Coding mistakes that could decrease accuracy of the moment:  
- Using beta barrel residues as selection, instead of transmembrane region

- Using .5, rather than an average, when no parameters are available (is this really a bad thing? The general principle would be, "if you don't know how some knowledge changes your probabilities, then pretend you don't know it")

What are these centers, structures, etc., "with 1qd5"? What files did I use on the paper I sent Vik?  
I might not get the modern moments, if I'm not using the modern centers.

I don't like the way I'm loading centers, anyway. Once I have the non-normalized moments, and a first batch of threaded moments, I'm going to change the selections and start calculating centers on the fly.

I don't think I like interacting with an alignment through an oracle, actually. I'd rather have a function of a seq record, and just use the oracle to pass along the alignment along with info about which is the pdb sequence. So, a class that inherits from the alignment class.

Thing is I find myself just pulling sequences out of the alignment to use the compare function. It would be better if the object just *was* an alignment.