Bio:
“Derek Wilson has a sufficiently overinflated sense of his own notoriety that he assumes you know who he is already. Nonetheless, grudgingly: Derek Wilson is a mass spectrometrist whose training began in Unionville’s high school for the Arts, where he double majored in Acting and Signing. Many things happened there that are now of little to no consequence and some things happened that are of great consequence. He then went to Trent University where he skinny-dipped in the Otonabee river and also completed a BSc thesis under the gentle tutelage of Prof. Stephen Rafferty. He then went to do a PhD in mass spectrometry with the very tall and equally talented German whom you may know (Lars Konermann) and after that he did a post-doc under uber-amyloidogenesis guru Chris Dobson at Cambridge, where he attempted (largely without success) to learn biophysical NMR. Realizing his mistake of believing you can ever do anything worthwhile with NMR, he returned to his mass spectrometry roots shortly after taking up a tenure track position at York university, where he has been ever since. He’s published a bunch of papers (almost 100, if you count the ones where he’s in the middle), got probably more funding than he strictly deserves, and has done some administrative things, like right now being the president of the Canadian Society for Mass Spectrometry. His science today is at least pretty ok.”

Talk Title:
Proteins Move and That’s Important When Developing Drugs That Target Them, Featuring Cancer, Neurodegenerative Disease, COVID and Hydrogen Deuterium Exchange Mass Spectrometry

Abstract:
“I’m not sure what I can add to the awesome title (see above), but suffice it to say that this talk will feature taking fundamental information about protein conformational
dynamics and translating it to drug discovery in the real world, with real-world impacts involving real-world money. Stories will include industry/academic battles against some of the absolute worst diseases ever, like cancer, neurodegenerative disease and yes, COVID. If methods float your boat, then you’ll be happy to know that we use our own special and (we would argue) super-powerful version of hydrogen deuterium exchange mass spectrometry that allows us to explore how proteins respond (structurally and dynamically) to drug candidates in unprecedented detail. What I can assure you is that there will be some pretty nice science and you probably won’t be all that bored.”