```
TEM2016_SelAC/1-263            1  HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCG  53
TEM2016_SelAC_Simulated/1-263 1  HPETRVKVKGAEECLGAGRGYIELDLNSGKILESFRPEERFPMRSTFKVLLCG  53
TEM2016_Consensus/1-263       1  HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCG  53
TEM2016_DMS/1-263             1  SEKVKMAVQQMEWRMGGHVGYFQIDIMDGDVLEAWRSKERFPMMSTMKVILCG  53
TEM2016_DMS_Simulated/1-263   1  HEKTKTKVRDAERRMGGRVGYLQIDIHDGDVLESFRQKERFPMMSTFKVILCG  53

TEM2016_SelAC/1-263            54 AVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSD  106
TEM2016_SelAC_Simulated/1-263 54 AELSRGDAGQEQLGRRIHYSQADEVEYSPVTEKHLTDGMTVRELCSAAVTMDD  106
TEM2016_Consensus/1-263       54 AVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSD  106
TEM2016_DMS/1-263             54 CILERVDNGFLKLQRKVKFQVNDLVAWSPITMMYIITGMTIQDLCDAAITLSD  106
TEM2016_DMS_Simulated/1-263   54 AILYRVDAGTEKLGRRVHFTVNDLVAYSPITSQYINDGMTIADLCDAAITLSD  106

TEM2016_SelAC/1-263            107 NTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPA  159
TEM2016_SelAC_Simulated/1-263 107 NTAADLLLTTIGGRGELTAFLHNMTDHVTRLARGAPELGEAIPGDECDTTMPI  159
TEM2016_Consensus/1-263       107 NTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPA  159
TEM2016_DMS/1-263             107 NTAANILLKELGGPIMLTMWMNMMGDMYTRLDRWEPYLNMAYEQDERDTTTPK  159
TEM2016_DMS_Simulated/1-263   107 NTAANILLKSLGGPIELTEYMNNMGDNVTRLDRWEPYLNAATPADERDTTTPK  159

TEM2016_SelAC/1-263            160 AMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGA  212
TEM2016_SelAC_Simulated/1-263 160 AMAQTLRGLLTEELLTLASRARLIDWMEADKVAGPLLRSCLPAGWFIADKSGA  212
TEM2016_Consensus/1-263       160 AMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGA  212
TEM2016_DMS/1-263             160 SMADTIKQMLKTHHLSFNSQQILISWMYMDKVAGPLLRQKIPADWYIADKSGA  212
TEM2016_DMS_Simulated/1-263   160 VMAKTIHELLKDHRLSKGSQQILIEWMKLDKVAGPLLRQAIPADWYIADKSGA  212

TEM2016_SelAC/1-263            213 GERGSRGIIAALGPDGKPSRIVVIYMTGSQATMDERNRQIAEIGASLIKHW  263
TEM2016_SelAC_Simulated/1-263 213 EVRGSGGIIAALGPDGKPSRIVVIYVTGRQATMDERSRQGEEIGASLIKRW  263
TEM2016_Consensus/1-263       213 GERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW  263
TEM2016_DMS/1-263             213 GDHGSRGIVALMGPNKHMERVIIIYMTGSNANMIQRNQWFKEIGKNIIKNW  263
TEM2016_DMS_Simulated/1-263   213 GKHGSRGIVAAIGPAGVASRVIIIYLTGSNNNMDARNQWFAEIGKNIIKNW  263
```