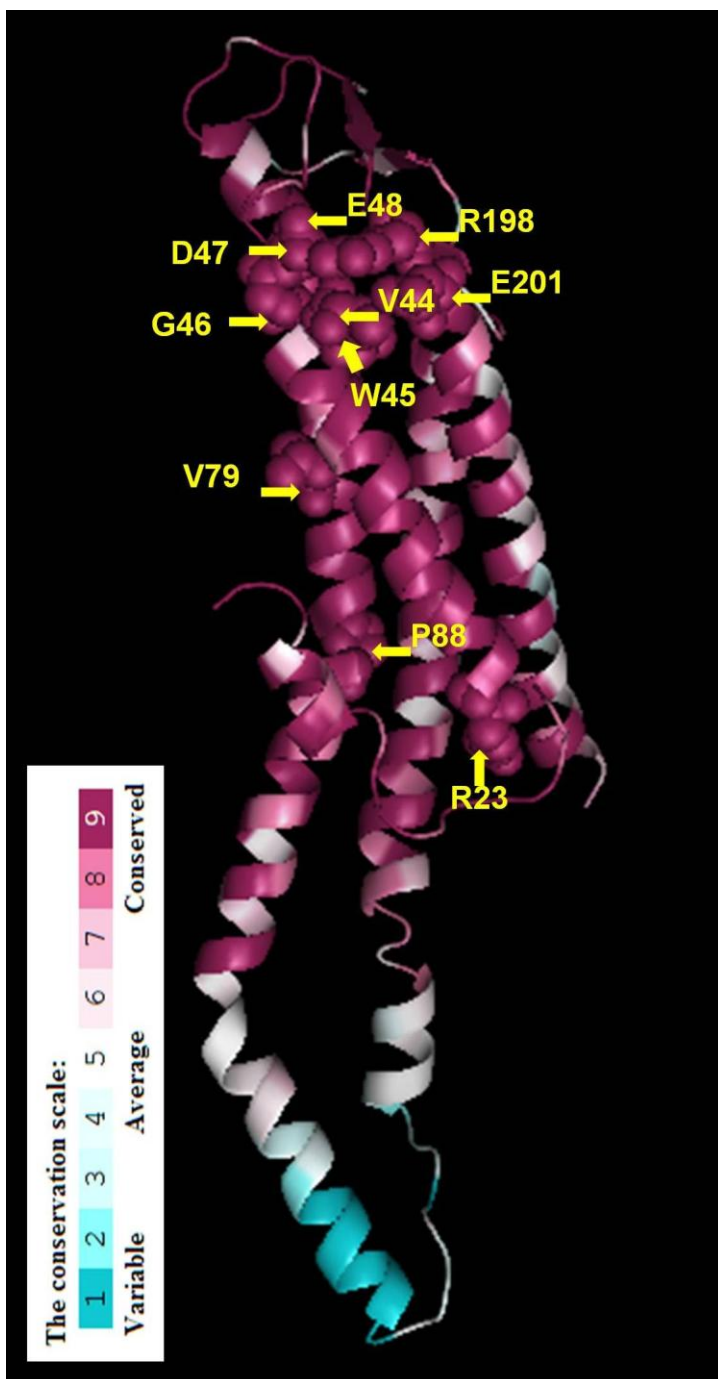
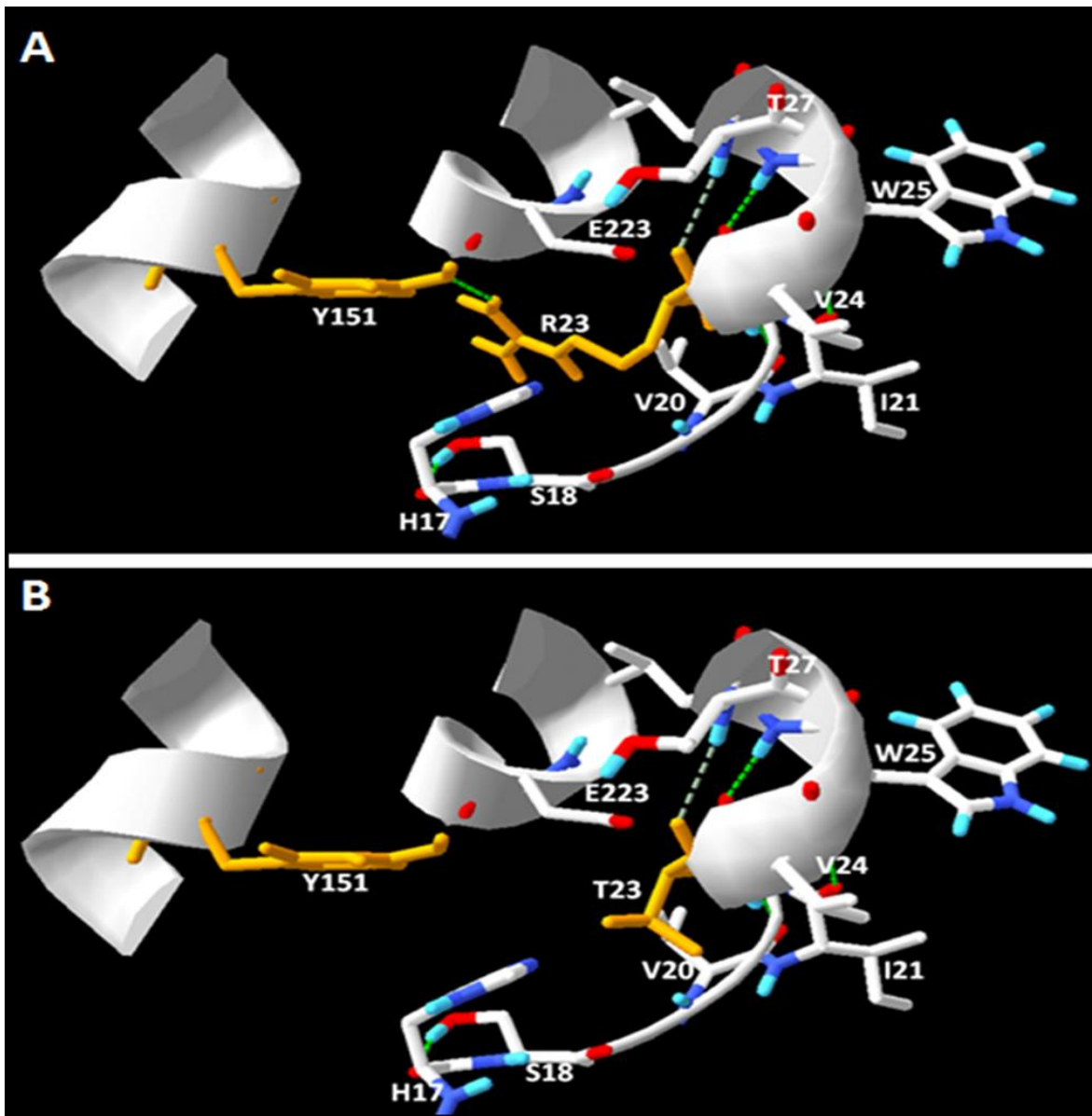


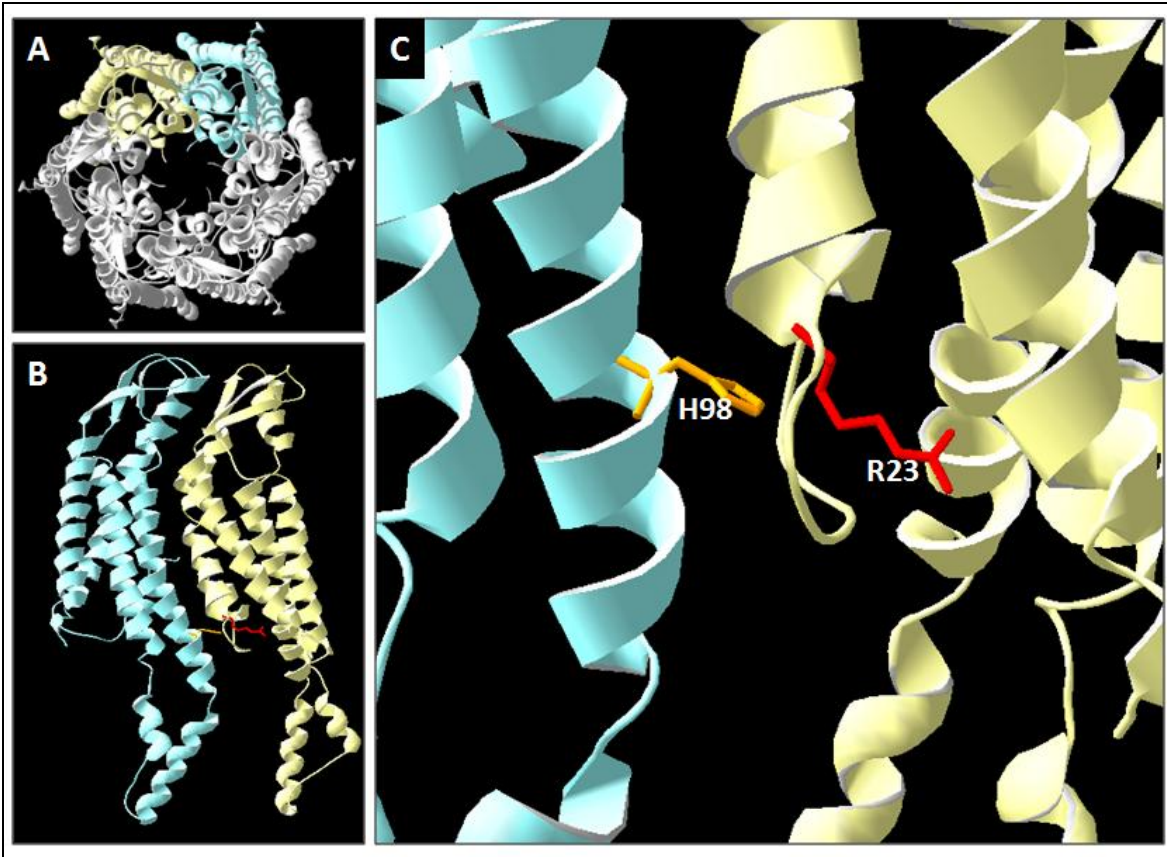
SUPPLEMENTARY FIGURES:



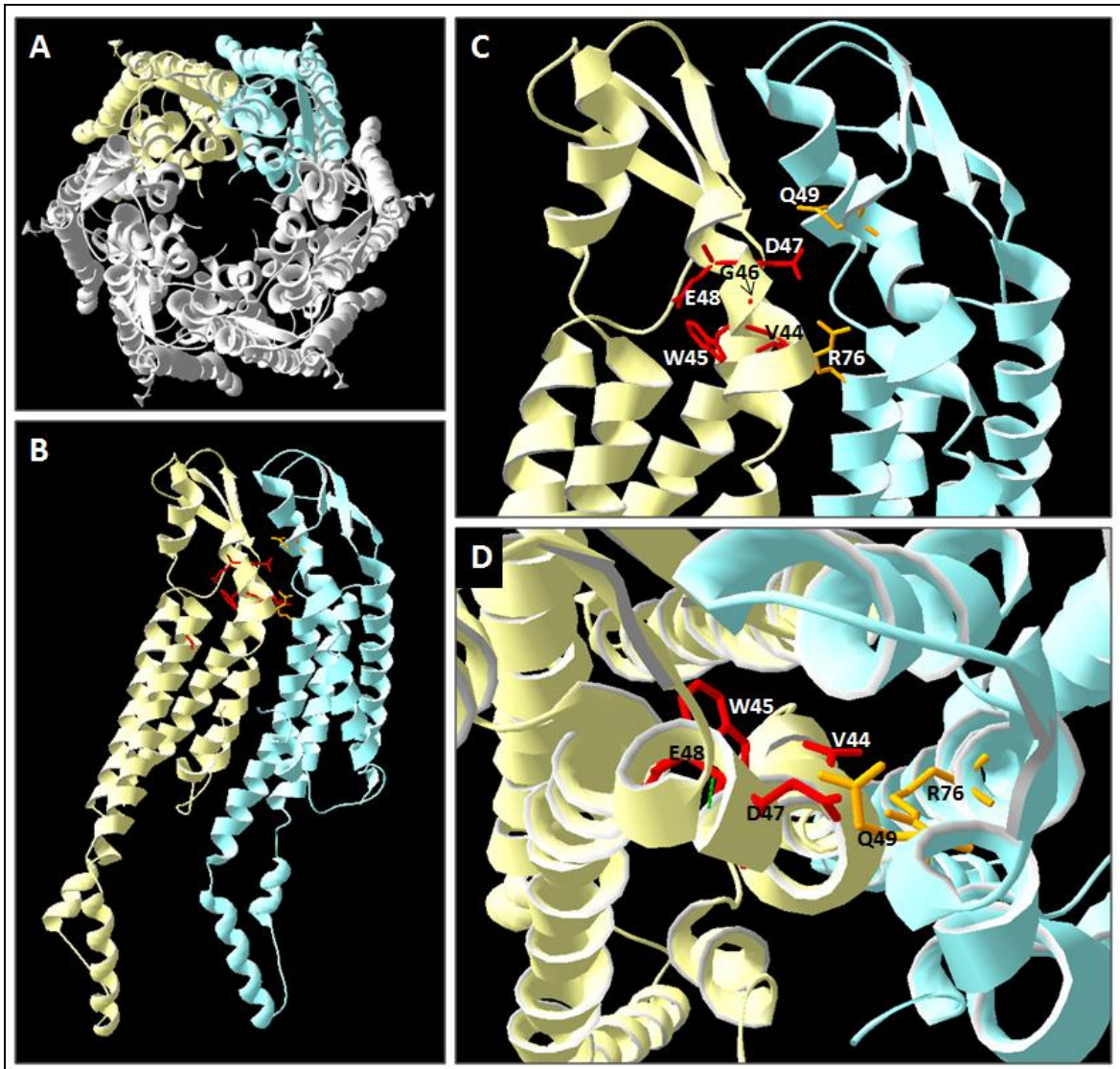
Supplemental Figure 1.



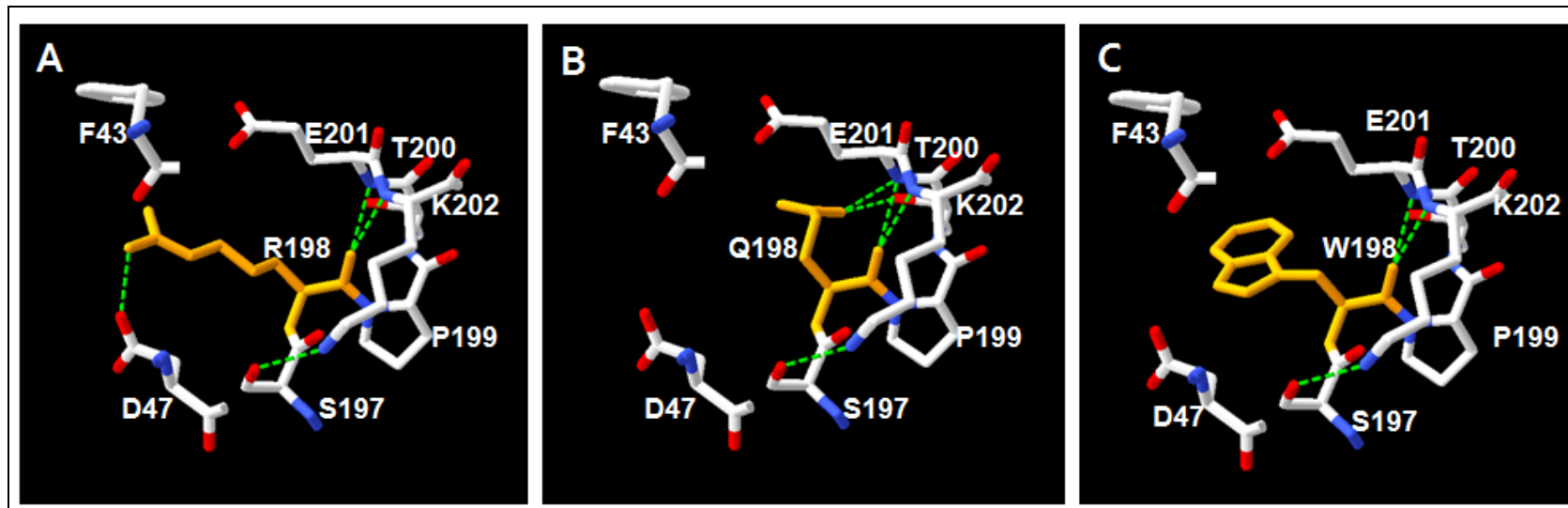
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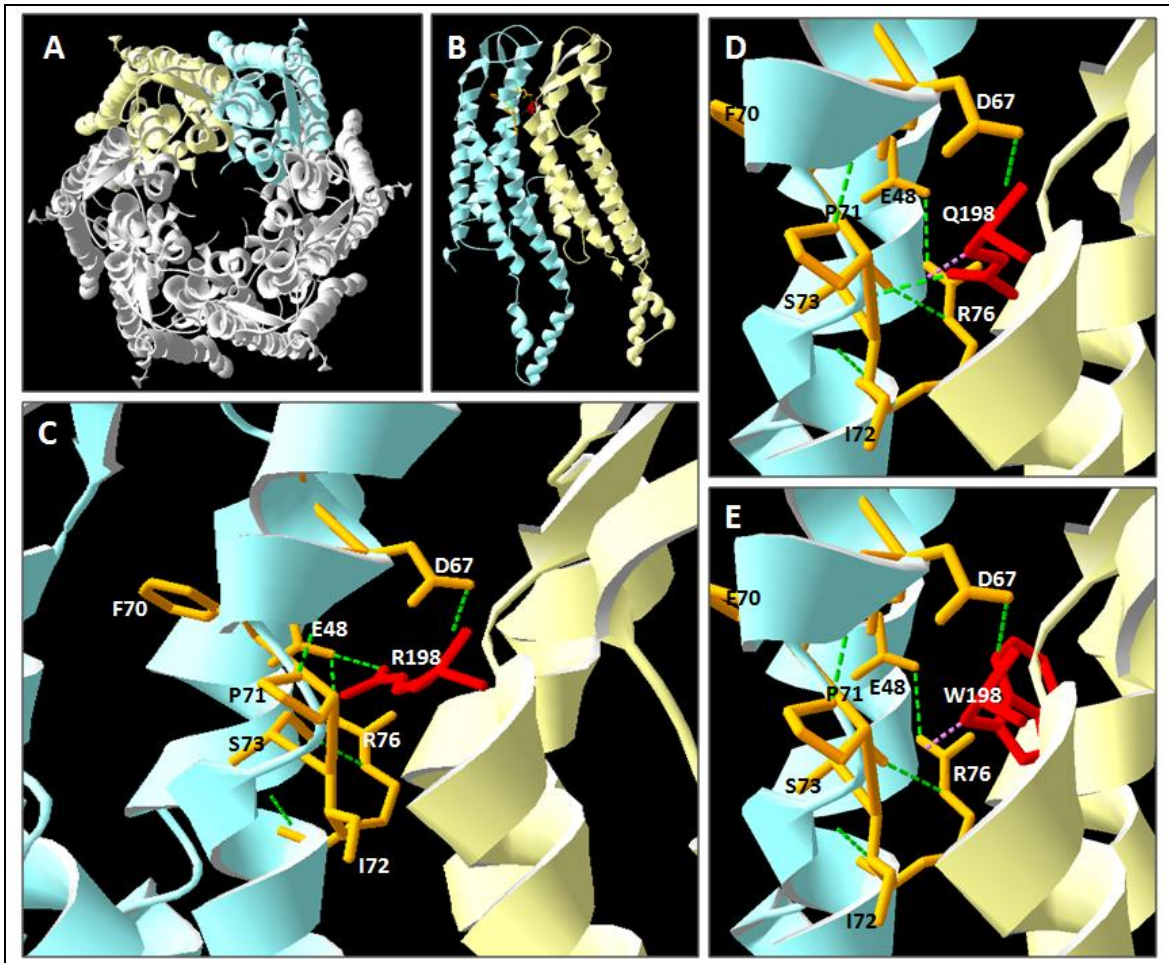
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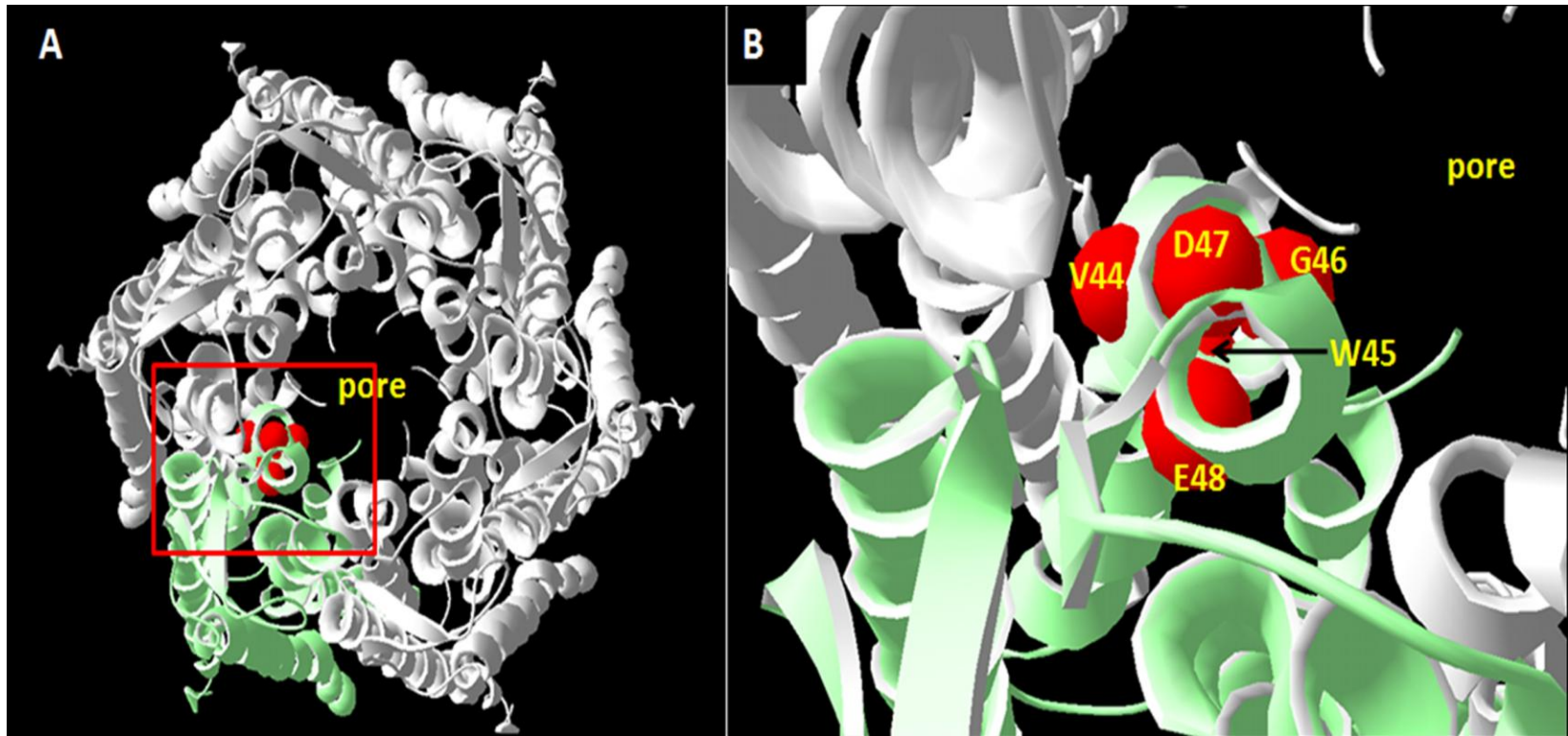
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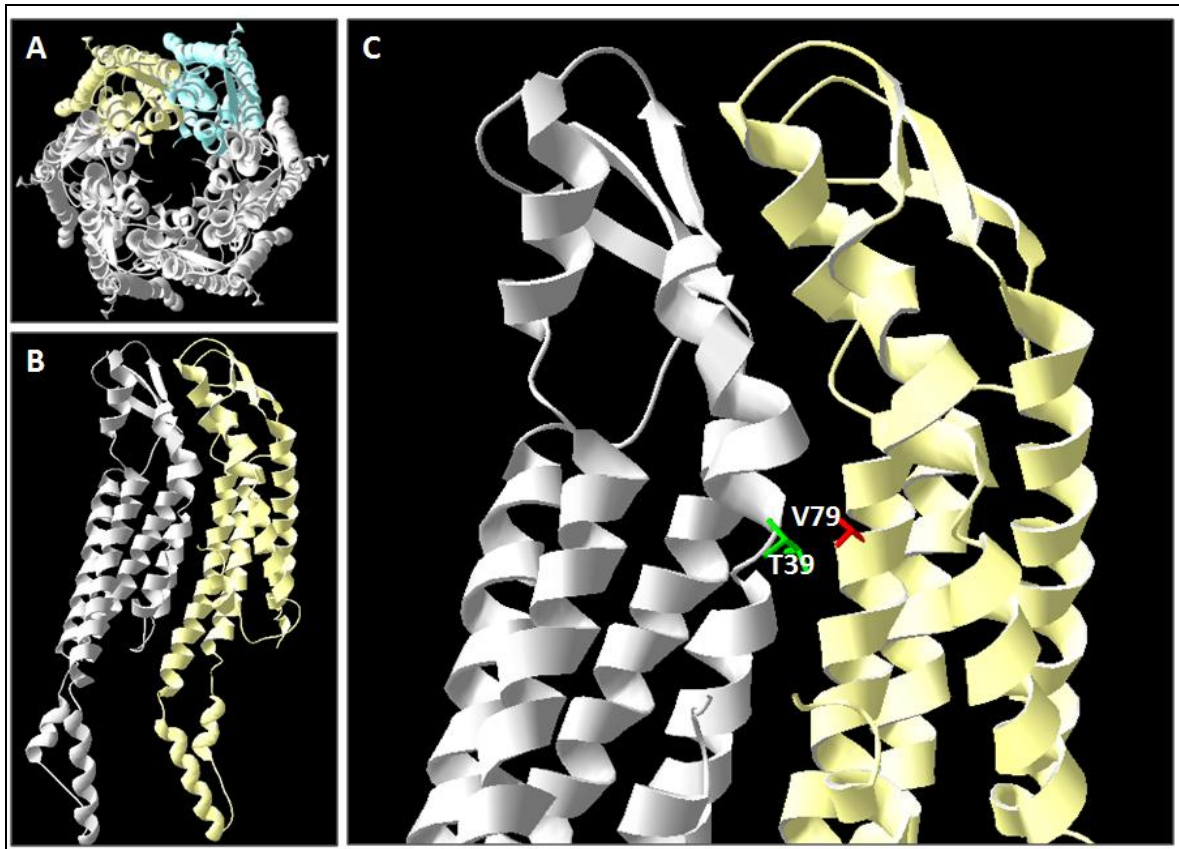
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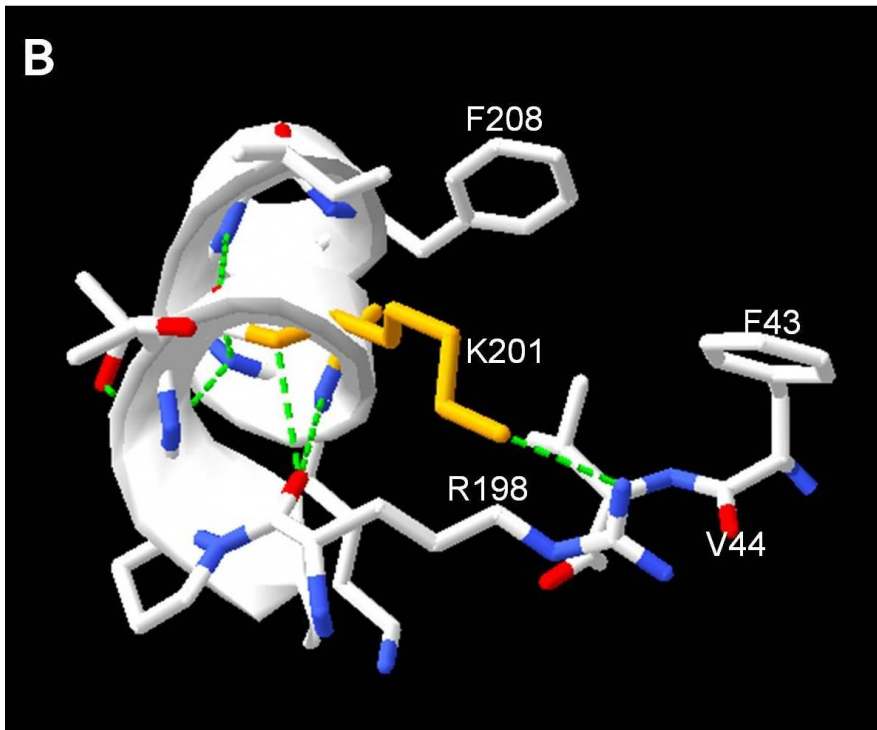
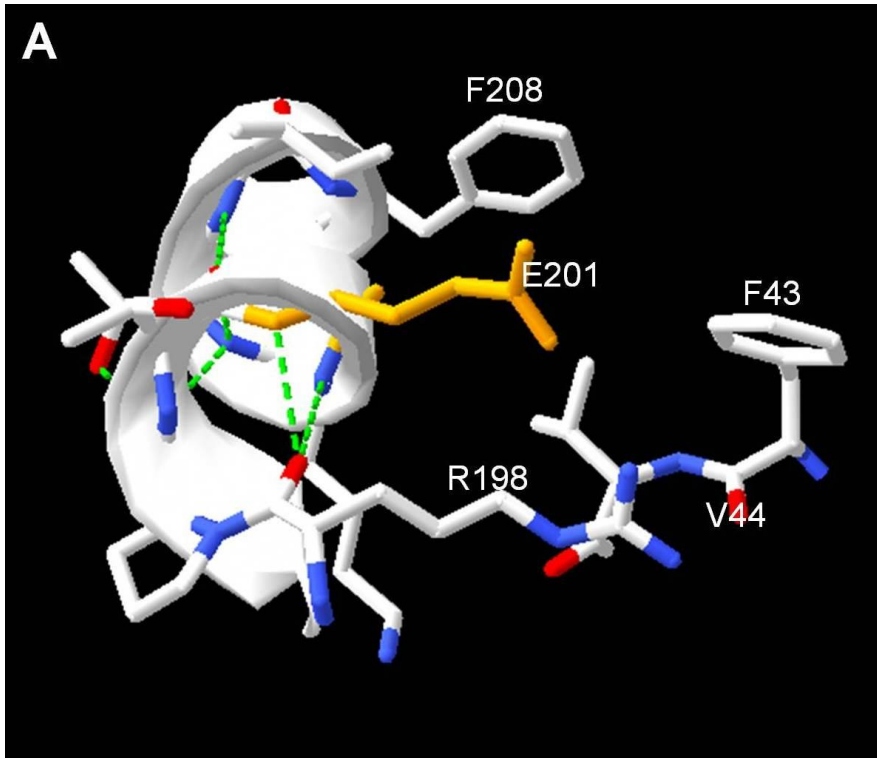
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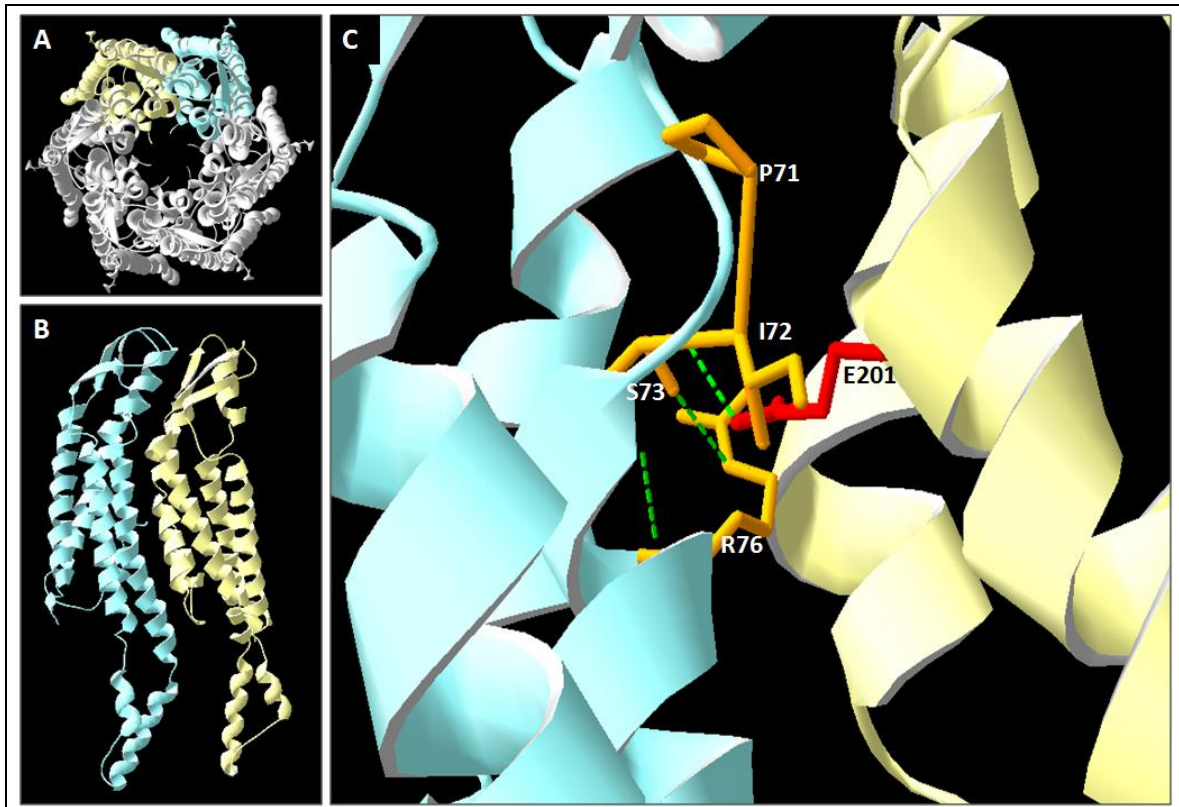
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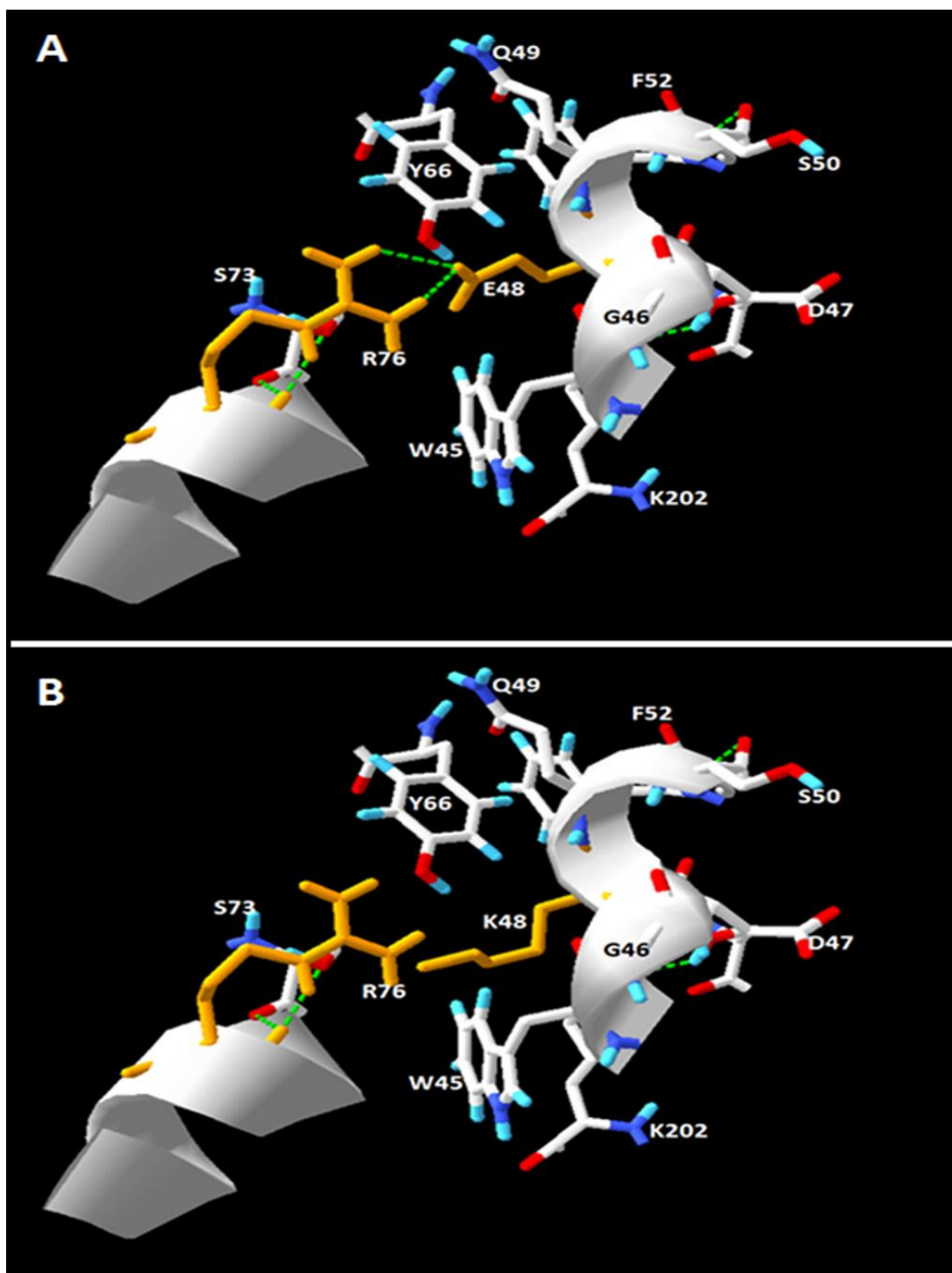
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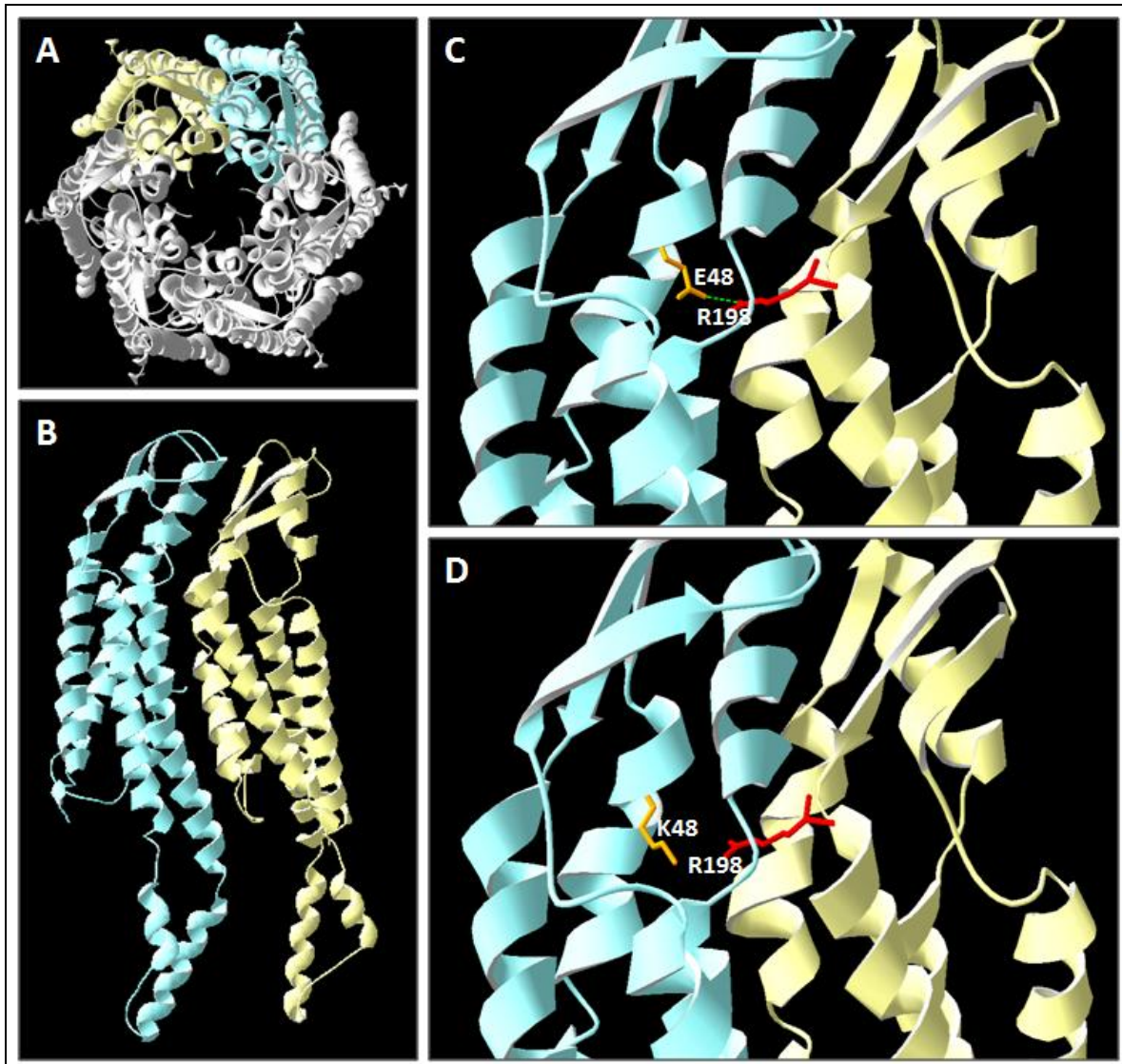
Supplemental Figure 9.



Supplemental Figure 10.



Supplemental Figure 11.



Supplemental Figure 12.

SUPPLEMENTARY FIGURE LEGENDS:

Supplemental Figure 1. The homology model of Cx50 color-coded according to evolutionary conservation.

Ribbon view of the Cx50 homology model is shown with the mutation-involving residues plotted on it. The structure is color-coded according to evolutionary conservation using the ConSurf server, with turquoise-through-maroon corresponding to variable-through-conserved positions (see color bar). PyMOL was used for visualization. All of the functionally characterized Cx50 mutations involve highly conserved residues. *Check supplementary text for multiple sequence alignment.*

Supplemental Figure 2. The 3-dimensional neighborhood (surrounding 4Å space) of R23 in normal Cx50 protein (homology model).

A. Residues lying within surrounding 4Å space of R23 are shown. R23 (TM1) has inter-helix H-bonding with side-chain of Y151 (TM3). B. The H-bond of R23 with Y151 is lost in the mutant R23T. Green and grey dotted lines indicate potential H-bonds (strong and weak, respectively) - computed using the SwissPDBViewer.

Supplemental Figure 3. The 3-dimensional neighborhood of R23 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in the hexameric complex – viewed from outer lipid-facing side. C. Mutation-involving residue R23 (red) in one subunit (yellow) and H98 (orange) of adjacent subunit (blue) lie within 4Å space.

Supplemental Figure 4. The 3-dimensional neighborhood of V44, W45, G46, D47 and E48 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in the hexameric complex – viewed from pore side. C. Mutation-involving residues 44-48 are shown (red) in one subunit (yellow); two residues (R76 & Q49 - orange) in adjacent subunit (blue) within surrounding 4Å space of the mutation-involving residues are shown. D. The intermolecular interface (involving residues 44-48 of one chain and R76 & Q49 of adjacent chain) is shown – viewed from the top. Side-chains of V44 & D47 point outwards, facing adjacent subunit; side-chains of W45 & E48 are directed towards the subunit. There is no inter-subunit H-bonding involving the residues.

Supplemental Figure 5. The 3-dimensional neighborhood (surrounding 4Å space) of R198 in normal Cx50 protein (homology model).

A. Residues lying within surrounding 4Å space of R198 are shown. B. R198Q leads to loss of 1 H-bond with D47 and gain of another H-bond with T200/E201. C. R198W leads to a loss of 1 H-bond with D47. Green lines indicate potential H-bonds - computed using the SwissPDBViewer.

Supplemental Figure 6. The 3-dimensional neighborhood of R198 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in the hexameric complex – viewed from outer lipid-facing side. C. Neighbouring residues in adjacent subunit (orange) that lie within surrounding 4Å space of R198 (red) are shown. R198 might form H-bond with E48 of adjacent subunit. Green dotted lines indicate potential H-bond - computed using the SwissPDBViewer. D. R198Q – the H-bond with E48 is

replaced with a new H-bond with S73; steric clash induced (pink dotted line). E. R198W – the H-bond with E48 is lost; steric clash induced.

Supplemental Figure 7. The 3-dimensional neighborhood of G46 in the oligomeric complex.

A. Docked model of hemichannel (constructed by SymmDock server) formed by symmetric docking of Cx50 subunits (Cx50 homology models). A single Cx50 subunit is colored light-green. Mutation-involving residues (red spheres) in the junction of TM1 and EC1 are localized in the docked model. B. Zoomed view of the residue-positions. G46 is a pore-exposed residue.

Supplemental Figure 8. The 3-dimensional neighborhood of V79 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in the hexameric complex – viewed from pore side. C. Mutation-involving residue V79 (red) in one subunit (yellow) and T39 (green) of adjacent subunit (grey) lie within 4Å space.

Supplemental Figure 9. The 3-dimensional neighborhood (surrounding 4Å space) of E201 in normal Cx50 protein (homology model).

A. Residues lying within surrounding 4Å space of E201 are shown. B. A new H-bond with side-chain of R198 is formed by the mutation E201K. Green dotted line indicates potential H-bond - computed using the SwissPDBViewer.

Supplemental Figure 10. The 3-dimensional neighborhood of E201 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in

the hexameric complex – viewed from outer lipid-facing side. C. P71, I72, S73 and R76 (orange) of adjacent subunit (blue) lie within surrounding 4Å space of E201 (red). E201 forms inter-molecular H-bonding with S73 of adjacent subunit.

Supplemental Figure 11. The 3-dimensional neighborhood (surrounding 4Å space) of E48 in normal Cx50 protein (homology model).

A. Residues lying within surrounding 4Å space of E48 are shown. E48 (TM1) has inter-helix H-bonding with R76 (TM2). B. The H-bond of E48 with R76 is lost in the mutant E48K. Green dotted lines indicate potential H-bonds - computed using the SwissPDBViewer.

Supplemental Figure 12. The 3-dimensional neighborhood of E48 in the oligomeric complex.

A. Docked model of hemichannel – viewed from the top. Two adjacent Cx50 subunits are colored. B. Two adjacent Cx50 subunits are shown to be arranged in similar relation as in the hexameric complex – viewed from outer lipid-facing side. C. R198 (red) of adjacent subunit (yellow) lies within surrounding 4Å space of E48 (orange). E48 has inter-molecular H-bonding with R198 of adjacent subunit. Green dotted line indicates potential H-bond - computed using the SwissPDBViewer. D. The H-bond of E48 with R198 is lost in the mutant E48K.

SUPPLEMENTARY TEXT:

CLUSTAL 2.1 multiple sequence alignment constructed by CLUSTALW2 server – 52% sequence similarity between human Cx50 protein sequence and human Cx26 protein sequence, which was used as template (PDB: 2ZW3) for homology modeling

```
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Cx50      MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFCNTQQPG 60
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2ZW3      CKNVCYDHYFPISHIRLWALQLIFVSTPALLVAMH-VAYRRHEKKRKFGEIKSEFK-- 116
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          * .:*          *:*.***:* ** . *:::***.*: .*:*.* * :

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Cx50      LYRCSRWPCPNVDCFVSRPTEKTIIFILFMLSVASVSLFLNVMEELGHLGLKGIRSAKRP 239
          * :*. *****.*****:**:***:*.:::*** ** :* :. . *:*

2ZW3      V 226
Cx50      V 240
          *
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CLUSTAL 2.0.10 multiple sequence alignment constructed by UNIREF90 – 150 non-redundant sequences homologous to human Cx50 were selected by PSI-BLAST and aligned

Input_protein_seq denotes human Cx50 protein sequence (NP_005258.2)

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UniRef90_H2UTF3_1_420 PSS--YP-----PNYTD-----VTAGSGAFLQPVAPPA
UniRef90_UPI000298F1F6_1_460 PSS--YP-----PNYTD-----VTAGSGAFLQPVAPPA
UniRef90_H3DE08_1_376 AGR-----AFGRR-----VQDGR-----PPAEPAS
UniRef90_Q8JFD2_1_434 PPTLSYP-----PDYTE-----VAVAGGAFLQPVVS---
UniRef90_H2T4Y1_1_438 PSALECL-----STYSSMNMAGRVAEEGGTYSPPEASLA
UniRef90_H2T4Y2_1_428 PS-----ARRVAEEGGTYSPPEASLA
UniRef90_H3BZL0_1_378 -----SGGNEGRSYPPEASLA
UniRef90_I3K1N0_1_478 PLVLDCL-----PAFGSVSVMGDGAEEGGAYSPPEFPT
UniRef90_H2LFL5_1_470 PSALNRL-----P-----EYANGNANASFMGDRAAEE
UniRef90_M7BWJ7_1_486 PSPAAFP---TVSPALPDSHTITPLLSSQTVPPYYAEATARAQP-AATTF
UniRef90_K7F163_1_492 PSPAVLP---AVPPALSDSRAITPLLSSQTVPPYYAEATARAQP-ATAVS
UniRef90_H0ZM32_1_512 PAPPVVVTTATPPPVLDPDTRAVTPLLAPVTMASYYATGAPRRRPPNTTS
UniRef90_H3AH16_1_396 -----SLHYPPFYAEATSGGHHGYPGAP
UniRef90_B0BM18_1_388 -----YYTDVAAALPVLHHAARFS
UniRef90_Q4S8R0_1_345 PSYN-----YYTGHFAVPEFFPTDSKY
UniRef90_I3KYH7_1_341 PNYN-----YFGHSAVPEFFPTDSKY
UniRef90_H2M0G7_1_345 PNYT-----YLTSHTLSHEFFSADSKF
UniRef90_H3A471_1_360 QHYP-----FFPSHGRPQYPYNPSLAAY
UniRef90_Q6GLA5_1_353 PHPY-----HYSPTKE-GSTFSPTLAF
UniRef90_UPI0002A4A1D5_1_346 PSYDD-----YFSGHCQVQPAFPPIPSY
UniRef90_S4RXA6_1_456 HSVKTSS-----QPISYTYQPPTDERNYDPPSFRT
UniRef90_P16863_1_360 CSSPT-----APMSPPGYKLVGTGERN--PSSCRN
UniRef90_H2LU51_1_404 CVGTSVGR-----KTTIPTAPSG---YTLLEKQG
UniRef90_I3KYL3_1_401 CMGTTVGR-----KSTIPTAPSG---YTLLEKQG
UniRef90_G3NC44_1_402 CVGTSVGR-----KTTIPTAPCG---YTLLEKQG
UniRef90_H2SSL2_1_392 CAGTSVAG-----KTTIPTAPCG---YTLLEKQG
UniRef90_UPI0002C46B7E_1_433 ---TSANS-----LKQLPSASD----YHLLVEKKT
UniRef90_G3ULF1_1_432 ---VSANS-----LKGLPSAPD----YNLLVEKKT
UniRef90_C9IYK1_1_407 ---TSANS-----LKRLPSAPD----YNLLVEKQT
UniRef90_H0Y0G7_1_436 ---TAANS-----LKRFPSAPN----YNLLVEKQT
UniRef90_L9JD22_1_408 ---TSANS-----LKRLPSAPD----YNLLVEKQT
UniRef90_F1N617_1_436 ---TSANS-----LKRLSSVPD----YSLLDVKQT
UniRef90_F1SV25_1_385 ---TSANS-----LKRLSSAPD----YSLLDVEKQT
UniRef90_L5JUH5_1_307 ---TSANS-----LKQLSSAPD----YNLLVEKQT
UniRef90_UPI00020369CA_1_441 SLGISATP-----QKTLPSVLSG---YAFLMEKQT
UniRef90_R4GLX1_1_405 SLGISATP-----QKTLPSVLSG---YAFLMEKQT
UniRef90_UPI00035A19E6_1_466 SLEIPTTP-----QKTLPCALSS---HTFLMEKQT
UniRef90_F6WA84_1_463 CLGTATNP-----PKTLPSAPIG---YTVLREKQM
UniRef90_G1SG18_1_430 MICSSLPD-----RISLLQANN----QQQGIRINV
UniRef90_UPI00032B0E64_1_413 MICSSLPE-----RISLFQANN----QKQGIQVNV
UniRef90_UPI0002C65D9D_1_412 MICSPLE-----KISLLQANN----QQQVIQVNV
UniRef90_F7CF28_1_383 MICSSLPE-----KISLLQANN----QQQVIQVNV
UniRef90_Q969M2_1_435 MICSSLPE-----RISPLQANN----QQQVIRVNV
UniRef90_L9JVZ3_1_406 MICSSLPE-----RMSLLQANN----QQQVIQVNV
UniRef90_I3M407_1_414 TICSSLPE-----RISPLQANN----QQQVIQVNV
UniRef90_L5JMB7_1_435 MICSPLE-----RTPVLQANS----QQQIILVNV
UniRef90_L8J083_1_417 MTCSPFPE-----KISLLQANN----QQQVIRVNV
UniRef90_UPI0002BCCFF6_1_421 MNCSPFPE-----GVSLQASN----QQQVFRVNV
UniRef90_F1RY20_1_421 MISPFPE-----RISLLQANN----QQQVIQVNV
UniRef90_UPI0002C59166_1_412 MICSPLE-----RISLLQANN----QQQVIQVNV
UniRef90_G3TBX7_1_436 MICSSLPK-----RIPLLQANN----QQQVIRVNV
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UniRef90_H3CDZ2_1_426
UniRef90_I3IZH7_1_440
UniRef90_E7F3P4_1_389

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VTHSLLHE-----NIALLLQPVPQPIWPEQQQVIGIDN

CIMSNSSP-----QSSYKLLPN-----QQGGLPVYL

VLTNSSPQ-----RLVQLTQMTCSALPDTHGETLAI
LLASSSPQ-----RLVQLTQVTCALPNTN-----AT
VLSNSSPQ-----RLIQLTQMTCSAMPETQVESQPL
FLTNSSPQ-----KQLHLTHTSLAMAPDGMVPLPI

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UniRef90_H2MUH4_1_428
UniRef90_UPI00022B4A0D_1_396
UniRef90_H3D8V1_1_361
UniRef90_G3NHJ7_1_420
UniRef90_Q503J6_1_391
UniRef90_F6QCF2_1_438
UniRef90_UPI00034FAB61_1_453
UniRef90_UPI0001DE8510_1_439
UniRef90_H3A837_1_370
UniRef90_G1KPB7_1_391
UniRef90_B0S6Z4_1_382
UniRef90_G1PZ72_1_426
UniRef90_UPI000155FB82_1_448
UniRef90_F6U7L2_1_428
UniRef90_UPI0002C6341D_1_440
UniRef90_M3Z8M0_1_445
UniRef90_G1Q1M8_1_411
UniRef90_G1PYG2_1_394
UniRef90_L5L5Q1_1_430
UniRef90_UPI0002BCF55A_1_410
UniRef90_P41987_1_407
UniRef90_J9JHI9_1_433
UniRef90_Q9Y6H8_1_435
UniRef90_G3QHB2_1_399

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PFSNK-----MASQQNIDNLAT-----
PFSNK-----MASQQNTDNLST-----
PFSNK-----MASQQNTDNLAT-----
PFSNN-----TASQQNTDNLAT-----
PFSNN-----MASQQNTDNLVT-----
PFSNK-----MASQQNTDNLAT-----
PFSNK-----LASQQNTDNLAT-----
PFSNK-----MASQQNTHNLAT-----
PFSNQ-----VASQQNTDNLAT-----
TFSTN-----TASQQNTDNLAT-----
RFSNN-----MASQQNTDNLAT-----
DFSNN-----MGSRKNPDTLAT-----
DFSNN-----MGSRKNPDALAT-----
PLKNN-----MASQQNTDNMAT-----
PFSNN-----TVSQNTDNLAT-----
HFSNN-----LASRQNTDNLAT-----
PFSNK-----MASQQNTANFAT-----
PFSNK-----MASQQNTANFAT-----
PFSNK-----MASQQNTANFAT-----
LHSHH-----LHHIHQTCQPFT--NH-----
FPSHL-----LVHQNSSENTVTEKNK-----
VETSP-----LPAKPFNQFEEKI-----
VETTP-----VSAKPFNQFEEKI-----
VETSP-----LSAKPFSQFAEKM-----
VETSP-----LSAKPFSQFEEKI-----
VQTSP-----LSAKPFSQFEEKT-----
VETSP-----LSAKPFAQFEEKM-----
VETSP-----LSAKPFGQFEEKM-----
VETSP-----LSAKPFSQFEEKM-----
VEASP-----LSAKPFSQFEEKV-----
VETTP-----LSAKPFHQFEEKI-----
VETSP-----LSAKPFSQFEEKI-----
VETSP-----LAAQPFQGFEEKV-----
VETRP-----LAATPFSRFEEKI-----
VETRP-----LAATPFSRFEEKI-----
VESSP-----LADKPFQFEEKM-----
VETAP-----PPS-SFNLDLDEKL-----
VEAGP-----PPS-SFKDLDEKL-----
VEPSP-----LPS-AFNEFEEKI-----
MEAGR-----GAS-PFHGLEEKG-----
MEAGR-----GAP-PFQGLEEKV-----
MEAGR-----GSP-PFQGLEEKV-----
MEAGR-----GPP-PFLGLEEKA-----
MEAGR-----LPA-SYEPFEEKSD-----
LEASP-----LPA-HFNGYDK-----
LEASP-----LPA-HFNGYDK-----
LEASP-----LPA-HFNGYDK-----
VETTP-----LPA-PFAGFEEKE-----
AETTP-----VPP-SLNEFEEKM-----
MEEGQ-----FFLPQLEKEQKSSQEAI-----
GEASP-----RSAQPFRLEERR-----
PGAPP-----PPTDFKMVALS-----EAHR
PGAPP-----PPTDFKMVALS-----EAHR
PGAPP-----PATDFKMVALS-----EAHG
PGAPP-----PATDFDMAALS-----EAPG
--APP-----PATDFNMAGLS-----QTQG
--APP-----PATDFNMAALS-----QTQG
PGAPL-----PATDVTKEALS-----EAQG
PEPPP-----P-----AALP-----GTPG
PEPPP-----P-----AALP-----GTPG
PGAPP-----L-----AADF-----HPAA
PGAPP-----PAADFKLLALT-----EARG
PGAPP-----PAADFRMLALT-----EARG

UniRef90_F7B1T8_1_432	PGAPP-----PAADFKLALTL-----EARG
UniRef90_L9L2D3_1_460	PGAPPG-----PAADFKVGALT-----EAQG
UniRef90_Q64448_1_417	PGAPL-----SPADFTVVTLN-----DAQG
UniRef90_G3H8J5_1_417	PEAPP-----PPADFTVVTLN-----DAQD
UniRef90_UPI0003333DA4_1_405	PGTTP-----PAADFTVVSLK-----EAQG
UniRef90_I3NC37_1_417	PGAPP-----PAADFKMVALN-----ESQG
UniRef90_H0XD37_1_430	PGAPP-----PAADFKVVALS-----EVPE
UniRef90_G1U3S9_1_407	G-QAL-----PTTEQNWAPTP-----VA
UniRef90_UPI00032AEFC1_1_413	P-PAG-----DSTEVALVAEPEKGRLL-----LPTS
UniRef90_UPI00034F30A8_1_402	PGAPL-----PTADFRVAQGG-----EAHG
UniRef90_UPI0003340A67_1_370	SGTPL-----PATDLGLEAPG-----EACV
UniRef90_UPI0002234D0E_1_449	PGAPP-----PPADFKMVPLS-----EEQG
UniRef90_G3TTN5_1_429	PGAPP-----PPADFKMVPLS-----EEQG
UniRef90_UPI0002C457ED_1_447	LGAPP-----PPTDFKMVALS-----EEQG
UniRef90_UPI000333D50E_1_427	PGAPP-----PPTDFKMVALA-----EERG
UniRef90_UPI0003343FBC_1_423	PGTTL-----PATNFKTVALA-----EVHG
UniRef90_F7G5V2_1_446	PGAPP-----QPTEFRMVTLPL-----EERS
UniRef90_G3VY19_1_428	PGAPP-----QPTEFRMVTLPL-----EERS
UniRef90_UPI000155BBAC_1_459	PGAPG-----PPTDFKVALG-----KERS
UniRef90_F7EY8_1_425	-----FKMAGLP-----KERS
UniRef90_I3KXW1_1_474	VPSA-----AEFKMDDLQEQESLQSSP-----
UniRef90_UPI00022B3AE8_1_449	VPSA-----AEFKMDDLQEQESLQSSP-----
UniRef90_UPI0002A48057_1_447	LSSA-----EE--MEALHQEESI HQAPP-----
UniRef90_H2MCD5_1_421	LSSA-----EE--MEALHQEESI HQAPP-----
UniRef90_H2UTF3_1_420	VPST-----TEFKTDDLQREPPRHQPS-----
UniRef90_UPI000298F1F6_1_460	VPST-----TEFKTDDLQREPPRHQPS-----
UniRef90_H3DE08_1_376	PP-----
UniRef90_Q8JFD2_1_434	APST-----AEFKMDPLREEL-----
UniRef90_H2T4Y1_1_438	VMSS-----PTGLKMD--GTVFHPDDFLLLEALPPSFCS-----
UniRef90_H2T4Y2_1_428	VMSS-----PTGLKMD--GTVFHPDDFLLLEALPPSFCS-----
UniRef90_H3BZL0_1_378	VMSS-----PASLKMD--GSAFHPDDLLEALPASFCG-----
UniRef90_I3K1N0_1_478	VTSLNAATTVPAGMKMD--STMFHPDDFLDAA--SFYS-----
UniRef90_H2LFL5_1_470	GASS-----PAVIFNPNMATTPTPELNLVRSPSFST-----
UniRef90_M7BWJ7_1_486	LADYP-----GAPPFSEEQHNATPTPTPTSIPTPTPTSIPT
UniRef90_K7F163_1_492	LAGYS-----GALPFAEELHKTATPIPASTPIPTPTLVPT
UniRef90_H0ZM32_1_512	MASYP-----AAPQVPEERHHAVTPTPISTPTPTPTPTPT
UniRef90_H3AH16_1_396	AADFK-----AMPPPAEPEPKPS-----
UniRef90_B0BM18_1_388	APDFK-----ITSVPEEALESPS-----
UniRef90_Q4S8R0_1_345	SVT-----EPGSAYSPPYS-----
UniRef90_I3KYH7_1_341	GMP-----EPNSAYSPPYN-----
UniRef90_H2M0G7_1_345	NVA-----EPNSAYNPYN-----
UniRef90_H3A471_1_360	PLPSM-----NENNSSFHPYN-----
UniRef90_Q6GLA5_1_353	PLSP-----SKTTSNVMS-----
UniRef90_UPI0002A4A1D5_1_346	DLSPLS-----KSTDSSFHPYH-----
UniRef90_S4RXA6_1_456	ATRDVLVAGGR-----LVAQGVGDQNWANWE-----EEE
UniRef90_P16863_1_360	YNKQASE-----QNWANYS-----AEQ
UniRef90_H2LU51_1_404	NGPN-----YPLLSASSAFVPIQ-----
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UniRef90_G3NC44_1_402	NGPA-----YPLLNASSAFVPIK-----
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UniRef90_H0Y0G7_1_436	HTAE-----YPSLNSSSVFQANL-----
UniRef90_L9JD22_1_408	HPAV-----YPSLNSSSAFQADP-----
UniRef90_F1N617_1_436	HTAG-----YPSLN-PSAFQTD-----
UniRef90_F1SV25_1_385	HRAV-----YPSLN-SSVYQTD-----
UniRef90_L5JUH5_1_307	HTAV-----YPSLN-LSAFQAD-----
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UniRef90_R4GLX1_1_405	DTAI-----YPVLNSAPVFQPVQ-----
UniRef90_UPI00035A19E6_1_466	DTML-----YPVLNSPSVFQSVQ-----
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UniRef90_UPI00032B0E64_1_413	PKSK-----AMWQIQPRQSEE-----
UniRef90_UPI0002C65D9D_1_412	PKSK-----TMWQIQPRQLEV-----
UniRef90_F7CF28_1_383	PKSK-----TMWQIQPRQLEV-----
UniRef90_Q969M2_1_435	PKSK-----TMWQIQPRQLEV-----
UniRef90_L9JVZ3_1_406	PKSK-----SMWQIQPRRLGI-----
UniRef90_I3M407_1_414	PKSK-----SIWQIQPPQLDV-----
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UniRef90_L8J083_1_417	PNSK-----TWHIIPQARQLDV-----
UniRef90_UPI0002BCCFF6_1_421	PNSK-----TTWQIQPRQLEV-----
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UniRef90_UPI0002C59166_1_412	PKSK-----TMWQSSQPMQLGV-----
UniRef90_G3TBX7_1_436	PKSE-----TIWQIQAKRLEV-----
UniRef90_G3GSS7_1_405	PRSK-----SMWQIPHPRQHEV-----

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UniRef90_M7BL54_1_431
UniRef90_UPI0002B44362_1_276
UniRef90_UPI000298933C_1_429
UniRef90_H3CDZ2_1_426
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UniRef90_E7F3P4_1_389

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P-----
NVSHQ-----NQEGSGA-TNQHPSHIG-----
SLSHQ-----NQEGSGN-ANQHPSHAC-----
NLALV-----APQNLEG-HNISRPSQ-----
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UniRef90_H3A837_1_370
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UniRef90_B0S6Z4_1_382
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-----EQVQGQEQIPMEG-FIHVRYGQ-----
-----EQVRGQEQTPPEG-FIQVRYGQ-----
-----EQVRGQDPLSRDG-FIHIHYDQ-----
-----EQVRGHEEMPPEG-FTHLRYAQ-----
-----EQVRGQEQAPGDG-FIHVRYAQ-----
-----EQVRGQEQVPEG-FIHVHYSQ-----
-----ERVRGREQVPEG-FIHIRYDQ-----
-----EQVQQGE--PG-----HIHYDQ-----
-----EMFPDQELISRDG-FIHMHYGQ-----
-----GEVFNQEIQPEG-FIHMHSYQ-----
-----EQVQGHERIPPEG-FIHIHYGE-----
-----EQVRGQERIPGED-FIHIHYGE-----
-----EQVQGREEAAGRA-FLHMQYAE-----
-----ERVHGQEDAAGEGPFIKSSYVE-----
-----ERVHSQEDAAGEGPFMKSSYME-----
-----ERVQSQDDIIGEGPFIQVNYTQ-----
-----ERVHSQEDAAGEGQFIQINYAQ-----
LAHQQNSVNMMAERHHSHDGLPAVDLFQMHHYGSPEARVR-----
IVAAVEEANFLQMSYSPPEWQSAQNGQIQDGVYLKSDSKCY-----
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UniRef90_H0WCZ7_1_358 -----KPDVP--SGVSSGH
UniRef90_G3X1A3_1_358 -----GPEMA--NGVPNAH
UniRef90_H0ZTI1_1_370 -----SPEVA--SECAAP-
UniRef90_P18860_1_369 -----SPEVA--SECAAP-
UniRef90_G1KPB5_1_370 -----NPEVR--NNSAPG-
UniRef90_K7FWT6_1_369 -----SPEAP--NDSAPH-
UniRef90_F1QL21_1_400 -----SEMTTP--STPSTPS
UniRef90_UPI0002A497DC_1_408 -----SPESRDNNCLQIQN
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UniRef90_UPI00027FC10C_1_397 -----TTEEQEKVAVPEGEKVPETPGVDKEGEKEEPOSEKVKSKQGL
UniRef90_L9JGQ0_1_441 -----TTEGQEKVAVPEGEKAETPGVEKDGEKEELQS-EVAKQGL
UniRef90_P28236_1_440 -----ATEGQEVVPAEAGEKVPETAGVGQESEKDELLAEEKASKQGL
UniRef90_G5BBL7_1_440 -----APEGQETVAVPDRERVETPGVGKEDEKEELQAEKVKTKQGL
UniRef90_M3XED1_1_440 -----TLEVQEAITEPEGERVETPGVGKEGEKEELQIEKVKTKQGL
UniRef90_L5K685_1_440 -----STEGQETLAVLEGEKVPETPEVGKEGEKDELQAEKVKQGL
UniRef90_F6VG96_1_441 -----STEGQETNDELEGDRVETPGAGKEGEKEELPAEKASKQGL
UniRef90_P55917_1_440 -----STEGQETTAVLEGEKVPETPKVGKEAEKEELQAEKVKSKQEL
UniRef90_UPI000329268E_1_442 -----STEGQEMVVVPEGEKIEPPEGEKQKGEELQAEVMSKQRV
UniRef90_G3UBH4_1_410 -----AVLEGEKGETPKVGKESEKEELQAEQISKQGL
UniRef90_I3N716_1_431 -----TLEGQDAVAVPDGDKVETPAVGKEGDKDELQAEKMTKPGI
UniRef90_G3X210_1_429 -----EMQEATVEQEEKEKVGTP-ERKAGE-----KQEL
UniRef90_F7BI06_1_372 -----QEEEEKAGTPVEMKAGD-----KQEL
UniRef90_UPI000333FA9E_1_424 -----TTEGQE--AVLEGENAESFPASAQAEKEELPAEKASKPGP
UniRef90_K7EY71_1_406 -----EEELE-----VKKMAAEQELPGEELPAVP-----
UniRef90_M7BCA4_1_394 -----EEEQE-----VEKVVVEEQEPPGEELPSVP-----
UniRef90_P36381_1_400 -----QEEPG-----VKKAEEEVVSDEVEGSPAP-----
UniRef90_H2MUH4_1_428 -----AEKVEEMADEDEEEVEEAENGEDAAPAEAGLEAT-----
UniRef90_UPI00022B4A0D_1_396 -----GATPAEAGTEAA-----
UniRef90_H3D8V1_1_361 -----AAEAP-----
UniRef90_G3NHJ7_1_420 -----VEKG-----ADEDLEVEEAGNGEGVNPPEETRMVET-----
UniRef90_Q503J6_1_391 -----LAVEADMEAS-----
UniRef90_F6QCF2_1_438 -----SPSVRAPSDRAPSERALSERAPTRAASEHAGSEHTPSVRT
UniRef90_UPI00034FAB61_1_453 -----SPSVRAPSDRAPSERALSERAPTRAASEHAGSEHTPSVRT
UniRef90_UPI0001DE8510_1_439 -----SPSVG--LDQSPNE-----PTPLRALPEQGNPNHTFPDPE
UniRef90_H3A837_1_370 -----GAEG-----FKEKAGVKVGEKHE-----
UniRef90_G1KPB7_1_391 -----ELPTEEPPREGD-----
UniRef90_B0S6Z4_1_382 -----RVSTEGRETPAVEGEASQVGKEGEGELPAEKVAKQRL
UniRef90_G1PZ72_1_426 -----NGNG-----SPLGESKLEVT-PDE-EEAVVTAV
UniRef90_UPI000155FB82_1_448 -----NGNG-----SPLGESKLEVT-PDE-EEAVVTAV
UniRef90_F6U7L2_1_428 -----NGNG-----SPWGEKKLEVT-PDE-EERAVATVV
UniRef90_UPI0002C6341D_1_440 -----NGNG-----SSLGESKLEVT-PDDGEEQPVTAV
UniRef90_M3Z8M0_1_445 -----NGDS-----SLLGESRLEVT-PDE-QQQAVT-AV
UniRef90_G1Q1M8_1_411 -----NGDS-----SLLGESRLEVT-PDE-QQQAVT-AV
UniRef90_G1PYG2_1_394 -----NGNG-----HSLGESSLAVTPDQ-GVPAVTSVP
UniRef90_L5L5Q1_1_430 -----GGAG-----SSGDS-----D-GEGAVT-AV
UniRef90_UPI0002BCF55A_1_410 -----GAAG-----SSGDS-----D-GEGAVT-AV
UniRef90_P41987_1_407 -----DGTGGGEPGLLLTGSRSLLGDSKLAVTPDD-AEQPVTTPA
UniRef90_J9JHI9_1_433 -----PLLLDGSG-----SSLEGSALAGTPEEEEE-QAVTTAA
UniRef90_Q9Y6H8_1_435 -----LLDGS-----SSLEGSALAGTPEEEEE-QAVTTAA
UniRef90_G3QHB2_1_399 -----LLDGS-----SSLEGSALAGTPEEEEE-QAVTTAA

UniRef90_F7B1T8_1_432	-----HLLLDGSG-----	SSLEGSALAGTPEEEEE-QAVTTAA
UniRef90_L9L2D3_1_460	----APLLLVDSG-----	SSLEDSALAVTPEEEEE-QAVTTAA
UniRef90_Q64448_1_417	-----DSSG-----	SSLQESALVVTPEEGE-QALATTV
UniRef90_G3H8J5_1_417	-----DSSG-----	SSLEESALVVTPEEGE-QALATTV
UniRef90_UPI0003333DA4_1_405	-----DSSG-----	SSLEESALAVTPEEEEEQALATTV
UniRef90_I3NC37_1_417	-----DRSG-----	SSLEESALAVTPEEEEE-QALTTTA
UniRef90_H0XD37_1_430	-----VEGSG-----	SSLEDSALAVTPEEEEEQAVTTAA
UniRef90_G1U3S9_1_407	-----DASG-----	SGSEEVPLGATPEEEEE-PAVTTAA
UniRef90_UPI00032AEFC1_1_413	-----DASR-----	SSSEEGPLGATPGEEEE-PAVTTAA
UniRef90_UPI00034F30A8_1_402	-----DSSG-----	SSLEGRVVRVGTPEAE-----A
UniRef90_UPI0003340A67_1_370	-----DSSG-----	SSLAGSARGGTPG-----
UniRef90_UPI0002234D0E_1_449	-----NGST-----	SSLGENKLEVTPEE-KVQAETTRV
UniRef90_G3TTN5_1_429	-----NGST-----	SSLGENKLEVTPEE-KVQAETTRV
UniRef90_UPI0002C457ED_1_447	-----NGST-----	SNLEESKLEVTPEE-EVQAGATRV
UniRef90_UPI000333D50E_1_427	-----NGST-----	SSLRGSKLEVCPEE-EVQAGATSV
UniRef90_UPI0003343FBC_1_423	-----GRAG-----	NRVLLVNGNGRSSADTPDAGEPAATNI
UniRef90_F7G5V2_1_446	-----VINGSSS-----	SLGATKSEVTSEG-EKQPGTTTV
UniRef90_G3VY19_1_428	-----LINGSSS-----	SLGAAKSEVNSEG-EKQPGTTTV
UniRef90_UPI000155BBAC_1_459	-----LVNGSSS-----	LGGGSGGEAEAG-EEWPGTTRV
UniRef90_F7EY8_1_425	-----NGGS-----	LGGGSGGEAEAG-EEWPGTTRV
UniRef90_I3KXW1_1_474	PGNASNAGSWDGGKS-----	EQDEGHV-----TTT-V
UniRef90_UPI00022B3AE8_1_449	-----SWDGGKS-----	EQDEGHV-----TTT-V
UniRef90_UPI0002A48057_1_447	-----ADIWGSGRS-----	MQEKGHI-----TTTTV
UniRef90_H2MCD5_1_421	-----SNIWGSGRS-----	MQEKGHI-----TTTTV
UniRef90_H2UTF3_1_420	-----TGSWGGGRK-----	ERGGENV-----STTRV
UniRef90_UPI000298F1F6_1_460	-----TGSWGGGRK-----	ERGGENV-----STTRV
UniRef90_H3DE08_1_376	-----WGGGTN-----	EQEGRRV-----STTRV
UniRef90_Q8JFD2_1_434	-----GGLST-----	GPEEGHV-----TTT-V
UniRef90_H2T4Y1_1_438	-----NSSSSSLQ-----	VPHDDVT-----VVTKA
UniRef90_H2T4Y2_1_428	-----NSSSSSLQ-----	EETNPPL-----PQGEQ
UniRef90_H3BZL0_1_378	-----STASCD-----	VPPDDVT-----VVTKA
UniRef90_I3K1N0_1_478	-----TTVITAPSK-----	VLHNDFT-----VVTRA
UniRef90_H2LFL5_1_470	-----LSIIAPEVR-----	AADEESP-----AVQNE
UniRef90_M7BWJ7_1_486	AVNSSSSTSLSRGSSS-----	KWDVEGEEATKEWPVSAACTTV
UniRef90_K7F163_1_492	AVSSSSSTSLSRGSSS-----	KWDVEGEEATKAWPLSVACTTV
UniRef90_H0ZM32_1_512	SANSGSSTSLSGASGS-----	KWDVEGAEELSGARPVSAACTTV
UniRef90_H3AH16_1_396	----GSSGSLGGGK-----	QGQEDGN-----VTTV
UniRef90_B0BM18_1_388	-----TEASGSS-----	ARAEDRP-----VTRFV
UniRef90_Q4S8R0_1_345	-----	-----TCPAF
UniRef90_I3KYH7_1_341	-----	-----SSPVL
UniRef90_H2M0G7_1_345	-----	-----SSPAS
UniRef90_H3A471_1_360	-----	-----GKAAP
UniRef90_Q6GLA5_1_353	-----	-----ELDQF
UniRef90_UPI0002A4A1D5_1_346	-----	-----AGSAP
UniRef90_S4RXA6_1_456	-----	-----SSAAVAAALAAALEDEAEVLTATV
UniRef90_P16863_1_360	-----	-----
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UniRef90_I3KYL3_1_401	-----	-----ETRSPPSDKQEEREDQSPPHEDL
UniRef90_G3NC44_1_402	-----	-----ETRSPPSDKQEEPEEQSSPPLERM
UniRef90_H2SSL2_1_392	-----	-----DTHSLPVDKHEEPEEP-----
UniRef90_UPI0002C46B7E_1_433	-----	-----IQHISSSNNEGTHKIFGKEVNDNQ
UniRef90_G3ULF1_1_432	-----	-----LQHINS-NNDGTHKISGKDVDNDQ
UniRef90_C9IYK1_1_407	-----	-----FQHISSNNKDKTHKIFGKELNGNQ
UniRef90_H0Y0G7_1_436	-----	-----LQPIGSNNKDKTHKIFGKEVNDNQ
UniRef90_L9JD22_1_408	-----	-----LGHIGSNNKDKTHKIFGKEVNDNQ
UniRef90_F1N617_1_436	-----	-----LQNISSSNKEDTHKLSGKEVNGNQ
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UniRef90_L5JUH5_1_307	-----	-----
UniRef90_UPI00020369CA_1_441	-----	-----TQNASTNCTEGLLARPGTEMRNSQ
UniRef90_R4GLX1_1_405	-----	-----TQNAGINCSEGLLGRPGTERRSSQ
UniRef90_UPI00035A19E6_1_466	-----	-----TQNASTNNNEGFLGQLWTEMHDAQ
UniRef90_F6WA84_1_463	-----	-----PANANLHSHSEGIISVVAEIGGTH
UniRef90_G1SG18_1_430	-----	-----IQHSGQQPDH-SSFVQNTTTIQSW
UniRef90_UPI00032B0E64_1_413	-----	-----IQHLGQQPNH-SSFALQNTASQSC
UniRef90_UPI0002C65D9D_1_412	-----	-----IQHLGQQPDH-SSFGLQNTLSQSC
UniRef90_F7CF28_1_383	-----	-----IQHLGQQPDH-SSFALQKTTQSC
UniRef90_Q969M2_1_435	-----	-----NQHLGQQSDH-SSFGLQNTMSQSW
UniRef90_L9JVZ3_1_406	-----	-----IQHRGQQQTH-SSFPHNTVPSQSW
UniRef90_I3M407_1_414	-----	-----IQHPGQQPCH-SSFGLRNTVPSQSW
UniRef90_L5JMB7_1_435	-----	-----IQHSGQHPDL-SSFGLQNTMSQSW
UniRef90_L8J083_1_417	-----	-----IQHPGQQPDH-SLFLQNIIRPHSW
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UniRef90_G3GSS7_1_405	-----	-----IQHPGQQPCH-SLFGSKNVMSQSW

UniRef90_UPI0003316158_1_413 -----LQHPGQHSGK--PFGPQNAKCHSW
UniRef90_G3WUN4_1_443 -----VQYFQQCKHQYQQGHPQSSFSRGG
UniRef90_F6W379_1_264 -----
UniRef90_M7BL54_1_431 -----EQHYRQLSNQHGLGQPSRHPSSSSE
UniRef90_UPI0002B44362_1_276 -----D-----PSAYNSKKS-
UniRef90_UPI000298933C_1_429 -----PH--VRPQYAG-PRATLVASHMEI
UniRef90_H3CDZ2_1_426 -----PH--VKPQYAG-PRATLVASHMEI
UniRef90_I3IZH7_1_440 -----PHGSGKPHYAG-PRPTLTGGHMEI
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UniRef90_UPI0002C691BE_1_358 RLPARG-----YQSDKRCLSK-----ASSKARSDDLVS
UniRef90_F7BKC0_1_358 RLPHC-----YQNDKPRLSK-----ASSKARSDDLVS
UniRef90_Q0VCR2_1_359 SLPHG-----YQSDKRRLSK-----ASSKARSDDLVS
UniRef90_G3TUX5_1_358 RLPHG-----YHSDKRRLSK-----ASSKARSDDLVS
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UniRef90_Q01231_1_358 RLPQG-----YHSDKRRLSK-----ASSKARSDDLVS
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UniRef90_G1KPB5_1_370 LLSNG-----YLPDKRRLSKTS---HASSKARSDDLVS
UniRef90_K7FWT6_1_369 QVSNG-----YFNEKRRLSKTS---HASSKARSDDLVS
UniRef90_F1QL21_1_400 SHPG-----FFRDKRRLSKTSG---TSSNRLRPSDLAV
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UniRef90_L9JGQ0_1_441 PAEKAPSLCPPEL-----TADDARPLSRLS---KASSRARSDDLTI
UniRef90_P28236_1_440 SAEKAPSLCPPEL-----TTDDNRPLSRLS---KASSRARSDDLTI
UniRef90_G5BBL7_1_440 SAEKAPSLCPPEL-----TADDTRPLSRLS---KASSRARSDDLTI
UniRef90_M3XED1_1_440 PVEKSPSLCPDP-----SRDDTRPLSRLS---KTSSRARSDDLTV
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UniRef90_F6VG96_1_441 PAEKAPSLCPPEL-----SGDDTRPLSRLS---KASSRARSDDLTI
UniRef90_P55917_1_440 TPEKAPSLCAEL-----PGEDTRPLSRLS---KASSRARSDDLTV
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UniRef90_G3UBH4_1_410 PAEKAPSLCAEV-----TTDETRPLSRLS---KASSRARSDDLTV
UniRef90_I3N7I6_1_431 SAEKAPSLCPPEL-----TAEARPLSRLS---KASSRARSDDLTI
UniRef90_G3X210_1_429 PVEKAP-LCPPEL-----AADDTRPLSRLS---KASSRARSDDLTV
UniRef90_F7BI06_1_372 PVEKIP-LCPPEL-----AADDTRPLSRLS---KASSRARSDDLTV
UniRef90_UPI000333FA9E_1_424 -----LLCAEL-----AADDPRALSRLS---KASSRARSDDLTV
UniRef90_K7EY71_1_406 -----AET--DTRPPSRLS---KTSSRARSDDLTV
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UniRef90_P36381_1_400 -----AELATDVRSLRSLRSL---KASSRARSDDLTV
UniRef90_H2MUH4_1_428 -----DTIDDSRPLSRLS---KASSRARSDDLTI
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UniRef90_Q503J6_1_391 -----ETIEDTRPLSSLS---KASSRARSDDLTV
UniRef90_F6QCF2_1_438 PSNSATPERVPSRAAS-----EHAPYSRSLRSLRSL---KASSRARSDDLTV
UniRef90_UPI00034FAB61_1_453 PSNSATPERVPSRAAS-----EHAPLDCAPSERAPSRAASEHAPS DRAPS
UniRef90_UPI0001DE8510_1_439 ALEPDIVEYEPLGPEMPLLNLEFIPDSRSLRSLRSL---KASSRARSDDLTV
UniRef90_H3A837_1_370 -----PLSRLS---KASSRARS-----
UniRef90_G1KPB7_1_391 -----MEDEQEPLGGNV---ALPSTADTRP---
UniRef90_B0S6Z4_1_382 -----EVDSLKTPTVLPEVLEEHSSEGESVEE--
UniRef90_G1PZ72_1_426 PAEKAPSPGAEL-----AGDDTRPLSRLS---KASSRARSDDLTV
UniRef90_UPI000155FB82_1_448 EMHAPPLPPTD-----PGRSSKASKSSG-----SRARPDDLAI
UniRef90_F6U7L2_1_428 EMHAPPLPPTD-----PGRSSKASKSSG-----SRARPDDLAI
UniRef90_UPI0002C6341D_1_440 AMHAPPLPPTD-----PGRSSKASKSSA-----GHARPDDLAV
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UniRef90_G1PYG2_1_394 EMHMPLLPTD-----PRRSSKASKASN-----SQARPNDLAI
UniRef90_L5L5Q1_1_430 DMHAPPLPAE-----PRRSSTASKASG-----GRARPSDLAI
UniRef90_UPI0002BCF55A_1_410 ELHAPPEL PAD-----PGRSSKASKSSG-----GRARASDLAI
UniRef90_P41987_1_407 ELHAPPEPPAD-----PGRSSKASKSSG-----GRARAGDLAI
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UniRef90_Q9Y6H8_1_435 QMHQPPLPLGD-----PGRASKASRASS-----GRARPEDLAI
UniRef90_G3QHB2_1_399 QMHQPPLLLGD-----PGRASKASRASS-----GRARPEDLAI

UniRef90_F7B1T8_1_432
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UniRef90_UPI0003340A67_1_370
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ELHTPPLLLVE-----PGRASKASKASS-----GRARPGDLTI
EMHSPLVLLD-----PGRSSKS---SN-----GRARPGDLAI
EMHSPLVLLD-----PGRSSKA---SS-----GRARPGDLAI
EMHNPPLLLLD-----PGRSSKA---SN-----RAKPGDLAI
EMHEPPLLLTD-----PGRSSKA---SS-----GRARPGDLAI
EMHVQPSEPADPADPADP---VDPGRSSKA---SS-----GRARPDDLAI
EMHAPPLEAD-----AGRCSKAS--G-----GRARPSDLAI
EMHAPPPLSAD-----AGRCSKAS--SS-----GRARPSDLAI
QVEAPAPLLGD-----TGRSSKAS--S-----GRAKPRDLAI
-VEAPALLPED-----PRRSSKAS--S-----GRAKPGDLAI
DMHVPLLLGD-----VGRASKASKSSS-----GWARADDLAI
DMHVPLLLGD-----VGRASKASKSSS-----GWARADDLAI
DTHMPPLLLGD-----VGQASKASKLSS-----GRPRADDLAI
DMHRPPLLLGD-----PGRASKTSRASSS-----GRLRADDLAI
ELHRPPLLLRD-----AGQSGKAS--SN-----RARPNDLAI
EMHAPPPLLVLD-----SRRLSKASKASS-----GRARSDDLAI
EMHAPPPLLLID-----TRRLSKASKSSS-----GRARSDDLAV
EIHESPLLLLD-----LRRLSKASKASS-----CRARSDDLAI
EIHESPLLLLD-----LRRLSKASKASS-----CRARSDDLAI
EMHEPPVMVSTD-----PRRLSRASKSSS-----IRARPSDLAV
EMHEPPVMVSTD-----PRRLSRASKSSS-----IRARPSDLAV
EMHEPPVTVRTD-----PRRLSRTSKSSS-----IRTRPSDLAV
EMHEPPVTVRTD-----PRRLSRTSKSSS-----IRTRPSDLAV
EMHEPPATAGVD-----PRRLSRASKSSS-----VRARPSDLAV
EMHEPPATAGVD-----PRRLSRASKSSS-----VRARPSDLAV
EMHDPPPAPGVD-----PRRLSRASKSSS-----VRARPSDLAV
EMHEPP-VIFTD-----ARRLSRASKASS-----VRARPNDLAV
EMHWPPASATT-----DIRKPSRASKCS-----VRARPDLLAV
HSMFPTLPRHTPL-----YALTPPSRASKCS-----VRARPDLLAV
EMHWPPASAAAT-----DIRKPSRASRSS-----VRARPDLLAV
EMHQPPAAAGT-----DNRKPSRASKSGG-----GRARPDLLAV
DATAEMHPPPA-----DTRRPSRACKYSG-----ARARPDLLAV
EMHEPPLLLID-----
EMHEPPLID-----
EMHEPPLLVDT-----RLSRASKSSS-----CRARSDDLAV
EMHEPPVPTDTR-----RL-----
EMHQPP-----
EGSADSQRRNS-----QSSKHS-----LQFPF-----
EMSIENQRRNS-----QSSKHS-----
EAPAESQRRNS-----QSSKHS-----
SSPSDNQRSSS-----RSTKHGNKAKP-----ED-----
EKQRLPSNRNR-----HSSNRSRPG-----
GSP--TQPRPG-----YSTKRS-----
QLHDPPLHSGGEH-----DIDLRLSRASS-----RVRSDDLQV

ECGSSEYPTLPVADTSSCPALSGIVRKSRRVSP-----
ERARSEYPTLPVSDASSSTVLSGITRKRTR-----
GCTSSEYPTLPV--ASSCATMSGAAKRSRRVSP-----
-LVTSEYPTLPVADATSCPTLSGITRKSRR-----
VRRERRENDGKDSERNHYSRG-----VTVDLENHMRQSPPKVFSPLPANCN
VKERENFGTDSERCHYSKG-----VSDLENHVSQSPQKVFSLPANCN
LMEKRETEGKDSKRNYYSRGRHSIPGVAIDGENNMRQSPQT-----
LREKTEIDGKDSKRN--SRGHCFIPGVAIDLGHIGQLPHTAFSMASTST
LREKREMNAGKSKRNHYSRDHCSIPGVVIDLENHMQSPQTT-----
LRGKRETDGKDSKRNHYFKGHCSSPGDAIELNHNHVGQSPQTAFLPANCN
VRGKRESDESDESKRNHYPRG-----

KEADQKHFLADTQNADTKTAR--NHLLEQLRSGRERRILHKFPHQEQQ--Q
KEADQKHFLAGAQNADTAPRS--FAEMLSQPP-----LQFPF-----
EEAEKHFLLVTONADTASTF--YLRSAEMPSQTSLQPGTTFPSTSRFRQ
KQENTTTGHQANFEAAVHLGYR--PEMPLGAALYPSLQPEMTFSPPTDCT
PGTTTTT---RHCPAYAVGTWKQSQDLEPLGEPLTDLHSDSSVRESGGWV
P-DTTAS---RHCPVYAAGTQKQDLEPSGEPATDLHS--YCRDSDSSV
LGTTTTAP---RHCPSTYIGTWEQPPQHPRSSGEPLTDFHS--HCRDSDGSV
LGSTTAP---RHCPSTYIGTWEQPPQHPRSSGEPLTDFHS--HCRDSDGSV
LGTTTTAP---RNCPSFAVGTWEQSDPEPSGEPLTDLHS--HCRDSEGS
LGKMTAS---RHCPSTYIGTWEQSDPEPSGEPLTDLHS--HCRDSEGS
LGATVAS---QHCPSTYIGTWEQSDPEPSGEPLTDMRS--HFKGSDGSV
LGETTAP---RHCPSTYIGTWEQSDPEPSGEPLTDFHN--HCRDSEGS
LGKMTAP---RHCPSTYIGTWEQSDPEPSGEPLTDLHS--HCRDSEGS
LGTMMAS---RHCLSHHTGPWERPQDLKPSGEPLTDLHS--HCRDSEGS
LGTEIAP---RHCPSTYIGTWEQSDPEPSGEPLTDLHS--HCRDSEGS
LERTTAP---EHCPSTYIGTWEQSDPEPSGEPLTDLHS--HCKDSDGSV
LGTMTAS---PHCPPSTLGTWERSHGQDASGKPLSDLQS--H-----

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UniRef90_UPI000298933C_1_429
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R-----
TERGSYLGSKASFLSRASESSDSR-----

RKHSR-----

SSPSDSTD-----
SNPSDSADS-----
ASPSDSGDCQSGTDNAS-----
