Alignment
Template: PDB code 3G5U (Chain A)
Target: human P-gp

Reference: Aller SG, Yu J, Ward A, Wenig Y, Chittaboina S, et al. (2009) Structure of P-glycoprotein reveals a molecular basis for poly-specific drug binding. Science 323: 1718-1722

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3G5U_A.pdb      ---------------------------------VSVLTMFRYAGWLDRLYMLVGTLAAII 27
human_P-gp      MDLEGDRNGGAKKKNFFKLNNKSEKDKKEKKPTVSVFSMFRYSNWLDKLYMVVGTLAAII 60
                                                 ***::****:.***:***:********

3G5U_A.pdb      HGVALPLMMLIFGDMTDSFASVGNVS---KNSTNMSEADKRAMFAKLEEEMTTYAYYYTG 84
human_P-gp      HGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMNLEEDMTRYAYYYSG 120
                **..******:**:*** **..**:.   .* ** *: :. .:* :***:** *****:*

3G5U_A.pdb      IGAGVLIVAYIQVSFWCLAAGRQIHKIRQKFFHAIMNQEIGWFDVHDVGELNTRLTDDVS 144
human_P-gp      IGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGELNTRLTDDVS 180
                ******:.********************::******.**********************

3G5U_A.pdb      KINEGIGDKIGMFFQAMATFFGGFIIGFTRGWKLTLVILAISPVLGLSAGIWAKILSSFT 204
human_P-gp      KINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTLVILAISPVLGLSAAVWAKILSSFT 240
                ***************:***** ***:**********************.:*********

3G5U_A.pdb      DKELHAYAKAGAVAEEVLAAIRTVIAFGGQKKELERYNNNLEEAKRLGIKKAITANISMG 264
human_P-gp      DKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKELERYNKNLEEAKRIGIKKAITANISIG 300
                **** *********************************:*******:***********:*

3G5U_A.pdb      AAFLLIYASYALAFWYGTSLVISKEYSIGQVLTVFFSVLIGAFSVGQASPNIEAFANARG 324
human_P-gp      AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASPSIEAFANARG 360
                ******************:**:* **************************.*********

3G5U_A.pdb      AAYEVFKIIDNKPSIDSFSKSGHKPDNIQGNLEFKNIHFSYPSRKEVQILKGLNLKVKSG 384
human_P-gp      AAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
                ****:************:**********:*****:*:**********:*********:**

3G5U_A.pdb      QTVALVGNSGCGKSTTVQLMQRLYDPLDGMVSIDGQDIRTINVRYLREIIGVVSQEPVLF 444
human_P-gp      QTVALVGNSGCGKSTTVQLMQRLYDPTEGMVSVDGQDIRTINVRFLREIIGVVSQEPVLF 480
                ************************** :****:***********:***************

3G5U_A.pdb      ATTIAENIRYGREDVTMDEIEKAVKEANAYDFIMKLPHQFDTLVGERGAQLSGGQKQRIA 504
human_P-gp      ATTIAENIRYGRENVTMDEIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIA 540
                *************:************************:********************

3G5U_A.pdb      IARALVRNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVIAHRLSTVRNADVIAG 564
human_P-gp      IARALVRNPKILLLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
                ******************************.******:**********************

3G5U_A.pdb      FDGGVIVEQGNHDELMREKGIYFKLVMTQT------------------------------ 594
human_P-gp      FDDGVIVEKGNHDELMKEKGIYFKLVTMQTAGNEVELENAADESKSEIDALEMSSNDSRS 660
                **.*****:*******:*********  **

3G5U_A.pdb      ---------------------------LDEDVPPASFWRILKLNSTEWPYFVVGIFCAII 627
human_P-gp      SLIRKRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTEWPYFVVGVFCAII 720
                                           ***.:**.*****:*** *********:*****

3G5U_A.pdb      NGGLQPAFSVIFSKVVGVFTNGGPPETQRQNSNLFSLLFLILGIISFITFFLQGFTFGKA 687
human_P-gp      NGGLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLLFLALGIISFITFFLQGFTFGKA 780
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3G5U_A.pdb       GEILTKRLRYMVFKSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGATGSRLAVIFQNI 747
human_P-gp       GEILTKRLRYMVFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNI 840
                 *************:********************************** ******* ***

3G5U_A.pdb       ANLGTGIIISLIYGWQLTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGSGKIATEA 807
human_P-gp       ANLGTGIIISFIYGWQLTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGAGKIATEA 900
                 **********:****************************************:*******

3G5U_A.pdb       IENFRTVVSLTREQKFETMYAQSLQIPYRNAMKKAHVFGITFSFTQAMMYFSYAACFRFG 867
human_P-gp       IENFRTVVSLTQEQKFEHMYAQSLQVPYRNSLRKAHIFGITFSFTQAMMYFSYAGCFRFG 960
                 ***********:***** *******:****:::***:*****************.*****

3G5U_A.pdb       AYLVTQQLMTFENVLLVFSAIVFGAMAVGQVSSFAPDYAKATVSASHIIRIIEKTPEIDS 927
human_P-gp       AYLVAHKLMSFEDVLLVFSAVVFGAMAVGQVSSFAPDYAKAKISAAHIIMIIEKTPLIDS 1020
                 ****:::**:**:*******:********************.:**:*** ****** ***

3G5U_A.pdb       YSTQGLKPNMLEGNVQFSGVVFNYPTRPSIPVLQGLSLEVKKGQTLALVGSSGCGKSTVV 987
human_P-gp       YSTEGLMPNTLEGNVTFGEVVFNYPTRPDIPVLQGLSLEVKKGQTLALVGSSGCGKSTVV 1080
                 ***:** ** ***** *. *********.******************************

3G5U_A.pdb       QLLERFYDPMAGSVFLDGKEIKQLNVQWLRAQLGIVSQEPILFDCSIAENIAYGDNSRVV 1047
human_P-gp       QLLERFYDPLAGKVLLDGKEIKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNSRVV 1140
                 *********:**.*:*******:********:***************************

3G5U_A.pdb       SYEEIVRAAKEANIHQFIDSLPDKYNTRVGDKGTQLSGGQKQRIAIARALVRQPHILLLD 1107
human_P-gp       SQEEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHILLLD 1200
                 * ************* **:***:**.*:*******************************

3G5U_A.pdb       EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVIQNGKVKEHGTHQQL 1167
human_P-gp       EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQL 1260
                 **********************************************:***:**********

3G5U_A.pdb       LAQKGIYFSMVSVQA----- 1182
human_P-gp       LAQKGIYFSMVSVQAGTKRQ 1280
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