

## Human ABCG1 Sequence

>sp|P45844|ABCG1\_HUMAN ATP-binding cassette sub-family G member 1 OS=Homo sapiens OX=9606 GN=ABCG1 PE=1 SV=3 (**NP\_004906.3**)  
MACLMAAFSVGTAMNASSYSAEMTEPKSVCVSVDEVVSSNMEATETDLLNGHLKKVDNNL  
TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFNSGELVAIMGPS  
GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV  
SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF  
DEPTSGLDSASCFQVVSMLKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGGQCVYRGK  
VCNLVPYLRDLGLNCPYHNPADFVMEVASGEYGDQNSRLVRVREGMCDSDHKRDLGGD  
AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSFSASCLTQFCILFKRTFLSIMRDS  
VLTHLRITSHIGIGLLIGLLYLIGNEAKKVLNSNGFLFFSMLFLMFAALMPTVLTFFLE  
MGVFLREHLNLYWSLKAYYLAKTMADVFPQIMFPVAYCSIVYWMTSQPSDAVRFVLFAL  
GTMTSLVAQSLGLLIGAASSTSLQVATFVGPVTAIPVLLFSGFFVSFDTIPTYLQWMSYIS  
YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELDVENAKLYLDFIVLGIFFI  
SLRLIAYFVRLRYKIRAER

### Sequence Alignment (5 representative mammalian species with human sequence in bold):

→ Conserved polar residues are highlighted based on conservation scores obtained from analysis and alignment of 950 mammalian ABCG1 sequences using **BLASTp**. The conservation scores were obtained by Consurf ([https://consurf.tau.ac.il/consurf\\_index.php](https://consurf.tau.ac.il/consurf_index.php)).

#### Highlighted residues conservation score key:

- conservation score of 7
- conservation score of 8
- conservation score of 9

**\*The residues chosen as the involved residues in the ABCG1 Polar relay that displayed polar linkages in a 3D setting.**

XP_030661937.1	MACLMAAFSVGTAMNASSYSAEMTEPKSVCVSVDEVVSSNMEAAETDLLNGHLKKVDNNL	60
XP_004062897.1	MACLMAAFSVGTAMNASSYSAEMMEPKSVCVSVDEVVSSNMEATETDLLNGHLKKVDNNL	60
PNJ42434.1	MACLMAAFSVGTAMNASSYSAEMMEPKSVCVSVDEVVSSNMEATETDLLNGHLKKVDNNL	60
<b>NP_004906.3</b>	<b>MACLMAAFSVGTAMNASSYSAEMTEPKSVCVSVDEVVSSNMEATETDLLNGHLKKVDNNL</b>	<b>60</b>
XP_003319138.2	MACLMAAFSVGTAMNASSYSAEMTEPKSVCVSVDEVVSSNMEATETDLLNGHLKKVDNNL	60
XP_030661937.1	TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFSSGELVAIMGPS	120
XP_004062897.1	TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFNSGELVAIMGPS	120
PNJ42434.1	TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFNSGELVAIMGPS	120
<b>NP_004906.3</b>	<b>TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFNSGELVAIMGPS</b>	<b>120</b>
XP_003319138.2	TEAQRFSLLPRRAAVNIEFRDLSYSVPEGPWWRKKGYKTLLKGISGKFNSGELVAIMGPS	120
XP_030661937.1	GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV	180
XP_004062897.1	GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV	180
PNJ42434.1	GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV	180
<b>NP_004906.3</b>	<b>GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV</b>	<b>180</b>
XP_003319138.2	GAGKSTLMNILAGYRETGMKGAVLINGLPRDLRCFRKVSCYIMQDDMLLPHLTVQEAMMV	180
XP_030661937.1	SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF	240
XP_004062897.1	SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF	240
PNJ42434.1	SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF	240
<b>NP_004906.3</b>	<b>SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF</b>	<b>240</b>
XP_003319138.2	SAHLKLOEKDEGRREMVKEILTALGLLSCANTRTGSLSGGQRKRLAIALELVNPPVMFF	240

XP_030661937.1	DEPTSGLDASCFQVVS LMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCVRGK	300
XP_004062897.1	DEPTSGLDASCFQVVS LMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCVRGK	300
PNJ42434.1	DEPTSGLDASCFQVVS LMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCVRGK	300
NP_004906.3	DEPTSGLDASCFQVVS LMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCVRGK	300
XP_003319138.2	DEPTSGLDASCFQVVS LMKGLAQGGRSIICTIHQPSAKLFELFDKLYVLSQGQCVRGK	300
XP_030661937.1	VCNLVPYLRDLGLNCPITYHNPA DFMVEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGD	360
XP_004062897.1	VCNLVPYLRDLGLNCPITYHNPA DFMVEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGD	360
PNJ42434.1	VCNLVPYLRDLGLNCPITYHNPA DFMVEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGD	360
NP_004906.3	VCNLVPYLRDLGLNCPITYHNPA DFMVEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGD	360
XP_003319138.2	VCNLVPYLRDLGLNCPITYHNPA DFMVEVASGEYGDQNSRLVRAVREGMCDSDHKRDLGGD	360
XP_030661937.1	AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSF SASCLTQFCILFKRTFLSIMRDS	420
XP_004062897.1	AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSF SASCLTQFCILFKRTFLSIMRDS	420
PNJ42434.1	AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSF SASCLTQFCILFKRTFLSIMRDS	420
NP_004906.3	AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSF SASCLTQFCILFKRTFLSIMRDS	420
XP_003319138.2	AEVNPFLWHRPSEEVKQTKRLKGLRKDSSSMEGCHSF SASCLTQFCILFKRTFLSIMRDS	420
XP_030661937.1	VLTHLRITSHIGIGLLIGLLYLIGIGNEAKKVL SNSGFLFFSMLFLMFAALMPTVLTFPLE	480
XP_004062897.1	VLTHLRITSHIGIGLLIGLLYLIGIGNEAKKVL SNSGFLFFSMLFLMFAALMPTVLTFPLE	480
PNJ42434.1	VLTHLRITSHIGIGLLIGLLYLIGIGNEAKKVL SNSGFLFFSMLFLMFAALMPTVLTFPLE	480
NP_004906.3	VLTHLRITSHIGIGLLIGLLYLIGIGNEAKKVL SNSGFLFFSMLFLMFAALMPTVLTFPLE	480
XP_003319138.2	VLTHLRITSHIGIGLLIGLLYLIGIGNEAKKVL SNSGFLFFSMLFLMFAALMPTVLTFPLE	480
XP_030661937.1	MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVRFVLFAAL	540
XP_004062897.1	MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVRFVLFAAL	540
PNJ42434.1	MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVRFVLFAAL	540
NP_004906.3	MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVRFVLFAAL	540
XP_003319138.2	MGVFLREHLNYWYSLKAYYLAKTMADVPFQIMFPVAYCSIVYWMTSQPSDAVRFVLFAAL	540
XP_030661937.1	GTMTSLVAQSLGLLIGAASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLOWMSYIS	600
XP_004062897.1	GTMTSLVAQSLGLLIGAASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLOWMSYIS	600
PNJ42434.1	GTMTSLVAQSLGLLIGAASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLOWMSYIS	600
NP_004906.3	GTMTSLVAQSLGLLIGAASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLOWMSYIS	600
XP_003319138.2	GTMTSLVAQSLGLLIGAASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLOWMSYIS	600
XP_030661937.1	YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELIVENAKLYLDFIVLGIFFI	660
XP_004062897.1	YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELIVENAKLYLDFIVLGIFFI	660
PNJ42434.1	YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELIVENAKLYLDFIVLGIFFI	660
NP_004906.3	YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELIVENAKLYLDFIVLGIFFI	660
XP_003319138.2	YVRYGFEGVILSIYGLDREDLHCDIDETCHFQKSEAILRELIVENAKLYLDFIVLGIFFI	660
XP_030661937.1	SLRLIAYFVLR YKIRAER678	
XP_004062897.1	SLRLIAYFVLR YKIRAER678	
PNJ42434.1	SLRLIAYFVLR YKIRAER678	
NP_004906.3	SLRLIAYFVLR YKIRAER678	
XP_003319138.2	SLRLIAYFVLR YKIRAER678	