min\_length (int): minimum number of matching residues in a segment

min\_percent (float): min percent identity of matching residues

similarity\_threshold (float): Threshold for similarity between segments

require\_equal\_start\_match (bool): require that all matching segments start at the same relative residue number for all members of an NCS group, trimming the matching region as necessary. This is, but not otherwise

maximize\_size\_of\_groups (bool): request that the scoring be set up to maximize the number of members in NCS groups (maximize\_size\_of\_groups=True) or that scoring is set up to maximize the length of the matching segments in the NCS group (maximize\_size\_of\_groups=False)

required\_chains (list):

min\_fraction\_domain (float): domain must be this fraction of a chain

initial\_rms (float): Guess of RMS among chains

match\_radius (float): Keep atoms that are within match\_radius of NCS-related atoms

min\_contig\_length (int): segments < min\_contig\_length rejected

smooth\_length (int): two segments separated by smooth\_length or less get connected

max\_rmsd\_domain (int): max rmsd of domains

min\_fraction\_represented (float): Minimum fraction of residues represented by NCS to keep. If less...skip ncs entirely