

HOMSA_6382064
RATNO_9910502
GALGA_71895941
TRICAS_91085409
DROME_25012594
APIME_61656214
cluster-39
phos-1A
phos-1
phos
phos-2
phos-6
phos-7
XC-69
cluster-175
cluster-155

LAKELKFVTLVFRHGD RSP --- IDTFPTDPIKE -SSWPQGGFGLTLQGMQEHYELGEGYIRKRYRKLNFSEYKHE -QVYIRSTDVR T LMSAMTNLAALFPPEGVSIGNW --- PILLWQPIPVHTVPSLE -DQLLYLPFRN -CPRFQ
QAKELKFVTLVFRHGD RSP --- IETFPNDPIKE -SSWPQGGFGLTLQGMQEHYELGEGYIRKRYRKLNFSEYKHE -QVYIRSTDVR T LMSAMTNLAALFPPEGISIGNW --- PRLLWQPIPVHTVPSLE -DRLLYLPFRN -CPRFQ
RPRSLRFATLVYRHGD RSP --- IKAYPRDPDFQE -SAWPQGGFGLMQVGMQRQWELGQALRRRYHGFLSASYRRQ -EIFIRSTDYD R T LMSAEANLAGLYPPEEQMQFN --- PNISWQPIPVHTVPSG -EMLLKFPALT -CPRYE
LGDLLISVVVYRHGD RTP --- IQPYPRDPYRNASFVPVGGGLTLNLGKQHFRLGQWLRLQRYGGFLSPHYSEK -DFSIRSTDVR T LMSAEANLAGLYPPKADQVW --- PALPWQPIPIHTSPELE -DNLLSMKKN -CPKYI
LPGQLKFVHHVYRHGD RTP --- VDPYPTDPWGD RKFMTWGD LTLNLGKQEHYDLGKWLNRNYSNLLPPIYSNE -NIYVQSTDVDR T LMSAQSNLAGYEPQGEDIGNW --- TDINWQPIPIHTSPELE -DPILAAKAP -CPAYD
VQAELKQINIVFRHGD R IPDEKNEMYPKDPYLYDYFPLRGERL TNSGKMREYQLGQFLRERYGDFLGDIIYTES -VSALSSFYD R TKMSLQLVLAALYPPNKLQQWN --- EDLNWQPIATKYLRRYEDNIFLPEDCLLFTFIELD
AEELKLFVFTVARGADYEA --- CDYKGGPMITKRDEKES -KL TENGKRNA FELGQKIGET YTKLGVSKWDP --- KTNFWPIAAPS KRAQSTSLITAAAGMEGDQSKRDKS W TDEELKKTTFPAVFAFFNYMNPRED CPKYF
AEELKLFVFTVARGADYEA --- CDYKGGPKITNKDEKES -KL TENGKRDA FELGQKIGET YTKLGVSKWDP --- KTNFWPIAAPS KRSQTS LITAAAGMEGDQSKRDKS W TDEELKKTTFPAVLAFSNYMNRE CPKFEY
AAEQLKFVFTVARGADYEV --- CDIPGGPKITNKDGKDS -KL TEEGKNTV YQLGVKVS ELYKSKLGVSKWDS --- SKNYWPIATNSRRSQISTSLITAGLEGDQSKRDKS W TDEELKKTSPFAMLQFWKFIDPAK CPKFF
ADD -LKFVFMARGGDFVA --- GDYAGGPKIINKEAKDS -EL TEQGKQEA FLGTLKSEL YTKLGVSKWDS --- KTTYWPVALS QKRTQVSTLITAGLEGDQSKRKNKAW TNEELKATSFPAMESFSRFIKPNE CPKYI
-----FPAMESFSRFIKPNE CPNYL
AKDNLQFVFTAKGQDHQA --- CNYPGGPKITNIEEPDS -EL TEDGKKEA YEFGQKLSEYSKRLGVTKWDS --- AQNYWAIAAIEKRTKKATLITAGVIAKRQSVTSKT W SDEELQKTSFPALNDFFRFINPQHC CPKYI
DDLELKFVFAVARGSAHP --- CDYPGGPVIFHMPPEQS -RLSWRGREDA YGGQEISDMYRQRLGVNHWSK --- KNYLSLGSYS LRTMQAALVLGAGLENKHYKINWQ W SEAKKSSTQFPAMQYLYKIYSSQK CPKFEY
-----SEAKKSSTQFPAMQYLYKIYSSQK CPNFF
DESSLQFLFIVARAGEIFPD -NYMMKADTNYEYKNYGFPAGELNKGKTSMYELGDKIKKMPYNFLNKQATRKNLLQVTAVGSEYTLSTREAALLVLKGLTRDKDKESVKIRK W SAKQLSTTRNDEFTDAASNFSYD -CPNYQ
NESTLKLFFVVARAGEVYPN -NYMIKACPKYEYANHGFPPGELNENGRISMYQLGHKLRLIYPEFLHRRYITKNLLKATAVGNKYTISTREGALLTLKGLRNNENMNKAINTRK W SAKRLSTTRNDEFTDAASGGYQS -CPNFF

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XC-69
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ELE-SETLKSEEFQKRLHPYKDFIATLGKLSGLHGQDLFIWSKVYDPLYCESVHNFTLPSWATEDMTKLRELSEL -SLLSLYGIHKQKEKSLRGGVLVNEILNHNK RATQIPSYK -----KLIMYSAHDTTVSGLQMAL
ELK-SETLKSEEFKLRLQPYKSFIDTLPSLSGFEDQDLFEIWSRLYDPLYCESVHNFTFRTWATEDAMTKLSELSEL -SLLSLYGIHKQKEKSLRGGVLVNEILNHNK RATQIPQKAR -----KLIMYSAHDTTVSGLQMAL
QLQ-NETRNSAEYINKTRDNLQLQYLMVANETGIRDSLESVWS -VYDTLFYEQAHKMFLPSWPTPDVMTQMKLKDF -GFEFLFGIHHRVEKARLGGVLLDHIIRKHLTKAANSAHQQL -----KLLVYSAHDTTLVALQMAL
SLL-TQLFLCTEFFANQRNRLYLAWSKNSGA-NITSLETLEYLNTLYTESLNKFLPWNT -SGVYP-EKMAPW-AHLSFATQGNRDLARLKTGPLFNEIEHFRN-ATKKIENFR -----KFLVYSAHDTTIANVLNTM
YEL-ASLESSPEFKALTEKHRLNFAYLSEKGG-RPVKTFDAISYLNNTLFENLNMTLPKWNT -KMYVGREELTYV-SNFAFATSSYTRKLARLKAQPLLDIFQRFKEKSSGSLKPDOR -----SMWVYSAHDTTVASVLNAL
R-----VLESPRGKYEFSKYDLKLLKLEWDTGK-NITTPWDYYIYIHTVLAEGSYGLTLPSWTN -NIFPRGELFDS -TVFTYNTINSTPLLLKLYGGPLLRIFTKHLDDVVSQTQKKRR -----KIYLFSGHEINIASVLHAL
E-----QLMMKKIKITILQKCGNSMIEKHHYDVTPEKHIWYETLKLKLTQHPSGDLDWVTDIMKNLKECS ---AEFTWMTATSSKTLRLQTGGLLIYDIFNDMNEILQGAQPHATGGKENKLSLFTAPDILIPKLAVF
Q-----QLRARENKIKITLQKCGNSMKEVKHHYESVNPNKPEHIWYETLKLKLTQHPSGDLDWVTDIMKNLKECS ---ARYTWMTATSSRALRKLTTGGLLIYDIFNDMNEILQGAQPPATGGKESKLSLFTVPLEILIPKLAVF
K-----EVSQQP-EIATTLQDCASQMVEVKHYDVTDPKQHVWLTYETLKKMKKQKPSKVEWASDDMMKMLRECS ---AKLNWLATTKTDTLRKLSGGLLSDILNDMKEITQGAQPHATGGTSNKLSLFTTTPQGLLIAKLAVF
E-----ELLMKQKQEISTILKECISVVQVQKSYSAVNVNLPQHILWLAYETLKLKLRQPPSSSTWMTDMLMKNLRECS ---AKITWLATTKTDTLRKLSGGLLNDLFDNDMQITQGAQPNAPGGKDSKLVNFTVSQFLVISQLAAF
K-----ELLAAQGEIITTVKECISVVQVQKSKYPAD/DEKMPQHILWLAYETLKLKLRQPPSSSTWMTDMLMKNLRECS ---AKITWLAAKTDTLRKLSGGLLNDLFDNDMQITQKQPQPNAPGGKETKLVNFTVSQFLVISQLAAF
K-----STLSKQNDINTILGKCEAALKTVKEHYPAVVK -PQHTWLVEYETFKRMKQKQKASNLWLTDIMKQLQACS ---AEITWFAATNSDEWRKISGGLLLDIFDLDQITQKQPQYPAPGGANNKMSLFTVPQVLVISHLAVI
QDVRSNFI RTHKLDPRLFYAYQIFTEDLAGINLSPQRRPEDIWLAYESMFNVFYSYKRRYHHKYRYWKLVRQFKKFSKELMNTSLATEDLRKMSGGAIHVHDLNMANTITKNKSINDRP ---DLKLAVALTAQGLVASVAV
-----VYEKVSFVTSLSKRLSAGRYVSQLLDDVDHLNRNKGETPDGK ---KMWLYGSTSPFLKSIMSAM
KEY-NQALTKFEFFKPNVKTRLERLIEMGSKSGD-EQNVIDMLRKDDTDNTKRLTKSLNENADAN-ITVENLTPLRDL-YELYCSDLSNLPPPKWLDADLWDSFHLLMRRYNAIYST-E-----KLRLLSGGPITVKYFLNKL
KKQ-KIALKKELMPK-----EKNRKPAD-ESTITD--EDINSKTKNLINKLNENTGAN-ITGDNLVALKYL-ADLYEATERSNLLLPKNYDEDMWISLHFLMRRYIEASVST-N-----DLRSLAGRMVYKFDFKLD

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phos
phos-2
phos-6
phos-7
XC-69
cluster-175
cluster-155

D-----VYNGLLPPYASCHLT ELYF-EKGEYFVEMYRNETQHEPYP---LMLPGCS-PSGCLP LERFAELGVGPVIP--QDWSTECMTTNSHQGTEDSTD--
E-----LYNGLLPPYASCHLT ELYF--DNGGTFVEMYRNETQNEPYP---LTLPGCT-HSCPLERFAELLDPVIP--QDWATECMGTNSHQASL--
D-----VYNKIQAP-YASCHLT ELYQEDDGNFSVEMFFRNESGKEFPF---LTI PGCC-QICPLQRFLELTDVPVP--QDWEQEQIASSMHDTLGVLGVLAVCGSIIIIIIIIIIITVLFRIQSQPPGYRHVSNEGEEQA-
G-----AFEYHCOPYASTIMFELRRNSS--FYLNVFYKNS--SQVQK---ITPGCCD-FQNDQFETJALLKPIVITRKQWDLCEQJLSNFR-YNHIFVYSSAIGFLVFTLVLVWVIAWFKHLKNSGNDYTRLAIDEVA
K-----LFELHSPPYTAQIMELLRHDETNTPLVSIFYKNIT-AEPLP---LDTPGCC-PSGPLKTLMNIIYEDVLP--VDWRECKLSLMTMMTYEEANLGTATGILILVIALLFASYGLMIYYRRR-NYKLYSSYSQMA
Q-----LYYPHVVEYSSIIIMVHEIGETHYKIVVYLGIPSEARE---LQLPGCE-VLCPLYKYLQIENVIIPSN--EELICDKRFVDESANNLSIEELDFVKLNLIRIAGTENK-----
MPPGTLDDNKEITPMDFYPEAGAHNLNTEMYEENGKWKIKLIYYNGKNQPGKT---IKLPNCE-EKCPFRKFQKQLQNFMINEEHKKSKGL-
TPKGTLDDKPVTPMNIYPEAGAYLDTMEYENGKWKIKLIYYNGKNQPGKT---IRLPDCE-EKCPFNKFKQLEKFMINEKDHE TLCKG-
MPPGATLDGKVTPSSEVYPEGATMNETYEDNGTWKVKLIYYEGDKPGKT---IKLPDCE-EKCPFQFQQILTKYAVNEQEHE TLCKSAQWP-
MEPGSKLNNKAVTASDIYPEDGSHVDIEMYQENNKWSVKLVVYSGDKDQPQT---ITLPGCC-EKCPYEQFKSALQKYKITDEEHQKAKN-
MEPGSKLNNKAVTASDIYPEDGSHVDIEMYQENNKWSVKLVVYSGDKDQPQT---ITLPGCC-EKCPYEQFKSALQKYKITDEEHQKAKN-
TPPGTKIGSKDVTAAQNIYPEDGAVNLNLFKGDKEWKKIVYVKGGEPPQT---IALPGCP-EKCPYNNKFQILQYVIAISDDDHKKACGFPA-
APNGTTLGGKPLGADDLPEHGAMQVIEVYKQGESSWKIKVLRYKNREECLKP---MVISGCENELQDYDKFSAVKGIDLEEKAHNLNCKMAQE-
GGD-----QQYHSENLPPYEGAGMFITEIYQKEVEQTFHVRHYSTNPNQIPISDKNVLKLRDCE-ELCEFDKFKDLMKPMYLSKDDADKECLE-
D-----KRKGKLEPCDTKLLLHIGYERTVVPFFAALAGEDGFEING---QYLLKTM-RAYEGGMFIEAHETDS---PYDGLRVLVYSEDLHAPVYEVASVECKYPCFSFRQLKKNLSEIAVDKEKWLQLTM-----
D-----KLAGRLEPCETKLLLHIGYERTVVPFFAALAGEDGFEING---LV-----

