% w/v	30% v/v	30% v/v
30	0.2 M Ammonium Sulfate	None	30% w/v PEG 8000	15% w/v	10% w/v	15% v/v	5% v/v
31	0.2 M Ammonium Sulfate	None	30% w/v PEG 4000	15% w/v	10% w/v	10% v/v	5% v/v
32	None	None	2.0 M Ammonium Sulfate	25% w/v	Emulsion (15%)	25% v/v	20% v/v
33	None	None	4.0 M Na Formate	10% w/v	5% w/v	10% v/v	10% v/v
34	None	0.1 M Na Acetate pH 4.6	2.0 M Na Formate	30% w/v	20% w/v	25% v/v	20% v/v
35	None	0.1 M Na HEPES pH 7.5	0.8 M Mono-Na Phosphate 0.8 M Mono-K Phosphate	25% w/v	Emulsion (30%)	25% v/v	20% v/v
36	None	0.1 M Tris HCl pH 8.5	8% w/v PEG 8000	35% w/v	30% w/v	30% v/v	30% v/v
37	None	0.1 M Na Acetate pH 4.6	8% w/v PEG 4000	30% w/v	30% w/v	35% v/v	20% v/v
38	None	0.1 M Na HEPES pH 7.5	1.4 M Na Citrate	10% w/v	Emulsion (15%)	10% v/v	5% v/v
39	None	0.1 M Na HEPES pH 7.5	2% w/v PEG 400, 2.0 M Ammonium Sulfate	15% w/v	Emulsion (15%)	30% v/v	15% v/v
40	None	0.1 M Na Citrate pH 5.6	20% w/v Isopropanol, 20% w/v PEG 4000	5% v/v	10% w/v	10% v/v	10% v/v
41	None	0.1 M Na HEPES pH 7.5	10% w/v Isopropanol, 20% w/v PEG 4000	15% w/v	15% w/v	20% v/v	15% v/v
42	0.05 Mono-K Phosphate	None	20% w/v PEG 8000	20% w/v	20% w/v	25% v/v	20% v/v
43	None	None	30% w/v PEG 1500	20% w/v	10% w/v	15% v/v	10% v/v
44	None	None	0.2 M Magnesium Formate	50% w/v	35% w/v	30% v/v	30% v/v
45	0.2 M Zinc Acetate	0.1 M Na Cacodylate pH 6.5	18% w/v PEG 8000	20% w/v	15% w/v	20% v/v	10% v/v
46	0.2 M Calcium Acetate	0.1 M Na Cacodylate pH 6.5	18% w/v PEG 8000	20% w/v	25% w/v	20% v/v	20% v/v
47	None	0.1 M Na Acetate pH 4.6	2.0 M Ammonium Sulfate	20% w/v	Emulsion (25%)	25% v/v	20% v/v
48	None	0.1 M Tris HCl pH 8.5	2.0 M Ammonium Phosphate	20% w/v	Crystals (35%)	25% v/v	20% v/v
49	1.0 M Lithium Sulfate	None	2% w/v PEG 8000	20% w/v	20% w/v	25% v/v	15% v/v
50	0.5 M Lithium Sulfate	None	15% w/v PEG 8000	20% w/v	15% w/v	25% v/v	10% v/v

Cryobuffers

The amount of cryoprotectant (glycerol, PEG 400, ethylene glycol, 1,2-propanediol) to add to all the Hampton I and II screens to make them into cryobuffers has been determined.

See McFerrin and Snell, J. Appl Cryst. 35, 538-545 (2002).

(b) Hampton Screen II

#	Salt	Buffer	Precipitant	Glycerol	PEG 400	EG	PG
1	2.0 M Sodium Chloride	None	10% w/v PEG 6000	20% v/v	20% v/v	20% v/v	15% v/v
2	0.01 M CTAB	None	0.5 M Sodium Chloride, 0.01 M Magnesium Chloride	40% v/v	35% v/v	35% v/v	25% v/v
3	None	None	25% v/v Ethylene Glycol	15% v/v	10% v/v	10% v/v	5% v/v
4	None	None	35% v/v Dioxane	25% v/v	25% v/v	20% v/v	15% v/v

Table 2 (continued)

#	Salt	Buffer	Precipitant	Glycerol	PEG 400	EG	PG
5	2.0 M Ammonium Sulfate	None	5% v/v Isopropanol	25% v/v	Emulsion (25%)	25% v/v	20% v/v
6	None	None	1.0 M Imidazole pH 7.0	35% v/v	30% v/v	35% v/v	25% v/v
7	None	None	10% w/v PEG 1000, 10% w/v PEG 8000	20% v/v	20% v/v	20% v/v	15% v/v
8	1.5 M Sodium Chloride	None	10% v/v Ethanol	30% v/v	25% v/v	25% v/v	20% v/v
9	None	0.1 M Na Acetate pH 4.6	2.0 M Sodium Chloride	25% v/v	20% v/v	25% v/v	20% v/v
10	0.2 M Sodium Chloride	0.1 M Na Acetate pH 4.6	30% v/v MPD	None	None	None	None
11	0.01 M Cobalt Chloride	0.1 M Na Acetate pH 4.6	1.0 M 1,6 Hexanediol	20% v/v	25% v/v	25% v/v	20% v/v
12	0.1 M Cadmium Chloride	0.1 M Na Acetate pH 4.6	30% w/v PEG 400	5% v/v	5% v/v	10% v/v	5% v/v
13	0.2 M Ammonium Sulfate	0.1 M Na Acetate pH 4.6	30% w/v PEG MME 2000	10% v/v	10% v/v	10% v/v	10% v/v
14	0.2 M K/Na Tartrate	0.1 M Na Citrate pH 5.6	2.0 M Ammonium Sulfate	25% v/v	Emulsion (10%)	25% v/v	15% v/v
15	0.5 M Ammonium Sulfate	0.1 M Na Citrate pH 5.6	1.0 M Lithium Sulfate	25% v/v	Emulsion (25%)	25% v/v	20% v/v
16	0.5 M Sodium Chloride	0.1 M Na Citrate pH 5.6	2% w/v Ethylene Imine Polymer	40% v/v	Emulsion (20%)	35% v/v	25% v/v
17	None	0.1 M MES pH 6.5	35% v/v <i>tert</i> -Butanol	20% v/v	25% v/v	15% v/v	15% v/v
18	0.01 M Ferric Chloride	0.1 M Na Citrate pH 5.6	10% v/v Jeffamine M-600	30% v/v	25% v/v	35% v/v	20% v/v
19	None	0.1 M Na Citrate pH 5.6	1.0 M 1,6 Hexanediol	5% v/v	5% v/v	5% v/v	10% v/v
20	None	0.1 M MES pH 6.5	1.6 M Magnesium Sulfate	20% v/v	15% v/v	20% v/v	10% v/v
21	0.2 M Na/K Phosphate	0.1 M MES pH 6.5	2.0 M Sodium Chloride	25% v/v	25% v/v	25% v/v	20% v/v
22	None	0.1 M MES pH 6.5	12% w/v PEG 20,000	35% v/v	25% v/v	30% v/v	25% v/v
23	1.6 M Ammonium Sulfate	0.1 M MES pH 6.5	10% v/v Dioxane	25% v/v	Emulsion (15%)	20% v/v	15% v/v
24	0.05 M Calcium Chloride	0.1 M MES pH 6.5	30% v/v Jeffamine M-600	None	None	None	None
25	0.01 M Cobaltous Chloride	0.1 M MES pH 6.5	1.8 M Ammonium Sulfate	25% v/v	Emulsion (20%)	25% v/v	20% v/v
26	0.2 M Ammonium Sulfate	0.1 M MES pH 6.5	30% w/v PEG MME 5000	10% v/v	10% v/v	10% v/v	10% v/v
27	0.01 M Zinc Sulfate	0.1 M MES pH 6.5	25% w/v PEG MME 500	10% v/v	10% v/v	10% v/v	10% v/v
28	None	None	1.6 M Sodium Citrate pH 6.5	None	None	None	None
29	0.5 M Ammonium Sulfate	0.1 M HEPES pH 7.5	30% v/v MPD	None	None	None	None
30	None	0.1 M HEPES pH 7.5	10% w/v PEG 6000, 5% w/v MPD	20% v/v	25% v/v	25% v/v	15% v/v
31	None	0.1 M HEPES pH 7.5	20% v/v Jeffamine M-600	15% v/v	10% v/v	15% v/v	10% v/v
32	0.1 M Sodium Chloride	0.1 M HEPES pH 7.5	1.6 M Ammonium Sulfate	25% v/v	Emulsion (25%)	25% v/v	20% v/v
33	None	0.1 M HEPES pH 7.5	2.0 M Ammonium Formate	30% v/v	30% v/v	30% v/v	25% v/v
34	0.05 M Cadmium Sulfate	0.1 M HEPES pH 7.5	1.0 M Na Acetate	25% v/v	25% v/v	30% v/v	20% v/v
35	None	0.1 M HEPES pH 7.5	70% v/v MPD	None	None	None	None
36	None	0.1 M HEPES pH 7.5	4.3 M Sodium Chloride	15% v/v	10% v/v	10% v/v	10% v/v
37	None	0.1 M HEPES pH 7.5	10% w/v PEG 8000, 8% v/v Ethylene Glycol	25% v/v	20% v/v	25% v/v	15% v/v
38	None	0.1 M HEPES pH 7.5	20% w/v PEG 10000	25% v/v	25% v/v	20% v/v	15% v/v
39	0.2 M Magnesium Chloride	0.1 M TRIS pH 8.5	3.4 M 1,6 Hexanediol	None	None	None	None
40	None	0.1 M TRIS pH 8.5	25% v/v <i>tert</i> -Butanol	25% v/v	25% v/v	30% v/v	20% v/v
41	0.01 M Nickel (II) Chloride	0.1 M TRIS pH 8.5	1.0 M Lithium Sulfate	25% v/v	20% v/v	25% v/v	15% v/v
42	1.5 M Ammonium Sulfate	0.1 M TRIS pH 8.5	12% v/v Glycerol	15% v/v	15% v/v	20% v/v	10% v/v
43	0.2 M Ammonium Phosphate	0.1 M TRIS pH 8.5	50% v/v MPD	None	None	None	None
44	None	0.1 M TRIS pH 8.5	20% v/v Ethanol	25% v/v	30% v/v	35% v/v	20% v/v
45	0.01 M Nickel (II) Chloride	0.1 M TRIS pH 8.5	20% w/v PEG MME 2000	20% v/v	20% v/v	20% v/v	15% v/v
46	0.1 M Sodium Chloride	0.1 M Bicine pH 9.0	20% w/v PEG MME 500	15% v/v	15% v/v	15% v/v	15% v/v
47	None	0.1 M Bicine pH 9.0	2.0 M Magnesium Chloride	5% v/v	5% v/v	5% v/v	5% v/v
48	2% v/v Dioxane	0.1 M Bicine pH 9.0	10% w/v PEG 20000	30% v/v	30% v/v	30% v/v	20% v/v

Cryobuffers contd.

Similarly the amount of cryoprotectant to add to the 1536 robot screen conditions has been determined but not yet published.

This information will be published shortly but is readily available from the high-throughput lab.

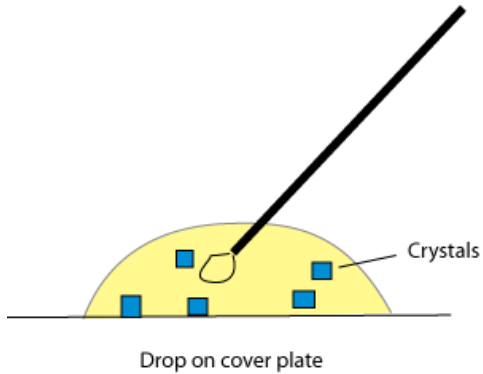
Cryo-buffers (make your own)

- Look for similar crystallization conditions in other publications.
- PEG < 4K – increase PEG, add small PEGs
- PEG > 4K – add small PEGs
- 30% of cases – add 15-25% glycerol
- MPD – increase MPD concentration
- Salt – add MPD and/or ethylene glycol or glycerol
- Salt – increase concentration/add salt
- Salt – exchange salts
- Note low salt concentrations need greater concentration of cryoprotectant than higher salt concentrations.
- Other cryoprotectants, DMSO, propanediol etc.
- Butanediol is very effective but expensive.
- (with thanks to Elspeth Garman for many tips).

Methods of cryoprotecting

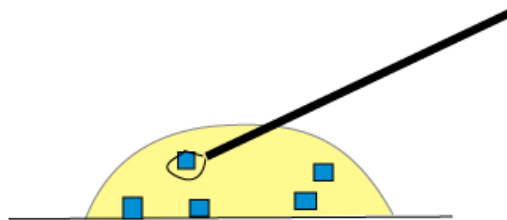
1. Grow in cryoprotectant conditions – usually results in the best diffracting crystals (choose a crystallization hit that is a cryoprotectant or can be cryoprotected with minimal addition of cryoprotectant). Always do this if you can.
2. Dialysis against a cryoprotectant solution. Tends to be slow and tedious, not recommended.
3. Rapid transfer into a cryoprotectant;
 - Straight into a final concentration.
 - Sweep through quickly then cryocool.
 - Sequential soaks in increasing concentrations. Different combinations of cryoprotectants can be used, e.g. glycerol and finally PEG 400 as in the case of insulin studies.
4. High pressure cooling.

Getting the crystal

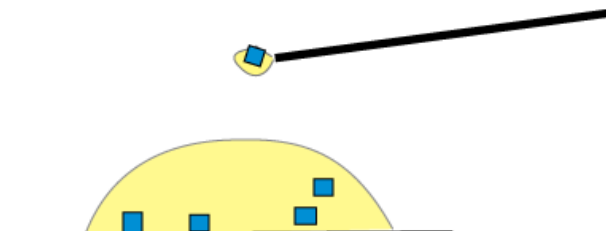


Ideally minimize the amount of liquid around the crystal while maintaining the crystal covered by the liquid

The loop size should be slightly larger than the crystal and used perpendicular to the liquid.



The loop should be brought up from below the crystal to capture the crystal.



The loop containing the crystal is rapidly raised and as quickly as possible transferred to the cold stream or plunged into liquid nitrogen/propane.

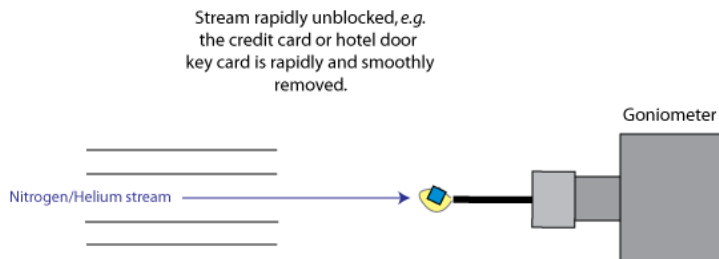
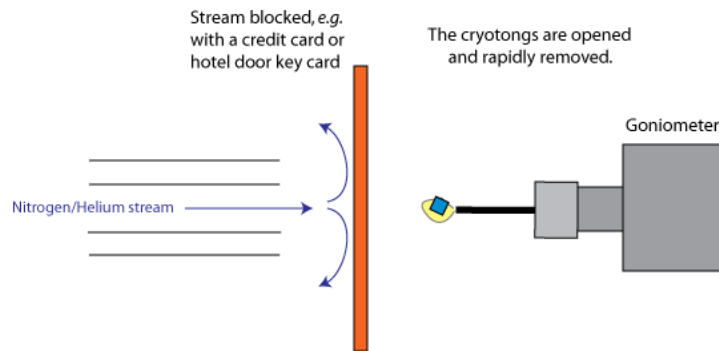
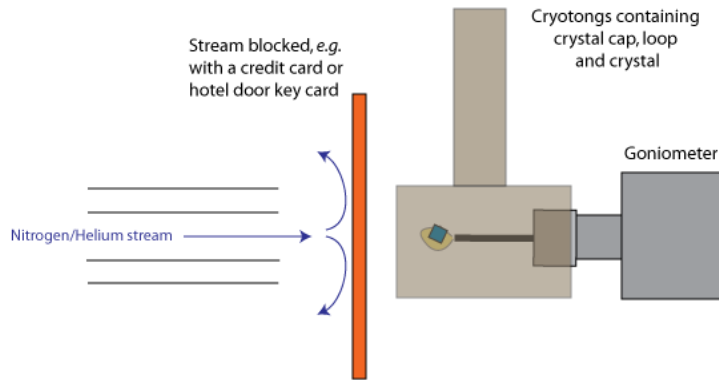
If more than one crystal is available more than one should be mounted and saved.

Flash cool as fast as possible

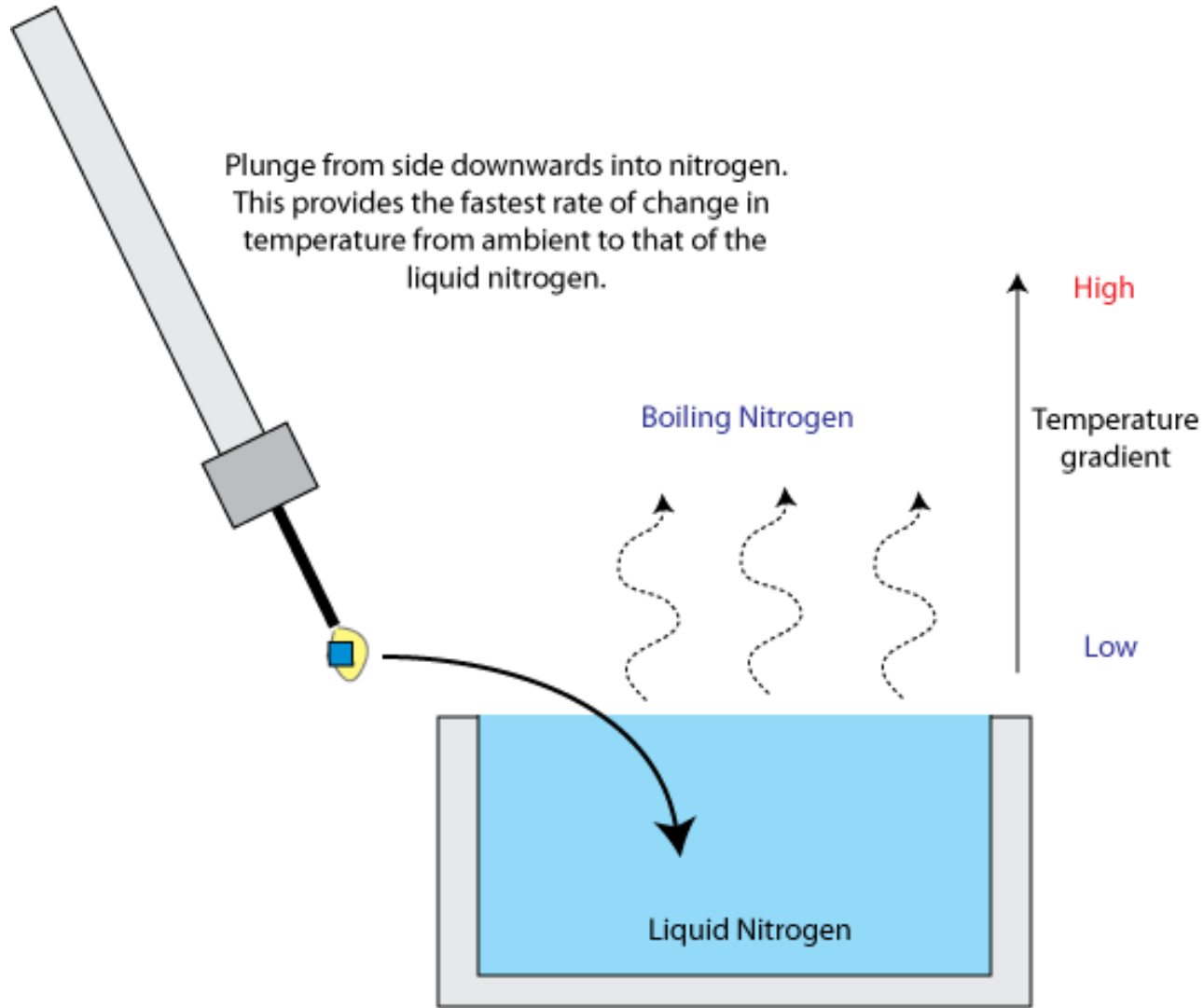
- Get the crystal into appropriate cryobuffer conditions if it is not already.
- Transfer the crystal directly into liquid nitrogen or into the cryostream remembering to block the stream first and release the block when the crystal is in place.
- This step has to be fast, both the transfer and the cooling moment. During transfer the small amount of liquid surrounding the crystal can evaporate.
- Why cover the cryostream?
 - This avoids the crystal being dehydrated by the nitrogen/air on the outside of the stream.
 - The crystal may be slow cooled as it passes into the stream forming ice
 - Whipping the cover away from the cryostream cools it fast.
- Use a standard pin length, preset to be close to the beam center and in the cryostream.

Note: Every step must be as rapid and smooth as possible to prevent turbulence

Flash cooling in the gas stream



Flash cooling by plunging



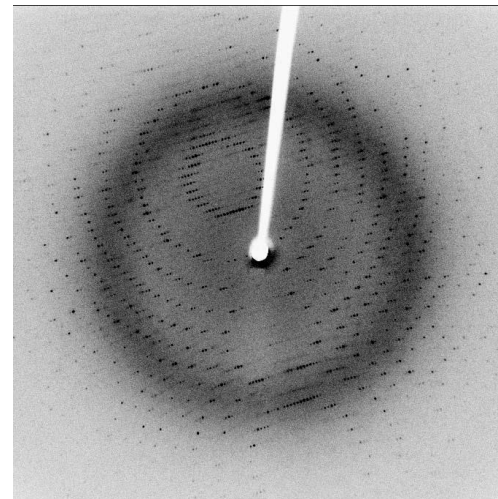
Does it diffract?

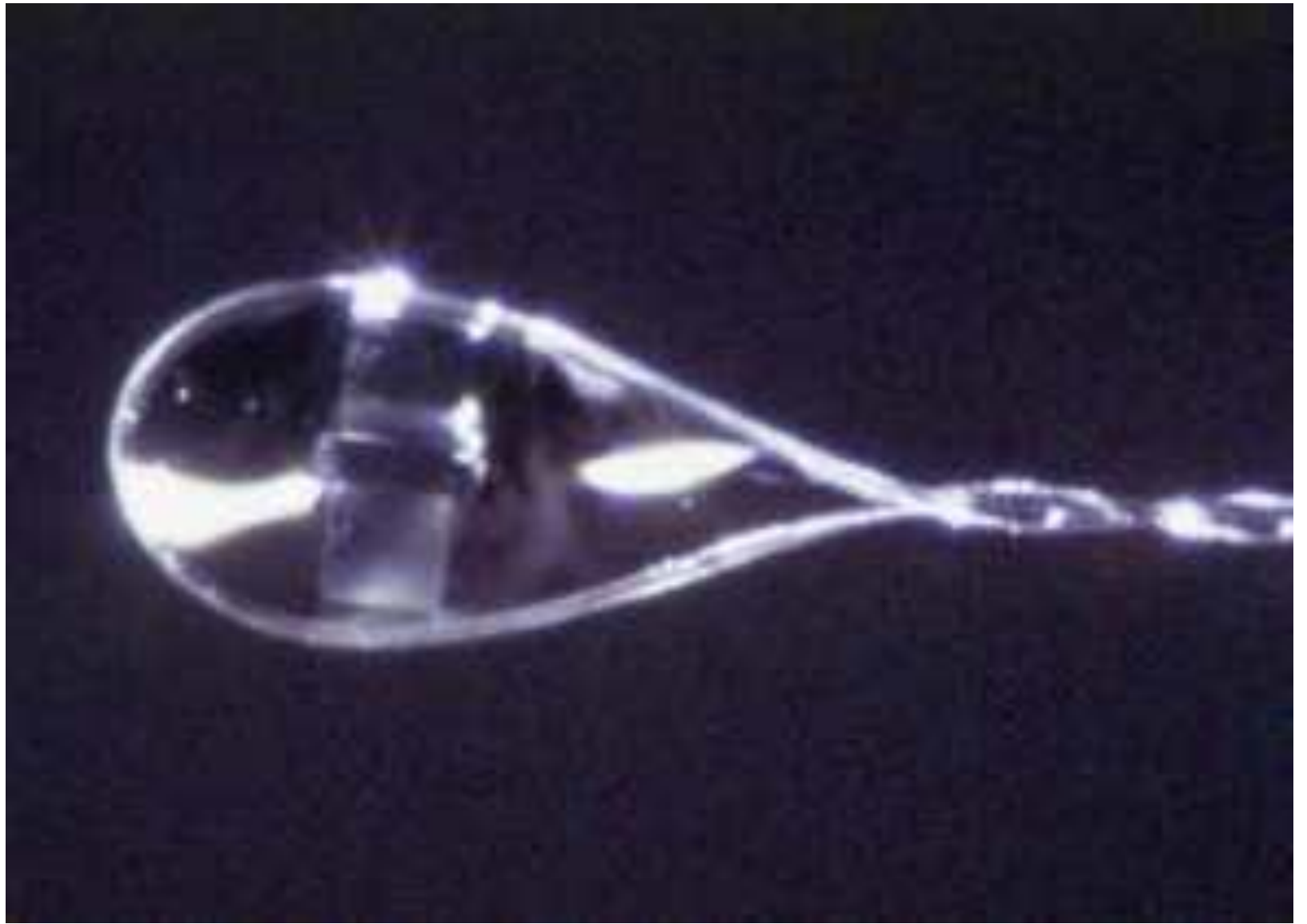
You cannot tell how well a crystal will diffract X-rays by looking at it.

There are many ugly ducklings.

The only way to tell is to put your crystal in front of an X-ray beam ... find the friendly crystallographer.

Or, screen crystals on the SSRL robot – not the ideal use of beamtime but very rapid, ~3-4 mins per sample.





Why do you want beamtime?

To get the initial data so that you can get funding to complete the study.

To solve the structure – use of multiple wavelengths or single defined wavelength to exploit anomalous scattering effects.

To extend the structural detail from beyond that currently available so that an mechanism/question/hypothesis etc. can be resolved.

All of the above.

Not to screen crystals – you will not get beamtime through standard proposal means to do this (my opinion that may be wrong)

Getting your beamtime

Note: First time users are currently requested to collect data at the beamline once or to attend a **training workshop** at the SSRL before they perform the experiment remotely.

Ways to get your beamtime

1. **Submitting a proposal.** Proposals can be submitted for single experiments, for a program (i.e. different research problems or projects scientifically linked or related to each other) or for rapid access ("hot" new projects).
2. Setting up **Participating Research Team** (PRT access)
3. **Scientific collaborations with SSRL staff**

A successful proposal

- A successful proposal has three components:
 1. Important structural target/s, and/or a novel and useful experiment
 2. Sound justification of the need for synchrotron time
 3. Experience and previous results (can you carry out the experiment)
- Many times the first and third component are well described but the second is weak as users may not have had too much synchrotron experience or do not take the time to think about that aspect.
- Make your proposal strong by balancing all three components.
- Contact the support staff beforehand for advice if you have any questions to ask. Most, with rare exceptions, do not bite.
- Make a reasonable estimate of time and a determination the appropriate beamlines that could be used. How much time does it take to screen, how much time does it take to collect data, how many samples do you have then ask for one shift extra?
- Look at other successful proposals if you can.

Justifications for Synchrotron Time

Examples include:

- A spectrum of energy (wavelength) unavailable in the laboratory. Required for anomalous diffraction experiments.
- An increased intensity to push the resolution limit further. What resolution do you have, why do you need to extend it further? What question cannot be answered at the current resolution?
- The ability to resolve longer unit cells. What can the system at home resolve, what can you expect to resolve at the synchrotron? Look into the beamline instrumentation, do a quick calculation.
- In the robotic case, study many samples much faster than at home. What percentage of crystals provide good diffraction, how many do you need to screen efficiently? What time would that take at home.
- Does the experiment requires many measurements in a rapid as possible time?
- Why remote time? Standard experiments, limited travel budget, save the funding agency money, enable you to do more?

Now you have your beamtime think about:

- Preparation – Things to do beforehand
- Filling – Putting samples in the cassette
- Shipping – Options and tips
- Screening – Quick look data collection
- Planning – Going from screening results to data collection
- Data collection – Tips and tricks
- Data backup – Getting it home
- Finishing – Acknowledgements, lessons and feedback

- Proper Preparation and Planning Prevents Poor Performance (PPPPPP)
 - Ice is the enemy
 - Liquid nitrogen boils off
- Keep it simple stupid (KISS)

Preparation

Robotic beamtime is no substitute for the real thing. To use robotic beamtime to its fullest potential you should try and ensure that at least one member of the team is competent in data collection at the synchrotron and understands the differences from home source collection. Personal contact with the beamline staff is also very useful for transferring the latest ideas, advice etc. In the case of Stanford this has the added benefit of having very nice restaurants....

Know your timeline

- Know which samples you plan to send (possibly pre-cool and store in cryovials to mount later).
- Inventory pins, loops, mounting equipment and do a dry run sufficiently ahead of the beamtime so that you can procure any missing items if necessary (two weeks).
- Check that you have liquid nitrogen available, a shipping dewar and a means to ship it (one week).
- Make up a log of samples as they are loaded, add this to the spreadsheet (several days).
- Keep the spreadsheet handy to upload immediately before data collection.

General Preparation

- Know where to find, read and understand the user guides.
 - These contain very useful practical tips and are updated regularly from comments received by users.
- Get details on the software available on the beamline and make sure you know how to use it. Print out the manuals and have them to hand.
- Make sure your remote access software works in advance and that you have an alternate plan if you should have network problems
 - Try and find a 24 hour Starbucks and kill internet access and caffeine needs at the same time 😊 Most users at HWI now collect data from home. DSL or cable internet access are more than sufficient.
- Know how to develop a good data collection strategy, how to integrate and scale the data. Be prepared to do this rapidly during screening and data collection.
- Know your crystal, screen it or others in the laboratory beforehand. If possible know the space groups and expected unit cells.
- Think about the sequence of experiments assuming that the experiment could end unexpectedly at any time (one advantage of robotic beamtime is that your sample can usually be saved for later if necessary).

User's Guide to Macromolecular Crystallography Experiments at SSRL - Microsoft Internet Explorer

Address http://smb.slac.stanford.edu/public/users_guide/manual/

Macromolecular Crystallography at SSRL powered by Google

Home | Site Map | Facilities | **User Guide** | Schedule | Forms | Research | News | Staff | Links

Next: [When you arrive at the beamline](#)

User's Guide to Macromolecular Crystallography Experiments at SSRL

- [When you arrive at the beamline](#)
- [Safety at the beamline](#)
 - [Safety procedures](#)
 - [Safety in the experimental hutch](#)
- [Mounting samples manually](#)
 - [Making room to safely mount samples](#)
 - [Mounting samples in the cryostream](#)
 - [Mounting crystals in capillaries](#)
 - [Sample illumination](#)
- [Using the SSRL Automated Mounting \(SAM\) system](#)
 - [Using the SSRL Sample Cassette Kit](#)
 - [Storing sample information: The Excel spreadsheet](#)
 - [Uploading an Excel spreadsheet](#)
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 - [Remote experiment support](#)
- [Problems? Before calling staff, please read the FAQs](#)
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 - [Sample mounting](#)
 - [Detectors](#)
 - [Problems during data collection](#)
 - [Data processing and graphics software](#)
 - [Remote access](#)
- [Before leaving...](#)
- [Referencing SSRL](#)
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- [Further reading](#)
 - [General](#)
 - [Automation](#)
 - [Detectors](#)
 - [Derivatives](#)
 - [Data collection](#)
 - [MAD/SAD](#)
 - [Crystallographic software \(phasing and refinement\)](#)
 - [Radiation damage](#)
 - [Crystal dehydration](#)
 - [Cryocrystallography](#)
 - [Crystal annealing](#)

http://smb.slac.stanford.edu/facilities/remote_access/webice/webice.pdf - Microsoft Internet Explorer

Address http://smb.slac.stanford.edu/facilities/remote_access/webice/webice.pdf

75%

Need to create PDF documents?

Web-Ice

July 25, 2006

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1

8.5 x 11 in

1 of 31

Done Internet

Preparation for Filling

Preparing pins

- Prepare a selection of pins and loops to suit crystal size.
- Prepare several at once.
- Select an appropriate loop to put in the pin.
- Glue the loop in the pin, 5 minute epoxy on the bottom of the loop holder to be inserted into the pin works well. Avoid getting epoxy on the outside of the copper mount.
- Check the loop under a calibrated microscope, make sure it is intact then write the size on the magnetic base.



Preparing for filling

- Make sure you have an excess of different size loops in standard height pins. Loops and pins can be cleaned and reused.
- Have loops and pins organized by size ready for mounting (see the 96 well organizers).
- Make sure the loop size can be read.
- If feasible, switch your entire laboratory over to SSRL compatible height pins. This will save problems later. Loops that are too short confuse the automatic centering and stop the process.
- Make sure the loops and pins are clean and the loop is solidly held in the pin (test and verify). A pair of pliers is a useful tool to have around.



Pouring dewar

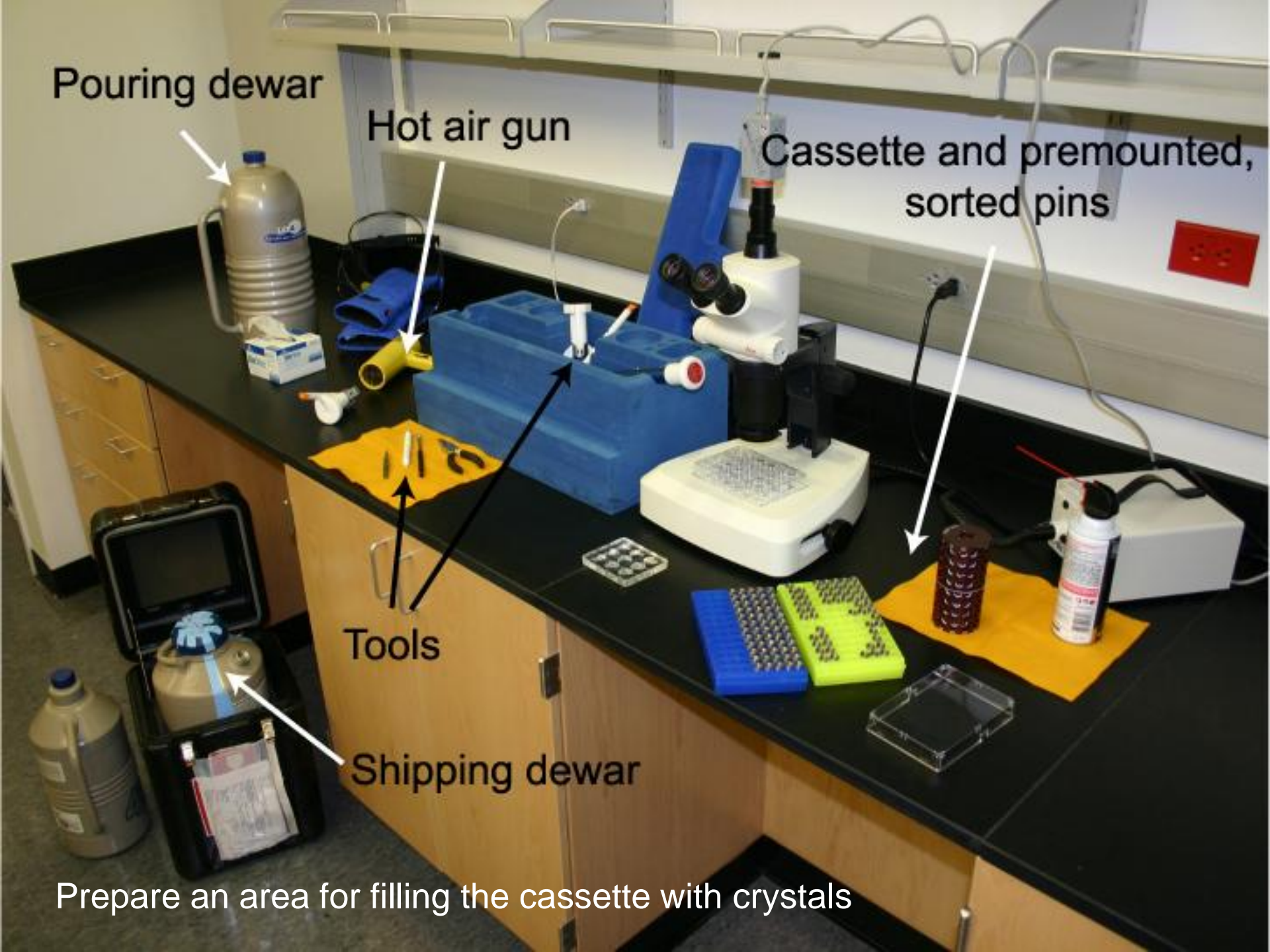
Hot air gun

Cassette and premounted, sorted pins

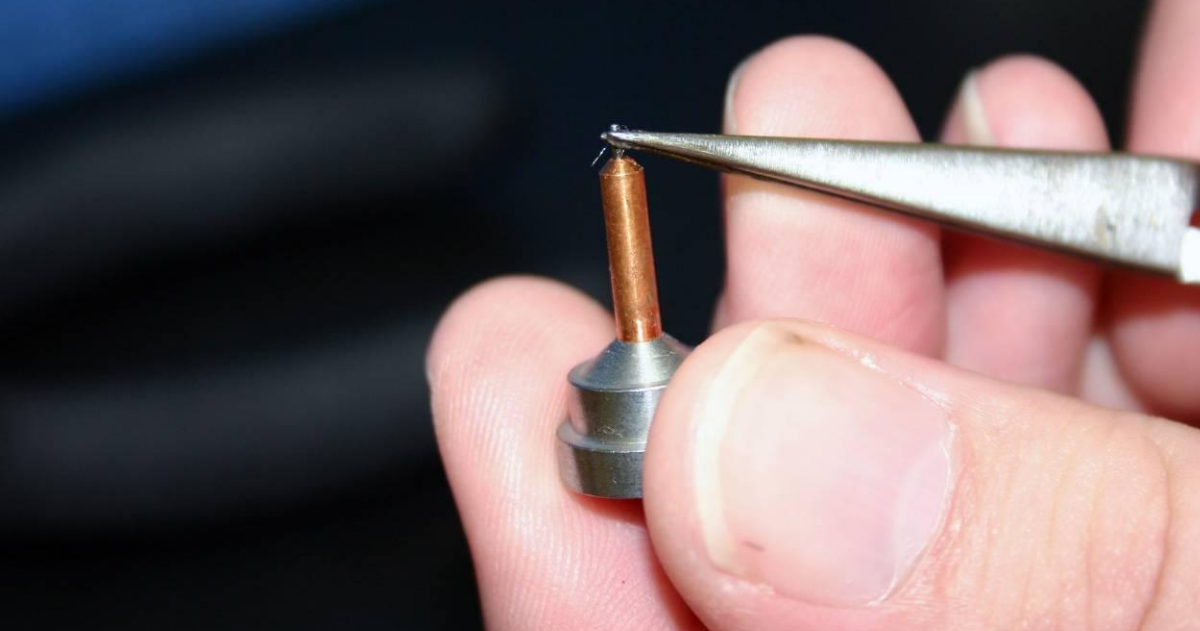
Tools

Shipping dewar

Prepare an area for filling the cassette with crystals



Testing Loops

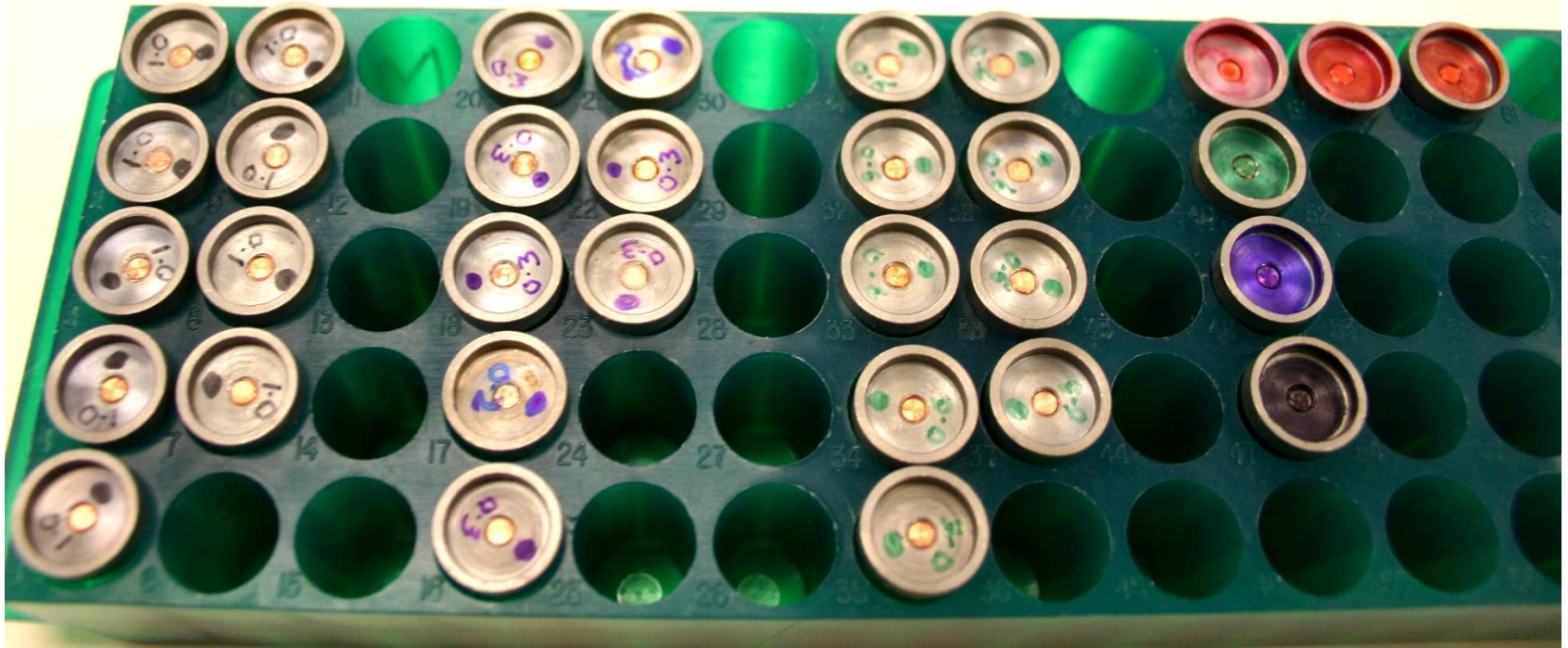


- Use forceps to test that the loop posts are firmly seated in the magnetic base
- If not, extract the loop with a pair of pliers and if the post is clean either re-glue the original loop or put a new one in its place.
- Test all loops before each data collection if reusing them (see last section).



Color code or identify loop sizes

- Better to use size indicator with color spot – less to remember
- Keep the loops organized for easy selection.



Preparing for filling

- Make sure liquid nitrogen is available for the filling.
- Use a phase separator on the liquid nitrogen delivery tube. These are available for approximately US \$50 and reduce the amount of gas released when transferring liquid nitrogen. They are good for both safety and economy reasons as the amount of nitrogen used seems lower with these.
- With practice and the use of a phase separator, a single 100 liter liquid nitrogen Dewar is sufficient for the filling of two shipping Dewars and four cassettes with nitrogen left over (commercially the cost of nitrogen for this is about US \$100).
- Have safe handling equipment available; gloves, face shield and safety glasses as appropriate to your institutions liquid nitrogen handling policy. .
- Have two or more pouring Dewars ready and a suitable funnel to help fill them.
- Have a cassette (cryocane) Dewar ready. This is useful for washing the cassettes and brief storage when emptying the shipping Dewar of liquid nitrogen.



A phase separator is a useful piece of equipment to fit on the end of a transfer hose. It cuts down significantly on the gas rather than liquid that is transferred, only costs about \$50 and seems to make our large Dewar last longer between refills.

Liquid should flow fairly rapidly. If not ice has formed inside the separator and it needs to be warmed and dried.



Preparing for filling (continued)

- If the shipping Dewars show evidence of ice allow them to warm and dry before use. Sometimes ice can build up if the Dewars are left dry but cold for a prolonged period.
- Before filling make sure the shipping Dewars have been fully charged and have not lost vacuum. Follow the manufacturers instructions for filling.
- Keep them filled with liquid until ready for shipping.
- Make sure the handle on the Dewar insert is firmly attached and the Dewar insert can be easily removed and replaced in the Dewar. The handle can come loose, this is not a disaster but it is useful to know before 'discovering it' during filling.
- Keep a spare microscope bulb and know where to find it.
- Keep a check list and follow it and amend it as necessary.
- Have a small sieve for removing ice from the liquid nitrogen in the blue reservoir.

Preparing for filling

- Have control crystals available, e.g. cryoprotected lysozyme, for each cassette. These can be used to tell if something untoward happened to the Dewar during shipping, e.g. if it were opened or tipped and warmed a little.
- A dry Dewar will keep below 100K for over two weeks if unopened (but don't let it).
- If available fill in a fume hood to create an updraft of boiling nitrogen and reduce ice formation.
- Have a log book ready to note down crystal details and position.
- Decide on the order of filling and cassettes to use.
- If shipping an odd number of cassettes remember that the styrofoam insert is not trash! If you lose this ship an empty cassette on top of the full one.
- Practice dry and if possible under liquid nitrogen.
- Have the microscope next to the filling reservoir.
- Make sure the cassette or cassettes are empty and clean. Sometimes the loop holder can come out of the pin and is still lodged in the cassette. Filling this position will cause severe problems.

Filling the cassette

(The first point where things can go wrong)



The number one
practical tip:

Ice is the Enemy

**Filling should be done
as rapidly as possible.**

Filling – Ice is the Enemy, Liquid Nitrogen Boils off

- Note the cassette number and order to be used.
- Make sure the shipping Dewar is still full of liquid nitrogen, top it off, keep it closed as much as possible.
- At all times assume the cassette could fall during transfer. Use cryogloves beneath it, not to hold it, but to catch it just in case.
- Each cassette contains 96 experiments. If several people are filling the result could only be as good as the worst skilled
- **Make sure the nitrogen level is maintained.**
- The blue lid covers the filling reservoir, it does not prevent boil off of the liquid nitrogen. If loading in a fume hood it is better not to use it.
- If floating ice appears put the cassette in the full shipping Dewar, empty and dry the reservoir and then replace the nitrogen.
- If in doubt, use fresh nitrogen.
- If frost appears on the cassette wash it by pouring liquid nitrogen over it.
- **Do not leave for a prolonged period, nitrogen boils off fast.**

Filling (continued)

- Keep the pouring Dewar filled.
- Use good illumination.
- Make notes during the filling and transfer them to the spreadsheet as soon as possible. Even better, enter them as filling.
- Cover the strong magnet on the wand with tape to remind you not to use it.
- Use two tool sets if you have them. Dry one set as you use the other set. Swap over every 4 crystals or sooner if needed.
 - Ice on the end of the tool can cause the pin to stick to the tool.
 - Ice in the guide tool can cause the crystal to hit the cassette edge.
- If the pin will not dismount push it back in then angle both the wand and guide tool. The pin should remain in the cassette (see next slide).





The magnet head can stick to the wand due to ice between the two. To overcome this push the magnet in with the wand following the guide tool, then tip both the wand and guide tool together. The magnet will remain in the cassette. New tools with a push release can also develop the same problem (with a similar solution).

Filling (continued)

- Mount several samples of each crystal.
- If possible use a little bit more cryoprotectant than needed.
- Empty the shipping Dewar at the last moment before have it picked up or take it to FedEx.
- Make sure all the liquid is emptied (follow the manufacturers instructions, e.g. invert, stand upright for some time, invert again etc.) A little liquid left can cause an amazing paperwork mountain if discovered. Future shipments would be jeopardized not to mention possible civil and criminal penalties – in the US they'll send you to Cuba.
- Wash the cassettes in liquid nitrogen if necessary to remove ice and then put them in the shipping Dewar.
- Tape the Dewar lid and write “Contains sample” on the tape (advice from the FedEx guy). Anyone who opens the lid will immediately assume you are shipping prize racehorse or bull products and leave it alone.

Shipping the cassette

(Another major point where things can go wrong)

Shipping – Contact the shipping company first!

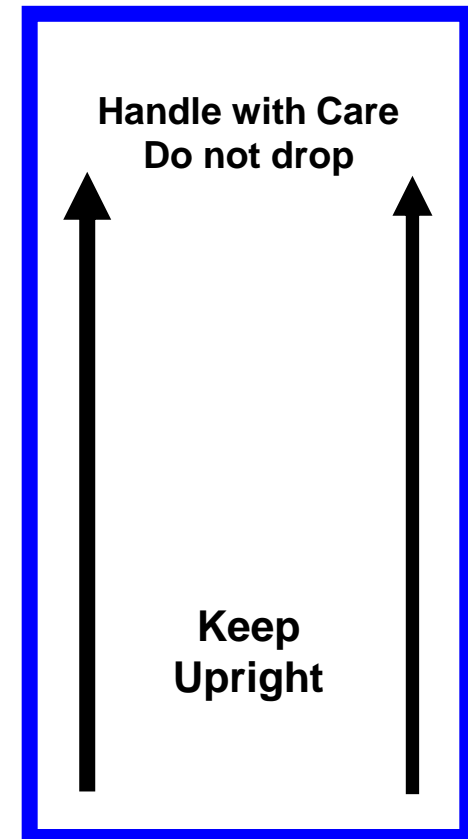
There are several ways to ship,

- Ground shipping in a dry Dewar (several days)
 - Ground shipping in a Dewar or dry shipper with liquid nitrogen (several days)
 - Overnight in a dry shipper (the usual method)
 - Overnight in a Dewar or dry shipper with liquid nitrogen.
- Shipping liquid nitrogen, *i.e.* in a Dewar or with the dry shipper filled with liquid requires lots of paperwork and a training course in the US. For further details see :
https://prosperitylms.com/req/fedex_student/
and
<http://www.fedex.com/us/services/options/express/dangerousgoods/seminars.html>



Shipping Dry (magic words)

- To avoid delays in shipping your Dewar (shipping dry) should have a label with the magic words “**Non-regulated**”, “**Not-restricted**” and “**Non-Hazardous**”.
- Any label signifying liquid nitrogen should be removed if shipping dry (your Dewar will be returned to you if this is not removed).
- For shipping in liquid nitrogen the rules are very different and beyond the scope of this workshop – please ask me later if you are interested in these details.
- Ship to arrive at least a day in advance of the beamtime and arrange to have the Dewar filled on arrival. At SSRL note that shipments are not accepted over the weekend so if your beamtime starts Monday aim to have the Dewar arrive on the Friday.



Shipping (continued)

- Track the shipment to ensure no surprises. First time Dewar shipments can be like a boomerang until the local FedEx office becomes used to the sight of those strange boxes.
- Label the Dewar with your name, similarly label the shipping box on the outside.
- Put the return shipping label inside the shipping box.
- Note: Our own experiences on icing during shipping have been mixed hence the use of a control crystal or several (this is also nice when you have a series of poor diffracting samples and your lysozyme, xylose isomerase or ribonulcease sample comes up and diffracts beyond 1A).

Avoiding Icing During Mounting

- One method that we use is to fill in a fume hood, fill rapidly and before inserting the cassette into the shipping Dewar wash the cassette with liquid nitrogen.
- Another method is to keep the cassette ports filled with dummy pins and only extract those pins before filling that port with a sample.
- A more complex but more useful technique is to pre-cool samples and store them under nitrogen using a cryo vial. These can then be transferred to the cassette rapidly on the day of filling. This is my preferred method of mounting as I can record a picture of the crystal cooled and check to see if ice buildup has happened as a result of shipping.

**Cryostream system
independent
from X-ray source**

Cryostream

Sample

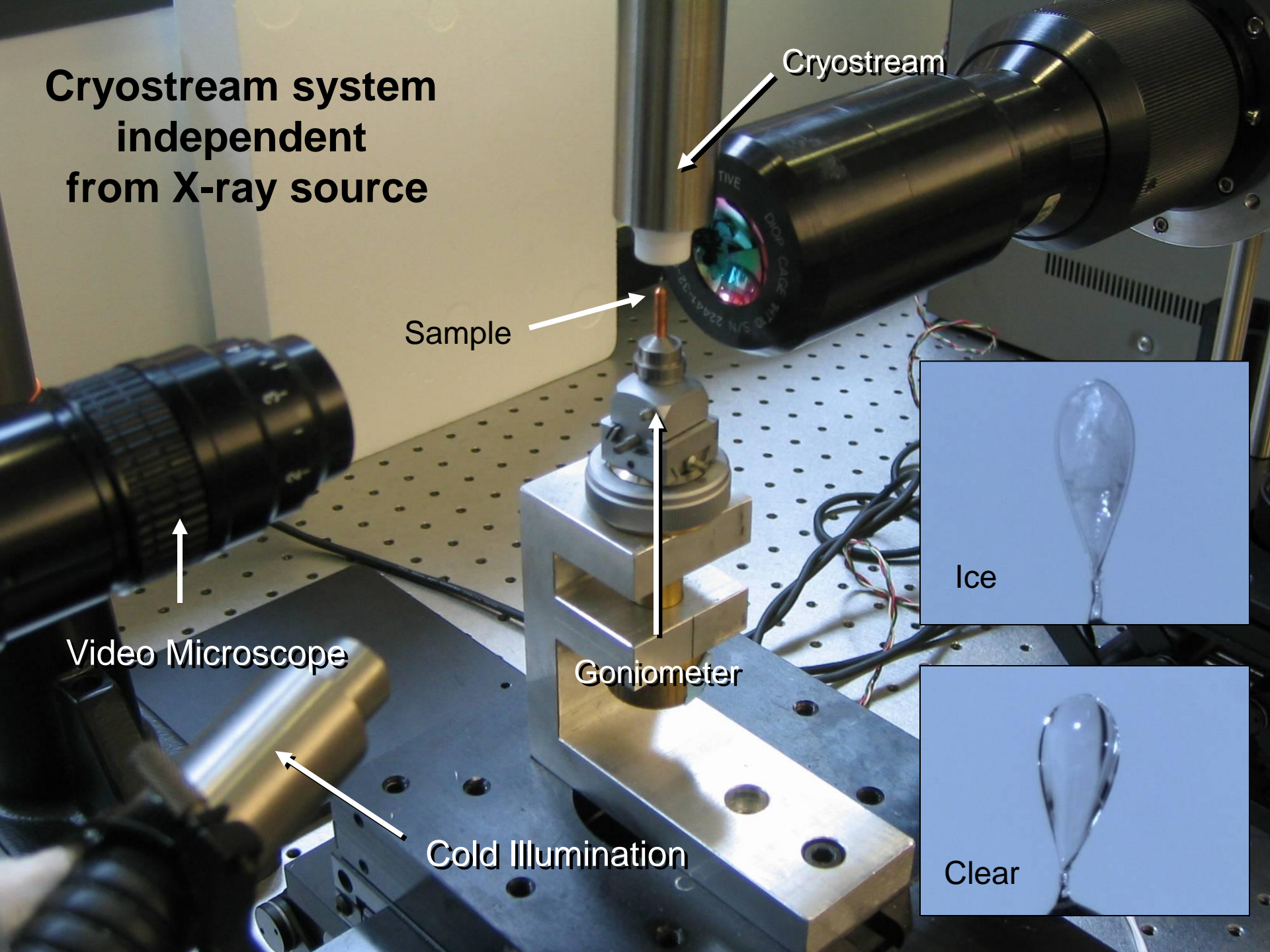
Video Microscope

Goniometer

Cold Illumination

Ice

Clear





Planning

(This will help make your experiment efficient)

Planning – Communication

- Contact the support staff before the run, let them know how many cassettes are planned.
- Share all the contact details of the team with each other and the support staff. Try and have one or at most two numbers where the person collecting data can be contacted at all times.
- Get the cell phone number for the support staff (tip, look on the website at SSRL using the browser available in the remote software).
- During available hours, 9:00 am – 9:00 pm California, don't be afraid to contact the support staff. Check if they will be taking calls outside these hours and if not, do not call.
- If you fail to contact your staff support look on the schedule to see who else is on support and try them next ... if it is urgent.
- Have a good communication plan within the team collecting data, especially if many different locations are being used. Instant messenger has worked quite well but a chat window available in Blu-Ice would be lovely 😊

At the synchrotron

(Setting up at home, screening and data collection)

Asimov's Laws of Robots

- Zero'th law – A robot must not merely act in the interests of individual humans, but of all humanity.
- First law – A robot may not harm a human being, or through inaction, allow a human being to come to harm.
- Second law – A robot must obey orders given by human beings except where such orders would conflict with preceding laws.
- Third law – A robot must protect its own existence as long as such protection does not conflict with the preceding laws.

...applied to remote data collection

- Zero'th law – A robot must not merely act in the interests of individual crystals, but in the best interests of the crystallographer.
- First law – A robot may not harm a crystal, or through inaction, allow a crystal to come to harm.
- Second law – A robot must obey orders given by crystallographers but may first question them if it senses evidence of sleep deprivation and lack of common sense.
- Third law – A robot must protect its own existence and reproduce at other beamlines as long as such protection does not conflict with the preceding laws....

Macromolecular Crystallography - Windows Internet Explorer

http://smb.slac.stanford.edu/

File Edit View Favorites Tools Help X Convert Select

Macromolecular Crystallography

Macromolecular Crystallography at SSRL

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SPEAR status
Beamline status
Support Staff Schedule
Beamline Information
PX users mailing list
Robosync
JCSG
SSRL
SLAC
Stanford University
Staff Area

Funding Agencies

Collaborative Research Institutions

Macromolecular Crystallography is a technique used to study biological molecules such as proteins, viruses and nucleic acids (RNA and DNA) to a resolution higher than ~5 Å. This high resolution helps elucidate the detailed mechanism by which these macromolecules carry out their functions in living cells and organisms. Protein molecules can crystallize under regulated conditions; the [crystals](#) are made up of multiple copies of the molecule arranged in a regular 3-dimensional lattice. The x-rays deflected ("scattered") by the atoms in equivalent positions in the crystal lattice concentrate into sharp intense spots ([crystal diffraction pattern](#)). The macromolecular structure can be determined by analysis of the intensities and positions of the diffraction spots.

The Macromolecular Crystallography Group at the [Stanford Synchrotron Radiation Laboratory](#), operates and develops beamlines providing state of the art macromolecular crystallography facilities and support for visiting researchers. Of the beamlines currently operational, three (BL9-2, BL1-5 and BL14-1) are designed for MAD experiments, two side stations (BL9-1, BL7-1 and BL11-1) are also MAD capable at slightly reduced energy resolution. BL12-2, with an undulator source, is optimized for microfocus applications, but can also be used for conventional experiments (MAD, screening, etc.). Researchers from universities, industry, and government laboratories around the world can gain access to the beamline facilities by submitting a [research proposal](#). [Updates on beamline facilities](#) and other user information are posted to the [px-ssrl mailing list](#).

News:
 Beamlines are being prepared for the 2009-2010 User Run
[Postdoctoral position available](#)

Beam Line	1-5	7-1	9-1	9-2	11-1	12-2	14-1
Flux @200 mA (p/s)	2.5x10 ¹⁰	2.8x10 ¹¹	7.2x10 ¹⁰	5.6x10 ¹¹	5.0x10 ¹¹	1.6x10 ¹²	7.2x10 ¹⁰
Experiment	MAD	MAD	MAD	MAD	MAD	Commissioning	MAD
Wavelength (Å)	0.85-2.06	0.97-1.76	0.77-0.98	0.85-2.06	0.82-1.17	0.72-1.86	0.95-2.06
Energy Range (keV)	6.0-14.5	7.0-12.7	12.6-16.2	6.0-14.5	10.6-15.1	6.67-17.2	6.0-13.0
Beam Size (µm)	100-200	50-200	50-250	50-200	50-300	20-200	100-200
Detector	Q315R	Q315R	Q315R	MAR325	MAR325	Pilatus6M	MAR325
Detector Size (mm ²)	315x315	315x315	315x315	325x325	325x325	431x448	325x325
Xtal-Detector (mm)	90-540	101-650	95-650	95-650	90-650	150-650	95-650
Throughput (images/minute)	20	20	20	13	13	90	13
BL phone (+1-650)	926-5215	926-5271	926-5291	926-5292	926-8648	926-5212	926-5141
Support phone (+1-650)	307-4151	283-4556	714-9411	714-9417	714-9414	714-9405	307-4151

Common Facilities

Remote Access	Remote access tools	Sample Database Spreadsheet templates	Remote Unix Desktop	Web-ICE
Beamline Hardware	Stanford Auto-Mounter (SAM)	Xe/Kr Incubation	Toolboard	Other Tools
Computing Resources	Control Software Blu-ICE	Computers	Software	Data Backup

[Technical questions: Webmaster](#) [Content questions: Mike Soltis](#)

Last modified: Thursday, 08-Oct-2009 15:31:52 PDT.

http://smb.slac.stanford.edu/public/research/index.shtml

Know your beamline

http://smb.slac.stanford.edu

Setting up at home

- It is possible to efficiently run the screening and data collection from a single computer but it is much easier to use two or three.
- One computer should be dedicated to the Blu-Ice control software. The other can be used for data processing, structural solution, refinement, web surfing etc.
- If using a computer with a small screen or low resolution the effective screen size needs to be increased so that software such as HKL2000 will run.
- Different session names should be used. If you have multiple users it is good to incorporate their name into the session name. That way you do not accidentally terminate their session instead of your own.
- If you loose connectivity the current process will not stop. Log in again and hit passive to gain control of the software.
- You cannot log into Blu-Ice until the support staff enable you and your beamtime.
- However, you can log into the “SSRL” computers and create a directory for the data collection.

Blu-Ice for data collection with HKL2000 processing

Web-Ice and beamline video system

Structural data processing (CCP4)



Strong Coffee

Phone to call staff

Screening

- Make sure your spreadsheet is uploaded and the appropriate directory is set for screening.
- One person needs to monitor screening throughout – failure of auto centering can stop the screening, crystals may be shot out of the beam etc.
- Scoring is fairly accurate however it should be checked for choosing the top samples to study:
 - Bad crystals may not be too bad. Icing can produce bad statistics but washing or even returning the crystal and remounting it effectively removes small amounts of surface icing.
 - Good crystals can be bad. Ice crystals can mislead scoring.
- The screening images can be integrated and a strategy determined however **if the crystal is returned to the Dewar and remounted the crystal position often changes**. Strategy will have to be run again.
- If it is a critical experiment collect data as soon as the screening shows a good crystal (see tips in data collection).

Screening – Keep it Simple

- Use good names for data directories. Process in a separate directory with a related name. Write these down in a logbook.
- Use the video cameras to troubleshoot – check the ion chambers, that the phi axis is correct and matches the software setting. Make sure the beam is coming through, *i.e.* no attenuation etc. then call the support staff. If out of hours call a more experienced person in the lab to have a look. If this does not do the trick go home and get some sleep and come back when the support staff are on call again.
- Generate a plan for data collection priority as screening progresses
- Each sample takes about 4 minutes (for a few seconds exposure time and two images). The largest part of this is mounting and dismounting.
- *It is quicker to center manually if you can keep up the pace and are ready to do this immediately after mounting (no longer an option).*
- Make sure you know what is happening and keep stuff happening, It is easy to be whiling away the time while screening has stopped for any number of reasons. Make notes on diffraction that looks good, compare with the automatic scoring routine.

Data Collection

- Follow a plan and know how to process the data before you collect it – practice with other data sets.
- Check the directory before collecting into it. Check the directory again, check you have the correct crystal, check the crystal and the directory!
- Plan on having rested before data collection. On a long run the person screening should get some sleep before starting data collection.
- Don't be greedy with resolution if collecting a MAD data set.
- Collect in dose mode but if you change beam size, dose needs renormalizing.
- Use a low (possibly medium) and high-resolution pass in that order if the data needs it. Low resolution can use a much shorter exposure time than high and can also use a wider oscillation range. Use about 20% resolution overlap depending on the number of reflections (a sufficient number must be common to scale the sets).
- Understand how to use distance, wavelength, oscillation and offset and the consequences in terms of data completeness where appropriate. Never think of the detector as square but use it as a round one (with no offset). Know the spectrum of the beamline and how to use it most effectively.

Data Collection (continued)

- For MAD data save the MAD scan data. Note down the wavelengths, and f' and f'' . Know the sequence, molecular weight and number of sites expected.
- Know how to make a good data strategy and the differences between an anomalous and a completeness strategy.
- Use testgen in Mosflm or equivalent to determine the most appropriate oscillation angle/s. Check out the program Best. Webice will also do this for you.
- Collect complete data sets, if more time is available collect even more data.
- Process your data as soon as it is collected even if the processing is a quick and dirty job. Make full use of the scripts available (have 2 people working during data collection). If cannot be immediately processed resolve the problem with the help of the support staff.
- There is no advantage to having the detector any closer than the edge of the diffraction. However the edge is difficult to determine by eye.
- If several people are collecting have a good communication plan.
- Let the support staff know if you are going to finish early.

Being polite (several projects during the same beamtime)

- If there are several projects collecting data remember that any waste of time by you eats into time that could be used productively by someone else.
- Don't waste time and have a plan beforehand on the priority of samples.
- Let others know the approximate time you will finish.
- Keep an eye on the data collection and process continuously so that any problems can be identified early on.
- If this is your critical experiment only when you are happy should you remove that crystal (and take a lower priority next time).
- Those who send salt shall be shot 😊

Finishing up

(Data transfer, sample return, pin cleaning etc.)

Transferring data

- It is best to process on the SSRL computers and ship the integrated intensities and log files back. The data will follow assuming you have requested it.
- It will take a few weeks for CD/DVD's to be received from the experimental run.
- Use descriptive names for the CD/DVD's. You, hopefully, will end up with a lot of them.

Choices to be made – sample return

- Cassettes can be left at SSRL. Remember this when collecting data. It may be better to spend more time collecting the best data set from one sample than several marginal datasets from another
- But, the more manipulation of the crystal that takes place the more chances to lose it!

Cleaning pins

- Pins and loops can be easily cleaned using a sonicator bath.
- We use a water wash followed by a 30% ethanol wash.
- The pins and loops are then dried and examined.
- Broken loops are pulled out of the pin and replaced with new loops.
- Loops still dirty are washed again.
- Best results are achieved using only a single layer of pins.
- About 80% of loops are reusable.



After the run

- Make notes of any problems and suggestions. Send them in the end of run report.
- Contact the support staff directly if you wish (email is best).
- A lot of effort goes into making the robotic system work well and ensuring the resulting data is the best possible -
 - acknowledge the support staff who helped out
 - reference appropriate publications about the robotic system and Blu-Ice
 - acknowledge SSRL
 - Get to know the habits of your support staff. When you see them encourage those habits, e.g. buy a beamline scientist a beer (or anything chocolate for particular individuals), say hello at meetings etc.
- Publish the paper, acknowledge the developments at SSRL that made it possible.
- Look forward to new developments.

**Two days
before
beamtime**

Email: Dewars
on the way, fill
when they
arrive please

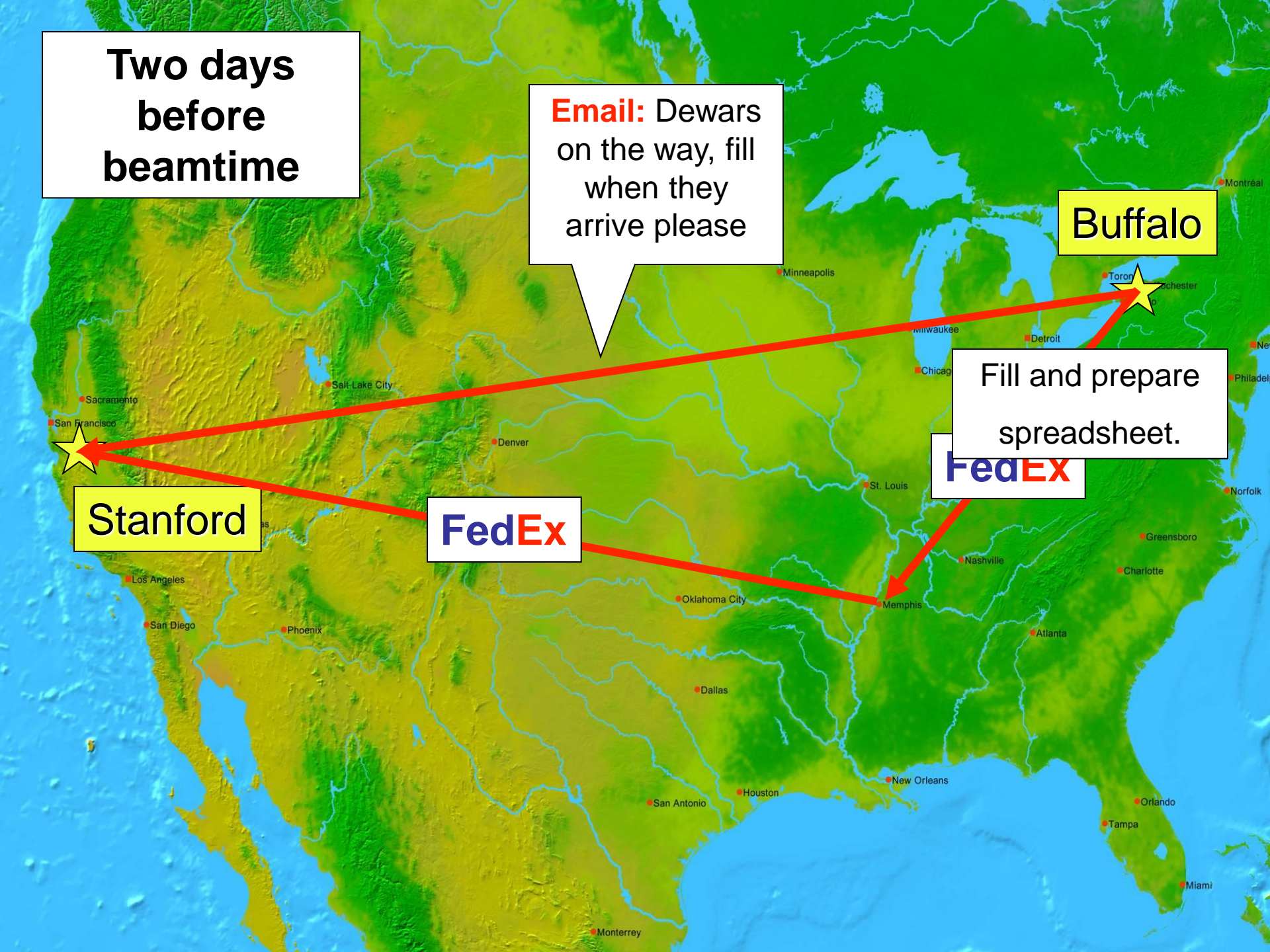
Buffalo

Fill and prepare
spreadsheet.

Stanford

FedEx

FedEx

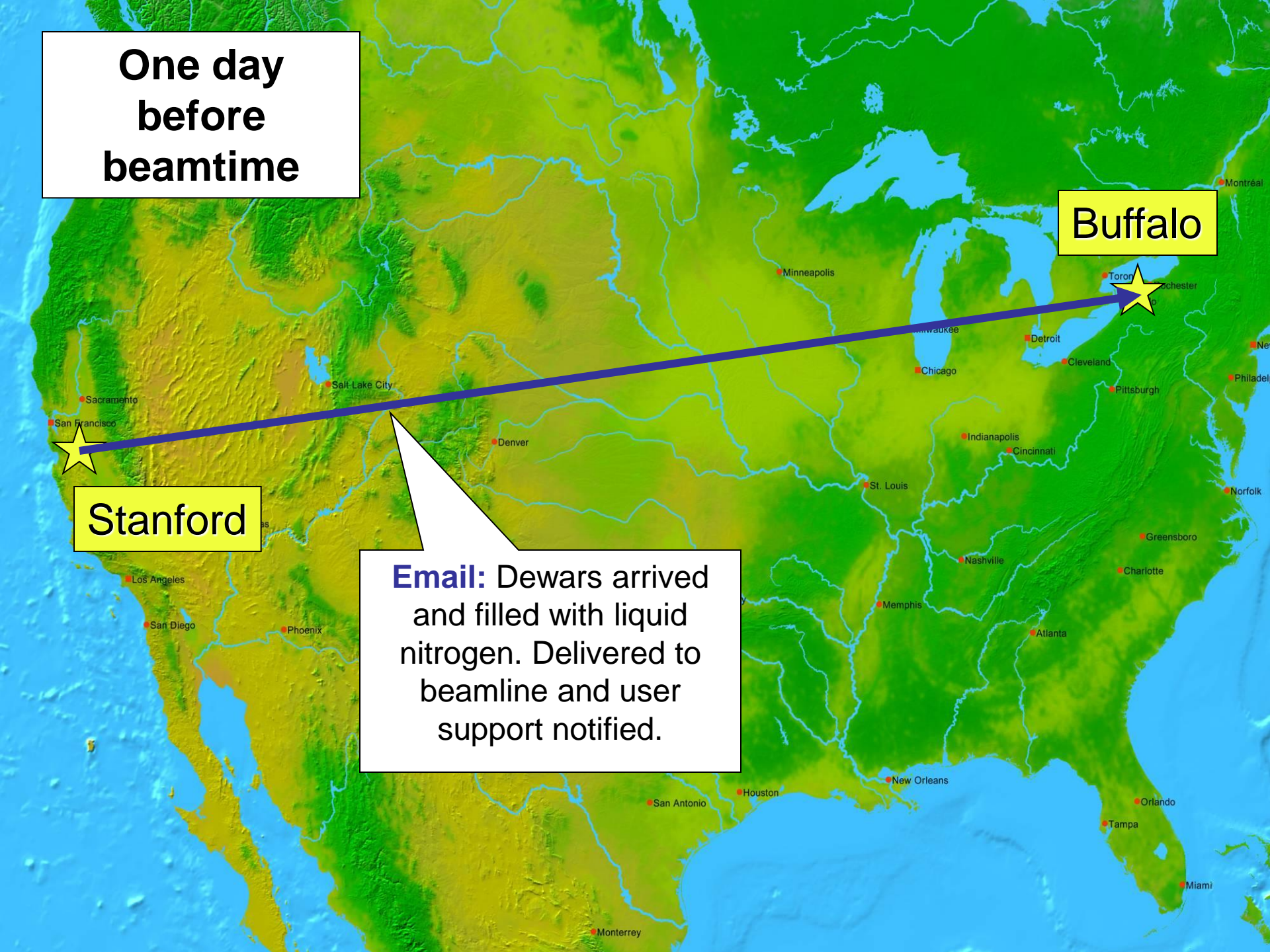


**One day
before
beamtime**

Buffalo

Stanford

Email: Dewars arrived
and filled with liquid
nitrogen. Delivered to
beamline and user
support notified.



**The day
of the
beamtime**

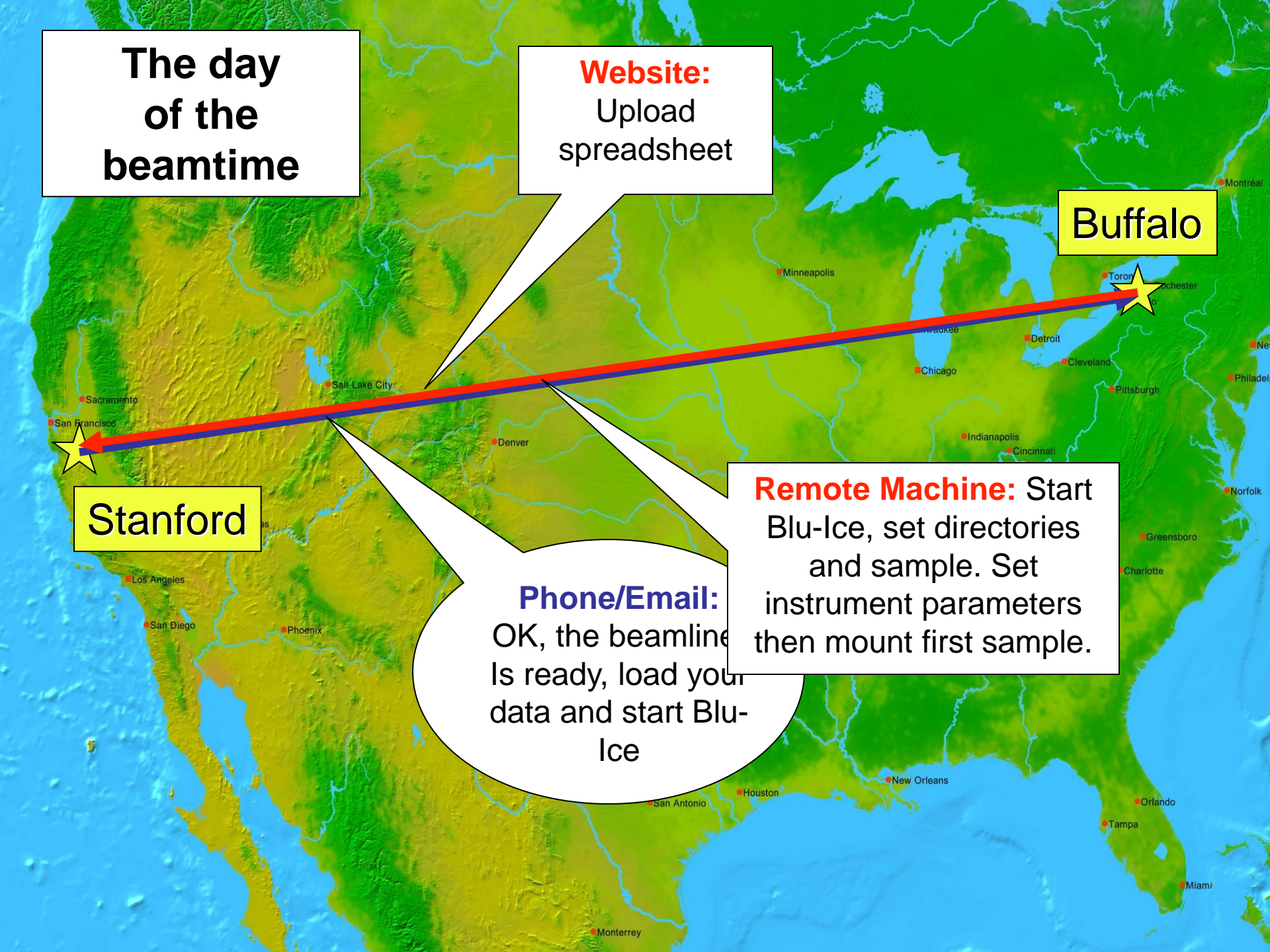
Website:
Upload
spreadsheet

Buffalo

Stanford

Remote Machine: Start
Blu-Ice, set directories
and sample. Set
instrument parameters
then mount first sample.

Phone/Email:
OK, the beamline
is ready, load your
data and start Blu-
Ice



**During
the
beamtime**

Automated
analysis of
crystals as
data is
collected

Remote machine:
Send images of crystal
centering

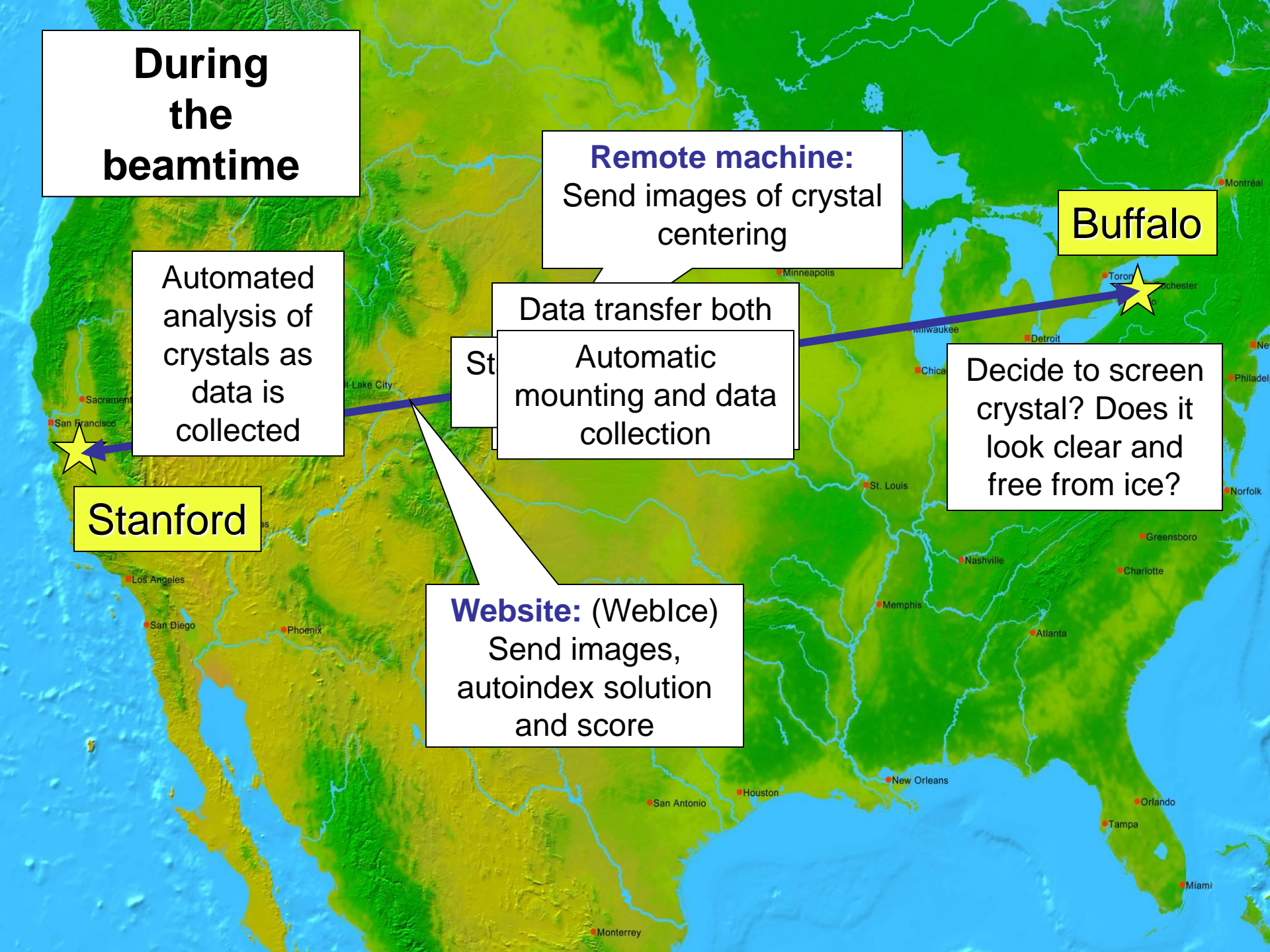
Buffalo

Data transfer both
Automatic
mounting and data
collection

Decide to screen
crystal? Does it
look clear and
free from ice?

Stanford

Website: (Weblce)
Send images,
autoindex solution
and score



**During
the
beamtime**

It looks great, can
you collect a MAD
data set and tell
Alice and Bob to
take a look?

Call collaborator,
from your
to be
. Take

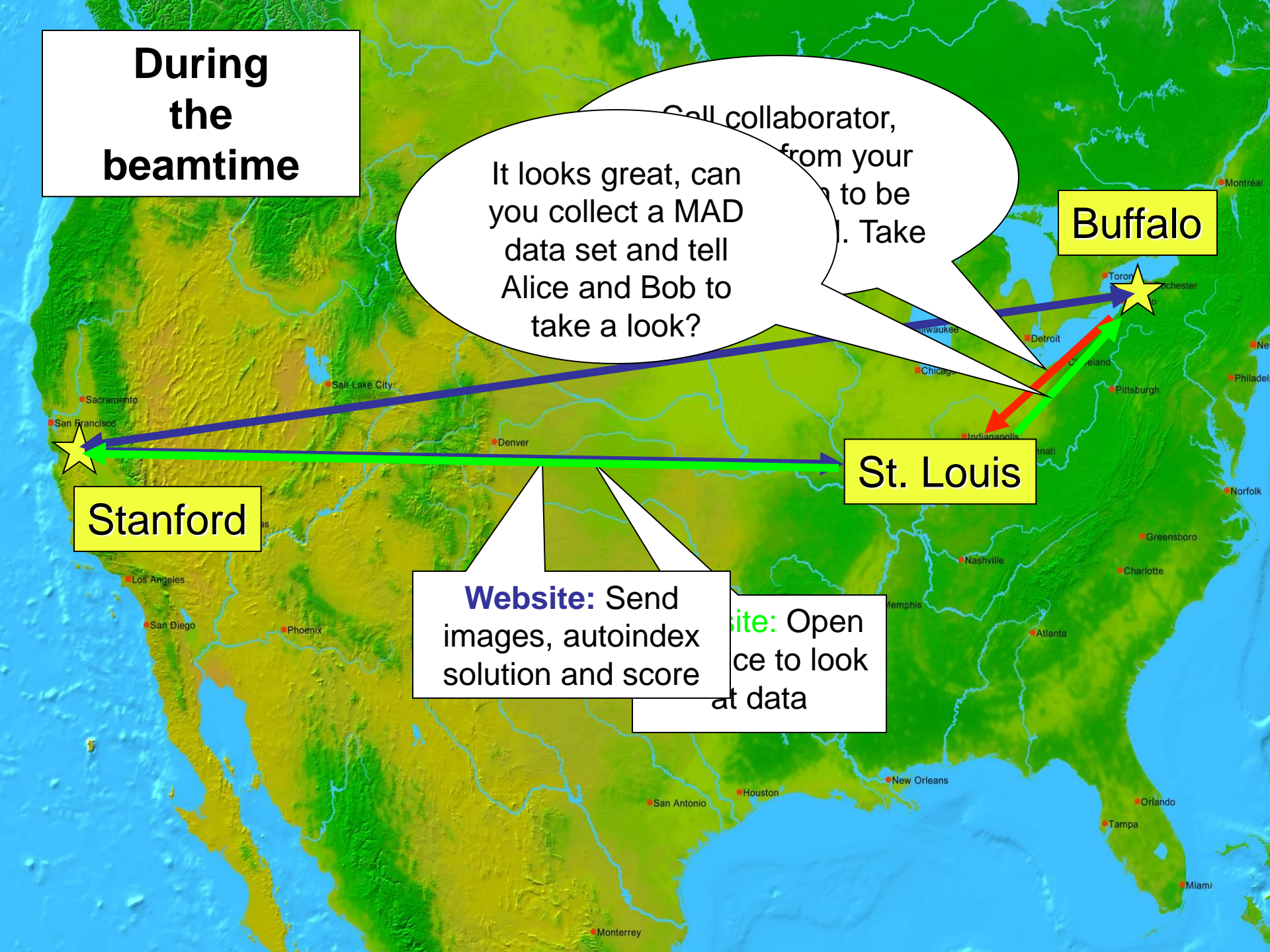
Buffalo

St. Louis

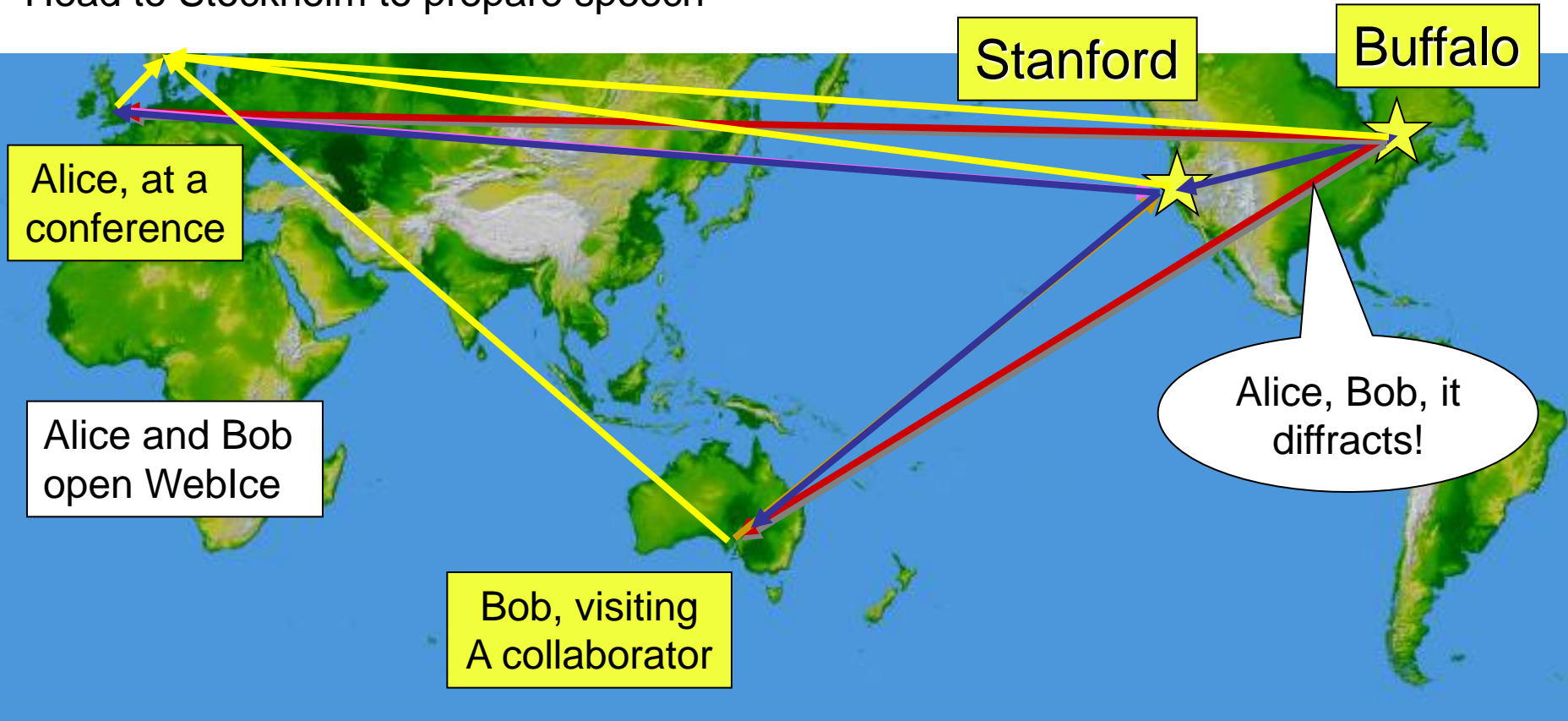
Stanford

Website: Send
images, autoindex
solution and score

Website: Open
page to look
at data



Head to Stockholm to prepare speech



Alice, at a conference

Alice and Bob open Weblce

Bob, visiting A collaborator

Stanford

Buffalo

Alice, Bob, it diffracts!

Maybe

Remember, "...the surest road to Stockholm is through a crystal tray."

Seringhaus & Gerstein, Science 315, 40-41 (2007)

Universal Laws of Remote Data Collection

- The most important experiment has the least amount of time available.
- Quick things never are.
- Unwatched nitrogen boils faster.
- Ice forms behind your back.
- When you think someone else is doing it, they are waiting for you.
- The computer will never tell you it is waiting.
- Planning to have something done early will get it done just in time. Planning for just in time will mean it will be late.
- The best crystal was the other one, not the one you collected data on.
- Whenever you set out to do something, something else must be done first.
- When all else fails, read the instructions.
- A difficult task will be halted near completion by one tiny, previously insignificant detail.
- Never trust modern technology. Trust it only when it is old technology.

The Universal Law of Remote Data Collection (from the synchrotron side)

The user will always want more.

Bottom Line

The system works well and is continuously evolving. Feedback to the synchrotron facility is a vital part of this evolution. Let them know what works well for you, what could work better, what doesn't work and what you would to see. Try it, see what works for you, optimize around that.

With a big word of
thanks to:

SSRL for developing this technology
and HWI for providing samples to make
use of it.



