

Datos suplementarios (1)

Estudio y caracterización de la dinámica celular
y morfogénesis de una estructura epitelial
primitiva en *Dictyostelium discoideum*

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Los alineamientos que se describen a continuación fueron obtenidos mediante los programas EMBOSS water (locales) y EMBOSS needle (globales). Relacionado con las secciones 3.2.2 y 3.3.3.

Parte 1: Alineamientos locales y globales de las proteínas de adhesión celular en Metazoos y sus homólogos en *D. discoideum* (Pág 3-28)

Parte 2: Alineamientos locales y globales de las proteínas de polaridad celular en Metazoos y sus homólogos en *D. discoideum* (Pág 29-42)

Moléculas de Adhesión Celular

- 1) Dd α -Actinina 1/Hs α -Actinina 2
- 2) DdCortexilina 1/Hs α -Actinina 4
- 3) DdAardvark/Hs β -Catenina
- 4) DdCoronina 7/HsCoronina 7
- 5) DdAbp120/HsFilamina
- 6) DdMiosina 7/HsMiosina 7
- 7) DdPaxilina/HsPaxilina
- 8) DdTM9 Proteína A/HsTM9SF4
- 9) DdRacI/HsRAC2
- 10) DdRacJ/HsRAC2
- 11) DdRacL/HsRAC1
- 12) DdFrmA/HsTalina 1
- 13) DdTalina A/HsTalina 2
- 14) Dd α -Catenina/HsVinculina

Moléculas de Polaridad Celular

- 15) Dd14-3-3/Hs14-3-3
- 16) DdRac1A/HsCdc42
- 17) DdRacB/HsCdc42
- 18) DDB_G0295485/HsCrb1
- 19) DdMarj-A/HsMark2
- 20) DdPakB/HsPak1
- 21) DdPakC/HsPak1
- 22) DdlrrA/HsScrib

[illegible]

[illegible]

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#####  
# Program: water  
# Rundate: Tue 28 Apr 2020 20:29:44  
# Commandline: water  
# -auto  
# -stdout  
# -asequence emboss_water-I20200428-202939-0515-62834091-p1m.asequence  
# -bsequence emboss_water-I20200428-202939-0515-62834091-p1m.bsequence  
# -datafile EBLOSUM62  
# -gapopen 10.0  
# -gapextend 0.5  
# -aformat3 pair  
# -sprtein1  
# -sprtein2  
# Align_format: pair  
# Report_file: stdout  
#####  
  
#  
# Aligned_sequences: 2  
# 1: ACTN4_HUMAN  
# 2: EMBOSS_001  
# Matrix: EBLOSUM62  
# Gap_penalty: 10.0  
# Extend_penalty: 0.5  
#  
# Length: 469  
# Identity:      138/469 (29.4%)  
# Similarity:    228/469 (48.6%)  
# Gaps:          87/469 (18.6%)  
# Score: 504.5  
#  
  
ACTN4_HUMAN      48 WEKQQRKTFTAWCNSHLRKAGTQIENIDEDFRDGLKLMLLLEVISGERLP      97  
                  ||..|.|.|||||.|.|.|.:|:::|.|||:|.|.:|.:...  
EMBOSS_001       6 WEIVQEKAFTAWVNSVLDRGGEKISDVGKDLSDGVKLIFFLELISSKKFN     55  
  
ACTN4_HUMAN      98 KPE--RGKMVRVHKINNPNKALDFIASK-GVKLVSIGAEIVDGNAMKMTLG     144  
                  |.. ..|.|:|.||..|||.|.: :|:|.||:|.|||.||  
EMBOSS_001      56 KKYDFEPKARINMIQNVALALKFLDEELKIKVQGIGSEDFVDNNKKMILG     105  
  
ACTN4_HUMAN     145 MIWTIIILRFAIQDISVEETSAKEGLLLWCQRKTAPYKNVNVQNFHISWKD     194  
                  .:||:....|.||...|:|||||||:..|.|.|.||:~|.||:~|  
EMBOSS_001     106 FLWTLRYRKYRIAVISEGDKSSEEGLLWLCKNTTTGYDGVNITSFTKSFRD     155  
  
ACTN4_HUMAN     195 GLAFNALIHRRHPELIEYDKLRKDDPVTNLNNAFEVAEKYLDIPKMLDAE     244  
                  |||||.|||.|:..||.....|:..|||.|||.|||.||:~|:~|  
EMBOSS_001     156 GLAFLALSHKFEPESFKFQEFAMDPIARLNAAFDAEKGLGVPKLLAE      205  
  
ACTN4_HUMAN     245 DIVNTARPDEKAIMTYVSSFYHAFSGAQ---KAETAANRICKVLAVNQEN     291  
                  :::. ...|:~:~|.|. |:|:~:~ ~. |:~|.::~..|| ..||  
EMBOSS_001     206 EVMR-GTTDERSLVLYTSLFFHAYRAKEEKARLESSKNEMANRLA-GLEN     253  
  
ACTN4_HUMAN     292 -----EHLMEDYEKLASDL--LEWIRRTIPWLED RVPQKTIQEMQQ      330  
                  |.:~:~:~|.|. | | .....|:~|:~:  
EMBOSS_001     254 SLESEKVSREQLIKQKDQLNSLLASLE ----- SEGAEREKRLRELEA     295  
  
ACTN4_HUMAN     331 KLEDFRDYRRVHKPPKVQ-----EKCQLEINF-----NTLQTK      363  
                  |:~:~:~:~|.~:~:~ ~:~|:~.. ~. |:~:  
EMBOSS_001     296 KLDELTKNLELEKLARMELEARLAKEKDRAILELKLAE AIDEKSKLEQQ      345  
  
ACTN4_HUMAN     364 LRLSNRP AFMPSEG-----KMVSDINNGWQHL---EQAEKG YEEWL      401  
                  :~:~:~:~:~| ..... ..|.|. | | .....:~:  
EMBOSS_001     346 IEATRIRGAAEAQGLGLLRKNLDTHVHDLLK-WQKLT MENSSSSSIDDI      394  
  
ACTN4_HUMAN     402 LNEIRRL---ERLDHLAEKFROKASIHEAWTDGKEAMLKHRDYETATLSD     448
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EMBOSS_001

395

IVEVSGLPFGEQVKHLATKL-----EAENLAI

421

ACTN4_HUMAN

449

IKALIRKHEAFESDLAAHQ

467

EMBOSS_001

422

MKLLNQK --- EDDLKAQK

436

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EMBOSS_001	382	ETVTQGGDDFTVKVQSP---EGPVDAQIKDNGDGSYDVEYKPTKGGDHTV	428
FLNA_HUMAN	457	HVTFAGVPIPRSPYTVTV-GQACNPSSACRAVGRGLQPKGVRVKETADFKV	505
EMBOSS_001	429	EVFLRGEPLAQGPTEVKILNSDSQNSYCD--GPGFEK--AQAKRPTEFTI	474
FLNA_HUMAN	506	YTKG-----AGSGELKVTVKGPKGEERVKQKDLGDGVYGFYYPMVPG	548
EMBOSS_001	475	HSVGA DNKPCAAGGDPFQVSISGPH-PVNVGITDNDGTYTVAYTPEQPG	523
FLNA_HUMAN	549	TYIVTITWGGQNIGRSPFEVKVGTECGNQKVRWGPGLGEGGVGKSADFFV	598
EMBOSS_001	524	DYEIQVTLNDEAIKDIPKSIHIKPAADPEKSYAEGPGLDGGECFQPSKFK	573
FLNA_HUMAN	599	VEAIGDD----VGTLGF--SVEGPSQAKIECDDKGDGSCDVRYWPQEAG	641
EMBOSS_001	574	IHAVDPDGVHRTDGGDGFVVITIEGPAPVDPVMVDNGDGTVDVEFEPKEAG	623
FLNA_HUMAN	642	EYAVHVLCSNEDIRLSPFMADIRDAPQDFHPDRVKARGPGLKGTGVAVNK	691
EMBOSS_001	624	DYVINLTLGDGDNVNGFPKTVTKPAPSAEHS---YAEGEGLVK--VFDNA	668
FLNA_HUMAN	692	PAEFT---VD---AKHGGKAPLRVQVQDNEGCPVEALVKDNGNGTYSCS	734
EMBOSS_001	669	PAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVDAKVTDNDNGTYGVV	718
FLNA_HUMAN	735	YVPRKPVKHTAMVSWGGSIPNSPFRVNV--GAGSHPNKVKVYGPVAKT	782
EMBOSS_001	719	YDAPVEGNYNVNVTLRGNPIKNMPIDVKICIEGANGEDSSFGSFTFTVAAK	768
FLNA_HUMAN	783	GLKAHEPTYFTVDCAEAGQGDVSIGIKAPGVVGPAAEADIDFDIIRNDND	832
EMBOSS_001	769	NKKGEVKTY-----GGD-----KFEVSITGPAE-EITLDAIDNQDG	803
FLNA_HUMAN	833	TFTVKYTPRGAGSYTIMVLFA DQATPTSPIR-VKVEPSHDASKVKA	877
EMBOSS_001	804	TYTAAYSLVGNGRFSTGVKLNKGHIEGSPFKQVLGNPGKKNPEVKS	849

```
#####
# Program: water
# Rundate: Tue 28 Apr 2020 22:51:15
# Commandline: water
#   -auto
#   -stdout
#   -asequence emboss_water-I20200428-225027-0383-61442869-p2m.asequence
#   -bsequence emboss_water-I20200428-225027-0383-61442869-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: MYH7_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1772
# Identity:      481/1772 (27.1%)
# Similarity:    776/1772 (43.8%)
# Gaps:          460/1772 (26.0%)
# Score: 1477.5
#

MYH7_HUMAN      71 VKEDQVMQQNPPKFDKIEDMAMLTFLHEPAVLNLDKDRYGSWMIYTYSGL 120
                  ::|...: |...|...|||...|...|...:|.|||.||...|||:|.
EMBOSS_001      1 MEDDDTL--NGEYFQPVEDMITLPILTEESLLNLMRYKKKEIYTYTGS 48

MYH7_HUMAN     121 FCVTVPYPYKWLVPVYTPEVVAAYRGKKRSEAPPHIFSISDNAYQYMLTDRE 170
                  ..|...|||:|.||:|...:|.:.|...|...|...|...|...|...:
EMBOSS_001      49 ILVAVNPYEILPIYTADIVKSYFAKSRNLMPLHIFAVSDAAFTNMIEEGK 98

MYH7_HUMAN     171 NQSILITGESGAGKTVNTRKVIQYFAVIAAIGDRSKKDQSPGKGTLEDQI 220
                  |||:|:|...|...|...|...|...|...|...|...|...|...|...|
EMBOSS_001      99 NQSIIISGESGAGKTESTKLIQYLAA-----RTNRHSQ-----VEQMI 137

MYH7_HUMAN     221 IQANPALEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEK 270
                  ::::|.|||||...|...|...|...|...|...|...|...|...|...|
EMBOSS_001     138 VESSPILEAFGNAKTI RNNNSSRFGKFIEIQFNREGHISGARIINYLLEK 187

MYH7_HUMAN     271 SRVIFQLKAERDYHIFYQILSNKKPELLDMLLITNNPYDYAFISQ-GETT 319
                  ||:..|...|...|...|...|...|...|...|...|...|...|...|
EMBOSS_001     188 SRISHQASSERNYHIFYQLLAGASDELKEKLLK-GEPEYHYLSQSGCIR 236

MYH7_HUMAN     320 VASIDDAEELMATDNADFVLGFTSEEKNSMYKLTGAIMHFGNMKFKLKQR 369
                  :.:|:|.|:.....|:|...|...|...|...|...|...|...|...|
EMBOSS_001     237 IENINDVEDFEHVKYAMNVLGLPEDKQFTIFSIVSAVLHIGNLKFEKSEK 286

MYH7_HUMAN     370 EEQAEPDGTGTEADKS ----AYLMGLNSADLLKGLCHPRVKVGNEYVTKG 414
                  :.:|| |:|:|. |...|...|...|...|...|...|...|...|
EMBOSS_001     287 TQGAE--GSEVSNKDTLKIIAQLLSVDPVKLETCLTIRHVLI-----RG 328

MYH7_HUMAN     415 QN -----VQQVIYATGALAKAVYERMFNWMVTRINATLETKQPRQYFIG 458
                  || |...|...|...|...|...|...|...|...|...|...|...|
EMBOSS_001     329 QNFVIPLKVNEAEDTRDSLAKALYGNVFNWLVVFINSKIHKPQKNSTFIG 378

MYH7_HUMAN     459 VLDIAGFEIFDFNSFEQLCINFTEKLLQQFFNHHMFVLEQEEYKKEGIEW 508
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EMBOSS_001	1179	IFSKVLHYMNSNPLVSKKDPADFYSPVKFILTKGLAIES-LRDEIYCQLI	1227
MYH7_HUMAN	1101	GSQLQKKLKEQLQARIEEL ----- EEELEAERTARAKVEKLRS DLS	1140
EMBOSS_001	1228::: .. :.. ..:: : KQSTSNPIQDLNIRVWELIHFTCTSTFPPTRKLIK YFAAYLKTTIQQSDVS	1277
MYH7_HUMAN	1141	RELEE-----ISERLEEAGGATSV ---QIEMNKKREAEFQKMRRDLE	1179
EMBOSS_001	1278	:...: .: :.: .. :.... .:: KSVKDSAQASYFILQRFTLNGARKQVPSVTELESIKENRPIFVRI-----	1322
MYH7_HUMAN	1180	EATLQHEATAAALRKKHADSV AELGEQIDNL-QRVKQKLEKEKSEFKLEL	1228
EMBOSS_001	1323 :..: :..... -----TATDGLKGLHIDSATTCESSNDLSQRSRM RVNSKENG F-----	1362
MYH7_HUMAN	1229	DDVTSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEETQRSVNDLTSQRA	1278
EMBOSS_001	1363: : :..: : -TIIESFNGIERDIAPTDKLC DVL-----SKVENLQATLS----- S	1397
MYH7_HUMAN	1279	KLQTENGELSRQLDEKEALISQLTRGKLYTQQLEDLKRQLEEEV KAKNA	1328
EMBOSS_001	1398	: .. :...: :.....: :....: : .. KIQVN---FKFVFKKKLFFDNITNNVPTTSINVEN ----- EF	1431
MYH7_HUMAN	1329	LAHALQSARHDCDLLREQYEEETEAKAELQRVLSKANSEVAQW----- RT	1373
EMBOSS_001	1432 :.....:.....:: :.. . YYHQLFNDLFNSNYCKDQYQISIGSLKLQFESSDYTDEIRAWLPNGRG	1481
MYH7_HUMAN	1374	KYETDAIQ RTE-----ELEEAKKKLAQRLQE---AEEAVEA	1406
EMBOSS_001	1482 :.. :.: :.. .: : KYFTTDIEKNRFD FINKYKSHKGLSPEDAKQM VQLLEKHPLANCSLVV	1531
MYH7_HUMAN	1407	VNAKCSSLEKTKHRLQNEIEDLMVDVERSNA AAAALDKKQRNFDKILA EW	1456
EMBOSS_001	1532 :.. :.: CEHQSES LYPKNFV-----LALNVNGINIYDPATSKMLESV-----	1568
MYH7_HUMAN	1457	KQKY-EESQSELESSQKEARSLSTELFKLKNAYEESLEHLETFKRENK NL	1505
EMBOSS_001	1569	.: .. : .. : .. :.. :..: --KYSNQSQQNLKSDDK---SVSIIL ----- ENKSTLQAFTGDVQKL	1605
MYH7_HUMAN	1506	QEEISDLTEQLGSSSGKTIHELE 1527	
EMBOSS_001	1606	... :..... :..: : VSLIKEYSLYLRNNAKYARALK 1627	

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EMBOSS_001	319	TSQVKDIDSTG--PTSRGTCGGCRKPIFGETIQAMGKFYHPEHFCCHNCQ	366
PAXI_HUMAN	389	EEIGSRNFFERDQGYPYCEKDYHNLFSPRCYYCNGPILDKVVTALDRTWHP	438
EMBOSS_001	367	NPLGTKNYYEQESLPHCEKCYQELFCARCAHCDEPISDRCITALGKKWHV	416
PAXI_HUMAN	439	EHFFCAQCGAFFGPEGFHEKD GKAYCRKDYFDMFAPKCGGCARAIENYI	488
EMBOSS_001	417	HHFVCTQCLKPFEGGNFFERDGRPYCEADFYSTFAVRCGGCNSPIRGECI	466
PAXI_HUMAN	489	SALNTLWHPCECFVCRECFTPFVNGSFFEHDGQPYCEVHYHERRGSLCSGC	538
EMBOSS_001	467	NALGTQWHPHEHFVCQYQKSFTNGQFFEFGGKPYCDVHYHQAGSVCSGC	516
PAXI_HUMAN	539	QKPITGR CITAMAKKFHPEHFVCAFLKQLNKGT FKEQNDKPYCQNCFLK	588
EMBOSS_001	517	GKAVSGRCVDALDKKWHPEHFVCAFCMNP LAGGSYTANNKPYCKGCHNK	566
PAXI_HUMAN	589	LF 590	
EMBOSS_001	567	LF 568	


```
#####
# Program: water
# Rundate: Tue 28 Apr 2020 23:03:18
# Commandline: water
#   -auto
#   -stdout
#   -asequence emboss_water-I20200428-230256-0088-65417630-p1m.asequence
#   -bsequence emboss_water-I20200428-230256-0088-65417630-p1m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: TM9S4_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 653
# Identity:      290/653 (44.4%)
# Similarity:    411/653 (62.9%)
# Gaps:          46/653 ( 7.0%)
# Score: 1466.5
#

TM9S4_HUMAN      13 LLFSLMCE--TSAFYVPGVAPINFHQNDPVEIKAVKLTSSRTQLPYEYYS      60
                  :|||:..  ...||:|:|.:.|.:.:.||.:.|||.||:|:|.
EMBOSS_001       12 ILFSIFLNHVNGIFYLPGMIPHDFAQGEEGAIKVNKITSVHTQIPYKYYQ      61

TM9S4_HUMAN      61 LP-FCQPSK-ITYKAENLGEVLRGDRIVNTPFQV-LMNSEKKCEVLCSQS      107
                  ||.|||.:|...|||:|.|||.|.:.:. .:..||:|.:.|
EMBOSS_001       62 LPGVCQPKEGIIDDTENLGEILLGDRIENSDYTFNFLTDGGKCKVINSES      111

TM9S4_HUMAN      108 NKPVTLTVEQSRLVAERITEDYYVHLIADNLPVATRLELYSNRDSDDKKK      157
                  ..|: :..|...:::|...|.||:|.|||...|.|
EMBOSS_001       112 CSPI-IKKEDLKVLEDRIQNQYRVHWLLDGLPVRQTGRLAS-----      151

TM9S4_HUMAN      158 EKDVQFEHGYRLGFTDV ----- NKIYLHNHLSFILYYHREDMEEDQE      199
                  :|.:.|||:..  .:|:|:|...:|  ....:
EMBOSS_001       152 -----DPGFDLGFMTLAEGQTVATAEKYLNHLEITIFYH -----SNPTD      191

TM9S4_HUMAN      200 HTYRVVRFEVIP---QSIRLEDLKADEKSSCTLPEGTNSSPQEIDPTKEN      246
                  :|.:.|.||:|. |...:|.:.|.....| |:....|. ....|.
EMBOSS_001       192 NTSRIVGFEIFPTSRQYKKVENWKGDTGDDC--PQYGENFEQLSVSVKEG      239

TM9S4_HUMAN      247 Q ---- LYFTYSVHWEEEDIKWASRWDTYL TMSDVQIHWFSIINSVVVF      291
                  :      :.:.|||.:.|.:.|.|||.|.:.:|...|||:|:|:|
EMBOSS_001       240 EDQERFVLWTYEVKYTPSPVLWNKRWDIYFESNDNSVHWFSILNSLMIVF      289

TM9S4_HUMAN      292 FLSGILSMIIIRTLRKDIANYNKEDDIE--DTMEESGWKL VHGDVFRPPQ      339
                  .|:..::|...|||:|...|.|.|. |.:.||:|...:|...|||.
EMBOSS_001       290 ILTVMVAMIIIRTLKKDIRRYSIDTSED RDSQEETGWKMIHGDVFRPPS      339

TM9S4_HUMAN      340 YPMILSSLLGSGIQLFCMILIVIFVAMLGMLSPSSRGALMTTACFLFMFM      389
                  :||:|...:|...:|.:.|.|.|.:.:|...:|.:.|. ....|:..
EMBOSS_001       340 HPMLLSVCIGSGVQIFSMTLITMIFAVLGLSPANIGGLATALIVLFVLS      389

TM9S4_HUMAN      390 GVFGGSAGRLYRTLKGHRWKKGAFACTATLYPGVVFGICFVLNCFIWGKH      439
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EMBOSS_001	390	AMFAGYFSTRVFTIFKGRNWKKNITIYALSMPGIIFGIFFFVNMFLRGAK	439
TM9S4_HUMAN	440	SSGAVPFPTMVALLCMWFGISLPLVYLGYFGRKQPYDNPVRTNQIPRQ	489
EMBOSS_001	440	SSAAVPFGTFASIIAMWFGISVPLVFLGSYFASKKVPEDPVRTNQIPRQ	489
TM9S4_HUMAN	490	IPEQRWYMNRFVGI LMAGILPFGAMFIELFFIFSAIWENQFYFLFGFLFL	539
EMBOSS_001	490	VPDQIWYMNPLYLSILMGGILPFGAVFIELHFILTSLWDNQFYIFGFLFI	539
TM9S4_HUMAN	540	VFIIILVVSCSQISIVMVYFQLCAEDYRWWRNFLVSGGSAFYVLVYAIFY	589
EMBOSS_001	540	VLMILIVTSAEISIVMCYFQLCAEDHHWWRSFLTAGSSSLYMFYISVSF	589
TM9S4_HUMAN	590	FVNKL DIVEFIPSLLYFGYTALMVLSFWLLTGTIGFYAAYMFVRKIYAAV	639
EMBOSS_001	590	F-RYLGITKFISLLDFSYSFIMSLAFAALTGTIGFYSCYFLVRKIYSSI	638
TM9S4_HUMAN	640	KID 642	
EMBOSS_001	639	HIN 641	

#-----
#-----


```
#####
# Program: water
# Rundate: Mon 18 Jan 2021 01:14:35
# Commandline: water
#   -auto
#   -stdout
# -asequence emboss_water-I20210118-011434-0305-92561731-p2m.asequence
# -bsequence emboss_water-I20210118-011434-0305-92561731-p2m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: RAC2_HUMAN
# 2: DDB0201669
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 194
# Identity:      72/194 (37.1%)
# Similarity:   111/194 (57.2%)
# Gaps:         17/194 ( 8.8%)
# Score: 302.5
#

RAC2_HUMAN      4 IKCVVVGDGAVGKTCLLISYT ----TNAFPGEYIPTVFDNYSANVMVDS      48
                  :|...:||..|||:|:..||:  |:.|.|... :.:|:..|...
DDB0201669     10 VKIFCLGDDGVGKSCVMNSYSSGGPLTSLFQGSEL--TWTDYTVSVTHNQ      57

RAC2_HUMAN     49 KPVNLGLWDTAGQEDYDRLRPLSYPTDVFLLICFSLVSPASYENVRAKWF      98
                  ||:|.|. |...|...|:..:..|.|||||||:|.|||:|:. ||.
DDB0201669     58 KPLKLRL-VIGDQNELRRIKQIEF--NDVFLICFSVDSKASYDNIE-KWN     103

RAC2_HUMAN     99 PEVRHHCPSTPIILVGTKLDLRDDKDTIEKLKEKKLAPITYPQGLALAKE     148
                  .|:|...|:..|||||||:||||:.....|  :.:|...|:..|||
DDB0201669    104 TEIRKILPTPNIIILVGTKIDLRKEGGELKK-----SIVTQEMGIEKAKE     147

RAC2_HUMAN    149 IDSVKYLECSALTQRGLKTVFDEAIRAVLCQPTRQQKRACSL      192
                  |:..||:|||..|..|:|.||||:|...:..:..|..|..|.|
DDB0201669    148 INAIKMECSTATYEGVKEVFDESINIYMTKKLYIQDLRKKSFL      191

#-----
#-----
```

```
#####
# Program: water
# Rundate: Mon 18 Jan 2021 01:32:42
# Commandline: water
#   -auto
#   -stdout
# -asequence emboss_water-I20210118-013240-0905-3266023-p1m.asequence
# -bsequence emboss_water-I20210118-013240-0905-3266023-p1m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#
# Aligned_sequences: 2
# 1: RAC1_HUMAN
# 2: DDB0201660
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 197
# Identity:      99/197 (50.3%)
# Similarity:    133/197 (67.5%)
# Gaps:          6/197 ( 3.0%)
# Score: 489.5
#
```

RAC1_HUMAN	1	MQAIKCVVVG DGAVGKTC LLISYTTNAFPGEYIPTVFDNYSANVMVDGKP	50
		. . : . . : : : 	
DDB0201660	1	MQYIKMVICG DGAVGKTS LLIAFASGEFPRDYQPTVFDNFS TLYMFQNK A	50
RAC1_HUMAN	51	VNLGLWDTAGQEDYDRLRPLSYPTDVF LICFSLVSPASFENVRAKWYPE	100
		. : : . . . : : : : . :	
DDB0201660	51	YNLGLFDTAGQEDFDRLRPLGYNDTDLFLICYSVINPPSYANVYDKWYSE	100
RAC1_HUMAN	101	VRHHC-PNTPIILVGTKLDLRDDKDTIEKLKEKKLTPITYPQGLAMAKEI	149
		: : : : : . . : : . : . . .	
DDB0201660	101	IKLYTGSEIPLILVGTQNDLRHDKATRETLALKQQAPISYEEGMMMRKRI	150
RAC1_HUMAN	150	GAVKYLECSALTQRGLKTVFDEAIRAVLCPPPVK ---- KRKRKCLLL	192
	 : : . . . : . : : : . . : :	
DDB0201660	151	GAKAFTECSVWSGKNVKQVFEEAIK-VYQDRQIEISKSKEKNNCIIL	196

```
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```


EMBOSS_001

1062 DTQCLTLDYEMGRIVLQTTESEEISSYLSYIDYIQTKLVGSQSF 1109

#-----

#-----


```
#####
# Program: water
# Rundate: Wed 29 Apr 2020 01:39:34
# Commandline: water
#   -auto
#   -stdout
#   -asequence emboss_water-I20200429-013936-0028-53012855-p1m.asequence
#   -bsequence emboss_water-I20200429-013936-0028-53012855-p1m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: VINC_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1138
# Identity:      218/1138 (19.2%)
# Similarity:    413/1138 (36.3%)
# Gaps:          330/1138 (29.0%)
# Score: 431.0
#

VINC_HUMAN      9 IESILEPVAQQISHLVIMHEEGEVDGKAIPDLTAPVAAVQAAVSNLVRVG      58
                  ::::|.|.:|...|.||:.....|.....|:...|...|.||:.....
EMBOSS_001      1 MDEVLEMIADAVSSLVVAITDSEEKNTLFGDMVPGVELIQQAVNGMAEAA      50

VINC_HUMAN     59 KETVQTTEDQILKRDMPPAFIKVENACTKLVQAAQMLQSDPYS-VPARDY     107
                  :|||.....: :.....:|:..|...|.....|:|: ||.:|
EMBOSS_001     51 EETVSLIDEEFIGQ-LESTSKQLKNSAGQLYHAVRAREDPWNRVPQKD-      98

VINC_HUMAN     108 LIDGSRGILSGTSDLLTFDEAEVRKIIRVCKGILEYLTVAEVVETMEDL     157
                  .|.....|.....|:|.....:.....|...|.....:|:..|
EMBOSS_001     99 AIKAAKQILQNVVLLVLIIEEQSNIKVLVNIAKKAAEGVRRIDEIENIKQL     148

VINC_HUMAN     158 VTYTKNLGPGMTKMAKMIDERQQELTHQHRVMLVNSMNTVKELLPVLIS     207
                  ..|.....:|.||.....|
EMBOSS_001     149 -----DVMIGDVNQLQNELVKRSQR-----      168

VINC_HUMAN     208 AMKIFVTTKNSKNQGIEEALKN -- RNFTVEKMSAEINEIIRVLQLTSW     253
                  :.:|.|.:.:.|:| .|...|:..|.....| :.
EMBOSS_001     169 -----RSEGSHPNPELRSKLEDIATMVNILSEQHQASARDVCR ----- NP      207

VINC_HUMAN     254 DEDAWASKDTEAMKRALASIDSKLNQAKGWLDRPSASPGDAGEQAIRQIL     303
                  .|:..||.:|.....|:|
EMBOSS_001     208 REETLRSKRSELSSKLLSAID-----      228

VINC_HUMAN     304 DEAGKVGELCAGKERREILGTCKMLGQMTDQVADLRARGQGSSPVAMQKA     353
                  :::.|.|:.....:|.....| |.....
EMBOSS_001     229 -----DLIYTIKLI FENNTKFVDLAFKWK---PVRTMAE      259

VINC_HUMAN     354 QQVSQGLDVLTA KVENAARKLEAMTNSKQSI AKKIDAAQNWLADPNGGPE     403
                  .:|:.....| :.:. :.:|.|:|. |...
EMBOSS_001     260 DEVTRASAVL---IDNL-----RTLPKSIEAG ----- NGPAA      288

VINC_HUMAN     404 GEEQIRGA---LAEARKIAELCDDPKERDDILRSLGEISALTSKLADLR      450
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EMBOSS_001	289	AREIVNAANLQISNAIIVANRCQDPVKKKMLLKQIEELKKLTPMLISAMK	338
VINC_HUMAN	451	QGKGDSPEARALAKQVATALQNLQTKTNRAVAN---SRPAKAAVHLEGKI	497
EMBOSS_001	339	PVL-ENPNDQEAQKHLESVIYSTQ-KASEALATAVVSSPAEI-----	378
VINC_HUMAN	498	EQAQRWIDNPTVDDRGVGQAAIRGLVAEGHRLANVMMGPYRQDLLAKCDR	547
EMBOSS_001	379	-----VAASGVSLA-----RDL-----	390
VINC_HUMAN	548	VDQLTAQLADLAARGESESPQARALASQLQDSLKDLKARMQEAMTQEVS	597
EMBOSS_001	391	-DSLEEATA----SGDKKRAQVILSHIPSAI-DKHIELANALLETITD	432
VINC_HUMAN	598	VFSDTTTPIKLLAVAATAPPDAPNREEVFDERAANFENHSGKLGATAEKA	647
EMBOSS_001	433	-----PG-----QRHQ-----	438
VINC_HUMAN	648	AAVGTANKSTVEGIQASVKTARELTPQVVSARILLRPNQNQAAYEHFET	697
EMBOSS_001	439	-----IKQSIERLQTLKPRIENANRAIANPNDEHARKNLSS	475
VINC_HUMAN	698	MKNQWIDNVEKMTGLVDEAIDTKSLLDASEEAIKKDLCKKVAMANIQPQ	747
EMBOSS_001	476	D----IKEAKKAIGQISQPYEVVSALNTK---IHNDLDSLICKIDEGGPD	518
VINC_HUMAN	748	MLVAGATSIARRANRILLVAKREVERSE-----DPKFREAVKAASDEL	790
EMBOSS_001	519	MQVKGVQYAKDIANSI----KKQIEAAEAYAQTITDPDRKKQVLDSEIQL	564
VINC_HUMAN	791	SKTISPVMVMDA-KAVAGNISDPGLQKSFLDGSRILGAVAKVREAFQPQE	839
EMBOSS_001	565	KK-LTPQLLEAIRACLANPDDKEARKRLDDVRRVKEASSNLSQVIQP--	611
VINC_HUMAN	840	PDFPPPPPDLEQLRLTDELAPPKPPLPEGEVPPPPPPPEEKDEEFPEQK	889
EMBOSS_001	612	-----TADELKEEK-----RKRNEEIIARIE	631
VINC_HUMAN	890	AGEVINQPMMAARQL---HDEARKWSSKPGIPAAEVGIGVVAEADAAD	935
EMBOSS_001	632	AEEKAKARALLKAAELARIEAEEKK-----RLAIIIEEEKRL	669
VINC_HUMAN	936	AAGFPVPPDMEDDYEPHELLMPSNQPVNQPIIAAAQSLHREATKWSSKGN	985
EMBOSS_001	670	AA-----EEEERKRAPKLVPPEG-PVNKAVFGAAADV---AQALESKVR	709
VINC_HUMAN	986	D-----IIAAAKRMALLMAEMSRVLRGGSGTKRALIQCAKDIKASDEV	1029
EMBOSS_001	710	DGTPLGILVQLSDEIAQQMALIASFAM--NGDVKGMITAARKIADTIKQV	757
VINC_HUMAN	1030	TRLAKEVAKQCTDKRIRTNLLQVCERIPTISTQLKILSTVKATMLGRTNI	1079
EMBOSS_001	758	QTQAKHIADNCTDPRCLKQNVLTCDGCGNFSTQLKILCAVKS-----	799
VINC_HUMAN	1080	SDEESEQATEMLVHNAQNLMSVKETVREAEAASIKIR	1117
EMBOSS_001	800	NDFNDPTAEEQLVTCAGLSGAVINLVKSSEAAASIKQR	837

#-----
#-----

```
#####
# Program: needle
# Rundate: Tue 28 Apr 2020 05:02:17
# Commandline: needle
#   -auto
#   -stdout
# -asequence emboss_needle-I20200428-050217-0143-71823977-p1m.asequence
# -bsequence emboss_needle-I20200428-050217-0143-71823977-p1m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: 1433Z_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 253
# Identity:      158/253 (62.5%)
# Similarity:    193/253 (76.3%)
# Gaps:          8/253 ( 3.2%)
# Score: 790.5
#

1433Z_HUMAN      1 MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKN      50
                  |:.|.|..|:|||||:|:|...|.|.|...|:|:|||||
EMBOSS_001       1 MTREENVYMAKLAEQARYEEMVEAMKKVAELDVELTVEERNLLSVAYKN      50

1433Z_HUMAN     51 VVGARRSSWRVSSIEQKTE--GAEEKQQMAREYREKIETELRDICNDVL      98
                  |:|:|:|:|:|:|:|:|:|.|.|...:|:|:|:|:|:|:|
EMBOSS_001     51 VIGARRASWRIISSIEQKEESKGNENHVKKIKEYKCKVEKELTDICNDIL     100

1433Z_HUMAN     99 SLLEKFLIPNASQAESKFYLYKMGDYRYLAEVAAGDDKKGIVDQSQQA     148
                  .:|..|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
EMBOSS_001    101 EVLESHLIVSSASGESKFYKMGDYFRYLAEFATGNPRKTSAESSLIA     150

1433Z_HUMAN    149 YQEAFEISKEMQPTHPIRLGLALNFSVFYIEILNSPEKACSLAKTAFDE     198
                  |:.|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
EMBOSS_001    151 YKAASDIAVTELPPTHPIRLGLALNFSVFYIEILNSPDRACNLAKTAFDD     200

1433Z_HUMAN    199 AIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDTQG-DEAEAGEGGEN--     245
                  |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
EMBOSS_001    201 AIAELDTLSEDSYKDSTLIMQLLRDNLTLWTSVHNMEKNQDGGDDQNEP     250

1433Z_HUMAN    246 ---      245
EMBOSS_001    251 GM*      253

#-----
#-----
```

```
#####
# Program: needle
# Rundate: Tue 28 Apr 2020 04:00:43
# Commandline: needle
#   -auto
#   -stdout
# -asequence emboss_needle-I20200428-040048-0313-27514751-p1m.asequence
# -bsequence emboss_needle-I20200428-040048-0313-27514751-p1m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: CDC42_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 195
# Identity:      127/195 (65.1%)
# Similarity:    151/195 (77.4%)
# Gaps:          4/195 ( 2.1%)
# Score: 684.0
#

CDC42_HUMAN      1 MQTIKCVVVG DGAVGKTC LLISYTTN KFPSEYV PTVFDNY AVTVMIGG EP      50
                  ||.|||||
EMBOSS_001       1 MQAIKCVVVG DGAVGKTC LLISYTTN AFPGEYI PTVFDNY SANVMVDG KP      50

CDC42_HUMAN     51 YTLGLFDT AGQEDYDR LRPLSYPT DVFLVCF SVVSPSS FENVKEK WVPE     100
                  ..|||:|
EMBOSS_001      51 INLGLWDT AGQEDYDR LRPLSYPT DVFLICFS IISPSSF ENVNGK WHPE     100

CDC42_HUMAN     101 ITHHCPKT PFLLVGTQ IDLRDDPS TIEKLAK NKQKPIT PETAEKL ARDLK     150
                  |.|.|..|. :|||:| :|:|..|. :.:|. :.|.|. :|.. :.:|.
EMBOSS_001      101 ICHHAPNV PIILVGT KLDMREDK ETQDRLK EKKLYP ISYEQGL AKMKEIN     150

CDC42_HUMAN     151 AVKYVECS ALTQKGLKN VFDEAILA ALEPPEPK KSRR--- CVLL-     191
                  |||:|
EMBOSS_001      151 AVKYLECS ALTQKGLK TVFDEAIR AVINPPL SKKKKSS GGCNIL*     195

#-----
#-----
```

```
#####
# Program: needle
# Rundate: Tue 28 Apr 2020 04:03:36
# Commandline: needle
#   -auto
#   -stdout
# -asequence emboss_needle-I20200428-040245-0656-76655243-p1m.asequence
# -bsequence emboss_needle-I20200428-040245-0656-76655243-p1m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: CDC42_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 196
# Identity:      121/196 (61.7%)
# Similarity:    155/196 (79.1%)
# Gaps:          5/196 ( 2.6%)
# Score: 662.5
#

CDC42_HUMAN      1  MQTIKCVVVGDGAVGKTCLLISYTTNKFSEYVPTVFDNYAVTMIGGEP      50
   |:|.|.|||||||||||||||||:|.||:|||||||||:..|:|:..
EMBOSS_001       1  MQSIKLVVVGDGAVGKTCLLISYTSNSFPTEYVPTVFDNYSANVMVDNKT      50

CDC42_HUMAN     51  YTLGLFDTAGQEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWPE     100
   .:|:|.|.|||||||||||||||||:|:|:|.:.|:|.|||.||
EMBOSS_001      51  VSLGLWDTAGQEDYDRLRPLSYPQTDVFLICFAIISQTSYTNVKSKWPE     100

CDC42_HUMAN     101 ITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLRDLK     150
   :|:|:|. ....:|:|:|.||:|. ....:|:|. ....:|:|:|.
EMBOSS_001      101 VTHHCPNCTIILVGTKCDLREDKESLEKLREKHQQPLTFQQGEQMAKEIK     150

CDC42_HUMAN     151 AVKYVECSALTQKGLKNVFDEAILAALEPPEP ---- KKSRRCVLL-      191
   |..|:|.|. ....:|:|:|. ....:|:|. ....:|:|.
EMBOSS_001      151 AFCYMECSALTQKGLKQVFDEAIKAVIFPDRDKATNKKNSKCSIL*      196

#-----
#-----
```

```
#####
# Program: water
# Rundate: Fri 22 Jan 2021 05:37:31
# Commandline: water
#   -auto
#   -stdout
# -asequence emboss_water-I20210122-053636-0196-90998482-p2m.asequence
# -bsequence emboss_water-I20210122-053636-0196-90998482-p2m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: CRUM1_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1521
# Identity:      321/1521 (21.1%)
# Similarity:    477/1521 (31.4%)
# Gaps:          661/1521 (43.5%)
# Score: 692.0
#

CRUM1_HUMAN      27 CNKNNTRCLSNSCQNNSTCKDFSNDNDSC--SDTANNLDKDCDNMKDPC      74
|::|..|..| |. | |...|:   || |..|. |..|. |.:.: |
EMBOSS_001      196 CSTSNGGCAHN-CAN--TAGSFT ---CSCRAGYTLNSDKKSCDINE-C      237

CRUM1_HUMAN      75 FSNPCQGSATCVNTPGERSFLCKCPPGYS-GT ----- ICETTIGSC      114
.:|.....|. |.: | |.|.|..||: || |..|. |..|. |
EMBOSS_001      238 STNNGGCNQVCTNSAG--SFACSCRAGYTLGTDKKTCVDINECSTNNGGC      285

CRUM1_HUMAN      115 GKN-----SCQ-----HGG---ICHQDPI      130
..| | | | | | | | | | | | | | | | | | | | | | | | | | | |
EMBOSS_001      286 AHNCANTAGSFTCSCRAGYTLNSDKKSCDINECSTNNGGCNQVCTNSAG      335

CRUM1_HUMAN      131 YPVCICPAGYA---GRFCEIDHDECASSPCQNGA---VCQDGIDGYSCF      173
...|. |. | | | | | | | | | | | | | | | | | | | | | | | | | |
EMBOSS_001      336 SFACSCNAGYSLGTDKKTC-TDINECSTN---NGGCNQVCTNSAGSFACS      381

CRUM1_HUMAN      174 CVPGY---QGRHCDLEVDECASDPCKNEATCLNEIGRYTCICPHNYS-G      218
|..| | | | | | | | | | | | | | | | | | | | | | | | | | | |
EMBOSS_001      382 CNSGYSLGTDKKTC-ADINECSTNNGGCNQVCTNSAGSFSCSCNSGYSLG      430

CRUM1_HUMAN      219 VN---CELEIDECWSQPCLNGA---TCQDALGAYFCDAPGF-LGDHCEL      261
.: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
EMBOSS_001      431 TDQKTC-ADINECSTN---NGGCNQICTNSVGSFSCSCNSGYSLGTDKKT      476

CRUM1_HUMAN      262 NTD--ECASQPCLHGG---LCVDGENRYSCNCTGSGFTGTHCETLMPL--      304
.| | | | | | | | | | | | | | | | | | | | | | | | | | | |
EMBOSS_001      477 CTDINECSTN---NGGCNQVCTNSAGSFSCSCNQGYLLGTDQKTCADINE      523
```


CRUM1_HUMAN	305	CWSKPCHNNATCEDSVNYTCHCWPGY--TGAQCEIDLNECNSNPCQSNG	352
EMBOSS_001	524	CDQKIC-GTANCTNTVGSYQCSCPSGYSFTGSSC-VDIDECSTN ---- NG	567
CRUM1_HUMAN	353	ECVELSSEKQYGRITGLPSSFYSYHESGYVCICQPGF ---- TGIHCEEDV	398
EMBOSS_001	568	GCAQVCT -----NSAGGFSCSCNSGYILSTDKKNC-NDI	600
CRUM1_HUMAN	399	NECSSNPCQNGG---TCENLPGNYTCHCPFDNLSRTFYGGRDCSDILLGC	445
EMBOSS_001	601	NECSTN---NGGCSQVCTNSAGSFSCSCNSGYLLST--DKKTCTD-----	640
CRUM1_HUMAN	446	THQQCL-NNGTCIPHFQDQGHGFSCLCPSGYTGSLCEIATTLSEFGDGFL	494
EMBOSS_001	641	-KNECLTNNGGCTQVCTNSVGSFSCSCNSGF-----	670
CRUM1_HUMAN	495	WVKSGSVTTKGSVCNIALRFQTVQPMALLFRSNRDVFKLELLSGYIHL	544
EMBOSS_001	671	-----	670
CRUM1_HUMAN	545	SIQVNNQSKVLLFISHNTSDGEWHFVEVIFAEAVTLTLIDDSCKE--KCI	592
EMBOSS_001	671	---ILNSNKL -----SCDDINEC-	685
CRUM1_HUMAN	593	AKAPTPLESDQSICAFQNSFLGGLPVGMTSNGVALLNFY--NMPSTPSFV	640
EMBOSS_001	686	-----DQKICG -----TANCTNIPGSYQCSCPSGYSFT	713
CRUM1_HUMAN	641	GCLQDIKIDWNHITLENISSGSSLNVKAGCVRKDWCESQPCQSRGRCINL	690
EMBOSS_001	714	G-----SGCIDIDECDQKIC-GTANCTNS	736
CRUM1_HUMAN	691	WLSYQCDCHRPYE--GPNCLEREYVAGRFGQDDSTGYVIFTLDESYGDTIS	738
EMBOSS_001	737	PGSYQCSCPSGYSFTGSSCI-----DIDEC SAD---	764
CRUM1_HUMAN	739	LSMFVRTLQPSGLLLALENSTYQYIRVWLERGR LAMLTNPSPKLVVKFVL	788
EMBOSS_001	765	-----NGGCSQICTNS-----	775
CRUM1_HUMAN	789	NDGNVHLISLKI KPYKIELYQSSQNLGFISASTWKIEKGDVIYIGGLPDK	838
EMBOSS_001	776	-----VGSFSCS-----	782
CRUM1_HUMAN	839	QETELNGGFFKGCIQDVRLNNQNLEFFPNPTNNASLNPVLVNVQTQGCAGD	888
EMBOSS_001	783	----CNSGF-----TLNSNKL -----SCDDI	799
CRUM1_HUMAN	889	NSCKSNPCHNGGVCHSRWDDFSCSCPALTS--GKACEEVQWCGFSPCPHG	936
EMBOSS_001	800	NECDQNICGTAN-CANSPGSYQCSCPNGYSFTGSGCIDIDEC-----	840
CRUM1_HUMAN	937	AQCQPVLQGFECIANAVFNGQSGQILFRSNGNITRELTNITFGFRTRDAN	986
EMBOSS_001	841	-----STDNGGCSQICTNSVGSFS-----	859
CRUM1_HUMAN	987	VIILHAEKEPEFLNISIQDSRLFFQLQSGNSFYMLSLTSLQSVNDGTWHE	1036
EMBOSS_001	860	-----	859
CRUM1_HUMAN	1037	VTLSMTDPLSQTSRWQMEVDNETPFVTSTIATGSLNFLKDNTDIYVGDR A	1086
EMBOSS_001	860	-----CSCDSGYTLNVDNK-----KSCDDI---DEC	882
CRUM1_HUMAN	1087	IDNIKGL-QGCLSTIEIGGIYLSYFENVHGF-INKPQEEQFLKISTNSVV	1134

EMBOSS_001	883	ISNNGGCDQKCAN---IPGSFGCYCNS--GFALNKNKKT-----	916
CRUM1_HUMAN	1135	TGCLQLNVCNSNPCLHGGNCEDI---YSSYHCSCPLGW----SGKHCEL	1176
EMBOSS_001	917	--CDDIDECSTN---NGDCGQICINQIGSYQCSCNLGFTLNQNNKNCD-	959
CRUM1_HUMAN	1177	NIDECFSN--PCIHGNCSDRVAAYHCTCEPGY----TGVNCEVDIDNCQS	1220
EMBOSS_001	960	DIDECLTNNGDCQH-VCKNLQGSFQCSCNSGYLLNQDNKKCD-DIDECST	1007
CRUM1_HUMAN	1221	HQCANGA---TCISHTNGYSCLCFGNFTGKFCRQSRLPSTVCGNEKTNLT	1267
EMBOSS_001	1008	D---NGGCIQVCTNSVGSFSCSCNSGFT---LNENKLS---CDDID---E	1045
CRUM1_HUMAN	1268	CYNGGN-----CTEFQTELKCMC-RPGFTGE--WCEKDIDECAS---	1303
EMBOSS_001	1046	CENGDNKCVGEFTSCQNTDGSYSCICPSNGFSNNSTYCE-DINECLSNEL	1094
CRUM1_HUMAN	1304	DPCVNGGLCQDLLNKFQCLC---DVAFAGE-RCEVDLADDLI-----	1341
EMBOSS_001	1095	NECSSNTICENRNGSYVCQCNPSDYSHSPFTCE---PKPIITNFYQKPF	1141
CRUM1_HUMAN	1342	-SDIFTTIG-----SVTVALLLILLLAIVASVVTSNKRATQGTYSPTS	1382
EMBOSS_001	1142	RSNIFVWQGINFVEFDTKVTIG-----EMICDYVTGNDTYTE---CSS	1181
CRUM1_HUMAN	1383	RQEKE---GSRVEMWNLMPPP	1400
EMBOSS_001	1182	REGKEVIGNVIVEANNILSDP	1202

#-----
#-----

EMBOSS_001	446	NNNNNNNNNNNNNNNNNNNTTTTNNATTTTPITSPIQNRNNEELDQEIE	495
MARK2_HUMAN	331	LMVSMGYTREEIQDSL VGQRYNEVMATYLLL-----	361
EMBOSS_001	496	ELVGLGFEREELCNSIRQNKYNDAASTYFLLQGKKLRESQQNQTDNAKKL	545
MARK2_HUMAN	362	-----GYKSSELEGDTITLKPR ---- PSADLTNS	386
EMBOSS_001	546	EKFYSEPLTIPAHVGENSPLIKYKRHHKRSNTVD-SPKSTNTPQYRSSNT	594
MARK2_HUMAN	387	SAPSPSHKVQRSVSANPKQRRF-----SDQAAG ----- PAIPT-	419
EMBOSS_001	595	QQNNHHHQQQQQQQQQQHHHTQQQNQQQSQQQYNNNNHNKPPTPTI	644
MARK2_HUMAN	420	-----SNSYSKKTQSNNNAENKRPEEDRESGRKASS-TAK	452
EMBOSS_001	645	VTTQASTTVNNHISINNNNNNNNNNNNSSTPGSNTVSSTQSSSINSS	694
MARK2_HUMAN	453	VPASPL-----PGLERKK ----- TTPTPSTNSVLSTSTNRSR	484
EMBOSS_001	695	VNPSPLCLSNAVPVSLREKLREKEATTTNTTTTTTTTTTTNTSSNNSS	744
MARK2_HUMAN	485	NSPLLERASLGQASIQNGKDSLTPGSRASASAAVSAARPRQHQKSM	534
EMBOSS_001	745	NQ-----SISSISPPTSTSPNLQPFSLASTANNN ----- NNNNNSN	780
MARK2_HUMAN	535	SASVHPNKASGLPPTESNCEVPRPSTA --- PQRVPVASPSAHNISSSG	579
EMBOSS_001	781	NNSNNNNNNNNNNNNNSLNSHIQRRATASSLQQQQMQQASNTRRLRSNSS	830
MARK2_HUMAN	580	GAPDRTNFPGRGVSSRSTFHAGQLRQV ----- RDQQNLPGY	614
EMBOSS_001	831	SVADQ-----SQRQ ---- ESRKLEDDWVIFEDYSNDGHRDGPKNYH	868
MARK2_HUMAN	615	VTPASPSGHSQGRRGASGSIFSFKTSKFVRRNLSFRFARRNLNEPESKDR	664
EMBOSS_001	869	LQPSSLSSHKKQK ---- SPVHSFLSSF--KNILKRSDDKSFNSSSSNNN	911
MARK2_HUMAN	665	V-----ETLRPHVVGSGGNDKE ----- KEEFR	686
EMBOSS_001	912	TNNNNTTTTSVSTNNTPTLTLEVDHQNSNNNNQQATSSSPNVTSPSSPSQQQ	961
MARK2_HUMAN	687	EAKPRSLRFTWSMKTSSMEPNEMMREIRKVL DANCQSELHEKYMLLCM	736
EMBOSS_001	962	QQEPRIVRFVFGVNTTTMKDAPELMQQVLKVVDTCIPHTKKAPFLIEC-	1010
MARK2_HUMAN	737	HGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANEL	786
EMBOSS_001	1011	-ETEG --- VRFSIEICRLPRLSVNGLKFKRIGGSSWRYKSICKDLLSQM	1055
MARK2_HUMAN	787	KL 788	
EMBOSS_001	1056	KL 1057	

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```
#####
# Program: water
# Rundate: Tue 28 Apr 2020 04:57:08
# Commandline: water
#   -auto
#   -stdout
# -asequence emboss_water-I20200428-045622-0049-35496111-p2m.asequence
# -bsequence emboss_water-I20200428-045622-0049-35496111-p2m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: PAK1_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 592
# Identity:      214/592 (36.1%)
# Similarity:    307/592 (51.9%)
# Gaps:          101/592 (17.1%)
# Score: 924.5
#

PAK1_HUMAN      2  SNNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTLNHGSKPLPPNPPEEKKKK      51
                  :||...:..||:|:|.||..                  |...:|
EMBOSS_001      308 NNNSSNATTSPSPSPVSNVG----- NKQDEEKK      335

PAK1_HUMAN      52  DRFYRSILPGDKTNKKKEKERPEISLPSDFEHTIHVGFDVAVTGEFTGMPE      101
                  .  :||...|.||:|:|. ....|...:|.|||...:| |||.|:|:
EMBOSS_001      336 G--FLSIFTNKKKNKDKKKEF-SVGSPFNVKHNHVNYSVTG-FEGLPK      381

PAK1_HUMAN      102 QWARLLQTSNITKSEQKKNQAVLDVLEFYNSKKTSSNSQKYMSFTDKSAE      151
                  :|...|:|.||:.....:|.|||:|:.....:|:
EMBOSS_001      382 EWEVILQSSGITREDVVEHSEVVIDVLDVDFHMQQQQQQAQQ-----      421

PAK1_HUMAN      152 DYNSSNALNVKAVSET-----PAVPPVSEDEDDDDDATPPPI      190
                  ...||..|:..:|..|...:.....:..|.||..
EMBOSS_001      422 ---EQQALMQKQMQQSGIPAHMLNNPKPPTIPIRDANKQPHNQLQPTPHQ      468

PAK1_HUMAN      191 APRPEHTKSVYTRSVEIPLVPTPTRDVATSPISPTENNTTPPDALTRNTE      240
                  .|:..|.:      :|   |:.....:|:.....:|..
EMBOSS_001      469 PPQHHHQ-----QP ---PQQHHHQQQQQHNNNNNNNNNNNNNNNN      506

PAK1_HUMAN      241 KQKKKPKMS-----DEEILEK----- L      257
                  .|:.....|      .|:|:|:
EMBOSS_001      507 NQQSAQQQSAGILSQQQEQLLEMMCGGAYDDEQYDLNNQPLPDETIVSL      556

PAK1_HUMAN      258 RSIVSVGDPKKKYTR-FEKIGQGASGTVYTAMDVATGQEVAIKQMNQQQ      306
                  ..:|...|:|.||.. ..|||:|:|.||:.....:|...:| |||.|:|:
EMBOSS_001      557 YDLVSQEDPTKLFGEGSTKIGEGAAGEVFVVTQLKTNNKVAIKKMPLNQQ      606

PAK1_HUMAN      307 PKKELIINEILVMRENKNPNIVNYLDSYLVGDELWVVMYLAGGSLTDVV      356
                  ..|   ||:..|:|:.....:|:|:| |||||.|||.||:..|:|:|:
EMBOSS_001      607 NMK-LIVTEIGIMKSCRHQNIIDYIDSYLVGDSLWVAMEFMGGGCLTEIL      655

PAK1_HUMAN      357 TE---TCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGMDGSV      403
```

EMBOSS_001	656	EQFNSVKLV	EQAIYVCAETLKGLAYIHSQ	HRIHRDIKSDNILLGSDGSV	705
PAK1_HUMAN	404	KLTDGFGCAQITPEQSKRST	MTMGTPYWM	APVTVTRKAYGPKVDIWSLGIM	453
EMBOSS_001	706	KLADFGYAAQLTKSKQKR	VTIVGTPYWM	APELIRGQNYDRKVDIWSLGIM	755
PAK1_HUMAN	454	AIEMIEGEPPYLNENPLRALY	LIATNGTPELQNP	EKLSAIFRDFLNRCLE	503
EMBOSS_001	756	AMEMAES	EPYPMSFPPLRALFLIT	TGKIPDLKDQNKWSDDFKDFVKKCLD	805
PAK1_HUMAN	504	MDVEKRGSAKELLQHQLK	IAKPLSSLTPLIAAAKEATKNNH	545	
EMBOSS_001	806	KDVENRPEAKVLLNHPFLK	TACNSNGLVPAIMEAKKA-KEAH	846	

PAK1_HUMAN	350	GSLTDVW---TETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNIL	396
EMBOSS_001	284	GCLTDILEAFDNIMSEIQIAYVVKETLKALQYIHS�HRIHRDIKSDNIL	333
PAK1_HUMAN	397	LGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVWTRKAYGPKVD	446
EMBOSS_001	334	LGSEGSVKIADFGYAAQLTQKQQRNTVVGTPYWMAPELIRGHYGVKVD	383
PAK1_HUMAN	447	IWSLGIMAIEMIEGEPYPYLNNPLRALYLIATNGTPELQNPEKLSAIFRD	496
EMBOSS_001	384	IWSLGIMMEMAEGEPYMDFPPLRALFLITTKGIPPLKETTQWSKTFQD	433
PAK1_HUMAN	497	FLNRCLEMDVEKRGSAKELLQHQLKIAKPLSSLTPLIAAAKEATKNNH	545
EMBOSS_001	434	FFSKCLDINVANRPDATDLLKHPFMDLACDSSEFKPLIQAARNV*----	478

#-----
#-----


```
#####
# Program: water
# Rundate: Tue 28 Apr 2020 04:43:42
# Commandline: water
#   -auto
#   -stdout
# -asequence emboss_water-I20200428-044242-0876-95986764-p2m.asequence
# -bsequence emboss_water-I20200428-044242-0876-95986764-p2m.bsequence
# -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#
# Aligned_sequences: 2
# 1: SCRIB_HUMAN
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 435
# Identity:      129/435 (29.7%)
# Similarity:    201/435 (46.2%)
# Gaps:          59/435 (13.6%)
# Score: 460.0
#

SCRIB_HUMAN      12 RHVESVDKRHCSLQAVPEEIYRYSRSLEELLLDANQLRELKPKFFRLLNL      61
                  |..|.|.|.|.:.:|..| .:..:|.|.|.|.:.:|.:.:|.:.
EMBOSS_001       15 RKREIVDLRKMNIKLPPTI--GALQCKELLLSENDLITPEEIGKLSKV      62

SCRIB_HUMAN      62 RKLGLSDNEIQRLPPEVANFMQLVELDVSRLNDI--PEIPESIKFCKALEI     109
                  .:..:|.|.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:
EMBOSS_001       63 EIIDFAKNRINYIPPEIGSLATLKLQFLSNNKLFYTPITPNIGALKNLTR     112

SCRIB_HUMAN      110 ADFSGNPLSRLPDGFTQLRSLAHLALNDVSLQALPGDVGNLANLVTLELR      159
                  .|.|.|.|.|.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:
EMBOSS_001       113 LDLSSNQLDDLPVEISNCEALEYLDISDNQLQSFPLEFGKLYNLQVFNC      162

SCRIB_HUMAN      160 ENLLKSLPASLSFLVKLEQLDLGGNDLEVL PDTLGALPNLRELWLDNRNL      209
                  :|.|.|.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|
EMBOSS_001       163 KNSLKS L PSEISGWVKLEELNVSNQLAFLPNQICLLGLLSTLNVGFNKL      212

SCRIB_HUMAN      210 SALP-----PELGNLRR-----      221
                  ..||                      |:|.|.:
EMBOSS_001       213 QQLPEELSSMVSLTNLDLKVNPPLQYVPQLSNLRQLKILSIRNLQITHLP      262

SCRIB_HUMAN      222 -----LVCLDVSEN-RLEELPAELGGLVLLTDLLLSQNLLRRLPDGI      262
                  |:|.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:
EMBOSS_001       263 LGLGLLSELIELDIRNPQLKEIPYDIATLINLQKLDLFGNNMRIVPREV      312

SCRIB_HUMAN      263 GQLKQLSILKVDQNRLC--EVTEAIGDCENLSELILTENLLMALPRSLGK      310
                  |.|.|.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|
EMBOSS_001       313 GNLINLQTLDLRQNKLTIIDNIPSEIGKLVNLKLLLSNLLIALPPEIAS      362

SCRIB_HUMAN      311 LTKLTNLNVDRNHLEALPPEIGGCVALSVLSLRDNRLAVLPPELAHTTEL      360
                  :..|.....|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|
EMBOSS_001       363 MKALKEFEASNNQLQAIPTEIGELSGLTGINLSGNKLTSSIPASFGNLSEL      412

SCRIB_HUMAN      361 HVLDVAGNRLQSLPFAL-----THNLKALWLAE      389
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EMBOSS_001

.:.|:..|:..|:..|:..|

413 QICDLKSNEIAELPTTLDGLKSCTKIDLSHNMLTE

|.:|:..|:..|:..|

447

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