

The unique structure of wild type carbonic anhydrase α CA1 from *Chlamydomonas reinhardtii*

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Supplementary DATA

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Supplementary Figure 1. A phylogenetic tree of all known α -type carbonic anhydrases produced using *ClustalX*.

CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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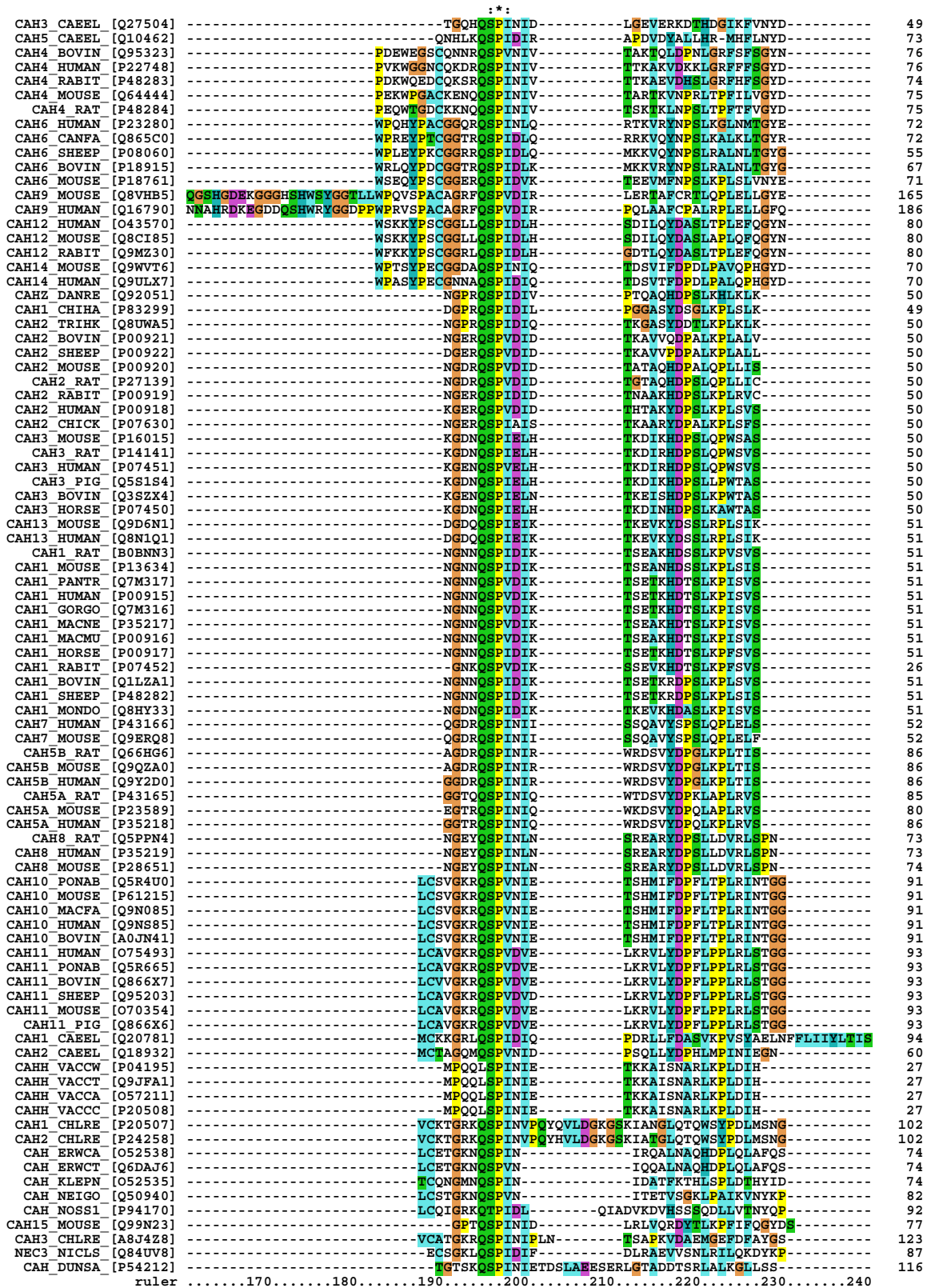
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CAH5 CAEEL [Q10462] -----MPSHLLVLSLLVALLVVSCGPGSDHGWCYDEN 33
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CAH4 HUMAN [P22748] -----MRMLLALLALSAARPSASAESHWCYEQ 28
CAH4 RABIT [P48283] -----MQLLFALLALGALRPLAGEELHWCEIQ 28
CAH4 MOUSE [Q64444] -----MQLLLALLALAVVAPST-EDSHWCYEQ 27
CAH4 RAT [P48284] -----MQLLLALLALAVVAPST-EDSHWCYEQ 27
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CAH6 CANFA [Q865C0] -----MRALALLALPLLGAQAQHGSLWTYS-E 27
CAH6 SHEEP [P08060] -----GHHVETWYS-E 10
CAH6 BOVIN [P18915] -----MTLFLFLLVVGQAQHEWTYS-E 22
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CAH9 HUMAN [Q16790] -----MAPLCPSPWLPPLIPAPAPGLVQLLLSLLLVVHPQRLPRMQED 46
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CAH12 MOUSE [Q8CI85] -----MPHRSRLRAVVLLLVILKKQPSSSAPLNGSKWTVFGP 37
CAH12 RABIT [Q9MZ30] -----MPVGLSRAAAVLLLVILKEQPSSSAPLNGSKWTVFGP 37
CAH14 MOUSE [Q9WVT6] -----MLFFALLKVTWILAADGGHWTVEGP 27
CAH14 HUMAN [Q9ULX7] -----MLFSALLLEVITWILAADGGQHWTVVEGP 27
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CAH2 TRIHK [Q8UWA5] -----MSHGWGYADH 10
CAH2 BOVIN [P00921] -----MSHHWGYGKH 10
CAH2 SHEEP [P00922] -----MSHHWGYGEH 10
CAH2 MOUSE [P00920] -----MSHHWGYSKH 10
CAH2 RAT [P27139] -----MSHHWGYSKS 10
CAH2 RABIT [P00919] -----MSHHWGYGKH 10
CAH2 HUMAN [P00918] -----MSHHWGYGKH 10
CAH2 CHICK [P07630] -----MSHHWGYDSH 10
CAH3 MOUSE [P16015] -----MAKEWGYASH 10
CAH3 RAT [P14141] -----MAKEWGYASH 10
CAH3 HUMAN [P07451] -----MAKEWGYASH 10
CAH3 PIG [Q5S1S4] -----MAKEWGYADH 10
CAH3 BOVIN [Q3SZX4] -----MAKEWGYADH 10
CAH3 HORSE [P07450] -----MAKEWGYADH 10
CAH13 MOUSE [Q9D6N1] -----MARLSWGYGEH 11
CAH13 HUMAN [Q8N1Q1] -----MSRLSWGYREH 11
CAH1 RAT [B0BNN3] -----MASADWGYDSK 11
CAH1 MOUSE [P13634] -----MASADWGYGSE 11
CAH1 PANTR [Q7M317] -----MASPDWGYDDK 11
CAH1 HUMAN [P00915] -----MASPDWGYDDK 11
CAH1 GORGO [Q7M316] -----MASPDWGYDDK 11
CAH1 MACNE [P35217] -----MASPDWGYDDK 11
CAH1 MACMU [P00916] -----MASPDWGYDDK 11
CAH1 HORSE [P00917] -----MAHSDWGYDSP 11
CAH1 RABIT [P07452] -----MASPDWGYDGE 11
CAH1 BOVIN [Q1LZA1] -----MASPDWGYDGE 11
CAH1 SHEEP [P48282] -----MANLNWSYEGE 11
CAH1 MONDO [Q8HY33] -----MTGHHGWGYGQD 12
CAH7 HUMAN [P43166] -----MTGHHGWGYGQD 12
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CAH5B MOUSE [Q9QZA0] -----MVVMNSLRVILQVSSCILLWRRFRVPLVPLRSCSLTCTYRNRNR 46
CAH5B HUMAN [Q9Y2D0] -----MLRAKMLGRGPYKPLAILLRHMGPLCA---TRPQHRWFQHSYAEKHSNC 45
CAH5A RAT [P43165] -----MLRRDRPKPLAILLRHVGLLCA---TPGQRWRWFQHSYAEKHSNC 40
CAH5A MOUSE [P23589] -----MLGRNTWTKSAFSLVQMWAPLWSRSMRPGRWCQRSCAWQNSNN 46
CAH5A HUMAN [P35218] -----MADLSFIEDAVAFPEKEDEEEEEEE-GVWGYEEG 34
CAH8 RAT [Q5PPN4] -----MADLSFIEDVAFPEKEDEEEEEEE-GVWGYEEG 34
CAH8 HUMAN [P35219] -----MADLSFIEDAVAFPEKEDEEEEEEE-GVWGYEEG 35
CAH8 MOUSE [P28651] -----MEIVWEVLFLLQANFIVCISAQONSPKIHGWNWAKKEVVQGSFV 44
CAH10 PONAB [Q5R4U0] -----MEIVWEVLFLLQANFIVCISAQONSPKIHGWNWAKKEVVQGSFV 44
CAH10 MOUSE [P61215] -----MEIVWEVLFLLQANFIVCISAQONSPKIHGWNWAKKEVVQGSFV 44
CAH10 MACFA [Q9N085] -----MEIVWEVLFLLQANFIVCISAQONSPKIHGWNWAKKEVVQGSFV 44
CAH10 HUMAN [Q9NS85] -----MCAAARLSAPRALVLAALGAAAHIGPAPDPEDWWSYKDNLQGNFV 46
CAH11 PONAB [Q5R4Z8] -----MCAAARLSAPRALVLAALGAAAHIGPAPDPEDWWSYKDNLQGNFV 46
CAH11 BOVIN [Q866X7] -----MCAAARLSAPRALVLAALGAAAHIGPAPDPEDWWSYKDNLQGNFV 46
CAH11 SHEEP [Q95203] -----MCGAARLSAPRALVLAALGAAAHIGPAPDPEDWWSYKDNLQGNFV 46
CAH11 MOUSE [Q70354] -----MCGAARLSAPRALVLAALGAAAHIGPAPDPEDWWSYKDNLQGNFV 46
CAH11 PIG [Q866X6] -----MRFECSHFPLFLIILTCHISPLKSSQ---NQWYSYSDSDFV 37
CAH1 CAEEL [Q20781] -----MIPWLLTACTIYPCVIG- 16
CAH2 CAEEL [Q18932] -----
CAHH VACCW [P04195] -----
CAHH VACCT [Q9JFA1] -----
CAHH VACCA [Q57211] -----
CAHH VACCC [P20508] -----
CAH1 CHLRE [P20507] -----MARTGALLLVALALAGCAQACTYKFGSPDPSKATVSGDHWHDGLN 45
CAH2 CHLRE [P24258] -----MARTGALLLVALALAGCAQACTYKFGSPDPSKATVSGDHWHDGLN 45
CAH ERWCA [Q52538] -----MKGKLSIALMLSVCFASASADS---VHWGVEGN 30
CAH ERWCT [Q6DAJ6] -----MKGKFSIALMLSVCFASASADS---VHWGVEGS 30
CAH KLEPN [Q52535] -----MKTSLGKAALLALSMPVTVFA---SHWSYEGE 30
CAH NEIGO [Q50940] -----MPRFPRLLPRLTAVLLLACAFSAAAAGN---HTHWGYTG 38
CAH NOSS1 [P94170] -----MSSLYRROLKLLGMSVLGFSFSSCVSPARAKTVNWGIGK 43
CAH15 MOUSE [Q99N23] -----MWALDFLLSFLLIQLAAQVSSGQWYDSDPK 33
CAH3 CHLRE [A8J4Z8] -----MRSAVLQRGQARRVSCRVDGSGVDSLPSHSASSARFLIDRRQLLTGAAASVITFVGCPCFLCKPGEARAAKAWYGEV 80
NEC3 NICLS [Q84UV8] -----MRMAAITKMLFISFLFSSVFLARSQEVDDSEFSYDEKSE 41
CAH DUNSA [P54212] -----MGSRRITLLGALFAVLAIAEGRLLTNNKAAEAETDVAVSSVAGSAGQLLVSEPHDNYE 63
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80

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CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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CAH4 HUMAN [P22748]	AESSNYPCLV	-----	38
CAH4 RABIT [P48283]	AS--NYSCLG	-----	36
CAH4 MOUSE [Q64444]	TKDPRSSCLG	-----	37
CAH4 RAT [P48284]	AKEPNSHCSG	-----	37
CAH6 HUMAN [P23280]	GALDEAH	-----	34
CAH6 CANFA [Q865C0]	GALDQVH	-----	34
CAH6 SHEEP [P08060]	GMLDEAH	-----	17
CAH6 BOVIN [P18915]	GVLDEKH	-----	29
CAH6 MOUSE [P18761]	DGVGSEQ	-----	33
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CAH12 MOUSE [Q8CI85]	AGEKN	-----	42
CAH12 RABIT [Q9MZ30]	DGERS	-----	42
CAH14 MOUSE [Q9WVT6]	HGQDH	-----	32
CAH14 HUMAN [Q9ULX7]	HGQDH	-----	32
CAHZ DANRE [Q92051]	DGPESWAESFPIA	-----	23
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CAH2 TRIHK [Q8UWA5]	NGPQKWCENFPIA	-----	23
CAH2 BOVIN [P00921]	NGPEHWHKDFPIA	-----	23
CAH2 SHEEP [P00922]	NGPEHWHKDFPIA	-----	23
CAH2 MOUSE [P00920]	NGPENWHKDFPIA	-----	23
CAH2 RAT [P27139]	NGPENWHKDFPIA	-----	23
CAH2 RABIT [P00919]	NGPEHWHKDFPIA	-----	23
CAH2 HUMAN [P00918]	NGPEHWHKDFPIA	-----	23
CAH2 CHICK [P07630]	NGPAHWHEHFPIA	-----	23
CAH3 MOUSE [P16015]	NGPDHWHELVPFA	-----	23
CAH3 RAT [P14141]	NGPEHWHELVPFA	-----	23
CAH3 HUMAN [P07451]	NGPDHWHELFPNA	-----	23
CAH3 PIG [Q58184]	NGPDHWHELVPFA	-----	23
CAH3 BOVIN [Q3SZX4]	NGPDHWHELFPNA	-----	23
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CAH1 HORSE [P00917]	NGPZEWVKLVPIA	-----	24
CAH1 RABIT [P07452]	-----	-----	24
CAH1 BOVIN [Q1LZA1]	NGPEHWGKLVPIA	-----	24
CAH1 SHEEP [P48282]	NGPEHWCKLHPFA	-----	24
CAH1 MONDO [Q8HY33]	NGPEHWSKLVPIA	-----	24
CAH7 HUMAN [P43166]	DGPEHWHKLVPIA	-----	25
CAH7 MOUSE [Q9ERQ8]	DGPEHWHKLVPIA	-----	25
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CAH5B MOUSE [Q9QZA0]	ALPPLWENLDLVP	-----	59
CAH5B HUMAN [Q9Y2D0]	ALHPLWESVDLVP	-----	59
CAH5A RAT [P43165]	ARRPLWTGPVSSP	-----	58
CAH5A MOUSE [P23589]	ARRPLWTGPVSSA	-----	53
CAH5A HUMAN [P35218]	TLHPLWTPVPSVP	-----	59
CAH8 RAT [Q5PPN4]	---VEWGLVFPDA	-----	44
CAH8 HUMAN [P35219]	---VEWGLVFPDA	-----	44
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CAH10 MOUSE [P61215]	FVPSFWGLVNSAWN	-----	58
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CAH10 HUMAN [Q9NS85]	FVPSFWGLVNSAWN	-----	58
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CAH11 PONAB [Q5R665]	PGPPFWGLVNAAWS	-----	60
CAH11 BOVIN [Q866X7]	PGPPFWGLVNAAWS	-----	60
CAH11 SHEEP [Q95203]	PGPPFWGLVNAAWS	-----	60
CAH11 MOUSE [O70354]	PGPPFWGLVNAAWS	-----	60
CAH11 PIG [Q866X6]	PGPPFWGLVNAAWS	-----	60
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CAHH VACCW [P04195]	-----	-----	-----
CAHH VACCT [Q9JFA1]	-----	-----	-----
CAHH VACCA [O57211]	-----	-----	-----
CAHH VACCC [P20508]	-----	-----	-----
CAH1 CHLRE [P20507]	GENWEGKDGAGNAW	-----	59
CAH2 CHLRE [P24258]	GENWEGKDGAGNFW	-----	59
CAH ERWCA [O52538]	GDPAHWGKLSPDFS	-----	44
CAH ERWCT [Q6DAJ6]	GDPAHWGKLSPDFS	-----	44
CAH KLEPN [O52535]	GSPHEHWGALNEEWK	-----	44
CAH NEIGO [Q50940]	DSPEWSGNLSEEFK	-----	52
CAH NOSS1 [P94170]	VGPEHWGELSPDFA	-----	57
CAH15 MOUSE [Q99N23]	CGPAHWKELAPACG	-----	47
CAH3 CHLRE [A8J4Z8]	AGPPTWKG	-----	88
NEC3 NICLS [Q84UV8]	NGPANWGNIRPDWK	-----	55
CAH DUNSA [P54212]	KVGFDTGGVGVN	-----	76
ruler90.....100.....110.....120.....130.....140.....150.....160	-----	-----

CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT



CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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CAH3 CAEEL [Q27504] -----HPIQ--GDIVNNGHSVQMT--PELRSEHPE 75
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CAH4 BOVIN [Q95323] -----MKHQ--WVYQNNGHTVMVL----LENKPS 99
CAH4 HUMAN [P22748] -----KKQT--WTYQNNGHSVVML----LENKAS 99
CAH4 RABIT [P48283] -----QREA--RLVENNGHSVMV----LGDVIS 97
CAH4 MOUSE [Q64444] -----QKQQ--WPIKNNQHTVEMT----LGGGAC 98
CAH4 RAT [P48284] -----QKKK--WEVKNNQHSVEMS----LGEDYI 98
CAH6 HUMAN [P23280] -----IQAG-EFFPMVNNGHTVQIS----LPTTMR 96
CAH6 CANFA [Q865C0] -----IQVG-EFFPMINNHTVQIS----LPTTMR 96
CAH6 SHEEP [P08060] -----LWHG-EFFVTNNGHTVQIS----LPTTMS 79
CAH6 BOVIN [P18915] -----LRQG-EFFMTNNGHTVQIS----LPTSMR 91
CAH6 MOUSE [P18761] -----KENL-EFTMTNNGHTVQIS----LPTSMY 95
CAH9 MOUSE [Q8VHB5] -----LQPLPELSLNNGHTVQLT----LPPGLK 190
CAH9 HUMAN [Q16790] -----LPPLPELRRLNNGHSVQLT----LPPGLE 211
CAH12 HUMAN [O43570] -----LSANKQFLLTNNGHSVRLN----LPPDMH 105
CAH12 MOUSE [Q8CI85] -----VSVEKLLNLTNDGHSVRLN----LNDMDY 105
CAH12 RABIT [Q9M230] -----VSADKQFNLTNDGHSVRLN----LPPDMY 105
CAH14 MOUSE [Q9WVT6] -----QLGTEPLDLHNNGHTVQLS----LPTTLH 95
CAH14 HUMAN [Q9ULX7] -----QPQTEPLDLHNNGHTVQLS----LPTTLH 95
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CAH1 CHIHA [P83299] -----YDFSNCLELLNNGHSFQVTFADDSHTLK 79
CAH2 TRIHK [Q8UWA5] -----YDPTSLDLLNNGHSFQVTFADDSHTMLT 80
CAH2 BOVIN [P00921] -----YGEATSRMVNNGHSFNVVEYDSDQKAVLK 80
CAH2 SHEEP [P00922] -----YEQAASRRMVNNGHSFNVVEYDSDQKAVLK 80
CAH2 MOUSE [P00920] -----YDKAASKSIVNNGHSFNVVEYDSDQNAVLK 80
CAH2 RAT [P27139] -----YDKVAASKSIVNNGHSFNVVEYDSDQFAVLK 80
CAH2 RABIT [P00919] -----YEHPISSRIINNNGHSFNVVEYDSDHKLVLK 80
CAH2 HUMAN [P00918] -----YDQATSLRLLNNGHSFNVVEYDSDQKAVLK 80
CAH2 CHICK [P07630] -----YDAGTAKAIVNNGHSFNVVEYDSDKSVLQ 80
CAH3 MOUSE [P16015] -----YDPPGSAKTILLNNGKICRVVFDDTYDRMMLR 80
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CAH1 RAT [B0BNN3] -----YNPATAKEIVNVGHSFHVVFDDSNQSVLK 81
CAH1 MOUSE [P13634] -----YNPATAKEIVNVGHSFHVVFDDSNQSVLK 81
CAH1 PANTR [Q7M317] -----YNPATAKEIVNVGHSFHVVFEDDNNRVLK 81
CAH1 HUMAN [P00915] -----YNPATAKEIVNVGHSFHVVFEDDNNRVLK 81
CAH1 GORGO [Q7M316] -----YNPATAKEIVNVGHSFHVVFEDDNNRVLK 81
CAH1 MACNE [P35217] -----YNPATAKEIVNVGHSFHVVFEDDNNRVLK 81
CAH1 MACMU [P00916] -----YNPATAKEIVNVGHSFHVVFEDDNNRVLK 81
CAH1 HORSE [P00917] -----YDPAATAKEIVNVGHSFQVKFEDSDNRVLK 81
CAH1 RABIT [P07452] -----YNPASAKEIVNVGHSFHVVFEDDSQSVLK 55
CAH1 BOVIN [Q1LZA1] -----YNPATAKEIVNVGHSFHVVFEDSDNRVLK 81
CAH1 SHEEP [P48282] -----YNPATAKEIVNVGHSFHVVFEDSDNRVLK 81
CAH1 MONDO [Q8HY33] -----YNPATAKEIVNVSHNFQVNFEDKDNQSVLK 81
CAH7 HUMAN [P43166] -----YEA CMSLSITNNGHSVQVDFNDDDRVVT 82
CAH7 MOUSE [Q9ERQ8] -----YEA CMSLSITNNGHSVQVDFNDDDRVVT 82
CAH5B RAT [Q66HG6] -----YDPAATCLHIWNNGYSLVEFEDSDTKSVIE 116
CAH5B MOUSE [Q9QZA0] -----YDPAATCLHIWNNGYSLVEFEDSDTKSVIE 116
CAH5B HUMAN [Q9Y2D0] -----YDPAATCLHWNNGYSLVEFEDSDTKSVIK 116
CAH5A RAT [P43165] -----YDAASCRYLWNTGYFFQVEFDDSCDESGIS 115
CAH5A MOUSE [P23589] -----YDAASCRYLWNTGYFFQVEFDDSCDESGIS 110
CAH5A HUMAN [P35218] -----YEAASCLYIWNNGYLFQVEFDDATEASGIS 116
CAH8 RAT [Q5PPN4] -----YVVCRDCEVTNDGHTIQVILKS---KSVLS 100
CAH8 HUMAN [P35219] -----YVVCRDCEVTNDGHTIQVILKS---KSVLS 100
CAH8 MOUSE [P28651] -----YVVCRDCEVTNDGHTIQVILKS---KSVLS 101
CAH10 PONAB [Q5R4U0] -----RKVSGTMYNTGRHVSLRLDK---EHLVNIS 118
CAH10 MOUSE [P61215] -----RKVSGTMYNTGRHVSLRLDK---EHLVNIS 118
CAH10 MACFA [Q9N085] -----RKVSGTMYNTGRHVSLRLDK---EHLVNIS 118
CAH10 HUMAN [Q9NS85] -----RKVSGTMYNTGRHVSLRLDK---EHLVNIS 118
CAH10 BOVIN [A0JN41] -----RKVSGTMYNTGRHVSLRLDK---EHLVNIS 118
CAH11 HUMAN [O75493] -----EKLRGTYLNTGRHVSFLPAP---RPVVNVS 120
CAH11 PONAB [Q5R665] -----EKLRGTYLNTGRHVSFLPAP---RPVVNVS 120
CAH11 BOVIN [Q866X7] -----EKLRGTYLNTGRHVSFLPAP---RPVVNVS 120
CAH11 SHEEP [Q95203] -----EKLRGTYLNTGRHVSFLPAP---RPVVNVS 120
CAH11 MOUSE [O70354] -----EKLRGTYLNTGRHVSFLPAS---RPVVNVS 120
CAH11 PIG [Q866X6] -----EKLRGTYLNTGRHVSFLPAP---RPVVNVS 120
CAH1 CAEEL [Q20781] -----LKLMLRYIFTCAHLFACNKKLGTWNRIFGANIAKFRAMVVYLIIFHAQVPLQVVEFVNTGQMVRRIRIGYSSKKPSVNTIT 174
CAH2 CAEEL [Q18932] -----IIVEAVFENTGQLPVVTVKDLNRPPTTINT 89
CAHH VACW [P04195] -----YNESKPTTIQNTGKLVRRINFRK---GYIS 53
CAHH VACCT [Q9JFA1] -----YNESKPTTIQNTGKLVRRINFRK---GYIS 53
CAHH VACCA [O57211] -----YNESKPTTIQNTGKLVRRINFRK---GYIS 53
CAHH VACCC [P20508] -----YNESKPTTIQNTGKLVRRINFRK---GYIS 53
CAH1 CHLRE [P20507] -----SVQVINNGHTIQVQWTYNYAGHAI 128
CAH2 CHLRE [P24258] -----SVQVINNGHTIQVQWTYNYAGHAI 128
CAH ERWCA [O52538] -----GTQQIINNNGHTIQVNVSS---GNLILL 98
CAH ERWCT [Q6DAJ6] -----GTQQIINNNGHTIQVNVSS---GNLILL 98
CAH KLEPN [O52535] -----GPITLINNNGHTIQAAALKTTADAI 100
CAH NEIGO [Q50940] -----SMVDVENNGHTIQVNYPEG---GNLLTV 107
CAH NOSS1 [P94170] -----LALHLINNNGKIVQVNYQP---GSYLKY 116
CAH15 MOUSE [Q99N23] -----APDPFVWLENDGHTVLLRVNSCQQNCPAI 106
CAH3 CHLRE [A8J4Z8] -----FEKCDVLTGHTMGOVNVFPAGNLAFI 150
NEC3 NICLS [Q84UV8] -----SNATLLNRGHDIMLRLLDDGGYLYKINE 113
CAH_DUNSA [P54212] -----SYQLSEVAINLEQDMQFSFNAPDEDLPQL 146
ruler .....250.....260.....270.....280.....290.....300.....310.....320
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CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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                                     *:..*
CAH3 CAEEL [Q27504] IYGGGLD-----QVYRLVQYHFHWG--ENDNEGSEHLGGRLYPAEHLHVVHQ-----GVED 124
CAH5 CAEEL [Q10462] IQGGGLK-----HRYKLAQPHLHWG--QNDAVGSEHAMGSLHYPAELHLVHVR--GLLKEALSR 158
CAH4 BOVIN [Q95323] IAGGGLS-----TRYQATQLHLHWS--RAMDRGSEHSFDCERFAMEMHIVHEKEKGLSNASQNF 158
CAH4 HUMAN [P22748] ISGGGLF-----AFYQAKQLHLHWS--DLFYKGSSESLDGEHFAMEMHIVHEKEKGRSRNVKAQD 154
CAH4 RABIT [P48283] ISGGGLF-----ARYRATQLHLHWS--QELDRGSEHSLDGERSAMEMHIVHQKETGTSG--NEVQD 158
CAH4 MOUSE [Q64444] IYGGDLF-----ARYEAVQLHLHWS--NGNDNGSEHSIDGRHFAMEMHIVHKK--LTS-----SKED 151
  CAH4 RAT [P48284] IFGGDLF-----TQYKAIQLHLHWS--EESNKGSEHSIDGKHFAEMHVVHKK--MTTGDQVQSD 155
CAH6 HUMAN [P23280] MTVA-DG-----TVYIAQGMHFWGGSASSEISGSEHTVDIRHVIIEHIVHYS--KYSYDIAQDA 155
CAH6 CANFA [Q86500] MMAS-DG-----TBYIAQGMHFWGGSASSEISGSEHTIDGIRFVAEIHIVHYS--KYSYDIAQHE 155
CAH6 SHEEP [P08060] MTTG-DG-----TQYLAQGMHFWGGSASSEISGSEHTVDMGRYVIEHIVHYS--KYSYEAQRE 138
CAH6 BOVIN [P18915] MTTT-DG-----SQYLLAKGMHFWGGSASSEISGSEHTVDMGRYVIEHIVHYS--KYSYEAQNE 150
CAH6 MOUSE [P18761] LETS-DG-----TEFISKAQPHFWGGRDWELSGSEHTIDGIRSIMAHVHFHMK--EYGYENAKDQ 154
CAH9 MOUSE [Q9VHB5] MALG-PG-----QEYRALQLHLHWG--TSDHPGSEHTVNGHRRPAEIHVVHLS--AFSELHVALGR 247
CAH9 HUMAN [P16790] MALG-PG-----REYRALQLHLHWG--AAGRPGSEHTVNGHRRPAEIHVVHLS--AFARVDVALGR 268
CAH12 HUMAN [O43570] IQGL-QS-----RYS-ATQLHLHWGNPNPH-GSEHTVSGQHFAAEHLHIVHYSNDLYPDASTASNK 163
CAH12 MOUSE [Q8CI85] IQGL-QP-----HHYRAEQLHLHWGNRNPNPH-GSEHTVSGKHFAAEHLHIVHYSNDLYPFSTASDK 164
CAH12 RABIT [Q9MZ30] LQGL-PR-----RYT-ATQLHLHWGNRNPNPH-GSEHTVGGQFAAEHLHIVHYSNDLYPDASTASNK 163
CAH14 MOUSE [P9WV76] LGGF-PS-----KYT-AAQLHLHWGQGSLE--GSEHQINSFAAEHLHVHYSYDQSQSYSLSAQAQK 153
CAH14 HUMAN [Q9ULX7] LGGF-PR-----KYV-AAQLHLHWGQKSGSPG-GSEHQINSFAAEHLHIVHYDSDSYSLSAEER 153
CAHZ DANRE [Q92051] GGPITG-----IYRLRQPHFWGSSDDK--GSEHTIAGTKFPCLEHLVHWN--TKYPNFGEAAASK 136
CAH1 CHIHA [P83299] GGPISG-----YRRLKQPHFWGASNDK--GSEHTVAGTKYPAELHLVHWN--TKYPIFGAAASK 135
CAH2 TRIHK [Q8UWA5] GGPISG-----KYRLKQPHFWGASDQK--GSEHTVAGTKYPAELHLVHWN--TKYPIFGAANK 136
CAH2 BOVIN [P00921] DGPLTG-----TYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
CAH2 SHEEP [P00922] DGPLTG-----TYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
CAH2 MOUSE [P00920] GGPISD-----SYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
  CAH2 RAT [P27139] GGPISG-----SYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
CAH2 RABIT [P00919] IQGLEG-----SYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
CAH2 HUMAN [P00918] GGPISD-----TYRLLVQPHFWGSSDDQ--GSEHTVDRKKYAAELHLVHWN--TKYGFDTAAQQ 136
CAH2 CHICK [P07630] GGALDG-----YRRLVQPHFWGSSDQ--GSEHTVGVKVDDELHIVHWN--VKYKFAEALKH 136
CAH3 MOUSE [P16015] GGPISG-----YRRLKQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--PKYPIFGAALKQ 136
  CAH3 RAT [P14141] GGPISG-----YRRLKQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--PKYPIFGAALKQ 136
CAH3 HUMAN [P07451] GGPISG-----YRRLKQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--PKYPIFGAALKQ 136
  CAH3 PIG [Q58184] GGPISG-----AVRLLVQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--SKYNFATALKH 136
CAH3 BOVIN [Q382X4] GGPISG-----YRRLKQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--SKYNFATALKH 136
CAH3 HORSE [P07450] GGPISG-----YRRLKQPHFWGSSDDH--GSEHTVGVKVAEELHLVHWN--PKYPIFGAALKQ 136
CAH13 MOUSE [Q9D6N1] GGPITG-----YRRLKQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH13 HUMAN [Q8N1Q1] GGPITG-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
  CAH1 RAT [P0BNN3] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 MOUSE [P13634] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 PANTR [Q7M317] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 HUMAN [P00915] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 GORGO [Q7M316] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 MACNE [P35217] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 MACMU [P00916] GGPISD-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 HORSE [P00917] DGPLPG-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 RABIT [P07452] GGPISD-----NRYLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 112
CAH1 BOVIN [Q1LZA1] GGPISG-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 SHEEP [P48282] GGPISG-----SYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH1 MONDO [Q8HY33] GGPISG-----SFRLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 138
CAH7 HUMAN [P43166] GGPISG-----YRRLKQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 139
CAH7 MOUSE [Q9ERQ8] GGPISG-----YRRLKQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 139
  CAH5B RAT [Q66H66] GGPISG-----NRYLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 173
CAH5B MOUSE [Q9QZAO] GGPISG-----NRYLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 173
CAH5B HUMAN [Q9Y2D0] GGPISG-----NRYLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 173
  CAH5A RAT [P43165] GGPISG-----HYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 172
CAH5A MOUSE [P23589] GGPISG-----HYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 167
CAH5A HUMAN [P35218] GGPISG-----HYRLLVQPHFWGSSDQ--GSEHTVGVKVAEELHVHWN--SKYPFVAAAE 173
  CAH8 RAT [Q5PPN4] GGPISG-----QEYFELYEVRPHFWGRENQR--GSEHTVNFKAFPMELHLHWNSLTFGSIDAVGK 159
CAH8 HUMAN [P35219] GGPISG-----HEFFELYEVRPHFWGRENQR--GSEHTVNFKAFPMELHLHWNSLTFGSIDAVGK 159
CAH8 MOUSE [P28651] GGPISG-----QEYFELYEVRPHFWGRENQR--GSEHTVNFKAFPMELHLHWNSLTFGSIDAVGK 160
CAH10 PONAB [Q5R4U0] GGPMT-----YSHRLEEIRLHFGESEDQ--GSEHLLNGQAFSGEVQLIHYNHELVTNVTAAKS 175
CAH10 MOUSE [P61215] GGPMT-----YSHRLEEIRLHFGESEDQ--GSEHLLNGQAFSGEVQLIHYNHELVTNVTAAKS 175
CAH10 MACFA [Q9N085] GGPMT-----YSHRLEEIRLHFGESEDQ--GSEHLLNGQAFSGEVQLIHYNHELVTNVTAAKS 175
CAH10 HUMAN [Q9NS85] GGPMT-----YSHRLEEIRLHFGESEDQ--GSEHLLNGQAFSGEVQLIHYNHELVTNVTAAKS 175
CAH10 BOVIN [A0JN41] GGPMT-----YSHRLEEIRLHFGESEDQ--GSEHLLNGQAFSGEVQLIHYNHELVTNVTAAKS 175
CAH11 HUMAN [O75493] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
CAH11 PONAB [Q5R665] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
CAH11 BOVIN [Q86627] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
CAH11 SHEEP [Q95203] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
CAH11 MOUSE [O70354] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
  CAH11 PIG [Q86626] GGPILL-----YSHRLESELRLFGARDGA--GSEHQINHGQFSAEVQLIHFQELYGNLSAASRG 177
CAH1 CAEEL [Q20781] GGPLYG-----YRIRVQRIDFHMGRKNEN--GSEHTINGRRFPMELVQLVAYNTDLYPNFTSAKS 232
CAH2 CAEEL [Q18932] GGPIMP-----YRKLHLIVHFGRADEGEKGS--GSEHTVDRVRFPAEIQLLAYNSALYPNFVAMTS 149
CAHH VACCW [P04195] GGPILPN-----EYVLSSLIHYWGKEDDY--GSEHLLDVKVYSGEINLVHWNKKKYSYBAKKH 110
CAHH VACCT [Q9JFA1] GGPILPN-----EYVLSSLIHYWGKEDDY--GSEHLLDVKVYSGEINLVHWNKKKYSYBAKKH 110
CAHH VACCA [O57211] GGPILPN-----EYVLSSLIHYWGKEDDY--GSEHLLDVKVYSGEINLVHWNKKKYSYBAKKH 110
CAHH VACCC [P20508] GGPILPN-----EYVLSSLIHYWGKEDDY--GSEHLLDVKVYSGEINLVHWNKKKYSYBAKKH 110
CAH1 CHLRE [P20507] AIPAMRNQNRIIVDVLMPNDASDRVAVTQPHFST--SEELLAGKIFPLELHIVHVKVTDLEACKGGCCFS 200
CAH2 CHLRE [P24258] AIPAMRNQNRIIVDVLMPNDASDRVAVTQPHFST--SEELLAGKIFPLELHIVHVKVTDLEACKGGCCFS 200
CAH ERWCA [O52538] DN-----ETFTLQCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 139
CAH ERWCT [Q6DAJ6] DN-----ETFTLQCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 139
CAH KLEPN [O52535] DG-----TFFLLQCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 141
CAH NEIGO [Q50940] NG-----RTYVTLKCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 148
CAH NOSS1 [P94170] AH-----QKFFLLQCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 157
CAH15 MOUSE [Q99N23] GQAGLPS-----PEYRLLQLHFWGSGPHQ--GSEHLLDVKVYSGEINLVHWNKKKYSYBAKKH 164
CAH3 CHLRE [A8J4Z8] GN-----MELELLCFHFWAP--SENEIDGKQFPLEGHFVYK--ADGALT 187
NEC3 NICLS [Q84UV8] T-----TQYKQLQLHFWHT--SENEIDGKQFPLEGHFVYK--ADGALT 147
CAH DUNSA [P54212] TIIGVVH-----TFKFFVQLHFWHT--SENEIDGKQFPLEGHFVYK--ADGALT 190
ruler .....330.....340.....350.....360.....370.....380.....390.....400
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CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

CAH3 CAEEL [Q27504]	IWTIFTEPVVTHDQLELFRQVODIEKRFI	225
CAH5 CAEEL [Q10462]	IWTVLAEPMATISHLHLLRQLHNKELVKS	261
CAH4 BOVIN [Q95323]	VMTVFQKPIQLHRDQILAFSOKLFYDDQK	263
CAH4 HUMAN [P22748]	VMTVFRFPIQLHREQILAFSOKLYYDKEIT	263
CAH4 RABIT [P48283]	VMTVFOEPIRLHRDQILAFSSKLYYDEK	259
CAH4 MOUSE [Q64444]	IWTVYKQPIKIHKNQFLFESKNLYYDEQK	256
CAH4 RAT [P48284]	IWTVFEKPIKIHKNQFLFESKLYYDEQK	260
CAH6 HUMAN [P23280]	HWFVLADFVKLSRTQVWKLNSLLDHRNK	257
CAH6 CANFA [Q865C0]	HWFVLVHHVRLSIOQVWKLNSLLDHNK	257
CAH6 SHEEP [P08060]	HWFVVDTVKLSKTOVEKLENSLLNHONK	240
CAH6 BOVIN [P18915]	HWFVVDTVKLSKTOIEKLENSLLNHONK	252
CAH6 MOUSE [P18761]	QWFLVLRDRVTLKSAQVVTIENSVMDDHNN	256
CAH9 MOUSE [Q8VHB5]	IWTVFNEIVKLSAKQLHTLSVSLWGPGRDS	348
CAH9 HUMAN [Q16790]	IWTVFNEIVMLSAKQLHTLSVSLWGPGRDS	369
CAH12 HUMAN [O43570]	LWTVFRNPVQISQEQLLALETALYCTHMDDPSP	267
CAH12 MOUSE [Q8CI85]	LWTVFRNPVQISQEQLLALETALYFTHMDDPTP	268
CAH12 RABIT [Q9MZ30]	LWTVFRNPVTISQEQLLALCTALYFTRADDPA	267
CAH14 MOUSE [Q9VWT6]	LWTVFNRRQISMGLEKLEQLSSTEDDPSEP	258
CAH14 HUMAN [Q9ULX7]	LWTVFYRRSQISMGLEKLEQLFSTEEEPKSL	258
CAHZ DANRE [Q92051]	IWTVLKEPISVSPAQMAKFRSLLFSSEGETPCC	239
CAH1 CHIHA [P83299]	IWTVCKEPISVSCEQMAKFRSLLFSAEGEPCC	238
CAH2 TRIHK [Q8UWA5]	IWTVCKQPISVSSEOMKFRSLLFTAEEKACC	239
CAH2 BOVIN [P00921]	IWTVLKEPISVSSQMLKFRSLNFNNAEGEPPELL	239
CAH2 SHEEP [P00922]	IWTVLKEPISVSSQMLKFRSLNFNNAEGEPPELL	239
CAH2 MOUSE [P00920]	IWTVLREPTIVSSEOMSHFRSLNFNNEEGDAEEA	239
CAH2 RAT [P27139]	IWTVLKEPITVSEOMSHFRSLNFNSEGEAEEL	239
CAH2 RABIT [P00919]	IWTVLKEPITVSEOMKFRSLNFNKAEPEEP	239
CAH2 HUMAN [P00918]	IWTVLKEPISVSEQVLKFRSLNFNSEGEPEEL	239
CAH2 CHICK [P07630]	IWTVLKEPITVSEOMCKLRGLCFSAENEPVCR	239
CAH3 MOUSE [P16015]	VWLLLKEPMTVSDQMAKLRSLFSAENEPVVP	239
CAH3 RAT [P14141]	VWLLLKEPMTVSDQMAKLRSLFSAENEPVVP	239
CAH3 HUMAN [P07451]	VWLLLKEPMTVSDQMAKLRSLFSAENEPVVP	239
CAH3 PIG [Q58184]	VWLLLKEPITVSDQMAKLRSLYSAENEPVVP	239
CAH3 BOVIN [Q38ZX4]	VWLLLKEPITVSDQIAKLRSLYSAENEPVVP	239
CAH3 HORSE [P07450]	VWLLLKEPITVSDQVAKLRSLFSAENEPVVP	239
CAH13 MOUSE [Q9D6N1]	IWTVLKEPISVSSQQLARFRSLLCTAEGESAAF	241
CAH13 HUMAN [Q8N1Q1]	IWTVLKEPISVSSQQLAKFRSLLCTAEGESAAF	241
CAH1 RAT [B0BNN3]	IWTVICKESISLSPQOLAQLRGLLSSAEGEPAVP	241
CAH1 MOUSE [P13634]	IWTVICKDSISLSPQOLAQLRGLLSSAEGESAVP	241
CAH1 PANTR [Q7M317]	IWTVICKESISVSEOLAQFRSLLSNVGDNAVP	241
CAH1 HUMAN [P00915]	IWTVICKESISVSEOLAQFRSLLSNVGDNAVP	241
CAH1 GORGO [Q7M316]	IWTVICKESISVSEOLAQFRSLLSNVGDNAVP	241
CAH1 MACNE [P35217]	IWTVICKESISVSEOLAQFRSLLSNVGDNPVP	241
CAH1 MACMU [P00916]	IWTVICKESISVSEOLAQFRSLLSNVGSNPVP	241
CAH1 HORSE [P00917]	IWTVICKENISVSSQQLSQFRSLLSNVGGKAVP	241
CAH1 RABIT [P07452]	IWTVICKDSISVSEOLAQFRSLLSNAEGEAAVP	215
CAH1 BOVIN [Q1LZA1]	IWTVIFKETISVSEOLAQFRSLLANAEGDREVV	241
CAH1 SHEEP [P48282]	IWTVIFKETISVSAEOLAQFRSLLANAEGDKEVC	241
CAH1 MONDO [Q8HY33]	IWTVIYREPIASSEOLAQFRSLLSTAEGEKASS	241
CAH7 HUMAN [P43166]	IWTVILREPICTISEROMGKFRSLLFTSEDDERIH	242
CAH7 MOUSE [Q9ERQ8]	IWTVILREPIRISEROMEKFRSLLFTSEDDERIH	242
CAH5B RAT [Q66HG6]	IWTVIKKQVPEVDHDDLEQFRTLLFTSEGEKEKR	276
CAH5B MOUSE [Q9QZA0]	IWTVIKKQVPEVDRDQLEQFRTLLFTSEGEKEKR	276
CAH5B HUMAN [Q9Y2D0]	IWTVIKKQVPEVDHDDLEQFRTLLFTSEGEKEKR	276
CAH5A RAT [P43165]	IWTVIVHKMPIEVSQSLSTFRLLFSGRGDEEV	275
CAH5A MOUSE [P23589]	IWTVIQKTPVEVSPSOLSTFRLLFSGRGDEEDV	270
CAH5A HUMAN [P35218]	IWTVIQKEPVEVAPPSOLSAFRTLLFSALGEEBKM	276
CAH8 RAT [Q5PPN4]	IWTVILFRYPLTISQLOIEEFRRRLRTHVKGAEIVGCD	267
CAH8 HUMAN [P35219]	IWTVILFRYPLTISQLOIEEFRRRLRTHVKGAEIVGCD	267
CAH8 MOUSE [P28651]	IWTVILFRYPLTISQMOIEEFRRRLRTHVKGAEIVGCD	268
CAH10 PONAB [Q5R4U0]	SWIIMNKPVYITRMOMHSLRLLSQNPSPQIFLS	281
CAH10 MOUSE [P61215]	SWIIMNKPVYITRMOMHSLRLLSQNPSPQIFLS	281
CAH10 MACFA [Q9N085]	SWIIMNKPVYITRMOMHSLRLLSQNPSPQIFLS	281
CAH10 HUMAN [Q9NS85]	SWIIMNKPVYITRMOMHSLRLLSQNPSPQIFLS	281
CAH10 BOVIN [A0JN41]	NWIIIMNKPVYITRMOMHSLRLLSQNPSPQIFLS	281
CAH11 HUMAN [O75493]	TWILIDRALNITSLQMHSRLLSQNPSPQIFQS	283
CAH11 PONAB [Q5R665]	TWILIDRALNITSLQMHSRLLSQNPSPQIFRS	283
CAH11 BOVIN [Q866X7]	TWILIDRALNITSLQMHSRLLSQNPSPQIFQS	283
CAH11 SHEEP [Q95203]	TWILIDRALNITSLQMHSRLLSQNPSPQIFQS	283
CAH11 MOUSE [O70354]	TWILIDRALNITSLQMHSRLLSQNPSPQIFQS	283
CAH11 PIG [Q866X6]	TWILIDRALNITSLQMHSRLLSQNPSPQIFQS	286
CAH1 CAEEL [Q20781]	IWTVILNLPPIPIKKEHFEEWSHLYLSMSEGAEKVY	336
CAH2 CAEEL [Q18932]	IWTVILNLPPIYIINDDLQIWNEMQKTETKQPEPSY	254
CAHH VACW [P04195]	VWIIFFPTPINIHSDDLSKFRLLSSSNHDGKPHY	214
CAHH VACCT [Q9JFA1]	VWIIFFPTPINIHSDDLSKFRLLSSSNHGGKPHY	214
CAHH VACCA [O57211]	VWIIFFPTPINIHSDDLSKFRLLSSSNHDGKPHY	214
CAHH VACCC [P20508]	VWIIFFPTPINIHSDDLSKFRLLSSSNHDGKPHY	214
CAH1 CHLRE [P20507]	LWHVMTQPRISFGQWNRRLAVGLKECNSTETAADAG	344
CAH2 CHLRE [P24258]	LWHVMTQPRISFGQWNRRLAVGEKCNSTETAADAG	348
CAH ERWCA [O52538]	RWLVLDHPVTASAEQISQFSSVMHH	228
CAH ERWCT [Q6DAJ6]	RWLVLDHPVTASAEQINQFSSVMHH	228
CAH KLEPN [O52535]	TRIVLKHPLTISAOAKFESHAMHH	230
CAH NEIGO [Q50940]	SWLVLTQYDHIDQAAEKFTRAVGS	236
CAH NOSS1 [P94170]	LWCVMATPIEASPAQIAKFSQMPF	246
CAH15 MOUSE [Q99N23]	LWTVFENTVPIGHAQVQFOAVLQTGPPGLHPRF	273
CAH3 CHLRE [A8J4Z8]	DWVFVMPQIKVPDQILDPMFRVGDNKT	290
NEC3 NICLS [Q84UV8]	VWIIDRKVKTVTRRQIKLLQEAHVHDG	245
CAH_DUNSA [P54212]	KWVVFKEARTVSAQVKVSEVTLAAHPBATVT	298
ruler490.....500.....510.....520.....530.....540.....550.....560	



CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

Accession	Species	Residue	Position
CAH3	CABEL	[Q27504]	246
CAH5	CABEL	[Q10462]	310
CAH4	BOVIN	[Q95323]	312
CAH4	HUMAN	[P22748]	312
CAH4	RABIT	[P48283]	308
CAH4	MOUSE	[Q64444]	305
CAH4	RAT	[P48284]	309
CAH6	HUMAN	[P23280]	306
CAH6	CANFA	[Q865C0]	305
CAH6	SHEEP	[P08060]	292
CAH6	BOVIN	[P18915]	304
CAH6	MOUSE	[P18761]	304
CAH9	MOUSE	[Q8VHB5]	415
CAH9	HUMAN	[Q16790]	439
CAH12	HUMAN	[Q43570]	331
CAH12	MOUSE	[Q8C185]	331
CAH12	RABIT	[Q9MZ30]	331
CAH14	MOUSE	[Q9WVT6]	315
CAH14	HUMAN	[Q9LXK7]	315
CAHZ	DANRE	[Q92051]	260
CAH1	CHHA	[P83299]	259
CAH2	TRHK	[Q8UWA5]	260
CAH2	BOVIN	[P00921]	260
CAH2	SHEEP	[P00922]	260
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CAH1	MACNE	[P35217]	261
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CAH1	HORSE	[P00917]	261
CAH1	RABIT	[P07452]	235
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CAH1	MONDO	[Q8HY33]	262
CAH7	HUMAN	[P43166]	264
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CAH15	MOUSE	[Q99N23]	324
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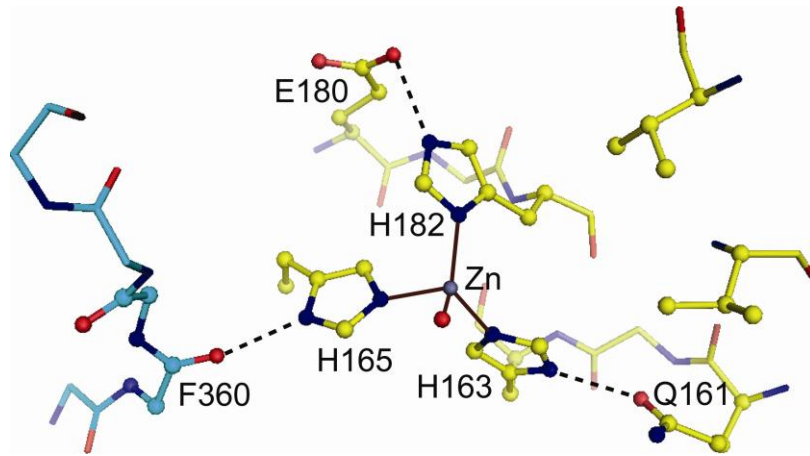
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CAHH VACCT [Q9JFA1]	-----	304
CAHH VACCA [O57211]	-----	304
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CAH1 CHLRE [P20507]	-----	377
CAH2 CHLRE [P24258]	-----	380
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CAH ERWCT [Q6DAJ6]	-----	244
CAH KLEPN [O52535]	-----	246
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CAH NOSS1 [P94170]	-----	264
CAH15 MOUSE [Q99N23]	-----	324
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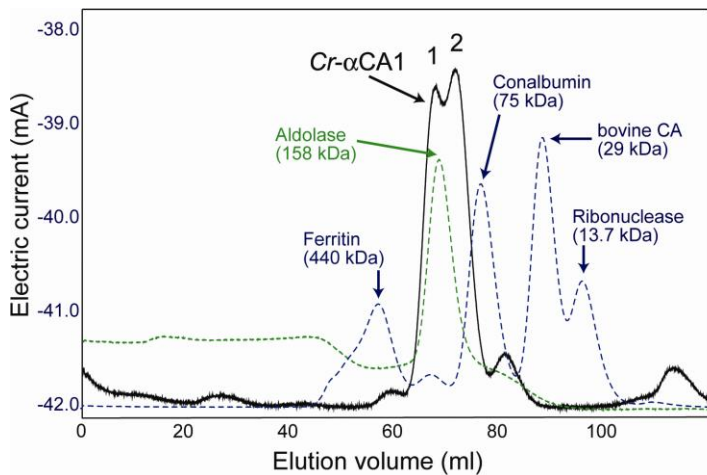
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CAH2 CHLRE [P24258]	-----	380
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CAH ERWCT [Q6DAJ6]	-----	244
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CAH NOSS1 [P94170]	-----	264
CAH15 MOUSE [Q99N23]	-----	324
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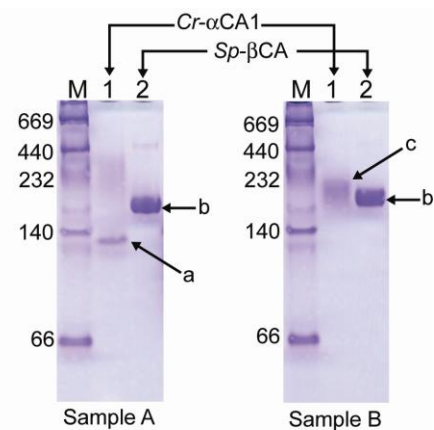
Supplementary Figure 2. *ClustalX* multiple sequence alignment.



Supplementary Figure 3. Three histidine residues capture a zinc atom to form the active site of Cr- CA1. Furthermore, the two histidine residues, H163 and H182, are supported by hydrogen bonds with the surrounding residues, Q161 and E180. The third histidine residue H165 is supported by a hydrogen bond with the carbonyl oxygen atom of F360 on the short peptide.



(a)



(b)

Supplementary Figure 4. A chromatogram of the gel-filtration step (a) and native-PAGE (b) of the purified *Cr*-CA1. In (a), Peaks (1) and (2) correspond to the molecular sizes of a dimer of the dimeric enzymes (159.2 kDa) and a single dimeric enzyme (79.6 kDa), respectively. In (b), lanes labeled M indicate the molecular-weight markers. Lanes 1 and 2 are for *Cr*-CA1 and for spinach CA, respectively. Arrows a, b and c indicate the bands for a dimer of the dimeric enzyme *Cr*-CA1 (159.2 kDa), an octamer of spinach CA (212kDa) and a trimer of the dimeric enzyme *Cr*-CA1 (238.8kDa), respectively. Sample A is *Cr*-CA1 just after purification and Sample B is Sample A that was stored for three months at 277 K. The difference observed in lane 1 between the two samples suggests that dimers of *Cr*-CA1 can form higher order oligomers