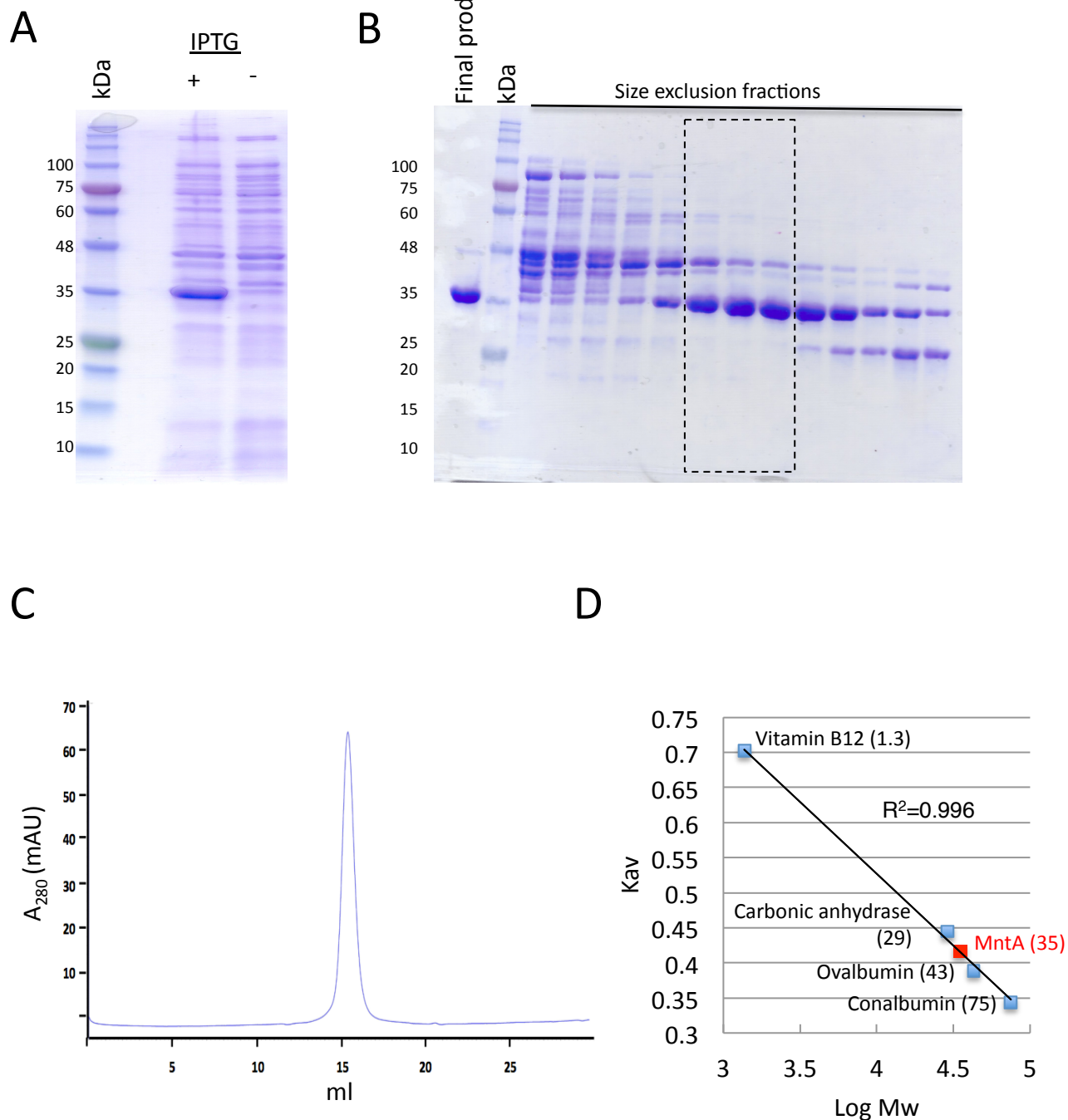
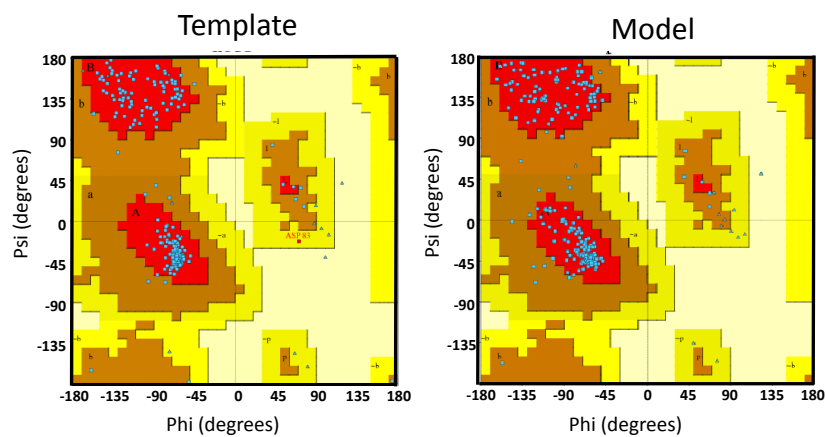


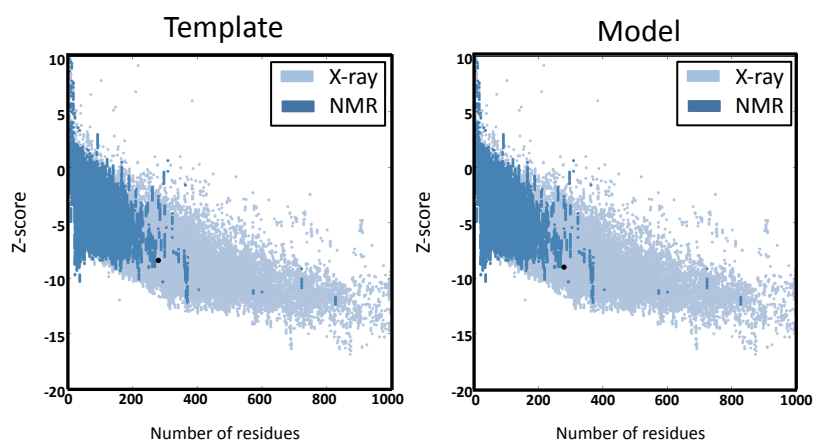


Supplementary Figure 1.

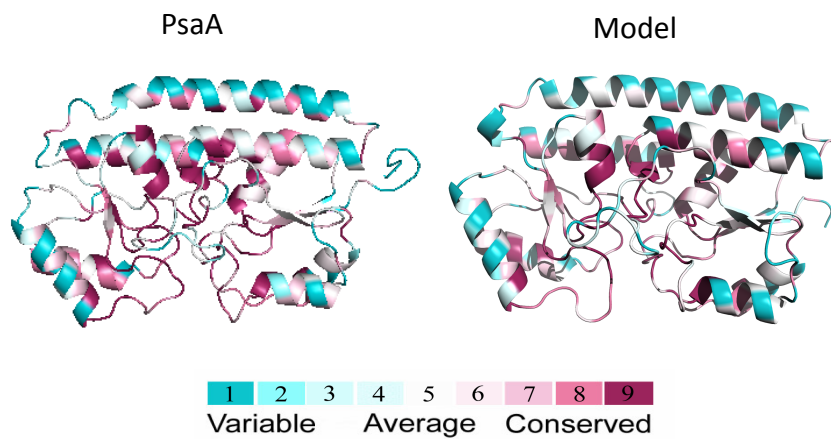
A



B



C



MntA: 1 ----MKFKNVVLSILCIFVFALTACSSN-----TN--GKEEGS--GKLKVVTYSIIYDMVKQIGGEKVEIHS-60
PsaA: 1 ----M-KKLGTLVLFLSAIILVACAS-----GKKDTTSGQKLKVATNSIIADITKNIAGDKIDLHS-58
TroA: 1 -----MIRERICACVLALGMLTGF-----THAFGSKDAAADGKPLVVTTIGMIADAVKNIAQGDVHLKG-59
ZnuA: 1 ----MLHKKTLFLFAALSAAALWGATQAA-----DAAVVASLKPVGFIASAIADGVTETEV-51
MntC: 1-MATSFASRGGLLASGLAIAFWLTGCGTAEVTTSNAPSEEVTAVTTEVQGETEEKKKVLTFTFTVLADMVQNVAGDKLVVES-80
MtsA: 1-----MGKRMSLILGAFLSVFLLVACSS-----TGTKTAKSDKLKVVATNSIIADMTKAIAGDKIDLHS-59

MntA: 61-LVPIGANPHEYDPLPKDVMKMTDADMVLYNGLNLEEGG-AWFKKLLKTANKSEKAPVYKVSEGV---EAIYLETKGLE--135
PsaA: 59-IVPIGQDPHEYEPLPEDVKKTSEADLIFYNGINLETGGNAWFTKLVENAKKTE-NKDYFAVSDGVDV---IYLEGQNEK--133
TroA: 60-LMGPGVDPHLYTATAGDVEWLGNADLILYNGLHLE-----TKMGEVFSKLRSRLVVAVSETIPVSQRLSLE----E--127
ZnuA: 52-LLPDGASEHDYSLRPSDVKRLQNADLVVWVGPEME----AFMQKPVSKLPGAK--QVTIAQLEDVKPLLMKSIHGDDDDH-125
MntC: 81-ITRIGAEIHGYEPTPSDVKQAQDADLILYNGMNLER----WFEQFLGNVKDVP----SVVLTEGIEPIP--IADGPYTD--149
MtsA: 60-IVPIGQDPHEYGPLPEDVEKTSNADVIFYNGINLEDGGQAWFTKLVKNAQKTK-NKDYFAVSDGIDV---IYLEGASEK--134

MntA: 136-----KEPDPHAWMNIKNGILYAENVKKALIKEDPKNKEFYTKNADNYVAELQKLHDET VNRIHQIPEEKRF-203
PsaA: 134-----GKEDPHAWLNLENGIIFAKNIAKQLSAKDPNNKEFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLI-201
TroA: 128-----AEFDPHVWFVDVKLWSYSVKAVYESLCKLLPGKTREFTQRYQAYQQQLDKLDAYVRRKAQSLPAERRVL-195
ZnuA: 126-DHAEKSDEDDHHHGDFNMHLWLSPEIARATAVAIHGKLVELMPQSRAKLDANLKDFEAQLASTETQVGNELA--PLKGKGY-203
MntC: 150-----KPNPHAWMSPRNALVYVENIRQAFVELDPD NAKYNNANAAYVSEQLKAIDRQLGADLEQVPANQRFL-216
MtsA: 135-----GKEDPHAWLNLENGI IYSKNIAKQLIAKDPKNKETYEKNLKAYVAKLEKLDKEAKSKFDAIAENKKLI-202

MntA: 204-ISSEGAFKYFGKAYDIKTGYIWEINSENQGTDPQIRDVSVSIQTNKVPALFVETSVDRRSMETV-----SKETNVPIAGT-278
PsaA: 202-VTSEGAFKYFSKAYGVPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVESSVDDRPMKTV-----SQDTNIPPIYAQ-276
TroA: 196-VTAIDAFGYFSRAYGFEVKGLQGVSTASEASAHDMQELAAAFIAQRKLPAIFIESSIPHKNV EALRDAVQARGHV VQIGGE-275
ZnuA: 204-FVFHDAYGYFEKQFGLTPLGHFTVNPEIQPGAQRLHEIRTQLVEQKATCVFAEPQFRPAVVESV-----ARGTSVRMGT--277
MntC: 217-VSCEGAFSYLARDYGMEEIYMWPINAEQQFTPKQVQTVIEEVKTNNVPTIFCESTVSDKGQKQV-----AQATGARFGGN-291
MtsA: 203-VTSEGCFKYFSKAYGVPSAYIWEINTEEEGTPDQISSLIEKLKVIKPSALFVESSVDRRP METV-----SKDSGIPPIYSE-277

MntA: 279-IFTDSLKGSGEDGDTY LKMMKWNIDTIINGLQK-----311
PsaA: 277-IFTDSIAEQGKEGDSYYSMMKYNLDKIAEGLAK-----309
TroA: 276-LFSDAMGDAGTSEGTYVGMVTHNIDTIVAALAR-----308
ZnuA: 278---LDPLGTNIKLGKTSYSEFLSQLANQYASCLKGD-----310
MntC: 292-LYVDSLSTEEGPVPTFLDLLEYDARVITNGLLAGTNAQQ-330
MtsA: 278-IFTDSIAKKGKPGDSY YAMMKWNLDKISEGLAK-----310