Fold it

Suzanne: When you've got it right you see your protein moving and changing shape and your score rushes up, your own player name rushes up through the ranks and, yeah, the adrenalin starts.

Charlie: It's like being a scientist when you get a paper published. That 10% of euphoria is supposed to take you through the 90% of banging your head against a brick wall.

David Baker: People put a huge amount of energy into playing games on computers so I think projects like this can channel that energy into solving real world problems, and that's a way in which everyone can contribute that really hasn't been there before.

Suzanne: I'm Suzanne Halitski and I'm an administrator in Manchester, and my folding gaming name is also Suzanne.

Charlie: Hallo I'm Charlie, I'm a bench technician and in my spare time I play Fold it. I used to be number two in the world my gaming tag is *CharlieFortsConscience* and I'm a member of the Contenders.

Charlie: It's essentially a 3-d jigsaw puzzle. You're given a protein which comprises of uh... a backbone and individual side-chains and by moving these around changing the interactions your score either goes up or down.

David Baker: Scientists are interested in working out three-dimensional structures of proteins because they help understand how the proteins carry out their jobs, what they do inside cells. The principle behind the prediction of protein structures on a computer is that we've known for a long time that all the information needed to determine the structure of a protein is in the amino acid sequence of the protein. So, from genome sequences we can translate those into amino acid sequences, using that genetic code, now we have this amino acid sequence. It turns out that the structure that proteins fold to is almost always the lowest energy structure for that amino acid sequence. So the structure prediction problem then is finding the lowest energy structure for that amino acid sequence and the reason it's hard is that there's so many different possible configurations. The big advantage that a human has is that they can look at a complicated thing like a big protein and sort of zoom in on the regions that probably most need to be reworked. And we give them visual cues: the regions that are high in energy locally are red and so they sort of stand out like "oh so you need to do something here".

Suzanne: To start with a protein that is so misshapen, it's ugly and it's red, and to work through that to a beautifully streamlined structure, where it's symmetrical and things are tucked in, and nothing is hanging out, of the sides, yeah, that is sort of the goal and that's what I like doing, to sort of help it in some ways to sort of be what it should be.

Charllie: A really good Fold-it player I think needs a number of skills. Problem-solving is obviously one of them I think, a slightly addictive personality, a little bit of stubbornness thrown in, and a little bit of luck on top. You don't necessarily need to have a scientific background to play, you just need to know what works and what doesn't and you can learn that within the game itself.

Suzanne: I'm an administrative worker in the rehab team. I'm just answering telephones, working on bespoke computer programmes, interacting with staff. It's very repetitive. When I go home, I become a different person. I just like to measure myself against something, and it's given me something that my everyday life hasn't given me. It's to just use abilities I didn't know I had.

Charlie: For me it's a guilty pleasure, and yet here I am involved in something that has real relevance in the scientific world. It makes you feel very proud of what you do, which is essentially a little hobby.

David Baker: You can imagine where you come home in the evening and you can either stay up all night playing Halo or you can be designing an HIV vaccine with people all around the world. I mean, which would you be happier saying you did when you went into work in the morning? People out there are discovering not only alternative protein structures but new approaches to solving the problem, so they're really doing scientific research even though most of the players don't really, are not practicing scientists.

Charlie: The computer versus human paradox, as it were, is ultimately we're going to fold ourselves out of the game. We're here to provide a sort of refinement to the uh... folding algorithms that protein servers use to try and do this automatically. As we get better and feed back to the Baker lab, the automated algorithms for the computers will get better and ultimately we'll be left with nothing to do.