ACA session planning template

Name, date, and time of your session goes here at the very top for easy reference

## ACA session chair info sheet - very helpful reference

https://acas.memberclicks.net/session-chair-information

# Key dates and deadlines:

**November/December**:

* Submit session description to ACA Headquarters
* Review scientific program
* Begin seeking funding

**January:**

* + Annual Meeting Webpage Launch
  + Registration Opens
  + Abstract Portal Opens

**March:**

* + Travel Grant Applications due @ the end of the month (specific date to be determined)

**April:**

* + Abstract submission deadline (specific date to be determined)
  + Sessions to be organized @ the end of the month (specific date to be determined)
  + Etter award winners to be selected by SIGs.

**May:**

* + Schedule of sessions to be confirmed (specific date to be determined)
  + Early Registration Ends May 31st

# Co-chairs

You, your co-chair, contact info, and SIG affiliations

# Session Description Brainstorming

## Idea 1

This session will focus on multiple aspects of etc etc.

## Idea 2

We will showcase many of the advances made in structural biology, etc

# Possible speakers

Think about a balance of early/mid/late career scientists, of women, minorities, etc

## Industry

People you’re thinking of, and who will contact them

## Academia (let’s get them sponsorship)

People you’re thinking of, who will contact them

* Invited talks. Guideline from Council: no more than 60% of # speakers/allotted time for invited speakers (i.e. at least 40% from general submissions)

## Contact matrix

| **Person** | **Category** | **Career level** | **contacted** | **response** | **email** |
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# Topics

Balance interests of cosponsoring SIGs

# Scheduling

5-7 speakers, depending on 20, 25, or 30 minute speaking slots

[Abstract site](https://ww2.aievolution.com/acas/index.cfm?do=usr.accountGateway&signInType=attendee&noAutoPick=1): https://ww2.aievolution.com/acas/index.cfm?do=usr.accountGateway&signInType=attendee&noAutoPick=1

[Here's a link to the 2022 draft program.](https://docs.google.com/spreadsheets/d/1hMyHVbRcueObuUkDNksMVNqXO76BJoNF1qAId6iAJcQ/edit#gid=814390968)

# Registration:

Put fees and deadlines here once released

# To-do:

* Items here

## Funding

# Practice Session

(Most relevant for virtual meeting)

## Speakers requesting funding assistance:

## Intros and so forth:

How you will introduce each speaker

# Session Summary

As a followup, you’ll need to write a session summary for *Reflections*. Here’s a sample:

In session 4.2.5 we explored applications of structural biology methods to drug discovery, including structure/function studies, hit validation, lead optimization challenges and fragments with a particular interest in examples involving a variety of techniques. We featured a mix of speakers representing both academic and industrial institutions who presented their work involving small molecule and antibody therapeutics. With over 70 participants, we had an engaging session that encapsulated the diverse role of structural biology and complementary biophysical techniques in drug discovery.

We opened our session with a crystallography-based talk from You Wang (Duke University) who described the X-ray crystal structure-guided optimization of a small-molecule fungal FTPase inhibitor. The second speaker, Md Rezaul Karim (Moffitt Cancer Center), presented some intriguing complementary crystallographic and SAXS studies to elucidate ligand-induced global conformational changes in TAF1 tandem bromodomains in the quest to find a dual TAF1-ATR inhibitor as a potential cancer therapeutic. Rachel Palte (Merck & Co) then moved us toward the macromolecular therapeutic realm with a mesmerizing talk about the analysis of paratopes and epitopes of 5 anti-hArg antibodies via cryo-EM structural studies of complexes consisting of antibodies bridging trimers of hArg1. Her team obtained local resolutions of 3.5 Å for these complexes, consisting of multiple hArg and mAb molecules, which are greater than 650 kDa in size.

After the coffee break we continued with more cryo-EM from Christine Jao (Genentech) who captivated us with how she utilized protein engineering and chimeras to advance drug discovery efforts for the Nav 1.7, a pain-sensing voltage-gated sodium channel. Next up and moving beyond small molecule therapies, Sandra Gabelli (Johns Hopkins School of Medicine) highlighted her group’s recent work towards developing bispecific antibodies and CAR-T cells that target intracellular cancer mutations via MHC-neoantigen complexes presented on the cell surface. Through the application of crystallography combined with cellular assays, biophysics and computation, it was a fascinating tale of how antibodies can distinguish between proteins differing by a single amino acid. Finally, the last two speakers in the session presented their work focusing on fragment-based drug discovery. Russell Judge (Abbvie) described his team’s path starting with a fragment hit for Bcl-XL and overcoming many challenges beyond potency to develop a first-in-class orally active inhibitor. Rod Hubbard (Vernalis and York University) wrapped up the presentations by spotlighting examples where NMR, SPR and high throughput crystallography were critical to advancing fragment-based lead discovery for several disease targets. We concluded the session with an interactive discussion covering the presentations as well as our experiences in structure-based drug discovery.

A huge thank you to our facilitators for their technical assistance: Emilia Arturo and James Moody; and to our sponsors for their generous support of the session: Constellation Pharmaceuticals, Dectris, Thermo Fisher Scientific, SPTLabtech, Anatrace/Molecular Dimensions.