Region parameters

Parameters for hierarchical sampling	
Each region is defined independently, and identified by ∼region[]	
parameter	*meaning*
\element_top_type{}	Type of element considered in the region. For RNA bases, use *region*.
\dependency_type{}	Independent or dependent. For now only independent is used.
\residues{}	List all residues in format *chain_id:residue_id* in the region. E.g. A:1.
\nres{}	Number of residues in the region.
\center{}	Center of region to define rigid body rotation and translation
\nrespair{}	Number of base-pairs in region.
\residue_pair{}	List all base-pairs in the region, of the format *chain_id:residue_id,chain_id:residue_id*. E.g. A:1,D:19.
\prop_trans_sig{}	Translation step size for rigid body motion.
\prop_rot_sig{}	Rotation step size for rigid body motion.
\prop_trans_sig_freeres{}	Translation step size for free residues in the region.
\prop_rot_sig_freeres{}	Rotation step size for free residues in the region.
\prop_trans_sig_respair{}	Translation step size for base-pairs in the region.
\prop_rot_sig_respair{}	Rotation step size for base-pairs in the region.
\prop_trans_sig_respair _internal{}	Translation step size for bases within each base-pair in the region.
\prop_rot_sig_respair _internal{}	Rotation step size for bases within each base-pair in the region.