Ubiquitylation of the Bardet-Biedl syndrome protein complex is essential for cilium assembly and signaling

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Appendix Figures

Table of Contents

Appendix Figure S1 Page 2

Appendix Figure S2 Page 3

Appendix Figure S3 Page 4

Appendix Figure S4 Page 5

Appendix Figure S5 Pages 6-10

Appendix Figure S6 Page 11



Appendix Figure S1. **A.** Schematic representation of human PJA2.The cysteine-rich region (RING) and the C-terminal rat clone 33 isolated by the yeast two-hybrid system are shown. Bait and pray fragment were indicated. **B,C** Immunoprecipitation of BBS2 (**B**) or BBS1 (**C**) from HEK293 cell lysates expressing HA-tagged BBS1 or BBS2 and ubiquitin-myc. Serum-deprived cells were left untreated or stimulated with FSK for 1 and 3 hours. Ubiquitinated BBS1 and BBS2 proteins and HA-tagged were detected. The precipitates were immunoblotted with anti-myc (ubiquitinated BBS1 or BBS2) and anti-HA antibodies. **D.** HEK293 cells were serum deprived for 24h, pretreated with cycloheximide (10μ m) and stimulated with foskolin (40μ m) at indicated time. BBS1 and BBS2 protein levels were detected with endogenous antibody as indicated.



Appendix Figure S2: Coarse –Grained model of the Ub-hBBSome in an open conformation. Beads (BB) are shown as spheres.



Appendix Figure S3: Atomic position Pearson Correlation Coefficient (aPCC) matrices calculated on **A** wt-hBBSome and **B** Ub-hBBSome after 5µs of CG-MD. Residues of each subunit are numbered as follows: BBS1 (S2-S568, blue rectangle),BBS2 (M570-V1285, green rectangle), BBS4 (F1288-L1683, cyan rectangle), BBS5 (M1685-S2025, light pink rectangle), BBS7 (M2026-A2740, yellow rectangle), BBS8 (M2742-F3239, orange rectangle), BBS9 (S3242-S4068, red rectangle), BBS18 (M4071-Q4122, purple rectangle). In particular, BBS18 presents a relatively high correlation (> 0.5) with BBS4 and BBS8, which is observed only in the Ub-hBBSome model. BBS18 also has high aPCC values with BBS1 and BBS2, which correlate with each other, too. BBS1 and BBS2 anticorrelate with BBS7 (aPCC < -0.5). The black rectangles highlight the zones showing high correlation between BB1, BBS4, BBS8 and BBS18 in Ub-hBBSome. The same areas are also highlighted in wt-hBBSome for the sake of comparison.



Appendix Figure S4: Superimposition between the bovine *b*BBS1 subunit of the apo (closed) form of the Cryo-EM *b*BBSome structure (PDB ID: 6vbu) (light-yellow surface) and the last CG-MD frame of: **A** CG model of the K143 Ubiquitinated *h*BBS1 (Ub-*h*BBS1 CG) (light-blue surface) and **B** CG model of the wild-type *h*BBS1 (wt-*h*BBS1 CG) (light-magenta surface). After 5 μ s of CG-MD, a more closed conformation of the Ub-*h*BBS1 CG can be observed, compared to the wt-*h*BBS1 CG.

hBBS1 6vbu_BBS1	MAATSSSDSDGGKGESEA	2 SKWLD <mark>AHYDP</mark> MANIHTFSA ANSKWLD <mark>SLSDS</mark> MANIHTFSA 20	CLALAD <mark>L</mark> HGDGEYKL <mark>VV</mark> GDLGI CLALAD <mark>F</mark> HGDGEYKL <mark>AM</mark> GDLGI	41 P P 60
hBBS1 6vbu_BBS1	<mark>GGQ</mark> QPRLKVLKG <mark>PLVMTE</mark> DGR <mark>Q</mark> PRLKVLKGHTLVSQ	61 SPLPALPAAAATFLMEQHEF KPLPDLPAAAVTFLMASHEF 80	82 PRTPALALASGPCVYVYKNLRP PRTPALALASGPCVYVYKNLKP 100 10	03 Y Y .21
hBBS1 6vbu_BBS1	FKFSLP <mark>Q</mark> LPPNPLEQDLV FKFSLP <mark>S</mark> LP <mark>T</mark> NPLEQDLV	124 INQAKED <mark>R</mark> IDPLTLKEMLE <mark>S</mark> I INQAKEDQIDPLTLKEMLE <mark>G</mark> I 143	142 1 RETAEEPLSIQSLRFLQLELSI REKAEVPLSVQSLRFLPLELSI 160 1	62 E E .80
hBBS1 6vbu_BBS1	MEAFVNQHKS <mark>NSIK</mark> RQTV MEAFVNQHKS <mark>K</mark> SI <mark>R</mark> RQTV	182 /ITTMTTLKKNLADEDAVSCL /ITTMTTLKKNLADEDAVSCL 200	202 2: VLGTENKELLVLDPEAFTILAI VLGTENKELLVLDPEAFTILAI 220 2/	22 K K 40
hBBS1 6vbu_BBS1	MSLPSVP <mark>V</mark> FLEVSGQFD\ MSLPSVP <mark>A</mark> FLEASGQFD\	242 /EFRLAAACRNGNIYILRRDS /EFRLAAACRNGSIYILRRDS 260	262 KHPKYCIEL <mark>S</mark> AQPVGL <mark>IR</mark> VHKV KRPKYCIELGAQPVGLVGVHKV 280 3	82 V V 800
hBBS1 6vbu_BBS1	LVVGS <mark>T</mark> QDSLHGFT <mark>H</mark> KGK LVVGS <mark>N</mark> QDSLHGFT <mark>Y</mark> KGK	302 KLWTVQMPAAIL <mark>T</mark> MNLLEQH RLWTVQMPAAILAMNLLEQH 320	322 ISRGLQAVMAGLANGEVRIYRDI ISRGLQAVMAALANEEVRIYHDI 340 340 340	42 K K 60
hBBS1 6vbu_BBS1	ALLNVI <mark>H</mark> TPDAVTSLCFG VLLNVI <mark>R</mark> TP <mark>E</mark> AVTSLCFG	362 GRYGREDNTLIMTT <mark>R</mark> GGGLI GRYGREDNTLIMTT <mark>L</mark> GGGLI 380	382 :KILKRTAVF <mark>V</mark> EGGSEVGPPPA :KILKRTAVF <mark>A</mark> EGG <mark>G</mark> EAGPPPS 400 4	02 Q Q 20
hBBS1 6vbu_BBS1	A <mark>M</mark> KLNVPRKTRLYVDQTL A <mark>I</mark> KLNVPRKTRLYVDQTL	422 REREAGTAMHRAFQTDLYLL REREAGTAMHRTFQADLYLL 440	442 RLRAARAYLQALESSLSPLST RLRAARAY <mark>V</mark> QALESSLSP <mark>V</mark> SL 460 4	162 T T 180
hBBS1 6vbu_BBS1	AREPLKLHAVVQGLGPTF AREPLKLHAVVQGLGPTF	482 KLTLHLQNTSTTRPVLGLLV KLTLHLQNTSTARPILGLV 500	502 /CFLYNEALYSLPRAFFKVPLL /CFLYNEVLYALPRAFFKVPLL 520 520 5	22 V V 40
hBBS1 6vbu_BBS1	PGLNYPLETFV <mark>E</mark> SLS <mark>N</mark> KO PGLNYPLETFV <mark>K</mark> SLS D KO	542 5ISDIIKVLVLREGQS <mark>A</mark> PLLS 5ISDIIKVLVLREGQS <mark>T</mark> PLLS 560	562 568 SAHVNMPGS SAHINMPMSEGLAAD 580 592	

В

hBBS2 6vbu_BBS2	570 MLLPVFTLKLRHKISPRM MLQPVFTLKLRHKISPRM 1	589 VAIGRYDGTHPCLAAATQ <mark>T</mark> G VA <mark>V</mark> GRYDGTHPCLAAATQ <mark>AG</mark> 20	609 KVFIHNPH <mark>TRN</mark> QH <mark>VSAS</mark> RVF KVFIHNPH <mark>SRSQHLGAP</mark> RVL 40	629 QS QS 60
hBBS2 6vbu_BBS2	PLESDVSLLNINQ <mark>A</mark> VSCL PLESDVSLLNINQ <mark>T</mark> VSCL	649 TAGVLNPELGYDALLVGTQT TAGVLNPELGYDALLVGTQT 80	669 NLLAYDVYNNSDLFYREVAD NLLAYDVYNNSDLFYREVAD 100	689 GA GA 120
hBBS2 6vbu_BBS2	<mark>N</mark> AIVLGTLGDI <mark>S</mark> SPLAII <mark>S</mark> AIVLGTLGDI <mark>T</mark> SPLAII	709 GGNCALQGFNHEG <mark>S</mark> DLFWTV GGNCALQGFNHEG <mark>N</mark> DLFWTV 140	729 TGDNV <mark>N</mark> SLALCDFDGDGKKE TGDNV <mark>H</mark> SLALCDFDGDGKKE 160	749 LL LL 180
hBBS2 6vbu_BBS2	VGSEDFDIRVFKEDEIVA VGSEDFDIRVFKEDEIVA	769 EM <mark>T</mark> ETEI <mark>V</mark> TSLCPMYGSRFG EM <mark>S</mark> ETEI <mark>I</mark> TSLCPMYGSRFG 200	789 YALSNGTVGVYDKT <mark>S</mark> RYWRII YALSNGTVGVYDKT <mark>A</mark> RYWRII 220	809 KS KS 240
hBBS2 6vbu_BBS2	KN <mark>H</mark> AMSIHAFDLNSDGV <mark>N</mark> KN <mark>Q</mark> AMSIHAFDLNSDGV <mark>C</mark>	829 ELITGWSNGKVDARSDRTGE ELITGWSNGKVDARSDRTGE 260	849 VIFKDNFSSAIAGVVEGDYRI VIFKDNFSSAIAGVVEGDYRI 280	869 MD ME 300
hBBS2 6vbu_BBS2	G <mark>HI</mark> QLICCSVDGEIRGYL G <mark>CQ</mark> QLICCSVDGEIRGYL	889 PGTAEMRGNLMD <mark>TSA</mark> EQDLI PGTAEMRGNLMD <mark>ISV</mark> EQDLI 320	909 RELSQKKQNLLLELRNYEEN/ RELSQKKQNLLLELRNYEEN/ 340	929 AK AK 360

hBBS2 6vbu_BBS2	930 949 969 AELASPLNEADGHRGIIPANTRLHTILSVSLGNETQTAHTELRISTSNDTIIRAVLIFAE AEL <mark>S</mark> SPLNEADGHRG <mark>V</mark> IPANTKHHTALSVSLG <mark>SEAQAAHAELC</mark> ISTSNDTIIRAVLIFAE 361 380 400 420
hBBS2 6vbu_BBS2	1049 GIFTGESHVVHPSIHNLSSSICIPIVPPKDVPVDLHLKAFVGYRSSTQFHVFESTRQLPR GVFAGESHVVHPSVHHLSSSVRIPITPPKDIPVDLHLKTFVGYRSSTQFHVFELTRQLPR 440 460 480
hBBS2 6vbu_BBS2	1069 FSMYALTSLDPASEPISYVNFTIAERAQRVVVWLGQNFLLPEDTHIQNAPFQVCFTSLRN FSMYALTSPDPASEPLSYVNFIIAERAQRVVMWLNQNFLLPEDTNIQNAPFQVCFTSLRN 500 520 540
hBBS2 6vbu_BBS2	1129 1149 1169 GGHLHIKIKLSGEITINTDDIDLAGDIIQSMASFFAIEDLQVEADFPVYFEELRKVLVKV GGQLYIKIKLSGEITVNTDDIDLAGDIIQSMASFFAIEDLQVEADFPVYFEELRKVLVKV 600 560 580 600
hBBS2 6vbu_BBS2	1189 DEYHSVHQKLSADMADHSNLIRSLLVGAEDARLMRDMKTMKSRYMELYDLNRDLLNGYKI DEYHSVHQKLSADMADNSNLIRSLLVQAEDARLMRDMKTMKNRYKELYDLNKDLLNGYKI 620 640 660
hBBS2 6vbu_BBS2	1249 RCNNHTELLG <mark>N</mark> LKAVNQAIQRAG <mark>R</mark> LRVGKPKNQVITACRDAIRSNNINTLFKIMRVG RCNNHTELLG <mark>S</mark> LKAVNQAIQRAG <mark>H</mark> LRVGKPKNQVITACRDAIRSNNINMLF <mark>R</mark> IMRVGTASS 680 700 717 721
hBBS4 6vbu_BBS4	1288 1319 FPILEKQNWLIHLHYIRKDYEACKAVIKEQLQ MAEEKLSARTQLPVSAESQKPVLKKAPEFPILEKQNWLIHLYYIQKDYEACKAVIKEQLQ 29 60
hBBS4 6vbu_BBS4	1339 1359 1359 1379 ET <mark>Q</mark> GLCEYAIYVQALIFRLEGNIQESL <mark>E</mark> LFQTCAVLSPQ <mark>S</mark> ADNLKQVARSLFLLGKHKAA ET <mark>H</mark> GLCEYAIYVQALIFRLEGNIQESL <mark>R</mark> LFQMCA <mark>F</mark> LSPQ <mark>C</mark> ADNLKQVARSLFLLGKHKAA 80 100 120
hBBS4 6vbu_BBS4	1399 IEVYNEAAKLNQKDWEI <mark>S</mark> HNLGVCYIYLKQF <mark>N</mark> KAQDQLHNAL <mark>N</mark> LNRHDLTYIMLGKI <mark>H</mark> LL IEVYNEAAKLNQKDWEI <mark>C</mark> HNLGVCYIYLKQF <mark>D</mark> KAQDQLHNAL <mark>H</mark> LNRHDLTYIMLGKIFLL 140 160 180
hBBS4 6vbu_BBS4	1459 EGDLDKAIEVYKKAVEFSPENTELLTTLGLLYLQLGIYQKAFEHLGNALTYDPTNYKAIL KGDLDKAIEIYKKAVEFSPENTELLTTLGLLYLQLGIYQKAFEHLGNTLTYDPTNYKAIL 200 220 240
hBBS4 6vbu_BBS4	AAGSMMQTHGDFDVALTKYRVVACAVPESPPLWNNIGMCFFGKKKYVAAISCLKRANYLA AAGSMMQTHGDFDVALTKYKVVACAVIESPPLWNNIGMCFFGKKKYVAAISCLKRANYLA 260 280 300
hBBS4 6vbu_BBS4	1579 PFDWKILYNLGLVHLTMQQYASAFHFLSAAINFQPKMGELYMLLAVALTNLED <mark>I</mark> ENAKRA P <mark>L</mark> DWKILYNLGLVHLTMQQYASAFHFLSAAINFQPKMGELYMLLAVALTNLED <mark>S</mark> ENAKRA 320 340 360
hBBS4 6vbu_BBS4	1639 YAEAVHLDKCNPLVNLNYAVLLYNQGEK <mark>KN</mark> ALAQYQEMEKKV <mark>S</mark> LLK <mark>DN</mark> SSLEFD <mark>S</mark> EMVEM Y <mark>E</mark> EAV <mark>R</mark> LDKCNPLVNLNYAVLLYNQGEK <mark>RD</mark> ALAQYQEMEKKV <mark>N</mark> LLK <mark>YS</mark> SSLEFD <mark>P</mark> EMVEV 380 400 420
hBBS4	1683 AQKL
6vbu_BBS4	AQKLGAALQVGEALVWTKPVKDPKSKHQTASTSKAAGFQQPLGSNQALGQAMSSAATCRK 424
hBBS4 6vbu_BBS4	LSSGAGGTSQLTKPPSLPLEPEPTVEAQPTEASAQTREK

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Appendix Figure S5

hBBS5	AYFADGNKQQDREPVFSEELGLAIEKLKDGFTLQGLWEVS- 2004 2025
6VBU_7 hBBS7	20 MDLNLNRADYLQVGVTSQKTMKLLPASKHRATQKVVVGDHDGIVMCFGMKKGEAVTVFKT MDLILNRMDYLOVGVTSOKTMKLIPASRHRATOKVVIGDHDGVVMCFGMKKGEAAAVFKT 2045 2085 2085
6VBU_7 hBBS7	80 LPG <mark>Q</mark> KIARLELGG <mark>AL</mark> NTPQEKIFIAAGSEIRGFTKRGKQFLSFETNLTESIKAMHISGSD LPG <mark>P</mark> KIARLELGG <mark>VI</mark> NTPQEKIFIAAASEIRGFTKRGKQFLSFETNLTESIKAMHISGSD 2105 2125 2145
6VBU_7 hBBS7	LFLSASYIYNHYCDCKDQHYYLSGDKINDVICLPVERLLREVPVLACQDRVLRVLQGSDV LFLSASYIYNHYCDCKDQHYYLSGDKINDVICLPVERLSRITPVLACQDRVLRVLQGSDV 2165 2185 2205
6VBU_7 hBBS7	200 TYEIEVPGPPTVLALHNGNGGDSGEDLLFGTSDGKLGLIQITTSKPIHKWEIRNEKKRGG MYAVEVPGPPTVLALHNGNGGDSGEDLLFGTSDGKLALIOITTSKPVRKWEIQNEKKRGG 2225 2245 2265
6VBU_7 hBBS7	300 ILC <mark>V</mark> DSFDIVGDGVKDLLVGRDDGMVEVY <mark>G</mark> FDNANEPVLRFDHTLSESVTSIQGGCVGKD ILC <mark>I</mark> DSFDIVGDGVKDLLVGRDDGMVEVY <mark>S</mark> FDNANEPVLRFDQMLSESVTSIQGGCVGKD 2325 2325
6VBU_7 hBBS7	320 GYDEIVVSTYSGWITGLTTEPVHKESGPGEELKENQEMQNKISSLRSELEQLQYKVLQER SYDEIVVSTYSGWVTGLTTEPIHKESGPGEELKINQEMONKISSLRNELEHLQYKVLQER 2345 2365 2385
6VBU_7 hBBS7	420 EKYQQSSQSSKAKSAVPSF <mark>SV</mark> NDKFTLNKDDASYSLILEVQTAIDNVLIQSDVPIDLLDV ENYQQSSQSSKAKSAVPSF <mark>GI</mark> NDKFTLNKDDASYSLILEVQTAIDNVLIQSDVPIDLLDV 2405 2425 2445
6VBU_7 hBBS7	440 DKNSAVVSFSSCDSESNDNFLLATYRCQANTTRLELKIRSIEGQYGTLQAYVTPRIQPKT DKNSAVVSFSSCDSESNDNFLLATYRCQADTTRLELKIRSIEGQYGTLQAYVTPRIQPKT 2465 2485 2505
6VBU_7 hBBS7	500 CQVRQYHIKPLSLHQRTHFIDHDRPMNTLTLTGQFSF <mark>SEL</mark> HSWVVFCMPEVPEKPPAGEC CQVRQYHIKPLSLHQRTHFIDHDRPMNTLTLTGQFSF <mark>AEV</mark> HSWVVFCLPEVPEKPPAGEC 2545 2545
6VBU_7 hBBS7	580 VTFYFQNTFLDTQLESTYRKGEGVFKSDNISTISILKDVLSKEATKRKINLNISYEINEV VTFYFQNTFLDTQLESTYRKGEGVFKSDNISTISILKDVLSKEATKRKINLNISYEINEV 2605 2605

Е

6VBU_5 YTSLIAVHRAYETSKMYRDFKLRSALIQNKQLRLLPQENVYNKINGVWNLSSDQGNLGTF hBBS5 FTSVMAVHRAYETSKMYRDFKLRSALIQNKQLRLLPQEHVYDKINGVWNLSSDQGNLGTF 180 180 6VBU_5 FITNVRIVWHANMNDSFNVSIPYLQIRSVKIRDSKFGLALVIESSQQSGGYVLGFKIDPV hBBS5 FITNVRIVWHANMNDSFNVSIPYLQIRSIKIRDSKFGLALVIESSQQSGGYVLGFKIDPV 180 180 6VBU_5 FITNVRIVWHANMNDSFNVSIPYLQIRSIKIRDSKFGLALVIESSQQSGGYVLGFKIDPV 1884 1904 6VBU_5 EKLQESVKEINSLHKVYSANPIFGVDYEMEEKPQPLEALTVKQIQDDVEIDSDDHTDAFV 1884 1904

341 AYFADGNKQQDREPVFSEELGLAIEKLKDGFTLQGLWEVMN

20

1704

40

1724

1744

MSVLDALWEDRDVRFDVSSQQMKTRPGEVLIDCLDSVEDTKGNNGDRGRLLVTNLRIVWH

MSVLDALWEDRDVRFDLSAQQMKTRPGEVLIDCLDSIEDTKGNNGDRGRLLVTNLRILWH

SLALPRVNLSIGYNCILNITTRTANSKLRGQTEALYVLTKCNSTRFEFIFTNLVPGSPRL

SLALSRVNVSVGYNCILNITTRTANSKLRGOTEALYILTKCNSTRFEFIFTNLVPGSPRL 1764 1784 1784 1804

6VBU_5 hBBS5

6VBU 5

hBBS5

6VBU 5

6VBU_7 hBBS7	520 SVKHTLKLIHPKLEYQLLLAKKVQLIDALKELQ SVKHTLKLIHPKLEYQLLLAKKVQLIDALKELQ 2645	00000000000000000000000000000000000000	660 ILEEADHLQEEY ILEEADHLQEEY 2685
6VBU_7 hBBS7	KKQPAHLERLYGMITDLF1 680 KKQPAHLERLYGMITDLF1DKFKFKGTNVKTKV 2705	700 PLLLEILDSYDQNAL PLLLEILDSYDQNAL 2725	715 IAFFDAA ISFFDAA 2740

F

G

6VBU_BBS8 hBBS8	MEPLLLAWSYFRRRRFQLCADLCTQMLEKSPCDQAAWILKARALTEMVYVDEIDVDEEGI MEPLLLAWSYFRRRKFQLCADLCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGI 2760 2780 2800
6VBU_BBS8 hBBS8	AEMILDENAIAQVPRPGTSLKLPGTNQTGGPSPAVRPVTQAGRPITGFLRPSTQSGRPGT AEMMLDENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITOAGRPITGFLRPSTQSGRPGT 2820 2840 2840 2860
6VBU_BBS8 hBBS8	160 IEQAIKTPRTAYTARPIASSSGRFVRLGTASMLTSPDGPFINLSRLNLAKYAQKPKLAKA MEQAIRTPRTAYTARPITSSSGRFVRLGTASMLTSPDGPFINLSRLNLTKYSQKPKLAKA 2880 2900 2920
6VBU_BBS8 hBBS8	200 LFEYIFHHENDVKTALDLAALSTEHSQYKDWWWKVQIGKCYYRLGLYREAEKQFKSALKQ LFEYIFHHENDVKTALDLAALSTEHSQYKDWWWKVQIGKCYYRLGMYREAEKQFKSALKQ 2940 2960 2980
6VBU_BBS8 hBBS8	260 QEMVDTFLYLAKVY <mark>I</mark> SLDQPLTALNLFKQGLDKFPGEVTLLCGIARIYEEMNNISSATEY QEMVDTFLYLAKVY <mark>V</mark> SLDQPVTALNLFKQGLDKFPGEVTLLCGIARIYEEMNNMSSAAEY 3000 3020
6VBU_BBS8 hBBS8	320 YKEVLKQDNTHVEAIACIGSNHFYTDQPEVALRFYRRLLQMGVYNCQLFNNLGLCCFYAQ YKEVLKQDNTHVEAIACIGSNHFYSDQPEIALRFYRRLLOMGIYNGQLFNNLGLCCFYAQ 3060 3080 3100
6VBU_BBS8 hBBS8	380 QYDMTLTSFERALSLAENEEEVADVWYNLGHVAVGTGDTNLAHQCFRLALVSNNQHAEAY QYDMTLTSFERALSLAENEEEAADVWYNLGHVAVGIGDTNLAHQCFRLALVNNNNHAEAY 3120 3140 3140
6VBU_BBS8 hBBS8	NNLAVLEMR <mark>R</mark> GHVEQAKALLQTASSLAPHMYEPHFNFATISDKIGDLQRSYAAAKKSEAA NNLAVLEMRKGHVEQARALLQTASSLAPHMYEPHFNFATISDKIGDLQRSYVAAQKSEAA 3180 3200 3220
6VBU_BBS8 hBBS8	FPDHVDTQHLIKQLEQHFAML FPDHVDTQHLIKQLRQHFA 3240
6VBU_BBS9 hBBS9	40 MSLFKARDWWST <mark>V</mark> LGDKEEFDQGCLCLADVDNTGNGQDKIIVGSFMGYLRIFNPHPVKTG -SLFKARDWWSTILGDKEEFDOGCLCLANVDNSGNGODKIIVGSFMGYLRIFSPHPAKTG 3260 3280 3300
6VBU_BBS9 hBBS9	120 DGAQAEDLLLEVHLRDPTLQVEVGKFVSGTEMLHLAVLHSRKLCVYSVSGTLGNVEHGNQ DGAQAEDLLLEVDLRDPVLQVEVGKFVSGTEMLHLAVLHSRKLCVYSVSGTLGNVEHGNQ 3320 3340 3360
6VBU_BBS9 hBBS9	YQ <mark>I</mark> KLMYEHNLQRTACNMTYGSFGGVKGRDLICIQS <mark>V</mark> DGMLMVFEQESYAFGRFLPGSLL CQMKLMYEHNLQRTACNMTYGSFGGVKGRDLICIQSMDGMLMVFEQESYAFGRFLPGFLL 3380 3400 3400 3420
6VBU_BBS9 hBBS9	200 PGPLAYSSRTDSFITVSSCHQVESYKYQVLAFATDADKRQETEQQKHGSGKRLVVDWTLN PGPLAYSSRTDSFLTVSSCQOVESYKYQVLAFATDADKRQETEQQKLGSGKRLVVDWTLN 3440 3460 3480

 6VBU_BBS9
 IGEQAIDICIVSFIQSASSVFVLGERNFFCLKDNGQIQFMKKLDYSPSCFLPYCSVSEGT

 hBBS9
 IGEQALDICIVSFNQSASSVFVLGERNFFCLKDNGQIRFMKKLDWSPSCFLPYCSVSEGT

 3500
 3540

 320
 340

 6VBU_BBS9
 INTLIGNHNNMLHIYQDVTLKWATQLPHVPVAVRVGCLHDLKGVIVTLSDDGHLQCSYLG

 hBBS9
 INTLIGNHNNMLHIYQDVTLKWATQLPHIPVAVRVGCLHDLKGVIVTLSDDGHLQCSYLG

 3560
 3580

6VBU_BBS9 hBBS9	380 420 TDPSLFQAPKVESRELNYDELDMELKELQKVIKNVNKSQDVWPLTEREDDLKVSAMVSPN 420 TDPSLFQAPNVQSRELNYDELDVEMKELQKIIKDVNKSQGVWPMTEREDDLNVSVVVSPN 3640 3640 3660
6VBU_BBS9 hBBS9	480 FDSVSQATDVEVG <mark>A</mark> DLVPSVTVKVTLKNRVALQKIKLSIYVQPPLVLTGDQFTFEFMAPE FDSVSQATDVEVG <mark>T</mark> DLVPSVTVKVTLQNRVILQKAKLSVYVQPPLELTCDQFTFEFMTPD 3680 3700 3720
6VBU_BBS9 hBBS9	520 MTRTVGFSVYLKGSYSPPELEGNAVVSYSRPTERNPDGIPRVSQCKFRLPLKLVCLPGQP LTRTVSFSVYLKRSYTPSELEGNAVVSYSRPTDRNPDGIPRVIQCKFRLPLKLICLPGQP 3740 3760 3780
6VBU_BBS9 hBBS9	SKTASHK <mark>L</mark> TIDTNKSPVSLLSLFPGFAKQS <mark>E</mark> DDQVNVMGFRFLGG <mark>SQVTL</mark> LASKTSQRYR SKTASHK <mark>I</mark> TIDTNKSPVSLLSLFPGFA <mark>S</mark> QSDDDQVNVMGFHFLGG <mark>ARITV</mark> LASKTSQRYR 3800 3820 3820 3840
6VBU_BBS9 hBBS9	IQSEQFEDLWLITNELI <mark>I</mark> RLQEYFEKQG <mark>I</mark> KDF <mark>T</mark> CSFSGSVPLEEYFELIDHHFELRINGE IQSEQFEDLWLITNELI <mark>L</mark> RLQEYFEKQG <mark>V</mark> KDF <mark>A</mark> CSFSGSIPLQEYFELIDHHFELRINGE 3860 3880 3800
6VBU_BBS9 hBBS9	700 720 KLEELLSERAVQFRAIQRRLL <mark>T</mark> RFKDKTPAPLQHLDTLLDGTYKQVIALADAVEENQ <mark>D</mark> NL KLEELLSERAVQFRAIQRRLLARFKDKTPAPLQHLDTLLDGTYKQVIALADAVEENQGNL 3920 3940 3960
6VBU_BBS9 hBBS9	740 780 FQSFTRLKSATHLVILLIGLWQKLSADQ <mark>I</mark> AILEAAFLPLQQDTQELGWEETVDAALSHLL FQSFTRLKSATHLVILLI <mark>A</mark> LWQKLSADQ <mark>V</mark> AILEAAFLPLQEDTQELGWEETVDAA <mark>I</mark> SHLL 3980 4000 4020
6VBU_BBS9 hBBS9	820 KTCLSKSSKEQALNLNSQLGIPKDTSQLKKHITLFCDRLAKGGRLCLSTDAAAPQTMVMP KTCLSKSSKEQALNLNSQLNIPKDTSQLKKHITLLCDRLSKGGRLCLS 4060 4068
6VBU_BBS9 hBBS9	GGCATIPESDLEGRSIDQDSSELFTNHKHLMVETPVPEVSPLQGVTE
6VBU_BBS18 hBBS18	MAETKSMFREVLPKQGQL <mark>20</mark> MAETKSMFREVLPKQGQLYVEDITTMVLCKPKLLPLKSLTLEKLEKMQQAAQDTIHQQEM MFREVLPKOGPLFVEDIMTMVLCKPKLLPLKSLTLEKLEKMHQAAQNTIROO 4084 4104 4122
6VBU_BBS18 hBBS18	TEKEQKITH

Appendix Figure S5: BBSome bovine and human sequence alignments, highlighting the different residue numbers between the experimental (PDB ID: 6vbu) and the human homology model used during CG-MD simulations. **A.** *b*BBS1/*b*BBS1; **B**. *b*BBS2/*b*BBS2; **C**. *b*BBS4/*b*BBS4; **D**. *b*BBS5/*b*BBS5; **E**. *b*BBS7/*b*BS7; **F**. *b*BBS8/*b*BBS8; **G**. *b*BBS9/*b*BBS9; **H**.

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bBBS18/hBBS18.



Appendix Figure S6: ARPE-19 cells were transiently transfected with Myc-tagged BBS1 variants or Myc-tagged BBS1- K143R. After 24h from transfection, cells were harvested and analyzed using a fluorescein isothiocynate (FITC) Annexin V Apoptosis Detection Kit and 7-AAD staining solution, according to the manufacturer's protocol.