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**Title:** Fast structure and positional ortholog searching and viral metagenome assembly

**Abstract:** I will give an update on Foldseek, which can perform structural similarity searches and alignment through the Uniprot50 and MGnify/ESM30 database of 95M structures in a few seconds on a single core, at a sensitivity similar to TMalign ([search.foldseek.com](http://search.foldseek.com)). At its core is the 3Di structural alphabet that we learned using a discrete variational autoencoder. I will also present SpaceDust, a tool for fast sequence- and structure-based searches of clusters of “positional orthologs” between genomes, as well as Penguin, our new strain-resolved viral metagenome assembler.