Name of parameter	Meaning
total_score	weighted average of all parameters
Transform_accept_ratio	How well the low resolution Monte Carlo stage worked. It is a number between 0 and 1 and is provided as a diagnostic
fa_elec	Coulombic electrostatic potential
fa_intra_rep	The repulsive energy within residues
fa_pair	Statistical residue-residue interaction potential. Very useful in protein-protein interactions
fa_rep	The repulsive portion of the Lenard-Jones potential. If high then there are clashes in the protein
if_X_hbond_bb_sc **if_X_hbond_sc**	Hydrogen bonding term between protein backbones and sidechain (ligand)
interface_delta_X	The energy of interactions between the ligand (chain X) and the protein
ligand_is_touching_X	1 if ligand is close to the protein, 0 otherwise
complex_normalized	Total score of the protein complex with the ligand (holo state) normalized by the number of residues
dG_cross	The energy of interaction between the two sides of the complex, calculated in the holo state (protein bound to ligand)
dG_separated	The energy of interaction between the two sides of the complex, calculated by taking the score of the holo state, then separating the two sides of the interface, optionally repacking, and then calculating the score in the separated state. This is particularly useful if you think you have an "induced fit" type situation, and want to correct for repacking in the absence of the ligand.
delta_unsatHbonds	How many unsatisfied hydrogen bonds are introduced by the design. Unsatisfied hydrogen bonds are ones where the atom is able to make a hydrogen bond but does not because it's blocked by other residues
Packstat	How well the protein is packed. values between 0-1 with 1 being better
sc_value	Shape complementary score. Values between 0-1 with 1 being better. It looks at the correspondence between normal vectors of the surfaces of the protein and ligand
side1_normalized **side2_normalized**	The energies of the two sides of the interface, possibly normalized by the number of residues