

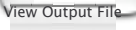
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ClustalW Results

Results of search	
Number of sequences	5
Alignment score	30009
Sequence format	Pearson
Sequence type	aa
ClustalW version	1.82
JalView	
Output file	clustalw-20050127-10461244.output
Alignment file	clustalw-20050127-10461244.aln
Guide tree file	clustalw-20050127-10461244.dnd
Your input file	clustalw-20050127-10461244.input
	

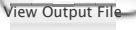
To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the JalView button, reload the page and check your browser settings to enable Java Applets.

Scores Table

Sort by Sequence Number 

SeqA	Name	Len(aa)	SeqB	Name	Len(aa)	Score
1	dlg_CG1725-PH	970	2	Sap97_dlg1	905	51
1	dlg_CG1725-PH	970	3	chapsyn-110_dlg2	839	50
1	dlg_CG1725-PH	970	4	Sap102_dlg3	849	48
1	dlg_CG1725-PH	970	5	PSD-95_dlg4	721	54
2	Sap97_dlg1	905	3	chapsyn-110_dlg2	839	70
2	Sap97_dlg1	905	4	Sap102_dlg3	849	64
2	Sap97_dlg1	905	5	PSD-95_dlg4	721	74
3	chapsyn-110_dlg2	839	4	Sap102_dlg3	849	64
3	chapsyn-110_dlg2	839	5	PSD-95_dlg4	721	70
4	Sap102_dlg3	849	5	PSD-95_dlg4	721	66

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

Sort by Sequence Number 

Alignment

CLUSTAL W (1.82) multiple sequence alignment

```
dlg_CG1725-PH      MPVKKQEAHRALELLEDYHARLSEPDRLRALRIAIERVIRIFKSRLFQALLDIQEFYELTL 60
Sap97_dlg1         MPVRKQDTQRALHLEERYSKLSQTEDRQLRSSIERVINIFQSNLQALIDIQEFYEVTL 60
chapsyn-110_dlg2   -----
Sap102_dlg3        -----MHKHQHCKCKPECYEVTR 18
PSD-95_dlg4        -----

dlg_CG1725-PH      LDDSKSIQKTAETLQIATKWEKDQGAVKIADFIKSSNLNRNCAYEFNNDASSNQTNQSA 120
Sap97_dlg1         LDNPCKVDHSHKQCEPVQPVTT----WEIASLPSTAVTSETLPGSLSPVPEKYRYQD-EEV 115
chapsyn-110_dlg2   -----QKYRYQD-EDG 10
Sap102_dlg3        LAALRRLEP-----PGYGD----WQVPDPYGPSSGNGASSGGYSSQTLPSQAGATP 67
PSD-95_dlg4        -----MDCLCIVTTKKYRYQD-EDT 19
                                     *

dlg_CG1725-PH      LNQNPIANNVSAQAQAEALSRTFKSELEEILNORMRIESDTENAKEPTVE----- 170
Sap97_dlg1         LPPEHISPQVTNEVLGPELVHVEKNLSEIENVHGFVSHSHSPIKPTAEVPPSSPIVPV 175
chapsyn-110_dlg2   -PHDHSPLRLTHEVRGPELVHVEKNLSQIENVHGYVLQSHISP----- 53
Sap102_dlg3        TPRTKAKLIPTGRDVGVPVPKVPVGKSTPKLNGSGPGWWEPECTCTN----- 113
PSD-95_dlg4        PPLEHSPAHLPN----- 31

dlg_CG1725-PH      -----QQQKQQQAQQRSSRSPPQQNPQQQGSKSRSGSQTVNGDDSWLYEDIQLERG 222
Sap97_dlg1         TPALVPVPESTVVLPSAPQANPPPVLVNTDSLETPTYVNGT-----DADYEFEEITLERG 230
chapsyn-110_dlg2   -----LKASPAPIIVNTDTLDTIPYVNGT-----EIEYEFEEITLERG 91
```

```

Sap102_d1gh3      -----RDWYEQASAPAPLLVNPEALEPFLSVNGS-----DGMFKYEEIVLERG 155
PSD-95_d1gh4      -----QANSPPVIVNTDTLEAPGVNGT-----EGEMEYEEITLERG 68
                  ::. . *  *.: : .*: : :*: * *

dlg_CG1725-PH      NSGLGFSIAGGTNDPHIGTDTSIYITKLISGGAADGRLSINDIIVSVNDVSVVDVPH 282
Sap97_d1gh1        NSGLGFSIAGGTNDPHIGDDSSIFITKIIITGGAAQDGRLRVNDCLRVNEADVVDVTHS 290
chapsyn-110_d1gh2  NSGLGFSIAGGTNDPHIGDDPGIFITKIIIPGAAADGRLRVNDCLRVNEVDVSEVSHS 151
Sap102_d1gh3       NSGLGFSIAGGTNDPHIVPDDPGIFITKIIIPGAAAMDGR LGVNDCLRVNEVDVSEVSHS 215
PSD-95_d1gh4       NSGLGFSIAGGTNDPHIGDDPSIFITKIIIPGAAQDGRLRVNDCLFVNEVDVREVTHS 128
                  ***** :*: *.:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

dlg_CG1725-PH      SAVDALKKAGNVVVLHVKKRKGTTATPAAGSAAGDARDSAASGPKVIEIDLKGGKGLGF 342
Sap97_d1gh1        KAVEALKEAGSIVRLYVKKRK-----PAS-----EKIMEIKLIKGPKGGLGF 331
chapsyn-110_d1gh2  KAVEALKEAGSIVRLYVRRRR-----PIL-----ETVVEIKLFGKPGKGLGF 192
Sap102_d1gh3       RAVEALKEAGPVVRLVRRRQ-----PPP-----ETIMEVNLLKGPKGGLGF 256
PSD-95_d1gh4       AAVEALKEAGSIVRLYVRRK-----PPA-----EKIIEIKLIKGPKGGLGF 169
                  *:***** :*: * * : * : * : * : * : * : * : * : *

dlg_CG1725-PH      SIAGGIGNQHIPGDNIGYVTKLMDGGAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELA 402
Sap97_d1gh1        SIAGGVGNQHIPGDNISIVTKIIEGGAHKDQKLQIGDKLLAVNS---VCLEEVTHEEA 387
chapsyn-110_d1gh2  SIAGGVGNQHIPGDNISIVTKIIEGGAQKDGRLQVGDRLMVNN---YSEEVTHEEA 248
Sap102_d1gh3       SIAGGIGNQHIPGDNISYITKIEGGAQKDGRLQIGDRLAVNN---TNLQDVRRHEEA 312
PSD-95_d1gh4       SIAGGVGNQHIPGDNISYVTKIIEGGAHKDQKLQIGDKLLAVNS---VGLEDVMHEDA 225
                  *****:*****.*:***::*:*: **:.*:***::*.. :*: * * *

dlg_CG1725-PH      VATLKSITDKVTLIIGKTQHLTTSASGGGGGLSSGQQLSQSQSLATSQSQSQVHQQQH 462
Sap97_d1gh1        VTALKNTSDFVYLKVAKPTSMYINDGYAPPDITNS---SSQSVNDHVPSSCLG----- 438
chapsyn-110_d1gh2  VAILKNTSDVVYLKVGKPTTIYMTDPYGPDDITHS---YSPMENHLLSGNNGTLE--- 301
Sap102_d1gh3       VASLKNTSDMVYLKVAKPGSIHLNDMYAPPDYAST---FTALADNHISHNSSLGLVGAVE 369
PSD-95_d1gh4       VAALKNTYDVVYLKVAKPSNAYLSDSYAPPDITTS---YSQHLDNEISHSSYLGTD--- 278
                  *: ** . * * * :*. . . . : : . :

dlg_CG1725-PH      ATPMVNSQSTEPSGSRYASTNVLAAPVPGTPRAVSTEDITR----- 502
Sap97_d1gh1        -----QTPTSPARYS-----PISKAVLGDEITR----- 462
chapsyn-110_d1gh2  ---YKTSLPPISPGRYS-----PIPKHMLGEDDYTRPPEPVYSTVNKICDPPASPR 349
Sap102_d1gh3       SKVTYPAPPQVPPTRYSS-----PIPRHMLAEEDFTTR----- 400
PSD-95_d1gh4       ---YPTAMTPTSPRRYS-----PVAKDLLGEEDIPR----- 306
                  . * * : * : * : * : * : * : * : * : *

dlg_CG1725-PH      -----EPRTI 507
Sap97_d1gh1        -----EPRKV 467
chapsyn-110_d1gh2  HYSPEVCDKSFLLSTPHYHLGLLPDSMTSHSQHSTATRQPSVTLQRAISLEGEPRKV 409
Sap102_d1gh3       -----EPRKI 405
PSD-95_d1gh4       -----EPRII 311
                  ***:

dlg_CG1725-PH      TIQKGFPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATHEE 567
Sap97_d1gh1        VLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLGSSELKRGDRIISVNSVDLRAASHEQ 527
chapsyn-110_d1gh2  VLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLGSSELKRGDQILSVNGIDLRGASHEQ 469
Sap102_d1gh3       ILHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLGSSELKRRGDRIISVNGVNLRNATHEQ 465
PSD-95_d1gh4       VIHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLGSSELKRGDQILSVNGVDLRNASHQ 371
                  ::*: . *****:***:*****.*:***::*:*: **:***:

dlg_CG1725-PH      AAQALKTSGGVVTLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LRRTTQKRSLYVR 626
Sap97_d1gh1        AAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSVSSGSGSLRTSQKRSLYVR 587
chapsyn-110_d1gh2  AAAALKGAGQVTTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKRSLYVR 529
Sap102_d1gh3       AAAALKRAGQSVTIVAQYRPEEYSRFEAKIHDLREQMMNSSMSSGSGSLRTSEKRSLYVR 525
PSD-95_d1gh4       AAIALKNAGQVTTIIAQYKPEEYSRFEAKIHDLREQLMNSSLGSGTASLRSNPKRGFYIR 431
                  * * * * : * :*:***:***:***:***:***:***:***:***:***:***:***:

dlg_CG1725-PH      ALFDYDPNRRDGLPSRGLPFFKHGDILHVTNASDDEWQARRVLGDNEDEQIGIVPSKRRW 686
Sap97_d1gh1        ALFDYDKTKDSGLPSQGLNFRFGDILHVINASDDEWQARRVTPDGEDEVGVIPSKRRV 647
chapsyn-110_d1gh2  AMFDYDKSKDSGLPSQGLSFKYGDILHVINASDDEWQARRVTLGDSEEMGVIPSKRRV 589
Sap102_d1gh3       ALFDYDRTDRDSCPLSQGLSFSYGDILHVINASDDEWQARRLVTFHGESEQIGIVPSKRRV 585
PSD-95_d1gh4       ALFDYDKTKDCGFLSQALSFFHFGDVLHVIDASDDEWQARRVHSDSETDDIGFIPSKRRV 491
                  * * * * . : * : * * * * : * * : * * * * * * . . : : * . : * * *

dlg_CG1725-PH      ERKMRARDRSVKFQGHAAANNLKDQSTLDRKKKNFTFSRKFPFMKSRDEKNEGSDQEP 746
Sap97_d1gh1        EKKERARLKTVKFNKTRGDK-----GEIPDDMGSKGLK 681
chapsyn-110_d1gh2  ERKKEARLKTVKFNKPG-----VIDSKGDI 615
Sap102_d1gh3       EKKEARLKTVKFHARTGMIESNRDF-----PGLSDDYYGAKNLK 625
PSD-95_d1gh4       ERREWSRLKAKDWGSSS-----GSQ--- 511
                  *: : * : : . . : .

dlg_CG1725-PH      FMLCYTQDDANAEGASEENVLSYEAQRLSINYTRPVIIILGPLKDRINDDLISEYDPKFG 806
Sap97_d1gh1        HVTSNASDSESSYRGQEEYVLSYEPVNNQEVNRYTRPVIIILGPMKDRVNDLISEFPDKFG 741
chapsyn-110_d1gh2  PGLGDGYGKTTLRGQEDLILSYEPVTRQEIYTRPVIIILGPMKDRINDDLISEFPDKFG 675
Sap102_d1gh3       GVTSTNTSDSESSKQEDAILSYEPVTRQEIYHARPVIIILGPMKDRVNDLISEFPDKFG 685
PSD-95_d1gh4       -----GREDVLSYETVTQMEVHYARPIIILGPTKDRANDDLISEFPDKFG 557
                  . * : : * * . : : * : * : * * * * * * * * : * : * *

dlg_CG1725-PH      SCVPHTTRPKREYEVGDRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 866
Sap97_d1gh1        SCVPHTTRPKRDYEVGDRDYHFVTSREQMEKDIQEHKFIAGQYNNHLYGTSVQSVRAVA 801
chapsyn-110_d1gh2  SCVPHTTRPKRDYEVGDRDYHFVISREQMEKDIQEHKFIAGQYNDNLYGTSVQSVRVA 735
Sap102_d1gh3       SCVPHTTRPRRDNEVDGQDYHFVVSREQMEKDIQDNKFIAGQFNDNLYGTSIQSVRAVA 745
PSD-95_d1gh4       SCVPHTTRPKREYIDGRDYHFVSSREKMEKDIQAHKFIAGQYNSHLYGTSVQSVREVA 617
                  *****: * : * : * * * * * * : * * * * : * : * * * * *

dlg_CG1725-PH      EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTTEEAKKTYERAIKM 926
Sap97_d1gh1        EKGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKL 861
chapsyn-110_d1gh2  ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPKSLEPLMEMNKRLTEEQAKKTYDRAIKL 795
Sap102_d1gh3       ERGKHCILDVSGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNRRQTYEQANKIFDKAMKL 805
PSD-95_d1gh4       EQGKHCILDVSANAVRRLQAHLHPAIFIRPSLENVLEINKRITEEQARKAFDRATKL 677
                  * * * * * * * : * : * * * : * : * : * : * : * : * : * : * : * : * : * : * :

dlg_CG1725-PH      EQEFGEYFTGVVQGDTEIEEYKVKSMIWSQSGPTIWWPSKESE 970
Sap97_d1gh1        EQEFTEHFTAIVQGDTELDIYNQVKQIEEQSGPYIWWPAKEKL 905
chapsyn-110_d1gh2  EQEFGEYFTAIVQGDTELDIYNQCKLVIEEQSGPFIWIPSKEKL 839
Sap102_d1gh3       EQEFGEYFTAIVQGDSEIEIYNKIKQIEDQSGHYIWWPSPEKL 849
PSD-95_d1gh4       EQEFTCFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWWPARERL 721
                  * * * * * * : : * : * : * : * : * : * : * : * : * : * : * : *

```

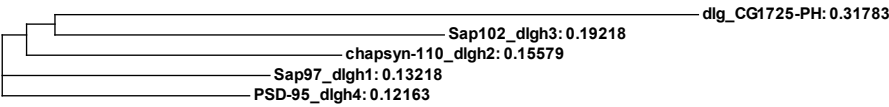
PLEASE NOTE: Showing colors on large alignments is slow.

Guide Tree

Show as Cladogram Tree Hide Distances View DND File

```
(
(
(
dlg_CG1725-PH:0.31783,
Sap102_dlg3:0.19218)
:0.01411,
chapsyn-110_dlg2:0.15579)
:0.01161,
Sap97_dlg1:0.13218,
PSD-95_dlg4:0.12163);
```

Phylogram



Show as Cladogram Tree Hide Distances View DND File

Right-click on the above tree to see display options.
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