

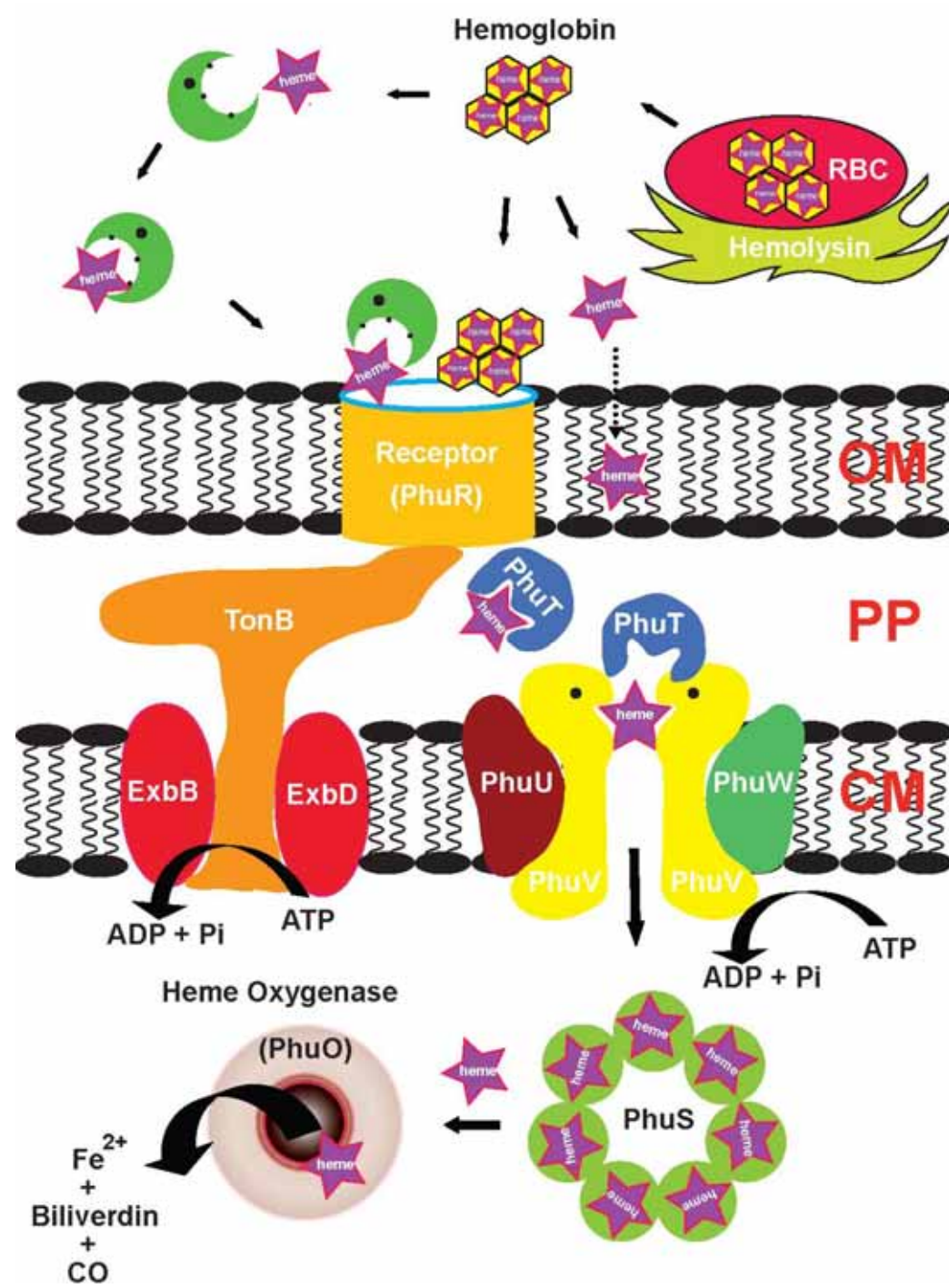
Periplasmic Heme Transport Protein



Yong Tong



Heme Acquisition System



Sequence Alignment of PhuT, ShuT, BtuF and FhuD

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PhuT  -----: : :-----.. :* : * *
ShuT  MNRRLYFIYNSNDNHDHSQFDKSSHIMPRIITRPFLFTPLTLCISAVASASKSTVKRKKLFTAVLALSWAFSVTAAERIVVAGGSLTELIYAMGAG-- 97
BtuF  -----MMPLGLFPLPRAAVV-----LLISLLTLPAAQAARVISLSPSTTELAYAAGLG-- 49
FhuD  -----MSGPLPISRRLTAMALSP-----LLWQMNIAHAAAIDPNRIVALEWLPVELLLALGIVPY 57
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....1

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PhuT  --SKLVGVDTTSQHPQALKQLPSVGYQRQLAAREGVLAALRPDILIGTEMGPPPVLKQLEGAGVRVETLS-AKPDLEALESNLKKGDLGVPRAEAA 142
ShuT  --ERVVGVDETTSTYPPETAALPHIGYWKQLSSEGILSLRPDSVITWADAGPQIVLDQLRAQKVNVTLPFVPATLEQMYANIRQLAKTLQVPEQGDAL 192
BtuF  --DKLVAVSAYSIDYPESAKKLEHVASWQGGINVERILALKPDLILAWRGGNPRPLDOLAALGIPIFYSD--PTHIDQIASDLDKLAQYSPHPEQAHQA 142
FhuD  GVADTINYRLVWSEPPLPESVIDVGLRTEPNLELLTETMKPSPMVWSAGYGPSPEMLARIAPGRGFNFSD-GKQPLAMARKSLTEMADLLNLQSAAEETH 154
00.....110.....120.....130.....140.....150.....160.....170.....180.....190.....

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PhuT  ELDYRQLRRQADWIAAAQKSQPAPGVLLVIGNAGGQLLVAGRNTGGDWVLNLRAGARNLATHE---GYKPISEVLAALDPVAVVIADRSLEGDAAR 236
ShuT  VTCINRRLERVQONVAAKKAP---VKAMPILSAGGSAPQVAGKGSVADAILSLAGAENVATHC---QYKSYSAESLIAANPEVIVVTISQMVDGDIR 283
BtuF  AEFROHVNTLRDRYARSQPK-----RTFLQFGTQPLFTSSGHTLQSEVVS LCGGENIFADSR--VPWPQVSREQVMTRKPVIVVSGTQSGVDNV 232
FhuD  LAQYEDFIRSMNRFVVKRGAR---PLLLTTLIDPRHMLVFGPNSLPQEIILDEYGI PNAWQGETNFWGSTAVSIDRLAAVKDVDVLCFDHDSKIDMDA 248
.200.....210.....220.....230.....240.....250.....260.....270.....280.....290....

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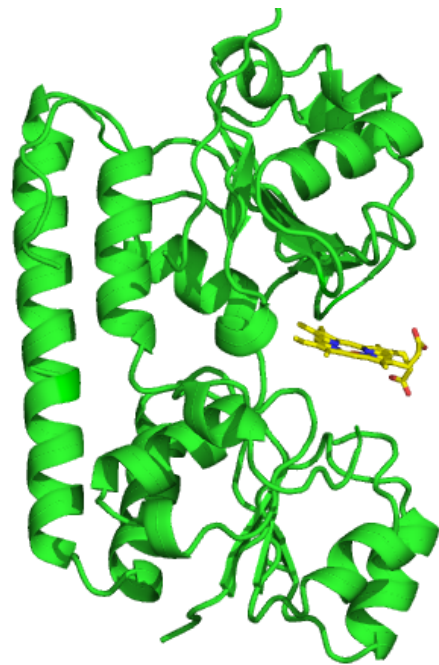
PhuT  *
ShuT  AALLKQNPGLAPTRAARDGRLLVLDPTLLVGGGLPRLPDGLAALSAAFYPSAKPLSTEAAH 297
BtuF  ---LRSIAGITHIAAWKNQRIITVDQNLILG-MGPRIADVVESLHQQLWFPQ----- 331
FhuD  AFWLPQL--VVPVIALNEDWFNRSRILLA--AQQLCQQMASIPTPVAESH----- 281
PhuT  ---LMATPLWQAMPFVRAGRFRQRPVAVWFYV--ATLSAMHFVRVLDNAIGGKA----- 297
...300.....310.....320.....330.....340.....350....

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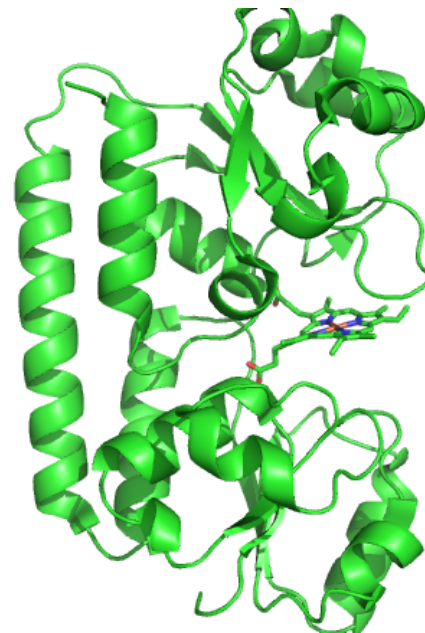
PhuT

PBD: 2R79



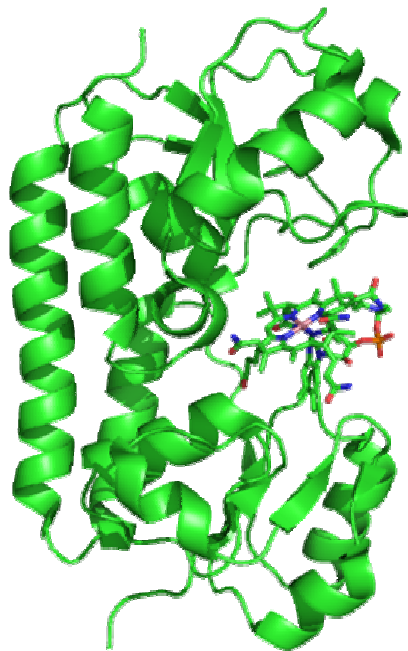
ShuT

PBD: 2R7A



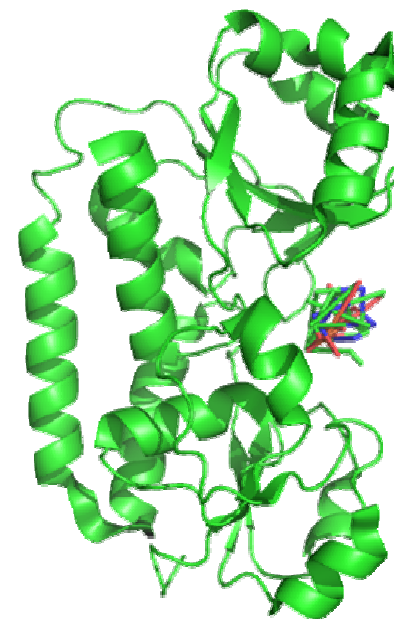
BtuF

PBD: 1N2Z



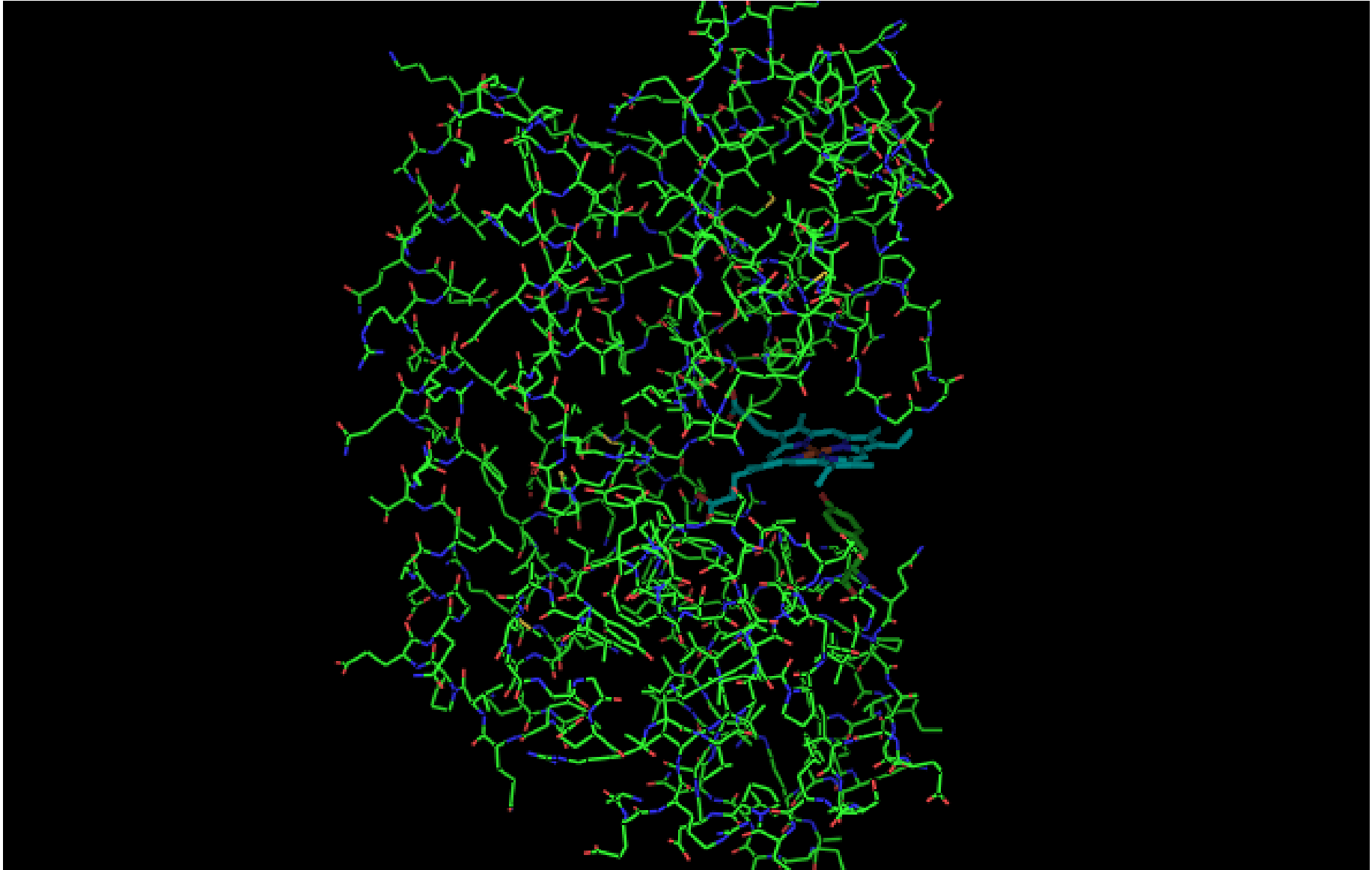
FhuD

PBD: 1K7S

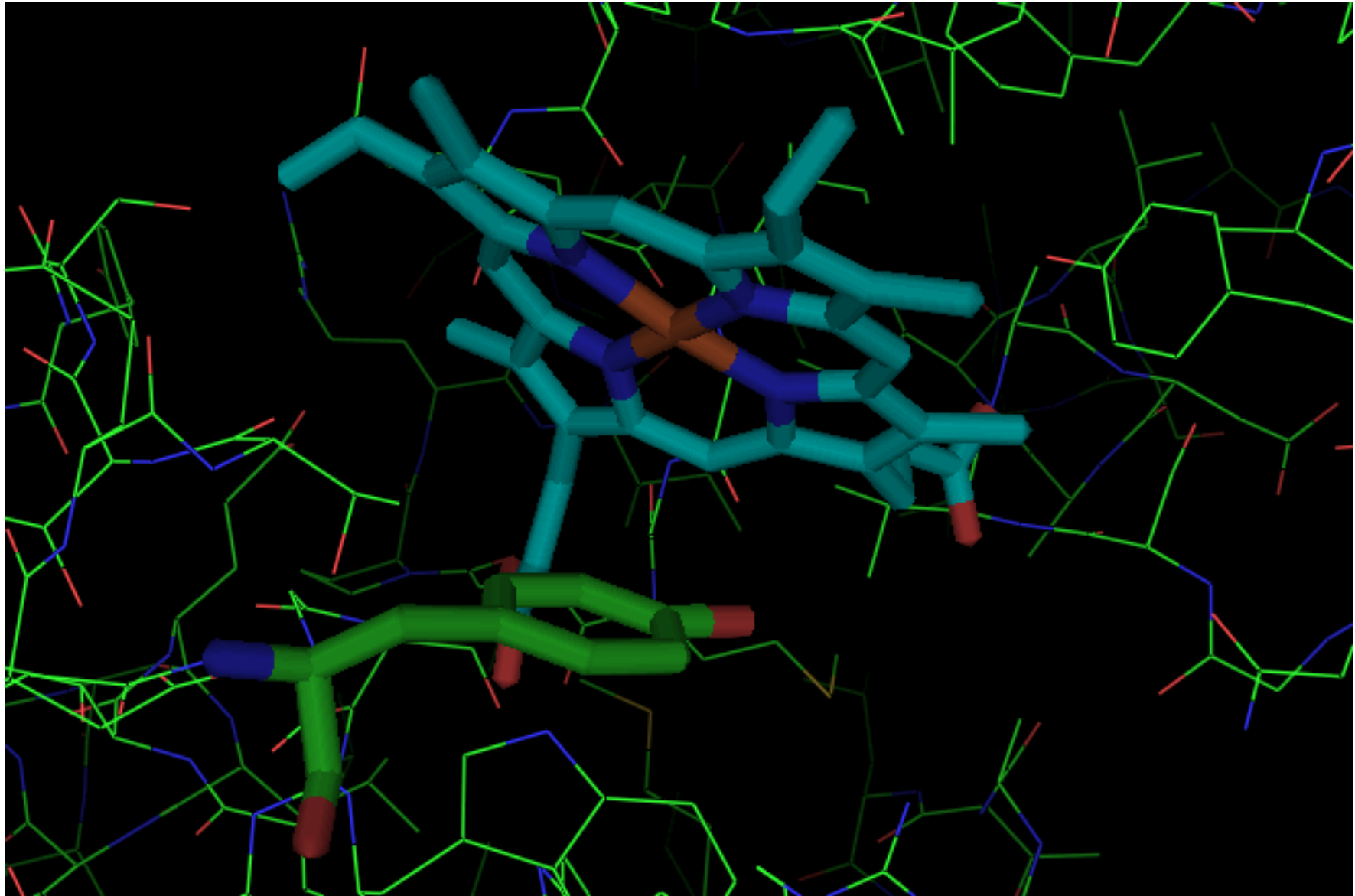


Go to Jmol

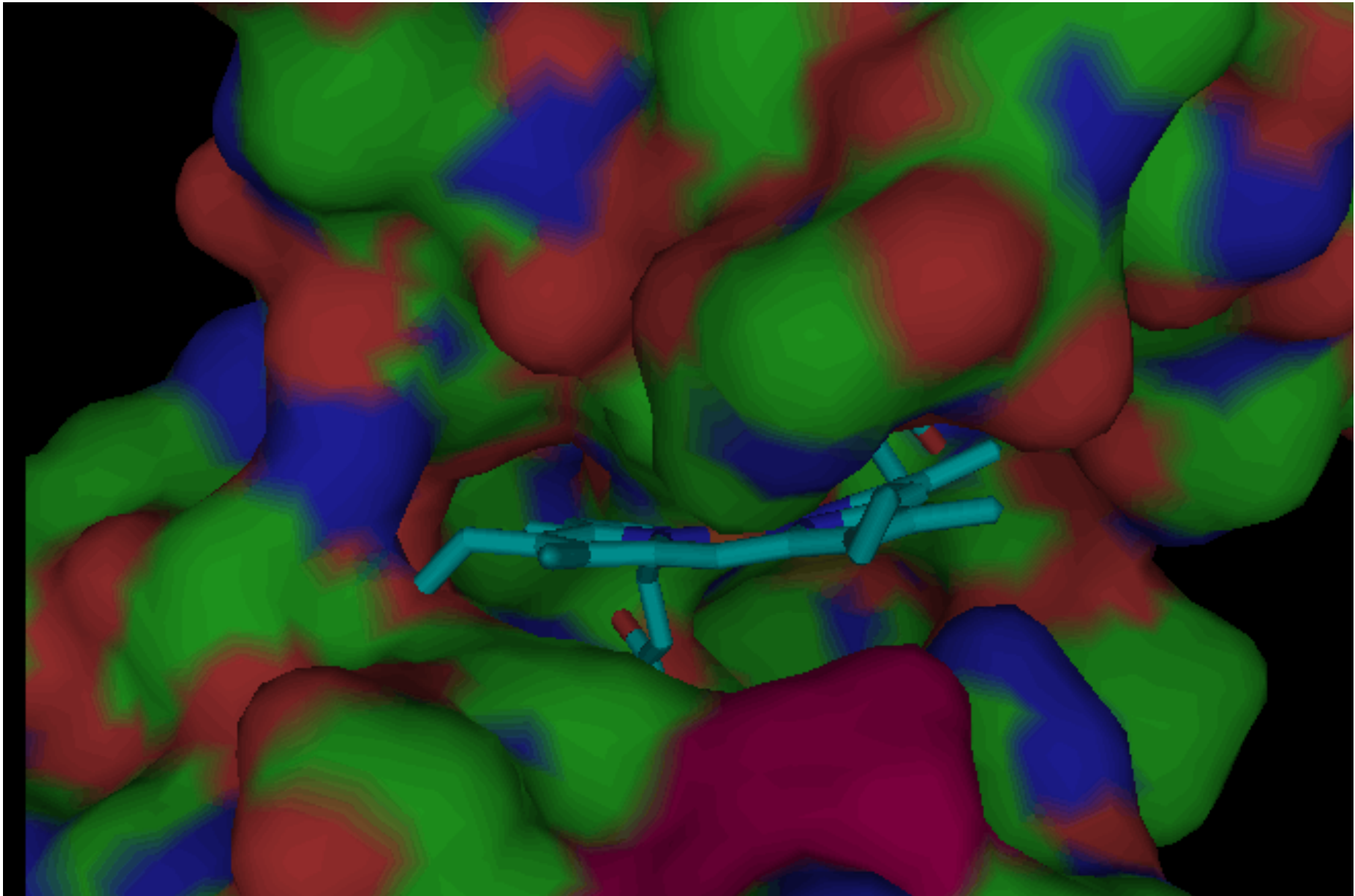
Periplasmic Binding Protein ShuT



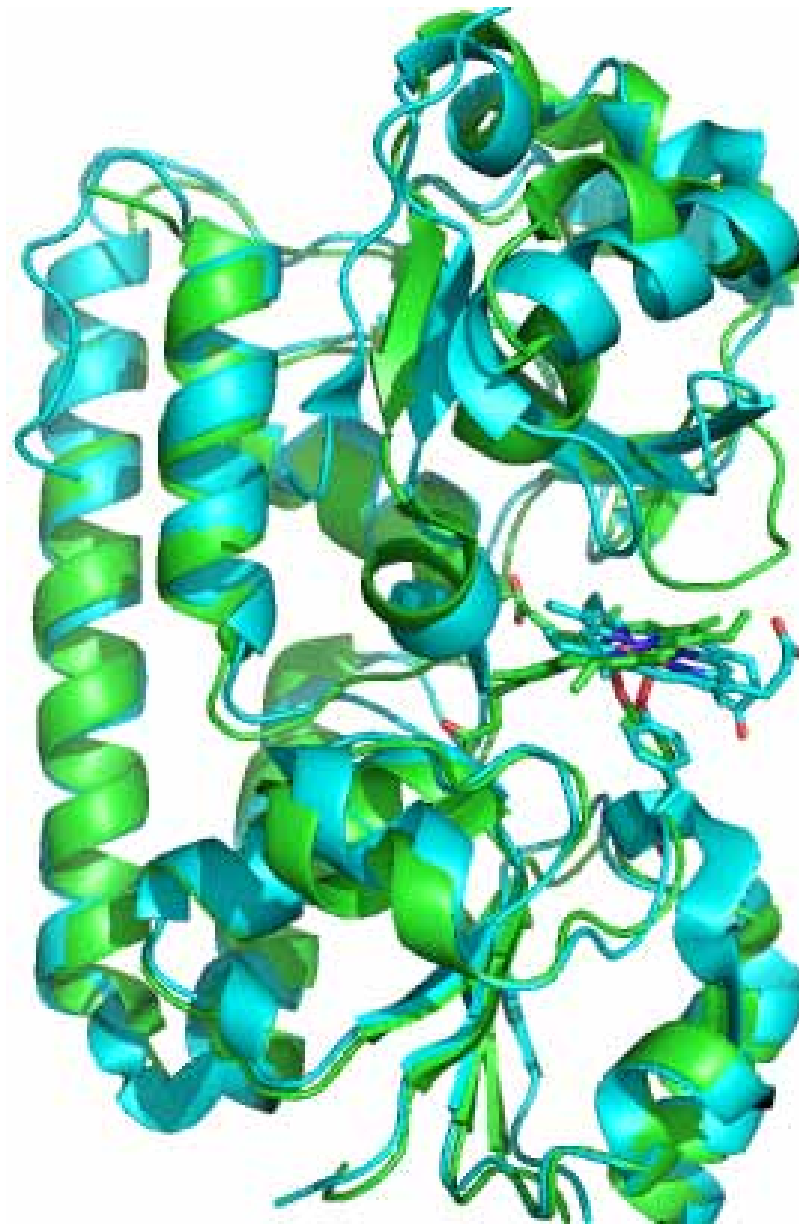
Periplasmic Binding Protein ShuT



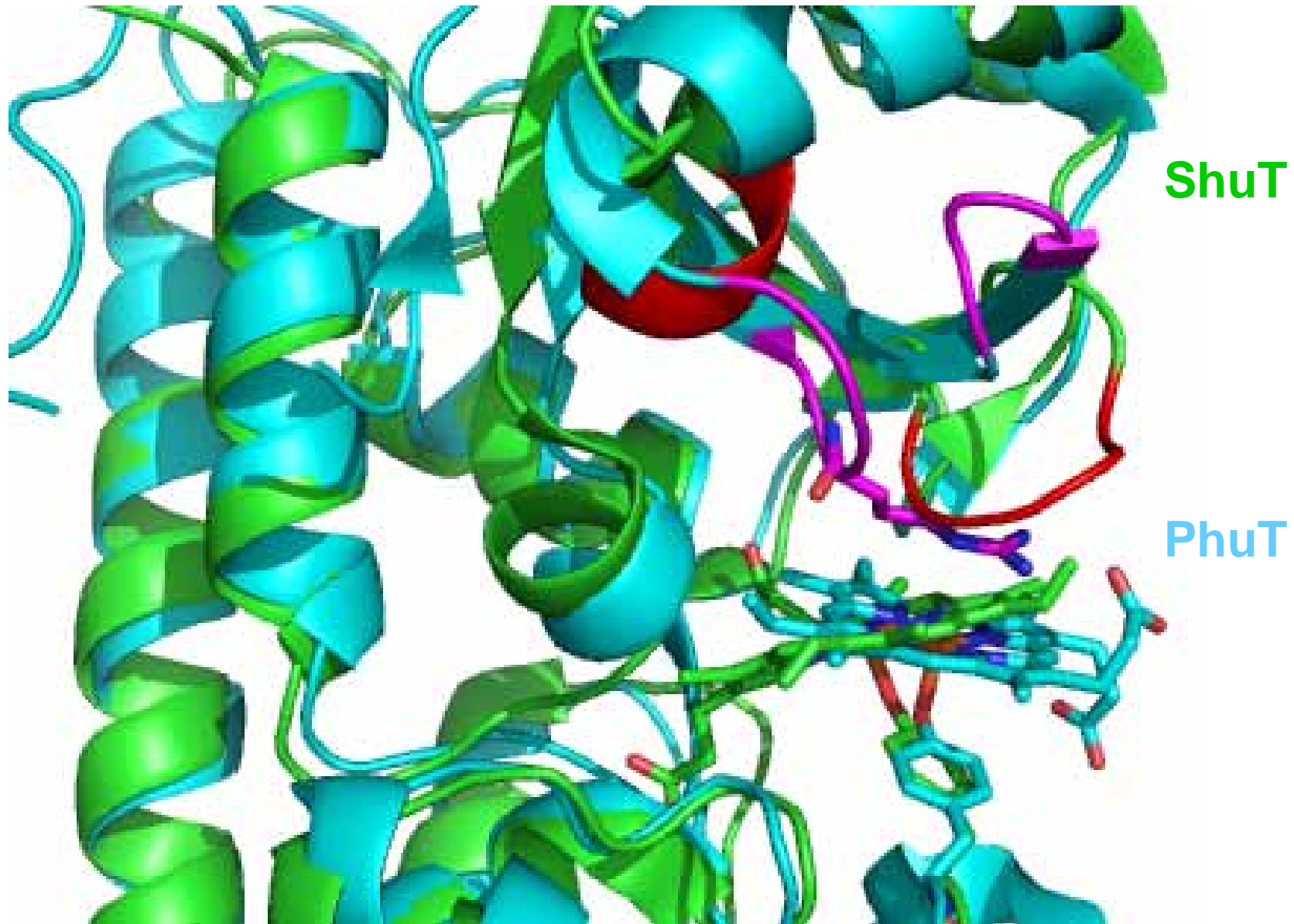
Periplasmic Binding Protein ShuT



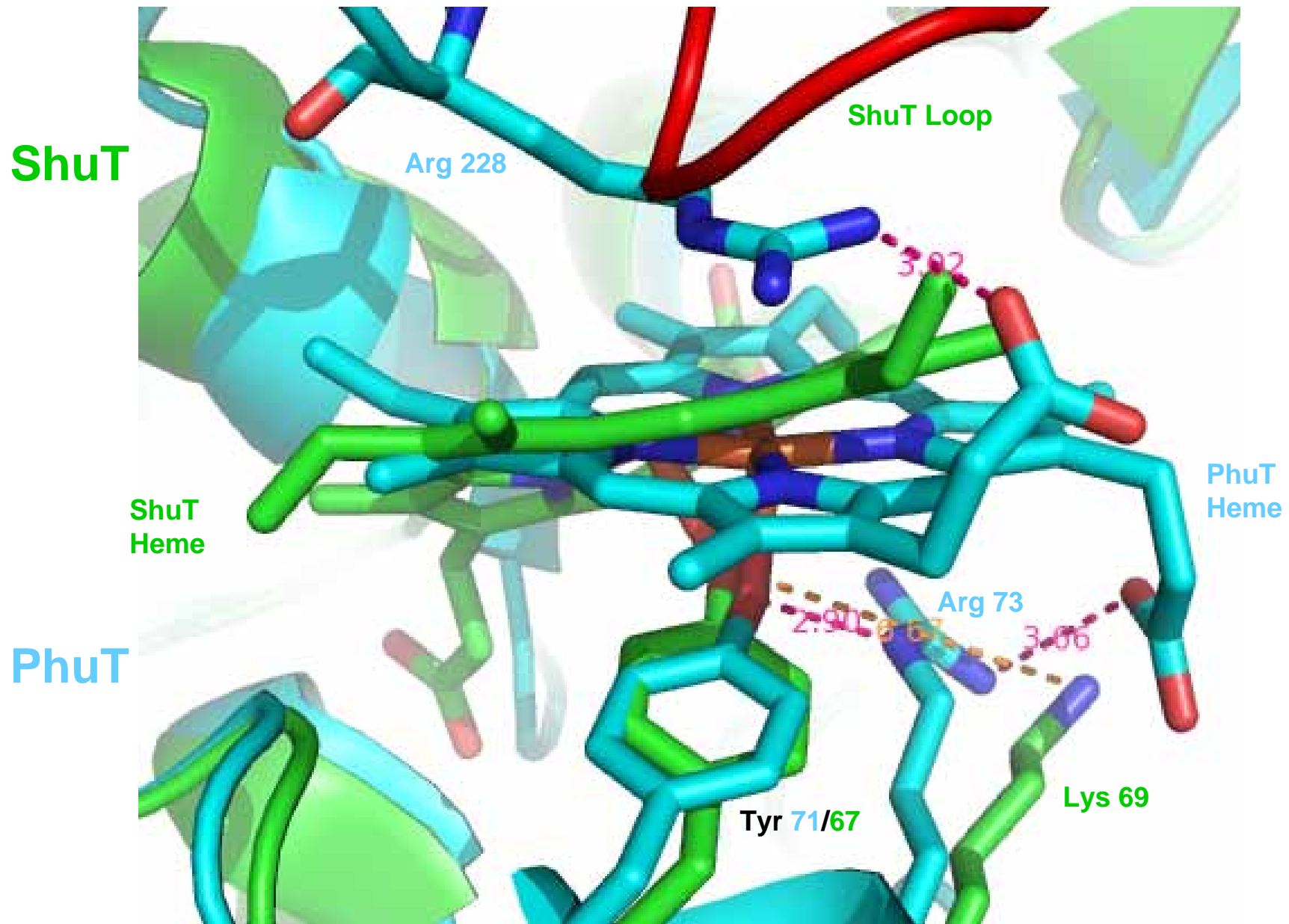
PhuT/ShuT structural alignment with PyMOL



PhuT/ShuT structural alignment with PyMOL



PhuT/ShuT structural alignment with PyMOL



Merry Christmas!



HAPPY HOLIDAYS

