

```

aram_Bac_su      59 RIAGIDLENRLNQEFGQAECLIIIPENEAGDVTADERSLIHVLHHTKQPTDVMIAVGSSTI
egsA_Arc_fu     44 NLVVVNLKETLKD--FEYDMLLVESAKMEEARKIVLRG-----GFADYDAVVGVGGGKV
egsA_Pyr_ab     43 KIAGESVKKAIRDE-FDVYSITVKKAHIGEVEKVEAKI-----RDYNIKWAIAVGGGSI
egsA_Aer_pe     48 SKYFERLRASLEAEGLTVGLKIIRDATVETAAEVAREA-----LESRIEVVAGLVGGGKS
egsA_Met_th     45 QIAGEAAIESLQAEGFVVDQVTVDDATMASVRNVQDGL-----DGVSVVLGVGGGKV
egsA_Sul_so     47 KKIADKVIENLPKD-AKYEVVEIDSATLDDVVMVEEVI-----KRISPSLLLGIGGGKV
Loki_GC14_Frg   12 NPTTNNINAGVDMG-----ELNNVDVILGVGGGSS
Loki_Baja1     31 ELLKPHVINDPSKIILNRSM--DIAHLEQLYSSLKK-----TIEESYSIIGIGGGTS
Loki_Baja2     32 EILEPKITTTPKFVVYNNNM--ALSHLEELYKSLRK-----FIKKDFSLIGIGGGSP
Loki_Baja3     32 EIIPKPLSKFPIKTI FNKYM--DINHLRLTYNNSEA-----IIEDSIAIVGIGGGTA
Thor_Baja      39 ERYQHLLEDVGTGTC-----PAWIMAPNNSTDQ-----VPEKADIVVGFGGGRS
Thor_AB        39 SEYSQLLES AIGKP-----CRWLMASTYRADTNT-----VLGNVDIVLGFGGGSS
Thor_MP11T     39 TEYAKRLETAIGKS-----CRWLIAS TYRANTNT-----VLGKVDIVLGFGGGSS
Thor_MP8T      39 SQYSTTLE EIVERP-----CKWIMGSAYPKNSPF-----SIGDVDIVIGFGGGAS
Thor_MP9T      39 SQYSTTLE EIVERP-----CKWIMGSAYPKNSPF-----SIGDVDIVIGFGGGAS
Thor_SMTZ145   39 AEYADRLETVIGRQ-----CRWLMASTYRANTNT-----VLGKVDIVLGFGGGSS
Thor_SMTZ183   39 STYKEEVEKLMGQE-----QTWFMVSEYQSGVPP-----ALLEKDIILGFGGGRS
Thor_SMTZ45    39 AAYREIVEDFMGGE-----VTWLLVSEYEKGFPS-----KASGKDIILGFGGGRS
consensus      61 iy erlee l ke                wings y                l vdivlgfGgGts

```

```

aram_Bac_su      119 HDIVRFAA-----FORDLPIFISYPTAPSVDGFTSAGAPIILYGTKTTIQTAKPSALFAD
egsA_Arc_fu     96 LDVSKVVS-----SELNASMISVPTTASHDGIASPVASFKEKPKISISTNPPSAVIAD
egsA_Pyr_ab     96 IDVTKLAS-----YRSGIPFISFPTTASHDGIASANASIRGIEAKTSIKARPPIAVIAD
egsA_Aer_pe    102 IDVAKYAS-----KRAGSVFVSIPTVASHDGIITSPFSSLKGFDFKPISRPAKAPFAITID
egsA_Met_th     97 IDVAKMSA-----TLEGLHFISVPTAASHDGIASPRASIRNNGEKTASLEASSPIGVIAD
egsA_Sul_so    100 IDVTKYAA-----FRNSLEFVSIPTSPSHDGIITSPFASIKGLQKPVSVKAKEPLAITAD
Loki_GC14_Frg   42 IDVAKCISVGI--MGDI AKNTFHL PDYANH-GIVPTAKDV-----
Loki_Baja1     81 CDTAKYLSWRFKKDMGMDLIDLMLPSIISVDAFLCSSI AVRSDNKVNYIGESTPKKIITID
Loki_Baja2     82 CDTAKYLAWKMANESKKKVDLFLMPSIISVDAFLCSSI AVRNVGNKVNYIGESAPPEILVD
Loki_Baja3     82 CDTAKYLTWKSQKQHTDIDLILIPSIISVDAFLCSSI AVRDNMKVNYIGDSYPEKILID
Thor_Baja      82 LDTAKLEA-----RDYDIDWISVPTAASHDGIASDVASVSHNGYRYSEKCKSPIAVAD
Thor_AB        84 LDVAKLIS-----RDTGIDWISIPTAASHDGIASEVASVSHNGYKYSEKCKGPLAVLAD
Thor_MP11T     84 LDVAKLIS-----RDTGISWISVPTAASHDGIASEVASVSHNGYKYSEKCKGPLAVIAD
Thor_MP8T      84 LDVAKLIA-----RDTDLDWISVPTAASHDGIASEVATVSHDGYRYSEKCKSPIAVIAD
Thor_MP9T      84 LDVAKLIA-----RDTDLDWISVPTAASHDGIASEVATVSHDGYRYSEKCKSPIAVIAD
Thor_SMTZ145   84 LDVAKLIS-----RDTGISWISVPTAASHDGIASEVASVSHNGYKYSEKCKAPLAVIAD
Thor_SMTZ183   84 IDTAKLLA-----RDTGLNWSVPTAASHDGIASDVASVSHNGYRYSVRCKSPIGVIAD
Thor_SMTZ45    84 IDTAKLLA-----RDTSLDWISVPTAASHDGIASDVASVSHNGYRYSEKCKSPIGVIAD
consensus      121 lDvaklia                rdtgldwisvPtaashdgiasdvasvshngykysekckspiaviad

```

```

aram_Bac_su      173 LDLLKAAPOSMAAGFGDMLGKITSLADWEISRHLAGEPYPSPAGAKIVQEFALAACIEHTE
egsA_Arc_fu     150 LNIIKNCPIRLLRSYGCDLVSNISSVKDWQLARDLVGEDYNEVAASIAVMPAQLMVSKAD
egsA_Pyr_ab     150 IEVIKTAPRRYLAAGVGDVINSITAVRDWKLAKLKG EYFSEYAAALSLMSAKM VIRDAE
egsA_Aer_pe     156 VDVI AEA PRRYNIAGFGDLIGKYTAVLDWRLAHKLRLEYGEYAASLALLSAKHVSQYAE
egsA_Met_th     151 TEIISRAPFRLLASGCADIISNYTAIMDWKLAHRLLNERYSESAAALSLMTAKMI IKSAD
egsA_Sul_so     154 IEILSLSPRRLINAGIGDTIGKIIAVRDWKLAKLRGEY YG DYTASLALMSAKHAFQCTK
Loki_GC14_Frg   79 MDLLKNFRRRY-----
Loki_Baja1     141 YNLIQKAPKYLNRAGVSDTISITSALGDWKL AHS ENNEPFDQKIFAQAITIAKDLMNARN
Loki_Baja2     142 YELIKKAPKFLNRAGVSDTISITSALGDWKL IAVKENNDNF DQSVFN RAREIAKDLMDART
Loki_Baja3     142 YELIKSAPKFLNRAGVSDTISITSALGDWLI SRKQTNERFDKTVFNEAKKIAIDLMDARN
Thor_Baja      136 IDIIEQAPDILRKAGTGDII CKISSLA EWRLAHEHNGENLQEPVFEMVESALNEVLK---
Thor_AB        138 TSIISRAPPRLRLAGLGDII CKTSSLA EWKLAHEVKNESFDDEVYSIVRKALDSVLA---
Thor_MP11T     138 TSIISKAPPRLKLAGLGDII CKTSSLA EWKLAHEVKDEPFDNEVYTI VKKALDSVLV---
Thor_MP8T      138 TSIISKAPPKLLKLAGLGDII CKTSSLA EWKLAHEVKDEAFHQEAYDLVYNSLTTILK---
Thor_MP9T      138 TSIISKAPPKLLKLAGLGDII CKTSSLA EWKLAHEVKDEAFHQEAYDLVYNSLTTILK---
Thor_SMTZ145   138 TSIISKAPPRLKLAGLGDII CKTSSLA EWKLAHEVAND EPNDEVYTI VKKALDSVLV---
Thor_SMTZ183   138 LSVIEKAPPSLTLAGIGDIVCKSSSLGEWRLAHEERNEPFEKRVYALVESALESVLQ---
Thor_SMTZ45    138 LSVIEKAPPKLLRLAGIGDIVCKASSLGEWRLA HARND EPNDRVYSLVKSALSVLQ---
consensus      181 lsiiskapprrlragvgdiicktssladwklahelk e fde vyslv al svl

```

```

aram_Bac_su      233 DIAMKTE TGIRVLMESLIVSGLVMLALDHSR PASGGEHHISHWIE MELMEKRRPQILHGA
egsA_Arc_fu     210 ELDLTLPPHLLMLLRGLTMSGVAIAFVGSSRPASGA EHKFSHALDYLGYGN---GTHGE
egsA_Pyr_ab     210 IIRLGNDEGVRKVIKALISSGVAMSIAGSSRPASGA EHLFSHALDLLDKP---ALHGE
egsA_Aer_pe     216 EIALGTREGYRVLLEALVSSGVSMCIAGSTR PASGSEHLFAHALHIVARNK---PLHGE
egsA_Met_th     211 AIKEGLEESARLAVKSLTSSGIAIISIAGSSRPASG SEHKFSHALDMTAPKP---ALHGE
egsA_Sul_so     214 IINKDIKYGVRMLMEALISSGVAMGMAGSTR PASGSEHLFAHA VELIHPEG---ILHGE
Loki_GC14_Frg   90 -----
Loki_Baja1     201 EIKDVTRRGIKALVDGFVREVALCSQWGNARPEEG SEHFLAYCIESITTHSH---YIHGQ
Loki_Baja2     202 EIKKVS DKGIKSLVQGFYNEVKLC EEWGNARPEEG SEHFLAYCLESITKKH---YIHGN
Loki_Baja3     202 KIRDVSEE GIKALTEGFFREVDLCEK WGNARPEEG SEHFLAYCIESITHDH---YIHGQ
Thor_Baja      193 -----NDSLETLLILAEINSGKAMNIAQSSRPCSGTEHAISHAMDRRCQN-----LHGI
Thor_AB        195 -----D DSLENLISAEIDAGRAMSIFGSSRPCSGTEHAISHAMDRSCSE-----LHGL
Thor_MP11T     195 -----D DGLETLIRAEIDAGRAMSIFGSSRPCSGTEHAISHALDIVCAD-----LHGL
Thor_MP8T      195 -----D DSFEALVRAEIDAGRAMSLAGSSRPCSGTEHAISHAMDRIQSD-----LHGL
Thor_MP9T      195 -----D DSFEALVRAEIDAGRAMSLAGSSRPCSGTEHAISHAMDRIQSD-----LHGL
Thor_SMTZ145   195 -----D DSLETLLISAEIDAGRAMSIFGSSRPCSGTEHAISHALDRVCAE-----LHGL
Thor_SMTZ183   195 -----D EGGLEALVRAEIDAGRAMSIFGSSRPCSGTEHAISHAMDRQCNE-----LHGL
Thor_SMTZ45    195 -----D ERLDLTVRAEIDSGRAMTIFGSSRPCSGTEHAISHAMDRGTTE-----LHGL
consensus      241 i degle lvraeidsgramsia gssrpcsgtehaishaldri e lHgl

```

```

aram_Bac_su      352 DEI GVGQDSVKN AFRHAHTL--RD- RCTGLR--IINENKTLINHGLYE-----
egsA_Arc_fu     304 KEIGLTREQVTEALMLATKL--RKK-RFTILE--AVKPTKEEFELVVEKTGVA--
egsA_Pyr_ab     299 YELGIDPEIIEAL TIAHKI--RPE-RYTILG--KEGLTREA AEKAAKITGVI--
egsA_Aer_pe     305 KELGVEDDEVVEAL TIAARI--RPE-RYTILG--EKGLTREA AEALARKKTGVI--
egsA_Met_th     300 AELGIDPEYIIEAL TMAHNI--RRE-RYTILG--DRGLTREA AERLAKITEVI--
egsA_Sul_so     303 KDLGLSDEEVIKAL TIAHTI--RPE-RYTILG--DRGLTWSSA EK IARVTKIID-
Loki_GC14_Frg   -----
Loki_Baja1     294 NSLSISSDILRSALKKIQTYVKKENLMYSIYN SPRLEINTPKIEETIRFITKI--
Loki_Baja2     295 EEQNISYASLQKAL LKVQDYVSEDLFYSIYN SPQLILSEEKVEEIIINFVKSL--
Loki_Baja3     295 QSNKIPL EVLREALNSVEKYVKNENLMYSIYN SPNLKLD DKKIDEIIQFIKTI--
Thor_Baja      280 AEMNMSRKLFLDDI HHALKIMKKRN-RYSVFE--HLD AKDDDILRACKNI NY--
Thor_AB        282 SEMKISTEQFIESIHQGLNIMKKRN-RYSVLT--HLDVDDSSLRSIMVELGY--
Thor_MP11T     282 SEMNITEGQFIDSIHGLSIMKKRN-RYSVLK--HLDVDDASLKSIMRDMGY--
Thor_MP8T      282 EGMNSSMSAFLEDIDHALKIMKKRD-RYSVLE--HLNVDTANLTKTLRDLGY--
Thor_MP9T      282 EGMNSSMSAFLEDIDHALKIMKKRD-RYSVLE--HLNVDTANLTKTLRDLGY--
Thor_SMTZ145   282 SEMNINEEQFIESIH HGLGIMERRK-RYSVLK--HLDVDDTSLRSVMRDLDY--
Thor_SMTZ183   282 GDLSLSESQLLDHIQHGLDIMORRD-RYSVLE--HLAVENTDILETLVTL EYNE
Thor_SMTZ45    282 DDIGISADQFLDYVNHALDIMNRRN-RYSVLQ--HQGADDTQILKTLKVLKYL--
consensus      361 eigis e fieal halkim rrd rysil hl lde iehvlr lgyi

```

- DHAP binding site
- NAD(P)H binding site
- Metal (Zn) binding site