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| Modeled NPA sequences |
| No. 15, Total Score: 124.88, Ligand Score: -3.77 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKWAQAGFEPSGKIHLGHYLQIKKMIDLQNAGFGTAITLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAIYVYGSEFQLDKDYTLNVYRLALKTTLKRARRSMELIAREDENPKVAEVIYPIMQVNSLHYAGADVAVGGMEQRKIHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLY |
| No. 19, Total Score: 23.55, Ligand Score: -3.93 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKAGQNGFEPSGKIHLGHYLQIKKMIDLQNAGFDMAVVLDDLGAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGSEFQLDKDYTLNVYRLALKTTLKRARRSMELIAREDENPKVAEVIYPIESVNALHYSGVDVAVGGMEQRKITMLARELLPKKVVAIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLA |
| No. 31, Total Score: -3.40, Ligand Score: -2.47 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIVFAPSGKIHLGHYLQIKKMIDLQNAGFDIIILLADLNAYMAQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGSEFQLDKDYTLNVYRLALKTTLKRARRSNELVAPEDENPKVVHVIAATNNANNAHYLGVDVAVGGMENRKSHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLA |
| No. 32, Total Score: -1.57, Ligand Score: -3.82 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAMAPSGKIHLGHYLQIKKMIDLQNAGFDIIIILDDLGAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYGSEFQLDKDYTLNVYRLALKTTLKRARRANELLAREDENPKVAQVIAPTTNVNAAHYLGVDVAVGGMENRKAHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLS |
| No. 40, Total Score: 11.67, Ligand Score: -4.33 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAHAPSGKIHLGHYLQIKKMIDLQNAGFDIIIILGDSVAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYSSELNLDKDYTLNVYRLALKTTLKRARRSAELNAREDENPKVAEVISSILSVAQTHGLGVDVAVGGMEARKAHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLH |
| No. 41, Total Score: 11.55, Ligand Score: -2.98 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKSAYIAFKPSGKIHLGHYLQIKKMIDLQNAGFDIIIFLGDSAAYDNQKGELDEIRKIGDYNKKVFEAMGLKAKYVYSSEINLDKDYTLNVYRLALKTTLKRARRANELNAREDENPKVAEVIAAIKGVGQGHKAGVDVAVGGMEARKMHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLQ |
| No. 43, Total Score: 66.36, Ligand Score: -5.05 |
| MDEFEMIKRNTSEIISEEELREVLKKDEKSASIGFEPSGKIHLGHYLQIKKMIDLQNAGFDIYIQLADLHAYLNQKGELDEIRKIGDYNKKVFEAMGLKAKYHYSSQYQLSKKSTLDTYRLALKTTLKRARRSMELIAREDENPKVAEVIYPINAVDQAGNSGSDVAVGGMEQRKIHMLARELLPKKVVCIHNPVLTGLDGEGNFIAVDDSPEEIRAKIKKAYCPAGVVEGNPIMEIAKYFLEYPLTIKRPEKFGGDLTVNSYEELESLFKNKELHPMDLKNAVAEELIKILEPIRKRLY |