```
OccD1          -------------------------DAFVSDQAEAKGFIEDSSLDLLLRNYYFNRDGKSG 35
OccD2          ----------------------------DEGEAKEGFIEGSSLQLLTRNYYFNHDRRHA 31
OccD3          ADEQENPPAPDNPSYAAEVQSIPSVAKPIKGQAGATGLVEGQSLTLTTRNFYSRENMKDS 60
OccD4          --------------------------EENAERSKEGFIEGSEVNLLLRNFYFNRDFRKG 33
OccD5          --------------------------------GDGGFVEDSELQFLARTYYFNRDYRDS 27
OccD6          ----------------------------NDQEAAKGFVEDSHLDLFFRNGYISRDYKHG 31
OccD7          -------------------------------ATEEAKAPDYLEWRLLNRNYFLYNDYRR- 28
OccD8          ----------DDSLGHRDNISTGLNQRQKAEMKVPPGFVEGSTLNGFIRNYYFARDNHDT 50

OccK1          ---------------------------------AEGGFLEDAKTDLVLRNYYFNRDFRDH 27
OccK2          ----------------------------GHVHAGQGFLEDAKASLTARNFHLHRNFVG- 30
OccK3          -------------------------------------DLVEDSHASLELRNFYFNRDFRQS 24
OccK4          -------------------------------------EFLADSSAHLDLRNFYQLRDYRQH 24
OccK5          ----------------------------------AGFLEDSKASLETRNFYMNRDFRD- 24
OccK6          -------------------------------------EFIKDSKASIELRNFYFNRDFRQE 24
OccK7          -------------------------------------EFFADGKAGLELRNFYFNRDYRQP 24
OccK8          ----------------------------------AGFIEDSKASLTLRNFYINTDNRNG 25
OccK9          ----------------------------------EGFIEDASVSLGLRNLYFNRDFRQP 25
OccK10         -------------------------------------AFLEDGSARLEARTVYFNRDFRDG 24
OccK11         ----------------------------------EGFLEDSRASLALRNFYMNRDFRD- 24
                                                          *. .   :

OccD1          ----SGDR-----------VDWTQGFLTTYESGFTQGTVGFGVDAFGYLGLKLDGT--SD 78
OccD2          SG-HDS-------------KEWAQGFIATFQSGYTPGVVGFGVDAYGMLGLKLDGG--GG 75
OccD3          FTFRIPKAGG-GSQRIHQRNAWVQGTVLKYSSGYTQGTVGFGFDVAAFNEIALERG--KG 117
OccD4          QSS-PAGGGY--------TEEWVQGFMANFSSGFTQGTLGVGIDAFAQLGVRLDSG--GG 82
OccD5          PNNAGRNRFKPRSERNGYREEATQGLRLQFASGYTPGSLGFGLDAHAMLGLQLDSG--GG 85
OccD6          ----RQDK-----------AEWGQAATATFTSGFTQGTVGVGVDAFGLYAVRLDGG--KG 74
OccD7          -ADAGR----------GYRKEWAHGLIVDLESAYTPGRVGFGLDLHGFAGFKLDGG--RG 75
OccD8          PSRRDQ-------------REWAQGLMLSFRSGYTDTPIGIGLDAHAFYGLRLDGG--GG 95

OccK1          ----DAGKSL--------VDEWAQGFILKFSSGYTPGTVGVGLDAIGLFGVKLNSG--RG 73
OccK2          ----DASQGK--------AEEWTQSFILDARSGFTQGSVGFGLDVLGLYSLKLDGG--KG 76
OccK3          ----GARDN---------ADEWAQGFLLRLESGFSEGTVGFGVDAIGLLGFKLDSG--SG 69
OccK4          ----DAPQSQ--------AGNWSQGFVLRLQSGFTGGPLGFGLDATGLLGVKLDSG--RG 70
OccK5          ----GPGQSK--------REEWAQGFILNLQSGYTQGTVGFGLDAMGMLGVKLDSG--RG 70
OccK6          ----GASQSK--------AEEWAQGFLLRYESGYTEGTIGFGVDAIGLLGVKLDSS--PD 70
OccK7          ----GASQSY--------SEEWAQGFLLRYESGYTEGLFGLGVDALGLLGVRLDSS--PE 70
OccK8          ----TASPSK--------QEEWGQGFILNYQSGFTQGTVGFGVDALGLLGVRLDGGGRAG 73
OccK9          ----GAAQSK--------QEEWAQGFLLQAKSGYTQGTLGLGVELIGQLGLKLDSS--PD 71
OccK10         SSANPQGASK--------REEAAQGFILDLRSGYTEGALGFGVDTLAMLGIKLDSS--PA 74
OccK11         ----GAGRAK--------SEEWAQGFLFDYRSGYTEGTLGVGLDLLGKLGVRLDSG--AG 70
                                     :.      *.::   .*.*.:  .   . *:

OccD1          KTGT----GNLPVMN----DGKP---RDDYSRAGGA-VKVRISKTMLKWGEMQPTAPVFA 126
OccD2          TGGT----SILPITSPSKEGYESGKAPDEFSSGGAA-LKIRAFDTELKLGDQFLSNPVVA 130
OccD3          RIGGG---GNRTLAN------SDGEALGEWSKLGVANIRLRASNTEFKAGRFLVNTPVFS 168
OccD4          RSGAGGSVDLLPYDD-------QGRPQDDYSRAGGA-VKLRWYGTVLRVGDVFPETPVIQ 134
OccD5          RTGT----GNLPVGA-------DGHPDHRYGKVGGA-LRLRHGETRLKYGQTTTSAPVFA 133
OccD6          RSGA----AGIDFFK----QGDSGSAADDLSKGGAA-VKFRISNTVLKYGDQMPSLPVLS 125
OccD7          HAGT----GLLPLDS-------SGDNASEYSDAGAA-LKLRLGESLLKVGEMTVETPVFD 123
OccD8          SGGA----GVLPLDS-------AGRPADSFSAAGAA-LKLRGLDSLLKIGDQLLENPVIA 143

OccK1          TSNS----ELLPLHD-------DGRAADNYGRVGVA-AKLRVSASELKIGEMLPDIPLLR 121
OccK2          TAGT----QLLPIHD-------DGRPADDFGRLAVA-GKLRVSNSELKIGEWMPVLPILR 124
OccK3          SGGT----GLLPADG------SAGGSQDDYAKLGLT-AKARVSNSLLKVGALHFKSPLVS 118
OccK4          RSND----GTLPFGA------NSKEPVDDYSHLGLT-AKLRYSQTQLQVGILMPQLPVAF 119
OccK5          RSGT----GLLPKD-------SDGRAPDTYSKLGLT-AKVKVSQSELKVGTLIPKLPSVQ 118
```

```
OccK6          RSGT----GLLKRDR------ETGRAQDDYGEAGIT-AKLRASKSTLKIGTLTPKLPVIM 119
OccK7          RSGS----GLLPYST------SDRRAAHDYSSLGLT-AKLRVSHSTLKIGTLMPRLPVVQ 119
OccK8          KSGLDRQPGTVFPLE------SNGEPVHDFASLGLT-AKAKVSNTEFRYGTLQPKLPVVT 126
OccK9          RAGS----GLLPRHA-------DGRAADDYARLGVA-PKLKLSNTELKLGELLPELPILL 119
OccK10         DSNS----GLLPSSGH-----DPRRSVDQYAKAGVA-GKMRFSQTQFRYGAMLPDMPLLK 124
OccK11         RSGT----GLLPLR-------DDGSAAGDYARLDAT-AKLRLSRSELKVGGLVPKLPTIQ 118
                 .                           .    :  : :   : :: *      *

OccD1          AGGSRLFPQTATGFQLQSSEFE-GLDLEAGHFTEGKEPTTVKSRGELYATYAGET----- 180
OccD2          GGESRMLPQTFRGVSLTNNSFE-DLTLTAG-QVSFTKYYNQSGHRRLGSYYG-----ELP 183
OccD3          YIDNRALPSSFTGFAVTSEELD-NLSLQAGSFRKVSPRTGS-GDEDMTTEYGTRQVK--- 223
OccD4          YGNSRLFPSSFRGFTLVNDSLAKGLTLQAGKLNSMTQPNSTSGSDDFYSFYTGRRID--- 191
OccD5          ASSNRTLAGMAYGLLLEDRSFD-GLLLEGGRFTAASGPGESKVRGDISTVYG----RLGA 188
OccD6          YDNSRLLPESYSGTLITSKEIE-GLELNAGRFT-------AESRKSAEGRDSGG------ 171
OccD7          TSDKRLQPQYARGFFLQSDDLD-RVRIQAGRFTAFKEQASSSGHGDFDG-YG----ASTA 177
OccD8          SGVSRMVPQSYRGVTLKNYHFR-ALELDAG-FVEATRLRNQSGHSHLTSGYGNGTKGGIA 201

OccK1          YDDGRLLPQTFRGFAVVSRELP-GLALQAGRFDAVSLRNSA-DMQDLSAWSAPTQK---- 175
OccK2          SDDGRSLPQTFRGGQLSANEIA-GLTLYAGQFRGNSPRNDA-SMQDMSLFGRPAAT---- 178
OccK3          ANDTRLLPELFRGALLDVQEID-GLTLRGAHLDRNKLNSSS-DYQVFSANRIGGR----- 171
OccK4          RDDVRLLPQTFDGALLTSSEIE-GLTLTAGQLWKSRTRESA-GSDDMYIMGRDKAH---- 173
OccK5          PNNGRIFPQIFEGALLTSKEIK-DLGFTAGRLEKTKIRDSS-DSEDLALNDKNGRFAGVS 176
OccK6          PNDSRLLPQTFQGGALNSMEID-GLTLDAGRLKKVNQRDSS-DNEDMTITGGGKRNIVVR 177
OccK7          FNDTRLHPQTFQGGLLEVNEID-GLALQFGQLRQVKQRDST-NAEDLGITRGNKRNVLAG 177
OccK8          YNDGRLLPVTFEGGQVTSTDLK-DFTLVAGQLEHSKGRNST-DNRSLSIAGANGSSASSR 184
OccK9          RNDGRLLPQTFQGGMLTSREIA-GLTLHGGQMRSLSQRNSS-DHQDLSVDGRGGAF---- 173
OccK10         YNDGRLLPTLFHGAQLTSEEIA-GLRFSATRLERYTARDSS-DAQDIRLHCKNKRYACDT 182
OccK11         PNYGRLFPQVFQGALLTSGELS-GLSLNLGRLTEVSQRNEA-GTSDLALFNRNRRFAGAA 176
                   *  .    *  :    :   . :

OccD1          ----AKSADFIGGRYAITDNLS-ASLYGAELEDIYRQYYLNSNYTIP-LASDQSLGFDFN 234
OccD2          GDRDSHHLSWLGGTWGGIEGFT-SSLYAAELQNVWKQYYADVDYTYE-IDDNWSLNPGAH 241
OccD3          ----GDRLNYLGGNYKPLDGLE-ISLYGSHFQDVWNQYYLGVTHDIGDLENGIALRTAFN 278
OccD4          ----SPWVAYAGGDYQATEHWS-VSLYGSRQKDAWDQYYAGTSFNYP-LDDKLSLLGGAN 245
OccD5          YPVRLDAVGFLGGQWQATERLQ-LSLYASRFDDIWQQAYFGASHRQP-LGGERALRVDLD 246
OccD6          ----LKSINVFGGKYAFTDHFN-ASLYASDVEDVLKKQYINLNYTIP-LQADQSLNFDFN 225
OccD7          G----SAIGFAGASLAASDNLS-GSLFAAQLDNVWRQVYLNMNLQR------AAFSLDGN 226
OccD8          ADRESPHIAWLGASYSAPGGSQ-ATLYSGRLEDIWNQHYLGLSQPWR-LSSQLTLTPWLH 259

OccK1          ----SDGFNYAGAEYRFNRERTQLGLWHGQLEDVYRQSYANLLHKQR-VGDW-TLGANLG 229
OccK2          ----SDRFDFAGGEYRFNGERSLLGLWNAELKDIYRQQYLQLQHSQP-LGDW-LLGANLG 232
OccK3          ----SDAFDFAGGDYRLTPALT-ASLHQGRLKDIYRQTFAGLVHTLD-LGGQRSLKSDLR 225
OccK4          ---ASDEFNLAGATYAFTPRLS-ASYYYGQLKDIYRQHYLGLLHTLP-LGEGLSLRSDLR 228
OccK5          ----ADHFDLGGLDYKLTDQLT-ASYHYSNLQDVYRQHFVGLLHSWP-IGPG-ELTSDLR 229
OccK6          SGLTSDKFDFAGGSYKWTDNLS-TSYHYGKLDNFYKQHYLGLVHTLP-IADKQSLKSDIR 235
OccK7          RHPGSDRFDFAGGTYRWSERLS-SSYHYANLEDFYRQHHLGVQHLLP-LADDQSLKSDIR 235
OccK8          D---SNKFYYAGGDYKVNKDLT-LQYYYGNLDDFYKQHFLGLIHNWQ-IGPG-VLKTDLR 238
OccK9          ----SDRFDYLGAEYRFNAERSQVGLWQARLQDIYRQDYYSLSHKQS-FGGW-RLGASVG 227
OccK10         T---GNRFDAYQLDYQVNDGLL-LQYAQGGLRNVYRQRYLGAVGKRQ-VGAG-KLSADLR 236
OccK11         Q---ADRFDLAGLDYRIAPDWT-GSYHYGELEQVYAQHFLGLKGRIG-IAAD-SLESDLR 230
                                            .   :   : .               :

OccD1          IYRTNDE----GKAKAG--------------------DISNTTWSLAAAYTLDA-HTFTL 269
OccD2          YYKTVDS----GDSLLG--------------------RIDNNTYSLHFAVGYRQ-HTVTA 276
OccD3          GYHTGDT----GAREAG--------------------YIDNDTWSLAFTLGHRA-HALTL 313
OccD4          YYKVKDQ----GRQVMG--------------------ELDNDIWSVRGGFAYGP-HQVLL 280
OccD5          AYRTRDS----GQSRFG--------------------RIDTLTSSLALGYEHGP-QRITL 281
OccD6          GYRTKLDSDFADQNFNG--------------------NRDNKIWSLAASYTIDA-HTFMI 264
```

```
OccD7          LYRTRDQ----GRSRAG--------------------AIDTLAYSLQLKYRVGA-QGFSL 261
OccD8          YYKTRDQ----GRSQLG--------------------RIDNDLYNAGLTLAGGG-QSLSL 294

OccK1          LFVDRDD----GAARAG--------------------EIDSHTVYGLFSAGIGL-HTFYL 264
OccK2          GFRGRDA----GSARAG--------------------KLDNRTVSALFSARYGL-HTLYL 267
OccK3          FARASED----GGFR----------------------ELDNRAFGALFSLRLGA-HAVAA 258
OccK4          YFDSGED----GAAIS--------------------GPVDNRNLNAMLTLRAGA-HAFGI 263
OccK5          FARSTDS----GSAKA--------------------GGIDNKSLNGMFTYSLGN-HAFGA 264
OccK6          WARSTDD----GSS----------------------NVDNKALNAMFTYSLGY-HAFGV 267
OccK7          WARSTDE----GGS----------------------RVNNRALNALFTYRLGG-HAFGL 267
OccK8          AFDSSSD----GKNGSRSGRADGYVSSGYYGSGVTKGEVDNRAFSGLFTYTVSG-HSIGA 293
OccK9          LFDTRDE----GAAKLG--------------------ELENRALTGFFSATRGG-HSLGA 262
OccK10         WFDSEDA----GAARAG--------------------KIDNRALSLLLAYAQGG-HTLSA 271
OccK11         LALSRDT----GGARG--------------------GRIDNRSFSGSLTYRLRNGQAFGL 266
                     .                                  ..              : .

OccD1          AYQKVHGDQPFDYIGFGRNG-SGAGGDSIFLANSV--QYSDFNGPGEKSWQARYDLNLAS 326
OccD2          VLQKVNGNTPFDYINQGD---------SIFLDNS--QQYSDFNGPNEKSWKLQYDYDFVA 325
OccD3          AYQQVDGNEYFDYVHET---------SAIFLANS---MLADYNSPNEKSAQIRYETDWSY 361
OccD4          SYQRNNGDDDFDYLRQT---------DSIYLDNS--IQYSDFNSPKERSLMLRYDLDMAA 329
OccD5          AYQRVHGEQPFDYMAFGDGR----SSASMVLANS--VGYSDFNGPGERSWQLRYDLDLGA 335
OccD6          AHQRNTGDTGYNYGWYQNAGGIGDGGTTIWLANS---YWSDFNAEDERSWQVSYALDFAK 321
OccD7          AYQRVHGDTPFDFVG-GD---------SIYLANS--IKYADFNGPGERSWQARYDLDLAP 309
OccD8          SLQKVDGDTPFDFIAQND---------RTFLYESNAMQYADFNGPGERSWKIQYQASLAF 345

OccK1          GLQKVGGDSGWQSVYG---------SSGRSMGND--MFNGNFTNADERSWQVRYDYDFVG 313
OccK2          GLQKVSGDDGWMRVNG---------TSGGTLAND--SYNASYDNPGERSWQLRYDFDFVG 316
OccK3          GYQRISGDDPYPYIAG----------SDPYLVNF--IQIGDFGNVDERSWQLRYDYDFGA 306
OccK4          GVQKMIGNDAFPVLNGY---------TTPYVANL--MAYQTFTRPQEKSWQLRYDYDFAG 312
OccK5          AWQRMNGDDAFPYLEG----------SNPYLVNF--VQVNDFAGPKERSWQLRYDYDFVG 312
OccK6          GYQKMSGDTGFAYING----------ADPYLVNF--IQIGDFANKDEKSWQARYDYNFAG 315
OccK7          GYQRMSGDSGFAYLAG----------TDPYLVNF--VQIGDFANKDERSWQLRYDYDFAA 315
OccK8          GYQILNGDSDFPFLNRGDGE-----GSTAYLITD--VQIGKFQRAGERTWQVRYGYDFAT 346
OccK9          GYQRMYGDDGMLYIAG---------TS-TPLVND--IQVRNFTSAGERSWQLRYDYDFVA 310
OccK10         GWQRMNGASSMPYLDG----------SNPYLANY--LQVNDFANPEERSWQLRYDFDLRS 319
OccK11         GYQRMSGDHGFPYLEG----------TDPYLVNF--GQYNDFAEAGESSWQLRYDCDFAP 314
                 *   *                       :          :    * :    *  .

OccD1          YGVPGLTFMVRYINGKD-------IDGTKMSDNNVGYKNYGYGEDGKHHETNLEAKYVVQ 379
OccD2          LGLPGLSASASYSRGK------LDLTRVDPDSPGYGGWYSADGKNAKHWERDLDLQYVVQ 379
OccD3          YGVPGLSTGVWYVKGWDIDG---THYDGDRNGAYGNYAEVRAQDGEKHHELGLMAAYKVQ 418
OccD4          FGVPGLSFMTRYGKGWD------ADYSNANSVYMRTDANGNPLTNQGRWERDVEVKYVVQ 383
OccD5          LGLPGLSLHALHARGR---------AGASASSAAESIYAGLYGRDGRHRENDLGFAYRVK 386
OccD6          YGVPGLTYRVAYVRGDN-------IKTAETSN-------------GKEREIFNQVQYVVQ 361
OccD7          FGLPGLSFMARYVSGRAIDGSHAPAGGAYNPLGADGRYRPLQGSGGKHWERDLDLRYLFA 369
OccD8          LAAPDWQFGAAYGRGQ------ADLTRVDPDSAGYGYLYNPNGKNAQHWERDLSLRYAFP 399

OccK1          LGWPGLIGMVRYGHGSN------ATTKAGSG--------------GKEWERDVELGYTVQ 353
OccK2          LGLPGLTFMTRYLHGDH------VRLAGVTDD-------------GSEWGRESELGYTLQ 357
OccK3          LGLPGLSFMSRYVSGDN------VARG-AAND-------------GKEWERNTDLGYVVQ 346
OccK4          LGLPGLNLMTRYVQGRD------IDRGAGRAD-------------DSEWERNTDLSYVIQ 353
OccK5          LGIPGLTFMTRYVKGDN------VELAGQSGE-------------GREWERNTELQYVFQ 353
OccK6          VGIPGLTFMTRYVKGDN------IDLLTTSGE-------------GKEWERDMDIAYVFQ 356
OccK7          IGLPGLTFMSRYLRGEH------IDLLDGGGR-------------GKEWERDTDIAYLVQ 356
OccK8          VGVPGLTFNTIYLSGD--------KIKTARGD-------------QSEWERDISLAYVIP 385
OccK9          LGIPGLTAMARYASGAH------ARTKAMDD--------------GRAWERDVDVAYVIQ 350
OccK10         VGVPGLSFMTRYVNGDH------IRLANGDE--------------GKEWERDIELKYIVQ 359
OccK11         LGVPGLSLMTRYFSGHG------AKPKGADG--------------SREWERDSDLRYVLQ 354
                                                                        * .
```

```
OccD1          SGPAKDLSFRIRQAWHRAN-----ADQG--EGDQNEFRLIVDYPLSIL- 420
OccD2          GGPAKDLSLRLRWATHRGTGGYSAVDN-----DIDEYRVIVDYPIDVF- 422
OccD3          NGPIKDSTFKLTYMMHKAS-------QNQIDGSVNELRLVSTFPFNLL- 459
OccD4          GGAAKDLAFRVRQATVRS---------DSFESDLDEVRLIVEYPLQVL- 422
OccD5          AGPLAGLALRASQAWHRGNASY--LDG-----DIDETRLVVDYSRSIW- 427
OccD6          SGPAKDLTLRLRSSFLRVS-----NDARSYNDDGNEIRAFVEYPFSVF- 404
OccD7          SGPFKDLSLNVSHLSHRANAAQ--AGD-----DIDRLYLIVEYPLKGSL 411
OccD8          AGPAKGLSVTLRWATHRPGEGYTAPGNTRGNSSSDEYRVVVDYPIRLL- 447

OccK1          SGPLARLNVRLNHASNRR--------SFNS--DFDQTRLVVSYPLSW-- 390
OccK2          SGAFKRLNVRWRNSSQRR--------DWGSNTRFDENRLIVSYPLSLL- 397
OccK3          SGPLKNLGVKWRNATVRS----------NFANDLDENRLILSYSLALW- 384
OccK4          SGPLKSVALKWRNITYRS----------RYGADLDENRFIVNYTLKLW- 391
OccK5          SGALKNLGIRWRNATFRS----------NFTRDIDENRLIVSYTLPIW- 391
OccK6          SGPLKNLGVKWRNATMRT----------NYTNDYDENRLIVSYTLPLW- 394
OccK7          SGPLKNLGIKLRNGTFRS----------DFGNDIDETRLIVSYALPLW- 394
OccK8          DGTFKGLGFTWKNASFRSGLPA--AGSSNNQRDQDENRLIVSYTLPLL- 431
OccK9          SGPLKNLGLRWRNAMLRS--------NHAA--DVDENRLILSYSLPLL- 388
OccK10         SGRFKDLSLRLRNATYRT-------DFERSARDVDEVRLIASYNLSLF- 400
OccK11         GGALKGLGLVWRNATYRS----------AFSRDIDENRLYLTYELPLF- 392
                *      .       :                 :.      :
```

Figure S1. CLUSTALW multiple sequence alignment of OccD/OccK channels. Invariant residues (*), highly conserved residues (:) and conserved residues (.) are shown at the bottom. The observed secondary structure elements for OccD1 and OccK1 are shown (β strands colored as blue arrows for OccD1 and as salmon arrows for OccK1; α-helices in red). The missing residues in the crystal structures are shown as hatched orange bars. The residues that line the pore constriction are highlighted in green. Amino acid residues that are part of the basic ladder are highlighted in pink. Pore lining basic residues that are also part of the basic ladder are highlighted in purple. The L7 insertion for OccD1 is highlighted in yellow and the N-terminal extension of OccD3 is shown in cyan.