Figure 1

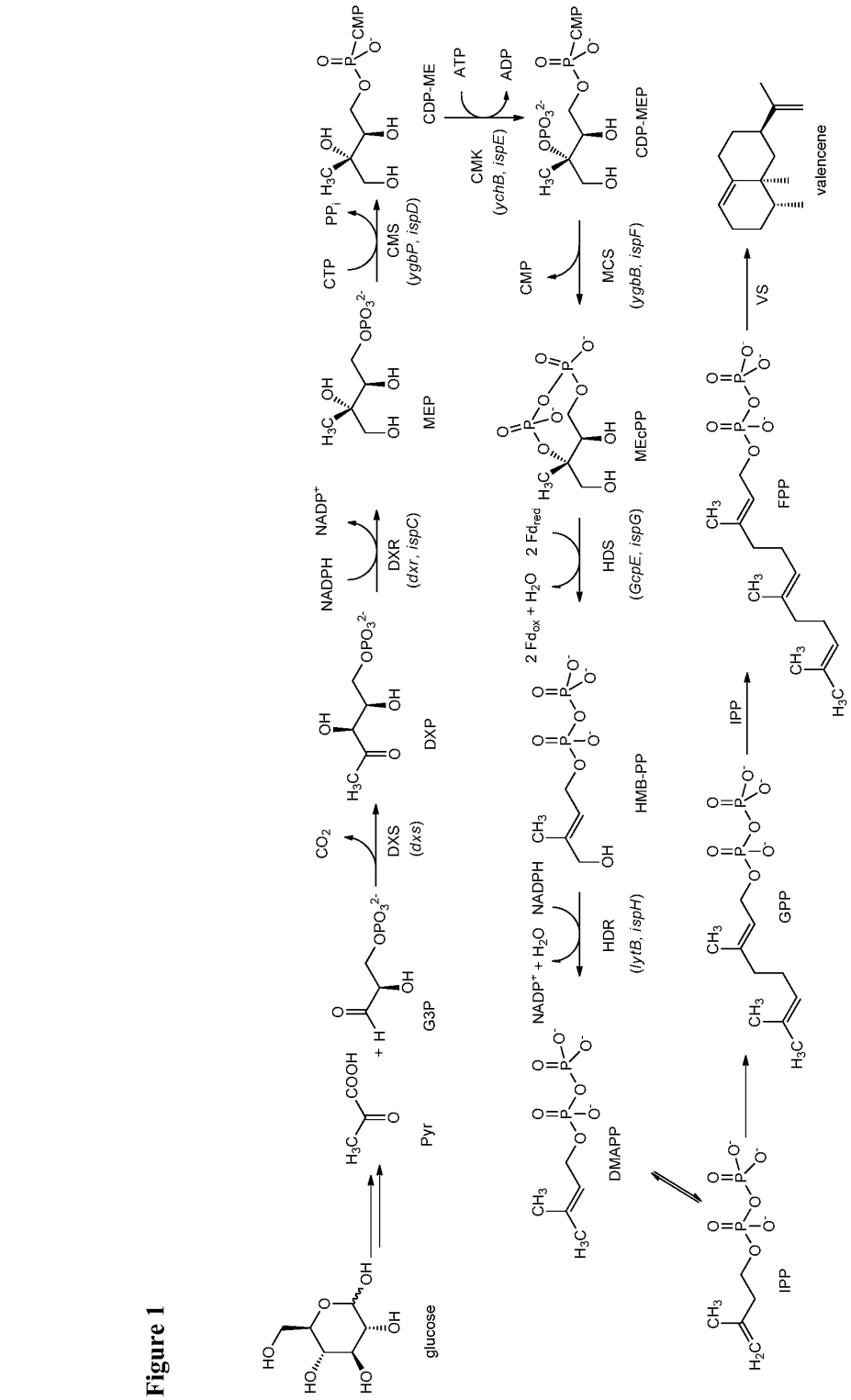

glucose
Pyr
G3P
DXS
(dxs)
DXP
DXR
(dxr, ispC)
MEP
CMS
(ygbP, ispD)
CDP-ME
CMK
(ychB, ispE)
CDP-MEP
MCS
(ygbB, ispF)
MEcPP
HDS
(GcpE, ispG)
HMB-PP
HDR
(lytB, ispH)
DMAPP
IPP
GPP
FPP
VS
valencene
ATP
ADP
CTP
PPi
CMP
NADPH
NADP+
CO2
NADP+ + H2O
2 Fdox + H2O
2 Fdred

Figure 2

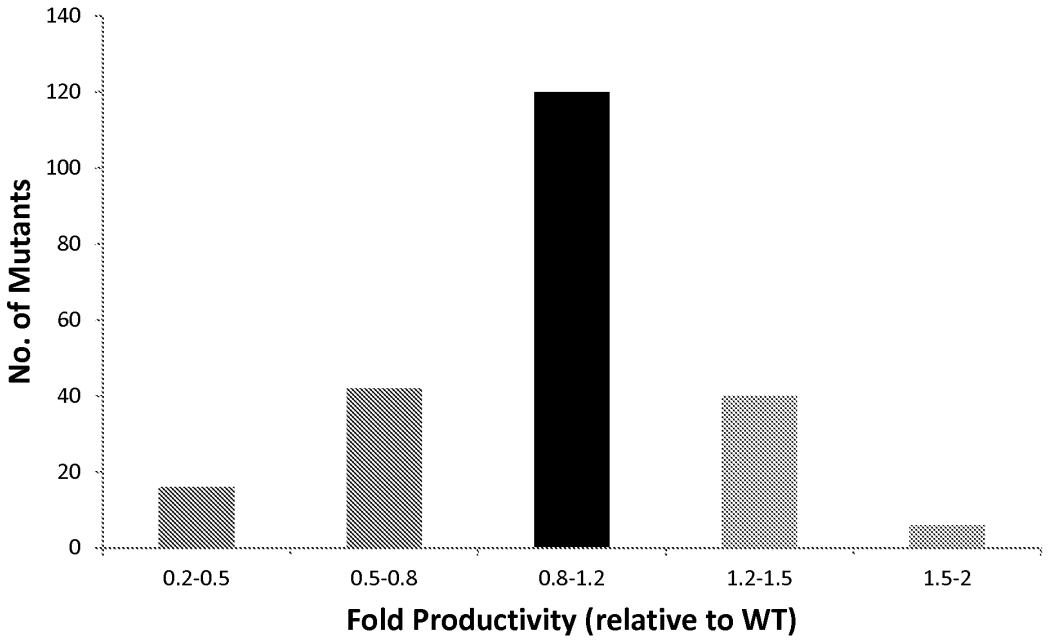

140
120
100
80
60
40
20
0
No. of Mutants
0.2-0.5
0.5-0.8
0.8-1.2
1.2-1.5
1.5-2
Fold Productivity (relative to WT)

Figure 3A

>VvVS [Vitis vinifera]

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TGATCTCAGACGTTCGTGGCATGCTGGGTCTGTATGAAGCTGCGCATCTGCGCGTCCACGGCGA
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TACTTTGCAGAAGCTAAATGGCTGCATGAAGAACACGTGCCGGCGTTCGAAGAATATATGCGCG
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TATCTAA (SEQ ID NO: 2)

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ELKLFIEAIEKWDESSINQLPEYMKLCFVALIDVYNEIEEEMEKEGNQYRIHYLKEVMKNQVRA
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TTCGTGGGTATGGGCGAGATCGTGACCAAAGAGGCATTCGACTGGGTGACGAGCGACCCGAAG
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CAGAAACGCGGTCACGTTACCAGCGCCGTGGAGTGCTACATGAAGCAGTACGGCGTGACAGAG
GAGCAAGTGTACAGCGAGTTCAAGAAACAAATCGAGAACGCCTGGCTGGACATCAACCAAGAG
TGCCTGAAACCGACCGCAGTGCCGATGCCTCTGTTAGCCCGTCTGCTGAATTTCACACGCACG
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ATCGCCAGTGTGTTCATCAACCCGGTGATCTAA (SEQ ID NO: 4)

>Vv2M1 | engineered valencene synthase

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GATCTAA (SEQ ID NO: 6)

>Vv1M5 | engineered valencene synthase

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ELKLFIEAIEKWDESSINQLPEYMKLCFVALIDVYNEIEEEMEKEGNQYRIHYLKEVMKNQVRA
YFAEAKWLHDEHVPAFEEYMRVALASSGYCLLAVTSFVGMGEIVTKEAFDWVTSDPKLMSSSNT
ITRLMDDIKSHKFEQKRGHVTSAVECYMKQYGVTEEQVYSEFKKQIENAWLDINQECLKPTAVP
MPLLARLLNFTRTMDVIYKEEDSYTHVGKVMRDNIASVFINPVI (SEQ ID NO: 7)

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GAGTTAAAGCTGTTCATCGAGGCAATCGAGAAGTGGGATGAGAGTAGCATCAACCAACTGCCGG
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GATCTAA (SEQ ID NO: 8)

>Vv2M5 | engineered valencene synthase

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GATCTAA (SEQ ID NO: 10)

>VS2 | engineered valencene synthase

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GYHLAEQVAHALNRPIRKGLERLEARWYISVYQDEAFHDKTLLELAKLDFNLVQSLHKEELSNL
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>CsVS | Citrus sinensus valencene synthase

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QRWNIEAVDMLPEYMKLIYRTLLDAFNEIEEDMAKQGRSHCVRYAKEENQKVIGAYSVQAKWFS

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Figure 3B

```
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VS2         MATQVSASSLAQIPQPKNRPVANFHPNIWGDQFITYTPEDK-VTRAKKEEQIEDLKKEVK 59
VvVS        MSTQVSASSLAQIPQPKNRPVANFHPNIWGDQFITYTPEDK-VTRACKEEQIEDLKKEVK 59
CsVS        MASGETF-----------RPTADFHPSLWRNHFLKGASDFKTVDHTATQERHEALKEEVR 49
            *::  :            **.*:***.:* ::*:. :.: * * :: .:*: * **:**:

Vv2M5       RKLTAAAVANPSQLLNFIDAVQRLGVAYHFEQEIEEALQHICNSFHDCNDMDGDLYNIAL 119
VS2         RKLTAAAVANPSQLLNFIDAVQRLGVAYHFEQEIEEALQHICNSFHDCNDMDGDLYNIAL 119
VvVS        RKLTAAAVANPSQLLNFIDAVQRLGVAYHFEQEIEEALQHICNSFHDCNDMDGDLYNIAL 119
CsVS        RMITDAEDK-PVQKLRLIDEVQRLGVAYHFEKEIGDAIQKLCPIYIDSNRAD--LHTVSL 106
            * :* *    * * *.:** **********:** :*:*::*  : *.*  *  *:.::*

Vv2M5       GFRLLRQQGYTISCDIFNKFTDERGRFKEALISDVRGMLGLYEAAHLRVHGEDILAKALA 179
VS2         GFRLLRQQGYTISCDIFNKFTDERGRFKEALISDVRGMLGLYEAAHLRVHGEDILAKALA 179
VvVS        GFRLLRQQGYTISCDIFNKFTDERGRFKEALISDVRGMLGLYEAAHLRVHGEDILAKALA 179
CsVS        HFRLLRQQGIKISCDVFEKFKDDEGRFKSSLINDVQGMLSLYEAAYMAVRGEHILDEAIA 166
             ******** .****:*:**.*:.****.:**.**:***.*****:: *:**.** :*:*

Vv2M5       FTTTHLKAMVES--LGYHLAEQVAHALNRPIRKGLERLEARWYISVY--QDEAFHDKTLL 235
VS2         FTTTHLKAMVES--LGYHLAEQVAHALNRPIRKGLERLEARWYISVY--QDEAFHDKTLL 235
VvVS        FTTTHLKAMVES--LGYHLAEQVAHALNRPIRKGLERLEARWYISVY--QDEAFHDKTLL 235
CsVS        FTTTHLKSLVAQDHVTPKLAEQINHALYRPLRKTLPRLEARYFMSMINSTSDHLCNKTLL 226
            *******::* .  :  :****: *** **:** * *****:::*:    .: : :****

Vv2M5       ELAKLDFNLVQSLHKEELSNLARWWKELDFATKLPFARDRLVEGYFWMMGVYFEPQYLRG 295
VS2         ELAKLDFNLVQSLHKEELSNLARWWKELDFATKLPFARDRLVEGYFWMMGVYFEPQYLRG 295
VvVS        ELAKLDFNLVQSLHKEELSNLARWWKELDFATKLPFARDRLVEGYFWMHGVYFEPQYLRG 295
CsVS        NFAKLDFNILLELHKEELNELTKWWKDLDFTTKLPYARDRLVELYFWDLGTYFEPQYAFG 286
            ::******:: .******.:*::***:***:****:******* ***  *.******  *

Vv2M5       RRILTKVIALTSILDDIHDAYGTPEELKLFIEAIEKWDESSINQLPEYMKLCYVALLDVY 355
VS2         RRILTKVIALTSILDDIHDAYGTPEELKLFIEAIEKWDESSINQLPEYMKLCYVALLDVY 355
VvVS        RRILTKVIAMTSILDDIHDAYGTPEELKLFIEAIERWDINSINQLPEYMKLCYVALLDVY 355
CsVS        RKIMTQLNYILSIIDDTYDAYGTLEELSLFTEAVQRWNIEAVDMLPEYMKLIYRTLLDAF 346
            *:*:*::  : **:** :***** ***.** **:::*: .::: ******* * :***.:

Vv2M5       NEIEEEMEKEGNQYRIHYLKEVMKNQVRAYFAEAKWLHDEHVPAFEEYMRVALASSGYCL 415
VS2         NEIEEEMEKEGNQYRIHYLKEVMKNQVRAYFAEAKWLHDEHVPAFEEYMRVALASSGYCL 415
VvVS        KEIEEEMEKEGNQYRVHYAKEVMKNQVRAYFAEAKWLHEEHVPAFEEYMRVALASSGYCL 415
CsVS        NEIEEDMAKQGRSHCVRYAKEENQKVIGAYSVQAKWFSEGYVPTIEEYMPIALTSCAYTF 406
            :****:* *:*.:: ::* **  :: : ** .:***: : :**::**** :**:*..* :

Vv2M5       LAVTSFVGMGEIVTKEAFDWVTSDPRIMSSSNTITRLMDDIKSHKFEQKRGHVTSAVECY 475
VS2         LAVTSFVGMGEIVTKEAFDWVTSDPRIMSSSNTITRLMDDIKSHKFEQKRGHVTSAVECY 475
VvVS        LATTSFVGMGEIATKEAFDWVTSDPKIMSSSNFITRLMDDIKSHKFEQKRGHVTSAVECY 475
CsVS        VITNSFLGMGDFATKEVFEWISNNPKVVKAASVICRLMDDMQGHEFEQKRGHVASAIECY 466
            : ..**:***::.***.*:*::.:*:::.::. * *****::.*:*********:**:***

Vv2M5       MKQYAVTEEQVYSEFKKQIENAWLDINQEC-LKPTAVPMPLLARLLNFTRTMDVIYKEED 534
VS2         MKQYAVTEEQVYSEFKKQIENAWLDINQEC-LKPTAVPMPLLARLLNFTRTMDVIYKEED 534
VvVS        MKQYGVSEEQVYSEFQKQIENAWLDINQEC-LKPTAVSMPLLARLLNFTRTMDVIYKEQD 534
CsVS        TKQHGVSKEEAIKMFEEEVANAWKDINEELMMKPTVVARPLLGTILNLARAIDFIYKEDD 526
             **:.*::*:. . *:::: *** ***:*  :***.*. ***. :**::*::*.****:*

Vv2M5       SYTHVGKTMRDNIASVFINPVI- 556
VS2         SYTHVGKTMRDNIASVFINPVI- 556
VvVS        SYTHVGKVMRDNIASVFINAVI- 556
CsVS        GYTHS-YLIKDQIASVLGDHVPF 548
            .***    ::*:****: : *
```

Figure 4A

>ZzHO [Zingiber zerumbet]

MEAISLFSPFFFITLFLGFFITLLIKRSSRSSVHKQQVLLASLPPSPPRLPLIGNIHQLVGGNPHR
ILLQLARTHGPLICLRLGQVDQVVASSVEAVEEIIKRHDLKFADRPRDLTFSRIFFYDGNAVVMTP
YGGEWKQMRKIYAMELLNSRRVKSFAAIREDVARKLTGEIAHKAFAQTPVINLSEMVMSMINAIVI
RVAFGDKCKQQAYFLHLVKEAMSYVSSFSVADMYPSLKFLDTLTGLKSKLEGVHGKLDKVFDEIIA
QRQAALAAEQAEEDLIIDVLLKLKDEGNQEFPITYTSVKAIVMEIFLAGTETSSSVIDWVMSELIK
NPKAMEKVQKEMREAMQGKTKLEESDIPKFSYLNLVIKETLRLHPPGPLLFPRECRETCEVMGYRV
PAGARLLINAFALSRDEKYWGSDAESFKPERFEGISVDFKGSNFEFMPFGAGRRICPGMTFGISSV
EVALAHLLFHFDWQLPQGMKIEDLDMMEVSGMSATRRSPLLVLAKLIIPLP (SEQ ID No: 13 | Wild Type)

MALLLAVFFFFITLFLGFFITLLIKRS*SR*SSVHKQQVLLASLPPSPPRLPLIGNIHQLVGGNPHRI
LLQLARTHGPLICLRLGQVDQVVASSVEAVEEIIKRHDLKFADRPRDLTF*SR*IFFYDGNAVVMTPY
GGEWKQMRKIYAMELLN*SR*RVKSFAAIREDVARKLTGEIAHKAFAQTPVINLSEMVMSMINAIVIR
VAFGDKCKQQAYFLHLVKEAMSYVSSFSVADMYPSLKFLDTLTGLKSKLEGVHGKLDKVFDEIIAQ
RQAALAAEQAEEDLIIDVLLKLKDEGNQEFPITYTSVKAIVMEIFLAGTETSSSVIDWVMSELIKN
PKAMEKVQKEMREAMQGKTKLEESDIPKFSYLNLVIKETLRLHPPGPLLFPRECRETCEVMGYRVP
AGARLLINAFAL*SR*DEKYWGSDAESFKPERFEGISVDFKGSNFEFMPFGAGRRICPGMTFGISSVE
VALAHLLFHFDWQLPQGMKIEDLDMMEVSGMSATRRSPLLVLAKLIIPLP (SEQ ID NO: 14)

ATGGCTCTGTTATTAGCAGTGTTCTTCTTTTTCATTACGCTGTTTCTGGGTTTCTTTATTACGCTG
CTGATTAAACGCTCGTCCCGTAGCTCTGTCCATAAACAGCAAGTGCTGCTGGCCTCTCTGCCGCCG
AGTCCGCCGCGCCTGCCGCTGATTGGCAACATCCATCAACTGGTGGGCGGCAACCCGCATCGTATT
CTGCTGCAACTGGCGCGTACCCACGGCCCGCTGATCTGCCTGCGTCTGGGTCAGGTTGATCAAGTG
GTTGCAAGTTCCGTGGAAGCTGTTGAAGAAATTATCAAACGTCACGACCTGAAATTTGCAGATCGT
CCGCGCGACCTGACCTTTAGCCGTATTTTCTTTTATGATGGTAACGCTGTCGTGATGACGCCGTAC
GGCGGTGAATGGAAACAGATGCGTAAAATCTATGCAATGGAACTGCTGAACAGCCGTCGTGTGAAA
TCTTTTGCGGCCATTCGTGAAGACGTTGCACGCAAACTGACCGGCGAAATCGCTCACAAAGCATTC
GCTCAGACGCCGGTCATTAACCTGTCTGAAATGGTGATGAGTATGATCAATGCGATTGTCATCCGC
GTGGCCTTTGGTGATAAATGTAAACAGCAAGCATACTTCCTGCATCTGGTGAAAGAAGCTATGTCC
TATGTTTCATCGTTTTCAGTCGCGGATATGTACCCGTCCCTGAAATTCCTGGACACCCTGACGGGC
CTGAAAAGCAAACTGGAAGGCGTTCACGGTAAACTGGATAAAGTCTTCGACGAAATCATCGCACAG
CGTCAAGCAGCGCTGGCGGCGGAACAGGCTGAAGAAGATCTGATTATCGACGTGCTGCTGAAACTG
AAAGATGAAGGCAACCAGGAATTTCCGATTACCTATACGTCAGTTAAAGCGATTGTCATGGAAATC
TTCCTGGCCGGCACCGAAACCAGCAGCAGCGTGATTGACTGGGTTATGAGTGAACTGATCAAAAAC
CCGAAAGCGATGGAAAAAGTGCAGAAAGAAATGCGTGAAGCCATGCAAGGCAAAACCAAACTGGAA
GAATCGGATATTCCGAAATTTAGCTACCTGAATCTGGTTATCAAAGAAACCCTGCGTCTGCATCCG
CCGGGTCCGCTGCTGTTCCCGCGTGAATGCCGCGAAACCTGCGAAGTGATGGGCTATCGTGTTCCG
GCGGGTGCCCGCCTGCTGATTAACGCATTTGCTCTGTCTCGTGATGAAAAATACTGGGGTTCCGAC
GCCGAATCATTTAAACCGGAACGCTTTGAAGGCATCTCTGTGGATTTCAAAGGTAGTAATTTTGAA
TTTATGCCGTTCGGCGCGGGCCGTCGTATTTGTCCGGGCATGACCTTTGGTATCTCCTCAGTTGAA
GTCGCGCTGGCCCATCTGCTGTTTCACTTCGATTGGCAACTGCCGCAAGGCATGAAAATTGAAGAT
CTGGACATGATGGAAGTCTCGGGTATGAGCGCAACCCGTCGTAGCCCGCTGCTGGTTCTGGCCAAA
CTGATTATCCCGCTGCCG (SEQ ID NO: 15)

>BsGAO [Barnadesia spinosa]

MELTLTTSLGLAVFVFILFKLLTGSKSTKNSLPEAWRLPIIGHMHHLVGTLPHRGVTDMARKYGSL
MHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLSPYGEYWRQLRKLCT
LELLSAKKVKSFQSLREEECWNLVKEVRSSGSGSPVDLSESIFKLIATILSRAAFGKGIKDQREFT
EIVKEILRLTGGFDVADIFPSKKILHHLSGKRAKLTNIHNKLDSLINNIVSEHPGSRTSSSQESLL
DVLLRLKDSAELPLTSDNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGK
ERIQEEDIQELSYLKLVIKETLRLHPPLPLVMPRECREPCVLAGYEIPTKTKLIVNVFAINRDPEY
WKDAETFMPERFENSPINIMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGAR
LDELDMSECFGATVQRKSELLLVPTAYKTANNSA (SEQ ID No: 16 | Wild Type)

MALLLAVFLGLAVFVFILFKLLTGSKSTKNSLPEAWRLPIIGHMHHLVGTLPHRGVTDMARKYGSL
MHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLSPYGEYWRQLRKLCT
LELLSAKKVKSFQSLREEECWNLVKEVRSSGSGSPVDLSESIFKLIATIL*SR*AAFGKGIKDQREFT
EIVKEILRLTGGFDVADIFPSKKILHHLSGKRAKLTNIHNKLDSLINNIVSEHPG*SR*TSSSQESLL
DVLLRLKDSAELPLTSDNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGK
ERIQEEDIQELSYLKLVIKETLRLHPPLPLVMPRECREPCVLAGYEIPTKTKLIVNVFAINRDPEY
WKDAETFMPERFENSPINIMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGAR
LDELDMSECFGATVQRKSELLLVPTAYKTANNSA (SEQ ID NO: 17)

ATGGCTCTGTTATTAGCAGTTTTCCTGGGCCTGGCTGTCTTCGTCTTTATCCTGTTCAAACTGCTG
ACCGGCTCAAAATCAACCAAAAATTCACTGCCGGAAGCATGGCGTCTGCCGATCATTGGCCACATG
CATCACCTGGTTGGCACGCTGCCGCATCGCGGTGTGACCGACATGGCGCGTAAATACGGCAGCCTG
ATGCATCTGCAACTGGGCGAAGTGAGCACCATTGTCGTCTCATCGCCGCGTTGGGCAAAAGAAGTG
CTGACGACGTATGATATTACCTTTGCGAATCGCCCGGAAACCCTGACCGGCGAAATTGTTGCGTAC
CACAACACGGATATTGTGCTGTCACCGTATGGCGAATACTGGCGCCAACTGCGTAAACTGTGCACG
CTGGAACTGCTGAGCGCCAAAAAAGTGAAAAGTTTTCAGTCGCTGCGTGAAGAAGAATGCTGGAAT
CTGGTGAAAGAAGTGCGTTCGAGCGGCTCAGGTTCCCCGGTCGATCTGTCGGAATCCATCTTTAAA
CTGATTGCAACCATTCTGAGCCGCGCAGCGTTTGGCAAAGGTATCAAAGATCAGCGTGAATTTACC
GAAATTGTGAAAGAAATCCTGCGCCTGACGGGCGGTTTTGATGTGGCGGATATTTTCCCGTCCAAA
AAGATCCTGCACCACCTGAGCGGCAAACGTGCGAAACTGACCAACATCCACAACAAACTGGATTCC
CTGATTAATAACATTGTTTCTGAACATCCGGGTTCGCGTACCTCGTCGAGCCAGGAAAGCCTGCTG
GATGTGCTGCTGCGCCTGAAAGATTCCGCGGAACTGCCGCTGACCTCGGACAATGTTAAAGCCGTG
ATCCTGGATATGTTCGGTGCGGGCACGGATACGTCGAGCGCCACGATTGAATGGGCGATCAGCGAA
CTGATCCGCTGCCCGCGTGCAATGGAAAAAGTGCAAACGGAACTGCGTCAAGCGCTGAATGGTAAA
GAACGCATTCAGGAAGAAGATATTCAGGAACTGTCCTATCTGAAACTGGTCATTAAAGAAACCCTG
CGCCTGCATCCGCCGCTGCCGCTGGTGATGCCGCGTGAATGTCGTGAACCGTGTGTCCTGGCGGGT
TACGAAATCCCGACCAAAACGAAACTGATTGTGAATGTCTTTGCCATCAATCGTGACCCGGAATAC
TGGAAAGATGCAGAAACCTTCATGCCGGAACGCTTTGAAAACAGCCCGATTAACATCATGGGTAGT
GAATATGAATACCTGCCGTTTGGCGCAGGCCGCCGTATGTGTCCGGGTGCAGCTCTGGGTCTGGCG
AATGTGGAACTGCCGCTGGCGCACATCCTGTATTATTTTAACTGGAAACTGCCGAATGGCGCTCGC
CTGGATGAACTGGATATGTCGGAATGCTTTGGCGCGACGGTCCAACGCAAAAGCGAACTGCTGCTG
GTCCCGACGGCATACAAAACGGCAAACAACTCCGCA (SEQ ID NO: 18)

>HmPO [Hyoscyamus muticus]

MQFFSLVSIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKLPLLGSMLHMVGGLPHHVLRDLAKKYGP
LMHLQLGEVSAVVVTSPDMAKEVLKTHDIAFASRPKLLAPEIVCYNRSDIAFCPYGDYWRQMRKIC
VLEVLSAKNVRSFSSIRRDEVLRLVNFVRSSTSEPVNFTERLFLFTSSMTCRSAFGKVFKEQETFI
QLIKEVIGLAGGFDVADIFPSLKFLHVLTGMEGKIMKAHHKVDAIVEDVINEHKKNLAMGKTNGAL
GGEDLIDVLLRLMNDGGLQFPITNDNIKAIIFDMFAAGTETSSSTLVWAMVQMMRNPTILAKAQAE
VREAFKGKETFDENDVEELKYLKLVIKETLRLHPPVPLLVPRECREETEINGYTIPVKTKVMVNVW
ALGRDPKYWDDADNFKPERFEQCSVDFIGNNFEYLPFGGGRRICPGISFGLANVYLPLAQLLYHFD
WKLPTGMEPKDLDLTELVGVTAARKSDLMLVATPYQPSRE (SEQ ID NO: 19 | Wild Type)

MALLLAVFFFSLVSIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKLPLLGSMLHMVGGLPHHVLRDLAKKYGP
LMHLQLGEVSAVVVTSPDMAKEVLKTHDIAFASRPKLLAPEIVCYNRSDIAFCPYGDYWRQMRKICVLEVLS
AKNVRSFSSIRRDEVLRLVNFVRSSTSEPVNFTERLFLFTSSMTCRSAFGKVFKEQETFIQLIKEVIGLAGG
FDVADIFPSLKFLHVLTGMEGKIMKAHHKVDAIVEDVINEHKKNLAMGKTNGALGGEDLIDVLLRLMNDGGL
QFPITNDNIKAIIFDMFAAGTETSSSTLVWAMVQMMRNPTILAKAQAEVREAFKGKETFDENDVEELKYLKL
VIKETLRLHPPVPLLVPRECREETEINGYTIPVKTKVMVNVWALGRDPKYWDDADNFKPERFEQCSVDFIGN
NFEYLPFGGGRRICPGISFGLANVYLPLAQLLYHFDWKLPTGMEPKDLDLTELVGVTAARKSDLMLVATPYQ
PSRE (SEQ ID NO: 20)

ATGGCTCTGTTATTAGCAGTTTTCTTCTTCTCCCTGGTCTCAATCTTTCTGTTCCTGTCCTTTCTG
TTCCTGCTGCGTAAATGGAAAAACTCAAACTCCCAATCGAAAAAACTGCCGCCGGGTCCGTGGAAA
CTGCCGCTGCTGGGCTCTATGCTGCACATGGTTGGCGGCCTGCCGCATCACGTTCTGCGTGATCTG
GCGAAAAAATATGGTCCGCTGATGCATCTGCAACTGGGCGAAGTCTCCGCCGTGGTTGTCACCTCA
CCGGATATGGCAAAAGAAGTGCTGAAAACGCATGACATTGCGTTCGCCTCCCGTCCGAAACTGCTG
GCCCCGGAAATTGTGTGCTACAACCGCTCAGATATTGCATTTTGTCCGTATGGTGACTACTGGCGT
CAAATGCGCAAAATTTGCGTCCTGGAAGTGCTGTCGGCCAAAAATGTGCGCAGCTTTAGCTCTATT
CGTCGTGATGAAGTTCTGCGTCTGGTTAACTTCGTCCGCAGTTCCACCTCGGAGCCGGTGAATTTT
ACGGAACGTCTGTTTCTGTTCACCTCATCGATGACCTGCCGTAGCGCATTTGGTAAAGTTTTCAAA
GAACAGGAAACCTTCATTCAACTGATCAAAGAAGTCATTGGCCTGGCCGGCGGTTTTGATGTGGCA
GACATCTTTCCGAGTCTGAAATTCCTGCATGTTCTGACCGGCATGGAAGGCAAAATTATGAAAGCT
CATCACAAAGTCGATGCGATTGTGGAAGACGTTATCAACGAACACAAGAAAAACCTGGCGATGGGC
AAAACGAACGGCGCACTGGGCGGTGAAGATCTGATCGACGTTCTGCTGCGTCTGATGAATGATGGC
GGCCTGCAATTTCCGATCACCAACGATAATATCAAAGCTATTATCTTTGATATGTTTGCGGCGGGC
ACCGAAACCAGCAGCAGCACCCTGGTGTGGGCGATGGTGCAGATGATGCGTAACCCGACGATTCTG
GCAAAAGCTCAAGCGGAAGTGCGCGAAGCCTTCAAAGGCAAAGAAACCTTTGATGAAAATGACGTT
GAAGAACTGAAATATCTGAAACTGGTCATCAAAGAAACGCTGCGTCTGCATCCGCCGGTTCCGCTG
CTGGTCCCGCGTGAATGCCGCGAAGAAACCGAAATTAACGGTTATACCATCCCGGTTAAAACGAAA
GTGATGGTTAATGTCTGGGCTCTGGGCCGTGATCCGAAATACTGGGATGACGCGGACAACTTTAAA
CCGGAACGCTTTGAACAGTGCTCTGTGGATTTCATCGGCAACAACTTTGAATATCTGCCGTTTGGC
GGTGGCCGTCGCATTTGTCCGGGTATCAGCTTCGGCCTGGCTAATGTTTATCTGCCGCTGGCGCAA
CTGCTGTACCACTTTGATTGGAAACTGCCGACCGGCATGGAACCGAAAGATCTGGACCTGACCGAA
CTGGTGGGCGTTACGGCAGCTCGTAAATCTGATCTGATGCTGGTTGCGACCCCGTACCAGCCGAGC
CGTGAA (SEQ ID NO: 21)

>LsGAO [Lactuca sativa]

MELSITTSIALATIVFFLYKLATRPKSTKKQLPEASRLPIIGHMHHLIGTMPHRGVMDLARKHGSL
MHLQLGEVSTIVVSSPKWAKEILTTYDITFANRPETLTGEIIAYHNTDIVLAPYGEYWRQLRKLCT
LELLSVKKVKSFQSIREEECWNLVKEVKESGSGKPINLSESIFTMIATILSRAAFGKGIKDQREFT
EIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTSIHKKLDNLINNIVAEHHVSTSSKANETLL
DVLLRLKDSAEFPLTADNVKAIILDMFGAGTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGK
EKIQEEDIQDLAYLNLVIRETLRLHPPLPLVMPRECREPVNLAGYEIANKTKLIVNVFAINRDPEY
WKDAEAFIPERFENNPNNIMGADYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGAS
HDQLDMTESFGATVQRKTELLLVPSF (SEQ ID NO: 22 | Wild Type)

MALLLAVFIALATIVFFLYKLATRPKSTKKQLPEA*SR*LPIIGHMHHLIGTMPHRGVMDLARKHGSL
MHLQLGEVSTIVVSSPKWAKEILTTYDITFANRPETLTGEIIAYHNTDIVLAPYGEYWRQLRKLCT
LELLSVKKVKSFQSIREEECWNLVKEVKESGSGKPINLSESIFTMIATIL*SR*AAFGKGIKDQREFT
EIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTSIHKKLDNLINNIVAEHHVSTSSKANETLL
DVLLRLKDSAEFPLTADNVKAIILDMFGAGTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGK
EKIQEEDIQDLAYLNLVIRETLRLHPPLPLVMPRECREPVNLAGYEIANKTKLIVNVFAINRDPEY
WKDAEAFIPERFENNPNNIMGADYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGAS
HDQLDMTESFGATVQRKTELLLVPSF (SEQ ID NO: 23)

ATGGCTCTGTTATTAGCAGTTTTCATCGCACTGGCTACCATCGTCTTCTTCCTGTATAAACTGGCA
ACGCGCCCGAAATCTACCAAAAAACAACTGCCGGAAGCGAGCCGTCTGCCGATTATCGGCCACATG
CATCACCTGATTGGCACCATGCCGCACCGTGGTGTCATGGATCTGGCCCGCAAACATGGCTCGCTG
ATGCATCTGCAACTGGGCGAAGTGAGCACCATTGTGGTTAGCTCTCCGAAATGGGCAAAAGAAATT
CTGACCACCTATGATATTACCTTTGCTAACCGCCCGGAAACCCTGACGGGCGAAATTATCGCGTAC
CATAATACGGACATTGTGCTGGCCCCGTATGGTGAATACTGGCGTCAACTGCGTAAACTGTGCACC
CTGGAACTGCTGTCCGTTAAAAAAGTCAAATCATTTCAATCGATTCGTGAAGAAGAATGTTGGAAC
CTGGTGAAAGAAGTTAAAGAAAGCGGCTCTGGTAAACCGATTAATCTGAGTGAATCCATCTTCACC
ATGATTGCGACGATCCTGAGTCGTGCGGCCTTTGGCAAAGGTATTAAAGATCAGCGCGAATTTACC
GAAATTGTCAAAGAAATCCTGCGTCAAACGGGCGGTTTCGATGTGGCAGACATTTTTCCGAGCAAA
AAATTCCTGCATCACCTGTCTGGCAAACGTGCTCGCCTGACCAGTATCCATAAAAAACTGGATAAC
CTGATCAACAATATCGTCGCGGAACATCATGTGAGCACCAGCAGCAAAGCGAATGAAACGCTGCTG
GATGTTCTGCTGCGCCTGAAAGACAGTGCCGAATTTCCGCTGACCGCAGACAACGTCAAAGCTATT
ATCCTGGATATGTTCGGTGCAGGCACCGATACCAGCAGCGCAACGGTGGAATGGGCCATTAGCGAA
CTGATCCGTTGCCCGCGCGCAATGGAAAAAGTTCAGGCAGAACTGCGTCAAGCTCTGAACGGTAAA
GAAAAAATCCAGGAAGAAGATATTCAAGACCTGGCCTATCTGAATCTGGTGATTCGTGAAACCCTG
CGTCTGCACCCGCCGCTGCCGCTGGTTATGCCGCGTGAATGCCGTGAGCCGGTGAACCTGGCGGGC
TATGAAATCGCCAATAAAACCAAACTGATCGTCAATGTGTTTGCGATTAACCGTGACCCGGAATAC
TGGAAAGACGCGGAAGCCTTTATCCCGGAACGTTTTGAAAACAATCCGAACAATATCATGGGTGCA
GATTATGAATACCTGCCGTTTGGCGCTGGTCGTCGCATGTGTCCGGGCGCAGCTCTGGGTCTGGCA
AACGTTCAACTGCCGCTGGCGAACATTCTGTACCATTTCAACTGGAAACTGCCGAATGGCGCGTCC
CACGATCAACTGGACATGACCGAATCATTTGGTGCCACCGTGCAACGTAAAACGGAACTGCTGCTG
GTTCCGAGCTTC (SEQ ID NO: 24)

>NtEAO [Nicotiani tabacum]

MQFFSLVSIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKIPILGSMLHMIGGEPHHVLRDLAKKYGP
LMHLQLGEISAVVVTSRDMAKEVLKTHDVVFASRPKIVAMDIICYNQSDIAFSPYGDHWRQMRKIC
VMELLNAKNVRSFSSIRRDEVVRLIDSIRSDSSSGELVNFTQRIIWFASSMTCRSAFGQVLKGQDI
FAKKIREVIGLAEGFDVVDIFPTYKFLHVLSGMKRKLLNAHLKVDAIVEDVINEHKKNLAAGKSNG
ALGGEDLIDVLLRLMNDTSLQFPITNDNIKAVIVDMFAAGTETSSTTTVWAMAEMMKNPSVFTKAQ
AEVREAFRDKVSFDENDVEELKYLKLVIKETLRLHPPSPLLVPRECREDTDINGYTIPAKTKVMVN
VWALGRDPKYWDDAESFKPERFEQCSVDFFGNNFEFLPFGGGRRICPGMSFGLANLYLPLAQLLYH
FDWKLPTGIMPRDLDLTELSGITIARKGGLYLNATPYQPSRE (SEQ ID NO: 25 | Wild Type)

MALLLAVFFFSLVSIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKIPILGSMLHMIGGEPHHVLRDL
AKKYGPLMHLQLGEISAVVVT*SR*DMAKEVLKTHDVVFA*SR*PKIVAMDIICYNQSDIAFSPYGDHWR
QMRKICVMELLNAKNVRSFSSIRRDEVVRLIDSIRSDSSSGELVNFTQRIIWFASSMTCRSAFGQV
LKGQDIFAKKIREVIGLAEGFDVVDIFPTYKFLHVLSGMKRKLLNAHLKVDAIVEDVINEHKKNLA
AGKSNGALGGEDLIDVLLRLMNDTSLQFPITNDNIKAVIVDMFAAGTETSSTTTVWAMAEMMKNPS
VFTKAQAEVREAFRDKVSFDENDVEELKYLKLVIKETLRLHPPSPLLVPRECREDTDINGYTIPAK
TKVMVNVWALGRDPKYWDDAESFKPERFEQCSVDFFGNNFEFLPFGGGRRICPGMSFGLANLYLPL
AQLLYHFDWKLPTGIMPRDLDLTELSGITIARKGGLYLNATPYQPSRE (SEQ ID NO: 26)

ATGGCTCTGTTATTAGCAGTTTTCTTCTTCTCCCTGGTCTCAATCTTCCTGTTCCTGTCCTTTCTG
TTCCTGCTGCGTAAATGGAAAAACTCTAATAGCCAATCCAAAAAACTGCCGCCGGGTCCGTGGAAA
ATTCCGATCCTGGGCTCTATGCTGCACATGATTGGCGGTGAACCGCATCATGTGCTGCGTGATCTG
GCGAAAAAATATGGTCCGCTGATGCATCTGCAACTGGGCGAAATCTCTGCGGTGGTTGTCACGAGT
CGTGACATGGCCAAAGAAGTGCTGAAAACCCATGATGTGGTTTTTGCATCTCGCCCGAAAATCGTT
GCTATGGATATTATCTGCTATAACCAGTCGGACATCGCGTTCAGCCCGTACGGTGATCACTGGCGT
CAAATGCGCAAAATTTGTGTCATGGAACTGCTGAACGCCAAAAATGTGCGCAGTTTTAGCTCTATT
CGTCGTGATGAAGTCGTGCGTCTGATTGATTCCATCCGCTCAGACAGTTCCTCAGGCGAACTGGTG
AATTTTACGCAGCGTATTATCTGGTTCGCATCGAGCATGACCTGCCGCTCGGCTTTTGGTCAGGTT
CTGAAAGGCCAAGATATTTTTGCGAAGAAAATTCGTGAAGTGATCGGTCTGGCCGAAGGCTTCGAT
GTTGTGGATATTTTTCCGACCTATAAATTCCTGCATGTCCTGAGCGGTATGAAACGCAAACTGCTG
AACGCGCACCTGAAAGTTGATGCCATTGTCGAAGACGTGATCAACGAACATAAGAAAAACCTGGCG
GCGGGTAAATCCAACGGCGCACTGGGCGGTGAAGATCTGATTGACGTGCTGCTGCGTCTGATGAAT
GATACCAGCCTGCAATTTCCGATCACCAACGACAACATTAAAGCGGTGATCGTTGATATGTTCGCG
GCGGGCACCGAAACCTCTAGTACCACGACCGTTTGGGCGATGGCCGAAATGATGAAAAACCCGTCG
GTGTTTACCAAAGCACAAGCGGAAGTGCGTGAAGCGTTTCGTGATAAAGTTAGCTTCGATGAAAAT
GATGTGGAAGAACTGAAATACCTGAAACTGGTGATTAAAGAAACGCTGCGTCTGCATCCGCCGAGC
CCGCTGCTGGTTCCGCGTGAATGCCGTGAAGATACCGACATTAACGGTTATACGATCCCGGCAAAA
ACCAAAGTCATGGTGAATGTTTGGGCTCTGGGCCGTGACCCGAAATACTGGGATGACGCAGAATCC
TTTAAACCGGAACGCTTTGAACAGTGCTCAGTGGATTTCTTTGGTAACAACTTTGAATTTCTGCCG
TTTGGCGGTGGCCGTCGCATTTGTCCGGGTATGTCCTTCGGCCTGGCGAACCTGTATCTGCCGCTG
GCCCAACTGCTGTACCACTTTGATTGGAAACTGCCGACGGGTATTATGCCGCGTGATCTGGACCTG
ACGGAACTGTCTGGCATTACCATCGCACGCAAAGGTGGCCTGTATCTGAATGCTACCCCGTACCAG
CCGAGTCGTGAA (SEQ ID NO: 27)

>CpVO [Citrus x paradisi]

MELPLKSIALTIVIVTVLTWAWRVLNWVWLRPKKLEKFLRQQGLKGNSYRLLFGDLKENSIELKEA
KARPLSLDDDIAIRVNPFLHKLVNDYGKNSFMWFGPTPRVNIMNPDQIKAIFTKINDFQKVNSIPL
ARLLIVGLATLEGEKWAKHRKLINPAFHQEKLKLMLPAFYLSCIEIITKWEKQMSVEGSSELDVWP
YLANLTSDVISRTAFGSSYEEGRRIFQLQAELAELTMQVFRSVHIPGWRFLPTKRNRRMKEIDKEI
RASLMGIIKNREKAMRAGEAANNDLLGILMETSFREIEEHGNNKNVGFSMNDVIEECKLFYFAGQE
TTSVLLNWTMVLLSKHQDWQERARQEVLQVFGNNKPDYDGLNHLKIVQMILYEVLRLYPPVTVLSR
AVFKETKLGNLTLPAGVQIGLPMILVHQDPELWGDDAVEFKPERFAEGISKAAKNQVSYFPFALGP
RICVGQNFALVEAKMATAMILQNYSFELSPSYVHAPTAVPTLHPELGTQLILRKLWCKNN (SEQ
ID NO: 28 | Wild Type)

MALLLAVFIALTIVIVTVLTWAWRVLNWVWLRPKKLEKFLRQQGLKGNSYRLLFGDLKENSIELKE
AKARPLSLDDDIAIRVNPFLHKLVNDYGKNSFMWFGPTPRVNIMNPDQIKAIFTKINDFQKVNSIP
LARLLIVGLATLEGEKWAKHRKLINPAFHQEKLKLMLPAFYLSCIEIITKWEKQMSVEGSSELDVW
PYLANLTSDVI*SR*TAFGSSYEEGRRIFQLQAELAELTMQVFRSVHIPGWRFLPTKRNRRMKEIDKE
IRASLMGIIKNREKAMRAGEAANNDLLGILMETSFREIEEHGNNKNVGFSMNDVIEECKLFYFAGQ
ETTSVLLNWTMVLLSKHQDWQERARQEVLQVFGNNKPDYDGLNHLKIVQMILYEVLRLYPPVTVLS
RAVFKETKLGNLTLPAGVQIGLPMILVHQDPELWGDDAVEFKPERFAEGISKAAKNQVSYFPFALG
PRICVGQNFALVEAKMATAMILQNYSFELSPSYVHAPTAVPTLHPELGTQLILRKLWCKNN (SEQ
ID NO: 29)

ATGGCTCTGTTATTAGCAGTTTTCATTGCTCTGACGATTGTTATTGTTACGGTGCTGACCTGGGCG
TGGCGTGTGCTGAACTGGGTTTGGCTGCGTCCGAAAAAACTGGAAAAATTTCTGCGCCAGCAAGGC
CTGAAGGGTAACAGCTATCGTCTGCTGTTCGGCGATCTGAAAGAAAATTCTATTGAACTGAAAGAA
GCGAAAGCCCGTCCGCTGAGTCTGGATGACGATATTGCAATCCGCGTTAACCCGTTTCTGCATAAA
CTGGTCAACGATTACGGCAAAAATTCTTTTATGTGGTTCGGTCCGACCCCGCGCGTGAACATTATG
AACCCGGATCAGATTAAAGCGATCTTTACGAAAATCAACGATTTCCAAAAAGTTAATAGCATTCCG
CTGGCGCGTCTGCTGATCGTCGGCCTGGCCACCCTGGAAGGTGAAAAATGGGCAAAACATCGCAAA
CTGATTAACCCGGCTTTTCACCAAGAAAAACTGAAACTGATGCTGCCGGCGTTCTATCTGTCCTGC
ATCGAAATTATCACGAAATGGGAAAAACAGATGTCAGTGGAAGGTAGCTCTGAACTGGACGTTTGG
CCGTATCTGGCCAATCTGACCAGCGATGTTATTTCTCGTACGGCATTTGGCAGTTCCTACGAAGAA
GGTCGTCGCATCTTCCAGTTACAGGCGGAACTGGCCGAACTGACCATGCAGGTTTTTCGTTCTGTC
CATATTCCGGGCTGGCGTTTCCTGCCGACGAAACGCAACCGTCGCATGAAAGAAATTGACAAAGAA
ATCCGCGCCAGTCTGATGGGTATTATCAAAAATCGTGAAAAAGCAATGCGCGCTGGCGAAGCGGCC
AACAATGATCTGCTGGGTATTCTGATGGAAACCAGCTTTCGTGAAATCGAAGAACACGGCAACAAT
AAAAACGTCGGTTTCAGCATGAATGACGTGATCGAAGAATGTAAACTGTTTTATTTCGCTGGCCAG
GAAACCACGTCAGTTCTGCTGAACTGGACGATGGTGCTGCTGTCGAAACATCAGGATTGGCAAGAA
CGTGCCCGCCAGGAAGTCCTGCAAGTGTTTGGCAACAATAAACCGGACTACGATGGTCTGAACCAC
CTGAAAATTGTGCAGATGATCCTGTATGAAGTTCTGCGTCTGTATCCGCCGGTGACGGTGCTGAGC
CGTGCGGTGTTTAAAGAAACCAAACTGGGTAATCTGACGCTGCCGGCAGGCGTCCAGATTGGTCTG
CCGATGATCCTGGTGCACCAGGACCCGGAACTGTGGGGCGACGATGCTGTGGAATTTAAACCGGAA
CGTTTCGCGGAAGGTATTAGTAAAGCAGCTAAAAATCAGGTTTCCTATTTTCCGTTCGCGCTGGGT
CCGCGTATTTGCGTCGGTCAAAACTTTGCACTGGTGGAAGCTAAAATGGCAACCGCTATGATCCTG
CAAAATTATAGCTTTGAACTGTCACCGAGCTATGTTCATGCGCCGACCGCCGTTCCGACGCTGCAC
CCGGAACTGGGCACGCAACTGATTCTGCGTAAACTGTGGTGTAAAAACAAT (SEQ ID NO: 30)

>AaAO [Artemesia annua]

MKSILKAMALSLTTSIALATILLFVYKFATRSKSTKKSLPEPWRLPIIGHMHHLIGTTPHRGVRDL
ARKYGSLMHLQLGEVPTIVVSSPKWAKEILTTYDITFANRPETLTGEIVLYHNTDVVLAPYGEYWR
QLRKICTLELLSVKKVKSFQSLREEECWNLVQEIKASGSGRPVNLSENVFKLIATILSRAAFGKGI
KDQKELTEIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTSLRKKIDNLIDNLVAEHTVNTSS
KTNETLLDVLLRLKDSAEFPLTSDNIKAIILDMFGAGTDTSSSTIEWAISELIKCPKAMEKVQAEL
RKALNGKEKIHEEDIQELSYLNMVIKETLRLHPPLPLVLPRECRQPVNLAGYNIPNKTKLIVNVFA
INRDPEYWKDAEAFIPERFENSSATVMGAEYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNW
KLPNGVSYDQIDMTESSGATMQRKTELLLVPSF (SEQ ID NO: 31 | Wild Type)

MALLLAVFIALATILLFVYKFATRSKSTKKSLPEPWRLPIIGHMHHLIGTTPHRGVRDLARKYGSL
MHLQLGEVPTIVVSSPKWAKEILTTYDITFANRPETLTGEIVLYHNTDVVLAPYGEYWRQLRKICT
LELLSVKKVKSFQSLREEECWNLVQEIKASGSGRPVNLSENVFKLIATIL*SR*AAFGKGIKDQKELT
EIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTSLRKKIDNLIDNLVAEHTVNTSSKTNETLL
DVLLRLKDSAEFPLTSDNIKAIILDMFGAGTDTSSSTIEWAISELIKCPKAMEKVQAELRKALNGK
EKIHEEDIQELSYLNMVIKETLRLHPPLPLVLPRECRQPVNLAGYNIPNKTKLIVNVFAINRDPEY
WKDAEAFIPERFENSSATVMGAEYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGVS
YDQIDMTESSGATMQRKTELLLVPSF (SEQ ID NO: 32)

ATGGCTCTGTTATTAGCAGTTTTCATCGCACTGGCAACCATTCTGCTGTTTGTGTATAAATTCGCT
ACCCGTTCCAAATCAACGAAAAAATCACTGCCGGAACCGTGGCGCCTGCCGATTATCGGTCACATG
CATCACCTGATCGGCACCACCCCGCATCGTGGCGTGCGTGATCTGGCACGCAAATATGGCTCGCTG
ATGCATCTGCAACTGGGTGAAGTCCCGACCATTGTGGTTAGCTCTCCGAAATGGGCGAAAGAAATC
CTGACCACCTATGATATTACCTTTGCCAACCGCCCGGAAACCCTGACGGGCGAAATCGTGCTGTAC
CACAATACGGATGTGGTGCTGGCGCCGTATGGTGAATACTGGCGTCAACTGCGTAAAATTTGCACC
CTGGAACTGCTGAGTGTGAAAAAAGTTAAATCTTTCCAGAGCCTGCGTGAAGAAGAATGTTGGAAC
CTGGTTCAAGAAATTAAAGCATCGGGCAGCGGTCGCCCGGTTAACCTGAGTGAAAATGTCTTTAAA
CTGATTGCTACCATCCTGTCCCGTGCGGCCTTCGGCAAAGGTATCAAAGATCAGAAAGAACTGACC
GAAATTGTCAAAGAAATCCTGCGCCAAACGGGCGGTTTTGATGTGGCGGACATTTTTCCGTCGAAA
AAATTCCTGCATCACCTGAGCGGTAAACGTGCCCGCCTGACCAGCCTGCGTAAGAAAATTGATAAC
CTGATCGACAATCTGGTCGCGGAACATACCGTGAACACGAGTTCCAAAACCAATGAAACGCTGCTG
GATGTGCTGCTGCGCCTGAAAGACTCCGCCGAATTTCCGCTGACCTCAGATAATATCAAAGCGATT
ATCCTGGATATGTTCGGTGCAGGCACCGATACCAGCAGCAGCACCATTGAATGGGCAATCTCAGAA
CTGATTAAATGCCCGAAAGCTATGGAAAAAGTCCAGGCAGAACTGCGCAAAGCTCTGAACGGCAAA
GAAAAAATCCATGAAGAAGATATTCAAGAACTGTCTTACCTGAACATGGTTATCAAAGAAACCCTG
CGTCTGCACCCGCCGCTGCCGCTGGTGCTGCCGCGTGAATGTCGCCAGCCGGTTAACCTGGCAGGC
TATAACATCCCGAATAAAACGAAACTGATCGTTAACGTCTTTGCTATTAACCGTGACCCGGAATAC
TGGAAAGACGCGGAAGCCTTTATCCCGGAACGCTTTGAAAACAGCAGCGCGACCGTGATGGGTGCC
GAATATGAATACCTGCCGTTTGGCGCGGGTCGTCGCATGTGTCCGGGCGCAGCTCTGGGTCTGGCA
AACGTGCAACTGCCGCTGGCTAATATCCTGTATCACTTCAACTGGAAACTGCCGAATGGCGTTAGC
TACGATCAAATTGACATGACCGAAAGCTCAGGTGCCACGATGCAACGCAAAACCGAACTGCTGCTG
GTGCCGTCCTTC (SEQ ID NO: 33)

>AtKO [Arabidopsis thaliana]

MAFFSMISILLGFVISSFIFIFFFKKLLSFSRKNMSEVSTLPSVPVVPGFPVIGNLLQLKEKKPHK
TFTRWSEIYGPIYSIKMGSSSLIVLNSTETAKEAMVTRFSSISTRKLSNALTVLTCDKSMVATSDY
DDFHKLVKRCLLNGLLGANAQKRKRHYRDALIENVSSKLHAHARDHPQEPVNFRAIFEHELFGVAL
KQAFGKDVESIYVKELGVTLSKDEIFKVLVHDMMEGAIDVDWRDFFPYLKWIPNKSFEARIQQKHK
RRLAVMNALIQDRLKQNGSESDDDCYLNFLMSEAKTLTKEQIAILVWETIIETADTTLVTTEWAIY
ELAKHPSVQDRLCKEIQNVCGGEKFKEEQLSQVPYLNGVFHETLRKYSPAPLVPIRYAHEDTQIGG
YHVPAGSEIAINIYGCNMDKKRWERPEDWWPERFLDDGKYETSDLHKTMAFGAGKRVCAGALQASL
MAGIAIGRLVQEFEWKLRDGEEENVDTYGLTSQKLYPLMAIINPRRS (SEQ ID NO: 34 | Wild Type)

MALLLAVFSMISILLGFVISSFIFIFFFKKLLSF*SR*KNMSEVSTLPSVPVVPGFPVIGNLLQLKE
KKPHKTFTRWSEIYGPIYSIKMGSSSLIVLNSTETAKEAMVTRFSSISTRKLSNALTVLTCDKSM
VATSDYDDFHKLVKRCLLNGLLGANAQKRKRHYRDALIENVSSKLHAHARDHPQEPVNFRAIFEH
ELFGVALKQAFGKDVESIYVKELGVTLSKDEIFKVLVHDMMEGAIDVDWRDFFPYLKWIPNKSFE
ARIQQKHKRRLAVMNALIQDRLKQNGSESDDDCYLNFLMSEAKTLTKEQIAILVWETIIETADTT
LVTTEWAIYELAKHPSVQDRLCKEIQNVCGGEKFKEEQLSQVPYLNGVFHETLRKYSPAPLVPIR
YAHEDTQIGGYHVPAGSEIAINIYGCNMDKKRWERPEDWWPERFLDDGKYETSDLHKTMAFGAGK
RVCAGALQASLMAGIAIGRLVQEFEWKLRDGEEENVDTYGLTSQKLYPLMAIINPRRS (SEQ ID NO: 35)

ATGGCTCTGTTATTAGCAGTTTTTTCGATGATTTCTATCCTGCTGGGCTTTGTTATCTCGTCCTTT
ATCTTTATCTTCTTCTTCAAAAAACTGCTGTCGTTTTCTCGTAAAAACATGTCCGAAGTTTCAACC
CTGCCGAGTGTCCCGGTGGTTCCGGGTTTTCCGGTTATCGGTAATCTGCTGCAGCTGAAAGAAAAG
AAACCGCATAAGACCTTCACGCGCTGGTCCGAAATCTATGGCCCGATCTACTCAATTAAAATGGGT
AGCTCTAGTCTGATTGTGCTGAACTCTACCGAAACGGCAAAAGAAGCTATGGTTACCCGTTTTTCC
TCAATTTCGACGCGCAAGCTGAGCAATGCGCTGACCGTCCTGACGTGCGACAAATCTATGGTGGCC
ACCAGTGATTACGATGACTTCCATAAACTGGTTAAGCGTTGTCTGCTGAACGGCCTGCTGGGTGCG
AATGCCCAGAAGCGTAAGCGCCACTATCGCGACGCCCTGATTGAAAACGTGTCGAGCAAACTGCAT
GCACACGCTCGTGATCATCCGCAGGAACCGGTCAATTTTCGCGCAATCTTCGAACACGAACTGTTT
GGCGTGGCGCTGAAACAAGCCTTCGGCAAGGATGTTGAATCGATTTACGTCAAAGAACTGGGCGTG
ACCCTGAGCAAAGACGAAATCTTTAAGGTCCTGGTGCATGATATGATGGAAGGTGCAATTGACGTT
GATTGGCGTGATTTCTTTCCGTATCTGAAATGGATTCCGAACAAGTCATTCGAAGCTCGCATTCAG
CAAAAACACAAGCGTCGCCTGGCAGTGATGAACGCTCTGATTCAGGATCGTCTGAAACAAAATGGC
TCTGAAAGTGATGACGATTGCTATCTGAATTTTCTGATGTCCGAAGCAAAAACCCTGACGAAGGAA
CAGATTGCTATCCTGGTTTGGGAAACCATTATCGAAACGGCGGACACCACGCTGGTCACCACGGAA
TGGGCGATCTACGAACTGGCCAAGCATCCGAGCGTTCAGGATCGCCTGTGCAAAGAAATTCAAAAC
GTCTGTGGCGGTGAAAAATTTAAGGAAGAACAGCTGTCGCAAGTGCCGTATCTGAATGGTGTTTTC
CACGAAACCCTGCGTAAATATAGCCCGGCACCGCTGGTCCCGATCCGTTACGCCCATGAAGATACC
CAGATTGGCGGTTATCACGTGCCGGCAGGCAGTGAAATTGCTATCAACATTTACGGTTGCAATATG
GACAAAAAGCGTTGGGAACGCCCGGAAGATTGGTGGCCGGAACGTTTTCTGGACGATGGCAAATAT
GAAACCTCTGATCTGCATAAGACGATGGCGTTCGGTGCAGGTAAACGTGTGTGTGCAGGTGCACTG
CAAGCAAGTCTGATGGCAGGCATCGCTATTGGTCGTCTGGTGCAAGAATTTGAATGGAAACTGCGC
GACGGCGAAGAAGAAAACGTTGATACCTATGGTCTGACGTCCCAGAAACTGTACCCGCTGATGGCC
ATTATCAATCCGCGTCGCTCA (SEQ ID NO: 36)

>*Sr*KO [Stevia rebaudiana]

MDAVTGLLTVPATAITIGGTAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLK
EKKPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTADKTM
VAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQS
ELFGLAMRQALGKDVESLYVEDLKITMNRDEIFQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFEN
TIQQMYIRREAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMV
TTEWAMYELAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRRHSPVPIIPLRHVH
EDTVLGGYHVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGS
LQALLTASIGIGRMVQEFEWKLKDMTQEEVNTIGLTTQMLRPLRAIIKPRI (SEQ ID NO: 37 | Wild Type)

MALLLAVFAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTFTRW
AATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTADKTMVAMSDYDDYH
KTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMRQ
ALGKDVESLYVEDLKITMNRDEIFQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR
REAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMY
ELAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLG
GYHVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALL
TASIGIGRMVQEFEWKLKDMTQEEVNTIGLTTQMLRPLRAIIKPRI (SEQ ID NO: 38)

ATGGCTCTGTTATTAGCAGTTTTTGCCGTCGCTCTGGCGGTAGCACTGATCTTCTGGTATCTGAAA
TCTTACACTAGCGCGCGCCGCTCTCAGTCCAACCACCTGCCGCGTGTGCCGGAAGTTCCGGGTGTG
CCACTGCTGGGCAACCTGCTGCAACTGAAAGAAAAGAAACCGTACATGACCTTTACCCGCTGGGCA
GCGACTTATGGTCCTATCTACAGCATTAAAACCGGCGCTACGTCTATGGTTGTGGTTTCTTCCAAC
GAAATCGCGAAAGAAGCCCTGGTGACTCGTTTCCAGTCCATTAGCACCCGCAACCTGTCCAAAGCG
CTGAAGGTTCTGACGGCTGACAAGACTATGGTGGCTATGAGCGACTATGATGACTACCACAAAACC
GTTAAACGTCACATCCTGACCGCAGTACTGGGTCCGAACGCACAGAAAAAACATCGCATCCACCGC
GACATTATGATGGATAACATCTCCACGCAGCTGCATGAGTTCGTTAAGAACAATCCAGAACAGGAA
GAGGTAGATCTGCGTAAAATTTTTCAGTCCGAACTGTTCGGTCTGGCTATGCGTCAGGCGCTGGGC
AAAGACGTTGAAAGCCTGTATGTCGAAGACCTGAAAATTACCATGAACCGTGATGAGATCTTCCAG
GTTCTGGTTGTAGATCCGATGATGGGCGCCATCGACGTGGATTGGCGTGACTTCTTTCCGTACCTG
AAATGGGTCCCGAACAAGAAGTTCGAAAACACCATCCAGCAAATGTACATCCGTCGTGAAGCGGTG
ATGAAAAGCCTGATCAAAGAACACAAAAAGCGTATTGCTTCTGGTGAGAAACTGAACTCCTACATC
GATTATCTGCTGTCCGAAGCGCAGACCCTGACCGACCAACAGCTGCTGATGTCTCTGTGGGAACCG
ATTATCGAAAGCAGCGACACCACTATGGTCACTACCGAATGGGCAATGTATGAGCTGGCCAAAAAC
CCGAAACTGCAGGATCGTCTGTACCGTGACATCAAAAGCGTTTGCGGCTCCGAGAAAATCACTGAA
GAACACCTGTCTCAGCTGCCGTACATCACTGCTATTTTCCACGAAACCCTGCGTCGCCATTCTCCG
GTTCCGATCATTCCGCTGCGTCACGTTCACGAAGATACTGTGCTGGGTGGTTACCATGTACCGGCA
GGCACTGAACTGGCTGTCAACATCTACGGCTGTAACATGGATAAAAACGTTTGGGAGAATCCTGAA
GAATGGAACCCGGAACGCTTCATGAAAGAGAACGAAACCATCGACTTCCAGAAAACGATGGCTTTC
GGCGGTGGTAAACGTGTGTGCGCAGGTTCTCTGCAGGCGCTGCTGACGGCGTCCATTGGTATCGGT
CGCATGGTACAGGAATTTGAATGGAAGCTGAAAGACATGACCCAAGAAGAGGTGAATACCATTGGT
CTGACTACCCAGATGCTGCGTCCACTGCGTGCAATCATCAAACCTCGTATT (SEQ ID NO: 39)

>PpKO [Physcomitrella patens]

MAKHLATQLLQQWNEALKTMPPGFRTAGKILVWEELASNKVLITIALAWVLLFVARTCLRNKKRL
PPAIPGGLPVLGNLLQLTEKKPHRTFTAWSKEHGPIFTIKVGSVPQAVVNNSEIAKEVLVTKFAS
ISKRQMPMALRVLTRDKTMVAMSDYGEEHRMLKKLVMTNLLGPTTQNKNRSLRDDALIGMIEGVL
AELKASPTSPKVVNVRDYVQRSLFPFALQQVFGYIPDQVEVLELGTCVSTWDMFDALVVAPLSAV
INVDWRDFFPALRWIPNRSVEDLVRTVDFKRNSIMKALIRAQRMRLANLKEPPRCYADIALTEAT
HLTEKQLEMSLWEPIIESADTTLVTSEWAMYEIAKNPDCQDRLYREIVSVAGTERMVTEDDLPNM
PYLGAIIKETLRKYTPVPLIP*SR*FVEEDITLGGYDIPKGYQILVNLFAIANDPAVWSNPEKWDPE
RMLANKKVDMGFRDFSLMPFGAGKRMCAGITQAMFIIPMNVAALVQHCEWRLSPQEISNINNKIE
DVVYLTTHKLSPLSCEATPRISHRLP (SEQ ID NO: 40 | Wild Type)

MALLLAVFTQLLQQWNEALKTMPPGFRTAGKILVWEELASNKVLITIALAWVLLFVARTCLRNKK
RLPPAIPGGLPVLGNLLQLTEKKPHRTFTAWSKEHGPIFTIKVGSVPQAVVNNSEIAKEVLVTKF
ASISKRQMPMALRVLTRDKTMVAMSDYGEEHRMLKKLVMTNLLGPTTQNKNRSLRDDALIGMIEG
VLAELKASPTSPKVVNVRDYVQRSLFPFALQQVFGYIPDQVEVLELGTCVSTWDMFDALVVAPLS
AVINVDWRDFFPALRWIPNRSVEDLVRTVDFKRNSIMKALIRAQRMRLANLKEPPRCYADIALTE
ATHLTEKQLEMSLWEPIIESADTTLVTSEWAMYEIAKNPDCQDRLYREIVSVAGTERMVTEDDLP
NMPYLGAIIKETLRKYTPVPLIP*SR*FVEEDITLGGYDIPKGYQILVNLFAIANDPAVWSNPEKWD
PERMLANKKVDMGFRDFSLMPFGAGKRMCAGITQAMFIIPMNVAALVQHCEWRLSPQEISNINNK
IEDVVYLTTHKLSPLSCEATPRISHRLP (SEQ ID NO: 41)

ATGGCTCTGTTATTAGCAGTTTTTACGCAACTGCTGCAACAATGGAATGAAGCTCTGAAGACGAT
GCCGCCGGGTTTTCGCACCGCTGGCAAAATTCTGGTGTGGGAAGAACTGGCAAGCAATAAAGTTC
TGATTACGATCGCACTGGCTTGGGTCCTGCTGTTTGTGGCTCGTACCTGCCTGCGCAATAAAAAG
CGTCTGCCGCCGGCAATCCCGGGCGGTCTGCCGGTGCTGGGCAACCTGCTGCAGCTGACGGAAAA
GAAACCGCATCGTACCTTTACGGCGTGGAGCAAGGAACACGGCCCGATTTTCACCATCAAAGTCG
GTTCGGTGCCGCAGGCTGTGGTTAACAATAGCGAAATTGCGAAAGAAGTCCTGGTGACCAAGTTC
GCCAGCATCTCTAAACGTCAAATGCCGATGGCACTGCGCGTCCTGACGCGTGATAAAACGATGGT
GGCTATGTCTGACTATGGCGAAGAACATCGCATGCTGAAAAAGCTGGTGATGACGAATCTGCTGG
GTCCGACCACGCAGAACAAAAATCGTAGTCTGCGCGATGACGCACTGATTGGCATGATCGAAGGT
GTTCTGGCGGAACTGAAGGCCAGTCCGACCTCCCCGAAAGTCGTGAACGTTCGCGATTATGTCCA
GCGTTCTCTGTTTCCGTTCGCGCTGCAGCAAGTGTTTGGCTACATTCCGGATCAAGTTGAAGTCC
TGGAACTGGGCACGTGTGTTTCTACCTGGGATATGTTCGACGCACTGGTTGTCGCTCCGCTGAGT
GCGGTTATTAACGTCGATTGGCGTGACTTTTTCCCGGCCCTGCGCTGGATTCCGAATCGTTCCGT
GGAAGATCTGGTGCGCACCGTTGACTTTAAGCGTAACTCAATTATGAAAGCCCTGATCCGTGCAC
AGCGTATGCGCCTGGCTAACCTGAAGGAACCGCCGCGCTGCTACGCAGATATTGCTCTGACCGAA
GCGACGCACCTGACCGAAAAACAACTGGAAATGAGTCTGTGGGAACCGATTATCGAATCCGCCGA
TACCACGCTGGTGACCTCAGAATGGGCTATGTATGAAATTGCGAAAAATCCGGATTGTCAGGACC
GTCTGTACCGCGAAATCGTGTCCGTTGCCGGCACGGAACGCATGGTTACCGAAGATGACCTGCCG
AACATGCCGTATCTGGGTGCAATTATCAAAGAAACGCTGCGCAAGTACACCCCGGTTCCGCTGAT
TCCGAGTCGTTTTGTCGAAGAAGATATCACCCTGGGCGGTTATGACATTCCGAAAGGTTACCAGA
TCCTGGTCAACCTGTTCGCGATTGCCAATGATCCGGCCGTTTGGTCGAACCCGGAAAAATGGGAC
CCGGAACGCATGCTGGCAAATAAAAAGGTGGATATGGGCTTTCGTGACTTCAGCCTGATGCCGTT
TGGCGCCGGTAAACGCATGTGCGCCGGTATCACCCAAGCAATGTTCATTATCCCGATGAATGTGG
CGGCCCTGGTTCAGCATTGTGAATGGCGCCTGAGCCCGCAAGAAATCTCTAACATCAACAACAAG
ATCGAAGATGTGGTTTACCTGACCACGCATAAACTGTCACCGCTGTCGTGCGAAGCAACCCCGCG
TATCAGCCACCGTCTGCCG (SEQ ID NO: 42)

>BmVO [Bacillus megaterium]

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE*S*
*R*FDKNLSQALKFVRDFAGDGLATSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAVQLVQKWE
RLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDDPA
YDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLI
AGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTIP
AFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGN
GQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSP
STEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREG
AVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKG
AENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH
GAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQ
IRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKE
QVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGY
GEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQ
GQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAF*SR*MPNQPKTYVQHVMEQDGKKLIEL
LDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAG (SEQ ID NO: 43)

ATGACGATTAAAGAAATGCCGCAACCGAAGACGTTTGGCGAACTGAAGAACCTGCCGCTGCTGAA
CACGGATAAGCCGGTGCAAGCCCTGATGAAGATTGCTGATGAACTGGGCGAAATCTTTAAATTCG
AAGCGCCGGGTCGTGTGACCCGTTATCTGAGCAGCCAGCGTCTGATTAAAGAAGCCTGCGATGAA
TCGCGCTTTGACAAGAACCTGAGCCAGGCACTGAAATTTGTTCGTGATTTCGCAGGTGACGGTCT
GGCCACCAGCTGGACGCATGAAAAGAACTGGAAAAAGGCCCACAATATTCTGCTGCCGTCGTTCA
GCCAGCAAGCAATGAAAGGCTACCATGCTATGATGGTCGATATCGCGGTTCAGCTGGTCCAAAAA
TGGGAACGTCTGAATGCGGACGAACACATTGAAGTGCCGGAAGATATGACCCGCCTGACGCTGGA
CACCATCGGTCTGTGTGGCTTTAACTATCGTTTTAATTCGTTCTACCGCGATCAGCCGCATCCGT
TCATTACCAGCATGGTGCGTGCGCTGGACGAAGCCATGAACAAACTGCAGCGTGCAAACCCGGAT
GACCCGGCGTATGATGAAAACAAGCGTCAGTTTCAAGAAGACATCAAAGTGATGAATGATCTGGT
TGACAAGATTATCGCAGATCGCAAAGCGAGCGGCGAACAGTCAGATGACCTGCTGACGCACATGC
TGAACGGCAAAGACCCGGAAACCGGTGAACCGCTGGATGACGAAAACATCCGTTATCAGATCATC
ACCTTTCTGATCGCAGGCCATGAAACCACGTCGGGTCTGCTGAGCTTTGCGCTGTACTTCCTGGT
CAAGAACCCGCACGTGCTGCAGAAAGCGGCCGAAGAAGCAGCTCGTGTGCTGGTTGATCCGGTTC
CGTCGTATAAACAGGTCAAGCAACTGAAATACGTGGGTATGGTTCTGAATGAAGCGCTGCGCCTG
TGGCCGACGATTCCGGCATTTAGCCTGTATGCTAAGGAAGATACCGTTCTGGGCGGTGAATACCC
GCTGGAAAAAGGCGATGAACTGATGGTCCTGATTCCGCAGCTGCATCGCGACAAAACCATCTGGG
GTGATGACGTGGAAGAATTTCGCCCGGAACGCTTCGAAAACCCGAGCGCGATTCCGCAGCATGCC
TTTAAACCGTTCGGCAATGGTCAACGTGCGTGCATCGGCCAGCAATTTGCGCTGCACGAAGCCAC
GCTGGTTCTGGGTATGATGCTGAAACATTTTGATTTCGAAGACCACACCAACTATGAACTGGATA
TTAAGGAAACCCTGACGCTGAAACCGGAAGGCTTCGTGGTTAAAGCGAAGTCTAAAAAGATTCCG
CTGGGCGGTATCCCGTCTCCGAGTACGGAACAGAGTGCCAAAAAGGTCCGTAAAAAGGCGGAAAA
CGCCCATAATACCCCGCTGCTGGTGCTGTATGGTTCTAACATGGGCACGGCAGAAGGCACCGCTC
GCGATCTGGCAGACATTGCTATGTCTAAAGGTTTTGCGCCGCAGGTGGCCACGCTGGATAGTCAT
GCAGGCAATCTGCCGCGTGAAGGTGCTGTCCTGATCGTGACCGCAAGCTACAACGGTCACCCGCC
GGATAATGCGAAGCAGTTCGTTGATTGGCTGGACCAAGCGTCGGCCGATGAAGTTAAAGGTGTCC
GCTATAGCGTGTTTGGCTGTGGTGACAAGAACTGGGCTACCACGTACCAGAAAGTTCCGGCGTTC
ATTGATGAAACGCTGGCGGCCAAAGGCGCAGAAAATATCGCTGATCGTGGTGAAGCAGACGCTTC
CGATGACTTTGAAGGCACCTATGAAGAATGGCGCGAACACATGTGGTCGGATGTGGCAGCTTACT
TCAACCTGGATATTGAAAACAGCGAAGACAATAAATCCACCCTGTCACTGCAGTTTGTTGATAGT
GCGGCCGACATGCCGCTGGCAAAGATGCACGGCGCTTTCTCCACGAATGTCGTGGCTTCAAAAGA
ACTGCAGCAACCGGGTTCGGCACGTAGCACCCGCCATCTGGAAATTGAACTGCCGAAAGAAGCCA
GCTATCAGGAAGGCGATCACCTGGGTGTGATTCCGCGTAACTACGAAGGCATCGTGAATCGTGTT
ACGGCCCGCTTTGGTCTGGATGCATCCCAGCAAATCCGCCTGGAAGCGGAAGAAGAAAAGCTGGC
GCATCTGCCGCTGGCCAAAACCGTCTCAGTGGAAGAACTGCTGCAGTATGTGGAACTGCAAGATC
CGGTTACCCGTACGCAGCTGCGTGCGATGGCGGCTAAGACCGTCTGCCCGCCGCACAAAGTGGAA
CTGGAAGCTCTGCTGGAAAAGCAGGCGTATAAAGAACAAGTGCTGGCGAAACGCCTGACCATGCT
GGAACTGCTGGAAAAGTACCCGGCCTGTGAAATGAAGTTCTCTGAATTTATCGCACTGCTGCCGT
CTATCCGTCCGCGTTATTACAGTATTAGTTCCTCACCGCGTGTGGATGAAAAACAGGCCAGTATC
ACCGTTTCTGTTGTCAGTGGCGAAGCATGGTCTGGCTATGGTGAATACAAGGGTATCGCAAGTAA
CTACCTGGCTGAACTGCAGGAAGGCGATACCATTACGTGCTTTATCTCTACGCCGCAAAGTGAAT
TTACCCTGCCGAAAGACCCGGAAACGCCGCTGATCATGGTTGGCCCGGGCACCGGTGTCGCACCG
TTTCGTGGTTTCGTGCAGGCACGCAAGCAACTGAAAGAACAGGGCCAATCCCTGGGTGAAGCGCA

TCTGTATTTTGGCTGTCGCTCACCGCACGAAGATTATCTGTACCAGGAAGAACTGGAAAACGCGC
AATCCGAAGGTATTATCACGCTGCATACCGCCTTCTCACGTATGCCGAATCAGCCGAAAACCTAC
GTCCAGCACGTGATGGAACAAGATGGCAAAAAGCTGATTGAACTGCTGGACCAGGGTGCGCATTT
TTATATCTGCGGTGATGGCAGCCAAATGGCACCGGCAGTGGAAGCAACCCTGATGAAATCCTACG
CAGATGTTCACCAGGTCTCAGAAGCAGACGCTCGTCTGTGGCTGCAGCAACTGGAAGAAAAGGGC
CGCTATGCGAAAGATGTTTGGGCCGGTTAA (SEQ ID NO: 44)

>PsVO [Pleurotus sapidus]

MRYGCAAVALFYLTAMGKLHPLAIIPDYKGSMAASVTIFNKRTNPLDISVNQANDWPWRYAKTCVL
SSDWALHEMIIHLNNTHLVEEAVIVAAQRKLSPSHIVFRLLEPHWVVTLSLNALARSVLIPEVIVP
IAGFSAPHIFQFIRESFTNFDWKSLYVPADLE*SR*GFPVDQLNSPKFHNYAYARDINDMWTTLKKFV
SSVLQDAQYYPDDASVAGDTQIQAWCDEMRSGMGAGMTNFPESITTVDDLVNMVTMCIHIAAPQHT
AVNYLQQYYQTFVSNKPSALFSPLPTSIAQLQKYTESDLMAALPLNAKRQWLLMAQIPYLLSMQVQ
EDENIVTYAANASTDKDPIIASAGRQLAADLKKLAAVFLVNSAQLDDQNTPYDVLAPEQLANAIVI
(SEQ ID NO: 45)

ATGCGTTATGGCTGTGCTGCTGTGGCTCTGTTCTATCTGACCGCTATGGGCAAACTGCACCCGCTG
GCTATTATCCCGGACTACAAGGGTAGCATGGCGGCCTCTGTCACCATTTTTAACAAACGTACGAAT
CCGCTGGATATCAGCGTTAACCAGGCAAATGACTGGCCGTGGCGCTATGCTAAGACGTGCGTGCTG
AGCAGCGATTGGGCGCTGCATGAAATGATTATCCACCTGAACAATACCCATCTGGTGGAAGAAGCC
GTCATTGTGGCAGCTCAGCGTAAACTGTCACCGTCGCACATCGTTTTTCGCCTGCTGGAACCGCAT
TGGGTGGTTACCCTGTCGCTGAACGCACTGGCTCGTAGCGTGCTGATCCCGGAAGTTATTGTCCCG
ATCGCGGGTTTCTCTGCCCCGCACATTTTTCAGTTCATCCGCGAATCTTTTACCAATTTCGATTGG
AAAAGTCTGTACGTCCCGGCGGACCTGGAATCGCGTGGCTTTCCGGTGGATCAGCTGAACAGCCCG
AAGTTCCATAATTATGCGTACGCCCGCGATATCAACGACATGTGGACCACGCTGAAAAAGTTTGTG
AGTTCCGTTCTGCAGGATGCCCAATATTACCCGGATGACGCAAGTGTGGCTGGTGATACGCAGATT
CAAGCATGGTGCGACGAAATGCGTTCCGGCATGGGTGCGGGCATGACCAACTTCCCGGAATCAATC
ACCACGGTTGATGACCTGGTCAATATGGTGACCATGTGTATTCACATCGCGGCCCCGCAGCATACG
GCGGTTAACTATCTGCAGCAATACTACCAAACCTTCGTCAGTAACAAGCCGTCCGCACTGTTCTCA
CCGCTGCCGACCTCTATTGCTCAGCTGCAAAAATACACGGAAAGTGATCTGATGGCAGCTCTGCCG
CTGAACGCGAAGCGTCAGTGGCTGCTGATGGCCCAAATTCCGTATCTGCTGTCGATGCAGGTGCAA
GAAGATGAAAACATCGTTACCTACGCGGCCAATGCGTCCACGGATAAAGACCCGATTATCGCATCA
GCTGGCCGCCAGCTGGCAGCTGACCTGAAAAAGCTGGCGGCCGTTTTTCTGGTCAACTCAGCCCAG
CTGGATGACCAAAATACCCCGTATGATGTGCTGGCACCGGAACAGCTGGCGAATGCCATTGTTATC
TAA (SEQ ID NO: 46)

>PoLO [Pleurotus ostreatus]

MAPTMSL*SR*SALKNVHLPYMVQHPEPTDCSTAMKHAAEGYDRARQMIAFLFDILDYESSVPQKFTP
EEKKEKYTWSHSDKFPPHLAIIPEDIDVPAYIIFSIVRLVQTLSIMSGIQCNERLAPGPEQNTMEK
LTKWNAERHKNQGWVKDMFNEPNIGLRNDWYTDAVFAQQFFTGPNPTTITLASDTWMKAFTEEAAS
QGKRDLISLFRSAPPNSFYVQDFSDFRARMGAKPDEELCATSDGGVTRYGCAAVALFYLPPTGELH
PLAIVPDYKGSMAASITLFNKRVDPSDASVDQANDWPWRYAKTCVLSADWVLHEMIIHLNNTHLVQ
EAVIVAVQRTLPDSHIVFRLLKPHWVVTLSLNAQARSVLIPEVIVPIAGFSELRIFQFVGHAFTNF
DWKALYVPTDLEFRGFPLDRLDDDKFHNYAYAKDIKDMWMALRKFVSSVLKDGKYYPDDSAVAADA
QIQDWCDEMRSEKGAGMKKFPESISTLDDLIDMVTMCIHIAAPQHTAVNYLQQYYQTFVPNKPSAL
FSPLPTLLSQLESYTESDLMAALPLGAKQEWLLMAQVPYLLSKEVEQDGNIVTYAGTASNNEDPII
AAAGKELSADLVILAGVFLKNSEKLDDQNTAYNVLAPDQLANAIVI (SEQ ID NO: 47)

ATGGCCCCGACGATGTCACTGTCTCGCTCCGCACTGAAGAATGTCCACCTGCCGTATATGGTCCA
ACACCCGGAACCGACCGATTGCAGCACCGCGATGAAACACGCGGCCGAAGGTTATGATCGTGCTC
GCCAGATGATTGCGTTTCTGTTCGACATCCTGGATTACGAAAGCTCTGTTCCGCAAAAATTTACC
CCGGAAGAAAAGAAAGAAAAATATACGTGGTCACACTCGGATAAGTTCCCGCCGCATCTGGCCAT
TATCCCGGAAGACATTGATGTGCCGGCATACATTATCTTTAGCATCGTTCGTCTGGTCCAGACCC
TGAGTATTATGTCCGGCATCCAATGCAACGAACGTCTGGCACCGGGGCCGGAACAGAATACGATG
GAAAAACTGACGAAGTGGAACGCGGAACGTCATAAAAATCAAGGCTGGGTCAAGGATATGTTTAA
CGAACCGAATATTGGTCTGCGCAACGACTGGTATACCGATGCTGTGTTCGCGCAGCAATTTTTCA
CGGGTCCGAATCCGACCACGATTACCCTGGCCTCTGATACGTGGATGAAAGCATTTACCGAAGAA
GCAGCTAGTCAGGGCAAGCGTGACCTGATCAGCCTGTTTCGCTCTGCCCCGCCGAACTCCTTCTA
CGTTCAGGACTTTTCAGATTTCCGTGCTCGCATGGGCGCGAAACCGGACGAAGAACTGTGCGCGA
CCTCTGATGGCGGTGTTACCCGTTATGGCTGTGCAGCAGTCGCACTGTTTTACCTGCCGCCGACC
GGTGAACTGCATCCGCTGGCCATTGTGCCGGATTATAAAGGCAGTATGGCAGCTTCCATCACGCT
GTTCAACAAGCGTGTGGACCCGTCAGATGCCTCGGTTGACCAGGCAAATGATTGGCCGTGGCGCT
ACGCTAAAACCTGTGTTCTGTCCGCGGATTGGGTCCTGCATGAAATGATTATCCACCTGAACAAT
ACCCATCTGGTGCAGGAAGCCGTCATTGTGGCAGTTCAACGTACGCTGCCGGATTCACACATCGT
TTTTCGCCTGCTGAAACCGCATTGGGTGGTTACCCTGTCGCTGAATGCCCAGGCACGTAGCGTTC
TGATCCCGGAAGTCATTGTGCCGATCGCGGGCTTCAGTGAACTGCGCATCTTTCAGTTCGTTGGT
CACGCCTTTACCAACTTCGACTGGAAAGCACTGTATGTCCCGACGGATCTGGAATTTCGTGGTTT
CCCGCTGGACCGCCTGGATGACGATAAGTTCCATAACTATGCTTACGCGAAGGACATTAAGGATA
TGTGGATGGCCCTGCGTAAGTTCGTGAGTTCCGTTCTGAAAGATGGCAAGTATTACCCGGACGAT
TCGGCTGTTGCAGCAGACGCGCAGATTCAAGACTGGTGCGATGAAATGCGCAGCGAAAAAGGCGC
GGGTATGAAAAAGTTCCCGGAAAGCATTTCTACCCTGGACGATCTGATCGATATGGTGACGATGT
GTATTCACATCGCAGCTCCGCAGCATACCGCCGTGAACTATCTGCAGCAATATTACCAAACGTTT
GTTCCGAATAAACCGTCAGCACTGTTCTCGCCGCTGCCGACCCTGCTGAGCCAGCTGGAATCTTA
CACGGAAAGTGATCTGATGGCGGCCCTGCCGCTGGGTGCTAAACAGGAATGGCTGCTGATGGCGC
AAGTGCCGTATCTGCTGTCTAAGGAAGTCGAACAGGATGGCAACATTGTGACCTACGCCGGTACG
GCAAGTAACAATGAAGATCCGATTATCGCAGCTGCGGGCAAAGAACTGTCCGCTGACCTGGTCAT
CCTGGCGGGTGTGTTTCTGAAAAACTCAGAAAAGCTGGACGATCAGAACACCGCCTATAATGTCC
TGGCACCGGATCAACTGGCCAATGCAATTGTGATCTAA (SEQ ID NO: 48)

>CiVO [Cichorium intybus]

MEISIPTTLGLAVIIFIIFKLLTRTTSKKNLLPEPWRLPIIGHMHHLIGTMPHRGVMELARKHGSL
MHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLAPYGEYWRQLRKLCT
LELLSNKKVKSFQSLREEECWNLVKDIRSTGQGSPINLSENIFKMIATILSRAAFGKGIKDQMKFT
ELVKEILRLTGGFDVADIFPSKKLLHHLSGKRAKLTNIHNKLDNLINNIIAEHPGNRTSSSQETLL
DVLLRLKESAEFPLTADNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGK
ERIQEEDLQELNYLKLVIKETLRLHPPLPLVMPRECREPCVLGGYDIPSKTKLIVNVFAINRDPEY
WKDAETFMPERFENSPITVMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYFNWKLPNGKTF
EDLDMTESFGATVQRKTELLLVPTDFQTLTAST (SEQ ID NO: 49 | Wild Type)

MALLLAVFLAVIIFIIFKLLTRTTSKKNLLPEPWRLPIIGHMHHLIGTMPHRGVMELARKHGSLMH
LQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLAPYGEYWRQLRKLCTLE
LLSNKKVKSFQSLREEECWNLVKDIRSTGQGSPINLSENIFKMIATIL*SR*AAFGKGIKDQMKFTEL
VKEILRLTGGFDVADIFPSKKLLHHLSGKRAKLTNIHNKLDNLINNIIAEHPGNRTSSSQETLLDV
LLRLKESAEFPLTADNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGKER
IQEEDLQELNYLKLVIKETLRLHPPLPLVMPRECREPCVLGGYDIPSKTKLIVNVFAINRDPEYWK
DAETFMPERFENSPITVMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYFNWKLPNGKTFED
LDMTESFGATVQRKTELLLVPTDFQTLTAST (SEQ ID NO: 50)

ATGGCTCTGTTATTAGCAGTTTTTCTGGCTGTCATTATCTTTATCATCTTCAAACTGCTGACCCGC
ACCACCTCGAAGAAAAACCTGCTGCCGGAACCGTGGCGTCTGCCGATTATCGGCCACATGCATCAC
CTGATTGGCACCATGCCGCACCGTGGTGTGATGGAACTGGCGCGCAAACATGGCTCACTGATGCAC
CTGCAGCTGGGTGAAGTGAGCACCATCGTGGTTAGCTCTCCGCGTTGGGCGAAAGAAGTTCTGACC
ACGTATGATATTACCTTTGCCAACCGCCCGGAAACCCTGACGGGCGAAATCGTGGCATACCATAAT
ACGGACATTGTTCTGGCTCCGTATGGTGAATACTGGCGTCAGCTGCGCAAACTGTGCACCCTGGAA
CTGCTGAGTAACAAAAAAGTCAAATCTTTTCAAAGTCTGCGTGAAGAAGAATGTTGGAATCTGGTG
AAAGATATCCGCTCCACCGGCCAGGGTTCACCGATCAACCTGTCGGAAAACATCTTCAAAATGATC
GCGACGATCCTGTCTCGTGCGGCCTTTGGCAAAGGTATTAAAGACCAAATGAAATTCACCGAACTG
GTTAAAGAAATCCTGCGCCTGACGGGCGGTTTTGATGTCGCAGACATTTTCCCGAGTAAAAAACTG
CTGCATCACCTGTCCGGCAAACGTGCTAAACTGACCAACATCCATAACAAACTGGATAACCTGATC
AACAACATTATCGCCGAACACCCGGGTAATCGTACCAGTTCCTCACAGGAAACGCTGCTGGATGTT
CTGCTGCGCCTGAAAGAAAGCGCAGAATTTCCGCTGACCGCGGACAATGTTAAAGCCGTCATTCTG
GATATGTTCGGTGCAGGCACCGACACGTCGAGCGCAACCATTGAATGGGCTATCTCTGAACTGATT
CGTTGCCCGCGCGCGATGGAAAAAGTGCAGACGGAACTGCGTCAAGCCCTGAACGGCAAAGAACGC
ATCCAGGAAGAAGATCTGCAAGAACTGAACTACCTGAAACTGGTTATCAAAGAAACCCTGCGCCTG
CATCCGCCGCTGCCGCTGGTCATGCCGCGTGAATGCCGCGAACCGTGTGTGCTGGGCGGTTATGAT
ATCCCGAGCAAAACCAAACTGATCGTCAACGTGTTTGCAATTAATCGTGACCCGGAATACTGGAAA
GACGCTGAAACCTTTATGCCGGAACGCTTCGAAAACAGCCCGATTACGGTTATGGGTTCTGAATAT
GAATACCTGCCGTTTGGTGCAGGTCGTCGCATGTGTCCGGGTGCAGCTCTGGGTCTGGCGAATGTC
GAACTGCCGCTGGCCCACATCCTGTATTACTTCAACTGGAAACTGCCGAATGGCAAAACCTTTGAA
GATCTGGACATGACCGAATCCTTCGGTGCAACGGTGCAACGCAAAACCGAACTGCTGCTGGTGCCG
ACGGATTTCCAAACGCTGACCGCATCAACG (SEQ ID NO: 51)

>HaGAO [Helianthus annuus]

MEVSLTTSIALATIVFFLYKLLTRPTSSKNRLPEPWRLPIIGHMHHLIGTMPHRGVMDLARKYGSL
MHLQLGEVSAIVVSSPKWAKEILTTYDIPFANRPETLTGEIIAYHNTDIVLAPYGEYWRQLRKLCT
LELLSVKKVKSFQSLREEECWNLVQEIKASGSGTPFNLSEGIFKVIATVL*SR*AAFGKGIKDQKQFT
EIVKEILRETGGFDVADIFPSKKFLHHLSGKRGRLTSIHNKLDSLINNLVAEHTVSKSSKVNETLL
DVLLRLKNSEEFPLTADNVKAIILDMFGAGTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGK
ERIKEEEIQDLPYLNLVIRETLRLHPPLPLVMPRECRQAMNLAGYDVANKTKLIVNVFAINRDPEY
WKDAESFNPERFENSNTTIMGADYEYLPFGAGRRMCPGSALGLANVQLPLANILYYFKWKLPNGAS
HDQLDMTESFGATVQRKTELMLVPSF (SEQ ID NO: 52 | Wild Type)

MALLLAVFIALATIVFFLYKLLTRPTSSKNRLPEPWRLPIIGHMHHLIGTMPHRGVMDLARKYGSL
MHLQLGEVSAIVVSSPKWAKEILTTYDIPFANRPETLTGEIIAYHNTDIVLAPYGEYWRQLRKLCT
LELLSVKKVKSFQSLREEECWNLVQEIKASGSGTPFNLSEGIFKVIATVL*SR*AAFGKGIKDQKQFT
EIVKEILRETGGFDVADIFPSKKFLHHLSGKRGRLTSIHNKLDSLINNLVAEHTVSKSSKVNETLL
DVLLRLKNSEEFPLTADNVKAIILDMFGAGTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGK
ERIKEEEIQDLPYLNLVIRETLRLHPPLPLVMPRECRQAMNLAGYDVANKTKLIVNVFAINRDPEY
WKDAESFNPERFENSNTTIMGADYEYLPFGAGRRMCPGSALGLANVQLPLANILYYFKWKLPNGAS
HDQLDMTESFGATVQRKTELMLVPSF (SEQ ID NO: 53)

ATGGCTCTGTTATTAGCAGTTTTCATCGCCCTGGCAACCATTGTCTTTTTCCTGTATAAACTGCTG
ACCCGTCCGACCTCATCTAAAAACCGTCTGCCGGAACCGTGGCGCCTGCCGATTATCGGCCACATG
CATCACCTGATTGGCACCATGCCGCACCGTGGTGTCATGGATCTGGCACGCAAATATGGCAGCCTG
ATGCATCTGCAACTGGGTGAAGTTTCTGCGATTGTGGTTAGCTCTCCGAAATGGGCCAAAGAAATT
CTGACCACCTATGATATTCCGTTTGCGAACCGCCCGGAAACCCTGACGGGCGAAATTATCGCATAC
CACAATACCGACATTGTGCTGGCTCCGTATGGTGAATACTGGCGTCAACTGCGTAAACTGTGCACG
CTGGAACTGCTGAGTGTTAAAAAAGTCAAAAGTTTCCAGAGCCTGCGTGAAGAAGAATGTTGGAAC
CTGGTTCAAGAAATTAAAGCGAGCGGCAGCGGCACCCCGTTTAATCTGAGTGAAGGTATTTTCAAA
GTGATTGCGACCGTGCTGAGCCGTGCGGCATTTGGTAAAGGTATCAAAGATCAGAAACAATTCACC
GAAATTGTCAAAGAAATCCTGCGCGAAACGGGCGGTTTTGATGTGGCGGACATCTTTCCGAGCAAA
AAATTCCTGCATCACCTGTCTGGCAAACGTGGTCGCCTGACCTCAATTCATAACAAACTGGATTCG
CTGATCAACAATCTGGTCGCCGAACATACCGTGAGCAAAAGCAGCAAAGTGAATGAAACGCTGCTG
GATGTCCTGCTGCGTCTGAAAAACTCGGAAGAATTTCCGCTGACCGCAGACAATGTGAAAGCTATT
ATCCTGGATATGTTCGGTGCAGGCACCGATACCAGCAGCGCAACGGTGGAATGGGCCATTAGCGAA
CTGATCCGTTGCCCGCGCGCAATGGAAAAAGTTCAGGCAGAACTGCGTCAAGCTCTGAACGGCAAA
GAACGCATTAAAGAAGAAGAAATCCAGGATCTGCCGTATCTGAATCTGGTTATTCGTGAAACCCTG
CGTCTGCATCCGCCGCTGCCGCTGGTCATGCCGCGTGAATGTCGCCAAGCAATGAACCTGGCTGGC
TATGACGTGGCAAATAAAACCAAACTGATCGTCAATGTGTTTGCGATTAACCGTGACCCGGAATAC

TGGAAAGACGCGGAAAGTTTTAACCCGGAACGCTTTGAAAACAGCAACACCACGATTATGGGTGCG
GATTATGAATACCTGCCGTTTGGCGCCGGTCGTCGCATGTGTCCGGGCAGCGCGCTGGGTCTGGCC
AACGTTCAACTGCCGCTGGCCAATATCCTGTATTACTTCAAATGGAAACTGCCGAATGGCGCCTCA
CACGATCAACTGGACATGACCGAATCGTTTGGTGCAACCGTGCAACGCAAAACGGAACTGATGCTG
GTTCCGTCTTTC (SEQ ID NO: 54)

Figure 4B

>n20yhcB-t29SrKO
MAWEYALIGLVVGIIIGAVAAWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTFT
RWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTADKTMVAMSDYDDY
HKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMRQ
ALGKDVESLYVEDLKITMNRDEIFQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRR
EAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYEL
AKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLGGYH
VPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLTASI
GIGRMVQEFEWKLKDMTQEEVNTIGLTTQMLRPLRAIIKPRI (SEQ ID NO: 55)

>n22yhcB-t30VO1c9
MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTF
TRWAATYGPIYSIKTGATSVVVVSSNEIAKEAMVTRFQSISTRNLSKALKVLTADKTMVAMSDYDD
YHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMR
QALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR
REAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYE
LAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGY
HVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIAS
IGIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 56)

>n22yhcB-t30VO1c12
MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTF
TKWAATYGPIYSIKTGATSMVVVSSNEIAKEAMVTRFQSISTRNLSKALKVLTADKQMVAMSDYDD
YHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMR
QALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR
REAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYE
LAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGY
HVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIAS
IGIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 57)

>n22yhcB-t30VO1b4
MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTF
TRWAATYGPIYSIKTGATSVVVVSSNEIAKEAMVTRFQSISTRNLSKALKVLTADKQMVAMSDYDD
YHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMR
QALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR
REAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYE
LAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGY
HVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIAS
IGIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 58)

>n20yhcB-t29VO1c11
MAWEYALIGLVVGIIIGAVAAWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTFT
KWAATYGPIYSIKTGATSMVVVSSNEIAKEAMVTRFQSISTRNLSKALKVLTADKQMVAMSDYDDY
HKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMRQ
ALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRR
EAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYEL
AKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGYH
VPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIASI
GIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 59)

>n22yhcB-t30VO1b6

MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTF
TKWAATYGPIYSIKTGATSVVVVSSNEIAKEAMVTRFQSISTRNLSKALKVLTADKTMVAMSDYDD
YHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMR
QALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR

REAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYE
LAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPIIPLRHVHEDTVLGGY
HVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIAS
IGIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 60)

>n22yhcB-t30VO1c6 (VO2)

MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEKKPYMTF
TKWAATYGPIYSIKTGATSVVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTADKQMVAMSDYDD
YHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQEEVDLRKIFQSELFGLAMR
QALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWRDFFPYLKWVPNKKFENTIQQMYIR
REAVMKSLIKEQKKRIASGEKLNSYIDYLLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYE
LAKNPKLQDRLYRDIKSVCGSEKITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGY
HVPAGTELAVNIYGCNMDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIAS
IGIGRMVQEFEWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI (SEQ ID NO: 61)

Figure 5A

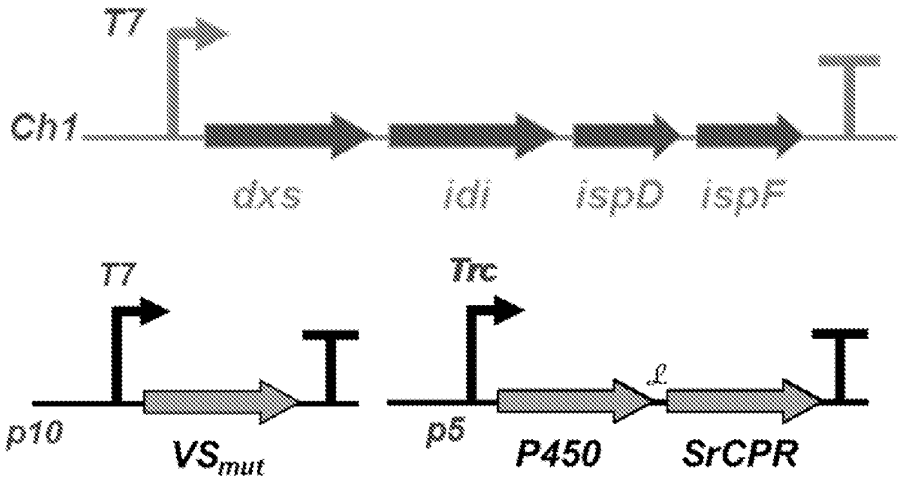


Figure 5B

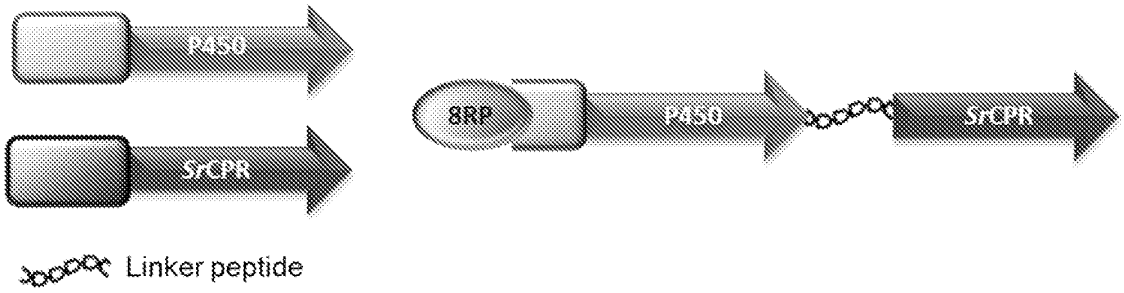


Figure 6A

>*Sr*CPR [Stevia rebaudiana]

MQSDSVKVSPFDLVSAAMNGKAMEKLNASESEDPTTLPALKMLVENRELLTLFTTSFAVLIGCLVF
LMWRRSSSKKLVQDPVPQVIVVKKKEKESEVDDGKKKVSIFYGTQTGTAEGFAKALVEEAKVRYEK
TSFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAANFYKWFTEGDDKGEWLKKLQY
GVFGLGNRQYEHFNKIAIVVDDKLTEMGAKRLVPVGLGDDDQCIEDDFTAWKELVWPELDQLLRDE
DDTSVTTPYTAAVLEYRVVYHDKPADSYAEDQTHTNGHVVHDAQHP*SR*SNVAFKKELHTSQSDRSC
THLEFDISHTGLSYETGDHVGVYSENLSEVVDEALKLLGLSPDTYFSVHADKEDGTPIGGASLPPP
FPPCTLRDALTRYADVLSSPKKVALLALAAHASDPSEADRLKFLASPAGKDEYAQWIVANQRSLLE
VMQSFPSAKPPLGVFFAAVAPRLQPRYYSISSSPKMSPNRIHVTCALVYETTPAGRIHRGLCSTWM
KNAVPLTESPDCSQASIFVRTSNFRLPVDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGSS
IFFFGCRNRKVDFIYEDELNNFVETGALSELIVAF*SR*EGTAKEYVQHKMSQKASDIWKLLSEGAYL
YVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW (SEQ ID NO: 62)

ATGCAGAGCGATTCTGTTAAAGTATCCCCGTTCGACCTGGTCTCTGCGGCTATGAACGGCAAAGCA
ATGGAGAAACTGAACGCGAGCGAATCTGAAGATCCAACCACCCTGCCGGCACTGAAAATGCTGGTA
GAAAACCGTGAACTGCTGACTCTGTTCACCACCTCCTTCGCCGTTCTGATTGGTTGCCTGGTCTTC
CTGATGTGGCGCCGTTCCTCTTCCAAGAAGCTGGTACAGGACCCGGTTCCTCAGGTGATCGTCGTT
AAAAAGAAAGAGAAGGAAAGCGAAGTCGATGACGGCAAAAAGAAGGTTTCCATTTTCTACGGTACT
CAGACCGGCACCGCTGAGGGTTTTGCCAAAGCACTGGTTGAAGAGGCAAAAGTGCGTTACGAAAAA
ACTTCCTTCAAAGTGATTGACCTGGACGACTATGCTGCGGATGATGATGAATACGAGGAAAAACTG
AAAAAAGAAAGCCTGGCCTTCTTCTTCCTGGCAACCTATGGCGATGGTGAACCGACCGACAACGCG
GCGAACTTCTACAAATGGTTTACCGAAGGCGACGACAAAGGTGAATGGCTGAAGAAACTGCAGTAT
GGTGTTTTCGGTCTGGGCAATCGCCAGTACGAACATTTTAACAAAATCGCAATCGTTGTTGATGAC
AAACTGACTGAAATGGGTGCGAAACGTCTGGTGCCGGTTGGCCTGGGTGACGATGATCAATGCATC
GAAGATGACTTCACCGCATGGAAAGAACTGGTTTGGCCGGAACTGGATCAGCTGCTGCGCGACGAA
GACGACACTTCCGTGACCACCCCGTATACCGCTGCAGTGCTGGAGTACCGTGTTGTTTACCACGAT
AAACCGGCGGACTCTTACGCCGAAGATCAGACTCACACTAACGGTCACGTCGTACATGACGCACAG
CACCCGTCTCGTAGCAATGTTGCGTTTAAGAAAGAGCTGCACACGAGCCAGTCCGACCGCTCTTGT
ACGCACCTGGAGTTCGATATCTCCCACACCGGTCTGTCCTATGAAACCGGTGACCATGTTGGCGTT
TACAGCGAAAACCTGAGCGAGGTAGTTGATGAAGCGCTGAAACTGCTGGGCCTGTCTCCAGACACC
TACTTTAGCGTGCATGCTGACAAGGAAGATGGTACTCCGATTGGCGGCGCTTCCCTGCCGCCACCG
TTTCCACCTTGCACTCTGCGTGATGCTCTGACTCGTTACGCTGATGTTCTGTCTAGCCCGAAAAAG
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GCGTCTCCGGCCGGCAAAGACGAATACGCGCAGTGGATTGTCGCTAACCAGCGCTCTCTGCTGGAA
GTGATGCAGTCCTTCCCGTCTGCCAAACCGCCACTGGGCGTGTTTTTCGCAGCTGTGGCTCCGCGC
CTGCAGCCGCGCTACTATTCTATCTCTAGCTCCCCGAAAATGAGCCCGAACCGCATCCACGTTACT
TGTGCTCTGGTTTACGAAACCACCCCTGCGGGCCGTATCCACCGTGGTCTGTGCTCTACGTGGATG
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AACTTCCGTCTGCCGGTGGACCCGAAAGTTCCTGTTATCATGATCGGTCCTGGCACGGGTCTGGCC
CCGTTTCGTGGTTTTCTGCAGGAGCGTCTGGCTCTGAAAGAATCCGGTACTGAGCTGGGCTCTTCC
ATCTTTTTCTTCGGTTGTCGTAACCGCAAAGTCGATTTCATCTATGAAGACGAACTGAACAACTTC
GTAGAGACTGGTGCACTGTCCGAACTGATTGTGGCATTCTCTCGTGAAGGCACGGCGAAAGAATAC
GTTCAACACAAAATGTCTCAGAAAGCGAGCGATATCTGGAAACTGCTGTCCGAGGGTGCGTATCTG
TATGTTTGTGGCGACGCGAAAGGCATGGCTAAAGATGTACACCGCACCCTGCACACCATTGTACAA
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TACCTGCGTGATGTATGGTAA (SEQ ID NO: 63)

>AtCPR [Arabidopsis thaliana]

MTSALYASDLFKQLKSIMGTDSLSDDVVLVIATTSLALVAGFVVLLWKKTTADRSGELKPLMIPKS
LMAKDEDDDLDLGSGKTRVSIFFGTQTGTAEGFAKALSEEIKARYEKAAVKVIDLDDYAADDDQYE
EKLKKETLAFFCVATYGDGEPTDNAARFSKWFTEENERDIKLQQLAYGVFALGNRQYEHFNKIGIV
LDEELCKKGAKRLIEVGLGDDDQSIEDDFNAWKESLWSELDKLLKDEDDKSVATPYTAVIPEYRVV
THDPRFTTQKSMESNVANGNTTIDIHHPCRVDVAVQKELHTHESDRSCIHLEFDI*SR*TGITYETGD
HVGVYAENHVEIVEEAGKLLGHSLDLVFSIHADKEDGSPLESAVPPPFPGPCTLGTGLARYADLLN
PPRKSALVALAAYATEPSEAEKLKHLTSPDGKDEYSQWIVASQRSLLEVMAAFPSAKPPLGVFFAA

IAPRLQPRYYSISSCQDWAP*SR*VHVTSALVYGPTPTGRIHKGVCSTWMKNAVPAEKSHECSGAPIF
IRASNFKLPSNPSTPIVMVGPGTGLAPFRGFLQERMALKEDGEELGSSLLFFGCRNRQMDFIYEDE
LNNFVDQGVISELIMAF*SR*EGAQKEYVQHKMMEKAAQVWDLIKEEGYLYVCGDAKGMARDVHRTLH
TIVQEQEGVSSSEAEAIVKKLQTEGRYLRDVW (SEQ ID NO: 64)

ATGACCAGCGCACTGTACGCAAGCGACCTGTTTAAGCAACTGAAGAGCATTATGGGCACCGATAGC
CTGAGCGATGATGTTGTCCTGGTCATTGCGACCACGAGCCTGGCACTGGTGGCTGGTTTTGTGGTT
CTGCTGTGGAAAAAGACCACGGCCGATCGTTCTGGCGAACTGAAACCGCTGATGATTCCGAAAAGT
CTGATGGCAAAGGACGAAGATGACGATCTGGATCTGGGCTCCGGTAAAACCCGTGTGTCAATCTTT
TTCGGTACCCAGACGGGCACCGCAGAAGGTTTCGCAAAAGCTCTGTCTGAAGAAATTAAGGCGCGC
TATGAAAAAGCGGCCGTTAAGGTCATCGATCTGGACGATTATGCAGCTGACGATGACCAGTACGAA
GAAAAACTGAAAAAGGAAACCCTGGCGTTTTTCTGCGTTGCCACCTACGGCGACGGTGAACCGACG
GATAACGCGGCCCGTTTTAGTAAATGGTTCACCGAAGAAAATGAACGCGACATTAAGCTGCAGCAA
CTGGCGTATGGCGTGTTTGCTCTGGGTAACCGTCAGTACGAACATTTCAACAAGATCGGTATCGTC
CTGGATGAAGAACTGTGTAAAAAGGGCGCGAAGCGCCTGATTGAAGTGGGCCTGGGTGATGACGAT
CAATCCATCGAAGACGATTTTAACGCCTGGAAAGAATCTCTGTGGAGTGAACTGGACAAACTGCTG
AAGGATGAAGACGATAAGAGCGTGGCGACGCCGTATACCGCCGTTATTCCGGAATACCGTGTCGTG
ACCCATGATCCGCGCTTCACCACGCAGAAAAGCATGGAATCAAATGTTGCGAACGGTAATACCACG
ATTGACATCCATCACCCGTGCCGTGTGGATGTTGCCGTCCAAAAAGAACTGCATACCCACGAATCG
GACCGTAGCTGTATCCACCTGGAATTTGATATTAGCCGCACGGGCATCACCTATGAAACGGGCGAC
CATGTGGGTGTTTACGCAGAAAACCACGTGGAAATTGTTGAAGAAGCTGGCAAACTGCTGGGTCAT
TCGCTGGATCTGGTTTTTAGCATCCACGCGGACAAGGAAGATGGTTCGCCGCTGGAAAGCGCAGTG
CCGCCGCCGTTCCCGGGTCCGTGCACCCTGGGTACGGGTCTGGCACGTTATGCAGATCTGCTGAAT
CCGCCGCGCAAATCCGCACTGGTGGCTCTGGCAGCTTACGCAACCGAACCGTCAGAAGCTGAAAAA
CTGAAGCATCTGACGTCGCCGGACGGTAAAGATGAATATAGCCAGTGGATTGTTGCGTCTCAACGC
AGTCTGCTGGAAGTCATGGCAGCATTTCCGTCGGCAAAACCGCCGCTGGGCGTGTTTTTCGCAGCT
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GTCCATGTGACCAGTGCACTGGTGTATGGTCCGACGCCGACCGGTCGCATTCACAAAGGCGTGTGC
TCTACCTGGATGAAAAACGCGGTTCCGGCCGAAAAGTCTCACGAATGTAGTGGTGCGCCGATTTTT
ATCCGTGCCAGTAACTTCAAACTGCCGTCCAATCCGTCAACCCCGATCGTTATGGTCGGTCCGGGT
ACGGGTCTGGCACCGTTTCGTGGTTTCCTGCAGGAACGCATGGCTCTGAAAGAAGATGGCGAAGAA
CTGGGTAGTTCCCTGCTGTTTTTCGGCTGCCGTAATCGCCAGATGGACTTCATCTACGAAGATGAA
CTGAACAACTTCGTCGATCAAGGTGTGATTTCCGAACTGATCATGGCATTTTCACGCGAAGGCGCT
CAGAAAGAATACGTCCAACATAAAATGATGGAAAAGGCGGCCCAAGTGTGGGATCTGATCAAAGAA
GAAGGCTATCTGTACGTTTGTGGCGACGCAAAGGGTATGGCTCGTGATGTCCATCGCACCCTGCAC
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ACCGAAGGCCGTTATCTGCGCGATGTTTGGTAA (SEQ ID NO: 65)

>TcCPR [Taxus cuspidata]

MQANSNTVEGASQGKSLLDI*SR*LDHIFALLLNGKGGDLGAMTGSALILTENSQNLMILTTALAVLV
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RYEKAVFKVVDLDNYAADDEQYEEKLKKEKLAFFMLATYGDGEPTDNAARFYKWFLEGKEREPWLS
DLTYGVFGLGNRQYEHFNKVAKAVDEVLIEQGAKRLVPVGLGDDDQCIEDDFTAWREQVWPELDQL
LRDEDDEPTSATPYTAAIPEYRVEIYDSVVSVYEETHALKQNGQAVYDIHHPCRSNVAVRRELHTP
LSDRSCIHLEFDISDTGLIYETGDHVGVHTENSIETVEEAAKLLGYQLDTIFSVHGDKEDGTPLGG
SSLPPPFPGPCTLRTALARYADLLNPPRKAAFLALAAHASDPAEAERLKFLSSPAGKDEYSQWVTA
SQRSLLEIMAEFPSAKPPLGVFFAAIAPRLQPRYYSISSSPRFAP*SR*IHVTCALVYGPSPTGRIHK
GVCSNWMKNSLPSEETHDCSWAPVFVRQSNFKLPADSTTPIVMVGPGTGFAPFRGFLQERAKLQEA
GEKLGPAVLFFGCRNRQMDYIYEDELKGYVEKGILTNLIVAF*SR*EGATKEYVQHKMLEKASDTWSL
IAQGGYLYVCGDAKGMARDVHRTLHTIVQEQESVDSSKAEFLVKKLQMDGRYLRDIW (SEQ ID
NO: 66)

ATGCAGGCTAATTCCAACACGGTGGAAGGTGCCTCCCAGGGGAAGAGCCTGCTGGACATATCTCGG
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GCTTTGATTTTGACAGAGAATTCGCAGAATTTGATGATTTTGACCACGGCTTTGGCTGTTTTGGTC
GCGTGTGTTTTCTTCTTCGTTTGGAGGAGGGGAGGATCGGATACGCAGAAGCCGGCGGTGAGACCG
ACGCCTCTGGTGAAGGAGGAAGATGAGGAGGAAGAAGACGATTCTGCAAAGAAGAAAGTCACGATT
TTCTTTGGGACACAGACTGGGACGGCCGAGGGATTTGCCAAGGCTCTAGCAGAAGAGGCAAAGGCA
AGATATGAGAAAGCTGTGTTTAAAGTCGTAGATTTGGACAACTATGCAGCAGATGATGAGCAGTAT
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ACTGACAATGCAGCAAGATTTTATAAGTGGTTTCTTGAGGGCAAGGAGAGGGAGCCATGGCTTTCT
GATCTCACTTATGGGGTGTTTGGATTAGGCAACAGACAATATGAACATTTTAATAAGGTGGCTAAA
GCAGTAGATGAAGTCTTAATTGAACAAGGTGCAAAGCGACTTGTTCCAGTGGGCCTTGGTGATGAT
GACCAATGCATTGAAGATGACTTTACTGCTTGGCGAGAGCAGGTTTGGCCTGAACTGGATCAGTTA
CTCCGGGATGAAGATGATGAGCCCACAAGTGCTACACCTTATACAGCTGCCATACCTGAGTATAGG
GTTGAAATTTATGATTCCGTGGTTTCAGTGTACGAGGAAACTCATGCTCTCAAGCAAAATGGCCAA
GCTGTTTATGATATCCATCACCCCTGCAGATCTAATGTGGCAGTGAGAAGAGAGCTTCATACACCT
TTGTCTGACCGCTCTTGCATCCATTTGGAATTTGATATATCAGACACTGGCCTTATATATGAGACA
GGAGATCATGTTGGTGTCCATACAGAAAACAGCATTGAAACTGTGGAGGAAGCAGCAAAGCTACTA
GGCTACCAATTGGACACTATATTCTCAGTCCACGGTGACAAAGAAGATGGCACGCCACTTGGAGGG
TCTTCTTTGCCACCACCTTTCCCTGGTCCATGCACCCTACGAACTGCTCTTGCTCGTTATGCTGAT
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GGTCCTGGAACTGGTTTTGCACCTTTTAGAGGTTTTTTGCAGGAAAGAGCAAAACTTCAAGAAGCT
GGTGAGAAGCTCGGTCCGGCTGTTTTATTTTTTGGGTGCAGGAATCGCCAAATGGACTACATTTAT
GAAGATGAGCTGAAGGGCTATGTGGAGAAAGGAATACTGACCAATCTCATTGTTGCTTTCTCTCGT
GAAGGAGCAACCAAAGAGTATGTCCAGCACAAGATGCTGGAAAAGGCATCCGATACCTGGAGTCTC
ATTGCTCAGGGTGGGTATCTTTATGTATGTGGTGATGCCAAGGGTATGGCTAGGGATGTACACAGG
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>AaCPR [Artemisia annua]

MAQSTTSVKLSPFDLMTALLNGKVSFDTSNTSDTNIPLAVFMENRELLMILTTSVAVLIGCVVVLV
WRRSSSAAKKAAESPVIVVPKKVTEDEVDDGRKKVTVFFGTQTGTAEGFAKALVEEAKARYEKAVF
KVIDLDDYAAEDDEYEEKLKKESLAFFFLATYGDGEPTDNAARFYKWFTEGEEKGEWLDKLQYAVF
GLGNRQYEHFNKIAKVVDEKLVEQGAKRLVPVGMGDDDQCIEDDFTAWKELVWPELDQLLRDEDDT
SVATPYTAAVAEYRVVFHDKPETYDQDQLTNGHAVHDAQHPCRSNVAVKKELHSPLSDRSCTHLEF
DISNTGLSYETGDHVGVYVENLSEVVDEAEKLIGLPPHTYFSVHADNEDGTPLGGASLPPPFPPCT
LRKALASYADVLSSPKKSALLALAAHATDSTEADRLKFLASPAGKDEYAQWIVASHRSLLEVMEAF
PSAKPPLGVFFASVAPRLQPRYYSISSSPRFAPNRIHVTCALVYEQTPSGRVHKGVCSTWMKNAVP
MTESQDCSWAPIYVRTSNFRLPSDPKVPVIMIGPGTGLAPFRGFLQERLAQKEAGTELGTAILFFG
CRNRKVDFIYEDELNNFVETGALSELVTAFSREGATKEYVQHKMTQKASDIWNLLSEGAYLYVCGD
AKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMAGRYLRDVW (SEQ ID NO: 68)

ATGGCGCAGTCTACCACCAGCGTGAAATTGTCCCCTTTTGATCTCATGACCGCTCTGCTGAATGGG
AAAGTCTCATTCGATACAAGCAACACAAGTGATACCAACATCCCTTTGGCGGTTTTTATGGAGAAT
AGAGAGTTACTCATGATTTTAACGACTTCCGTGGCCGTGCTCATTGGGTGCGTCGTCGTACTTGTC
TGGCGCCGGTCAAGTAGCGCAGCAAAGAAGGCGGCGGAGTCCCCGGTTATCGTCGTCCCAAAGAAG
GTTACAGAGGACGAGGTGGACGACGGACGCAAAAAAGTGACGGTATTCTTTGGTACACAGACCGGA
ACCGCGGAAGGATTTGCTAAAGCGCTGGTGGAAGAAGCTAAAGCCCGTTACGAAAAAGCGGTATTC
AAAGTGATAGACCTGGATGACTATGCGGCAGAGGACGACGAGTACGAGGAAAAATTGAAAAAAGAA
TCTCTTGCGTTCTTTTTTCTCGCCACTTACGGCGATGGAGAACCTACTGATAATGCGGCTCGGTTT
TATAAGTGGTTCACTGAGGGTGAAGAAAAAGGTGAATGGCTGGACAAATTGCAGTACGCAGTATTT
GGACTCGGGAATCGTCAATATGAACATTTTAACAAAATTGCTAAGGTCGTCGATGAAAAACTGGTT
GAGCAGGGTGCGAAACGTCTGGTCCCGGTTGGAATGGGCGATGACGACCAGTGCATTGAAGACGAC
TTTACAGCATGGAAGGAACTGGTGTGGCCGGAACTGGACCAACTTTTGCGTGACGAGGATGACACA
TCTGTAGCTACGCCGTACACTGCTGCGGTAGCCGAGTATAGGGTCGTTTTTCACGATAAACCGGAA
ACCTACGACCAAGACCAGCTCACAAATGGTCATGCAGTACATGATGCGCAACATCCTTGCAGGTCA
AATGTGGCGGTGAAGAAAGAGCTGCACAGTCCTCTGTCAGATCGTTCTTGCACCCACCTGGAATTT
GACATATCCAATACGGGCCTTTCGTATGAAACCGGAGATCACGTTGGTGTCTATGTTGAAAATCTG
TCGGAAGTGGTTGATGAGGCGGAAAAACTTATCGGTCTGCCGCCTCATACGTACTTTTCAGTCCAC
GCTGATAATGAAGACGGAACCCCGCTGGGTGGCGCATCGTTACCCCCACCCTTTCCACCATGCACT
CTGCGTAAGGCGCTTGCCAGTTATGCTGATGTTTTGTCTAGTCCCAAAAAGAGTGCACTTCTCGCA
CTGGCGGCCCATGCCACTGATAGTACAGAGGCCGACAGGCTGAAATTTCTGGCGTCACCAGCGGGA
AAAGACGAATACGCCCAATGGATCGTTGCCAGTCATCGGTCTTTACTGGAAGTGATGGAAGCGTTC
CCTTCCGCTAAGCCACCTCTGGGGGTCTTTTTCGCTAGTGTGGCACCCCGTCTACAGCCCCGGTAT

TACTCAATATCTAGCTCACCCAGATTTGCTCCGAATAGAATACACGTAACATGCGCGCTGGTCTAT
GAGCAGACCCCAAGTGGACGGGTGCATAAAGGGGTTTGTTCTACCTGGATGAAGAACGCCGTCCCA
ATGACCGAGTCTCAGGATTGTTCCTGGGCACCTATATATGTTAGAACATCAAACTTTCGACTGCCA
AGTGACCCGAAAGTTCCGGTAATTATGATAGGTCCAGGAACAGGGCTGGCTCCCTTTCGCGGGTTC
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ACTCAGAAAGCCTCAGATATATGGAACCTGCTGTCGGAGGGAGCCTATCTTTATGTTTGCGGTGAT
GCAAAAGGAATGGCCAAAGATGTCCACCGGACCCTCCACACTATTGTGCAGGAACAGGGTTCATTA
GACTCAAGTAAAGCCGAACTTTACGTAAAAAATCTACAGATGGCGGGCCGTTACCTCCGTGACGTT
TGGTAA (SEQ ID NO: 69)

>AtCPR1 [Arabidopsis thaliana]

MATSALYASDLFKQLKSIMGTDSLSDDVVLVIATTSLALVAGFVVLLWKKTTADRSGELKPLMIPK
SLMAKDEDDDLDLGSGKTRVSIFFGTQTGTAEGFAKALSEEIKARYEKAAVKVIDLDDYAADDDQY
EEKLKKETLAFFCVATYGDGEPTDNAARFYKWFTEENERDIKLQQLAYGVFALGNRQYEHFNKIGI
VLDEELCKKGAKRLIEVGLGDDDQSIEDDFNAWKESLWSELDKLLKDEDDKSVATPYTAVIPEYRV
VTHDPRFTTQKSMESNVANGNTTIDIHHPCRVDVAVQKELHTHESDRSCIHLEFDISRTGITYETG
DHVGVYAENHVEIVEEAGKLLGHSLDLVFSIHADKEDGSPLESAVPPPFPGPCTLGTGLARYADLL
NPPRKSALVALAAYATEPSEAEKLKHLTSPDGKDEYSQWIVASQRSLLEVMAAFPSAKPPLGVFFA
AIAPRLQPRYYSISSSPRLAPSRVHVTSALVYGPTPTGRIHKGVCSTWMKNAVPAEKSHECSGAPI
FIRASNFKLPSNPSTPIVMVGPGTGLAPFRGFLQERMALKEDGEELGSSLLFFGCRNRQMDFIYED
ELNNFVDQGVISELIMAFSREGAQKEYVQHKMMEKAAQVWDLIKEEGYLYVCGDAKGMARDVHRTL
HTIVQEQEGVSSSEAEAIVKKLQTEGRYLRDVW (SEQ ID NO: 70)

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GTGTTACTGTGGAAGAAGACTACCGCAGATAGGAGTGGTGAATTGAAACCGCTGATGATCCCAAAA
AGTCTGATGGCCAAAGATGAGGATGATGATCTGGATCTTGGATCAGGGAAGACGCGAGTCAGTATT
TTTTTCGGGACCCAGACGGGCACCGCGGAGGGCTTCGCCAAAGCTCTGTCCGAGGAAATAAAGGCC
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ACCGATAATGCAGCTAGGTTTTACAAGTGGTTTACCGAGGAGAACGAACGAGATATAAAGTTACAG
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GTTCTGGATGAGGAATTGTGCAAAAAGGGTGCAAAACGGCTGATAGAGGTGGGTCTAGGTGACGAT
GATCAATCTATAGAAGACGATTTTAATGCGTGGAAAGAGAGCTTATGGAGTGAACTGGATAAGCTC
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GTGACACACGATCCGAGGTTTACAACCCAAAAATCTATGGAGTCTAATGTCGCCAATGGCAACACA
ACGATTGATATTCACCACCCCTGTCGTGTTGACGTGGCTGTTCAAAAAGAACTTCATACACACGAA
AGTGACCGAAGTTGCATACACTTGGAATTTGACATTAGTCGCACCGGAATTACGTATGAAACTGGT
GATCACGTGGGTGTATACGCAGAAAATCATGTCGAAATAGTAGAAGAAGCTGGCAAACTGCTGGGA
CATTCACTCGATCTAGTGTTTAGTATACATGCCGATAAAGAGGATGGCAGCCCATTGGAAAGTGCC
GTCCCTCCGCCGTTTCCTGGACCGTGTACTCTGGGGACGGGACTCGCCCGCTATGCTGACCTGTTA
AACCCCCCTCGTAAAAGCGCCCTTGTGGCCCTGGCGGCATACGCAACTGAACCGAGCGAAGCGGAG
AAGCTGAAACATCTGACATCACCGGATGGCAAAGACGAGTATAGTCAGTGGATAGTAGCCTCTCAG
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GCTATCGCACCTCGGCTCCAGCCGCGCTATTACAGCATATCTTCAAGTCCCCGCTTAGCACCGTCT
CGTGTCCATGTCACTTCTGCGTTGGTTTATGGTCCGACTCCAACAGGTCGCATCCACAAAGGTGTC
TGTTCAACCTGGATGAAAAACGCGGTGCCCGCGGAGAAATCTCATGAGTGCAGTGGTGCACCTATT
TTTATCCGCGCAAGTAACTTCAAACTCCCTTCTAATCCGAGCACGCCCATTGTGATGGTTGGCCCA
GGCACTGGCCTTGCTCCGTTTCGCGGTTTTCTACAGGAGCGGATGGCCCTTAAAGAAGATGGGGAA
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GCTCAGAAAGAGTATGTCCAACACAAGATGATGGAAAAAGCGGCACAAGTGTGGGATCTTATTAAA
GAAGAAGGCTATCTTTATGTATGTGGGGATGCGAAAGGTATGGCCCGTGATGTCCATCGCACCCTG
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CAAACAGAGGGTCGTTACCTTCGCGACGTGTGGTAA (SEQ ID NO: 71)

>AtCPR2 [Arabidopsis thaliana]

MASSSSSSSTSMIDLMAAIIKGEPVIVSDPANASAYESVAAELSSMLIENRQFAMIVTTSIAVLIG
CIVMLVWRRSGSGNSKRVEPLKPLVIKPREEEIDDGRKKVTIFFGTQTGTAEGFAKALGEEAKARY
EKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEPTDNAARFYKWFTEGNDRGEWLKNL
KYGVFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQVGLGDDDQCIEDDFTAWREALWPELDTILR
EEGDTAVATPYTAAVLEYRVSIHDSEDAKFNDINMANGNGYTVFDAQHPYKANVAVKRELHTPESD
RSCIHLEFDIAGSGLTYETGDHVGVLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPISSSLP
PPFPPCNLRTALTRYACLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSL
LEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCST
WMKNAVPYEKSENCSSAPIFVRQSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESGVELG
PSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKASDIWNMISQGA
YLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW (SEQ ID NO: 72)

ATGGCGTCCAGCAGTTCATCGAGTTCTACAAGCATGATCGATCTGATGGCCGCTATTATCAAAGGG
GAACCCGTAATTGTCTCTGATCCAGCAAATGCCTCGGCATACGAGTCGGTGGCTGCCGAATTATCA
TCTATGTTAATTGAAAATAGACAATTTGCCATGATTGTGACAACTTCTATTGCTGTGCTGATAGGT
TGCATCGTCATGCTCGTGTGGCGCCGTAGCGGATCAGGCAACTCAAAGCGCGTCGAGCCTTTGAAA
CCCCTGGTTATCAAACCGCGAGAGGAGGAAATCGATGATGGCAGAAAAAAGGTTACTATCTTTTTT
GGCACACAGACGGGGACAGCGGAAGGTTTCGCGAAAGCACTCGGAGAGGAAGCGAAAGCCCGATAC
GAGAAAACACGGTTCAAAATTGTGGATCTGGATGACTATGCGGCTGATGATGATGAGTATGAAGAA
AAACTGAAAAAAGAAGATGTGGCGTTTTTTTTTCTTGCCACTTATGGCGACGGAGAGCCCACCGAT
AATGCAGCGCGGTTTTACAAGTGGTTCACCGAAGGAAATGATCGGGGAGAATGGTTAAAAAATCTG
AAATACGGTGTGTTCGGTCTTGGCAATCGCCAATATGAGCATTTTAATAAAGTCGCGAAAGTGGTC
GATGATATATTGGTAGAACAGGGCGCTCAGCGCCTCGTCCAGGTGGGGCTTGGCGACGATGATCAG
TGCATAGAAGATGATTTTACTGCATGGCGTGAAGCGCTGTGGCCGGAGCTGGACACCATTTTACGT
GAAGAGGGCGATACAGCAGTGGCAACCCCGTACACGGCTGCCGTCTTAGAGTATCGTGTGTCCATT
CATGATAGCGAGGATGCCAAATTCAATGACATCAATATGGCGAATGGAAATGGGTACACCGTGTTT
GACGCGCAGCACCCGTATAAGGCAAACGTTGCAGTCAAGAGGGAACTGCATACTCCTGAAAGTGAT
CGCAGTTGCATCCACCTGGAGTTCGATATTGCGGGATCAGGTTTAACGTACGAAACGGGCGACCAC
GTAGGTGTGCTGTGCGACAATCTTTCAGAGACAGTGGACGAAGCTCTGCGCCTGCTGGATATGAGC
CCGGATACCTATTTTAGCTTGCACGCTGAGAAAGAAGATGGGACTCCAATTAGCAGTAGCTTACCT
CCACCCTTTCCGCCGTGTAATTTGCGTACCGCCCTTACGCGCTATGCGTGTCTGCTGAGTTCGCCA
AAGAAGTCGGCCCTTGTGGCACTGGCGGCACATGCAAGTGACCCGACCGAGGCGGAGAGGCTGAAA
CATCTGGCTTCTCCAGCGGGCAAAGATGAATACAGCAAATGGGTGGTAGAATCACAGCGTTCCCTA
CTAGAAGTAATGGCCGAATTTCCCTCAGCTAAACCACCGCTGGGAGTGTTCTTTGCGGGCGTTGCT
CCCCGCTTGCAACCACGCTTTTATTCAATTAGCTCAAGTCCTAAGATAGCGGAAACACGGATACAT
GTAACTTGCGCATTGGTTTATGAAAAAATGCCAACCGGGAGGATACATAAAGGCGTATGTTCAACC
TGGATGAAAAATGCTGTGCCATACGAAAAGTCGGAGAATTGCTCCTCTGCCCCAATTTTCGTGCGT
CAAAGCAACTTTAAACTGCCGAGTGATTCAAAGGTGCCTATTATTATGATAGGCCCTGGTACAGGA
CTCGCCCCGTTTCGTGGTTTTCTTCAAGAAAGACTGGCTCTGGTCGAATCAGGCGTGGAATTAGGA
CCCTCCGTGTTATTTTTTGGCTGCCGCAACCGTCGAATGGACTTCATCTATGAAGAAGAATTGCAA
CGTTTTGTGGAGTCAGGCGCTCTGGCGGAACTATCCGTCGCCTTTAGTAGAGAAGGCCCAACCAAA
GAATACGTACAGCATAAGATGATGGATAAAGCGAGCGACATTTGGAATATGATCTCACAAGGGGCG
TACCTGTACGTATGTGGAGATGCCAAAGGAATGGCACGAGACGTACATAGATCGTTGCATACTATT
GCTCAAGAACAGGGAAGCATGGATTCGACTAAAGCAGAAGGCTTTGTTAAAAATCTACAGACATCT
GGTCGCTATCTGCGTGACGTGTGGTAA (SEQ ID NO: 73)

>ATR2 [Arabidopsis thaliana]

MASSSSSSSTSMIDLMAAIIKGEPVIVSDPANASAYESVAAELSSMLIENRQFAMIVTTSIAVLIG
CIVMLVWRRSGSGNSKRVEPLKPLVIKPREEEIDDGRKKVTIFFGTQTGTAEGFAKALGEEAKARY
EKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEPTDNAARFYKWFTEGNDRGEWLKNL
KYGVFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQVGLGDDDQCIEDDFTAWREALWPELDTILR
EEGDTAVATPYTAAVLEYRVSIHDSEDAKFNDITLANGNGYTVFDAQHPYKANVAVKRELHTPESD
RSCIHLEFDIAGSGLTMKLGDHVGVLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPISSSLP
PPFPPCNLRTALTRYACLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSL
LEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCST
WMKNAVPYEKSEKLFLGRPIFVRQSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESGVEL
GPSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKASDIWNMISQG
AYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW (SEQ ID NO:
74)

ATGGCGAGCAGTTCGTCCTCCTCTTCTACCAGTATGATCGATCTGATGGCCGCTATTATAAAAGGA
GAACCAGTCATTGTGTCTGATCCTGCAAACGCATCAGCCTACGAATCTGTGGCTGCTGAACTGTCC
TCGATGCTGATCGAAAATCGCCAATTTGCAATGATTGTTACAACCAGCATCGCTGTTCTTATCGGG
TGTATTGTCATGCTGGTTTGGCGGCGGAGTGGCAGCGGCAATTCTAAAAGAGTGGAGCCACTGAAG
CCTCTGGTAATCAAACCCCGCGAAGAAGAAATCGATGATGGACGTAAGAAAGTTACAATTTTTTTT
GGTACACAGACAGGTACAGCAGAGGGCTTTGCCAAAGCTCTTGGAGAAGAAGCAAAAGCTCGATAT
GAGAAAACACGCTTCAAGATCGTCGATCTGGATGACTACGCGGCAGACGACGATGAGTACGAAGAA
AAACTCAAAAAAGAGGATGTGGCTTTTTTTTTCCTGGCAACTTATGGGGACGGCGAGCCTACCGAC
AATGCAGCGCGGTTTTACAAATGGTTTACCGAAGGCAATGATAGAGGGGAGTGGCTCAAAAATCTC
AAATACGGAGTTTTCGGATTGGGGAATAGACAATACGAACACTTTAATAAGGTTGCGAAAGTGGTA
GATGATATTCTGGTCGAGCAGGGCGCGCAACGTTTAGTACAGGTCGGCCTGGGTGATGACGACCAG
TGCATCGAAGATGACTTTACGGCCTGGCGAGAAGCGCTCTGGCCGGAATTAGATACAATCCTTCGG
GAAGAGGGGGACACTGCTGTCGCTACCCCGTACACTGCCGCAGTGCTGGAATATCGTGTTTCAATA
CATGATTCGGAAGATGCCAAGTTTAATGACATCACCCTGGCAAACGGCAACGGATATACCGTATTT
GACGCTCAACATCCGTATAAGGCCAATGTAGCAGTAAAGCGGGAACTCCATACTCCCGAAAGTGAC
AGAAGTTGCATCCATCTGGAGTTCGATATAGCGGGAAGCGGACTGACTATGAAACTGGGAGATCAT
GTAGGGGTCCTGTGCGATAATTTGAGCGAAACCGTTGACGAAGCGCTCCGGCTTTTAGATATGTCC
CCTGATACTTATTTCTCTTTGCACGCCGAGAAGGAAGATGGTACACCTATATCCTCCTCGCTGCCG
CCGCCTTTTCCACCATGTAATCTGCGTACGGCCTTGACTAGGTATGCATGTCTTCTTAGCTCCCCG
AAAAAGTCCGCACTGGTAGCGTTGGCAGCTCATGCCAGCGATCCCACGGAGGCAGAGCGTTTAAAA
CACCTGGCGAGTCCTGCTGGCAAAGATGAATACAGCAAATGGGTGGTTGAGTCGCAGAGGTCCCTG
CTGGAAGTCATGGCTGAATTTCCGTCTGCGAAACCGCCTCTGGGAGTTTTCTTCGCAGGAGTAGCC
CCACGTTTACAACCGCGTTTCTATTCTATTTCTTCCTCCCCCAAGATCGCGGAAACTCGAATACAC
GTAACGTGCGCATTGGTGTATGAAAAGATGCCAACTGGTCGTATCCACAAGGGAGTGTGCTCAACC
TGGATGAAAAACGCCGTTCCGTATGAAAAATCGGAAAAATTGTTTTTGGGTAGACCCATATTCGTT
CGGCAGTCAAACTTTAAACTACCTTCTGATAGCAAGGTTCCGATTATTATGATTGGACCGGGTACT
GGCCTGGCGCCGTTCCGTGGTTTCCTGCAAGAACGGTTGGCGCTGGTGGAATCCGGCGTGGAACTT
GGGCCATCGGTTTTGTTTTTCGGGTGCCGCAATCGTCGCATGGACTTCATCTACGAGGAAGAACTC
CAGCGTTTTGTCGAAAGCGGTGCCCTTGCTGAATTGTCCGTTGCATTCAGCCGCGAAGGTCCAACT
AAGGAGTATGTGCAGCACAAAATGATGGACAAAGCGAGCGATATTTGGAATATGATTAGCCAGGGC
GCATACCTTTATGTGTGCGGTGATGCTAAGGGAATGGCGCGCGATGTCCATAGATCTTTACATACC
ATTGCACAGGAGCAGGGCTCTATGGATTCAACAAAAGCTGAAGGTTTTGTGAAAAACCTTCAGACC
AGCGGGCGGTATCTTCGCGATGTTTGGTAA (SEQ ID NO: 75)

>SrCPR1 [Stevia rebaudiana]

MAQSDSVKVSPFDLVSAAMNGKAMEKLNASESEDPTTLPALKMLVENRELLTLFTTSFAVLIGCLV
FLMWRRSSSKKLVQDPVPQVIVVKKKEKESEVDDGKKKVSIFYGTQTGTAEGFAKALVEEAKVRYE
KTSFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAANFYKWFTEGDDKGELLKKLQ
YGVFGLGNRQYEHFNKIAIVVDDKLTEMGAKRLVPVGLGDDDQCIEDDFTAWKELVWPELDQLLRD
EDDTSVTTPYTAAVLEYRVVYHDKPADSYAEDQTHTNGHVVHDAQHPSRSNVAFKKELHTSQSDRS
CTHLEFDISHTGLSYETGDHVGVYSENLSEVVDEALKLLGLSPDTYFSVHADKEDGTPIGGASLPP
PFPPCTLRDALTRYADVLSSPKKVALLALAAHASDPSEADRLKFLASPAGKDEYAQWIVANQRSLL
EVMQSFPSAKPPLGVFFAAVAPRLQPRYYSISSSPKMSPNRIHVTCALVYETTPAGRIHRGLCSTW
MKNAVPLTESPDCSQASIFVRTSNFRLPVDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGS
SIFFFGCRNRKVDFIYEDELNNFVETGALSELIVAFSREGTAKEYVQHKMSQKASDIWKLLSEGAY
LYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW (SEQ ID NO: 76)

ATGGCTCAGAGCGATTCTGTTAAAGTATCCCCGTTCGACCTGGTCTCTGCGGCTATGAACGGCAAA
GCAATGGAGAAACTGAACGCGAGCGAATCTGAAGATCCAACCACCCTGCCGGCACTGAAAATGCTG
GTAGAAAACCGTGAACTGCTGACTCTGTTCACCACCTCCTTCGCCGTTCTGATTGGTTGCCTGGTC
TTCCTGATGTGGCGCCGTTCCTCTTCCAAGAAGCTGGTACAGGACCCGGTTCCTCAGGTGATCGTC
GTTAAAAAGAAAGAGAAGGAAAGCGAAGTCGATGACGGCAAAAAGAAGGTTTCCATTTTCTACGGT
ACTCAGACCGGCACCGCTGAGGGTTTTGCCAAAGCACTGGTTGAAGAGGCAAAAGTGCGTTACGAA
AAAACTTCCTTCAAAGTGATTGACCTGGACGACTATGCTGCGGATGATGATGAATACGAGGAAAAA
CTGAAAAAAGAAAGCCTGGCCTTCTTCTTCCTGGCAACCTATGGCGATGGTGAACCGACCGACAAC
GCGGCGAACTTCTACAAATGGTTTACCGAAGGCGACGACAAAGGTGAATTGCTGAAGAAACTGCAG
TATGGTGTTTTCGGTCTGGGCAATCGCCAGTACGAACATTTTAACAAAATCGCAATCGTTGTTGAT
GACAAACTGACTGAAATGGGTGCGAAACGTCTGGTGCCGGTTGGCCTGGGTGACGATGATCAATGC
ATCGAAGATGACTTCACCGCATGGAAAGAACTGGTTTGGCCGGAACTGGATCAGCTGCTGCGCGAC
GAAGACGACACTTCCGTGACCACCCCGTATACCGCTGCAGTGCTGGAGTACCGTGTTGTTTACCAC
GATAAACCGGCGGACTCTTACGCCGAAGATCAGACTCACACTAACGGTCACGTCGTACATGACGCA

CAGCACCCGTCTCGTAGCAATGTTGCGTTTAAGAAAGAGCTGCACACGAGCCAGTCCGACCGCTCT
TGTACGCACCTGGAGTTCGATATCTCCCACACCGGTCTGTCCTATGAAACCGGTGACCATGTTGGC
GTTTACAGCGAAAACCTGAGCGAGGTAGTTGATGAAGCGCTGAAACTGCTGGGCCTGTCTCCAGAC
ACCTACTTTAGCGTGCATGCTGACAAGGAAGATGGTACTCCGATTGGCGGCGCTTCCCTGCCGCCA
CCGTTTCCACCTTGCACTCTGCGTGATGCTCTGACTCGTTACGCTGATGTTCTGTCTAGCCCGAAA
AAGGTTGCGCTGCTGGCGCTGGCCGCACATGCTTCTGACCCGTCTGAAGCTGACCGTCTGAAATTC
CTGGCGTCTCCGGCCGGCAAAGACGAATACGCGCAGTGGATTGTCGCTAACCAGCGCTCTCTGCTG
GAAGTGATGCAGTCCTTCCCGTCTGCCAAACCGCCACTGGGCGTGTTTTTCGCAGCTGTGGCTCCG
CGCCTGCAGCCGCGCTACTATTCTATCTCTAGCTCCCCGAAAATGAGCCCGAACCGCATCCACGTT
ACTTGTGCTCTGGTTTACGAAACCACCCCTGCGGGCCGTATCCACCGTGGTCTGTGCTCTACGTGG
ATGAAAAATGCCGTGCCGCTGACCGAATCCCCGGACTGCTCTCAGGCGTCCATCTTCGTGCGTACC
TCTAACTTCCGTCTGCCGGTGGACCCGAAAGTTCCTGTTATCATGATCGGTCCTGGCACGGGTCTG
GCCCCGTTTCGTGGTTTTCTGCAGGAGCGTCTGGCTCTGAAAGAATCCGGTACTGAGCTGGGCTCT
TCCATCTTTTTCTTCGGTTGTCGTAACCGCAAAGTCGATTTCATCTATGAAGACGAACTGAACAAC
TTCGTAGAGACTGGTGCACTGTCCGAACTGATTGTGGCATTCTCTCGTGAAGGCACGGCGAAAGAA
TACGTTCAACACAAAATGTCTCAGAAAGCGAGCGATATCTGGAAACTGCTGTCCGAGGGTGCGTAT
CTGTATGTTTGTGGCGACGCGAAAGGCATGGCTAAAGATGTACACCGCACCCTGCACACCATTGTA
CAAGAACAAGGCTCTCTGGATAGCTCCAAGGCAGAACTGTACGTGAAAAACCTGCAGATGTCTGGC
CGTTACCTGCGTGATGTATGGTAA (SEQ ID NO: 77)

>SrCPR2 [Stevia rebaudiana]

MAQSESVEASTIDLMTAVLKDTVIDTANASDNGDSKMPPALAMMFEIRDLLLLILTTSVAVLVGCFV
VLVWKRSSGKKSGKELEPPKIVVPKRRLEQEVDDGKKKVTIFFGTQTGTAEGFAKALFEEAKARYE
KAAFKVIDLDDYAADLDEYAEKLKKETYAFFFLATYGDGEPTDNAAKFYKWFTEGDEKGVWLQKLQ
YGVFGLGNRQYEHFNKIGIVVDDGLTEQGAKRIVPVGLGDDDQSIEDDFSAWKELVWPELDLLLRD
EDDKAAATPYTAAIPEYRVVFHDKPDAFSDDHTQTNGHAVHDAQHPCRSNVAVKKELHTPESDRSC
THLEFDISHTGLSYETGDHVGVYCENLIEVVEEAGKLLGLSTDTYFSLHIDNEDGSPLGGPSLQPP
FPPCTLRKALTNYADLLSSPKKSTLLALAAHASDPTEADRLRFLASREGKDEYAEWVVANQRSLLE
VMEAFPSARPPLGVFFAAVAPRLQPRYYSISSSPKMEPNRIHVTCALVYEKTPAGRIHKGICSTWM
KNAVPLTESQDCSWAPIFVRTSNFRLPIDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGSS
ILFFGCRNRKVDYIYENELNNFVENGALSELDVAFSRDGPTKEYVQHKMTQKASEIWNMLSEGAYL
YVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW (SEQ ID NO: 78)

ATGGCGCAATCTGAAAGTGTTGAGGCCAGTACCATCGACCTTATGACGGCAGTGTTGAAGGATACA
GTTATTGACACTGCAAATGCTTCAGATAACGGCGATTCTAAAATGCCTCCTGCGCTTGCGATGATG
TTCGAGATCCGCGATCTTCTGCTGATCCTTACCACATCAGTAGCGGTGCTGGTGGGATGCTTTGTG
GTACTCGTGTGGAAACGTTCGTCGGGCAAAAAATCAGGTAAGGAGCTGGAACCGCCTAAGATTGTC
GTACCGAAACGCCGACTGGAACAAGAAGTTGATGATGGCAAAAAAAAAGTGACTATATTTTTTGGG
ACACAGACAGGCACAGCGGAGGGATTTGCGAAAGCCTTATTCGAGGAGGCGAAGGCACGTTACGAG
AAAGCAGCTTTTAAAGTCATTGATCTGGATGACTATGCAGCAGACCTAGATGAATACGCAGAGAAA
CTGAAAAAAGAAACTTATGCGTTTTTCTTCCTGGCCACATACGGAGACGGTGAACCGACGGACAAT
GCCGCCAAGTTTTATAAGTGGTTCACTGAAGGGGATGAGAAAGGTGTATGGCTTCAGAAATTGCAA
TACGGAGTGTTCGGACTAGGAAATCGGCAATATGAGCACTTTAATAAAATAGGCATAGTAGTAGAC
GATGGGCTAACCGAGCAGGGGGCCAAACGGATTGTACCCGTGGGCCTGGGGGACGATGATCAGTCT
ATTGAGGATGATTTTAGTGCTTGGAAAGAGCTTGTTTGGCCTGAACTGGACTTACTCCTGCGTGAT
GAAGACGATAAAGCGGCAGCGACTCCATACACGGCAGCAATCCCCGAGTATAGAGTCGTATTCCAT
GATAAACCGGATGCTTTCTCTGATGACCATACCCAAACTAATGGTCATGCGGTCCATGATGCACAA
CATCCCTGCCGCAGCAATGTAGCGGTGAAAAAGGAGCTGCATACGCCTGAAAGTGATCGCTCATGT
ACGCATCTGGAGTTTGATATTTCACACACAGGTCTTAGCTACGAGACTGGAGATCACGTCGGAGTC
TATTGCGAAAATCTGATCGAAGTGGTTGAAGAGGCCGGGAAACTGTTGGGACTAAGTACAGATACT
TATTTTTCTTTACATATAGATAACGAGGATGGTTCCCCACTTGGCGGTCCATCTCTTCAGCCTCCA
TTCCCACCATGTACCTTACGCAAAGCGCTGACTAACTACGCAGATCTGCTGTCTAGCCCAAAGAAA
TCAACGCTTCTGGCGTTGGCTGCTCATGCCTCAGATCCGACCGAAGCTGATCGCCTTCGTTTTCTG
GCATCCCGAGAAGGTAAAGATGAATATGCAGAATGGGTGGTAGCGAATCAGCGTTCTTTGCTGGAA
GTCATGGAGGCATTCCCCAGCGCGCGCCCTCCGCTGGGTGTTTTCTTCGCAGCGGTGGCCCCGCGG
CTCCAGCCGCGTTATTATTCAATTAGCAGTTCTCCTAAGATGGAACCTAATCGAATCCATGTAACA
TGTGCATTGGTCTATGAGAAAACGCCGGCTGGCCGCATCCATAAAGGTATATGTAGCACATGGATG
AAAAATGCAGTACCCCTCACGGAGTCCCAGGATTGTAGTTGGGCGCCGATATTTGTTCGGACGAGC
AATTTTAGACTTCCTATAGACCCAAAGGTTCCAGTTATTATGATTGGTCCTGGCACCGGACTTGCG
CCATTCCGGGGGTTTCTGCAAGAAAGACTGGCTCTGAAAGAAAGCGGTACAGAACTCGGCTCCAGT

ATATTGTTTTTCGGCTGTCGCAACCGGAAAGTAGATTATATATATGAAAACGAGCTGAATAACTTC
GTTGAAAATGGTGCCCTGTCTGAACTCGATGTCGCTTTTTCGCGAGATGGCCCGACAAAAGAATAC
GTGCAGCATAAAATGACCCAGAAAGCAAGTGAAATCTGGAATATGCTGTCAGAAGGGGCATATCTG
TATGTGTGCGGAGATGCAAAGGGCATGGCCAAAGACGTTCACAGAACCTTGCATACCATAGTACAA
GAGCAGGGCTCTCTGGATAGCTCAAAAGCCGAGCTGTACGTGAAAAATCTCCAGATGAGTGGACGC
TACCTGAGGGATGTTTGGTAA (SEQ ID NO: 79)

>SrCPR3 [Stevia rebaudiana]

MAQSNSVKISPLDLVTALFSGKVLDTSNASESGESAMLPTIAMIMENRELLMILTTSVAVLIGCVV
VLVWRRSSTKKSALEPPVIVVPKRVQEEEVDDGKKKVTVFFGTQTGTAEGFAKALVEEAKARYEKA
VFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAARFYKWFTEGDAKGEWLNKLQYG
VFGLGNRQYEHFNKIAKVVDDGLVEQGAKRLVPVGLGDDDQCIEDDFTAWKELVWPELDQLLRDED
DTTVATPYTAAVAEYRVVFHEKPDALSEDYSYTNGHAVHDAQHPCRSNVAVKKELHSPESDRSCTH
LEFDISNTGLSYETGDHVGVYCENLSEVVNDAERLVGLPPDTYFSIHTDSEDGSPLGGASLPPPFP
PCTLRKALTCYADVLSSPKKSALLALAAHATDPSEADRLKFLASPAGKDEYSQWIVASQRSLLEVM
EAFPSAKPSLGVFFASVAPRLQPRYYSISSSPKMAPDRIHVTCALVYEKTPAGRIHKGVCSTWMKN
AVPMTESQDCSWAPIYVRTSNFRLPSDPKVPVIMIGPGTGLAPFRGFLQERLALKEAGTDLGLSIL
FFGCRNRKVDFIYENELNNFVETGALSELIVAFSREGPTKEYVQHKMSEKASDIWNLLSEGAYLYV
CGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW (SEQ ID NO: 80)

ATGGCGCAATCTAATTCTGTGAAAATCTCTCCATTGGATCTGGTTACAGCACTCTTTAGCGGGAAG
GTACTGGATACAAGTAACGCCAGTGAAAGCGGGGAATCCGCGATGCTGCCAACAATCGCGATGATC
ATGGAAAATCGGGAACTGCTAATGATTCTGACAACGTCTGTAGCAGTTTTAATCGGTTGCGTTGTG
GTTCTGGTGTGGCGTCGATCATCCACGAAAAAGAGCGCATTAGAACCGCCTGTTATCGTAGTACCA
AAAAGAGTTCAGGAGGAAGAGGTGGATGATGGGAAAAAAAAAAGTCACCGTTTTCTTCGGGACCCAA
ACTGGTACGGCAGAAGGTTTTGCGAAAGCACTGGTCGAAGAGGCGAAAGCCCGCTATGAGAAGGCG
GTTTTTAAGGTTATTGACCTTGATGACTATGCGGCGGACGATGATGAATACGAAGAAAAATTAAAG
AAAGAATCACTTGCCTTTTTTTTTTTGGCAACATACGGTGATGGCGAGCCGACTGATAACGCGGCA
CGGTTTTACAAATGGTTTACCGAAGGCGACGCGAAGGGGGAGTGGTTGAACAAGTTACAGTACGGT
GTGTTCGGCTTGGGGAACCGCCAGTACGAGCACTTTAACAAGATAGCTAAAGTTGTCGATGATGGT
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GATGATTTTACGGCTTGGAAGGAGTTAGTTTGGCCGGAACTGGACCAACTGCTGCGCGATGAGGAT
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CCTGATGCGCTGAGTGAGGACTATTCGTATACTAACGGCCATGCCGTTCACGATGCACAGCACCCG
TGCCGTTCTAATGTCGCCGTAAAAAAGGAACTGCATAGCCCGGAGTCGGACCGCAGTTGTACCCAT
CTGGAGTTTGATATTTCAAATACCGGGCTGAGTTACGAAACGGGCGATCACGTTGGCGTGTACTGT
GAGAATCTAAGCGAGGTTGTTAACGATGCAGAACGACTGGTCGGTTTGCCTCCAGATACTTATTTC
TCGATCCACACTGATAGCGAAGATGGCTCTCCACTCGGGGGGGCGAGTCTGCCGCCCCCGTTTCCC
CCGTGTACGCTGAGAAAGGCCCTTACATGTTATGCAGATGTACTCTCTTCCCCCAAAAAAAGTGCC
TTGCTCGCATTAGCAGCCCACGCTACCGATCCCTCGGAAGCAGATCGTCTGAAATTCTTGGCATCG
CCGGCGGGCAAAGATGAATACAGCCAATGGATAGTTGCAAGTCAGCGCAGTCTCTTAGAAGTGATG
GAAGCGTTTCCGTCCGCAAAGCCGTCCTTAGGTGTGTTTTTCGCGTCCGTGGCACCGCGTCTTCAG
CCTAGATATTACAGCATTAGTTCCTCTCCAAAAATGGCCCCGGACCGTATTCACGTGACTTGTGCT
CTTGTATATGAGAAAACCCCGGCAGGTCGTATTCACAAAGGCGTGTGCAGCACCTGGATGAAGAAT
GCAGTGCCGATGACCGAAAGCCAGGATTGTTCATGGGCGCCAATCTATGTCAGGACAAGTAATTTC
AGACTTCCGTCTGATCCTAAAGTTCCAGTCATAATGATTGGCCCCGGCACGGGACTGGCTCCTTTT
CGTGGTTTCCTGCAAGAGCGCTTGGCACTGAAAGAAGCAGGCACTGACCTGGGACTGTCCATCCTG
TTCTTTGGGTGCCGTAATCGTAAGGTCGATTTTATATATGAAAATGAATTGAACAACTTTGTAGAA
ACAGGCGCATTATCCGAACTGATCGTAGCTTTTAGTAGAGAGGGGCCGACGAAAGAATATGTACAA
CACAAGATGTCTGAGAAGGCTTCGGATATATGGAACCTGCTCTCTGAGGGTGCCTATCTGTACGTT
TGCGGTGATGCCAAAGGAATGGCCAAAGATGTGCACCGCACTTTACATACAATCGTCCAAGAGCAG
GGTAGCTTGGACTCATCTAAAGCTGAACTGTATGTGAAGAACTTACAGATGAGCGGGCGCTATTTG
CGAGATGTTTGGTAA (SEQ ID NO: 81)

>PgCPR [Pelargonium graveolens]

MAQSSSGSMSPFDFMTAIIKGKMEPSNASLGAAGEVTAMILDNRELVMILTTSIAVLIGCVVVFIW
RRSSSQTPTAVQPLKPLLAKETESEVDDGKQKVTIFFGTQTGTAEGFAKALADEAKARYDKVTFKV
VDLDDYAADDEEYEEKLKKETLAFFFLATYGDGEPTDNAARFYKWFLEGKERGEWLQNLKFGVFGL
GNRQYEHFNKIAIVVDEILAEQGGKRLISVGLGDDDQCIEDDFTAWRESLWPELDQLLRDEDDTTV
STPYTAAVLEYRVVFHDPADAPTLEKSYSNANGHSVVDAQHPLRANVAVRRELHTPASDRSCTHLE
FDISGTGIAYETGDHVGVYCENLAETVEEALELLGLSPDTYFSVHADKEDGTPLSGSSLPPPFPPC
TLRTALTLHADLLSSPKKSALLALAAHASDPTEADRLRHLASPAGKDEYAQWIVASQRSLLEVMAE
FPSAKPPLGVFFASVAPRLQPRYYSISSSPRIAPSRIHVTCALVYEKTPTGRVHKGVCSTWMKNSV
PSEKSDECSWAPIFVRQSNFKLPADAKVPIIMIGPGTGLAPFRGFLQERLALKEAGTELGPSILFF
GCRNSKMDYIYEDELDNFVQNGALSELVLAFSREGPTKEYVQHKMMEKASDIWNLISQGAYLYVCG
DAKGMARDVHRTLHTIAQEQGSLDSSKAESMVKNLQMSGRYLRDVW (SEQ ID NO: 82)

ATGGCGCAGTCAAGCAGTGGATCAATGAGCCCTTTCGATTTTATGACCGCTATAATAAAAGGTAAA
ATGGAGCCAAGTAATGCGTCTTTAGGAGCGGCAGGTGAAGTCACAGCAATGATACTTGATAATAGG
GAGCTGGTTATGATTCTGACGACCAGCATTGCAGTGCTGATCGGTTGCGTTGTAGTGTTCATTTGG
CGTCGTTCATCATCCCAGACCCCTACCGCGGTGCAGCCATTAAAACCACTTTTAGCGAAGGAAACA
GAGAGCGAAGTAGACGATGGCAAACAGAAAGTAACTATCTTTTTTGGTACTCAAACTGGAACCGCT
GAAGGTTTCGCGAAAGCGCTCGCAGACGAGGCCAAAGCACGGTATGATAAAGTCACTTTTAAAGTG
GTTGATCTGGACGATTATGCCGCAGATGACGAAGAATATGAAGAAAAGCTGAAGAAGGAAACGTTA
GCATTCTTTTTTCTTGCGACGTATGGAGATGGTGAACCTACTGACAATGCTGCAAGGTTTTATAAG
TGGTTTCTGGAAGGTAAAGAACGCGGAGAATGGCTTCAGAATCTAAAATTTGGTGTGTTTGGTTTA
GGCAACCGTCAGTATGAGCATTTCAATAAAATTGCCATTGTGGTTGATGAAATCCTTGCAGAACAA
GGTGGTAAGCGTCTCATTTCAGTTGGCCTGGGCGATGATGATCAGTGTATTGAGGATGACTTTACT
GCCTGGAGGGAATCGCTGTGGCCGGAGCTAGATCAGTTATTACGCGATGAGGATGATACTACGGTT
TCTACGCCGTATACCGCCGCGGTGCTGGAATACAGAGTCGTTTTTCATGATCCGGCAGATGCCCCA
ACTCTCGAAAAAAGCTACAGCAACGCTAACGGGCATAGCGTGGTTGATGCGCAACATCCGTTACGG
GCAAATGTTGCCGTCAGACGGGAGTTGCATACTCCTGCGTCTGACCGCTCATGTACCCATCTGGAA
TTTGATATATCTGGTACTGGCATCGCATACGAGACGGGTGATCATGTTGGCGTGTATTGCGAGAAT
CTTGCAGAGACGGTAGAAGAAGCGTTGGAACTTTTAGGTCTTTCCCCGGATACATACTTCTCCGTA
CACGCAGATAAAGAGGACGGTACGCCTCTCTCAGGCTCATCTCTCCCGCCGCCATTTCCACCGTGC
ACTTTACGTACAGCCCTGACGTTACATGCTGACTTACTGTCTTCCCCAAAGAAATCTGCATTGCTC
GCGCTTGCAGCTCATGCATCAGACCCCACTGAAGCTGATCGATTGCGGCACCTAGCAAGCCCTGCG
GGCAAGGACGAATACGCTCAGTGGATAGTTGCTAGTCAGCGTTCCTTGCTGGAAGTGATGGCGGAG
TTCCCCAGTGCCAAGCCCCCGCTGGGAGTATTCTTCGCATCGGTTGCTCCAAGATTGCAGCCCCGG
TACTACTCTATTTCTTCTTCCCCAAGAATAGCGCCGTCTCGCATACACGTGACCTGCGCGTTAGTT
TACGAGAAAACACCTACGGGCAGAGTACACAAAGGAGTTTGCTCCACTTGGATGAAAAACTCAGTG
CCCTCTGAAAAGAGTGATGAATGTTCATGGGCACCAATTTTCGTACGACAGAGCAACTTTAAACTG
CCCGCCGATGCGAAAGTACCCATAATTATGATTGGTCCAGGAACGGGTCTGGCACCATTTCGCGGC
TTCCTCCAGGAGCGGCTTGCATTGAAAGAAGCAGGGACAGAACTGGGACCTTCCATATTATTTTTT
GGGTGCCGCAACAGCAAAATGGACTATATATACGAGGATGAACTGGATAATTTTGTACAGAATGGG
GCACTCTCTGAACTCGTGTTGGCGTTCTCACGTGAAGGTCCTACCAAAGAGTATGTGCAACATAAG
ATGATGGAGAAAGCCTCAGATATATGGAACCTTATTTCACAGGGAGCTTATTTGTATGTGTGCGGG
GACGCAAAAGGCATGGCGCGTGATGTGCACCGCACGTTACATACCATCGCTCAGGAGCAGGGGTCA
TTAGATAGCTCAAAAGCAGAGAGTATGGTGAAGAATCTTCAGATGTCAGGCAGATACCTGCGCGAT
GTCTGGTAA (SEQ ID NO: 83)

Figure 6B

```
AtCPR2          MASSSSSSSTSMIDLMAAIIKGE-PVIVSDPANASAYESVAAELSSMLIENRQFAMIVTT 59
ATR2            MASSSSSSSTSMIDLMAAIIKGE-PVIVSDPANASAYESVAAELSSMLIENRQFAMIVTT 59
AaCPR           MAQSTTSVKLSPFDLMTALLNG---KVSFDTSNTSDTN----IPLAVFMENRELLMILTT 53
AtCPR           --MTSALYASDLFKQLKSIMGTDS-----------------------LSDDVVLVIATT 34
AtCPR1          -MATSALYASDLFKQLKSIMGTDS-----------------------LSDDVVLVIATT 35
                   :::    . :. : :::                            :.:  . :* **

AtCPR2          SIAVLIGCIVMLVWRRSGSGNSKRVE-PLKPLVIKPREEE----IDDGRKKVTIFFGTQT 114
ATR2            SIAVLIGCIVMLVWRRSGSGNSKRVE-PLKPLVIKPREEE----IDDGRKKVTIFFGTQT 114
AaCPR           SVAVLIGCVVVLVWRRSSSAAKKAAESPVIVVPKKVTEDE----VDDGRKKVTVFFGTQT 109
AtCPR           SLALVAG-FVVLLWKKTTADRSGELKPLMIPKSLMAKDEDDDLDLGSGKTRVSIFFGTQT 93
AtCPR1          SLALVAG-FVVLLWKKTTADRSGELKPLMIPKSLMAKDEDDDLDLGSGKTRVSIFFGTQT 94
                *:*:: * .*:*:*::: :  .   :  :        :::    :..*:.:*::******

AtCPR2          GTAEGFAKALGEEAKARYEKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEP 174
ATR2            GTAEGFAKALGEEAKARYEKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEP 174
AaCPR           GTAEGFAKALVEEAKARYEKAVFKVIDLDDYAAEDDEYEEKLKKESLAFFFLATYGDGEP 169
AtCPR           GTAEGFAKALSEEIKARYEKAAVKVIDLDDYAADDDQYEEKLKKETLAFFCVATYGDGEP 153
AtCPR1          GTAEGFAKALSEEIKARYEKAAVKVIDLDDYAADDDQYEEKLKKETLAFFCVATYGDGEP 154
                ********** ** ******: .*::*******:**:******** :*** :********

AtCPR2          TDNAARFYKWFTEGNDRGEWLKNLKYGVFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQ 234
ATR2            TDNAARFYKWFTEGNDRGEWLKNLKYGVFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQ 234
AaCPR           TDNAARFYKWFTEGEEKGEWLDKLQYAVFGLGNRQYEHFNKIAKVVDEKLVEQGAKRLVP 229
AtCPR           TDNAARFSKWFTEENERDIKLQQLAYGVFALGNRQYEHFNKIGIVLDEELCKKGAKRLIE 213
AtCPR1          TDNAARFYKWFTEENERDIKLQQLAYGVFALGNRQYEHFNKIGIVLDEELCKKGAKRLIE 214
                ******* ***** :::.  *.:* *.**.***********:. *:*: * ::**:**:

AtCPR2          VGLGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSEDAKF 294
ATR2            VGLGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSEDAKF 294
AaCPR           VGMGDDDQCIEDDFTAWKELVWPELDQLLRDEDDTSVATPYTAAVAEYRVVFHD-KPETY 288
AtCPR           VGLGDDDQSIEDDFNAWKESLWSELDKLLKDEDDKSVATPYTAVIPEYRVVTHDPRFTTQ 273
AtCPR1          VGLGDDDQSIEDDFNAWKESLWSELDKLLKDEDDKSVATPYTAVIPEYRVVTHDPRFTTQ 274
                **:*****.*****.**:* :*.*** :*::*.*.:*******.: ****  ** .  .

AtCPR2          NDINMANGNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLTYETGDHVG 354
ATR2            NDITLANGNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLTMKLGDHVG 354
AaCPR           DQDQLTNG--HAVHDAQHPCRSNVAVKKELHSPLSDRSCTHLEFDISNTGLSYETGDHVG 346
AtCPR           KSMESNVANGNTTIDIHHPCRVDVAVQKELHTHESDRSCIHLEFDISRTGITYETGDHVG 333
```

```
AtCPR1      KSMESNVANGNTTIDIHHPCRVDVAVQKELHTHESDRSCIHLEFDISRTGITYETGDHVG 334
            ..     .   :. * :** : :***::***:  ***** ******: :*:: : *****

AtCPR2      VLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPIS-SSLPPPFP-PCNLRTALTRYA 412
ATR2        VLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPIS-SSLPPPFP-PCNLRTALTRYA 412
AaCPR       VYVENLSEVVDEAEKLIGLPPHTYFSVHADNEDGTPLGGASLPPPFP-PCTLRKALASYA 405
AtCPR       VYAENHVEIVEEAGKLLGHSLDLVFSIHADKEDGSPLE-SAVPPPFPGPCTLGTGLARYA 392
AtCPR1      VYAENHVEIVEEAGKLLGHSLDLVFSIHADKEDGSPLE-SAVPPPFPGPCTLGTGLARYA 393
            *  :*  * *:** :*:. . .  **:**::***:*:  :::***** **.* ..*: **

AtCPR2      CLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSLLEVMAEFPSA 472
ATR2        CLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSLLEVMAEFPSA 472
AaCPR       DVLSSPKKSALLALAAHATDSTEADRLKFLASPAGKDEYAQWIVASHRSLLEVMEAFPSA 465
AtCPR       DLLNPPRKSALVALAAYATEPSEAEKLKHLTSPDGKDEYSQWIVASQRSLLEVMAAFPSA 452
AtCPR1      DLLNPPRKSALVALAAYATEPSEAEKLKHLTSPDGKDEYSQWIVASQRSLLEVMAAFPSA 453
             :*..*:****:****:*::.:**:*:**.*:** *****::*:* *:******  ****

AtCPR2      KPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCSTWMKN 532
ATR2        KPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCSTWMKN 532
AaCPR       KPPLGVFFASVAPRLQPRYYSISSSPRFAPNRIHVTCALVYEQTPSGRVHKGVCSTWMKN 525
AtCPR       KPPLGVFFAAIAPRLQPRYYSISSCQDWAPSRVHVTSALVYGPTPTGRIHKGVCSTWMKN 512
AtCPR1      KPPLGVFFAAIAPRLQPRYYSISSSPRLAPSRVHVTSALVYGPTPTGRIHKGVCSTWMKN 513
            **********.:********:*****.    *  .*:***.**** *:**:**********

AtCPR2      AVPYEKSENCSS-APIFVRQSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESGV 591
ATR2        AVPYEKSEKLFLGRPIFVRQSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESGV 592
AaCPR       AVPMTESQDCSW-APIYVRTSNFRLPSDPKVPVIMIGPGTGLAPFRGFLQERLAQKEAGT 584
AtCPR       AVPAEKSHECSG-APIFIRASNFKLPSNPSTPIVMVGPGTGLAPFRGFLQERMALKEDGE 571
AtCPR1      AVPAEKSHECSG-APIFIRASNFKLPSNPSTPIVMVGPGTGLAPFRGFLQERMALKEDGE 572
            ***  :*..    **::* ***:***:...*::*:**********************:*  * *

AtCPR2      ELGPSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKASD 651
ATR2        ELGPSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKASD 652
AaCPR       ELGTAILFFGCRNRKVDFIYEDELNNFVETGALSELVTAFSREGATKEYVQHKMTQKASD 644
AtCPR       ELGSSLLFFGCRNRQMDFIYEDELNNFVDQGVISELIMAFSREGAQKEYVQHKMMEKAAQ 631
AtCPR1      ELGSSLLFFGCRNRQMDFIYEDELNNFVDQGVISELIMAFSREGAQKEYVQHKMMEKAAQ 632
            ***.::**********:*****:**:.**:  *.::**  ******.  ********  :**::

AtCPR2      IWNMISQGAYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW 712
ATR2        IWNMISQGAYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW 713
AaCPR       IWNLLSEGAYLYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMAGRYLRDVW 705
AtCPR       VWDLIKEEGYLYVCGDAKGMARDVHRTLHTIVQEQEGVSSSEAEAIVKKLQTEGRYLRDVW 692
```

```
AtCPR1      VWDLIKEEGYLYVCGDAKGMARDVHRTLHTIVQEQEGVSSSEAEAIVKKLQTEGRYLRDVW 693
              :*:::.: .*********:****:****.***  .:.*::**  **:**  *******
```

Figure 6C

```
SrCPR2  MAQSESVEASTIDLMTAVLKDTVIDTANASDNGDSKMPPALAMMFEIRDLLLILTTSVAV 60
SrCPR3  MAQSNSVKISPLDLVTALFSGKVLDTSNASESGESAMLPTIAMIMENRELLMILTTSVAV 60
SrCPR   -MQSDSVKVSPFDLVSAAMNGKAMEKLNASESEDPTTLPALKMLVENRELLTLFTTSFAV 59
SrCPR1  MAQSDSVKVSPFDLVSAAMNGKAMEKLNASESEDPTTLPALKMLVENRELLTLFTTSFAV 60
           **:***: *.:**::* :....::. ***:. :.    *:: *:.* *:** ::***.**

SrCPR2  LVGCFVVLVWKRSSGKKSGKELEPPKIVVPKRRLEQEVDDGKKKVTIFFGTQTGTAEGFA 120
SrCPR3  LIGCVVVLVWRRSSTKKS--ALEPPVIVVPKRVQEEEVDDGKKKVTVFFGTQTGTAEGFA 118
SrCPR   LIGCLVFLMWRRSSSKKLVQDPVPQVIVVKKKEKESEVDDGKKKVSIFYGTQTGTAEGFA 119
SrCPR1  LIGCLVFLMWRRSSSKKLVQDPVPQVIVVKKKEKESEVDDGKKKVSIFYGTQTGTAEGFA 120
        *:**.*.*:*:*** **     *  *** *:  *.**********::*:**********

SrCPR2  KALFEEAKARYEKAAFKVIDLDDYAADLDEYAEKLKKETYAFFFLATYGDGEPTDNAAKF 180
SrCPR3  KALVEEAKARYEKAVFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAARF 178
SrCPR   KALVEEAKVRYEKTSFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAANF 179
SrCPR1  KALVEEAKVRYEKTSFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPTDNAANF 180
        ***.*****.****: ************** *** ******: **********************.*

SrCPR2  YKWFTEGDEKGVWLQKLQYGVFGLGNRQYEHFNKIGIVVDDGLTEQGAKRIVPVGLGDDD 240
SrCPR3  YKWFTEGDAKGEWLNKLQYGVFGLGNRQYEHFNKIAKVVDDGLVEQGAKRLVPVGLGDDD 238
SrCPR   YKWFTEGDDKGEWLKKLQYGVFGLGNRQYEHFNKIAIVVDDKLTEMGAKRLVPVGLGDDD 239
SrCPR1  YKWFTEGDDKGELLKKLQYGVFGLGNRQYEHFNKIAIVVDDKLTEMGAKRLVPVGLGDDD 240
        ******** **  *:**********************. **** *.* ****:*********

SrCPR2  QSIEDDFSAWKELVWPELDLLLRDEDDKAAATPYTAAIPEYRVVFHDKP-DAFSDDHTQT 299
SrCPR3  QCIEDDFTAWKELVWPELDQLLRDEDDTTVATPYTAAVAEYRVVFHEKP-DALSEDYSYT 297
SrCPR   QCIEDDFTAWKELVWPELDQLLRDEDDTSVTTPYTAAVLEYRVVYHDKPADSYAEDQTHT 299
SrCPR1  QCIEDDFTAWKELVWPELDQLLRDEDDTSVTTPYTAAVLEYRVVYHDKPADSYAEDQTHT 300
        *.*****:**********.*******.::.:******: *****:*:** *: ::* : *

SrCPR2  NGHAVHDAQHPCRSNVAVKKELHTPESDRSCTHLEFDISHTGLSYETGDHVGVYCENLIE 359
SrCPR3  NGHAVHDAQHPCRSNVAVKKELHSPESDRSCTHLEFDISNTGLSYETGDHVGVYCENLSE 357
SrCPR   NGHVVHDAQHPSRSNVAFKKELHTSQSDRSCTHLEFDISHTGLSYETGDHVGVYSENLSE 359
SrCPR1  NGHVVHDAQHPSRSNVAFKKELHTSQSDRSCTHLEFDISHTGLSYETGDHVGVYSENLSE 360
        ***.*******.*****.******:.:**********************.*** *

SrCPR2  VVEEAGKLLGLSTDTYFSLHIDNEDGSPLGGPSLQPPFPPCTLRKALTNYADLLSSPKKS 419
SrCPR3  VVNDAERLVGLPPDTYFSIHTDSEDGSPLGGASLPPPFPPCTLRKALTCYADVLSSPKKS 417
SrCPR   VVDEALKLLGLSPDTYFSVHADKEDGTPIGGASLPPPFPPCTLRDALTRYADVLSSPKKV 419
```

```
SrCPR1      VVDEALKLLGLSPDTYFSVHADKEDGTPIGGASLPPPFPPCTLRDALTRYADVLSSPKKV 420
            **::* :*:**..*****:* *.***:*:**.** ********** ***:******

SrCPR2      TLLALAAHASDPTEADRLRFLASREGKDEYAEWVVANQRSLLEVMEAFPSARPPLGVFFA 479
SrCPR3      ALLALAAHATDPSEADRLKFLASPAGKDEYSQWIVASQRSLLEVMEAFPSAKPSLGVFFA 477
SrCPR       ALLALAAHASDPSEADRLKFLASPAGKDEYAQWIVANQRSLLEVMQSFPSAKPPLGVFFA 479
SrCPR1      ALLALAAHASDPSEADRLKFLASPAGKDEYAQWIVANQRSLLEVMQSFPSAKPPLGVFFA 480
            :**********:**:*****:****  *****::*:**.*********::****:*.****** 

SrCPR2      AVAPRLQPRYYSISSSPKMEPNRIHVTCALVYEKTPAGRIHKGICSTWMKNAVPLTESQD 539
SrCPR3      SVAPRLQPRYYSISSSPKMAPDRIHVTCALVYEKTPAGRIHKGVCSTWMKNAVPMTESQD 537
SrCPR       AVAPRLQPRYYSISSSPKMSPNRIHVTCALVYETTPAGRIHRGLCSTWMKNAVPLTESPD 539
SrCPR1      AVAPRLQPRYYSISSSPKMSPNRIHVTCALVYETTPAGRIHRGLCSTWMKNAVPLTESPD 540
            :**********************.*******:*:**********:*** *

SrCPR2      CSWAPIFVRTSNFRLPIDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGSSILFFG 599
SrCPR3      CSWAPIYVRTSNFRLPSDPKVPVIMIGPGTGLAPFRGFLQERLALKEAGTDLGLSILFFG 597
SrCPR       CSQASIFVRTSNFRLPVDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGSSIFFFG 599
SrCPR1      CSQASIFVRTSNFRLPVDPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGSSIFFFG 600
            ** *.*:********** ********************:**:** **:***

SrCPR2      CRNRKVDYIYENELNNFVENGALSELDVAFSRDGPTKEYVQHKMTQKASEIWNMLSEGAY 659
SrCPR3      CRNRKVDFIYENELNNFVETGALSELIVAFSREGPTKEYVQHKMSEKASDIWNLLSEGAY 657
SrCPR       CRNRKVDFIYEDELNNFVETGALSELIVAFSREGTAKEYVQHKMSQKASDIWKLLSEGAY 659
SrCPR1      CRNRKVDFIYEDELNNFVETGALSELIVAFSREGTAKEYVQHKMSQKASDIWKLLSEGAY 660
            *******:***:********.******  *****:*.:*********::***:**::****** 

SrCPR2      LYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW 710
SrCPR3      LYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW 708
SrCPR       LYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW 710
SrCPR1      LYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELYVKNLQMSGRYLRDVW 711
            ************************************************** 
```

Figure 6D

```
ATR2        MASSSSSSSSTSMIDLMAAIIKGEPVIVSDPANASAYESVAAELSSMLIENRQFAMIVTTS 60
AtCPR2      MASSSSSSSSTSMIDLMAAIIKGEPVIVSDPANASAYESVAAELSSMLIENRQFAMIVTTS 60
PgCPR       MAQSSSGS-MSPFDFMTAIIKG------KMEPSNAS--LGAAGEVTAMILDNRELVMILTTS 53
AaCPR       MAQSTTSVKLSPFDLMTALLNGKVS-FDTSNTSDTN-----IP-LAVFMENRELLMILTTS 54
SrCPR3      MAQSN-SVKISPLDLVTALFSGKV--LDTSNASESGESAMLPTIAMIMENRELLMILTTS 57
SrCPR       MAQSD-SVKVSPFDLVSAAMNGKA--MEKLNASESEDPTTLPALKMLVENRELLTLFTTS 57
SrCPR2      MAQSE-SVEASTIDLMTAVLKDTV--IDTANASDNGDSKMPPALAMMFEIRDLLLLITTS 57
AtCPR1      MATSALVASDLFKQLKSIMGTDS-------------------------------LSDDVVLVIATTS 36
            ** *          :: :  ..                 ..    .  : ***

ATR2        IAVLIGCIVMLVWRRSGSGNSKRVEPLKP---LVIKPR----EEEIDDGRKKVTIFFGTQTG 115
AtCPR2      IAVLIGCIVMLVWRRSGSGNSKRVEPLKP--LVIKPR----EEEIDDGRKKVTIFFGTQTG 115
PgCPR       IAVLIGCVVVFIWRRSSSQTPTAVQPLKP--LLAKET----ESEVDDGKQKVTIFFGTQTG 108
AaCPR       VAVLIGCVVVLVWRRSSSAAKKAAESF-------VTVVPKKVTEDEVDDGRKKVTVFFGTQTG 110
SrCPR3      VAVLIGCVVVLVWRRSS-TKKSALEPP-----VIVVPKRVQEEEVDDGKKKVTVFFGTQTG 112
SrCPR       FAVLIGCLVFLMWRRSS--SKKLVQDPVPQ---VIVVKKKEKESEVDDGKKKVSIFYGTQTG 114
SrCPR2      VAVLVGCFVVLVWKRSS-GKKSGKELEPP---KIVVPKRPLEQEVDDGKKKVTIFFGTQTG 114
AtCPR1      LALVAG-FVVLLWKKTTADRSGELKPLMIPKSLMAKDEDDDLDLGSGKTRVSIFFGTQTG 95
             .*:: *  .*.::*:::        .          :  ::..*:  :*::*:*****

ATR2        TAEGFAKALGEEAKARYEKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEPT 175
AtCPR2      TAEGFAKALGEEAKARYEKTRFKIVDLDDYAADDDEYEEKLKKEDVAFFFLATYGDGEPT 175
PgCPR       TAEGFAKALADEAKARYDKVTFKVVDLDDYAADDEEYEEKLKKETLAFFFLATYGDGEPT 168
AaCPR       TAEGFAKALVEEAKARYEKAVFKVIDLDDYAAEDDEYEEKLKKESLAFTFLATYGDGEPT 170
SrCPR3      TAEGFAKALVEEAKARYEKAVFKVIDLDDYAADDDEYEEKLKKESLAFFFLATYGDGEPT 172
SrCPR       TAEGFAKALVEEAEARYEKTSFKVIDLDDYAADDDEYEEKLKKESLAFTFLATYGDGEPT 174
SrCPR2      TAEGFAKALFEEAKARYEKAAFKVIDLDDYAADLDEYAEKLKKETYAFTFLATYGDGEPT 174
AtCPR1      TAEGFAKALSEEIKARYEKAAVKVIDLDDYAADDDQYEEKLKKETLAFFCVATYGDGEPT 155
            ********** :* * **:*. .*::********** ::*  ******  ***  :*********

ATR2        DNAARFYKWFTEGNDRGEWLKNLKYGVFGLGNRQYEHFNKVAKVVDDILVEQGAQRLVQV 235
AtCPR2      DNAARFYKWFTEGNDRGEWLKNLKYGVFGLGNEQYEHFNKVAKVVDDILVEQGAQRLVQV 235
PgCPR       DNAARFYKWFLEGKERGEWLQNLKFGVFGLGNRQYEHFNKIAIVVDEILAEQGGKRLISV 228
AaCPR       DNAARFYKWFTEGEEKGEWLDKLQYAVFGLGNRQYEHFNKIAKVVDEKLVEQGAKRLVPV 230
SrCPR3      DNAARFYKWFTEGDAKGEWLNKLQYGVFGLGNRQYEHFNKIAKVVDDGLVEQGAKRLVPV 232
SrCPR       DNAANFYKWFTEGDDKGELLKKLQYGVFGLGNRQYEHFNKIAIVVDDKLTEMGAKRLVPV 234
SrCPR2      DNAARFYKWFTEGDEKGVWLQKLQYGVFGLGNRQYEHFNKIGIVVDDGLTEQGAKRIVPV 234
AtCPR1      DNAARFYKWFTENEDRDIKLQQLAYGVFALGNRQYEHFNKIGIVLDEELCKKGAKRLIEV 215
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                 *****.*****  *  .  :.   *.:*  :.**.**************:.  *:*: *  : *.:*:: *

ATR2             GLGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSE---DAK 293
AtCPR2           GLGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATFYTAAVLEYRVSIHDSE--DAK 293
PgCPR            GLGDDDQCIEDDFTAWRESLWPELDQLLRDEDDTTVSTPYTAAVLEYRVVFHDPA---DAP 286
AaCPR            GMGDDDQCIEDDFTAWKELVWPELDQLLRDEDDTSVATPYTAAVAEYRVVFHDKP---ETY 288
SrCPR3           GLGDDDQCIEDDFTAWKELVWPELDQLLRDEDDTTVATPYTAAVAEYRVVFHEKP--DAL 290
SrCPR            GLGDDDQCIEDDFTAWKELVWPELDQLLRDEDDTSVTTPYTAAVLEYRVVYHDKFA-DSY 293
SrCPR2           GLGDDDQSIEDDFSAWKELVWPELDLLLRDEDDKAAATPYTAAIPEYRVVFHDKP--DAF 292
AtCPR1           GLGDDDQSIEDDFNAWKESLWSELDKLLKDEDDKSVATPYTAVIPEYRVVYHDPRFTQK 275
                 *:*****.*****.**:* :*.*** :*::*.*.::.******.: ****  *:

ATR2             FNDITLANGNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLTMKLGDHV 353
AtCPR2           FNDINMANGNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLTYETGDHV 353
PgCPR            TLEKSYSNANGHSVVDAQHPLRANVAVRRELHTPASDRSCTHLEFDISGTGIAYETGDHV 346
AaCPR            DQDQ-LTN--GHAVHDAQHPCRSNVAVKKELHSPLSDRSCTHLEFDISNTGLSYETGDHV 345
SrCPR3           SEDYSYTN--GHAVHDAQHPCRSNVAVKKELHSPESDRSCTHLEFDISNTGLSYETGDHV 348
SrCPR            AEDQTHTN--GHVVHDAQHPSRSNVAFKKELHTSQSDRSCTHLEFDISHTGLSYETGDHV 351
SrCPR2           SDDHTQTN--GHAVHDAQHPCRSNVAVKKELHTPESDRSCTHLEFDISHTGLSYETGDHV 350
SmESNVAN--GNTTIDIHHPCRVDVAVQKELHTHESDRSCIHLEFDISRTGITYETGDHV 333
                   :  :*  *   . * :** : :**.::***:  ***** ******: :*::: : ****

ATR2             GVLCDNLSETVDEALRLLDMSPDTYFSLHAEKEDGTPIS-SSLPPPFP-PCNLRTALTRY 411
AtCPR2           GVLCDNLSETVDEARLLLDMSPDTYFSLHAEKEDGTPIS-SSLPPPFP-ECNLRTALTRY 411
PgCPR            GVYCENLAETVEEAELLGLSPDTYFSVHADKEDGTPLSGSSLPPPFP-PCTLRTALTLH 405
AaCPR            GVYVENLSEVVDEAEKLIGLPPHTYFSVHADNEDGTPLGGASLPPPFP-PCTLRKALASY 404
SrCPR3           GVYCENLSEVVNDAEELVGLPPDTYFSIHTDSEDGSPLGGASLPPPFP-ECTLRKALTCY 407
SrCPR            GVYSENLSEVVDEALKLLGLSPDTYFSVHADKEDGTPIGGASLPPPFP-PCTLRDALTRY 410
SrCPR2           GVYCENLIEVVEEAGKLLGLSTDTYFSLHIDNEDGSPLGGPSLQPPFP-PCTLRKALTNY 409
AtCPR1           GVYAENHVEIVEEAGKLLGHSLDLVFSIHADKEDGSPLE-SAVPPPFPGPCTLGTGLARY 392
                 **  :*  * *:;* .*:. .  .  **:* :.***:*:  .:: **** **.*  .*: :

ATR2             ACLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSLLEVMAEFPS 471
AtCPR2           ACLLSSPKKSALVALAAHASDPTEAERLKHLASPAGKDEYSKWVVESQRSLLEVMAEFPS 471
PgCPR            ADLLSSPKKSALLALAAHASDPTEADRLRHLASPAGKDEYAQWIVASQRSLLEVMAEFPS 465
AaCPR            ADVLSSPKKSALLALAAHATDSTEADRLKFLASPAGKDEYAQWTVASHRSLLEVMEAFPS 464
SrCPR3           ADVLSSPKKSALLALAAHATDPSEADRLKFLASPAGKDEYSQWIVASQRSLLEVMEAFPS 467
SrCPR            ADVLSSPKKVALLALAAHASDPSEADRLKFLASPAGKDEYAQWIVANQRSLLEVMQSFPS 470
SrCPR2           ADLLSSPKKSTLLALAAHASDPTEADRLRFLASREGKDEYAEWVVANQRSLLEVMEAFPS 469
AtCPR1           ADLLNPPRKSALVALAAYATEPSEARKLKHLTSFDGKDEYSQWIVASQRSLLEVMRAFPS 452
                 * :*..*:* :*:****:*::.:***::*:..*:*  *****::*:* .:******  ***
```

```
ATR2        AKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCSTWMK 531
AtCPR2      AKPPLGVFFAGVAPRLQPRFYSISSSPKIAETRIHVTCALVYEKMPTGRIHKGVCSTWMK 531
PgCPR       AKPPLGVFFASVAPRLQPRYYSISSSPRIAPSRIHVTCALVYEKTPTGRVHKGVCSTWMK 525
AaCPR       AKPPLGVFFASVAPRLQPRYYSISSSPRFAPNRIHVTCALVYEQTPSGRVHKGVCSTWMK 524
SrCPR3      AKPSLGVFFASVAPRLQPRYYSISSSPKMAPDRIHVTCALVYEKTPAGRIHKGVCSTWMK 527
SrCPR       AKPPLGVFFAAVAPRLQPRYYSISSSPKMSPNRIHVTCALVYETTPAGRIHRGLCSTWMK 530
SrCPR2      ARPPLGVFFAAVAPRLQPRIYSISSSPKMEPNRIHVTCALVYEKTPAGRIHKGICSTWMK 529
AtCPR1      AKPPLGVFFAAIAPRLQPRYYSISSSPRLAPSRVHVTSALVYGPTTPGRIHKGVCSTWMK 512
            *:*. *******.:********:********:;    *:***.****    *;**:*:*:******

ATR2        NAVPYEKSEKLFLGRPIFVRQSNFKLPSDSKVPIIMIGPGTGLAPFRGFLQERLALVESG 591
AtCPR2      NAVPYEKSENCSS-APIFVRQSNFKLFSDSKVPIIMIGPGTGLAPFRGFLQERLALVESG 590
PgCPR       NSVPSEKSDECSW-APIFVRQSNFKLPADAKVPIIMIGPGTGLAPFRGFLQERLALKEAG 584
AaCPR       NAVPMTESQDCSW-APIYVRTSNFRLPSDPKVPVIMIGPGTGLAPFRGFLQERLAQKEAG 583
SrCPR3      NAVPMTESQDCSW-APIYVRTSNFRLFSDPKVPVIMIGPGTGLAPFRGFLQERLALKEAG 586
SrCPR       NAVPLTESPDCSQ-ASIFVRTSNFRLPVDPKVPVIMIGPGTGLAPFRGFLQERLALKESG 589
SrCPR2      NAVPLTESQDCSW-APIFVRTSNFRLPIDPKVPVIMIGPGTGLAPFRGFLQERLALKESG 588
AtCPR1      NAVPAEKSHECSG-APIFIRASNFKLPSNPSTPIVMVGPGTGLAPFRGFLQERMALKEDG 571
            *:**  :*  .      .*:;* ***:** ;... *:;*;*********************:*  * *

ATR2        VELGPSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKAS 651
AtCPR2      VELGPSVLFFGCRNRRMDFIYEEELQRFVESGALAELSVAFSREGPTKEYVQHKMMDKAS 650
PgCPR       TELGPSILFFGCRNSKMDYIYEDELDNFVQNGALSELVLAFSREGPTKEYVQHKMMEKAS 644
AaCPR       TELGTAILFFGCRNRKVDFIYEDELNNFVETGALSELVTAFSREGATKEYVQHKMTQKAS 643
SrCPR3      TDLGLSILFFGCRNRKVDFIYENELNNFVETGALSELIVAFSREGPTKEYVQHKMSEKAS 646
SrCPR       TELGSSIFFFGCRNRKVDFIYEDELNNFVETGALSELIVAFSREGTAKEYVQHKMSQKAS 649
SrCPR2      TELGSSILFFGCRNRKVDYIYENELNNFVENGALSELDVAFSRDGPTKEYVQHKMTQKAS 648
AtCPR1      EELGSSLLFFGCRNRQMDFIYEDELNNFVDQGVISELIMAFSREGAQKEYVQHKMMEKAA 631
             :** ::::******  ::*:***:**:.**: * .::**  ****:*. ********  :**:

ATR2        DIWNMISQGAYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW 713
AtCPR2      DIWNMISQGAYLYVCGDAKGMARDVHRSLHTIAQEQGSMDSTKAEGFVKNLQTSGRYLRDVW 712
PgCPR       DIWNLISQGAYLYVCGDAKGMARDVHRTLHTIAQEQGSLDSSKAESMVKNLQMSGRYLRDVW 706
AaCPR       DIWNLLSEGAYLYVCGDAKGMAKDVHRILHTIVQEQGSLDSSKAELVVKNLQMAGRYLRDVW 705
SrCPR3      DIWNLLSEGAYLYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELVVKNLQMSGRYLRDVW 708
SrCPR       DIWKLLSEGAYLYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELVVKNLQMSGRYLRDVW 711
SrCPR2      EIWNMLSEGAYLYVCGDAKGMAKDVHRTLHTIVQEQGSLDSSKAELVVKNLQMSGRYLRDVW 710
AtCPR1      QVWDLIKEEGYLYVCGDAKGMARDVHRTLHTIVQEQBGVSSSEAEAIVKKLQTEGRYLRDVW 693
            ::*.::.: .**************:****:****.*** .:.*::**  **:**  ********
```

Figure 7

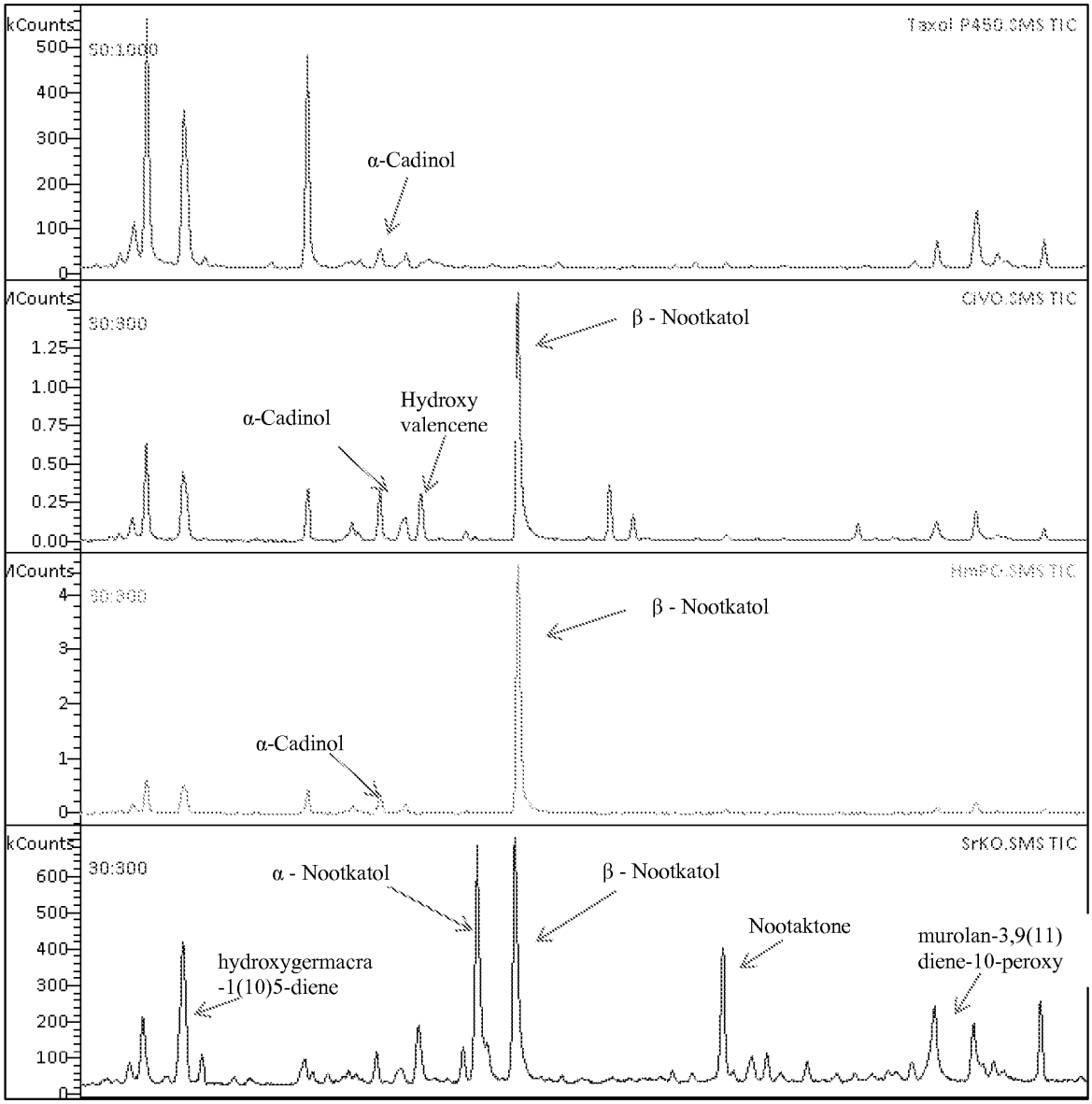

kCounts
500
400
300
200
100
0
50:1000
Taxol P450.SMS TIC
α-Cadinol
MCounts
1.25
1.00
0.75
0.50
0.25
0.00
50:300
CIVO.SMS TIC
β - Nootkatol
α-Cadinol
Hydroxy
valencene
MCounts
4
3
2
1
0
50:300
HmPC.SMS TIC
β - Nootkatol
α-Cadinol
kCounts
600
500
400
300
200
100
0
30:300
SrKO.SMS TIC
α - Nootkatol
β - Nootkatol
Nootaktone
murolan-3,9(11)
diene-10-peroxy
hydroxygermacra
-1(10)5-diene

Figure 8A

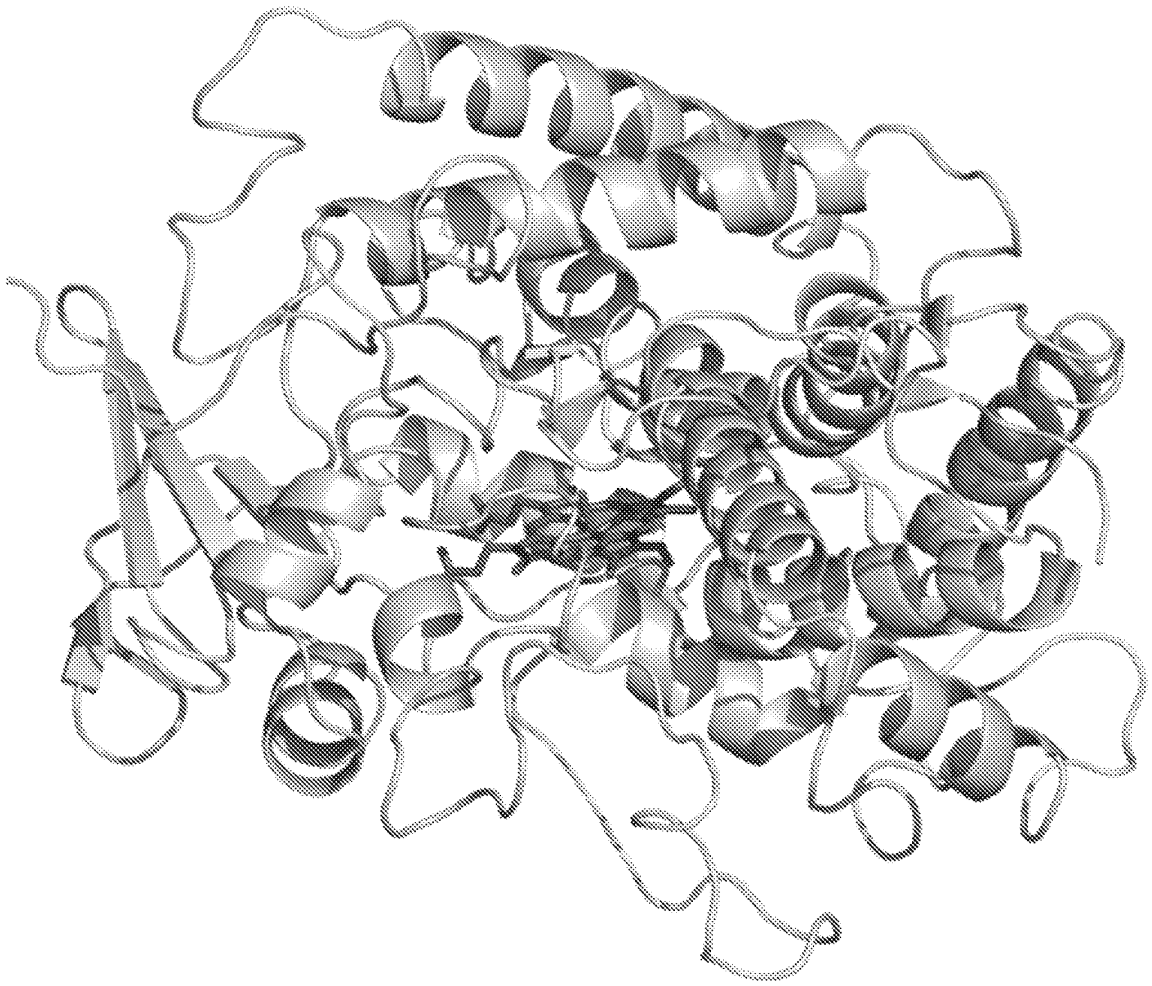
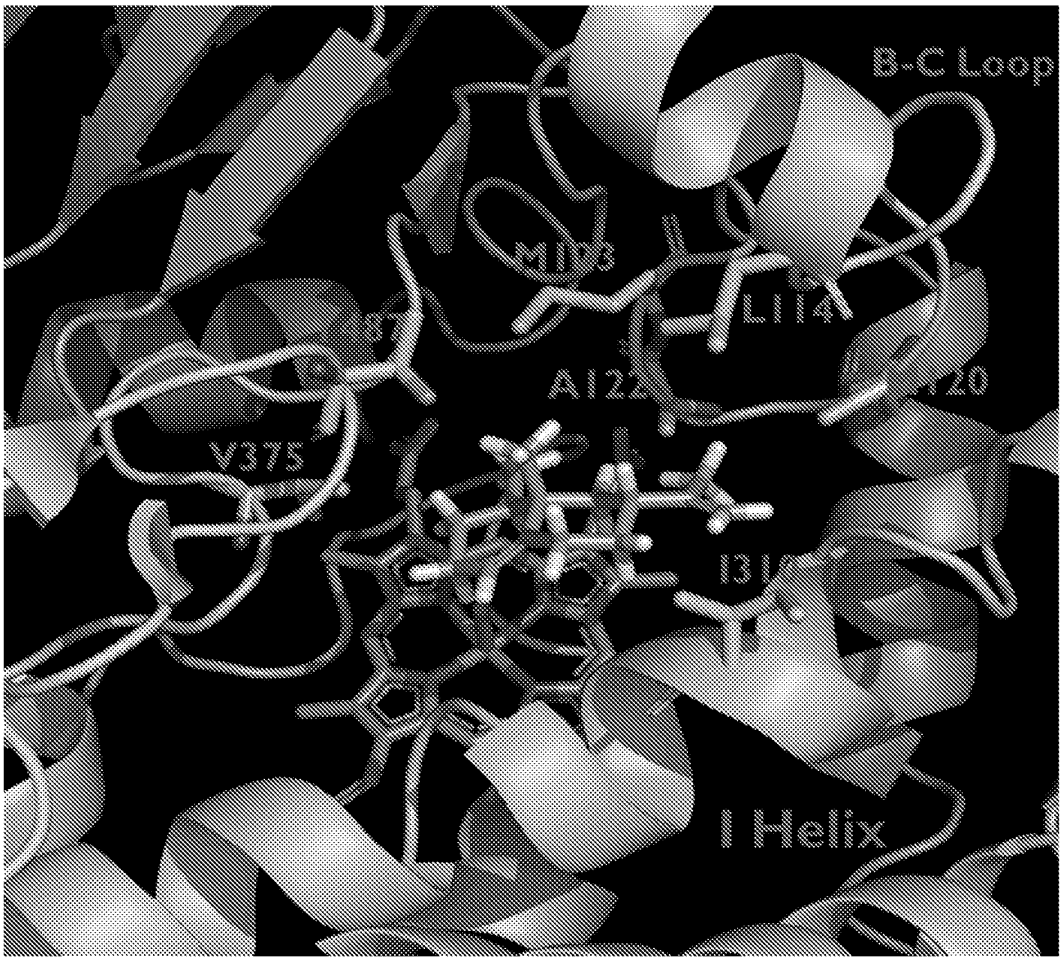
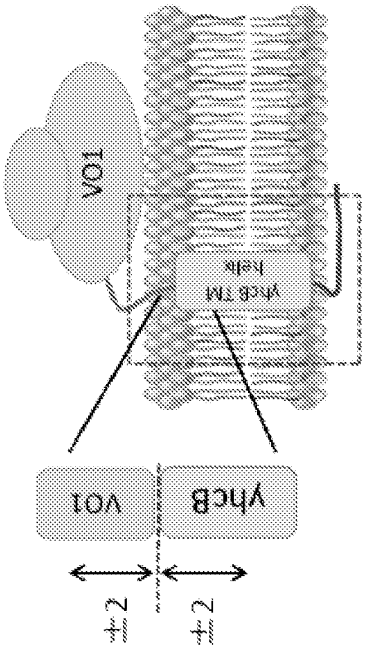


Figure 8B





	n20yhcB	n21yhcB	n22yhcB	n23yhcB	n24yhcB
t28VOR1	n20yhcB_t28VO1	n21yhcB_t28VO1	n22yhcB_t28VO1	n23yhcB_t28VO1	n24yhcB_t28VO1
t29VOR1	n20yhcB_t29VO1	n21yhcB_t29VO1	n22yhcB_t29VO1	n23yhcB_t29VO1	n24yhcB_t29VO1
t30VOR1	n20yhcB_t30VO1	n21yhcB_t30VO1	Current	n23yhcB_t30VO1	n24yhcB_t30VO1
t31VOR1	n20yhcB_t31VO1	n21yhcB_t31VO1	n22yhcB_t31VO1	n23yhcB_t31VO1	n24yhcB_t31VO1
t32VOR1	n20yhcB_t32VO1	n21yhcB_t32VO1	n22yhcB_t32VO1	n23yhcB_t32VO1	n24yhcB_t32VO1

Figure 9

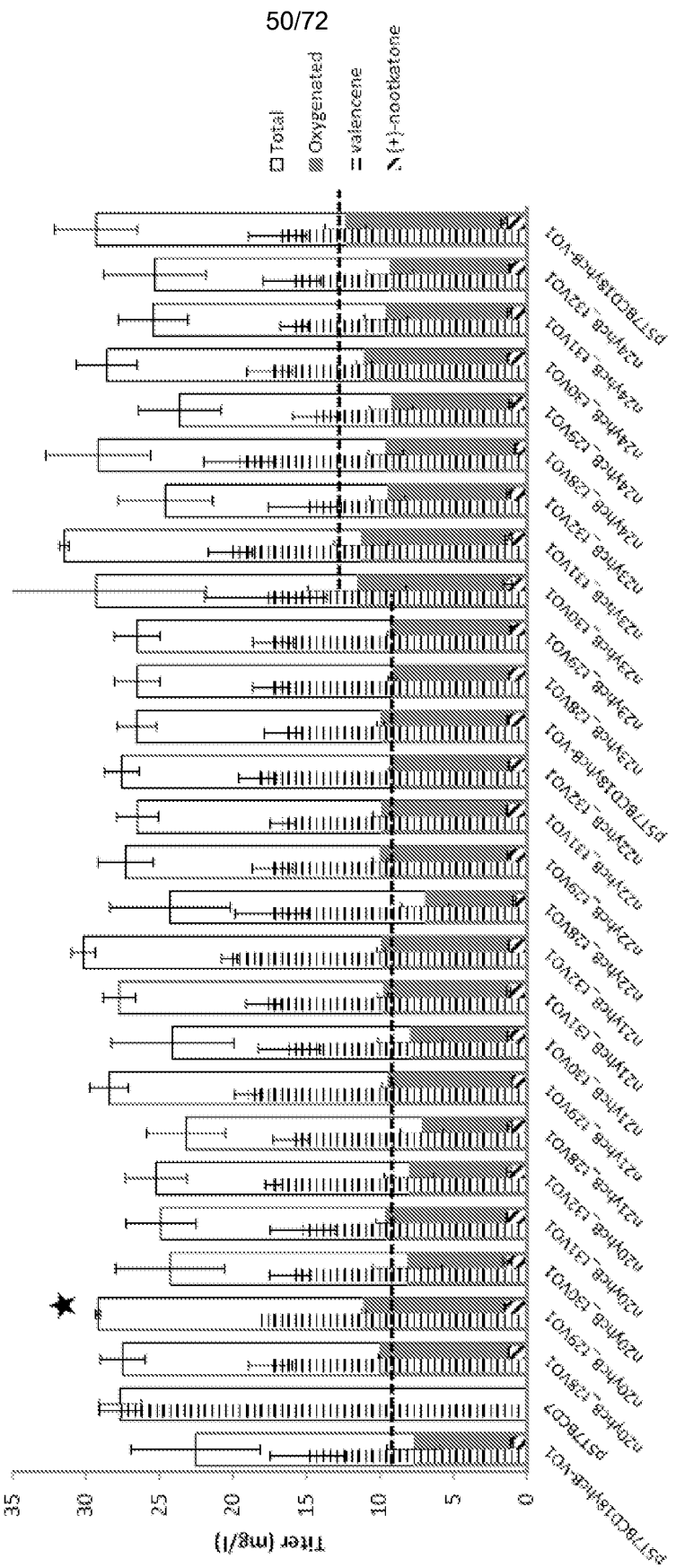

Total
Oxygenated
valencene
(+)-nootkatone
Titer (mg/l)
0
5
10
15
20
25
30
35
pST7BCD18yhcB-V01
pST7BCD7
n26yhcB_t28V01
n26yhcB_t29V01
n26yhcB_t30V01
n26yhcB_t31V01
n26yhcB_t32V01
n21yhcB_t28V01
n21yhcB_t29V01
n21yhcB_t30V01
n21yhcB_t31V01
n21yhcB_t32V01
n22yhcB_t28V01
n22yhcB_t29V01
n22yhcB_t31V01
n22yhcB_t32V01
pST7BCD18yhcB-V01
n23yhcB_t28V01
n23yhcB_t29V01
n23yhcB_t30V01
n23yhcB_t31V01
n23yhcB_t32V01
n24yhcB_t28V01
n24yhcB_t29V01
n24yhcB_t30V01
n24yhcB_t31V01
n24yhcB_t32V01
pST7BCD18yhcB-V01

Figure 10

Figure 11

#	(+)-nootkatone Downstream Pathway Enzymes
1	Valencene synthase (VS)
2	Valencene oxygenase (VO)
3	P450 reductase (CPR)
4	Alcohol dehydrogenase (ADH)

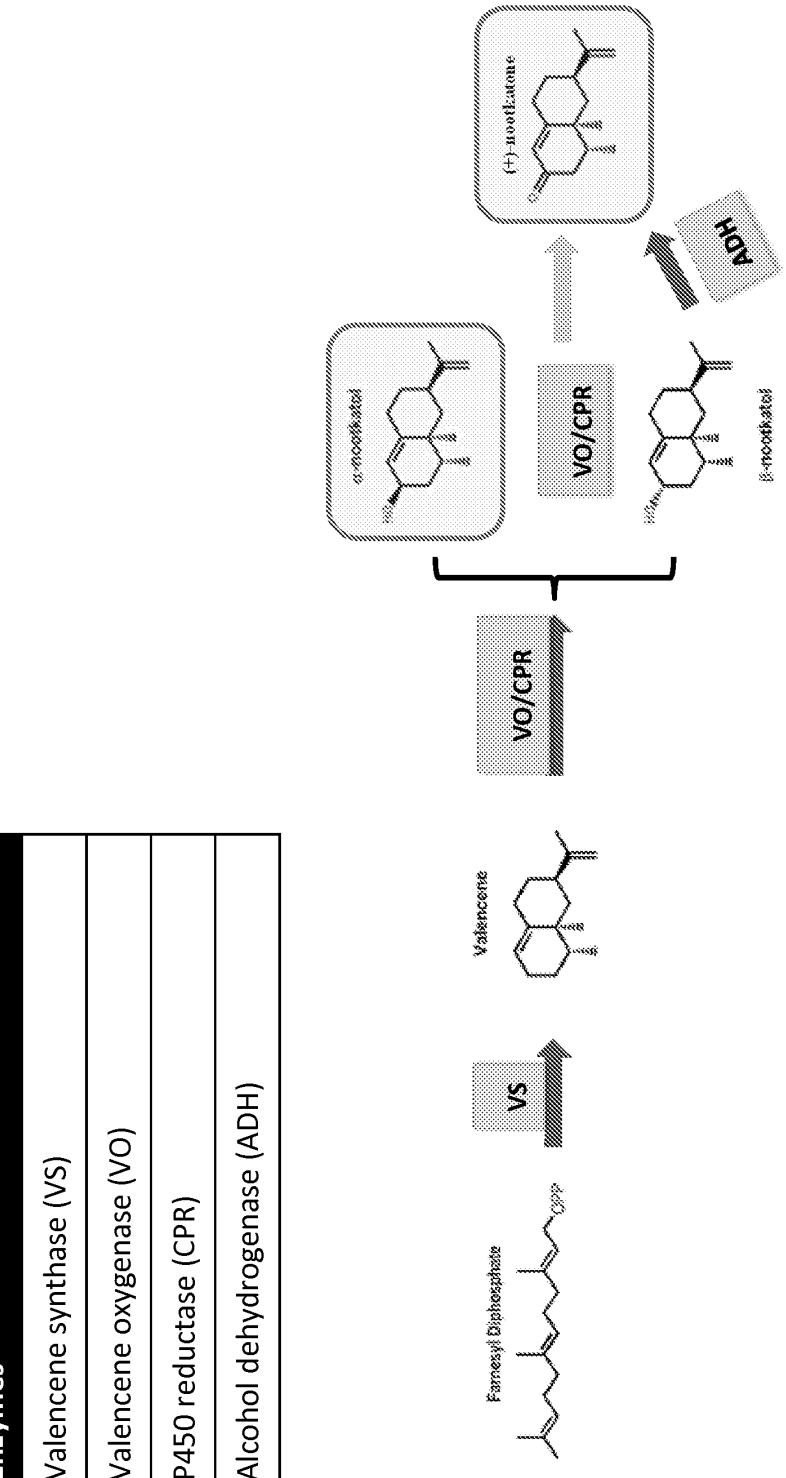


Figure 12

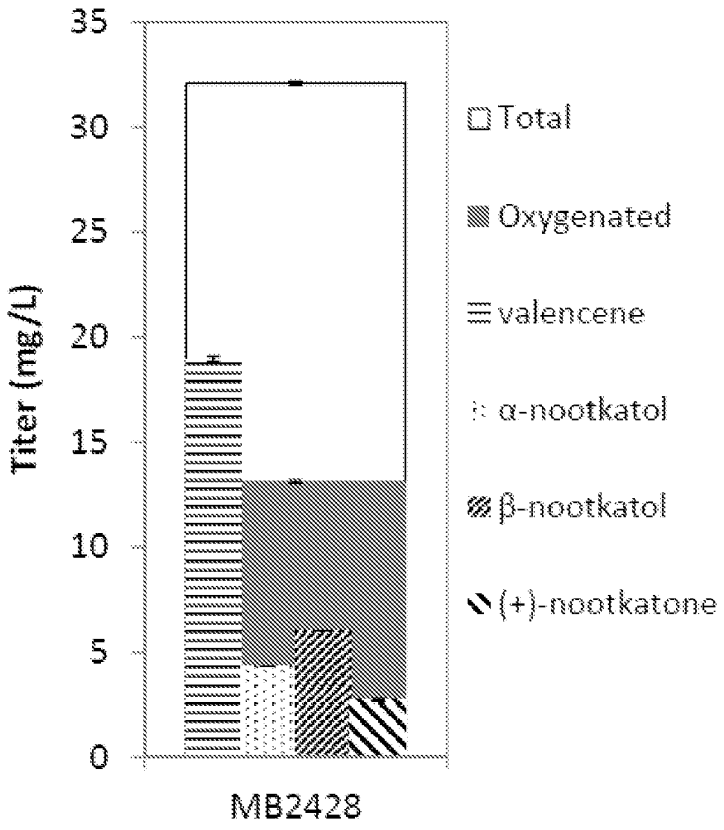
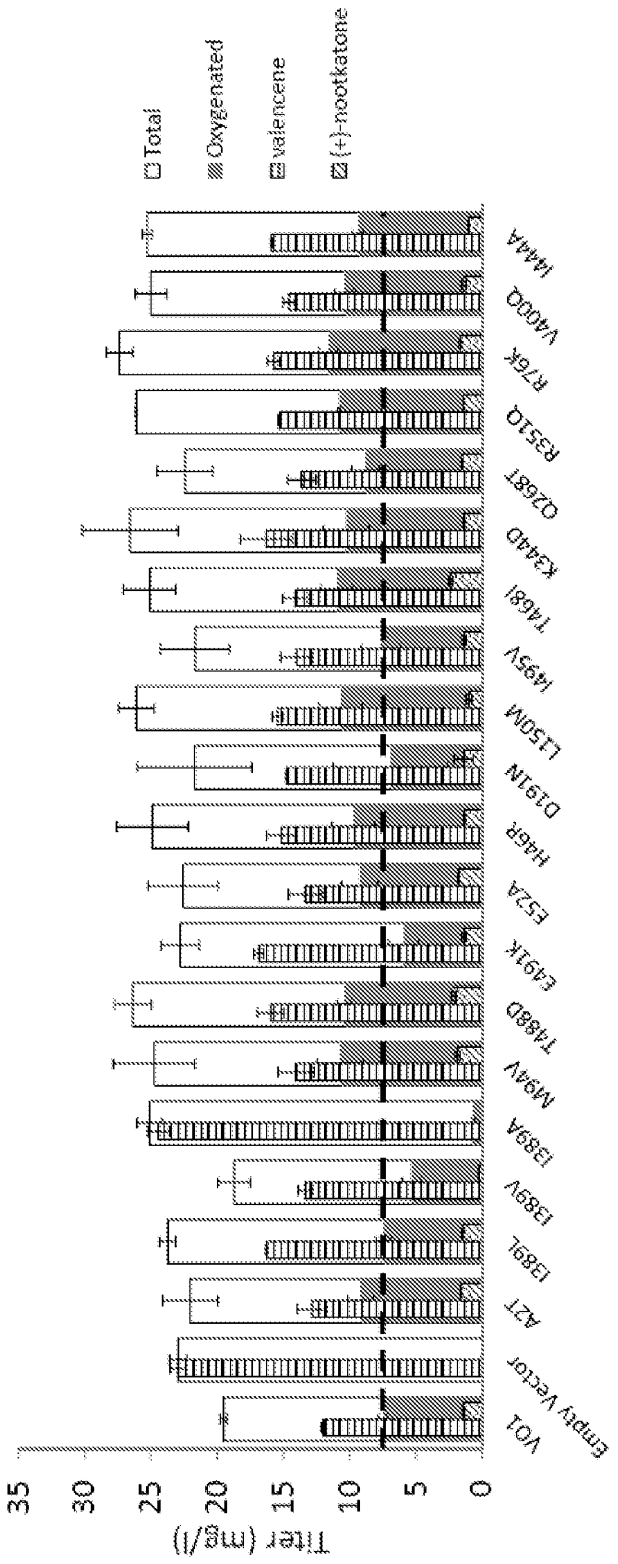

35
30
25
20
15
10
5
0
Titer (mg/L)
MB2428
Total
Oxygenated
valencene
α-nootkatol
β-nootkatol
(+)-nootkatone

Figure 13A


Total
Oxygenated
valencene
(+)-nootkatone
Titer (mg/l)
0
5
10
15
20
25
30
35
VO1
Empty Vector
A2T
I389L
I389V
I389A
M94V
T488D
L491K
E52A
H46R
D19N
L150M
I495V
T468I
K344D
Q268T
R351Q
R76K
V400Q
I444A

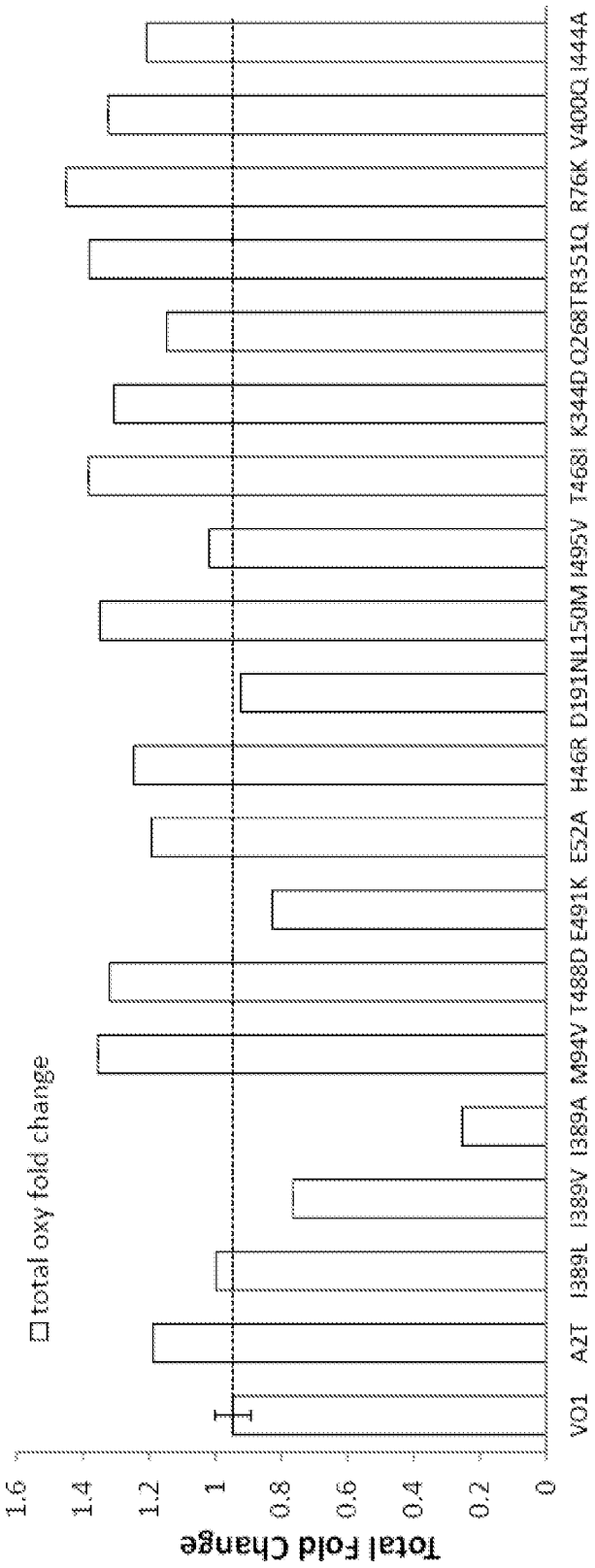
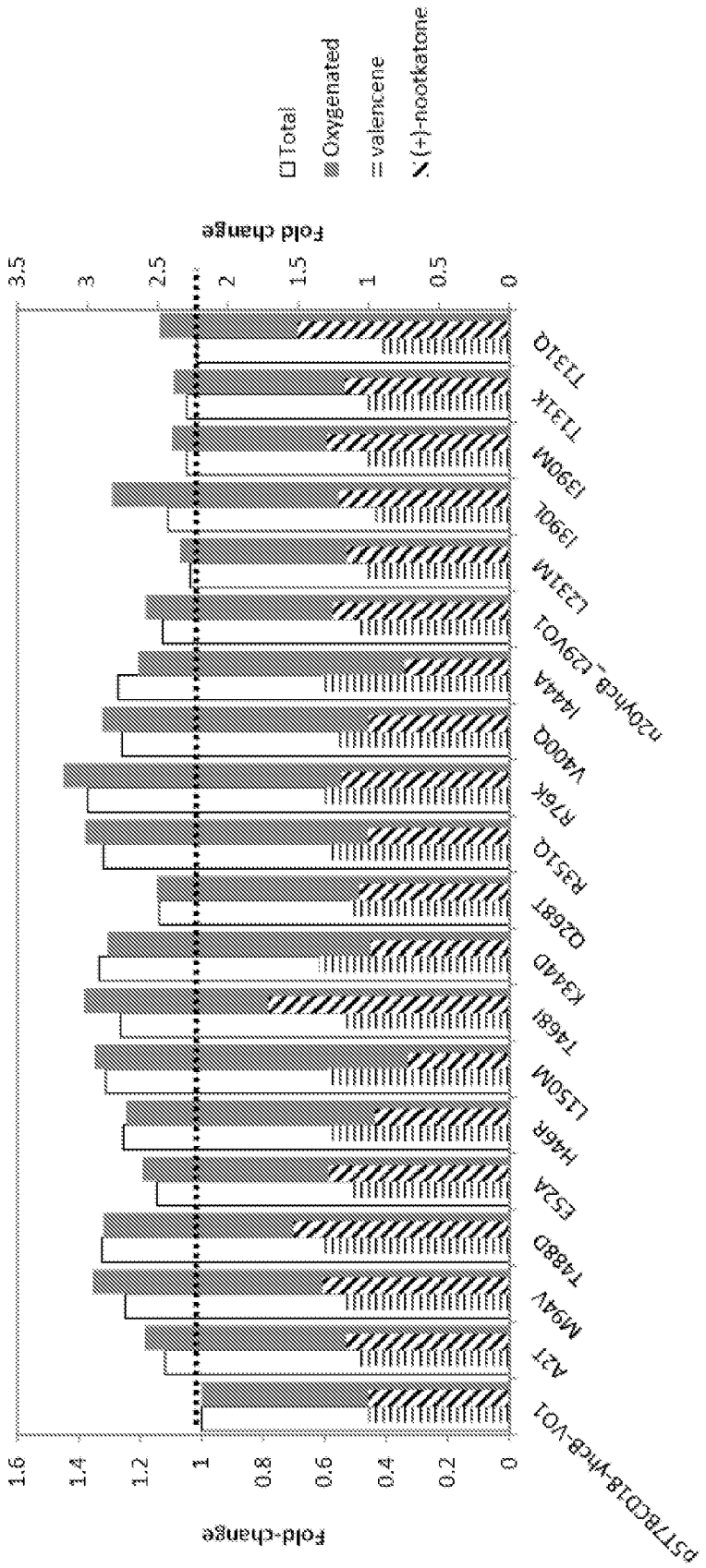

Total Fold Change
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
total oxy fold change
VO1
A2T
I389L
I389V
I389A
M94V
T488D
E491K
E52A
H46R
D191N
L150M
I495V
T468I
K344D
Q268R
T351Q
R76K
V400Q
I444A

Figure 13B

Figure 14


Total
Oxygenated
valencene
(+)-nootkatone
Fold change
Fold-change
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
0.5
1.5
2.5
3
3.5
pSTTBdCD18-Vhcb-V01
A2T
M9AV
T48SD
E52A
H46R
L150M
T468I
K344D
Q268T
R351Q
R76K
V400Q
I444A
n20yhcb_I29VQ1
L231M
I390L
I390M
T131K
T131Q

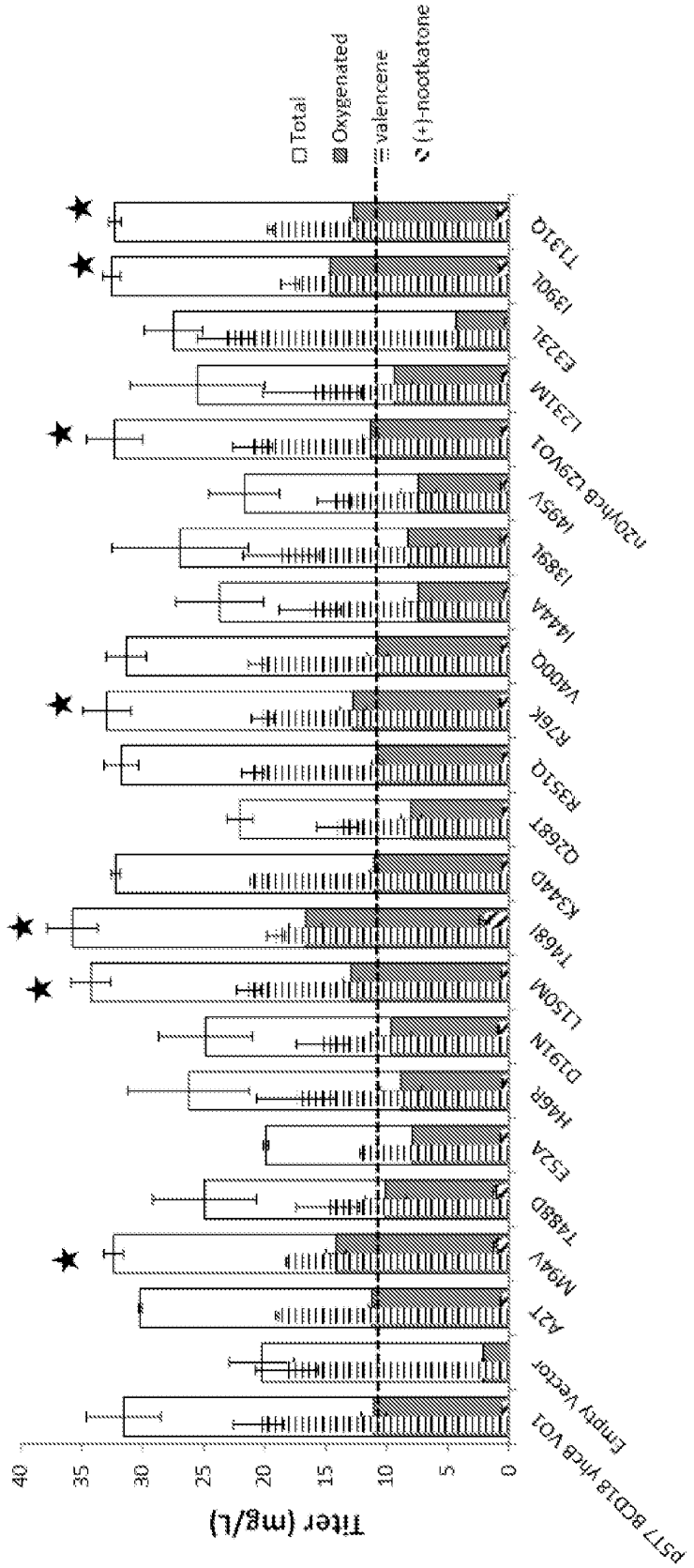

Total
Oxygenated
valencene
(+)-nootkatone
Titer (mg/L)
0
5
10
15
20
25
30
35
40
pST7 BCD1B vhcB VO1
Empty Vector
A2T
M94V
T488D
E52A
H46R
D19N
L150M
T468I
K344D
Q268T
R351Q
R76K
V400Q
I444A
I389L
I49SV
n20vhcB L29VO1
L231M
E232L
I390L
T131Q

Figure 15

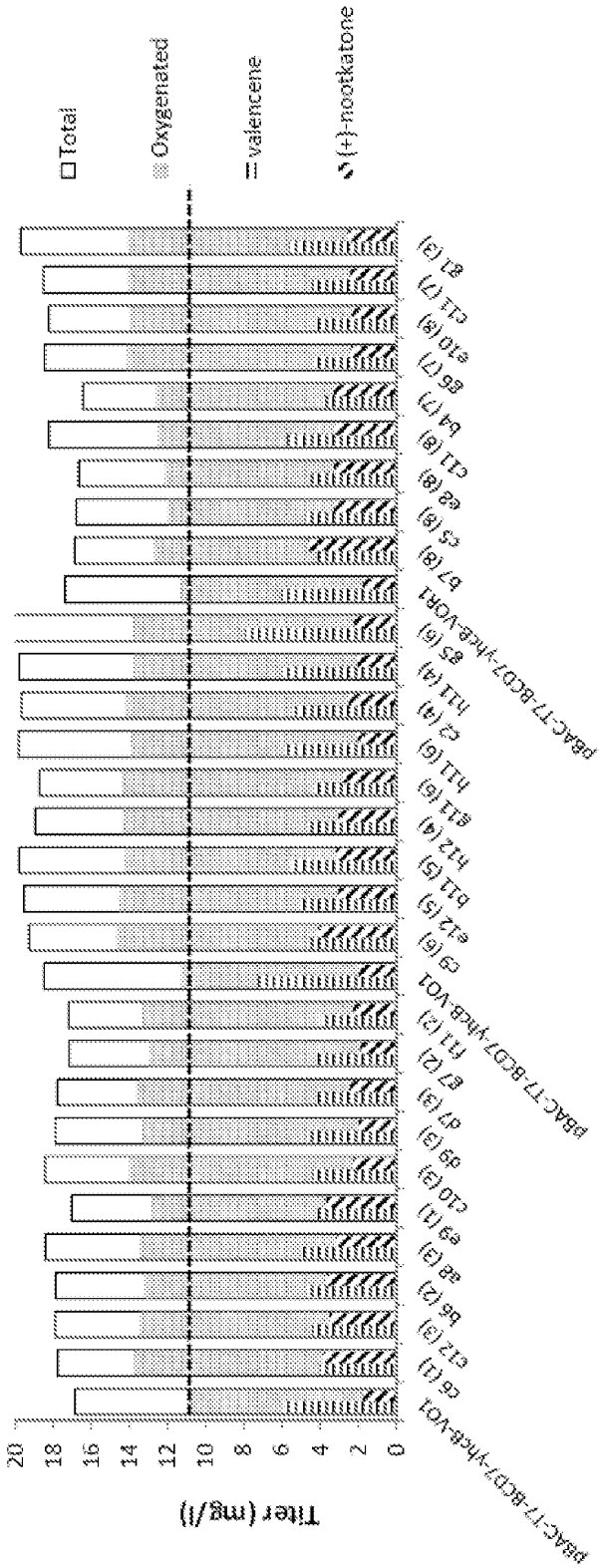

Total
Oxygenated
valencene
(+)-nootkatone
Titer (mg/l)
0
2
4
6
8
10
12
14
16
18
20
pBAC-T7-BCD7-yhcB-VOR1
pBAC-T7-BCD7-yhcB-VOR
c6 (1)
c12 (3)
b6 (2)
a8 (3)
e9 (1)
c10 (3)
d9 (3)
d7 (3)
f7 (2)
f11 (2)
c9 (6)
e12 (5)
b11 (5)
b12 (4)
a12 (6)
h11 (6)
c2 (4)
h11 (4)
f5 (6)
b7 (8)
c5 (8)
e8 (8)
c11 (8)
b4 (7)
f6 (7)
e10 (8)
c11 (7)
g1 (3)

Figure 16A

Figure 16B

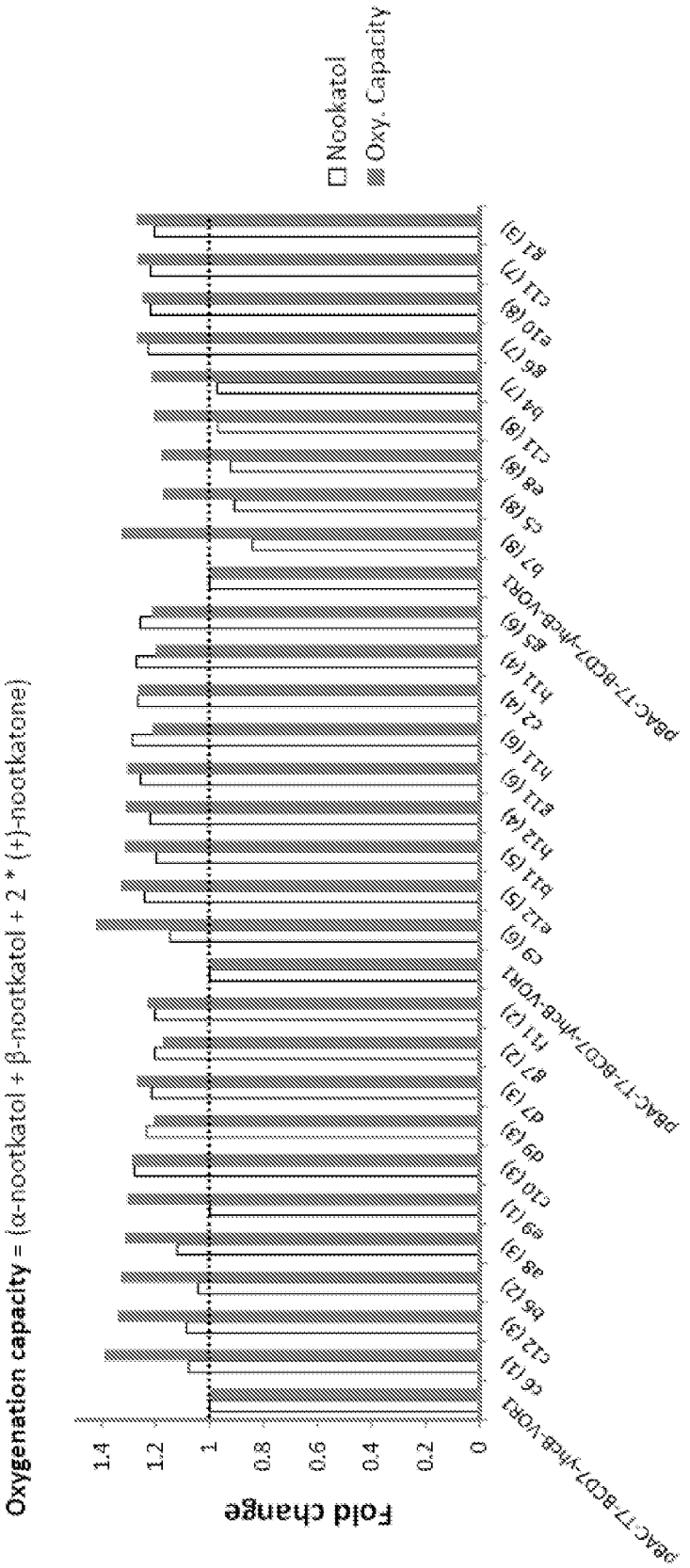
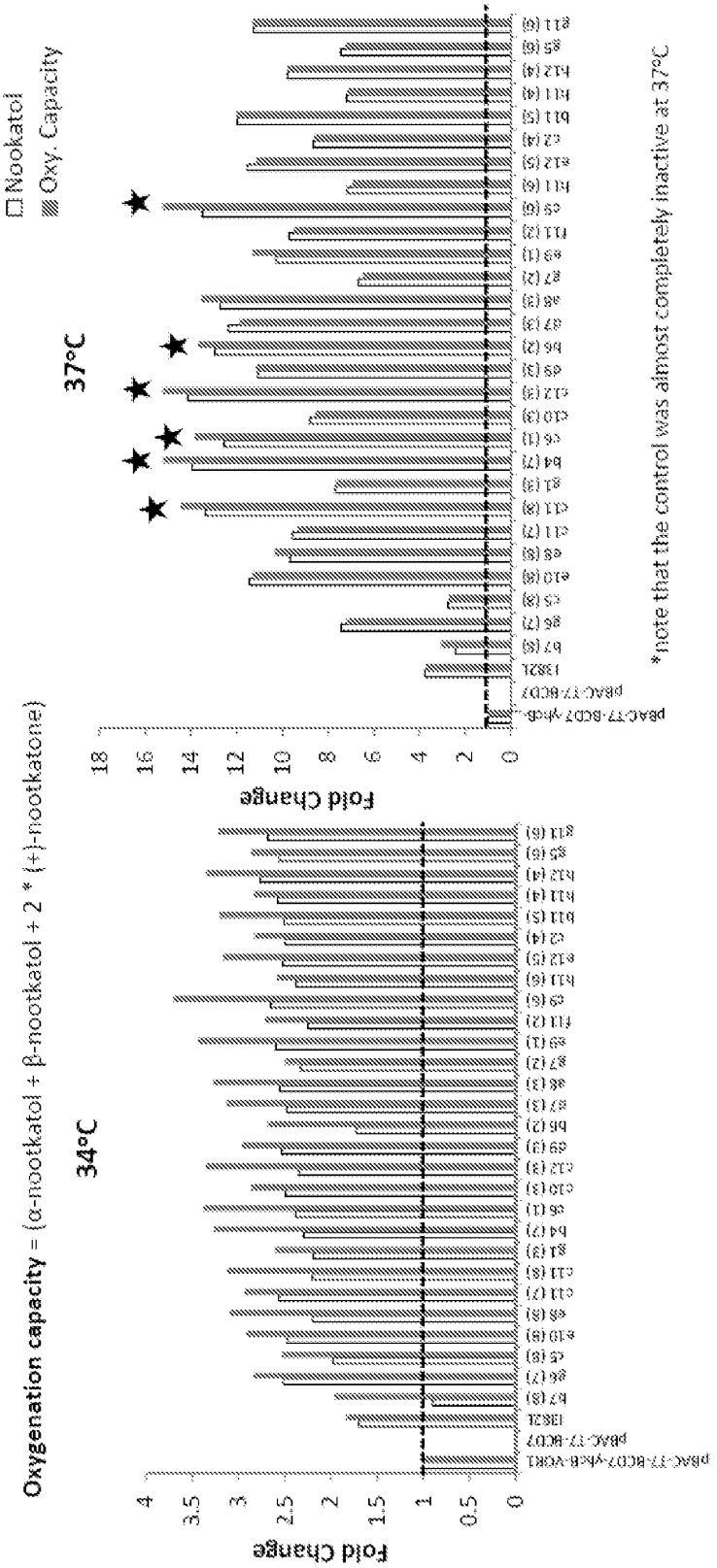

Oxygenation capacity = (α-nootkatol + β-nootkatol + 2 * (+)-nootkatone)
Fold change
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Nookatol
Oxy. Capacity
pBAC-T7-BCD7-yhcB-VOR1
c6 (1)
c12 (3)
b6 (2)
a8 (3)
e9 (1)
c10 (3)
d9 (3)
d7 (3)
g7 (2)
f11 (2)
c9 (6)
e12 (5)
b11 (5)
h12 (4)
g11 (6)
h11 (6)
c2 (4)
h11 (4)
g5 (6)
b7 (8)
c5 (8)
e8 (8)
c11 (8)
b4 (7)
e6 (7)
e10 (8)
c11 (7)
g1 (3)

Figure 17


Oxygenation capacity = (α-nootkatol + β-nootkatol + 2 * (+)-nootkatone)
34°C
37°C
Nookatol
Oxy. Capacity
Fold Change
*note that the control was almost completely inactive at 37°C

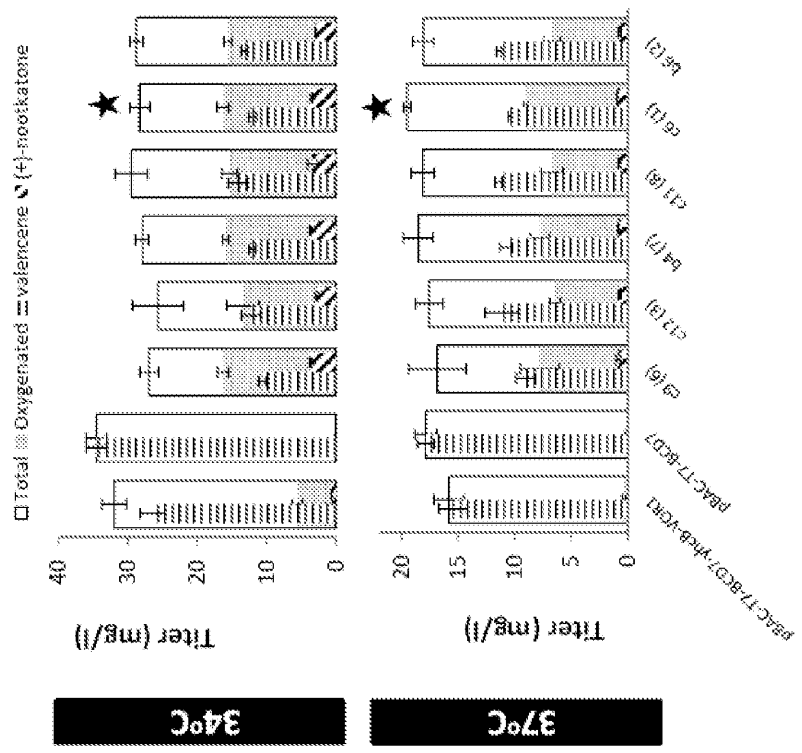

37°C
34°C
Titer (mg/l)
Titer (mg/l)
0
5
10
15
20
0
10
20
30
40
pBAC-T7-BCD7-yhcb-VCN1
pBAC-T7-BCD7
c9 (6)
c13 (8)
be4 (7)
c11 (8)
c6 (1)
be (2)
Total Oxygenated valencene (+)-nootkatone

Figure 18

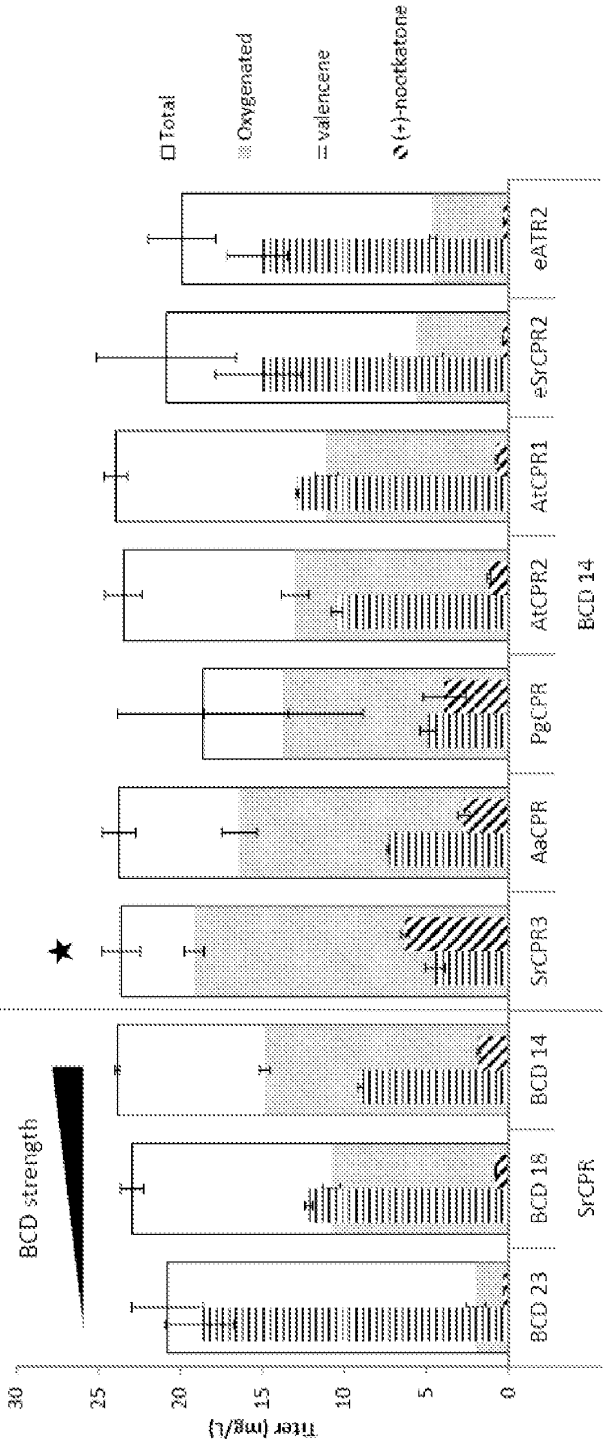

Total
Oxygenated
valencene
(+)-nootkatone
Titer (mg/L)
0
5
10
15
20
25
30
BCD strength
BCD 23
BCD 18
BCD 14
SrCPR
SrCPR3
AaCPR
PgCPR
AtCPR2
AtCPR1
eSyCPR2
eATR2
BCD 14

Figure 19

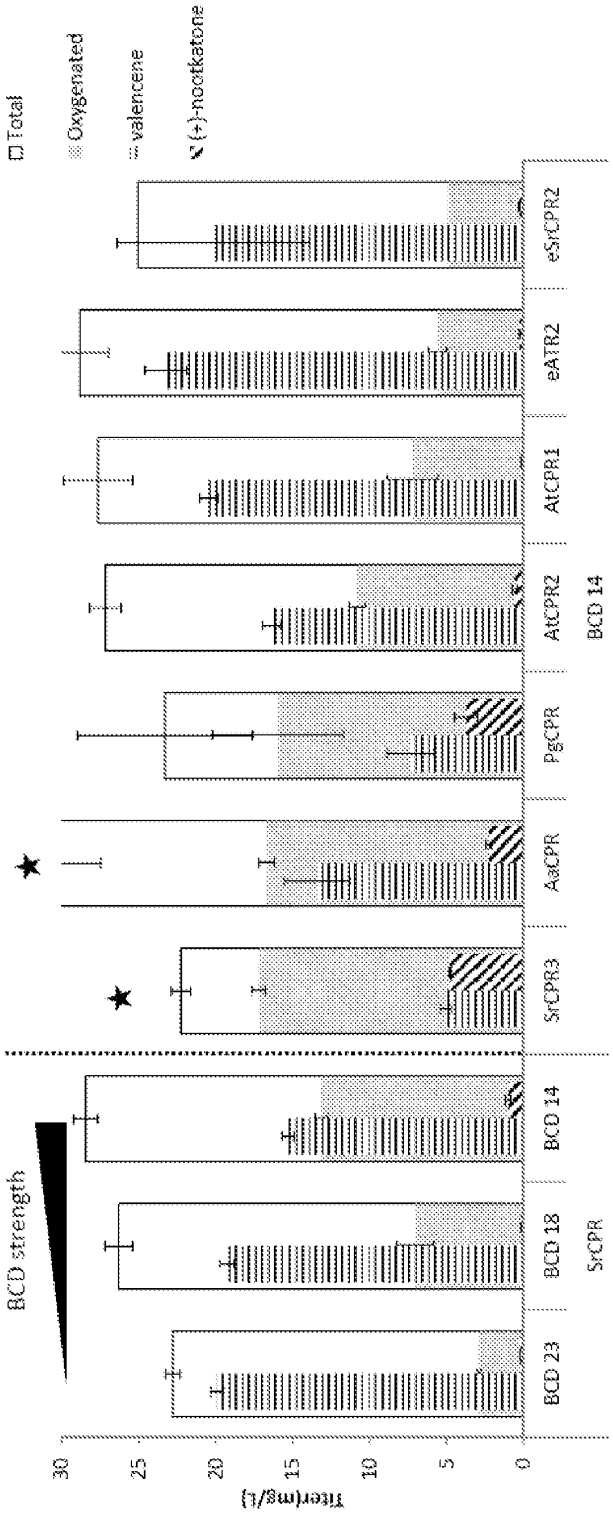

Total
Oxygenated
valencene
(+)-nootkatone
BCD strength
BCD 23
BCD 18
BCD 14
SrCPR
SrCPR3
AaCPR
PgCPR
AtCPR2
AtCPR1
eATR2
eSrCPR2
BCD 14
Titer(mg/L)
30
25
20
15
10
5
0

Figure 20

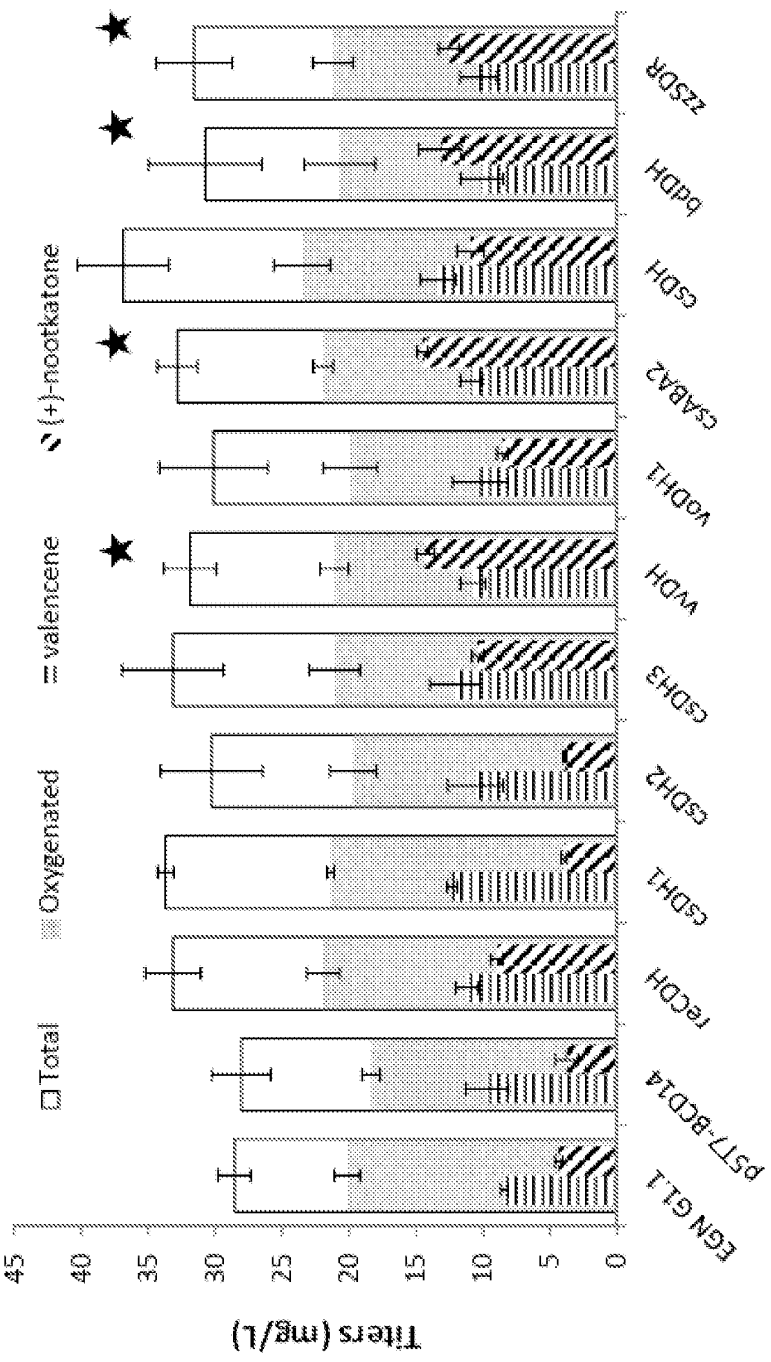

Titers (mg/L)
0
5
10
15
20
25
30
35
40
45
Total
Oxygenated
valencene
(+)-nootkatone
EGN GL1
pST7-BCD14
IeCDH
CsDH1
CsDH2
CsDH3
VDH
VoDH1
CsADA2
CsDH
bdDH
zSDR

Figure 21

Figure 22A

>ReCDH [Rhodococcus erythropolis]

MARVEGQVALITGAARGQGRSHAIKLAEEGADVILVDVPNDVVDIGYPLGTADELDQTAKDVEN
LGRKAIVIHADVRDLESLTAEVDRAVSTLGRLDIVSANAGIASVPFLSHDIPDNTWRQMIDINL
TGVWHTAKVAVPHILAGERGGSIVLTSSAAGLKGYAQISHYSAAKHGVVGLMRSLALELAPHRV
RVNSLHPTQVNTPMIQNEGTYRIFSPDLENPTREDFEIASTTTNALPIPWVESVDVSNALLFLV
SEDARYITGAAIPVDAGTTLK (SEQ ID NO: 84)

ATGGCCCGTGTGGAAGGTCAAGTGGCTCTGATTACCGGCGCTGCTCGTGGTCAAGGTCGTAGTC
ATGCGATTAAACTGGCGGAAGAAGGCGCGGATGTGATTCTGGTTGACGTCCCGAATGATGTGGT
TGACATCGGCTATCCGCTGGGTACGGCAGATGAACTGGACCAGACCGCTAAAGATGTTGAAAAC
CTGGGTCGTAAGGCGATTGTCATCCATGCCGATGTGCGCGACCTGGAATCACTGACGGCAGAAG
TGGATCGTGCTGTTAGTACCCTGGGCCGCCTGGACATTGTTTCCGCAAATGCTGGTATCGCCAG
CGTCCCGTTTCTGTCTCACGATATTCCGGACAACACCTGGCGTCAGATGATTGATATCAATCTG
ACGGGCGTCTGGCATACCGCGAAAGTGGCCGTTCCGCACATTCTGGCCGGTGAACGCGGCGGTT
CCATCGTTCTGACCAGCTCTGCGGCCGGCCTGAAAGGTTATGCACAAATTAGTCATTACTCCGC
AGCTAAGCACGGCGTCGTGGGTCTGATGCGTTCACTGGCACTGGAACTGGCTCCGCATCGTGTC
CGCGTGAACTCGCTGCACCCGACGCAGGTGAACACCCCGATGATTCAAAATGAAGGCACGTATC
GTATCTTTAGCCCGGATCTGGAAAACCCGACCCGCGAAGACTTCGAAATTGCGTCTACCACGAC
CAATGCCCTGCCGATCCCGTGGGTGGAATCAGTTGATGTCTCGAACGCACTGCTGTTCCTGGTT
AGCGAAGACGCACGTTACATTACCGGTGCAGCAATCCCGGTGGATGCCGGTACGACCCTGAAGT
AA (SEQ ID NO: 85)

>CsDH [Citrus sinensus]

MATPPISSLISQRLLGKVALVTGGASGIGEGIVRLFHRHGAKVCFVDVQDELGYRLQESLVGDK
DSNIFYSHCDVTVEDDVRRAVDLTVTKFGTLDIMVNNAGISGTPSSDIRNVDVSEFEKVFDINV
KGVFMGMKYAASVMIPRKQGSIISLGSVGSVIGGIGPHHYISSKHAVVGLTRSIAAELGQHGIR
VNCVSPYAVPTNLAVAHLPEDERTEDMFTGFREFAKKNANLQGVELTVEDVANAVLFLASEDAR
YISGDNLIVDGGFTRVNHSFRVFR (SEQ ID NO: 86)

ATGGCAACGCCGCCGATTTCATCCCTGATTTCACAACGCCTGCTGGGTAAAGTCGCCCTGGTCA
CGGGTGGTGCTTCTGGTATTGGTGAAGGCATCGTGCGTCTGTTTCACCGTCATGGCGCGAAAGT
GTGCTTTGTTGATGTGCAGGATGAACTGGGCTACCGTCTGCAAGAATCTCTGGTGGGCGACAAA
GATTCAAACATCTTTTATAGCCACTGTGATGTCACCGTGGAAGACGATGTGCGCCGCGCTGTGG
ATCTGACCGTGACGAAATTCGGTACGCTGGATATTATGGTCAATAACGCGGGTATTAGTGGCAC
CCCGTCCAGCGATATTCGTAATGTTGATGTGAGCGAATTTGAAAAAGTGTTTGATATTAACGTC
AAAGGCGTGTTTATGGGCATGAAATATGCCGCGAGCGTGATGATCCCGCGCAAACAGGGTAGCA
TCATCTCCCTGGGTTCTGTTGGCAGCGTGATCGGTGGCATTGGCCCGCACCATTATATCAGCTC
GAAACATGCGGTTGTGGGCCTGACCCGCAGCATTGCAGCGGAACTGGGTCAGCATGGCATTCGT
GTGAACTGTGTGTCTCCGTATGCGGTTCCGACCAATCTGGCGGTTGCACACCTGCCGGAAGATG
AACGTACCGAAGATATGTTTACGGGCTTCCGTGAATTTGCGAAAAAGAATGCCAACCTGCAAGG
TGTTGAACTGACCGTCGAAGATGTGGCCAATGCGGTGCTGTTTCTGGCCAGCGAAGATGCACGC
TACATTAGCGGTGATAATCTGATCGTTGATGGCGGCTTTACCCGTGTGAACCACTCATTTCGTG
TTTTCCGTTAA (SEQ ID NO: 87)

>CsDH1 [Citrus sinensus]

MSKPRLQGKVAIIMGAASGIGEATAKLFAEHGAFVIIADIQDELGNQVVSSIGPEKASYRHCDV
RDEKQVEETVAYAIEKYGSLDIMYSNAGVAGPVGTILDLDMAQFDRTIATNLAGSVMAVKYAAR

VMVANKIRGSIICTTSTASTVGGSGPHAYTISKHGLLGLVRSAASELGKHGIRVNCVSPFGVAT
PFSAGTINDVEGFVCKVANLKGIVLKAKHVAEAALFLASDESAYVSGHDLVVDGGFTAVTNVMS
MLEGHG (SEQ ID NO: 88)

ATGTCAAAACCGCGTCTGCAAGGCAAAGTGGCTATTATTATGGGTGCTGCGTCTGGCATCGGTG
AAGCTACGGCTAAACTGTTCGCTGAACATGGCGCATTTGTGATTATCGCTGATATTCAGGACGA
ACTGGGCAACCAGGTGGTTAGCTCTATCGGCCCGGAAAAAGCGTCTTATCGTCACTGCGATGTG
CGTGATGAAAAACAGGTTGAAGAAACCGTCGCGTATGCGATTGAAAAATACGGCAGCCTGGATA
TTATGTACTCCAATGCGGGCGTGGCCGGTCCGGTTGGCACGATTCTGGATCTGGACATGGCCCA
ATTCGACCGTACCATCGCAACGAACCTGGCTGGTAGTGTTATGGCAGTCAAATATGCGGCCCGT
GTCATGGTGGCGAATAAAATTCGCGGTAGCATTATCTGTACCACGAGTACCGCCTCCACGGTGG
GCGGCAGCGGCCCGCACGCCTATACCATTAGCAAACACGGTCTGCTGGGCCTGGTTCGTTCAGC
AGCTTCGGAACTGGGTAAACATGGCATCCGCGTGAACTGCGTTAGCCCGTTTGGTGTTGCGACC
CCGTTCTCTGCCGGTACGATTAACGATGTCGAAGGCTTTGTCTGTAAAGTGGCGAATCTGAAAG
GCATCGTCCTGAAAGCGAAGCATGTGGCCGAAGCGGCCCTGTTCCTGGCAAGCGATGAATCTGC
TTATGTGAGCGGTCACGACCTGGTGGTGGATGGTGGCTTTACGGCAGTTACGAATGTCATGTCA
ATGCTGGAAGGTCACGGCTAA (SEQ ID NO: 89)

>CsDH2 [Citrus sinensus]

MSNPRMEGKVALITGAASGIGEAAVRLFAEHGAFVVAADVQDELGHQVAASVGTDQVCYHHCDV
RDEKQVEETVRYTLEKYGKLDVLFSNAGIMGPLTGILELDLTGFGNTMATNVCGVAATIKHAAR
AMVDKNIRGSIICTTSVASSLGGTAPHAYTTSKHALVGLVRTACSELGAYGIRVNCISPFGVAT
PLSCTAYNLRPDEVEANSCALANLKGIVLKAKHIAEAALFLASDESAYISGHNLAVDGGFTVVN
HSSSSAT (SEQ ID NO: 90)

ATGTCAAACCCGCGTATGGAAGGCAAAGTCGCACTGATTACGGGCGCAGCATCTGGTATCGGTG
AAGCAGCAGTCCGTCTGTTCGCTGAACATGGTGCGTTTGTCGTGGCGGCAGATGTGCAAGACGA
ACTGGGTCATCAGGTGGCGGCATCTGTGGGTACGGACCAGGTGTGCTACCATCACTGCGATGTG
CGCGATGAAAAACAAGTGGAAGAAACCGTGCGTTATACCCTGGAAAAATACGGCAAACTGGATG
TCCTGTTTTCAAACGCGGGCATCATGGGTCCGCTGACCGGCATTCTGGAACTGGATCTGACCGG
CTTCGGTAACACGATGGCAACCAATGTGTGCGGTGTTGCCGCGACCATTAAACACGCGGCACGC
GCAATGGTGGACAAAAACATTCGCGGTAGCATTATCTGCACCACCAGCGTGGCTTCATCGCTGG
GTGGCACCGCGCCGCACGCATACACCACGAGCAAACACGCACTGGTGGGCCTGGTTCGTACGGC
ATGTTCGGAACTGGGTGCGTATGGCATTCGTGTGAACTGTATCAGCCCGTTTGGTGTTGCAACG
CCGCTGTCTTGCACGGCCTATAACCTGCGCCCGGATGAAGTGGAAGCAAACTCATGCGCACTGG
CGAACCTGAAAGGTATTGTGCTGAAAGCGAAACACATTGCGGAAGCAGCGCTGTTCCTGGCGAG
CGATGAAAGCGCGTATATTAGCGGTCATAATCTGGCGGTGGATGGTGGTTTCACGGTGGTTAAT
CATTCAAGTTCGTCGGCGACGTAA (SEQ ID NO: 91)

>CsDH3 [Citrus sinensus]

MTTAGSRDSPLVAQRLLGKVALVTGGATGIGESIVRLFHKHGAKVCVVDINDDLGQHLCQTLGP
TTRFIHGDVAIEDDVSRAVDFTVANFGTLDIMVNNAGMGGPPCPDIREFPISTFEKVFDINTKG
TFIGMKHAARVMIPSKKGSIVSISSVTSAIGGAGPHAYTASKHAVLGLTKSVAAELGQHGIRVN
CVSPYAILTNLALAHLHEDERTDDARAGFRAFIGKNANLQGVDLVEDDVANAVLFLASDDARYI
SGDNLFVDGGFTCTNHSLRVFR (SEQ ID NO: 92)

ATGACGACGGCTGGTTCGCGTGACAGTCCGCTGGTCGCTCAACGCCTGCTGGGCAAAGTGGCCC
TGGTTACGGGTGGTGCTACCGGCATTGGTGAAAGTATCGTGCGTCTGTTTCATAAACACGGCGC
GAAAGTTTGCGTGGTTGATATTAACGATGACCTGGGCCAGCATCTGTGTCAAACCCTGGGTCCG
ACCACCCGTTTCATTCACGGCGATGTTGCAATCGAAGATGATGTGAGCCGTGCGGTTGATTTTA
CCGTCGCCAACTTCGGTACGCTGGACATTATGGTGAACAATGCCGGTATGGGCGGTCCGCCGTG

CCCGGATATTCGTGAATTTCCGATCTCGACCTTTGAAAAAGTCTTCGACATTAACACCAAAGGC
ACGTTCATCGGTATGAAACATGCGGCCCGCGTGATGATTCCGAGTAAAAAAGGTAGTATTGTCA
GCATTAGCAGCGTGACCAGCGCGATTGGCGGCGCGGGTCCGCACGCCTATACCGCGAGCAAACA
TGCGGTGCTGGGCCTGACGAAATCTGTCGCGGCGGAACTGGGCCAGCACGGTATTCGTGTCAAC
TGTGTGTCTCCGTACGCCATCCTGACCAATCTGGCGCTGGCCCATCTGCACGAAGATGAACGTA
CGGATGACGCGCGTGCGGGTTTTCGTGCATTCATTGGTAAAAACGCTAATCTGCAAGGTGTTGA
TCTGGTCGAAGATGACGTGGCGAATGCCGTTCTGTTTCTGGCATCAGATGACGCTCGCTATATC
TCGGGCGATAACCTGTTCGTGGATGGCGGCTTCACCTGTACCAATCACTCCCTGCGTGTGTTCC
GTTAA (SEQ ID NO: 93)

>VvDH [Vitis vinifera]

MAATSIDNSPLPSQRLLGKVALVTGGATGIGESIVRLFLKQGAKVCIVDVQDDLGQKLCDTLGG
DPNVSFFHCDVTIEDDVCHAVDFTVTKFGTLDIMVNNAGMAGPPCSDIRNVEVSMFEKVFDVNV
KGVFLGMKHAARIMIPLKKGTIISLCSVSSAIAGVGPHAYTGSKCAVAGLTQSVAAEMGGHGIR
VNCISPYAIATGLALAHLPEDERTEDAMAGFRAFVGKNANLQGVELTVDDVAHAAVFLASDEAR
YISGLNLMLDGGFSCTNHSLRVFR (SEQ ID NO: 94)

ATGGCCGCAACGAGCATTGATAATTCTCCGCTGCCGAGTCAACGTCTGCTGGGTAAAGTCGCAC
TGGTCACGGGTGGCGCTACGGGTATTGGCGAAAGCATCGTGCGTCTGTTTCTGAAACAGGGTGC
TAAAGTGTGCATTGTGGACGTGCAAGATGACCTGGGCCAGAAACTGTGCGATACCCTGGGTGGC
GATCCGAACGTTAGCTTTTTCCATTGCGATGTGACCATCGAAGATGATGTGTGCCATGCAGTTG
ATTTTACCGTCACGAAATTCGGCACCCTGGATATTATGGTGAACAATGCGGGTATGGCAGGTCC
GCCGTGCTCGGACATCCGCAACGTGGAAGTCAGCATGTTTGAAAAAGTGTTTGATGTGAATGTG
AAAGGTGTTTTCCTGGGCATGAAACATGCAGCCCGCATTATGATTCCGCTGAAAAAAGGCACCA
TTATCAGCCTGTGTTCAGTTTCCAGCGCTATCGCGGGCGTTGGTCCGCACGCATATACGGGTAG
CAAATGCGCAGTGGCGGGTCTGACGCAATCGGTCGCAGCAGAAATGGGTGGTCATGGCATTCGC
GTGAACTGTATCAGCCCGTATGCAATCGCAACGGGTCTGGCGCTGGCACATCTGCCGGAAGATG
AACGCACGGAAGATGCAATGGCGGGTTTCCGTGCGTTTGTGGGTAAAAATGCGAATCTGCAAGG
TGTTGAACTGACCGTGGATGATGTGGCGCACGCAGCGGTGTTTCTGGCAAGCGATGAAGCACGT
TACATCTCTGGTCTGAATCTGATGCTGGACGGCGGCTTTTCGTGTACCAACCACTCGCTGCGTG
TCTTTCGCTAA (SEQ ID NO: 95)

>VvDH1 [Vitis vinifera]

MSTASSGDVSLLSQRLVGKVALITGGATGIGESIARLFYRHGAKVCIVDIQDNPGQNLCRELGT
DDACFFHCDVSIEIDVIRAVDFVVNRFGKLDIMVNNAGIADPPCPDIRNTDLSIFEKVFDVNVK
GTFQCMKHAARVMVPQKKGSIISLTSVASVIGGAGPHAYTGSKHAVLGLTKSVAAELGLHGIRV
NCVSPYAVPTGMPLAHLPESEKTEDAMMGMRAFVGRNANLQGIELTVDDVANSVVFLASDEARY
VSGLNLMLDGGFSCVNHSLRVFR (SEQ ID NO: 96)

ATGTCAACGGCTTCCTCGGGTGATGTGTCGCTGCTGTCGCAACGCCTGGTCGGTAAAGTCGCTC
TGATTACGGGTGGTGCAACGGGCATTGGTGAATCGATTGCGCGTCTGTTTTACCGTCATGGTGC
GAAAGTGTGCATCGTTGACATTCAGGATAATCCGGGTCAAAACCTGTGCCGTGAACTGGGCACC
GACGATGCGTGCTTCTTTCACTGCGATGTGAGCATTGAAATCGATGTGATTCGTGCTGTTGACT
TTGTGGTTAACCGCTTTGGTAAACTGGACATTATGGTTAATAACGCGGGCATCGCAGATCCGCC
GTGCCCGGATATTCGCAACACCGATCTGAGCATTTTTGAAAAAGTGTTCGATGTGAACGTGAAA
GGCACCTTTCAGTGTATGAAACACGCAGCGCGCGTTATGGTGCCGCAGAAAAAAGGTAGCATTA
TCAGCCTGACCTCGGTGGCGAGCGTGATTGGTGGCGCGGGTCCGCACGCCTATACGGGTAGCAA
ACACGCGGTTCTGGGTCTGACGAAAAGCGTTGCGGCAGAACTGGGTCTGCATGGTATTCGCGTG
AACTGTGTGAGTCCGTATGCAGTTCCGACGGGTATGCCGCTGGCACATCTGCCGGAATCGGAAA
AAACCGAAGATGCGATGATGGGTATGCGTGCATTTGTGGGTCGTAATGCCAACCTGCAAGGTAT
TGAACTGACCGTGGACGATGTCGCAAATAGCGTCGTGTTTCTGGCGTCGGATGAAGCGCGTTAT

GTTAGCGGTCTGAACCTGATGCTGGACGGCGGCTTCTCGTGTGTCAACCACTCGCTGCGTGTGT
TTCGCTAA (SEQ ID NO: 97)

>CsABA2 [Citrus sinensus]

MSNSNSTDSSPAVQRLVGRVALITGGATGIGESTVRLFHKHGAKVCIADVQDNLGQQVCQSLGG
EPDTFFCHCDVTKEEDVCSAVDLTVEKFGTLDIMVNNAGISGAPCPDIREADLSEFEKVFDINV
KGVFHGMKHAARIMIPQTKGTIISICSVAGAIGGLGPHAYTGSKHAVLGLNKNVAAELGKYGIR
VNCVSPYAVATGLALAHLPEEERTEDAMVGFRNFVARNANMQGTELTANDVANAVLFLASDEAR
YISGTNLMVDGGFTSVNHSLRVFR (SEQ ID NO: 98)

ATGTCCAATAGCAACTCTACGGATTCGTCGCCGGCAGTCCAACGCCTGGTCGGTCGTGTCGCCC
TGATTACGGGTGGTGCAACGGGTATTGGCGAAAGCACGGTGCGCCTGTTTCATAAACATGGCGC
GAAAGTGTGTATTGCCGACGTTCAGGATAACCTGGGTCAGCAAGTGTGTCAGAGTCTGGGTGGC
GAACCGGATACCTTTTTCTGCCATTGTGATGTGACGAAAGAAGAAGATGTGTGTAGCGCAGTTG
ATCTGACCGTGGAAAAATTTGGCACCCTGGACATTATGGTGAACAATGCGGGTATTAGCGGCGC
ACCGTGCCCGGACATTCGTGAAGCCGATCTGAGCGAATTTGAAAAAGTTTTCGACATCAACGTG
AAAGGCGTGTTTCACGGCATGAAACATGCAGCGCGTATTATGATCCCGCAAACCAAAGGCACCA
TTATCAGCATTTGCTCCGTGGCTGGTGCGATTGGTGGCCTGGGTCCGCACGCATATACCGGCTC
CAAACATGCAGTCCTGGGCCTGAACAAAAACGTGGCCGCGGAACTGGGCAAATACGGTATCCGT
GTGAATTGCGTCAGCCCGTATGCTGTTGCCACCGGCCTGGCTCTGGCACACCTGCCGGAAGAAG
AACGTACCGAAGATGCAATGGTGGGCTTTCGTAATTTTGTGGCACGCAACGCGAATATGCAAGG
CACCGAACTGACGGCGAATGATGTGGCAAACGCGGTCCTGTTTCTGGCCTCTGATGAAGCCCGT
TATATCAGCGGCACGAATCTGATGGTGGATGGCGGTTTTACCTCGGTCAATCACTCGCTGCGTG
TCTTCCGTTAA (SEQ ID NO: 99)

>BdDH [Brachypodium distachyon]

MSAAAAVSSSSSPRLEGKVALVTGGASGIGEAIVRLFRQHGAKVCIADVQDEAGQQVRDSLGDD
AGTDVLFVHCDVTVEEDVSRAVDAAAEKFGTLDIMVNNAGITGDKVTDIRNLDFAEVRKVFDIN
VHGMLLGMKHAARVMIPGKKGSIVSLASVASVMGGMGPHAYTASKHAVVGLTKSVALELGKHGI
RVNCVSPYAVPTALSMPHLPQGEHKGDAVRDFLAFVGGEANLKGVDLLPKDVAQAVLYLASDEA
RYISALNLVVDGGFTSVNPNLKAFED (SEQ ID NO: 100)

ATGTCCGCTGCTGCCGCCGTGTCCTCCTCATCGTCGCCGCGTCTGGAAGGCAAAGTCGCTCTGG
TTACGGGTGGTGCGTCAGGTATCGGCGAAGCCATTGTGCGCCTGTTCCGTCAACATGGTGCCAA
AGTGTGTATCGCGGATGTCCAAGACGAAGCGGGCCAACAGGTCCGTGATAGCCTGGGTGACGAT
GCCGGTACGGATGTGCTGTTTGTGCATTGCGACGTTACCGTGGAAGAAGATGTGTCACGCGCGG
TGGATGCCGCTGCGGAAAAATTCGGCACCCTGGACATTATGGTGAACAACGCAGGTATTACGGG
CGACAAAGTGACGGACATTCGCAACCTGGATTTCGCTGAAGTCCGTAAAGTGTTCGACATCAAT
GTGCACGGTATGCTGCTGGGCATGAAACATGCGGCCCGCGTGATGATTCCGGGTAAAAAAGGCT
CGATTGTGAGCCTGGCATCGGTCGCAAGCGTTATGGGTGGTATGGGTCCGCACGCATATACCGC
AAGCAAACACGCGGTTGTGGGTCTGACGAAAAGCGTTGCACTGGAACTGGGCAAACATGGTATT
CGTGTCAACTGTGTGAGCCCGTATGCAGTTCCGACCGCACTGTCAATGCCGCACCTGCCGCAGG
GCGAACATAAAGGTGATGCGGTGCGTGATTTCCTGGCGTTTGTTGGCGGTGAAGCGAATCTGAA
AGGTGTCGATCTGCTGCCGAAAGATGTTGCACAGGCGGTTCTGTATCTGGCAAGCGACGAAGCG
CGCTATATTTCTGCGCTGAATCTGGTGGTTGATGGCGGTTTTACGAGCGTGAATCCGAATCTGA
AAGCATTTGAAGACTAA (SEQ ID NO: 101)

>ZzSDR [Zingiber zerumbet]

MRLEGKVALVTGGASGIGESIARLFIEHGAKICIVDVQDELGQQVSQRLGGDPHACYFHCDVTV
EDDVRRAVDFTAEKYGTIDIMVNNAGITGDKVIDIRDADFNEFKKVFDINVNGVFLGMKHAARI

MIPKMKGSIVSLASVSSVIAGAGPHGYTGAKHAVVGLTKSVAAELGRHGIRVNCVSPYAVPTRL
SMPYLPESEMQEDALRGFLTFVRSNANLKGVDLMPNDVAEAVLYLATEESKYVSGLNLVIDGGF
SIANHTLQVFE (SEQ ID NO: 102)

ATGCGTCTGGAAGGCAAAGTGGCTCTGGTCACGGGCGGTGCGTCGGGTATTGGCGAATCTATTG
CTCGTCTGTTTATTGAACACGGTGCAAAAATTTGCATCGTGGATGTCCAGGATGAACTGGGTCA
ACAGGTCTCTCAGCGTCTGGGTGGCGATCCGCACGCCTGTTATTTCCACTGTGATGTGACCGTG
GAAGATGACGTTCGTCGCGCGGTGGATTTTACGGCGGAAAAATATGGCACCATTGACATTATGG
TTAACAATGCGGGCATTACGGGCGATAAAGTGATCGATATTCGTGATGCGGATTTCAACGAATT
TAAAAAAGTGTTCGACATTAACGTGAATGGTGTCTTTCTGGGCATGAAACACGCAGCGCGTATT
ATGATCCCGAAAATGAAAGGCTCCATCGTTTCGCTGGCGTCCGTTAGCTCGGTGATTGCTGGTG
CAGGTCCGCATGGCTATACCGGCGCAAAACATGCGGTTGTGGGTCTGACCAAAAGCGTTGCAGC
CGAACTGGGTCGTCATGGTATTCGCGTGAACTGCGTTTCGCCGTATGCGGTGCCGACGCGCCTG
TCAATGCCGTATCTGCCGGAATCGGAAATGCAGGAAGATGCACTGCGCGGCTTTCTGACCTTTG
TGCGTAGCAATGCGAACCTGAAAGGCGTTGATCTGATGCCGAATGATGTGGCGGAAGCTGTTCT
GTATCTGGCGACCGAAGAAAGCAAATATGTTTCAGGTCTGAATCTGGTTATTGACGGCGGCTTC
TCCATCGCTAATCATACCCTGCAAGTGTTTGAATAA (SEQ ID NO: 103)

Figure 22B

```
CsDH3          MTTAGSRDSPLVAQRLLGKVALVTGGATGIGESIVRLFHKHGAKVCVVDIN--------- 51
VvDH           MAATSIDNSPLPSQRLLGKVALVTGGATGIGESIVRLFLKQGAKVCIVDVQ--------- 51
VvDH1          MSTASSGDVSLLSQRLVGKVALITGGATGIGESIARLFYRHGAKVCIVDIQ--------- 51
CsABA2         MSNSNSTDSSPAVQRLVGRVALITGGATGIGESTVRLFHKHGAKVCIADVQ--------- 51
CsDH           MATPPIS--SLISQRLLGKVALVTGGASGIGEGIVRLFHRHGAKVCFVDVQ--------- 49
BdDH           -MSAAAAVSSSSSPRLEGKVALVTGGASGIGEAIVRLFRQHGAKVCIADVQ--------- 50
ZzSDR          -------------MRLEGKVALVTGGASGIGESIARLFIEHGAKICIVDVQ--------- 38
CsDH1          ----------MSKPRLQGKVAIIMGAASGIGEATAKLFAEHGAFVIIADIQ--------- 41
CsDH2          ----------MSNPRMEGKVALITGAASGIGEAAVRLFAEHGAFVVAADVQ--------- 41
ReCDH          ------------MARVEGQVALITGAARGQGRSHAIKLAEEGADVILVDVPNDVVDIGYP 48
                              *: *:**:: *.* * *.. .  : ..** :  .*:

CsDH3          ----DDLGQHLCQTLG----PTTRFIHGDVAIEDDVSRAVDFTVANFGTLDIMVNNAGMG 103
VvDH           ----DDLGQKLCDTLGG--DPNVSFFHCDVTIEDDVCHAVDFTVTKFGTLDIMVNNAGMA 105
VvDH1          ----DNPGQNLCRELG---TDDACFFHCDVSIEIDVIRAVDFVVNRFGKLDIMVNNAGIA 104
CsABA2         ----DNLGQQVCQSLGG--EPDTFFCHCDVTKEEDVCSAVDLTVEKFGTLDIMVNNAGIS 105
CsDH           ----DELGYRLQESLVGDKDSNIFYSHCDVTVEDDVRRAVDLTVTKFGTLDIMVNNAGIS 105
BdDH           ----DEAGQQVRDSLGDDAGTDVLFVHCDVTVEEDVSRAVDAAAEKFGTLDIMVNNAGIT 106
ZzSDR          ----DELGQQVSQRLGGDP--HACYFHCDVTVEDDVRRAVDFTAEKYGTIDIMVNNAGIT 92
CsDH1          ----DELGNQVVSSIGP---EKASYRHCDVRDEKQVEETVAYAIEKYGSLDIMYSNAGVA 94
CsDH2          ----DELGHQVAASVGT---DQVCYHHCDVRDEKQVEETVRYTLEKYGKLDVLFSNAGIM 94
ReCDH          LGTADELDQTAKDVENLG--RKAIVIHADVRDLESLTAEVDRAVSTLGRLDIVSANAGIA 106
                   *: .                  * **    .:   *  .    * :*::  ***:

CsDH3          GPPCPDIREFPISTFEKVFDINTKGTFIGMKHAARVMIPS-KKGSIVSISSVTSAIGGAG 162
VvDH           GPPCSDIRNVEVSMFEKVFDVNVKGVFLGMKHAARIMIPL-KKGTIISLCSVSSAIAGVG 164
VvDH1          DPPCPDIRNTDLSIFEKVFDVNVKGTFQCMKHAARVMVPQ-KKGSIISLTSVASVIGGAG 163
CsABA2         GAPCPDIREADLSEFEKVFDINVKGVFHGMKHAARIMIPQ-TKGTIISICSVAGAIGGLG 164
CsDH           GTPSSDIRNVDVSEFEKVFDINVKGVFMGMKYAASVMIPR-KQGSIISLGSVGSVIGGIG 164
BdDH           GDKVTDIRNLDFAEVRKVFDINVHGMLLGMKHAARVMIPG-KKGSIVSLASVASVMGGMG 165
ZzSDR          GDKVIDIRDADFNEFKKVFDINVNGVFLGMKHAARIMIPK-MKGSIVSLASVSSVIAGAG 151
CsDH1          G-PVGTILDLDMAQFDRTIATNLAGSVMAVKYAARVMVANKIRGSIICTTSTASTVGGSG 153
CsDH2          G-PLTGILELDLTGFGNTMATNVCGVAATIKHAARAMVDKNIRGSIICTTSVASSLGGTA 153
ReCDH          SVPFLSH-DIPDNTWRQMIDINLTGVWHTAKVAVPHILAGERGGSIVLTSSAAGLKGYAQ 165
               .       :       . :  *  *     * *.  ::     *:*:   *. .  .

CsDH3          PHAYTASKHAVLGLTKSVAAELGQHGIRVNCVSPYAILTNLA----LAHLHEDERTDDAR 218
VvDH           PHAYTGSKCAVAGLTQSVAAEMGGHGIRVNCISPYAIATGLA----LAHLPEDERTEDAM 220
VvDH1          PHAYTGSKHAVLGLTKSVAAELGLHGIRVNCVSPYAVPTGMP----LAHLPESEKTEDAM 219
CsABA2         PHAYTGSKHAVLGLNKNVAAELGKYGIRVNCVSPYAVATGLA----LAHLPEEERTEDAM 220
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CsDH      PHHYISSKHAVVGLTRSIAAELGQHGIRVNCVSPYAVPTNLA----VAHLPEDERTEDMF 220
BdDH      PHAYTASKHAVVGLTKSVALELGKHGIRVNCVSPYAVPTALS----MPHLPQGEHKGDAV 221
ZzSDR     PHGYTGAKHAVVGLTKSVAAELGRHGIRVNCVSPYAVPTRLS----MPYLPESEMQEDAL 207
CsDH1     PHAYTISKHGLLGLVRSAASELGKHGIRVNCVSPFGVATPFS----AGTIN--------- 200
CsDH2     PHAYTTSKHALVGLVRTACSELGAYGIRVNCISPFGVATPLS----CTAYNLRP------ 203
ReCDH     ISHYSAAKHGVVGLMRSLALELAPHRVRVNSLHPTQVNTPMIQNEGTYRIFSPDLENPTR 225
                 *  :* .: ** :. . *:. : :***.:: *  : * :

                                                                        
CsDH3     AGFRAFIGKNANLQGVDLVEDDVANAVLFLASDDARYISGDNLFVDGGFTCTNHSLRVFR--- 278
VvDH      AGFRAFVGKNANLQGVELTVDDVAHAAVFLASDEARYISGLNLMLDGGFSCTNHSLRVFR--- 280
VvDH1     MGMRAFVGRNANLQGIELTVDDVANSVVFLASDEARYVSGLNLMLDGGFSCVNHSLRVFR--- 279
CsABA2    VGFRNFVARNANMQGTELTANDVANAVLFLASDEARYISGTNLMVDGGFTSVNHSLRVFR--- 280
CsDH      TGFREFAKKNANLQGVELTVEDVANAVLFLASEDARYISGDNLIVDGGFTRVNHSFRVFR--- 280
BdDH      RDFLAFVGGEANLKGVDLLPKDVAQAVLYLASDEARYISALNLVVDGGFTSVNPNLKAFED-- 282
ZzSDR     RGFLTFVRSNANLKGVDLMPNDVAEAVLYLATEESKYVSGLNLVIDGGFSIANHTLQVFE--- 267
CsDH1     -DVEGFVCKVANLKGIVLKAKHVAEAALFLASDESAYVSGHDLVVDGGFTAVTNVMSMLEGHG 262
CsDH2     DEVEANSCALANLKGIVLKAKHIAEAALFLASDESAYISGHNLAVDGGFTVVNHSSSSAT--- 263
ReCDH     EDFEIASTTTNALPIPWVESVDVSNALLFLVSEDARYITGAAIPVDAGTTLK------------ 277
                .                :    :  .:::: ::*.:::: *::.  : :*.* :
```

Figure 23A

```
8rp-t20SrKO         -----MALLLAVFAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEK
8rp-t20VO0          -----MALLLAVFAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEK
n22yhcB-t30VO1      MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNRLPRVPEVPGVPLLGNLLQLKEK
n22yhcB-t30VO2      MAWEYALIGLVVGIIIGAVAMRWYLKSYTSARRSQSNHLPRVPEVPGVPLLGNLLQLKEK
                         **:  *..: :... : ***************:**********************

8rp-t20SrKO         KPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTA
8rp-t20VO0          KPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTA
n22yhcB-t30VO1      KPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTA
n22yhcB-t30VO2      KPYMTFTKWAATYGPIYSIKTGATSVVVVSSNEIAKEALVTRFQSISTRNLSKALKVLTA
                    *******:*****************:**********************************

8rp-t20SrKO         DKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQE
8rp-t20VO0          DKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQE
n22yhcB-t30VO1      DKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQE
n22yhcB-t30VO2      DKQMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEFVKNNPEQE
                    ** ************************************************************

8rp-t20SrKO         EVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEIFQVLVVDPMMGAIDVDWR
8rp-t20VO0          EVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEIFQVLVVDPMMGAIDVDWR
n22yhcB-t30VO1      EVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWR
n22yhcB-t30VO2      EVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEILQVLVVDPMMGAIDVDWR
                    ****************************************:*********************

8rp-t20SrKO         DFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTL
8rp-t20VO0          DFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEHKKRIASGEKLNSYIDYLLSEAQTL
n22yhcB-t30VO1      DFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEQKKRIASGEKLNSYIDYLLSEAQTL
n22yhcB-t30VO2      DFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEQKKRIASGEKLNSYIDYLLSEAQTL
                    ************************************:************************

8rp-t20SrKO         TDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSEKITEEHLS
8rp-t20VO0          TDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSEKITEEHLS
n22yhcB-t30VO1      TDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSEKITEEHLS
n22yhcB-t30VO2      TDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSEKITEEHLS
                    ************************************************************

8rp-t20SrKO         QLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLGGYHVPAGTELAVNIYGCNMDKNVWEN
8rp-t20VO0          QLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLGGYHVPAGTELAVNIYGCNMDKNVWEN
n22yhcB-t30VO1      QLPYITAIFHETLRKHSPVPIIPLRHVHEDTQLGGYHVPAGTELAVNIYGCNMDKNVWEN
n22yhcB-t30VO2      QLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGYHVPAGTELAVNIYGCNMDKNVWEN
                    ***************:******:********* ****************************

8rp-t20SrKO         PEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEFEWKLKDMT
8rp-t20VO0          PEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEFEWKLKDMT
n22yhcB-t30VO1      PEEWNPERFMKENETADFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEFEWKLKDMD
n22yhcB-t30VO2      PEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIASIGIGRMVQEFEWKLKDMT
                    *************** ************************ ********************

8rp-t20SrKO         QEEVNTIGLTTQMLRPLRAIIKPRI
8rp-t20VO0          QEEVNTIGLTNQMLRPLRAIIKPRI
n22yhcB-t30VO1      QEEVNTIGLTNQMLRPLRAIIKPRI
n22yhcB-t30VO2      QEEVNTIGLTNQMLRPLRAIIKPRI
                    **********:***************
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Figure 23B

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VO2         MDAVTGLLTVPATAITIGGTAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLG
VO1         MDAVTGLLTVPATAITIGGTAVALAVALIFWYLKSYTSARRSQSNRLPRVPEVPGVPLLG
SrKO        MDAVTGLLTVPATAITIGGTAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLG
VO0         MDAVTGLLTVPATAITIGGTAVALAVALIFWYLKSYTSARRSQSNHLPRVPEVPGVPLLG
            ************************************************:**************

VO2         NLLQLKEKKPYMTFTKWAATYGPIYSIKTGATSVVVVSSNEIAKEALVTRFQSISTRNLS
VO1         NLLQLKEKKPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLS
SrKO        NLLQLKEKKPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLS
VO0         NLLQLKEKKPYMTFTRWAATYGPIYSIKTGATSMVVVSSNEIAKEALVTRFQSISTRNLS
            ***************:*****************:**************************

VO2         KALKVLTADKQMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEF
VO1         KALKVLTADKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEF
SrKO        KALKVLTADKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEF
VO0         KALKVLTADKTMVAMSDYDDYHKTVKRHILTAVLGPNAQKKHRIHRDIMMDNISTQLHEF
            ********** ************************************************

VO2         VKNNPEQEEVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEILQVLVVDPMM
VO1         VKNNPEQEEVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEILQVLVVDPMM
SrKO        VKNNPEQEEVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEIFQVLVVDPMM
VO0         VKNNPEQEEVDLRKIFQSELFGLAMRQALGKDVESLYVEDLKITMNRDEIFQVLVVDPMM
            ************************************************:*********

VO2         GAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEQKKRIASGEKLNSYIDY
VO1         GAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEQKKRIASGEKLNSYIDY
SrKO        GAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEHKKRIASGEKLNSYIDY
VO0         GAIDVDWRDFFPYLKWVPNKKFENTIQQMYIRREAVMKSLIKEHKKRIASGEKLNSYIDY
            ********************************************:****************

VO2         LLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSE
VO1         LLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSE
SrKO        LLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSE
VO0         LLSEAQTLTDQQLLMSLWEPIIESSDTTMVTTEWAMYELAKNPKLQDRLYRDIKSVCGSE
            ************************************************************

VO2         KITEEHLSQLPYITAIFHETLRKHSPVPILPLRHVHEDTVLGGYHVPAGTELAVNIYGCN
VO1         KITEEHLSQLPYITAIFHETLRKHSPVPIIPLRHVHEDTQLGGYHVPAGTELAVNIYGCN
SrKO        KITEEHLSQLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLGGYHVPAGTELAVNIYGCN
VO0         KITEEHLSQLPYITAIFHETLRRHSPVPIIPLRHVHEDTVLGGYHVPAGTELAVNIYGCN
            ************************:*******:********** ********************

VO2         MDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLIASIGIGRMVQEF
VO1         MDKNVWENPEEWNPERFMKENETADFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEF
SrKO        MDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEF
VO0         MDKNVWENPEEWNPERFMKENETIDFQKTMAFGGGKRVCAGSLQALLTASIGIGRMVQEF
            ************************ ************************ ************

VO2         EWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI
VO1         EWKLKDMDQEEVNTIGLTNQMLRPLRAIIKPRI
SrKO        EWKLKDMTQEEVNTIGLTTQMLRPLRAIIKPRI
VO0         EWKLKDMTQEEVNTIGLTNQMLRPLRAIIKPRI
            ******* **********.***************
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