```
logo
NTDB id 47888 NMAA RS11770 WP 010981060.1  MLCPEKMSGMAGQYPYGVRSGLRRNGLKLWDIHFRMTRFIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINAASQQE  85
NTDB id 1127 NGFG RS10560 WP 003703428.1   .....................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINAASQQE  62
NTDB id 1126 NGFG RS09375 WP 003703428.1   .....................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINAASQQE  62
NTDB id 1125 NGFG RS07215 WP 003703428.1   .....................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINAASQQE  62
NTDB id 1108 NGFG RS06525 WP 003703428.1   .....................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINAASQQE  62
consensus                                                       **!*!**  ***!***!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
logo
NTDB id 47888 NMAA RS11770 WP 010981060.1  LEALPGIGPAKAKAIAEYRAQNGAFKSVDDLTKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPADKK  154
NTDB id 1127 NGFG RS10560 WP 003703428.1   LEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1126 NGFG RS09375 WP 003703428.1   LEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1125 NGFG RS07215 WP 003703428.1   LEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1108 NGFG RS06525 WP 003703428.1   LEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
consensus                                  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!
```

X non conserved
X similar
X ≥ 50% conserved