

RR Sec. signal

vcrA_Dmc_Q69GM4 1 ---MSKFHKTISRDFMKGLGLAGAGIGA-----VAASAPV-FHDIDE
tceA_Dmc_Q9KIP5 1 -M-----SEKYHSTVTRRDFMKRLGLAGAGAGALGAAVLAENNLPHFHKDVEDD
bvcA_Dmc_Q5YD55 1 -----MHNHCTISRDFMKGLGLAGAGIGA-----ATSVMPN-FHDLDE
cprA_Ddh_Q9XD04 1 -----MENNEQRQQTGMNRRSFLKVG-----AATTMGVIGAIKA--PAKVAN
prdA_Dsp_Q3LHG0 1 -MDREKENT-LDQKEEKRSVGISRRNFFKASGIAAGVAALG----LVTKSQPV-YAQQES
rdhA_Dha_B8FVX4 1 -M-----KMNLDRRSFLKASLVSAVAASAAAASAAKETFAPL-TAEAAE
pceA_Dha_Q8GJ31 1 -M-----GEINRRNFKLVSVILGAAAAVASASAVKGMVSP-L-VADAAD
cprA_Dch_Q8RQC9 1 -MTRSGKMEKLLKNEESKALSINRRNFKLIG-----AATTAMGLIGAVKSS-SQVAAA
cprA_Dha_P81594 1 -----MENNQRQSGMSRRSFLKVG-----AATTMGVIGAIKA--PAKVAN
pceA_Smu_W6EQP0 1 -M-----EKKKPELSRRDFGKLIIGGAAVTIAPFG-VPGANAAEKEKNAAE
Rdh_Fer_p1 1 -----WENHPL
Thor_SMTZ145 1 -MYVKTDLG-DSSKCTIECLGACQQ-----IHGDDSP-LSIQE-N
Thor_MP11T 1 -MYVKSNLG-DSSKCFECLYACQR-----IHGEDPPL-SIQQDN
Thor_AB 61 LMFVRTDTG-DPSSCNHECLDACRR-----VHGDESP-LSFQEGP
Thor_SMTZ183 1 -MQVLEDLG-KPDKCDRECVEACIQ-----QHGRNAPL-RFADGD
Thor_MP8T 1 -MYISKTLC-NPQVCKYECRTACSQ-----IHGDDSP-LGFGKES
Thor_MP9T 1 -MYISKTLC-NPQVCKYECRTACSQ-----IHGDDSP-LGFGKES
Thor_Baja 1 -VIIDKDLG-DPRKCNQACVVACQR-----IHGENAPL-IYTQGA
Loki_Baja2 1 -MNKNQN-
Loki_GC14_1 1 -M-
Loki_GC14_2 1 -M-
Loki_Baja3 1 -MKKASDI-
consensus 61 m i rr f k g lkg pl a

cluster (Thor 3)

vcrA_Dmc_Q69GM4 300 LNKRTGGI--AGAGSYTVYKDFARVGTLVQMFIKYLYGHALY--WPIGWG-PGGCFTTF
tceA_Dmc_Q9KIP5 335 RFKYAHSI--PMDPCSCIAYPLFTEVEARIQOFIAGLGYNSMG--GVEAWGPGSAFGNL
bvcA_Dmc_Q5YD55 306 RFKRSLGW--SLDASSMIAYPQMAFNNGRRVQTFLLKALGYOGLG--GDVAMWGPAGFVGM
cprA_Ddh_Q9XD04 225 TMWASTGYDGISGAMSMQSYFTSGCIAVIMAKYIRTLGYNARXHHAKNYEA-IMPVCIMA
prdA_Dsp_Q3LHG0 244 MLKYAPTT--LSEATVGTTEYSQMAESAGKMAEFIRGLGYNALP--MGNDAS-LSVPIAID
rdhA_Dha_B8FVX4 320 AYRTAPSV--LQGAAPGKSYSNMGEVAYKVASFLREIYGNVAVP--SGNDTG-MSVPIAVQ
pceA_Dha_Q8GJ31 320 AIRTSPSV--ISSATVGSYSNMAEYAVIAVFLRKLGYAAP--CGNDTG-ISVPMVAVQ
cprA_Dch_Q8RQC9 236 TTLASTGYDGISGAMSFQSYHATGNIAVILAQYIRTLGYNARAHHAKNYEA-IMPVAVIA
cprA_Dha_P81594 225 TMWASTGYDGISGAMSMQSYFTSGCIAVILAKYIRTLGYNARAHHAKNYEA-IMPVCIMA
pceA_Smu_W6EQP0 266 MMQTAPNS--MACATTAFQYSRMCMFDMWLQCFIRYMGYYAIP--SCNGVG-QSVAFAVE
Rdh_Fer_p1 87 M-----QGDIAGFYSKMAIIVAGSLAEFLRALGFTA-----PYAIS
Thor_SMTZ145 236 AIATSPSF--TSSAATALGYSTMAFVELELAAFIQRLLGYNAMS--CGNNDV-LSVPIAID
Thor_MP11T 237 AIATSPTF--TSSAATALGYSTMAFVELELAAFIQRLLGYNAIT--CGNDVS-LSVPIAID
Thor_AB 299 AIATSPAF--ASSAAVGFGYSMAFVEIELELAAFIQRLLGYRAMT--SGNDVS-LSVPIAID
Thor_SMTZ183 239 GISTSPAF--PSALSTAVGYSKMAFVEIELELAAFIRRLGFRVAVP--CGNDIA-LSVPLAID
Thor_MP8T 238 AIATSPTF--TSSAATGLGYSKMAFIEAELASFIRRMGYNAMT--CGNEVG-LSVPLAID
Thor_MP9T 238 AIATSPTF--TSSAATGLGYSKMAFIEAELASFIRRMGYNAMT--CGNEVG-LSVPLAID
Thor_Baja 233 GLAASPAP--AAQAASSIGYSKMAFVEIQLSSLIIRRMGYHALA--CGNDVA-LSVPLAID
Loki_Baja2 191 AISTAPAQ--QAAAAASLAYSMAFVTSCLGFEFIRNMGYKALQ--CGNDTG-LSIPLAID
Loki_GC14_1 181 AISTAPAQ--PAAAAASLAYSMAFVTSCLGFEFIRNMGYRALQ--CGNDTA-LSIPLAID
Loki_GC14_2 181 SISTAPAQ--PAAAAASLAYSMAFVTSCLGFEFIRNMGYRALQ--CGNDTA-LSIPLAID
Loki_Baja3 176 GINCAPTF--LEFASAGLGYSKMSTIACMAQFIRNMGYRALP--CANDTA-LSIPLAID
consensus 541 ai tspgw sgaasgigYskmaf v la fir lGynal cgndmg lsvpiaid

vcrA_Dmc_Q69GM4 410 CVSGGVHOEDEPTWDS--GNWNVQGYLGYRTDWSGCH-----NOCGMCQSSCPF
tceA_Dmc_Q9KIP5 447 CPTQAI SHE-GPRYDS--PHWDCVSGYEGWHLDYHKC-----INCTICEAVCPF
bvcA_Dmc_Q5YD55 418 CPSNAIQVG-PPQWNS--NRWDNTPGYLGYRLNWGR-----VLCTNCETYCPF
cprA_Ddh_Q9XD04 340 CPNDAITFDEDEPIE-----YNGYLRWNSDFKKTERTTNEEGSSCGTCLKVCWPW
prdA_Dsp_Q3LHG0 354 CPSESIKSKDPPSDKV--ACASNNPMMKKWYVNTWTCLNQVWENG--GGCNI CLSACPY
rdhA_Dha_B8FVX4 430 CPAQAISHVKDPVWLQPEDCTPSENPYTEKWQFDSQRCLSFAYNG--GDCGSCI AVCSW
pceA_Dha_Q8GJ31 430 CPAQAISHKEDKVLQPEDCEVAENPYTEKWHLDSNRCSFAYNG--SPCSNCAVCSW
cprA_Dch_Q8RQC9 351 CPGEAITDRDHVE-----YNGYLRWNSDMKKCAVFRRTTNEEGSSCGRCMKVCPW
cprA_Dha_P81594 340 CPNEAISFDEDEPIE-----YNGYLRWNSDFRKTERTTNEEGSSCGTCMKVCPW
pceA_Smu_W6EQP0 376 CPSKAITEG-PRTEEG--RSIHNSGKLOWQNDYKCLGYWPESG--GYCGVAVVAVCPF
Rdh_Fer_p1 176 CPAKAIP--PSWK-----YKWHVDVEKC-EYWCKSG--NLGCVVVRVCPY
Thor_SMTZ145 349 CPSQSI PYGKEQTWSG--NSPSNNPGIKKWIYINVERCYGFWDNG--SECSNCIRSCPY
Thor_MP11T 350 CPSQSI PYGKEQSWSG--NSISNNPMMKKWYVNVDSYGFWDNG--SECSNCIRSCPY
Thor_AB 412 CPSQSI PYGKEQTWEG--TTISNNPGIKKWIYVEVESYGFWDNG--SDCSNCIRSCPY
Thor_SMTZ183 352 CPSQSI PSGLTRTWAG--ATRSNNPGIKKWIYVNPETCYGFWDNG--SDCSNCIRSCPY
Thor_MP8T 351 CPSKSI PFGKERTLKG--KTI SNNSGIKKWIYVNVETCYGFWDNG--SECSNCIRSCPY
Thor_MP9T 351 CPSKSI PFGKERTLKG--KTI SNNSGIKKWIYVNVETCYGFWDNG--SECSNCIRSCPY
Thor_Baja 346 CPSQSI PYDKEQSWKG--TSKSNNPGVKKWIYVDVESYGFWDNG--GECSCNCIRSCPY
Loki_Baja2 304 CEVNAIPEEKNPTWNR--QSI SNNSEALKYIYVNVKCFEWFVENS--SDCGKCI AACPF
Loki_GC14_1 294 CETKAITEEREPSFKG--KNI SNNSGIKKWIYINAEKCFEWFVENS--SDCGKCI AACPF
Loki_GC14_2 294 CETNAISKEVQPSFKG--NNI SNNSGIKKWIYTDAAEKCFEWFVENS--SDCGSCI ATCPF
Loki_Baja3 289 CDFGAI SNNDSPTYQP--YSKSNNSGTKKWIYVDVEKCYDGVVHYS--SDCAKCIKACPF
consensus 661 Cpsqaip ekeptw g tvsnnpgmkkwyvdvekCy fvweng sdcgnCiksCpy

cluster 2

vcrA_Dmc_Q69GM4 40 LVSSEANS-----TKDQPWYVKH
tceA_Dmc_Q9KIP5 48 LLSAGKAL-----EGDHANKVNNHPWVVT
bvcA_Dmc_Q5YD55 40 VISAASAET-----SSLSGKSLNNFPWYVKE
cprA_Ddh_Q9XD04 42 AAETMNYV-----PGPTNARSKLRPVH--
prdA_Dsp_Q3LHG0 54 ESAIVNF-----AVQEVDSQPYNLP-
rdhA_Dha_B8FVX4 43 IIAPIRE-----TAEFPYQV--
pceA_Dha_Q8GJ31 42 IVAPITE-----TSEFPYKV--
cprA_Dch_Q8RQC9 52 ATDTLNYV-----PGRKSQNSKLRPHEH--
cprA_Dha_P81594 42 AAETLNYV-----PGSGKIRSKLRPVH--
pceA_Smu_W6EQP0 47 IRQQFAM-----TAGSPIIV--
Rdh_Fer_p1 7
Thor_SMTZ145 37 RYPIINLEKCTRCLACVRDCPLGAIVIN-----QMPHKA-QLSEIGVNKTTYCYPYDV--
Thor_MP11T 38 SQPKINHETCTKCLSCIRECPLEAIIIE-----ERQVEDS-KPSRMRTFRMTGYFPYQV--
Thor_AB 99 DHPVINLETCTVCLACVRVCLDAIKAE-----RATTEGPIDAVEASAFHVSDYVPYEV--
Thor_SMTZ183 38 RFPTIENG-CTICLACVRECPYGAITSSFADGHLKRRNV-GARGHRRPRIM-LRPYEA--
Thor_MP8T 38 LYPVIDEGTCTECLACVRACPLNAISIS-----EHPDTFFPEPIPPPVPAPISSERPYEV--
Thor_MP9T 38 LYPVIDEGTCTECLACVRACPLNAISIS-----EHPDTFFPEPIPPPVPAPISSERPYEV--
Thor_Baja 38 HALTYNLGRCTECLSLRACTKGAITAS-----KISTKKT-SASSEHDSLS-IHPYEV--
Loki_Baja2 7
Loki_GC14_1 2
Loki_GC14_2 2
Loki_Baja3 8
consensus 121 m t py v

cluster (Thor 4)

vcrA_Dmc_Q69GM4 354 DGQGEQGRTG-AAIHWKFGSSQRGSERVITDLPPIAETPP--IDAGMFEFCKTCYICRDV
tceA_Dmc_Q9KIP5 391 SGLGEQSRVS-SIIEPRYGSNTKGSRLMLTDLPLAETKP--IDAGIREFCKTCGICAEH
bvcA_Dmc_Q5YD55 362 SGLSEQCRAA-NEISPKYGSATKGSNRLVCDLPMVETKP--IDAGIHKFCETCGICTTV
cprA_Ddh_Q9XD04 284 AGLGELSRGTDCAIHPRRLGYRHKVA-AVTDLPLAPDKP--IDFGLLDFCRVCKKCADN
prdA_Dsp_Q3LHG0 299 AGLGELGRHG-LLVHPEYGSVSRIS-KVLTDLPLAPDKP--ISFGAAEF CRTCMKCAEA
rdhA_Dha_B8FVX4 375 AGLGEAGRSQ-QLITQKYGPRVRIA-KVYTDLELVPDKP--INIGAREFCRLCLKCADV
pceA_Dha_Q8GJ31 375 AGLGEAGRNG-LLITQKFGPRHRIA-KVYTDLELAPDKP--RKFQVREFCRLCKKCADA
cprA_Dch_Q8RQC9 295 AGLGELSRGTGSTIHPRMGFRHVA-AVTDLPLAPDKP--IDFGLQDFCRICGKCAEN
cprA_Dha_P81594 284 AGLGELSRGTGDSATHPRLGFRHVA-AVTDLPLAPDQP--LDFGLLDFCRVCKKCADN
pceA_Smu_W6EQP0 321 AGLGQASRMG-ACITPEFGPNVRLT-KVFTNMPVLPDKP--IDFGVTEFCETCKKCAEA
Rdh_Fer_p1 122 AGLGEYSRMG-LLITKKGPRVRL--KVFTDTPKADKP--VRFQVYEFCLCKKCAEK
Thor_SMTZ145 291 AGLGQYGRHG-LLITKQYGRVRIA-KVLTDMPLLRDYPDENFCKAVVRFCECTCKKCAT
Thor_MP11T 292 AGLGQYGRHG-LLITKQYGRVRIA-KVLTNMPLLRDYPDENFCKAVVRFCECTCKKCAT
Thor_AB 354 AGLGQYGRHG-LLITKEFGPRVRIA-KVLTDMPLQRDYPDEGFCCKSVIRFCETCEKCAAT
Thor_SMTZ183 294 AGLGQYGRHG-LLITKEYGPRVRIA-KVLTDMPLLPDCEPTGFCFAVLRFCETCEKCAHH
Thor_MP8T 293 AGLGQYGRHG-LLISKPYGPRVRIA-KVLTDMPLIPDSDLDFCRAVVRFCETCERCAQM
Thor_MP9T 293 AGLGQYGRHG-LLISKPYGPRVRIA-KVLTDMPLIPDSDLDFCRAVVRFCETCERCAQM
Thor_Baja 288 AGLGQYGRHG-LLITKEYGPRVRIA-KVLTDMPLIPDSDLDFCRAVVRFCETCERCAQM
Loki_Baja2 246 AGLGQYGRHG-LLITPEFGPRVRIA-KVFTNMPKSDNPNIKFIEKLLKCYCKNCTKCAEA
Loki_GC14_1 236 AGLGALGRIG-LLITPEFGPRVRIA-KVFTDPLPISDEVNKDFIHKVENFCCKRCKCANA
Loki_GC14_2 236 GGLGALGRIG-LLITPEFGPRVRIA-KVFTDPLPISDKPNEKFIHKVENFCCKRCKCANA
Loki_Baja3 231 AGLGALGRIG-LLITKDFGPRVRIA-KVLTDMPLIPDSDLDFCRAVVRFCETCERCAQM
consensus 601 aGlge gR g llitp yGprvria kvltldplvpdkp f gvlefCktC kCad

cluster 1

- Aminoacids binding to chlorinated compounds
Corronoid binding sites
conserved Fe-S cluster binding sites