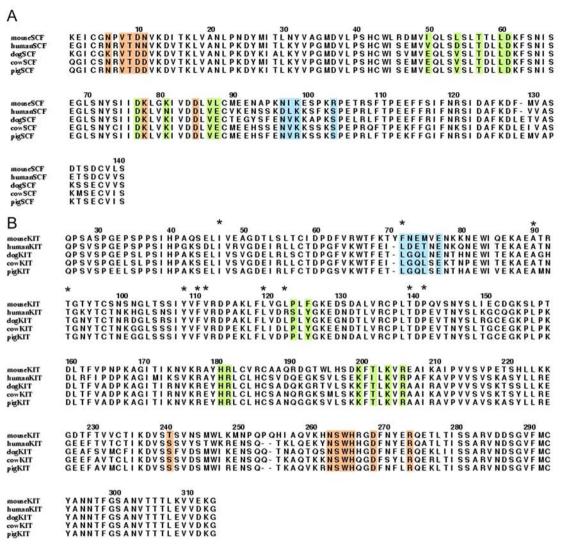


depicted as tubes and and KIT as surface. The crystal structure differs substantially from modled SCF/KIT complex, mostly because the templates used in modeling, e.g., the VEGF/FLT1complex and VCAM, have significant differences from SCF/KIT.



Supplementary Figure S2. Sequence alignment of SCF (A) and KIT (B) across species. Residues involved in ligand/receptor interactions are shaded in blue, green and orange for site 1, site 2 and site 3 respectively. KIT resides involved in D1-D2 hydrophobic interactions are marked with "\*".



Supplementary Figure S3. Structure-based sequence alignment between 4-helix bundle ligands that bind to class III RTKs. SCF residues involed in KIT binding, as derived from the SCF/KIT complex, are shaded in green. MCSF residues biochemically defined as receptor-binding important are shaded in orange. FLT3L residues biochemically defined as receptor-binding important are shaded in blue.