
Modeled NPA sequences

No. 15, Total Score: 124.88, Ligand Score: -3.77

MDEFEMIKRNTSEIISEEELREVLKKDEKWAQAGFEPGKIHLGHYLQIKKMIDLQNAGFGTAITLADLHAYLNQKGELDEIRKIGDYNKKVFEAMG
LKAIYVYGSEFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIMQVNSLHYAGADVAVGGMEQRKIHMLARELLPKKVVCIH
PVLTLGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKILE
PIRKRLY

No. 19, Total Score: 23.55, Ligand Score: -3.93

MDEFEMIKRNTSEIISEEELREVLKKDEKAGQNGFEPGKIHLGHYLQIKKMIDLQNAGFDMAVVLDLGGAYLNQKGELDEIRKIGDYNKKVFEAM
GLKAKYVYGSEFQLDKDYTLNVYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPIESVNALHYSVDVAVGGMEQRKITMLARELLPKKVVAIH
NPVLTGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKIL
EPIRKRLA

No. 31, Total Score: -3.40, Ligand Score: -2.47

MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIVFAPSGKIHLGHYLQIKKMIDLQNAGFDIILLADLNAYMAQKGELDEIRKIGDYNKKVFEAMGL
KAKYVYGSEFQLDKDYTLNVYRLALKTTTLKRARRSNELVAPEDENPKVVHVIAATNNAHAYLGVVDVAVGGMENRKSHMLARELLPKKVVCIH
NPVLTGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKIL
EPIRKRLA

No. 32, Total Score: -1.57, Ligand Score: -3.82

MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAMAPSGKIHLGHYLQIKKMIDLQNAGFDIILLDDLGGAYLNQKGELDEIRKIGDYNKKVFEAMGL
AKYVYGSEFQLDKDYTLNVYRLALKTTTLKRARRANELAREDENPKVAQVIAPTTNVNAAHYLGVVDVAVGGMENRKAHMLARELLPKKVVCIH
NPVLTGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKIL
EPIRKRLS

No. 40, Total Score: 11.67, Ligand Score: -4.33

MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAHAPSGKIHLGHYLQIKKMIDLQNAGFDIILLGDSVAYLNQKGELDEIRKIGDYNKKVFEAMGL
AKYVYSSELNLDKDYTLNVYRLALKTTTLKRARRSAELNAREDENPKVAEVISILSVAQTHGLGVVDVAVGGMEARKAHMLARELLPKKVVCIHNP
VLTGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKILEP
IRKRLH

No. 41, Total Score: 11.55, Ligand Score: -2.98

MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAFKPSGKIHLGHYLQIKKMIDLQNAGFDIIFLGDAAAYDNQKGELDEIRKIGDYNKKVFEAMGL
AKYVYSSEINLDKDYTLNVYRLALKTTTLKRARRANELNAREDENPKVAEVIAAIKGVGQGHKAGVDVAVGGMEARKMHMLARELLPKKVVCIH
PVLTLGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKILE
PIRKRLQ

No. 43, Total Score: 66.36, Ligand Score: -5.05

MDEFEMIKRNTSEIISEEELREVLKKDEKSASIGFEPGKIHLGHYLQIKKMIDLQNAGFDIYIQLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGL
KAKYHYSSQYQLSKSTLDYRLALKTTTLKRARRSMELIAREDENPKVAEVIYPINAQAGNSGSDVAVGGMEQRKIHMLARELLPKKVVCIHNP
VLTGLDGEENFIAVDDSPPEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESFLKKNELHPMDLKNVAEELIKILEP
IRKRLY
