

Supplemental Information

Figures legends for supplemental figures

Figure S1 Sequence alignment of Pdr5p with other fungal transporters. Pdr5p and 19 sequences from the PFamA database are aligned. The numbers above the columns are the absolute alignment positions. They are not residue numbers. The alignment begins with amino acid 149 of Pdr5p.

Figure S2 Structural-based sequence alignment of nucleotide binding domains. The NBDs of 20 structures from the Protein Databank (PDB) and the two NBDs from Pdr5p are organized in a structure-based alignment. Major sequence motifs are indicated above the columns. The ABC signature motif is designated as the C loop in this figure. The sequence names of proteins other than Pdr5p are the PDB codes.

Figure S3 Hydrophobicity profiles of Pdr5p and Sav1866. The Kyte-Doolittle scale was used on the entire alignment (left) and on Pdr5p and Sav1866 alone (right). The upper graphs are of TMD1 and the lower are of TMD2. The red circle indicates the misalignment between Pdr5p and Sav1866.

Figure S4 Hydrophobicity profiles of Pdr5p and mouse Pgp. The Kyte-Doolittle scale was used on the entire alignment (left) and on Pdr5p and Mouse Pgp alone (right). The upper graphs are of TMD1 and the lower are of TMD2.

Figure S5 Separation of the NBDs in the open conformation. The NBDs are further apart in the open conformation than in the closed conformation. The distance between residues G338 and S1039 increases from 5.9 Å to 24 Å in the open conformation.

Figure S6 The portal between helices 3 and 4. The open conformation allows access to the substrate-binding pocket of Pdr5p. Helices 3 and 4 are numbered. Measurements were made from the same pair of residues for each conformation.

Figure S7 Pdr5p as a true dimer. (A) A schematic showing the relationship of major motifs around the two ATP-binding sites. Letters in Figure S7A designate Walker A [A], Walker B [B], the C-loop [C], and the D-loop [D]. The sequences of the motifs are shown. White letters are canonical residues and black letters are aberrant residues. All aberrant residues surround ATP site 1. The aberrant arginine from the D-loop of ATP site 2 appears to interact only with ATP site 1 (see text for details). (B) A proposed true Pdr5p dimer. Two Pdr5p molecules (green and magenta) are opened into N-terminal and C-terminal halves. The N-terminal half of one monomer associates with the C-terminal half of the other. (C) A schematic depicting the events leading to a true Pdr5p dimer. After opening, one monomer rotates on top of the other so that N-terminal and C-terminal domains are associated.

Figure S8 Pdr5p TMDs in the open and closed conformations. (A) The closed conformation model based on Sav1866. The TMDs are opened to the extracellular environment. (B) The open conformation model based on mouse Pgp. The TMDs are closed to the extracellular environment. Numbers in both parts indicate the residues tested by mutagenesis (see text for details).

Figure S9 Sequence alignment of the TMDs of Pdr5p and mouse Pgp. The alignments were corrected for hydrophobicity.

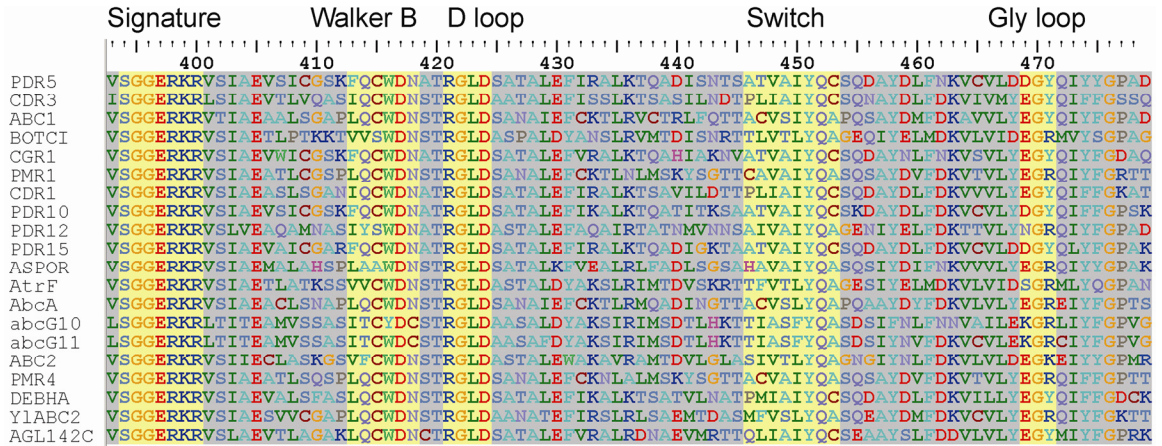
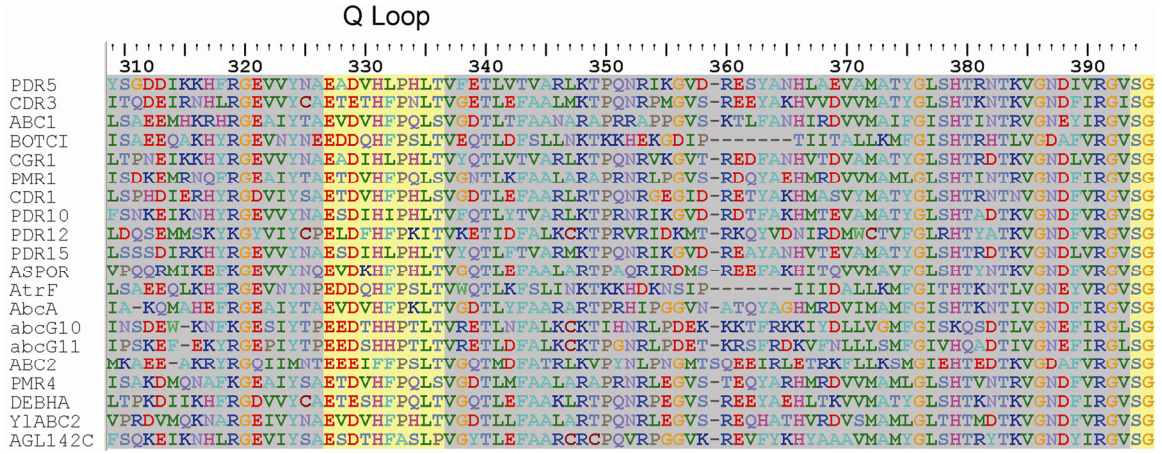
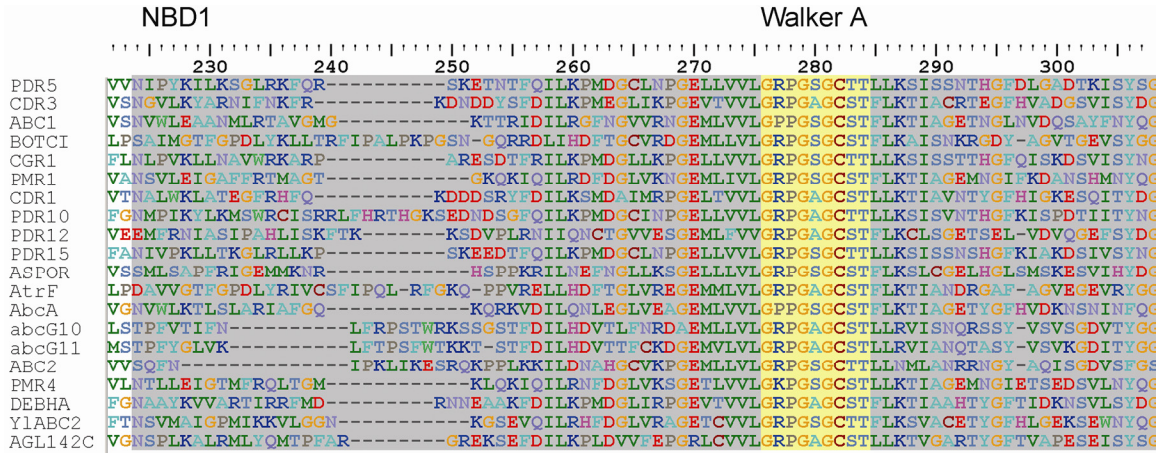
Figure S10 Sequence alignment of the TMDs of Pdr5p and Sav1866. The alignments were corrected for hydrophobicity.

Figure S11 MIC assay of TMD Mutants. Strains were tested on tritylimidazole (Trityl). WT denotes wild-type and $\Delta pdr5$ denotes the pdr5 deletion mutant.

Figure S12 Interfaces between TMDs and NBDs. (A) Sav1866p, (B) the Pdr5p open conformation model based on Sav1866p, (C) Pgp, and (D) the Pdr5p closed conformation model based on Pgp.

Supplementary Figure S1

Multiple Sequence Alignment of Pdr5



480 490 500 510 520 530 540 550 560

PDR5 KAKKVFEDMGVYCPSPQTTADFLTSVTSPSERT---LNKMDLKKGIHIPQTPKEMNDYVWKSPNYKELMKVEVDQRLLN-DEEAS---

CDR3 RAAAYFKKMGVYCPDRQTTADFLTSVTSIPAERI---INKEYLDRGKIKVQTPIDMVEYWHNSEYKQLREIIDEYLDNCEYNDQ---

ABC1 EAKQYFVNLGFCPCPAR-TTDFLTSMTADPHERI---VRPGFEGK---APRTPEEFAIAWENSABEYALQADIEYKSSHPINQPD---

BOTCI DAKKVFERIGYVCPKRTTADFLTACTDPAERR---FOKDFEGP---IPKGPVELEKAFRESEDYRLLOQEDVESYERMLHETDHAD---

CGR1 HAKVYFQRMGVCPPKRTIIPDFLTSVTSIPAERR---INKEYLDRGKIKVQTPIDMVEYWHNSEYKQLREIIDEYLDNCEYNDQ---

PMR1 EAREYFVTMGVYCPDRQTTADFLTSVTSIPAERV---VKPGFEGK---VPRTPDFEFAKGNKNSAAYKELQKEIDDYNTQYPTGGES---

CDR1 KAKYVFEDMGVYCPDRQTTADFLTSVTSIPAERE---PLPGYEDK---VPRTPDFEFAKGNKNSAAYKELQKEIDDYNTQYPTGGES---

PDR10 QAKKVFQRMGVCPEPQTTADFLTSVTSIPAERI---KDKMVKHGIIMIQTAYEMNQYWIQSEEVKQLQVQVNHKLDT-DSSQQ---

PDR12 KAVGYFQRMGWKPNRMTSAEFLTSVTVDFENRTLDIKPGYEDK---VPKSSSEFEEYWLNSEDYQELLRTYDDYQSRHFVNET---

PDR15 DAKKVFQDMGVCPPRQTTADFLTSVTSIPAERI---ISKEFIEKGTTRVPQTPKDMAEYWLQSESYKLNLIKIDIDSTLEK-NTDEA---

ASPOR DAKSYFERQGWVCPDRQTTADFLTSVTSIPAERK---ARPGMENQ---VPRTPAEDEFAAYWRKSPQYKQLMSEI SHYEQEHPLEEEEGDA---

AtrF KAREYFVNLGFCPCPKSTTADFLTSVTSIPAERK---FQPGREAS---TPKTPPEELEAVFRNSEYTKTICDEVASYEKKLQTDQED---

AbcA MAKHYFLQMGVYCPDRQTTADFLTSMTSHLERV---VQPGYEDR---VPRTPDFEFAARWKAQSPQRAQLMHIKSYNAKFFALDGEY---

abcG10 LAKQYFLDLGFCDECPKSTPDLFGVTVNPQERK---VRPGFEGR---APETSSDFEKAWKSSDLYQVMLQQOLEYEKKIELE-QPS---

abcG11 MAKQYFMSLGFCECPKSTPDLFGVTVNPQERI---IKKGFEGR---TPETSADFEAWKNSDIYRDQLOEQEYEBELIERT-QPK---

ABC2 EARPFMEMLGFCDDGANVADFLGVTVPTEPK---VRDEMCLK---FPRTAGAIRSEYEQTAVHDQATEYNY-YP---TTEBAQTK---

PMR4 EARPYFEDMGVYCPDRQTTADFLTSVTSIPAERV---IRPGFEGR---APITPDDFAEAWKSTARAKLGEIEYENYKPYKGGSS---

DEBHA QAKLYFLFMGVCPCPQTTADFLTSVTSIPAERV---VRPGYENK---VPRTPPEEFTYQWNSPERKALLGEIDDYLNKNTDNEER---

Y1ABC2 EAKQYFLDLGFCDCADRQTTADFLTSVTSIPAERI---IRPGVESR---VPRTPDDEFEKWLSEARQLLDIDEFNNEFVGGPA---

AGL142C LAKGYFLRMGWVCPDRQTTADFLTSVTSIPAERK---SQPGYEDK---VPRTPAREFYEWLRSPEHAVAMKQIQRIIAEAKTDAA---

TMD 1

570 580 590 600 610 620 630 640 650

PDR5 --REAIKEAHIKAKQSKRARPSSPYTVSMMQVKLLIRNMWRLLRNIGFTLMLIGCSMLILSMPTKIM--KKDTSTTYFRSS---

CDR3 --KQKIFEANNAKKAKHTYKSSSYTVSLPMQVRIIMKRWDRMRDIIIVPLSTVAGNIAMLILSSVFNL---QPNSSSYFRUS---

ABC1 --AEAFRKSRAAQGRGQRPNSPYTVSLTQQTKLCLWRGKRLLDPTLTVGLAANTLM LVISSIFNL---QMTSSFPQRJA---

BOTCI D-ARQFKASVEETKSKTVGPRSPYTVSFRQVLLTKREVELTLDKTYLTKTIIISNLIYGLSHHQ---SSNTLGNFRJG---

CGR1 --KEEIKEAHIKAKQSKRARPSSPYTVSMMQVKLLIRNMWRKNSASVTLQVFNAMMILSMPTKIQ--KSSADTYFRJA---

PMR1 --FQQFVESRKAQSKGQRAKSPYTVSVLBOVQICVTRGQRRLKSDYSLTISALIGNTIMLIVGSVYQL---PDDVTSFYSRJA---

CDR1 --RETYRESHVAKQSNTRPASPYTVSLPMQVRGV RNLRMKDPSIPIFSVFGQIVMLLILSSVFNL---SQTTGSFYRJA---

PDR10 --REQIKNAHIKAKQSKRARPSSPYTVSLTQVQLILIRDWRIKDPSIQLTVLSHAMLILSMPTKVM--LSTTTTTYFRJA---

PDR12 --RDRLDVAKHQRQQGQRENSQVFNWLTQVLCMIRGQRKDDSTTKV LSSLIKLIIISMFKIDDKSQSTAGYSRJA---

PDR15 --RNIIIRDAAHKAQAKRAPPSSPYVNVNMMQVKLLIRNMWRMKSASVTLWQVIGNSVMAMILSMPTKVM--KKDTSTTYFRJA---

ASPOR DALATFQOKKREIQAKHTRPQSPYLLSVMQIKLNMKRNQRVWADISSTVSTVISQIIMLIISSVYGT---PD TAGFTAKJA---

AtrF D-TRRFQKTVAQSKSRIVSKSSYTVSFRQVLCVQREWLLW-DKTSLYTKFIIISNLIYSSLYGT---SLDTSGNFRJG---

AbcA --LDKFKQSRRAQQAQQRVSSPYTVSLVQOVKLCWRGQRKLDPSVTISSLFNTIISLIVISIFYNL---KDTSTFPQRJA---

abcG10 S-TN-FIEQIRNENSKTNPKSIYTTSTHTQVRLI RNSQIIWDRRLISKISIIIVQTVIASLFTNM---KSDVTLNFRJG---

abcG11 K-VA-FVQVRRVANSKTNFKKSQYTTSTVTVQVILKRNKLVLDKQMSKLSVLIQSVIASLFTNM---DDDTGLNFRJG---

ABC2 K-TKLFQEGIAHEKDKGLPASSSPYTVSHTQVTRCIRKQGIIVDKTTFIKQSTIVQLIAGSLYNA---PDTTGLNFRJG---

PMR4 --YDAFVDARRAAQAKSQRVKSYPYTVSVRQKISLCVTRGQRRLDYSLTATLIGNFIMSLIVGSVFNL---PDTSSTFYRJA---

DEBHA --LQQFKDANHTKQSNHLRASPYPYTVSMMQVKLLIRNMRTKDPSTITIGVFNIVMLIISIFYNL---EDTGSFYRJA---

Y1ABC2 --LDNFMGLRKDAQAKHTRVQSPYTVSFMQTRLCWRGLRIKDMSTDIITVFNIVMLVLSMPTNM---PQTTESFYRJA---

AGL142C --REQLRDHHIVRQARHVKSSPYTVSFMQRIIVDRNWQRRLDPSVLSIVATSIMLILSCLLNL---KPDNTSLNFRJG---

660 670 680 690 700 710 720 730

PDR5 AMPTAILNAPSSSLEIFSLERPITEKHRTYSLHPSDAPASVLSSEIPSKLII VCPNIIFFFLVD RRNGGVPTFFLLINIVIA---

CDR3 VMTYALLNAPSSSLEIFSLERIVOKHREKALPPMDIIGSIIISDPLKVVCSVLPNLILFMVFKREPGAEFFLLISCS---

ABC1 LLFPACLLNGPLAALBILILAQREIVEKHDRALHPSERVSMCLDMPKVENIVPNLVTMAMLRREPGAEFFLLISGAT---

BOTCI TLEFSILLGWLGSLMLKVGCRBEIISRHKDAFRPSVVV RVVQDPLLLLQVPPSIVVFTITGLDQKRIIVLVIILT---

CGR1 AMPTAILNAPSSSLEIFSLERPITEKHRTYSLHPSDAPASVLSSEIPPKIVTILFNIIFFFLVNRDAGRFFFLINIVIA---

PMR1 LLFPVLLNAPSSSLEIFSLERPIVEKHKKALRPSHPPEEISSMCLDMPKILNITFNVTLTMTGLRQAGAEFFMLFSVIT---

CDR1 AMPTAVLNAPSSSLEIMSLERPIVEKHKKALRPSDELASIISELVVKLMSMSPNFTVMVFRRRRPPGAEFFVLMCIWC---

PDR10 AMPTAILNAPSSSLEIFSLERPIVEKHKKALRPSDAPASVLSSEIPPKLATVTPNIPYFLNLRKRDGAEFFLLIINIIT---

PDR12 MLPTVLLNAPSSSLEIFSLERIGNSSSREPIVVKHKSISMHLSESLQEIIEPTKVIVILCLITWIPMKEGAEFFILLLTV---

PDR15 AMPTAILNAPSSSLEIFSLERPIVEKHKKALRPSDAPASVLSSEIPPKLATVCPNIIFFFLVD RRNGGVPTFFLLINIVIA---

ASPOR TLEFPVLLMALIMGEINSLSQRPIVEKHNSTAFHPATEIACVVS DIPVKVI VVFNLILFLALGHRSAQFFLLLVTVIV---

AtrF ALFPYSILLGWLGLELMPVTRIVRHKEAFTRPSVSI RVMVDPAIFCMVVPPTIIMFTMLGDLVASKFIPLFLVYTT---

AbcA LLFPVLLMALCELEMLTLAQRPIIEKHSRHALHPSERFSSMIMDLPKILNITSNIVLTMTMLRREPGAEFFVPTSIL---

abcG10 RIYAAILNAPVSAEELGLTYRRILQKHSAMRPSLHI MVITDIPLTAIQVTIISVIVFTMGLQVDAKFTIILPTIPGS---

abcG11 AILSVIAPNALSISEMMPYRRVLOKHKKALRPSLHI QVVTDIPLTAIQVLSIIATFMGLQVDAKFTIICITLLGA---

ABC2 SCTLNLLNALSISEMMPYRRVLIKHKSNRHPAFCIQAIDIPVILVQVLSLILFTMVLMTSAGHPTWIIIVAT---

PMR4 LLFPVLLMALCELEMLTLAQRPIVEKHKRAPHHPAEALSMCLDVPKIANSFTNIPLFTMTHLRREGGPFTTWIPLVLT---

DEBHA AMPTAVLNAPSSSLEIFSLERPIVEKHKKALRPSDAPASIIITELPKITCLAFNLVFMVFRRRRAGNFFFLVNVTA---

Y1ABC2 LLFPAILNAPASILEILSLERPIVDKQRNAMHPADLAIITTFPTKTLIVSVLTIPTMNLRRREVPPTIPLVSLLC---

AGL142C ALPTVLLNAPSSSLEIMSLERIVKHKSNRHPAFCIQAIDIPVILVQVLSLILFTMVLMTSAGHPTWIIIVAT---

740 750 760 770 780 790 800 810 82

PDR5 INIV VFMMSHL RCVSLTKTLE M VPSM LLL LSM TGF IPKKILR--WSKWIW INPLAYL ESLLINE HGIK PC -
CDR3 IS CSTL MSHL RTIGATNSL E MTPSSLLLT LSTSGE IPVT MLE---WCKWIRWVNPVAYE LISNE HGRVDCS-
ABC1 ISFIVL MSMM RTI SMSRSLSQ M VPM A I L I L I I T G F V I P L D M L P---WCRWLW NIDILAYS ESLLINE HGRQRTCT-
BOTCI F I L T T I C I T S L R M F A L S P S I D D V R T S G I L N L L I I T G F V I P K P Q L V S E I W G W L Y I N P L S Y S E A G I S D E F N K I T C A P
CGR1 INVI VFMSHL RCVSLTKTLE M VPSM LLL LSM TGF IPRTKMLG---WSKWIW INPLAYL ESLMVNE HDRRIPC-
PMR1 FSI VFTLMSMI RTI SVSRTLSQLVPA I L I L L V I T G F T I P T R M L G---WSRWMN IDP VAYE S E T L I V N E H G R I P P C I P
CDR1 MCIWCTVMSHL RSI S V S T S I S M T P A T V L L L M V I T G F V I P T P S M L G---WSRWMN IDP VAYE S E T L I V N E H G R I P P C I P
PDR10 INIIVVFMSHL RCI S V S K T L P Q M V P S V L L L A F A M T G F I P R V O M L G---WSKWIW S I M P L S Y L E S L M I N E H G R I P P C I P
PDR12 F L L I V Q Q C T S F I K V A T M S K S V D A H V S G L V M L C V I A G F V L P I Q E M H H---W I R W L H I N P L T Y A S E S L V S T E H H R E M L C S -
PDR15 INVI VFTLHL RCVSLTKTLE M VPSM LLL LSM TGF IPRTKMLG---WSIWIW INPLAYL ESLMINE HDRRIPC-
ASPOR V T I V M V M S V R T M A I T Q T V S Q M L A G I L I L L I V T G F V L P V P S M H P---W E W I H I L N P I Y A E M L I A N E H G R D I C S -
AtrF F V I T T F S I T S L R M P A A L S P T I D D V R S E I L N I L V I V S V I P K Q L I D G S I W G W L F V N P I A Y S E A V L T N E S D R I M D C P
AbcA F S I L L T L M S M F R S M S L S R S L V Q L P S A V L L L L S M T G F I P T G M L G---W R W I A I N P I S Y S E S L M I N E H N R D P C M -
abcG10 T I F S T L S M V A T R L N L S P S L V S Q N I L N V I L M T Y G G Y S I P K N K M H P---W S W Y W I N P S P K A L M A N E R G D M N T C D
abcG11 I L L P A S L C T A L R C F G Y L C P S M I A Q N I S N V I I M L T T S G T T I P I P K M H P---W P S W R H I N I T Y A K A L M A N E E G L D N C K -
ABC2 I V V A T T C M T A L R A I S A R P S T D S A S K V S E L I I S A T I M Y H G M I Q K P R M H P---W V W L W I D P M A Y S D A I L S N E H K I I P C V G
PMR4 F S V L T T F M S M I R T I S A S R S L S Q L V P A V L I L M V I T G F V I P T R M L G---WSRWMN IDP VAYE S E T L I V N E H G R I P P C I P
DEBHA V N F T L M S M L R T I G S S T K S L S Q M T P A S I L L L L T I T G F V I P T P K M L G---W C R W I N I L D P I G A Y E A L I V N E H G R D E C S -
Y1ABC2 F S L L C T M M S M I R T I G S V T K T L E Q L P A S I I I L V I T G F S L P I S M H G---W R W I N W L N P V A Y E A V M V N E R N R E I C S -
AGL142C V S L T A T V M S H L R S V S A C K T L V M P A S L L L L L A V V G F V I P Q K M I L G---W S R W L F L N P I R I M E M V A N E D O R I E C S -

820 830 840 850 860 870 880 890 900

PDR5 --E VPRFP--AY---ANISSTEVCIVVGI--VPG---QD VLDD IRGTQYTHKDKWRSGI MA VVFFTV LILCEIN
CDR3 --NIVPSG--GY---P-KTGNVVC SIGI--LPG---E KVDGLYKLAN DSYSNVWRIFGLMA IILFGTTI FVQTN
ABC1 --E VPR FEPG--GDLSGTRVCG VGS-VAG---QP VSGED LYSSTR ESANKWRIFGILIA MIF CSRWLPRPMC
BOTCI PDQIVPSG---GVTNPEQVC STGA-EVG---SLVSG RLEQSFNRSRHLWRIFGIVL IIVT IATEVA
CGR1 --T IPRG--AY---NDVTGTERVC SVGA-RPG---ND VLDD FLKESD EHKHKWRSGV MA VVFFTV LILCEIN
PMR1 PESTIPAGD--SY---ADVRFN KICS KGA-VAG---QNVVSE IYTT SFQSN SHRWR MCMIG MVT MVT LVGTEI
CDR1 --Q VPSGP--GY---ENISRSNQCVC VGS-VPG---NEMVSGTNYL GAYQYNSHKWRIFGIVL IILFTEIN
PDR10 --Q I P S G P--N Y---V N T G E D V T C S L G S--I P G---N N V S G D D I Q T N Y S R H K K W R S V G I L A I I P L L I L F C E I N
PDR12 --L V P S G P--G Y---E G I S I A N Q V C D A G I--V K G---N L V S G D S I L H Q Y H F A Y K H W R W G V I V W T F G I V P V I L S E L
PDR15 --Q I P A G P--A Y---Q N I T G T Q R V C S V G A--Y P G---N D V L G D D F L K E S D E H K K W R S G I M A V V F F T V L I L C E I N
ASPOR --Q I P A--Y---P N L S E N S V C S S A G--K A G---Q R I S G D D I Q V N I Q T Y S G H V W R I F G I L I A L V G M M I T I A T E L N
AtrF P S Q L V P Q G P---G V D P R T Q E C L P G S--E L E---R R V S G S R L E E S F O T R S H L W R I F G V V I A T V L L I V T V L M E L
AbcA --D V P S G--P G Y---T D V L N I R V C S T V R S--V P G---Q A I V N G N A T I E S A Y S T A S H K W R I G V I P A M L L G A V I V A T D I
abcG10 D O T I P N G N Y I S N G S T M S Q D Q R C P S A G I--I E Q M V N G E F V A G S N Y I D A L D K S D D R T L V I I T L W W I F V I I M I A L E L
abcG11 --E S I P Y G P A Y Q G--S E D A T R I C L P L G G I--E Q---G S L T K G D T M D K T L S P A T E M S Q N V I I V C W V T V V C M M A M E I
ABC2 G P N I V P S G P---G P T D S G Q A C K V G S V P S---Q T V D D L L L--S L S Y S H S V W R N S G I W W W A V L V I T I F T T K W
PMR4 A-NIVPSG--AY---D S T S M E R I C S T V G A--Q S G---S T D V S G T L V L E E S T G M T K H L W R I F G I L I A L L V M S T I L A T E I
DEBHA --Q V P S G P--G Y---P T S G D S I I C S V G S--V A G---R D V T G D Y I N E Q T V T W S H R W R I W G I V A V V P F L V V H I M I C E I N
Y1ABC2 --M V P S G G--A Y---E N V S L D R S C L V G I--E P G---L R V N E D I P I N Q S Y E T Y N H L W R M C I L G I I P F G A L P A V E I
AGL142C --R M V P D S--F Y---E G F P I S I K V C L S V G I--V P G---Q S V M G T R I E T A Y S N T K K W M I W G I V L A Y A F F L A V L I L I E I N

910 920 930 940 950 960 970 980 990

PDR5 EG KQKGEILVFRSIVKRMKRGVLT EK--NAN---DPENVGER--SDLSSDRKMLQESSEESD-----TYG-
CDR3 KSSISKGETLVFRRKNIRKMRKM--EE---DEEAYMDGMAPLDFSGSTEISDYSYDYM-----
ABC1 ERKRSKGEVLFRRGQRPAAIKDAKT-----DPEAGPPKVGGA VVAANMT--GENAG-----
BOTCI DPTGGGGALEFKRSKAAK-NKVKAE NAT-----PDEENS PASTSPVPTSGASSNTLEPPQE-----
CGR1 EG KQKGEMLVFRSIVKRMKKEGKIRDK---TKMHTDKNDIENNS EITSNATNEKNMLQDTYDENAD-----SESI
PMR1 SE KSKGEVLLFRRGYAPKNSGNSDG-----DVEQTHGVSSAEKKD GAGSGGEQESA-----
CDR1 KG MOKGEIVLFLKGLSKLKKHKRKTAA SNKG---DIEAGPVAGKLDYQDEAEAVNNEKFTTEKG-----
PDR10 EG KQNGEMLVFRSIVKRMKKGIVSEK KKKNOPTLSTDAEKDVE MNNNSSATDSRFLRDSDAAIMGNDKTVAK EHYSSPSSAS
PDR12 KPVEGGGDL LLYKRGHMP ELGTEN-----ADARTASREEMMEALNGPNVDLEK-----
PDR15 EG KQKGEMLVFRSIVKRIKQLKKEGKLEK---HRP---GDIENNAGSSPD SATTEKKILDD S--SEGSD-----SSSD
ASPOR SSTSTAEVLVFRRGHEPAYLRDTSKK-----PDAESA VELSAMKPTTESGEGDMS-----
AtrF SFVGGGGALVFRKSKRAK-KLATQT TQ---NDEEKVDVG---DKAALSRGEAM SASNGE-----
AbcA TEKKPKGEILVFRGHKALKKGSDE-----DLEGGG---GRSATVEKIG--SDGLA-----
abcG10 DWTSGGMPHKVYKRGKAPKIN-----DDEERQON-----AMVENATSK-----
abcG11 DHTSGGYTHKVYKKGKAPKMN-----DVEEEKQON-----AIVAKATS N-----
ABC2 KLSSENGPSLLIPREQSKLVNAVROVDEEG-----QVSSESGHVSEKD-DATVNAQSDNNSTDDTA-----
PMR4 SEKRSKGEVLLFRRGYQPAHAAG-EG-----DLEKSSQPSAVAKTDES---TPSTT-----
DEBHA KG MOKGEILLFRKALKKRRR---RN-----DIESGNIEKISP DYNNDNVTDNEMES-----
Y1ABC2 QG KSKGEVLFVRKEHIKKORKEKNG-----DIESGVTMAGEKGTQESSES--SNTSI-----
AGL142C KSMOKGEMAVLFRSTLKKIKKQNKKAIN-----CDIEFGNAPKESSTIGSDQRELIQR-----

NBD2 Walker A

	1000	1010	1020	1030	1040	1050	1060	1070
PDR5	-----	EIGLSKSEALFHWRLNLC	EVQIKAEFRRILNNDV	GWVKPGTTLTALMGASGAGKTTLLDCLAE	RVTMGVIT-GDILVN			
CDR3	-----	R-----	KLLDTSNIFHWRNLTV	VVKIKSEERVILNNDV	GWVKPGEVTALMGASGAGKTTLLNALS	ERLTTGVITSGTRMVN		
ABC1	-----	FIQRQTSTFGWRDVC	EVQIKKETRRILDHVD	GWVKPGTTLTALMGVSGAGKTTLLDCLAD	RSMGVIT-GEMLVD			
BOTCI	-----	ALKDITGSESVFTWENVE	YVPIVGGERRILNNGV	NGYKPGIMVVALMGASGAGKTTLLNLTLS	QRQKTGVVT-GDMLVD			
CGR1	-----	ITSGSRGGSPQVGLSKSEALF	HWQNLCDVPIKTEVRRILNNDV	GWVKPGTTLTALMGASGAGKTTLLDCLAE	RTTMGVIT-GDMVNV			
PMR1	-----	AIQRQTSIFQWODVC	DVHIKNEERRILDHVD	GWVKPGTCTALMGVSGAGKTTLLDVLAT	RVTMGVVS-GEMLVD			
CDR1	-----	STGSDVFPENREIFFWRDLTY	QVKIKKEDRVILDHVD	GWVKPGQITALMGASGAGKTTLLNCL	SERVTTGIITDGERLVN			
PDR10	-----	SQSNFSFSKSDDELSKSQALF	HWKNLCDIPIKNGKRRILNNDV	GWVKPGTTLTALIGASGAGKTTLLDCLAE	RTTMGLIT-GDVAVD			
PDR12	-----	VIAEKDVFTWNHLDY	TIPYDGA	TRKLLSDVFGYVVKPKMTALMGESGAGKTTLLNVL	AQRINMGVIT-GDMLVN			
PDR15	-----	DNAG-----	LGLSKSEALFHWRLNLC	DVPIKGGORRILNNDV	GWVKPGTTLTALMGASGAGKTTLLDCLAE	RVTMGVIT-GNIIVD		
ASPOR	-----	IIPPKDIFFTWRDVC	DIETKGEPRRILDHVS	GWVKPGTTLTALMGVSGAGKTTLLDVL	AHRTSMGVIT-GDMVNV			
AtrF	-----	SFKRISSSDRIFTWSNVE	YVPIVNGTRKLLNNGV	NGYAKPGVMIALMGASGAGKTTLLNLT	LAQRQKMGVVT-GDFLVD			
AbcA	-----	MIERQTALFQWKDVC	DIKIKKENCRILDHVD	GWVKPGILTALMGVSGAGKTTLLDVLAT	RTTMGLIIS-GEMLVD			
abcG10	-----	MKDILKMRSCFTWNH	IHYTVQLNGKDLLLNDV	EGWIKPGQMTALMGSSGAGKTTLLDVL	AKRKTMGVVT-GKCLLN			
abcG11	-----	MKDILHMDGGIFTWQ	NIYRVKVGGERLLLDNIE	GWIKPGQMTALMGSSGAGKTTLLDVL	AKRKTMGVVE-GDSHLN			
ABC2	-----	AQGNLIRNSSVFTW	NLCYVTKIPSGDRLLDNV	QGWVKPGNLTALMGSSGAGKTTLLDVL	AQRKTBE	GIR-GSIQVD		
PMR4	-----	AIQRQTALFQWEDVC	DIKIKGEPRRILDHVS	GWVKPGTCTALMGVSGAGKTTLLDVL	ATRTTMGVVT-GQMLVD			
DEBHA	-----	KLPSAGDIFHWRELTY	QVKIKSEERVILNNDV	GWVKPGQVTALMGASGAGKTTLLNALS	DRLTS	GVITSGTRMVN		
Y1ABC2	-----	LQAQRGLYQWKDVC	DIKVKDEERRILNNDV	GWVKPGTTLTALMGASGAGKTTLLDVL	ADRKSTGVVT-GEMLVN			
AGL142C	-----	IGSDSIFHWRLNLC	DIQIKNETRRILNNDV	GWVKPGTTLTALMGYSGAGKTTLLDVL	ANRVRVGVVT-GNIIVD			

Q Loop Signature

	1080	1090	1100	1110	1120	1130	1140	1150	1160	
PDR5	GIPRDKS	FRSISGYC	QQDLHLK	TATVRES	SLRFSAYLRQPA	EVSI	EEKRYVEEVI	KILEMEKYA	DAVVGV--AGEGLNVEQRKRLT	
CDR3	GGELDSS	QRSISGYV	QQDLHLE	TSTVRE	ALKSARLRQPN	SVSIAEK	DYVEKI	IDLLEMRT	VDAIVGV--PGEGLNVEQRKRLT	
ABC1	GHQRDAS	FQRKTYGYV	QQDLHLQ	TTVRE	ALNFSALLRQPA	HVPRAEK	LAVDEVIR	LLDMQEYA	DAVVGV--PGEGLNVEQRKRLT	
BOTCI	GRPLGTAF	QRGTGFC	QMDLH	DTTIRE	ALELSAILRQ	HEVT	RAEKI	EYVDKI	IDLLELQDMQDALVR-----SLSVQRKRV	
CGR1	GRPRDTS	FRSISGYC	QQDLHLK	TATVRES	SLRFSAYLRQ	PSSVSI	EEKRYVE	AVIKILEM	ETYA	DAVVGV--PGEGLNVEQRKRLT
PMR1	GRPRDQS	FQRKTYGYV	QQDLHLH	TTVRE	ALRFSAILRQ	PRHVS	HOEKLD	YVEEVI	KLGMETHYA	DAVVGV--PGEGLNVEQRKRLT
CDR1	GHALDSS	FQRSISGYV	QQDVHLPT	STVRE	ALQFSAYLRQ	SNKIS	KEKDDY	VDYVID	DLLEMTDYA	DAIVGV--AGEGLNVEQRKRLT
PDR10	GRPRDQS	FRSISGYC	QQDLHLK	TATVRES	SLRFSAYLRQ	DDVSI	EEKDKY	VEEVI	EVLEMKLYA	DAIVGV--PGEGLNVEQRKRLT
PDR12	AKPLPAS	FNRS	CGYVAQAD	NEMAE	ELSVRES	LRFAAEL	RQSSVPLE	EKRYVEKI	IITLQMONYA	EALVGK--TCRGLNVEQRKRLT
PDR15	GRRLDES	FRSISGYC	QQDLHLK	TATVRES	SLRFSAYLRQ	PSSVSI	EEKRYVEEVI	KILEM	QOYSDAVGV--AGEGLNVEQRKRLT	
ASPOR	GRGLDQS	FQRSTGYV	QQDLHLE	TATVRES	SLRFSALLRQ	PNVSI	QEKDYVED	VRMLK	MEDEPA	EAIVGV--PGQGLNVEQRKRLT
AtrF	GRPLGAD	FQRGTGFC	QMDLH	DNSTIRE	ALEFTSALLRQ	DRNVSK	QEKLDY	VQIIDL	LELNDIQDAIIG-----SLNVEQRKRV	
AbcA	QQRDES	FQRKTYGA	QQDLHLH	TATVRE	ALEFTSALLRQ	SAHV	PROEKIDY	VEVI	KLLDMTEYA	DAIVGV--PGEGLNVEQRKRLT
abcG10	GKELNID	ERITGYVE	QMDVHNP	GLTVRE	ALRFSAKLRQ	EPVSL	ESLQDKRYVE	QVLEMMEM	KHLGDALIG	SLTGTGISVEERKRLT
abcG11	GRELEID	ERITGYVE	QMDVHNP	GLTVRE	ALRFSAKLRQ	EPVSL	ESLQDKRYVE	QVLEMMEM	KHLGDALIG	SLTGTGISVEERKRLT
ABC2	GRPLFVS	QRSAGY	CEQLD	VEATATVRE	ALEFTSALLRQ	PRDT	PREEK	LAVNTI	IDLLELHDA	DTLIGE--VGAGLSVEQRKRV
PMR4	GNPTDQS	FQRSTGYV	QQDLHLH	TSTVRE	ALRFSAYLRQ	PATV	SRQEKI	AYADEVI	KLLGMEAYA	DAIVGV--PGEGLNVEQRKRLM
DEBHA	GHELDAS	FQRSISGYV	QQDLHLQ	TSTVRE	ALRFSAYLRQ	PSV	PKSEK	DYVDYI	IRLLEMEKYA	DAVVGV--SGEGLNVEQRKRLT
Y1ABC2	GEHRDGS	FQRKTYGYV	QQDLHAT	TATVRES	LEFTSALLRQ	PSSI	PESEK	LAVDEVIR	ILEMETYA	DAVVGV--PGEGLNVEQRKRLT
AGL142C	GHLRDT	SFQRKTYGYC	QQDLHG	RTQTVR	DALKFSAYLRQ	POSISRAEK	NAYVEDI	IKLLGMEAYA	DAVVGV--TGEGLNVEQRKRLT	

Walker B D loop Switch Gly loop

	1170	1180	1190	1200	1210	1220	1230	1240	1250			
PDR5	IGVELTAK	PKLLVFLDE	PTSGLD	SQTAW	SICQLMK	KLANHGQA	ILCTIHQPSA	ILMQE	EDRLLFM	QRGGKTVYFGDL	EGGCKTMIDY	
CDR3	I AVELVARE	KLLVFLDE	PTSGLD	SQTAW	SICLIR	KLANHGQA	ILCTIHQPSA	ILLEE	EDRLLLLQ	KG-ETVYF	GEFGANCHTLLEY	
ABC1	IGVELAAK	PPLLVFLDE	PTSGLD	SQTAW	ILDLE	KLTKSQA	ILCTIHQPSA	MLFQ	REDRLLFL	AKGGKTVYFGD	IENSKIMIDY	
BOTCI	IGVELAAK	PNLLVFLDE	PTSGLD	SQSAYS	IVRFL	KMLSAAGQA	IVWSIHQPS	SVLIQ	QEDMILA	LNPGGNTSYFG	FPVGENGSAVVKY	
CGR1	IGVELAAK	PKLLVFLDE	PTSGLD	SQTAW	ATCQLMK	KLANHGQA	ILCTIHQPSA	MLMQE	EDRLLFL	LQKGGQTVYFGD	LKGGCKTMIKY	
PMR1	IGVELAAK	POLLVFLDE	PTSGLD	SQTSW	SILDID	LTKEGQA	ILCTIHQPSA	MLFQ	REDRLLFL	LAKGGRTVYFGEI	GEHSSTLSNY	
CDR1	IGVELVA	KPKLLVFLDE	PTSGLD	SQTAW	SICL	MRKLADHGQA	ILCTIHQPSA	LIMQ	EDRLLFL	LQKGGRTAYFGEI	GENCQTMINY	
PDR10	IGVELAAK	PKLLVFLDE	PTSGLD	SQTAW	STCQLMK	KLADSRQA	ILCTIHQPSA	ILMQE	EDRLLFL	LQEGGQTVYFGD	LKGGCKTMINY	
PDR12	IGVELVA	KPSLLVFLDE	PTSGLD	SQSAYS	IVQFMR	LADSSQA	ILCTIHQPSA	TLQ	QEDRLLLL	LKGGKMYYFGD	IGPNSBTLKY	
PDR15	IGVELAAK	PKLLVFLDE	PTSGLD	SQTAW	DTCQLMK	KLADHGQA	ILCTIHQPSA	ILMQE	EDRLLFL	LQKGGQTVYFGD	LEGGCKTMIDY	
ASPOR	IGVELAAK	PKLLVFLDE	PTSGLD	SQSSWA	ICAP	LRRLADSGQA	VLCTIHQPSA	ILFQQ	FDQLLFL	LARGGKTVYFGPI	QNSNTLLNY	
AtrF	IGVELAAK	PSLLVFLDE	PTSGLD	SQA	AFSIVRFL	KLKLSLGA	ILCTIHQPS	SMLIQ	QEDMILA	LNPGGNTFYFGP	VHGGDGVIKY	
AbcA	IGVELAAK	POLLVFLDE	PTSGLD	SQTSW	AILD	LLDKLKN	GQA	ILCTIHQPSA	MLFQ	REDRLLFL	LQAGGRTVYFGEI	IQNSQILIDY
abcG10	IGIELVAK	PHI-LFL	DEPTSGLD	SQSSYN	IVKIR	KLADAG	MPLVCTIHQPS	SVLE	YEDRILL	LAKGGKTVYFGD	IEKSKTLTSY	
abcG11	IGVELVAK	PQI-LFL	DEPTSGLD	SQSSYN	IKIR	KLADAG	MPLVCTIHQPS	SVLE	YEDRILL	LAKGGKTVYFGD	IEKSKTLTSY	
ABC2	IGVELVSK	PSILIFL	DEPTSGLD	SQSA	YHTVRFL	RKLAAV	GQAVL	VTIHQPSA	QLFQ	EDTLLLL	LAKGGKTVYFGEI	GDQAKVVKEY
PMR4	IGVELAAK	POLLVFLDE	PTSGLD	SQTSW	SILDIE	LTKEGQA	ILCTIHQPSA	MLFQ	REDRLLFL	LARGGRTIYFGEI	GENSSTLSNY	
DEBHA	IGVELVA	KPKLLVFLDE	PTSGLD	SQTAW	SICLIR	KLADHGQA	ILCTIHQPSA	ILLQ	EDRLLFL	LQGGKTVYFGD	LGDNQOTLIDY	
Y1ABC2	IGVELAAK	PPELLVFLDE	PTSGLD	SQTAW	SIVKLL	KLKLANHGQA	ILCTIHQPSA	ILFQ	EDRLLFL	LASGGRTVYFGD	IQSSILLEY	
AGL142C	IGVELVAK	PPELLVFLDE	PTSGLD	SQTAW	SICQLIK	KLNVHGQA	ILCTIHQPSA	ILMQE	EDRLLLL	SNGGRTVYFGPI	LEGGCKTMIQY	

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CDR3 ASKCPQHANPAEWMLEVVGAAPGTQA--NQDYEVWRNSSEYRAVQNEHLHREEMPGLAS-----GEKEPDTNQATAASFWKC
ABC1 GFPCPDHANPAEWMLEVVGAAPGTTS--DIDWHQAWRESPECADVHAELEDRLKEQVNTPT-----PPTEDKASVRETAAPFHQC
BOTCI V-QCPPLKNVAEFILETAAKGGKRRDGGKINWNEEWNLSNENKTVMQEIVRIKSEROKIA-----APEASSQREKOSFVTLQ
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PDR10 AHKCPDANPAEWMLEVVGAAPGTHA--SQDYFAIWRDSEYREMQKELDWMERELPKRT-----EGSSNEEQKEPATSTLVC
PDR12 GMKCGVSENPAEVILNCIGAGATASV--NSDWHDLWLASPECAARAEEVEELHRTLPGRA-----VNDDEPLATRTAASVMPFC
PDR15 AHKCPDANPAEWMLEVVGAAPGSHA--TQDYEVWRNSSEYRAVQNEHLHREEMKELNLPGRS-----KEPTAEHEKHPAASLVC
ASPOR ARKADDEANPAEWMLEIVNAGTNSSE--ENWFDVWRNSSEYRAVQNEHLHREEMKELNLPGRS-----DKNDESWSKSEFAMPFWVC
AtrF V-VCPFSKNVAEFILETAAKATTTKDGKKIDWNEEWRNSSEYRAVQNEHLHREEMKELNLPGRS-----VTETGSPYEFANSTMPFC
AbcA APPCPDANPAEWMLEVVGAAPGSHS--SINWFEWRNSSEYRAVQNEHLHREEMKELNLPGRS-----FRTTSSGQKREKDSYREFAAPPWVC
abcG10 VRSCTESENPAEVILEAIGAGTNPQV--STIDWPEVWRNSSEYRAVQNEHLHREEMKELNLPGRS-----DQDHGPPREPATSIWVC
abcG11 VRPCTESENPAEYILEATGAGVHGKS--DVNWPEAWKQSPRELADISRELAALKKEGGAQQYKP-----RSDGPAREWSSQSTWVC
ABC2 A-A-CPTENPAEHEMIDVVSQ--QLSQGK--DWDVWLASPEYANMTTELDRIDEAASKP-----PGTVDDGNEPATTLWVC
PMR4 AHHLTPGENPAEWMLEVVGAAPGTHS--DIDWPKVWRNSSEYRAVQNEHLHREEMKELNLPGRS-----AAVDHPPEPATSIWVC
DEBHA APKCPDANPAEWMLEVVGAAPGSHA--SQDYFDVWINSSEYRAVQNEHLHREEMKELNLPGRS-----KDDSPESMKTFAAPPWVC
Y1ABC2 ADPCPKANPAEWMLEVVGAAPGSHA--KRDWPEVWVAESPERAEKRELEDEMARTVERVQTN--TTERDSTGYSDSDQVAVGWVVC
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TMD2

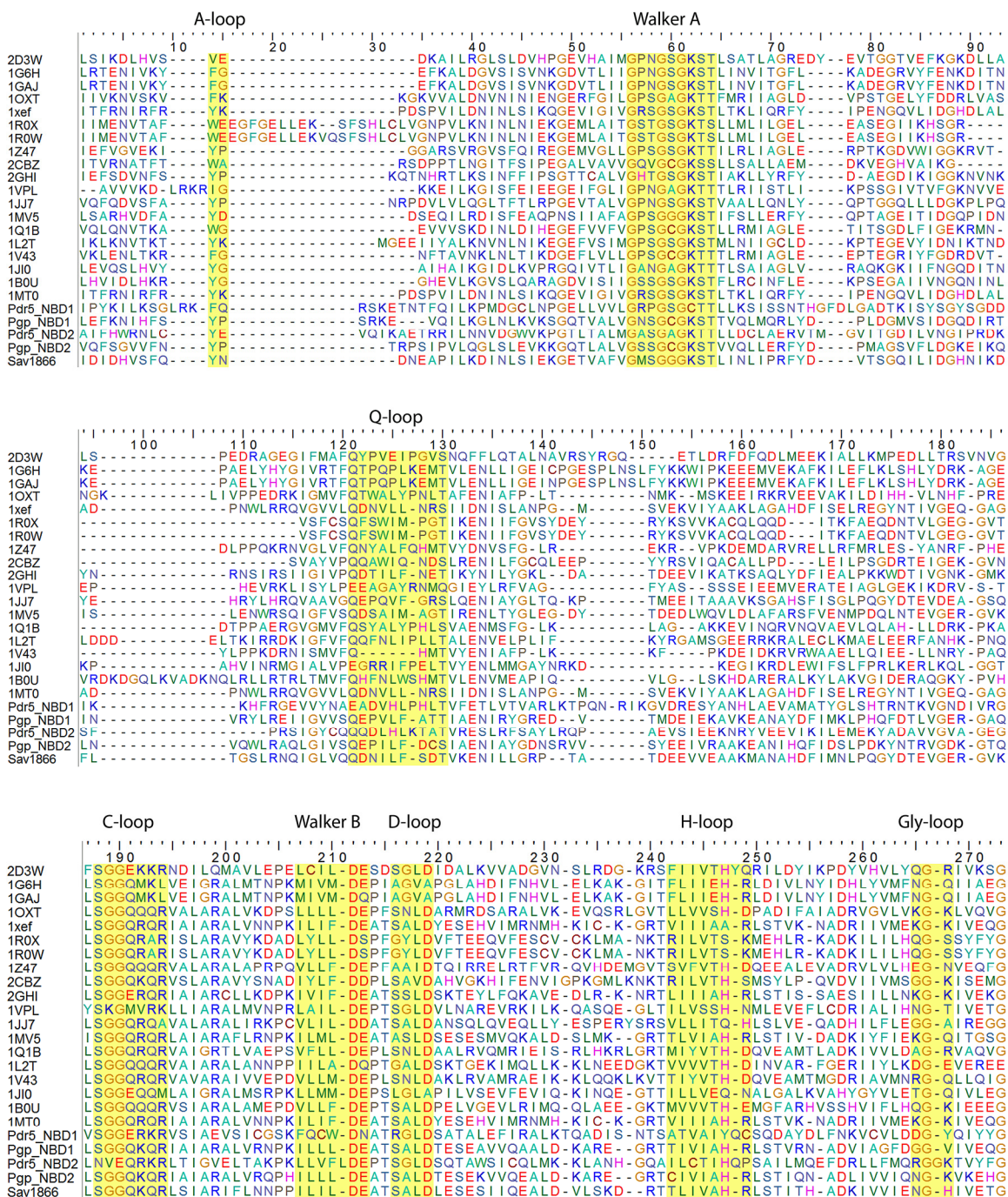
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CDR3 IIVVHRLQQWRTPSYIISKFMVLCSLNGFTTIKSONSMQLKQMLSIISMVVLTTLQQVPLVPTQRDLERERPSF
ABC1 IYVPHRVQQWRTPSYIKALCVLPLIGFVYDPAINTQQQLQNCMLIIPNLTIVGQLVQQTMPHFVPTQRDLERERPSF
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CGR1 FQLVCVRLQQWRTPDLWSKFIITFNQLIGFTTFTKDHITLQLQNCMLSIIMTVIIPNPILQQLPSPVQQRDLERERPSF
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CDR1 PLLVSWRIVQWRSPSYISKIILVVSMLNGFSTFKKINMQQLQNCMLSPVMPPIPNLTLVQQLPSPVQQRDLERERPSF
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PDR12 IKCVLRLTQWRDPSILKLTSTVILGPNFTWQLHRSIIDMQRMFTSLIILIPPTIVAVPKYQRLEWERLPSF
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ASPOR LQVTRVQQWRSPDLWSKFIITFNQLIGFTTFTKDRSLQQLQNCMLSIIMTVIIPNPILQQLPSPVQQRDLERERPSF
AtrF TLLLTAKRIQQWRDPSYIKLVSVIIGPNFTWMLNSIIMQDRMSIIMLIMIPVVLNSIVPKYINRALWEAREYPSF
AbcA LQVQCVRVQQWRSPSYISKFLCVLSLIVGFSLHTPNTIQQLQNCMLIIPNLTIVGQLVQQTMPHFVPTQRDLERERPSF
abcG10 TWEV KRLLIWWRDMSYVIGIFTPQASGLIIGFTFWNLDLSSDMNQRPVIEILILEILYIIPQPLIQKATK-KDAS
abcG11 TKEV KRLLIWWRDPSYIKLVSVIIGPNFTWMLNSIIMQDRMSIIMLIMIPVVLNSIVPKYINRALWEAREYPSF
ABC2 IKLVQRMVSLRNDVYVWKLHISLWGFSTFWMKDSDLQKLKLTINNIYVAVLQCLPLIHRRI-RETRKSH
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CDR3 KTFSWLAIIAQITAEIPYQVLAITISFSPWYVPLRNQVYSGVTHRQVLMWMLMTLM IYSSTLQICISWNQ--LDVAANW
ABC1 KVYSWKVMLSQIIVEIPWNSLIMVIMPCWYVPELERNILDOVTERSLFLWGLIETSTFTDLMIAGE--TAEAGGI
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abcG11 KTFSWPEAISIVVEIPYVISEIETICSWTAQLEHKTSD-----DEQTYEYWIIMMTCVSEGOVMVQI--NMFTAMLI
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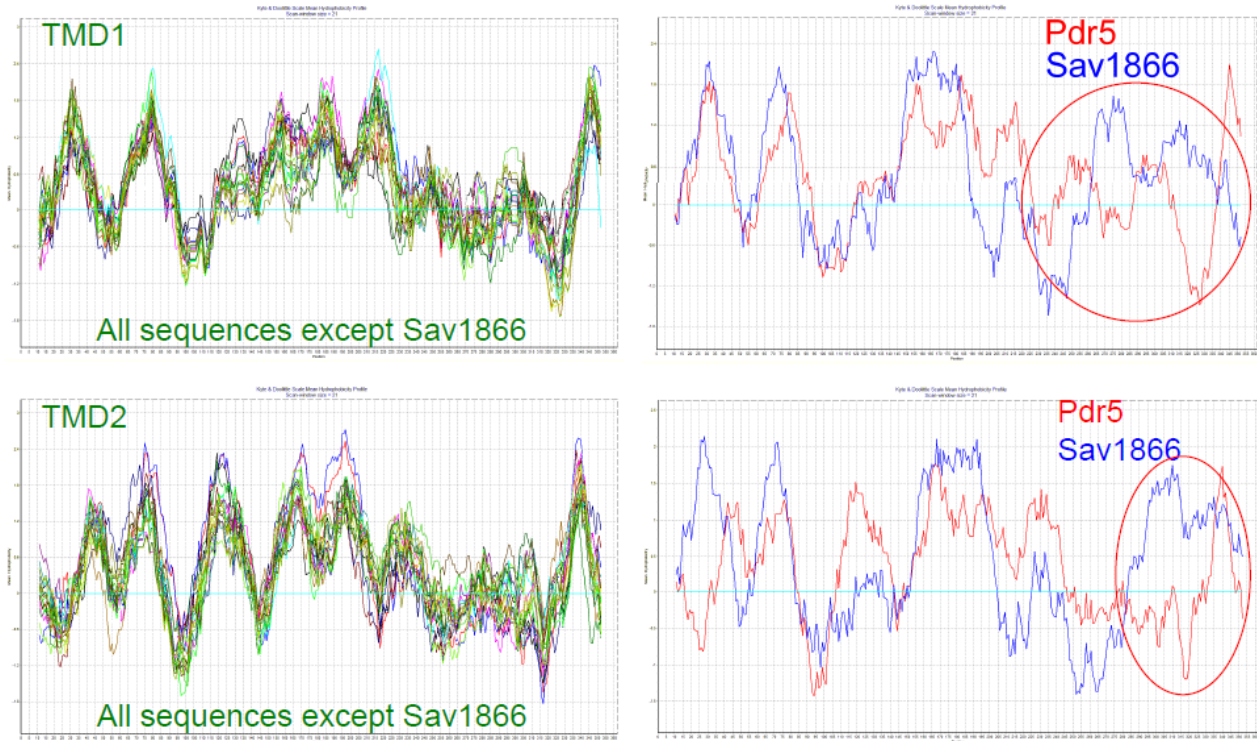
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CDR3	YAAWISLLLTISMI	CGVI	TKDSMPK	WV-	L	RCP	PLTALTS	MMS	IGL	DS	VKC	APTE	ILTP	PPQ	TPV	-	QK	OD	M	
ABC1	AGGIANLPTSLCLI	CGVL	NPD	MPR	WI-	M	RVSP	PTTIVS	LL	SV	VAN	SEV	RC	SN	EL	LD	DP--	LN	C	
BOTCI	VISHVLPPTTFVM	GL	FGV	VRP	ISQ	ISV	WRW	LFV	VNP	AT	YWI	GGII	ATLS	N	VPI	EC	SN	EA	Y	
CGR1	TAAHIGSLMPTM	LS	CGVM	TPD	MPR	WI-	M	RVSP	PLTYLID	LL	ST	GV	N	VD	IR	CS	N	TEL	V	
PMR1	TGGNLANLLPTSLCLI	CGVL	TPDK	MPH	WI-	M	RVSP	PTLVLS	ML	ST	GT	SG	K	V	EC	S	V	ELL	H	
CDR1	NAANLATLLPTMCLN	CGVL	QPD	VLP	WI-	M	RCP	PTLVQ	ML	ST	GL	NT	V	K	C	ER	E	V	S	
PDR10	NAANLASLLPTMSLS	CGVL	TPN	ILP	WI-	M	RVSP	PLTYLID	LL	SV	GL	AN	S	V	C	SS	N	ELL	K	
PDR12	SASMINSLFL	MLL	CGIL	QPRE	KMP	WRR	RLM	N	V	S	P	T	V	V	Q	L	V	T	P	
PDR15	TAAHIGSLMPTM	LS	CGVM	TPK	VMP	WI-	M	RVSP	PLTYMID	LL	LG	V	N	VD	V	K	C	S	N	
ASPOR	TAS	I	V	V	L	L	M	S	L	T	C	G	V	M	T	P	L	P	E	W
AtrF	VISHVLPPTTFVM	CGV	IVR	PRD	PV	WK	W	M	V	N	P	V	W	L	R	V	I	S	S	
AbcA	NAGLGNLLPTLCLL	CGVL	TPD	QLP	WI-	M	RVSP	PTLVLS	ML	S	V	G	I	S	N	T	N	V	I	
abcG10	LAAQILPPLLVLML	L	CGVL	VY	EQ	IP	N	FW	K	V	H	S	N	P	C	R	F	L	E	
abcG11	PMILPLPLIV	LPL	CGVM	V	P	P	S	S	I	P	T	W	R	W	V	H	N	P	C	
ABC2	VLAN--	P	V	V	I	G	L	V	S	CG	S	V	L	V	P	T	Q	I	Q	
DEBHA	TGGNLANLLPTSLCLI	CGVL	TKE	MPE	WV-	M	RVSP	PTLVLS	ML	ST	GT	V	S	G	AD	V	C	E	V	
Y1ABC2	NAANLASLLPTMCLT	CGIL	SSD	SMPR	WI-	M	RCP	PTLVLS	ML	S	V	L	S	V	A	L	S	D	V	
AGL142C	PAAILANVPTMCLIF	SG	V	L	V	K	L	P	R	WI-	W	M	L	S	P	V	T	L	V	

	1610	1620	1630	1640	1650	1660	1670	1680	
PDR5	-----L	KTG	LT	DEN--	T	D	C	S	F
CDR3	-----I	AG	G	LL	N	PE--	T	D	C
ABC1	-----S	T	T	I	P	G	L	R	I
BOTCI	-----S	A	G	V	G	L	T	N	P
CGR1	-----V	A	G	T	G	L	T	D	P
PMR1	-----G	L	V	V	N	G	T	Q	V
CDR1	-----F	A	G	G	P	E	T	R	N
PDR10	-----S	T	G	T	G	L	L	D	S
PDR12	-----N	N	T	G	L	V	N	P	T
PDR15	-----L	A	G	T	G	L	S	D	P
ASPOR	-----M	A	G	G	Q	L	S	N	P
AtrF	-----I	K	N	G	L	L	N	P	D
AbcA	-----N	L	G	G	L	A	D	E	M
abcG10	-----Y	G	I	V	R	V	I	K	D
abcG11	-----K	P	S	G	V	E	S	A	T
ABC2	-----P	S	V	D	L	I	N	P	S
PMR4	-----V	A	G	G	L	Q	N	P	M
DEBHA	-----F	A	G	G	L	I	S	D	N
Y1ABC2	-----G	S	A	G	L	V	S	S	A
AGL142C	-----N	A	E	S	V	L	L	N	P

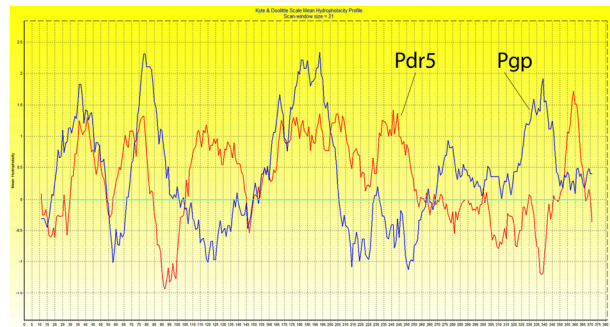
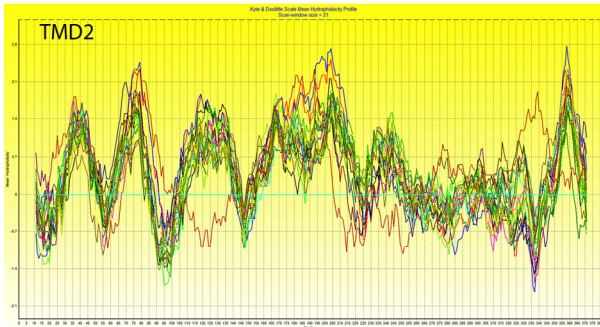
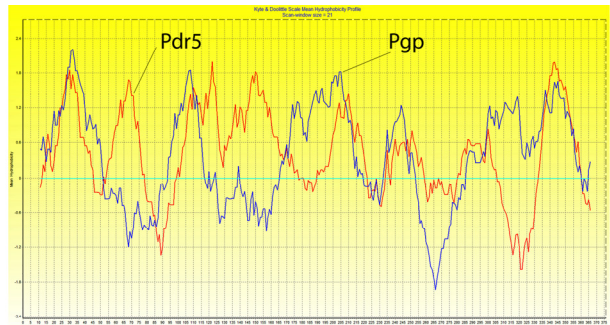
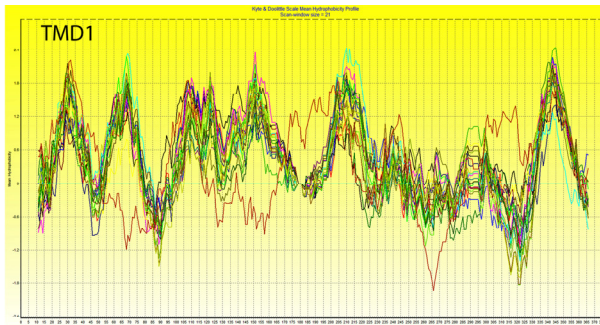
Supplementary Figure S2



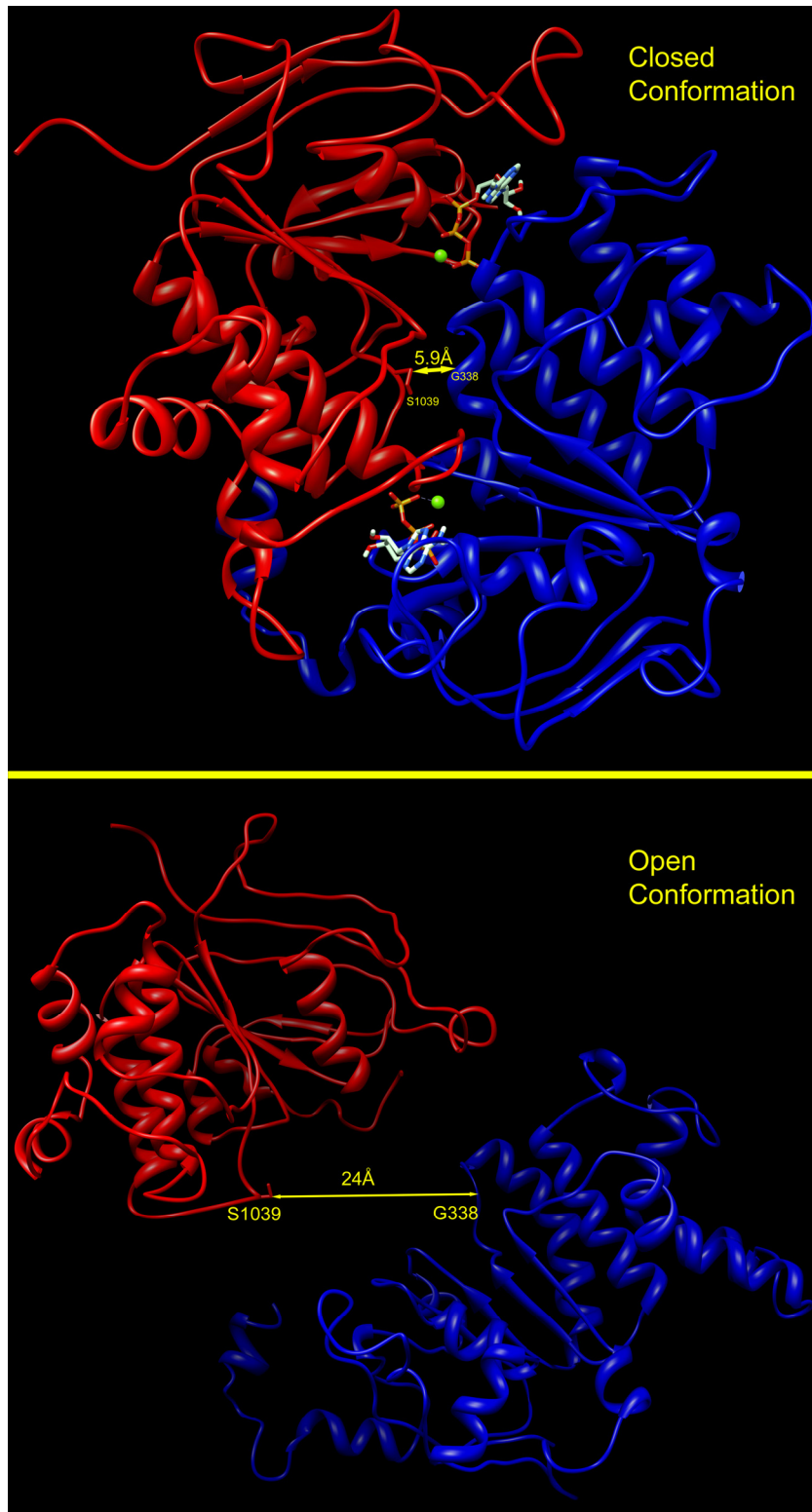
Sav1866: Hydrophobicity Profiles



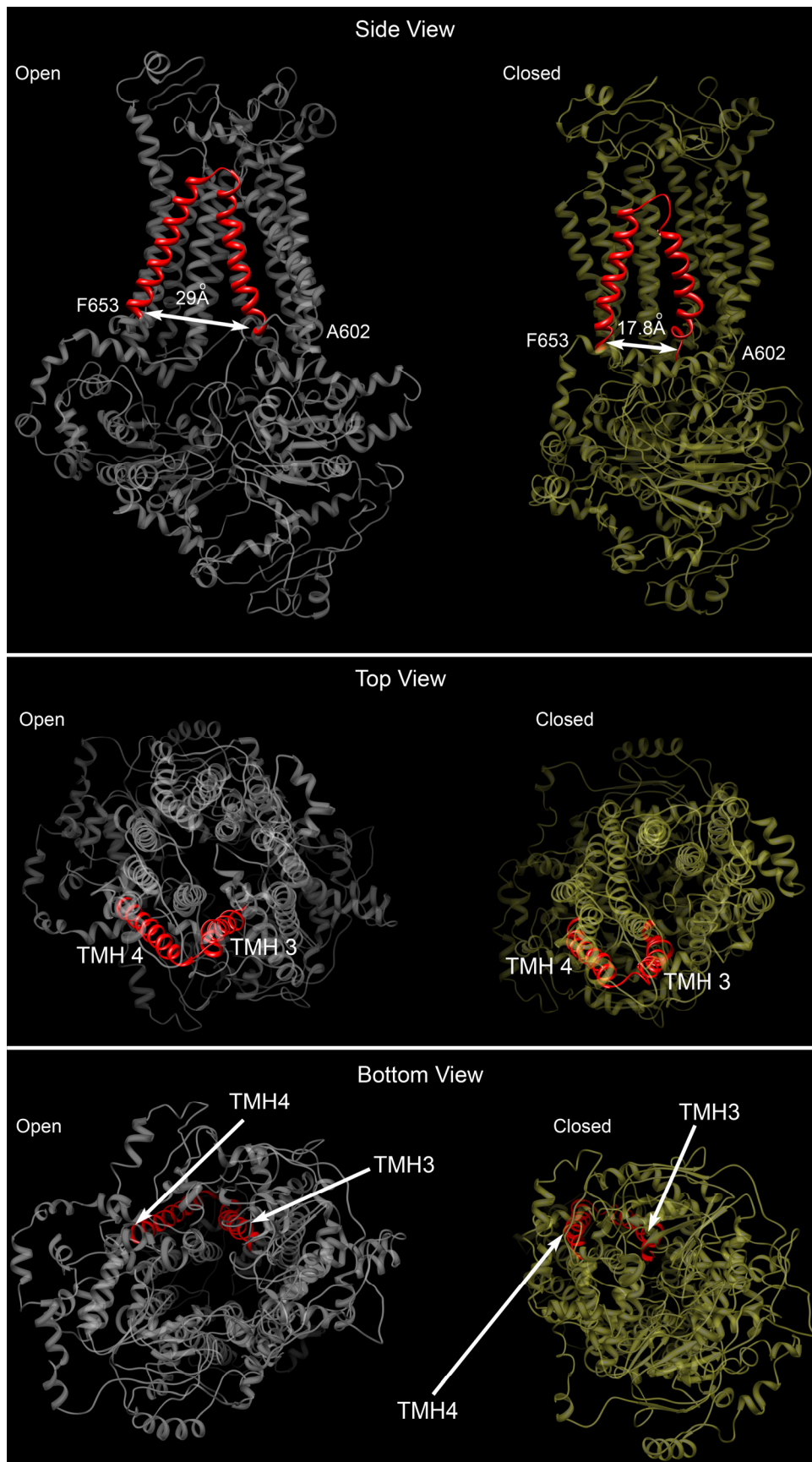
Supplementary Figure S4



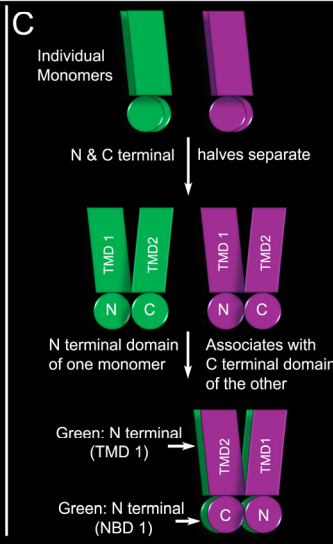
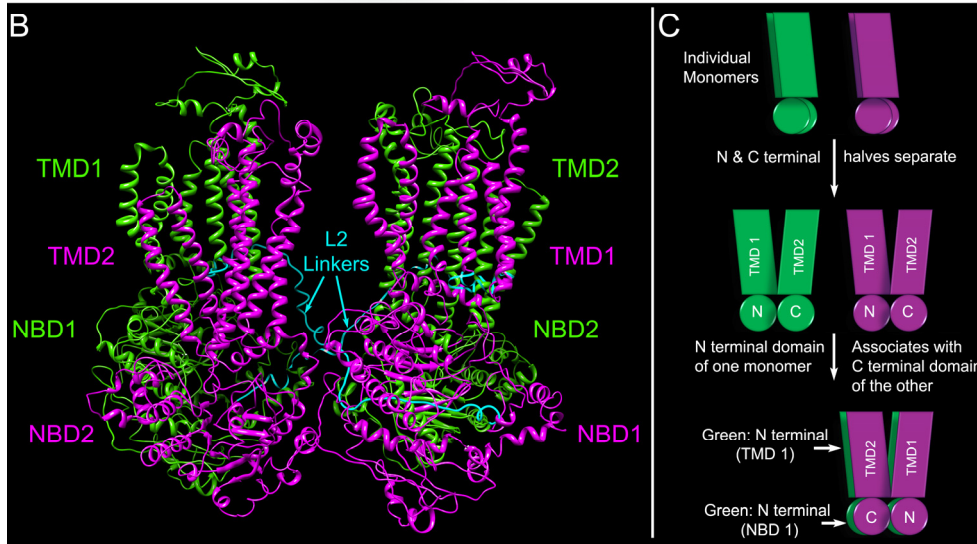
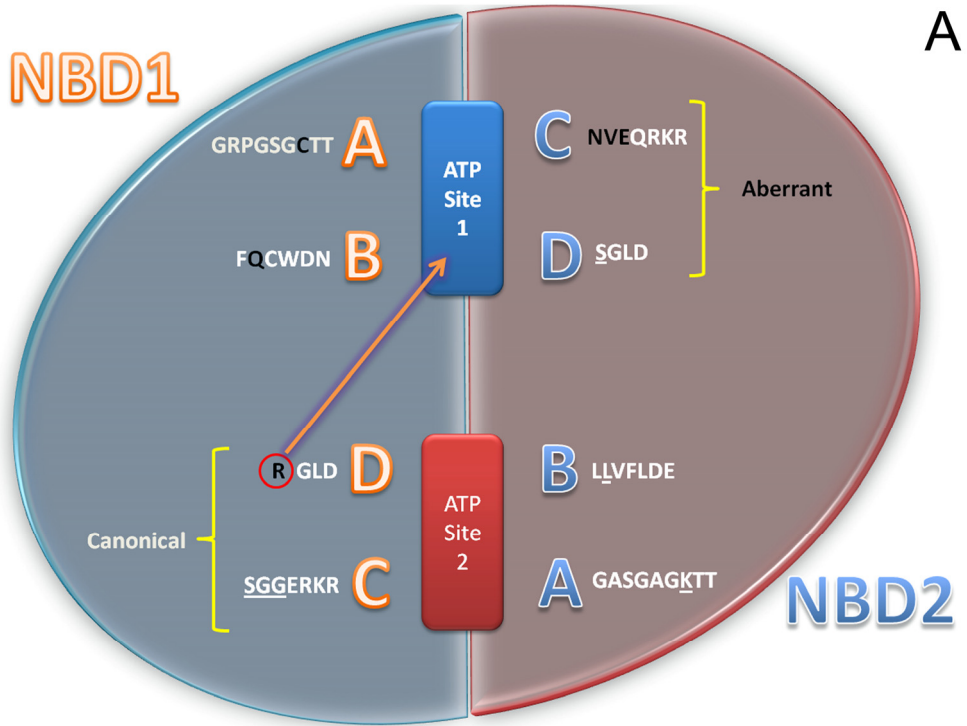
Supplementary Figure S5



Supplementary Figure S6

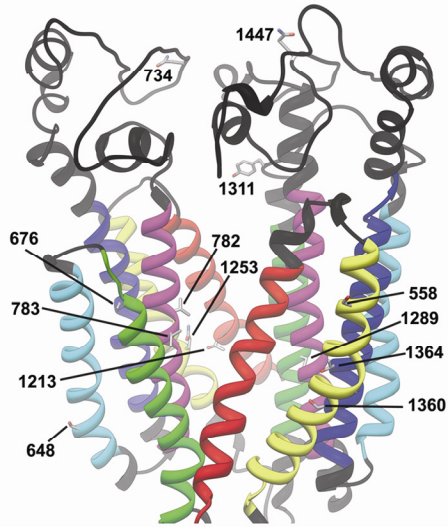


Supplementary Figure S7

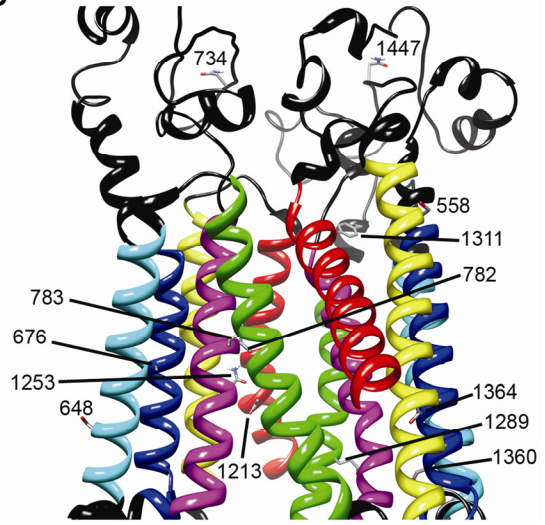


Supplementary Figure S8

A



B



Supplementary Figure S9

TMD1

```

PDR5 10 20 30 40 50 60 70 80
Pgp  MQVKYLLIRNWRRLRNNIGFTLFMI LGNC SMALILGSMFFKIMKKGD--TSTFYFR
      VSVLTMFRYAGW-LDRLYMLVGTLAAIIHGVALPLMMLIFGDM-TDSFASVGNVSKNSTNMS
      EADKRAMFAKLEEEEMTTYAYYY

PDR5 90 100 110 120 130 140 150 160
Pgp  -GSAMFFAILFNAPSSLLEIFSLYEARPITEKHRTYSLSYHPSADAFASVLSLEIPS-
      TGI GAGVLIVAYIQVSWFCLAA-GRQIHKI-RQK-FFHAIMNQEIG--WFDVHDV
      GELNTRLTDDVSKINEGIGDKIGMFFQA

PDR5 170 180 190 200 210 220 230 240 250
Pgp  IIAVCFNIIFYFLVDFRRNGGVFFFYLLINIVAVFSMS--HLF--RCVGSLT-
      MATFFGGFIIGFTRGWKLTLVILAISPVLGLSAGIWA-KILSSFIDKELHAYAKAGAVA
      EEVLAAIRTVIAFGGQKKELEERYNN

PDR5 260 270 280 290 300 310 320 330
Pgp  ---KTLSEAMVPASMLLLALSMTGFAIPKKKILRWKWIWYINPLAYLFESLLINEFHGI
      NLEEKARLGIKKAITANISMGAFFLLIYASYALAFWYGTSLVI--
      KFPCA EYVPRGPAYA

PDR5 340 350 360 370 380 390 400
Pgp  NISSTESVCTVVGAVPGQDYVLGDDFIRGTYYHDKDKWRGFGIGMAYVVFVYLF
      LCEYNEGAK
      SKEYSIGQVLTVFFSVLIGAFVSGQASPNIE
  
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TMD2

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PDR5 10 20 30 40 50 60 70 80
Pgp  LVSIRLFQQYWRSPDYLWSKFILTIFNQLFIFGFTFF--KA----GTSLQGLQNQ-MLAV
      FMFTVIFNPILQQ-YL-PSF
      WRILKLNSTEW--PYFVVGFICAIINGGLQPAFSVIFSKVVGVFTNGGPPETQRQNSN
      LFSLLFLILGIIISFITFFLQGGFT

PDR5 90 100 110 120 130 140 150 160
Pgp  VQQRDLYEARERPSRTFSWIS-
      FGKAG--EILTKRLRYMFKSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGATGSR
      LAVIFQNIANLGTGIIISLIYGW

PDR5 170 180 190 200 210 220 230 240
Pgp  FYSNASAAQGLHERGALFWLFSCAFYVYVGSMLLVISFNQVAE-
      Q-----LTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGSCKIATEAIE
      ENFRVTVVSLTREKQFETMYAQ

PDR5 250 260 270 280 290 300 310 320
Pgp  ---SAANLASLLFTMSLSFCGVMTPPSAMPFRWIFMYRVSPITYFIQALLAVGVAN
      DVKCADYELELFTPPSG
      SLQIPYRNAMKKAHVFGITFSFTQAM--MYFSYAAAFRFGAYLVTTQLMTFENVLLV-

PDR5 330 340 350 360 370 380 390 400
Pgp  MTCGQYMEPYLQLAKTGYLTDENATDTCSFQCI STTNDYLANVNSFYSERWRNYGIF
      ICYIAFNFIAGVFFYWLARVPKKN
      FSAIVFGAMAVGQVSSFPDYAKATVSA
  
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Supplementary Figure S10

TMD1

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PDR5 10 20 30 40 50 60 70 80
2HYD 10 20 30 40 50 60 70 80
M Q V K Y L L I R N M W R L R N - N I G F T L F M I L G N C S M A L I L G S M F F K I M K K - - G D T S T F - - - - Y F R G S A M F F A I L F N A F S S
M I K R Y L - - - Q F V K P Y K Y R I F A T I I V G I I K F G I P M L I - P L L I K Y A I D G V I N N H A L T T D E K V H H L T I A I G I A L F I F V I R P P - -

PDR5 90 100 110 120 130 140 150 160
2HYD 90 100 110 120 130 140 150 160
L L E I F S L Y E A - - - - R P I T E - K H R T Y - - - - S L Y H P - - S A D A F A S - - - - V L S E I P S K L - - I I A V C F N I I F Y F
- I E F I R Q Y L A Q W T S N K I L Y D I R K K L Y N H L Q A L S A R F Y A N N Q V G Q V I S R V I N D V E Q T K D F I L T G L M N I W L D C I T I I A L S I M F

PDR5 170 180 190 200 210 220 230 240
2HYD 170 180 190 200 210 220 230 240
L V D F R R N G G V F F F Y L L I N I V A V F S M S H L F - R C V G S L T K T -
F L D V K L T - L A A L F I F P F Y I L T V Y V F F G R L R K L T R E R S Q A L A E V Q G F L H E R V Q G I S V V K S F A I E D N E A K N F D K K N T N F L T R A L

PDR5 250 260 270 280 290 300 310 320
2HYD 250 260 270 280 290 300 310 320
- - - - - L S E A M V P A S M L L L A L S M Y T G F A I P K K K I L R - - - W S K W I W Y I N P L A Y L F E S L L I N E F H G I K F P C A - - E Y
K H T R W N A Y S F A A I N - T V T D I G P I I V I - G V G A Y - - L A I S -

PDR5 330 340 350 360 370 380 390 400 41
2HYD 330 340 350 360 370 380 390 400 41
V P R G P - - A Y A N I S S - - - T E S V C T V V - G A V P - G - - - Q D Y V L G D D F I R G T Y Q Y Y H K D K W R G F G - I G M A Y V V F F F V Y L F L C
- - - - - G S I T V G - - - - - T L A A F V G Y L E L L F G P L R R L - V A

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TMD2

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PDR5 10 20 30 40 50 60 70 80
2HYD 10 20 30 40 50 60 70 80
F S Q S I I Y Q T K L V S I R L F Q Q Y W R S P D Y L W S K F I L T I F N Q L F I G F T F F - - - - K A G - - - - - T S L Q G L Q N Q M - L A V F M F
M I K R Y L Q F V K P Y K - - - - - Y R I F A T I I V G I I - - - K - F G I - P M L I P L L I K Y A I D G V I N N H A L T T D E K V H H L T I A I G I A L F I F

PDR5 90 100 110 120 130 140 150 160
2HYD 90 100 110 120 130 140 150 160
T V I F N P - - I L Q Q Y L P S F V Q Q R D L Y E A R E R P S R T F S W I S - - - - - F I F A Q I F V E V P W N I L
V I V R P P I E F I R Q Y L A Q W T S N K I L Y D I R K K L - - - Y N H L Q A L S A R F Y A N N Q V G Q V I S R V I N D V E Q T K D F I L T G L M N I W L D C I T I I I

PDR5 170 180 190 200 210 220 230 240 250
2HYD 170 180 190 200 210 220 230 240 250
A G T I A Y F I Y Y Y P I G F Y S N A S A A G Q L H E R G A L F W L F S C A F Y V Y V G S M G L L V I S F N Q V A E S -
A L S I M F F L - - - - - D - - - - - V K L T L A A L F I F P F Y I L T V Y V F F - - - - - G R L R K L T R E R S Q A L A E V Q G F L H E R V

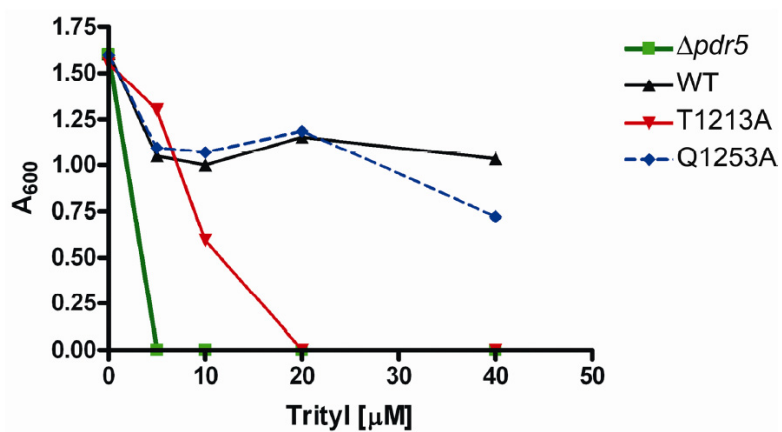
PDR5 260 270 280 290 300 310 320 330
2HYD 260 270 280 290 300 310 320 330
G G I S V V K S F A I E D N E A K N F D K K N T N F L T R A L K H T R W N A Y S F A A I N T V T D I G P I I V I G V G - A Y -

PDR5 340 350 360 370 380 390 400 410 42
2HYD 340 350 360 370 380 390 400 410 42
V G V A N V D V K C A D Y E L L E F T P P S G M T C G Q Y M E P Y L Q L A K T G Y L T D E N A T D T C S F C Q I S T T N D Y L A N V N S F Y S E R W R N Y G I F I C Y I
- - - - - L A I S G S I - - - - - T V G T - - - - - L A A F V

PDR5 0 430 440
2HYD 0 430 440
- A F N Y I A G V F F Y W L A R V P K K N G K L S K K
G Y L E L L F G P L R R L V A S F T T L T Q S F A S M

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Supplementary Figure S11



Supplementary Figure S12

