

pdeA1-Gx 1 LAQGMQLHYQIQVR--THTLEISGVEALSRWHPHLGNLPSRFFAVAEELGQIEAIGRWSLEACRQVVKDRDQIHVPT--VAVNSAVHFRNRALPEHAAALKDHN--KPSRLT
pdeA2-Gx 1 SKGMNLHYQIQVE--TMTGELSGVEALSRWHPHLGNLPSRFFAVAEELGQIEAIGRWSLEACSQVVKDRDQIVRPT--VAVNSAVHFRNRALPEHAAALKHG--LPDRLT
pdeA3-Gx 1 LAKGMNLHYQIQVR--THTLEISGVEALSRWHPHLGNLPSRFFAVAEELGQIEAIGRWSLEACRQVVKDRDQIHVPT--VAVNSAVHFRNRALPEHAAALKHH--LPDRLT
YahA-EC 1 LENHEKHWIQVFC--AQITGTGCELVRMHPHTGCGTGFIFLAESGLIVITRQLKQTADIMPVKHILPDNFNGINVSAGCLAAGFEKCLNLYKLG--NDKILV
BphG-RS 1 EESQHLVYQPIALNPEITERVGEALRMHPHLHCAQPGTGFIFLAESGLIVITRQLKQTADIMPVKHILPDLKNNVSLQIARPDLEKARADLAQVDP--PRHALC
VteA-VC 1 FLRDHIFNYIQD--FRSGAMVGEALRYEHTHTGMSSAVFLLEQLGHEKLETVESVSALASG---ADLQSVNLSQRNQQS--ICDPLAICERYG--PASKLT
VCA0785-vc 1 LRNDLLEVFQPKVS--MKTQRNVGAEALRMKHPVLGELSNETLHMAEQGLIFEVGHFVHQALKASDML-AYCPT-FCJAINVSSVQKNSGFEVQRDLALYC--FAHQLE
YhjH-Se 1 WLQERAYTQPIYQ---TCGRMAYELLTVTHPLN---PSQRLPDRYFLEITVSHRMEVVKQIDLAKADDFIEHGLLSVNDGPTLIALRQPKLRQLERL---WLR
Gcpe-Se 1 LENDQLHYQPKI---TWRGEVRSLEALVRMQSPERGLTPELFFSYAEELTVPGRWVLEVVRQLAKRDKINLR--VAVNSARQADQFTALQKALYDLN---EYCPD
Gcpe-Se 1 LERQELHYQPKI---APAGPTVGFLEALRMHPKQGVNDDQFPLAEKGLIVTGSWVLEACRQREHLQYDLWS--VAVNSALQEOPGLVDTTRSIARHS--TRDLDI
Dds-EC 1 ISNNQKLVYQPIF--AETGELYGIEALRMHPHLHCHP*PSRFFLAEEIGETENIGRWVLEACRQAEARSONTHIPA--SVMISALHFRSNQ--PNQSDAHAWG--DGHQIT
YfgF-EC 1 LEHNHFFMAQPIITG---MRGDVYHELELRKGENDELISDQSFLEPVAHEFQLSSSDMMVLEITLQFVAENRAKIPDAHR--AINISVTSVCCARFPVEVSQLEAKYQ--TEAWQLI
YegE-EC 1 IKENQMHLAHGVASPRIPERANLWISIKLWS--CEGEIIDEQTERRSFDPALSHADRRVHEFFQQAKAVAS---KGISISLPSVAVGLSSATLVNDLEQENSP--PPRLLH

pdeA1-Gx 115 VEITBSVMNDNSRDTEEVQSTIRNICCGISMDDEFTGYSISRLTRIPTEIKIDRSFNDFEYDTNAQAATMAVITGTSRIGTITVTEGVEEQORDILEKLNCDVYGGYEAAPLA
pdeA2-Gx 115 VEITBSVMNDSSSETEEVHARRLDVGSMDDFGTGYSISRLTRIPTEIKIDRSFNDFEYDTNAQAATMAVITGTSRIGTITVTEGVEEQMRILEELHCDVYGGYEAAPLA
pdeA3-Gx 115 VEITBSVMNDNSRDTEEVQSTIRNICCGISMDDFGTGYSISRLTRIPTEIKIDRSFNDFEYDTNAQAATMAVITGTSRIGTITVTEGVEEQMRILEELHCDVYGGYEAAPLA
YahA-EC 115 LETERNPVPTEARAI--DLSHQHNTIFA--DDFTGATYRYLQAFDFKIDKSFQMASVDEISGHVDNIVELARKGSIIVAEGETEQADLIGKGVFIQGYLYSPVPLA
BphG-RS 119 LEITETSIS--DEAVSEALISRALGVRAIDDEFTGYSIACLRRLPVDVKLDRAFGGHTAAQDHQIFAATVGHADIKVAEGTETLDLALRAAGADFAQGFHAAAPLS
VteA-VC 110 LEITHEVYNGTPTSLANARIMYGVGISDDEFTGYSIAGQLAQIPFTEIKIDRSFHDLATNYKHQQLTNMCLLAQSLGHCVVEGVENEETWQYRQLGCDVYGGYEAAPLA
VCA0785-vc 114 LEITSGLVDEPTASDINRHTLGVLSIDDEFTGYSIAGYKIPEDGKIDRSFLEQESSEDQELVRSMLHAKKLNVMVEGTES--TOEQELEQGCDVYGGYEAAPLA
YhjH-Se 108 FEVEHIRIP---KDSFASCEFGPLWDDFTGGMANFASLSEAYDYKIAELVMLRQSPERGLTFSQLHMMRYCRGVLEGVETPEWRDQNSPAFAAGQMFISRPAP
Gcpe-Se 113 VEITBSCTENDTLALSVQQSGLGQHLDDFTGYSISQLARIPIDAKLIDAFRDIHKQPLSLSVRAIVAQAALNQTAEGVENAKEDAFITKNGVNERQGFLLAKPMP
Gcpe-Se 115 LETETTTAVNKPEQSVAILTRITEMGVKASIDDEFTGYSISLYLKRIPACEIKIDRAFHELSEAGDGTVAATVAALAKALNQTVAEGVENEETQQFLTQLGCHTQGFLLGKPRP
Dds-EC 115 VEITBSMMEHDETEIFKRIQIRDMGVGISVDDFTGYSISLVSIPVTEIKIDKSFDRCLTEKRILALEAITSGQSLNITVAEGVEIKETFEMLRKIHCRVYGGYFISRLP*

YfgF-EC 112 FEVITBSNATNVKQAITQHTQELGCOTADDEFTGYSIYARLKNMADLITKIDGSEIRNTVSNLSDYQIVASITCHIRMKKTLVAEYVENEETREAVLSLGDVYGGYEAAPLA
YegE-EC 114 LIPAEALID---HAESVQLRLAGCRVLSQVGRDLQIENSKANMADYLIDGECANQQNLMDEHITIIQGHQRGKTAGVWVPLVMDT--SGIGVDLLEGEVADAAQ

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Girgis et al., Figure S10.