

PhCAC16.5 1 -----
Aacys-prot 1 -MGNGRITVLLSIVLISVAPSGSCSAGEWPSGGQPEDVAGGVGGQELFERMMEKHKRVVAHPGEKARRANLNLAFVRRKNAEGRRAPSSGGQV
McTHIOLPROT 1 --MATNSMTLILFLTYVSYSLSTKLPSEFSLLEGQENDILSSAKVSDLEGKWKELHCKTYCHEEENLRLLENFKKSKFVMEKNSERKS--ELDHTV
GhCYSPTROT 1 ---MGFQRNLGFFLLASLSSLSSLPSEFIVEHEIDAFLSERVLELQQWKEKHKRVVRAHEBAKREHENFKGNLKYILENAKRKAN-KWEHVV
DcCYSPTROT 1 ----MKMILSLSLSLAAAVTAADMSIITYDQTHAVG---STDVIMAAVESWLVKHKKSYNALGKKEQRFQIFKDNFLYIDQNAAKDR----SFKL
ZmCYSPTROT 1 MAASTTAAAAASLILLVSLAAADMSIVSYGE-----RSDEBARRMYAEMMAAGRTYNAVGEERRMQVEFDNLRVIDAANAADAG-VHSFRL
ZoCYSPTROT 1 MASFVAVVLLFLSSSALTAVSVVPLDILTLLKQAWAAPAGRSDEEVRILIQEVRVKKRPAENDDQYVGYRLEVFENLRFVDEANAADRG-EHAYRL

PhCAC16.5 1 -----NAIVTGLISLSAQELV
Aacys-prot 100 GNNVFADLSNEEFREYVSSRVLKKAAGEGRARRRAGEGVVAGCQAPASLDWRKAGAVTAVKQDCGSCWAFSITGAMEGINAITTGLISLSAQELV
McTHIOLPROT 97 GLNKFADLSNEEFKEMYSKVKGRSRNELKMGVVKRMSVSSRTCDAPSLDWRDGGVITPKDQCGCSCWAFSITGAMEGINAATATGDLTILSEQELV
GhCYSPTROT 97 GLNKFADLSNEEFKAYLSKVKPINKGITLS--RMRKQVQSCDAPSLDWRNYGVVAVKDCGSCWAFSITGAMEGINAVTGDILISLSAQELV
DcCYSPTROT 89 GLNKFADLSNEEFKSKYTGIRTID---SRKKVSGKSRYASLAGESIPESVDWREHGAVASVKDQCGCSCWAFSITGAMEGINAATGKLIILSEQELV
ZmCYSPTROT 92 GLNKFADLSNEEFKRYVIGARTIP---QRERKLG--ARYAADNEILPESVDWRAHGAVAEVKDCGSCWAFSITGAMEGINQIVTGDILISLSAQELV
ZoCYSPTROT 100 GNNVFADLSNEEFKARLRDLSL---GRSTSGEISIQYLREGDVLPSLDWRKAGAVAVKQDCGSCWAFSITGAMEGINQIVTGDILISLSAQELV

PhCAC16.5 18 NCDSTLYGCGGGMPSAFEWIINNGGIDSADYPYTAIQG---TNTITKEKTKVVIDEYQDVAQ--ESALLCAAQPVSVGIDGSSIDFQLYGGIY
Aacys-prot 200 DCDTINEGCGGGMPSAFEWIINNGGIDSEANYPYTAQADS--VNTITKEEKVVSIDYEDVAT--ESALLCAAQPVSVGIDGSSIDFQLYGGIY
McTHIOLPROT 197 DCDTLYGCGGGMPSAFEWIINNGGIDSEDDYPYTAQADS---TNTITKEEKVVSIDYEDVAT--ESALLCAAQPVSVGIDGSSIDFQLYGGIY
GhCYSPTROT 194 ECDTINNYGCGGGMPSAFEWIINNGGIDSESDYPYTAQ---VDGTNTITKEEKVVSIDYEDVAT--ESALLCAAQPVSVGIDGSSIDFQLYGGIY
DcCYSPTROT 186 DCDTINNYGCGGGMPSAFEWIINNGGIDSEADYPYTAQDQ---CDYVKNKAKVVIDSYEDVPEYDERALQKAAANQPTVAIEASCRDFQFDSGIF
ZmCYSPTROT 187 DCDTINNYGCGGGMPSAFEWIINNGGIDSEKDYPTKCTDGR---CDVKNKAKVVIDSYEDVPEYDERALQKAAANQPTVAIEASCRDFQFDSGIF
ZoCYSPTROT 197 DCDTINNYGCGGGMPSAFEWIINNGGIDSEADYPYTAQDQ---TNTITKEEKVVSIDYEDVAT--ESALLCAAQPVSVGIDGSSIDFQLYGGIY

PhCAC16.5 113 DDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
Aacys-prot 296 DDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
McTHIOLPROT 295 NDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
GhCYSPTROT 289 DDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
DcCYSPTROT 283 TDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
ZmCYSPTROT 284 TDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE
ZoCYSPTROT 293 TDCSSENFNDVHDHAVLVVGYGSGDDHYWILKNSWGTSGWMEGYAYIKRNTDISYGVCLINSMASYPTKESSSPP-----YSPALFPFPFSPSE

PhCAC16.5 208 CGDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK
Aacys-prot 396 CGDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK
McTHIOLPROT 395 CGDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK
GhCYSPTROT 369 -SVLHRTFFNFTHHISITK-----
DcCYSPTROT 370 CDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK
ZmCYSPTROT 371 CDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK
ZoCYSPTROT 384 CDYYSFGSIGQTCCELELIGVCFIQGCCPYENVCCKDKSEYCCPSGYSVCSNQCMLKEYGDYLGVAARKRRKAKYKLSNSTSTKLTMEMDQHLQWK

PhCAC16.5 307 RNEFLEMLKVQLIKKTLRLSNGSRY
Aacys-prot 495 RDGVAALR-----
McTHIOLPROT 494 RNPFAAAA-----
GhCYSPTROT -----
DcCYSPTROT -----
ZmCYSPTROT -----
ZoCYSPTROT -----