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HEADER      ModPipe Model of GI 115833068                2018-01-2
TITLE       Model of Sequence 2 from patent US 7105656
SOURCE
EXPDTA      THEORETICAL MODEL, MODELLER SVN 2018/01/27 03:13:33
AUTHOR      URSULA PIEPER, BENJAMIN WEBB, EASHWAR NARAYANAN, ANDREJ SALI
REMARK 220  Original ID: MDR1_HUMAN_MUT
REMARK 220  EXPERIMENTAL DETAILS
REMARK 220  EXPERIMENT TYPE: THEORETICAL MODEL
REMARK 220  METHOD: HOMOLOGY MODELING
REMARK 220  PROGRAM: MODPIPE
REMARK 220  SEQUENCE IDENTITY:                89.00
REMARK 220  GA341 SCORE:                      1.00
REMARK 220  EVALUE:                          0
REMARK 220  MPQS:                            1.9388
REMARK 220  zDOPE SCORE:                     -0.33
REMARK 220  TSVMOD METHOD:                   NA
REMARK 220  TSVMOD RMSD:
REMARK 220  TSVMOD NO35:
REMARK 220  TEMPLATE PDB:                   5ko2
REMARK 220  TEMPLATE CHAIN:                 A
REMARK 220  TARGET LENGTH:                 1280
REMARK 220  TARGET BEGIN:                  29
REMARK 220  TARGET END:                   1276
REMARK 220  TEMPLATE BEGIN:                28
REMARK 220  TEMPLATE END:                 1272
REMARK 220  MODPIPE RUN:                   MW-hPGPmutantG185V
REMARK 220  MODPIPE MODEL ID:              444f339089431267be00029d242df5ac
REMARK 220  MODPIPE ALIGN ID:             fdb3ed07482b784b780105ef8458cc3e
REMARK 220  MODPIPE SEQUENCE ID:          60d39a16bd58385778d9588e6f45244eMDLETKRQ
REMARK      6 MODELLER OBJECTIVE FUNCTION:    7692.9263
REMARK      6 MODELLER BEST TEMPLATE % SEQ ID: 88.861
REMARK      6 GENERATED BY MODPIPE VERSION SVN.r1610
HELIX       1   1 VAL      36 TYR      42 1              7
HELIX       2   2 TRP      45 LEU      85 1             41
HELIX       3   3 ILE      98 ARG     157 1             60
HELIX       4   4 ILE     160 VAL     165 1              6
HELIX       5   5 VAL     168 ILE     186 1             19
HELIX       6   6 ASP     188 PHE     267 1             80
HELIX       7   7 LYS     272 LYS     279 1              8
HELIX       8   8 GLU     282 LEU     322 1             41
HELIX       9   9 ILE     328 ASP     370 1             43
HELIX      10  10 SER     434 MET     440 1              7
HELIX      11  11 ILE     458 THR     460 1              3
HELIX      12  12 VAL     463 ILE     469 1              7
HELIX      13  13 ILE     484 ARG     489 1              6
HELIX      14  14 MET     497 ALA     507 1             11
HELIX      15  15 TYR     510 LYS     515 1              6
HELIX      16  16 GLY     533 ARG     547 1             15
HELIX      17  17 THR     563 ARG     577 1             15
HELIX      18  18 LEU     589 ASN     594 1              6
HELIX      19  19 HIS     612 GLU     618 1              7
HELIX      20  20 ILE     621 THR     630 1             10
HELIX      21  21 PHE     697 ASN     704 1              8
HELIX      22  22 TRP     708 ARG     741 1             34
HELIX      23  23 PRO     745 ARG     798 1             54
HELIX      24  24 VAL     801 ASP     805 1              5
HELIX      25  25 THR     811 TYR     853 1             43
HELIX      26  26 TRP     855 GLU     902 1             48
HELIX      27  27 PHE     904 LEU     910 1              7
HELIX      28  28 GLU     913 ALA     965 1             53
HELIX      29  29 PHE     971 PHE     994 1             24
HELIX      30  30 TYR     998 GLU    1013 1             16
HELIX      31  31 LYS    1076 GLU    1084 1              9
HELIX      32  32 VAL    1106 HIS    1112 1              7
HELIX      33  33 ILE    1127 GLY    1134 1              8
HELIX      34  34 GLN    1142 ALA    1152 1             11
HELIX      35  35 HIS    1155 SER    1160 1              6
HELIX      36  36 GLY    1178 ARG    1192 1             15
HELIX      37  37 THR    1208 ARG    1222 1             15
HELIX      38  38 LEU    1234 ASN    1239 1              6
HELIX      39  39 HIS    1257 GLN    1263 1              7
HELIX      40  40 ILE    1266 ALA    1275 1             10
SHEET       1   1 1 LEU     392 ARG     395 0
SHEET       2   2 1 LEU     415 VAL     417 0

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[illegible]

[illegible]