

0000000000000001111111111111111100111111111111111111111111111111111100
0000000000000000000000000000000011111111111111110000000000000000000000
00

> P06781 RHO2_YEAST

MSEKAVRRKLVIIIGDGACGKTSLLYVFTLGKFPQYHPTVVFENYVTDCRVDGIKVSLLTLDWTAGQE
EYERLRPFSYSKADIILIGFAVDNFESLINARTKWADEALRYCPDAPIVLVGLKKDLRQEAHFKEN
ATDEMVPIDAKQVARAIGAKKYMESALTGEGVDDVFEVATRTSLLMKKEPGANCCIIIL
00
00
00

> P02662 CAS1_BOVIN

MKLLILTCLVAVALARPKHPIKHQGLPQEVNENLLRFFVAPFPEVFGKEKVNELSKDIGSESTED
QAMEDIKQMEAESISSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAE
ERLHSMKEGIHAQQKEPMIGVNQELAYFYPELFRQFYQLDAYPSGAWYYVPLGTQYTDAPSFSDIP
NPIGSENSEKTTMPLW
00
111111111111111100
0000000111111111100000011111111110000000000000000000000000000000
000001111111111111

> P13811 ELBH_ECOLI

MNKVKFYVLFALLSSLCAHGAPQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIITFKSG
ATFQVEVPGSQHIDSQKKAIERMKDTRLRITYLTETKIDKLCVWNNKTPNSIAAISMEN
00
11111000
11

> P04156 PRIO_HUMAN

MANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRYPGQSPGGNRYPPQGGGGWGQPHGGGWG
QPHGGGWGQPHGGGWGQPHGGGWGQGGGTHSQWNKPSKPKTNMKHMAGAAAAGAVVGGGLGGYMLGS
AMSRPIIHFGSDYEDRYRENMHRYPNQVYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTTKGENF
TETDVKMMERVVEQMCITQYERESQAYYQRGSSMVLFSPPVILLISFLIFLIVG
00
00
11
11
11
11

> P87020 PRA1_CANAL

MNYLLFCLFFAFSVAAPVTVTRFVNASPTGYDWRADWVKGFIDSSCNATQYNQLSTGLQEAQLLA
EHARDHTLRFSGSKSPFFRKYFGNDTASAEVVGHFENVVGADKSSILFLCDDLDDKCKNDGWAGYWR
GSNHSDQTIICDLSFVTRRYLSQLCSGGYTVSKSKTNIFWAGDLLHRFWHLKLSIGQLVIEHYADTY
EEVLELAQENSTYAVRNSNSLIYYALDVYAYDVTIPGEGCNGDGTSYKKSDFSSFFEDSDSGSDSGA

> Q08137 OSPC2_BORBU

MKKNTLSAILMTLFLFISCNNSGKGGDSASTNPADESAGPNLTEISKKITDSNAFVLAVKEVETL
VLSIDELAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAI STLITEKLSKLNLEELKTEIAKAKKC
SEEF TNKLKSGHADLGKQDATDDHAKAA I LKTHATTDKGAK EFKDLFESVEGLL KAAQVALTNSVK
ELTSPVVAESP KKP

00
00
00
000011111111111

> Q39967 ALL5_HEVBR

ASVEVES AATALPKNETPEVTKAEETKTEEPAAPPASEQETADATPEKEEPTAAPAEPEAPAPETE
KAEVEKIEKTEEPAPEADQTTPEEKPAEPEPVAE EEPKHETKETETEAPAAPAEGEKPAEEKPI
TEAAETATTEVPVEKTEE

000000000000011111111011111111111101111111111111111111111111111111110000000000
00000011111111111000011111111111100000000000000000000000000000000000000011
1111111111100000000

> O82803 SRPP_HEVBR

MAEEVEEERLKYLD FVRAAGVYAVDSFSTLYLYAKDISGPLKPGVDTIENVVKT VVTPVYYI PLEA
VKFVDKTV DVS VTS LDG VVPV I KQVSAQTY SVAQDAPRIVLDVASSVFNTGVQEGAKALYANLEP
KAEQYAVITWRALNKLPLVPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRVSSYLPLLPT EKITKV
FGDEAS

0111111111111111111111100000000000111111111110011111111111100000000011111111
11111000000000000000111111111110000000011111111111000001111111111100000
00000000000000000000000000001111111111100000000000000000000000000000
000000

> Q9ZMZ4 UREA_HELPJ

MKLTPKELDKLMLHYAGELARKRKEKGIKLN YVEAVALISAHIMEEARAGKKTAAELMQEGRTLLK
PDDVMDGVASMIHEVGIEAMFPDGT KLVT VHTPIEANGKLVPGELFLKNEDITINEGKKAVSVKVK
NVGDRPVQIGSHFHF FEVNRCLDFDREKTFGKRLDIASGTAVRFEPGEEKSVELIDIGGNRRIFGF
NALVDRQADNESK KIALHRAKERGFHGAKSDDNYVKTIKE

11111111111100
0000000000000000000000111111111111111110000000000000000000111111111111
11100011111111111100
000

> P03126 VE6_HP V16

MHQKRTAMFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP
YAVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDKQRF
HNIRGRWTGRCMSSCRSSRTRRETQL

GGWSSKPRKGMGTNLSVNPPLGFFPDHQLDPVFGANSNNPDWDFNPIKDHWPAANQVGVGAFGPGF
TPPHGGVLGWSPQAQGMLTPVSTIPPPASANRQSGRQPTPI SPPLRDSHPQAMQWNSTAFHQALQD
PRVRGLYFPAGGSSSGTVNPAPNIASHISSISARTGDPVTNMENTSGFLGPLPVLQAGFFLLTRI
LTIPQSLDSWWTSLNFLGGSPVCLGQNSRSPTSNSHSPTSCPPICPGYRWMCLRRFIIFLFI LLLCL
IFLLVLLDYQGMLPVCPLILGSTTTSTGPCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPSSWA
FAKYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSAIWMMWYWGPSLYSIVSSFIPLLPIFFCLW
VYI

00
00
00
00
00
00
000

> Q40240 MPA5A_LOLPR

MAVQKYTVLFLRRGPRGGPGRSYAADAGYTPAAAATPATPAATPAGGWREGDDRRAEAAGGRQRL
ASRQPWPPLPTPLRRTSSRSPSPSPRASSPTSAAKAPGLIPKLDTAYDVAYKAAEAHPRGQV
RRLRHCPHRSLRVIAGALEVHAVKPATEEVLAAKIPTGELQIVDKIDA AFKIAATAANAAPTNDKF
TVFESAFNKALNECTGGAMRPTSSSPSRPRSSRPTPPPSPAPEVKYAVFEAALTKAITAMTQAQ
KAGKPAAAAATAAATVATAAATAAAVLPPPLL VQSLISLLIYY

00
00
00
000111111111111000
11111100
000

> P04405 GLYG2_SOYBN

MAKLVLSLCFLLFSGCFALREQAQQNECQIQKLNALKPDNRIESEGGFIETWNPNNKPFQCAGVAL
SRCTLNRNALRRPSYTNQGPQEIYIQQNGIFGMI FPGCPSTYQEPQESQQRGRSQRPD RHQKVHR
FREGDLIAVPTGVAWWMYNNEDTPVVAVSII DTNSLENQLDQMPRRFYLAGNQEQEFLKYQQQQQG
GSQSQKQKQEEENEENEGSNILSGFAPEFLKEAFVNMQIVRNLQGENEEEDSGAIVTVKGGLRV TAP
AMRKPPQEEEDDDDEEQPQC VETDKGCQRQSKRSRNGIDETICTMRLRQNIQNSSPDIYNPQAGS
ITTATSLDFPALWLLKLSAQYGLRKNAMFVPHYTLNANSIIYALNGRALVQVNCNGERVF DGEL
QEGGV LIVPQNFVAVAKSQSDNF EYVSFKTNDRPSIGNLAGANSLLNALPEEVIQHTFNLKSQQAR
QVKNNNPFSFLVPPQESQRRAVA

001111111111111100
00
00
11111100

GARAALWECGCATLGASFQYAQSKPKVEELNVLCNASEFTINKPKGYVGAEFPLNITAGTEAATGT
KDASIDYHEWQASLALSRYRLNMFTPYIGVKWSRVSFADDTIRIAQPKLAEAILDVTTLNRTTAGKG
SVVSAGTDNELADTMQIVSLQLNKMKSRSKSCGIAVGTITVDADKYAVTVEARLIDERAAHVNAQFR
F

00
00
00
00
00
00
0

> P21793 PGS2_BOVIN

MKATIIIFLLVAQVSWAGPFQOKGLDFDFMLEDEASGIGPEEHFPEVPEIEPMGPVPCPFRQCCHLRVV
QCSDLGLEKVPKDLPPDTALLDLQNNKITEIKDGDGFKNLKNLHTLILINNKISKISPGAFAPLVKL
ERLYLSKNQLKELPEKMPKTLQELRVHENEITKVRKSVFNGLNQMIIVVELGTNPLKSSGIENGAFAQ
GMKKLSYIRIADTNITTIPQGLPPSLTELHLDGNKITKVDAASLKGLNNLAKLGLSFNSISAVDNG
SLANTPHLRELHLNKNLKVPGGLADHKYIQVVYLHNNNISAIKSNDFCPPGYNTKKASYSYSGVSL
FSNPVQYWEIQPSTFRCVYVRAAVQLGNYK

00
00
00
00
001111111111111100
00

> P15310 PHLC1_CLOPE

MKRKICKALICATLATSLSWAGASTKVYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPESVRKNL
EILKENMHELQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPDTGESQIRKFSAL
ARYEWQRGNKQATFYLGEMHYFGDIDTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTAGCK
TNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSHSWDDWDYAAKVTLAN SQGTAGYI
YRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGTDDYMYFGIKTKDGKTQEWEMDNPGNDFMTG
SKD TYTFKLK DENL KIDDIQNMWIRKRKYTAFPDAYK PENIKI IANGKV VVDK DINEWISGNSTYN
IK

00
00000011111100
00
00000111111100
11111000
00

> Q8X7B6 TRPB_ECO57

TLLNPFYFGFEGGMYVPQILMPALRQLEEFVSAQKDPEFQAQFNDLLKQNYAGRPTALTKCQNITA
GTNTTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKTE I IAETGAGQHGVASALASALLGLKCRIY
MGAKDVERQSPNVFRMLMGAEV I PVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHPYPT
IVREFQRMIGEETKAQILEREGR LPDAVIACVGGGSNAIGMFADF INETNVGLIGVEPGGHGIETG
EHGAPLKHGRVGIYFGMKAPMMQTEDGQIEESYSISAGLDFPSVGPQHAYLNSTGRADYVSI TDDE
ALEAFKTLCLHEGI I PALESSHALAHALKMMRENPEKEQLLVNLSGRGDKDI FTVHDILKARGEI
00
00
00
00
0000011111111111111100
00

> P42375 CH60_PORGI

MAKEIKFDMESRDLLKKGVDALANAVKVTLGPKGRNVILSKTYGAPHITKDGVSVAKEIELECPFE
NMGALVKEVASKTND DAGDGT TATILAQSI IGVGLKNVTAGANPMDLKR GIDKAVKAVVTHIAG
MAKEVGDDFQKIEHVAKISANGDENIGSLIAEAMRKVKKEGVITVEEAKGTDTTVEVVEGMQFDRG
YISPYFVTNTDKMEVQ MENPFILYDKKISVLKEMLP ILEQTVQTKPLLI IAEDIDSEALATLVV
NRLRGLSLKICAVKAPGFGDRRKAMLEDIA ILTGGTVISEETGLKLENATMDMLGTAEKVTVDKDNT
TIVNGAGNKEG IASRITQ IKAQ IENTTS DYDREKLQERLAKLAGGVAVLYVGAASEVEMKEKKDRV
EDALSATRAAIEEGTVPGGGTAYIRAI AALEGLKGENEDET TGIEIVKRAIEEPLRQIVANAGKEG
AVVVQKVKEGKDDFGYNARTDVFENLYTTGVIDPAKVTRVALENAASIAGMFLTTECVIADKKEDN
PAAPAMPGGMGMGMGM

0000000000111111111100
000001111111111100
000000001111111111000000000111111111111111100000000000000111111
111100000000000000000111111111100000000000000000000000000000111
11111100000011111111111100
00001111111111111000000000000011111111111111110000000000000000
00000000000000000000011111111100000011111111110000000000000000
0000000000000000000000000111111111000011111111110000000000000000
0000000000000000

> Q00663 CARP_CANTR

MATIFLFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKRSDVPTT
LINEGPSYAADI VVGSNQQKQTVVIDTGSSDLWVVDTDAECQVTYSGQTNNFCKQEGTFDPSSSSS
AQNLNQDFSIEYGDLTSSQGSFYKDTVGFGGISIKNQFADVTTTSVDQGIMGIGFTA VEAGYNLY
SNVPVTLKKQGI INKNAYS CDLNSEDA STGKI I FGGVDNAKYTGTLTALPVTSSVELRVHLGSINF
DGTSVSTNADVVLDSGTTITYFSQSTADKFARIVGATWDSRNEIYRLPSCDLSGDAVVNFDQGVKI

DLGNGLKAIWQVEQKASIAGTDSGWGNRQSFIFGLKGGFGKLRVGRRLNSVLKDTGDINPWDSKSDYL
GVN KIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGRHNSESYHAGFNKNGGFFVQYGGAYKR
HHQVQEGLNIEKYQIHRLVSGYDNDALYASVAVQQQDAKLT DASNSHNSQTEVAATLAYRFGNVTP
RVSYAHGFKGLVDDADIGNEYDQVVVGAEYDFSKRTSALVSAGWLQEGKGENKFVATAGGVGLRHK
F

000000000000000000000000000000000111111111111111111000000000000000
0111111111111111111111111111111111000000000000000000000000000000
000000000000001111111111111111111100000011111111111100000000000000
0001111111111
111111111111111100
0

> P10332 OM1E_CHLPS

MKKLLKSALLFAATGSALSLOALPVGNPAPESLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYG
DYVFDRLVKVDVNKTFSGMAATPTQATGNASNTNQPEANRPNIAYGRHMQDAEWF SNA AFLALNI
WDRFDIFCTLGASNGYFKSSAAFNLVGLIGFSATSSTSTELPMQLPNVGI TQGVVEFYTDTSFSW
SVGARGALWECGCATLGAEFQYAQSNPKIEVLNVTSSPAQFVIHKPRGYKGASSNFPLPITAGTTE
ATDTKSATIKYHEWQVGLALSRLNMLVPYIGVNWSRATFDADTIRIAQPKLKSEILNITWNP SL
LGSTTTLPNNGGKDVLS DVLQIASIQINKMKS RKACGVAVGATLIDADKWSITGEARLINERAAHM
NAQFRF

00
00
00
00
00
00
000000000000000001111111111110000000000000000000000000000000000000
000000

> P23114 OM1N_CHLTR

MKKLLKSVLVFAALSSASSLQALPVGNPAPESLMIDGILWEGFGGDPCDPCCTTWCD AISMRVGYG
DFVFDRLVKTDVNKEFQMGAEPTSDTAGLSNDPTTNVARPNPAYGKHMQDAEMFTNAAYMALNIW
DRFDVFC TLGATTGYLKGNSASFNLVGLFGTKTQSTNFNTAKLPNTALNQAVVELYTDTTFAWSV
GARAALWECGCATLGASFQYAQSKPKVEELNVLCDASEFTINKPKGYVGAEFPLDITAGTEAATGT
KDASIDYHEWQASLALSRLNMFTPYIGVKWSRVSFADTIRIAQPKLAEAVLDVTTLNPTIAGKG
SVVASGSENELADTMQIVSLQLNKMKS RKSCGIAVGTTIVDADKYAVTVETRLIDERAAHVNAQFR
F

00
00
00
00

EQMFTRHFFNLGGKMGDTIPDELYIKSTSVPTPGSHVYTSTPSGSMVSSEQQLFNKPYWLRRAQGH
NNGMCWGNRVFLTVVDTTRSTNVSLCATEASDTNYKATNFKEYLRHMEEYDLQFIFQLCKITLTPE
IMAYIHNMDPQLLEDWNFGVPPPPSASLQDTRYRYLQSQAITCQKPTPPKPTDPYASLTFWDVDLS
ESFSMDLDQFPLGRKFLLRGAMPTVSRKRAAVSGTTPPTSKRKRVR

00
00
00
00
0000000000000000000111111000
00
00
00

> P00183 CPXA_PSEPU

TTETIQSNANLAPLPPHVPEHLVDFDFMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIAT
RGQLIREAYEDYRHSSECFPIPREAGEAYDFIPTSMPPPEQRQFRALANQVVGMPVVDKLENRIQ
ELACSLIESLRPQGQCNTEDYAEPFPIRIFMLLAGLPEEDI PHLKYLTDQMTRPDGSMTFAEAKE
ALYDYLIPIIEQRRQKPGTDAISIVANGQVNGRPITSDEAKRMCGLLLVGGLD TVVNFLSFSMEFL
AKSPEHRQELIERPERIPAACEELLRRFSLVADGRILTSDYEFHGVQLKKGQDQILLPQMLSGLDER
ENACPMHVDFSRQKVSHTTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFS IAPGAQIQHKSGIV
SGVQALPLVWDPATTKAV

0000001111111000
11111100
000000001111110111111000
00
11111100
00
111100000011111100

> P04012 VL1_HP11

MWRPSDSTVYVPPPNPVSKVVATDAYVKRTNIFYHASSRLLAVGHPYYSIKKVNTVVPKVSQYQ
YRVFKVVLDPDNKFALPDSSSLFDPTTQRLVWACTGLEVGGRGQPLGVGVSGHPLLNKYDDVENSQGY
GGNPGQDNRVNVGMDYKQTQLCMVGCAPPLGEHWGKGTQCSNTSVQNGDCPPLELITSVIQDGMV
DTGFGAMNFADLQTNKSDVPLDICGTVCKYPDYLQMAADPYGDRLFFYL RKEQMFARHFFNRAGTV
GEPVPD DLLVKGGNNRSSVASSIYVHTPSGSLVSSEAQLFNKPYWLQKAQGHNNGICWGNHLFVTV
VDTTRSTNMTLCASVSKSATYTNSDYKEYMRHVVEEFDLQFIFQLCSITLSAEVMAYIHTMNPSVLE
DWNFGLSPPPNGTLEDTRYVQSQAITCQKPTPEKEKQDPYKDMSEVNLKEKFSSSELDQFPLGR
KFLQSGYRGRTSARTGIKRPVAVSKPSTAPKRKRKTKK

00
00

NVSEDVRDNVSVDYKQTQLCILGCAPAIGEHWAKGTACKSRPLSQGDCPPLELKNTVLEDGDMVDT
GYGAMDFSTLQDTKCEVPLDICQSICKYPDYLQMSADPYGDSMFFCLRREQLFARHFWRAGTMGD
TVPQSLYIKGTGMPASPGSCVYSPSPSGSIVTSDSQLFNKPYWLHKAQGHNNGVCWHNQLFVTVVD
TTPSTNLITICASTQSPVPGQYDATKFKQYSRHEEYDLQFIFQLCTITLTADVMSYIHSMNSSILE
DWNFGVPPPPTTSLVDTYRFVQSVAITCQKDAAPAENKDPYDKLKFWNVDLKEKFSLDLDQYPLGR
KFLVQAGLRKPTIGPRKRSAPSATTSSKPAKRVRVRARK

00
00
00
00
00
000111111000
00
00
00

> P19542 OM1L_CHLTR

MKKLLKSVLVFAALSSASSLQALPVGNPAPESLMIDGILWEGFGGDCDPCDCTTWCDALSMRMGYYG
DFVFDRVLQTDVNKEFQMGAKPTATTGNAAAPSTCTARENPAYGRHMQDAEMFTNAAAYMALNIWDR
FDVFCTLGATSGYLKGNASAFNLVGLFGDNENQSTVKKDAVPNMSFDQSVVELYTDTTFAWSVGAR
AALWECGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGKEFPLDLTAGTDAATGTKDA
SIDYHEWQASLALSRLNMFTPYIGVKWSRASFDADTIRIAQPKLATAIFDITTLNPTIAGAGEVK
ANAEGQLGDTMQIVSLQLNKMKSRSKSCGIAVGTIIVDADKYAVTVETRLIDERAHVNAQFRF

00
00
00
00
00
00
00

> P77793 YDDV_ECO57

MEMYFKRMKDEWTGLVEQADPPIRAKAAEIAVAHAHYLSIEFYRIVRIDPHAEFLSNEQVERQLK
SAMERWIINVLSAQVDDVERLIQIQHTVAEVHARIGIPVEIVEMGFRVLKKILYPVIFSSDYSAE
KLQVYHFSINSIDIAMEVMTRAFTFSDSSASKEDENYRIFSLLENAAEEKERQIASILSWEIDIIY
KILLDSDLGSSSLPLSQADFGLWFNHKGRHYFSGIAEVGHISRLIQDFDGFIFNQTMRNTRNLNRS
RVKFLQIRNTVSQIITLLRELFEEVSRHEVGMDVLTKLLNRRFLPTIFKREIAHANRTGTPLSVL
IIDVDKFKEINDTWGHNTGDEILRKVSQAFYDNVRSSDYVFRYGGDEFIIVLTEASENETLRTAER
IRSRVEKTKLKAANGEDIALSLSIGAAMFNHGPDYERLIQIADALYIAKRRGRNRVWLKASL

00
11

QYNNETLKIKNGDLTKELNKTRQELANKQOESKENEKALNELLEKTVKDKIAKEQENKETIGTLKK
ILDETVKDKIAKEQENKETIGTLKKILDETVKDKLAKEQKSKQNI GALKQELAKKDEANKISDASR
KGLRRDLASREAKKQLEAEHQKLEEQNKI SEASRKGLRRDLASREAKKQLEAEQQKLEEQNKIS
EASRKGLRRDLASREAKKQVEKALEEANSKLAALEKLNKELEESKKLTEKEKAELQAKLEAEAKA
LKEQLAKQAEELAKLRAGKASDSQTPDTKPGNKAVPGKGQAPQAGTKPNQNKAPMKETKRQLPSTG
ETANPFFTAALVMATAGVAAVVKRKEEN

00
00
00
00
11111111111111110000000000000001111111111111111110000000000000000
00
00
00

> P08342 VL2_BPV4

MVRAARRKRASEDDLYRGCRCMGQDCPIDIKNKYEHNTLADRILKQVSSFLYFGQLGISSGKGTGGS
TGYTPLGGRGGGGVTSGKGANVVRPTVIVDALGPTGVPIDPAVPDSSIVPLLESSGGSTTLDPG
AEIEIIAEVHPPPVYEGPEVTIGDIEEPPILEVVPETHPTSRVRSTTSKHDNPAFTAYVASAQLPG
ETSASDNVYILHGFNGDFVQADPEGDTIFEEI PLEEFVPMPPSTSTPTSSFRSVLNKFQRRLY
NRKLVQQVKITNRNTFLKQPSQFVQWFEFNPAYVDDSLSLIFQQDLDEVSAAPDADFQDIVKLSRP
VFTTKEGLVRLSRLGQRGTIKTRMACK

000000000000000000000000011111111111111111100000000000000000000000
0000000000000000000000000111
11
111111111100
00
00

> P23421 OM1B_CHLTR

MKKLLKSVLVFAALSSASSLQALPVGNPAPESLMIDGILWEGFGGDPCTTWVDAISMRYGYG
DFVFDRVLKTDVNKEFQMGAKPTTTTGNVAVPSTLTARENPAYGRHMQDAEMFTNAACMALNIWDR
FDVFCTLGASSGYLKGNSASFNLVGLFGNENQTKVSNVAFVPMNSLDQSVVELYTDATAFAWSVGA
RAALWECGCATLGASFQYAQSKPKVEELNVLCAAEFTINKPKGYVGKELPLDLTAGTDAATGTKD
ASIDYHEWQASLALSRYLNMFTPYIGVKWSRASFDADTIRIAQPKSAETIFDVTTLNPTIAGAGDV
KTS AEGQLGDTMQIVSLQLNKMKSRSKSCGIAVGTIIVDADKYAVTVETRLIDERAHVNAQFRF

00
000000000000000000000000011111111111100000000000000000000000000000
000001111111111111110000000111111111111111111111111111111111111111
00

SITLQQQLKELTAPDENIPAKILSYNRANRAVAAILCNHQRAPPKTFEKSMMNLQTKIDAKKEQLAD
ARRDLKSAKADAKVMKDAKTKKVVESKKAQVQRLEEQLMKLEVQATDREENKQIALGTSKLNLYLDP
RITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADEDYEF

00
00
00
00000011
00
00000000000000000111
11
00
11
00
00
00
00

> P43238 ALL12_ARAHY

MRGRVSPMLLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACESRCKLE
YDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDDDRRQPRREEGGRWGPAGPREREREEDWRQP
REDWRRPUSHQQPRKIRPEGREGEQEWGTPGSHVREETSRRNPFYFPSRRFSTRYGNQNGRIRVLQR
FDQRSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHAL
RIPSGFISYILNRHDNQLNRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSTRNTLEAAFNAEFN
EIRRVLLEENAGGEQEERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSVSKKGSEEEGDITN
PINLREGEPPDLNNGFKLFEVKPKKPNQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVKGT
GNLELVAVRKEQQQRGRREEEDEDEEEEGSNREVRRYTARLKEGDVFIMPAAHPVAINASSELHL
LGFGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIKQKESHFVSARPQSQSQSP
SSPEKESPEKEDQEEENQGGKGPLLSILKAFN

0000000000000000000000000111
0000000000000000000000000111
11
00
0000000000000000000000000111
11
11
11
11
11
0111

> P02458 CO2A1_HUMAN

MIRLGAPQSLVLLTLLVAAVLRCQGQDVRQPGPKGQKGEPPGDIKDIVGPKGPPGPGQGPAGEQGPRG

PGPPGPAGEKGS PGADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGF PGLPGPSGEPGKQGPSGA
S GERGPPGPMGPPGLAGPPGESGREGAPGAEGSPGRDGS PGAKGDRGETGPAGPPGAPGAPGAPG
VGPAGKSGDRGETGPAGPAGVPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGRGFSGLQGPPGP
PGSPGEQGPS GASGPAGPRGPPGSAGAPGKDG LNLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGP
PGPPSAGFDFSLPQPPQEKAHDGGRYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKN
PARTCRDLKMCHSDWKS GEYWIDPNQGCNLDAIKVFCN METGETCVYPTQPSVAQKNWYISKNP KD
KRHVWFGESMTDGFQFEYGGQGS DPADVAIQ LTFRLMSTEASQNITYHCKNSVAYMDQQTGNLKK
ALLLKSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKT VIEYKTTKTSRLPIIDVAPLDV GADQ
EFGFDVGPVCF L

00
00
00
00
00
00
0000000011111111111000
00
00
00
00
00
00
00
00
00
00
00
00
00
00
00
000000000000

> P32553 VP2_AHSV4

MASEFGILMTNEKFDPSLEKTICDVIVTKKGRVKHKEVDGVCGYEWDETNRH RFG LCEVEHDMSISE
FMYNEIRCEGAYPIFPRYIIDTLKYEFIDRNDHQIRVDRDDNEMRKILIQPYAGEMYFSPECYPS
VFLRREARSQKLDRIRNYIGKRVEFYEEESKRKAILDQNKMSKVEQWRDAVNERIVSIEPKRGECY
DHGTDIIYQFIKKLRF GMMYPHYVVLHSDYCVPNKGGTSIGSWHIRKRTEGD AKASAMYS GKGPL
NDLRVKIERDDL SRETIIQII EYGKKFNSSAGDKQGNISIEKLVEYCDFLTTFVHAKKKEEGEDDT

