SEQ: FASTA formatted domain sequences

PXD: Preliminary XML formatted coordinate DB with annotated domains

**needle:** EMBOSS package global domain alignment

ALI: Pairwise sequence alignments

**3Dpurge:** RMSD superposition of aligned domain sequences, purge domains that fail cutoff

SEQ: Updated sequences

PXD: Updated coordinate DB

**RADAR:** Suboptimal self-alignment and internal repeat detection

REP: Internal repeat alignments

**3Dmask:** RMSD superposition of aligned repeats, mask repeat residues that fail cutoff

**validate:** validate final XML database against schema

XDB: XML formatted coordinate DB with annotated domains

**Nh3D:** Final list of non-homologous domains