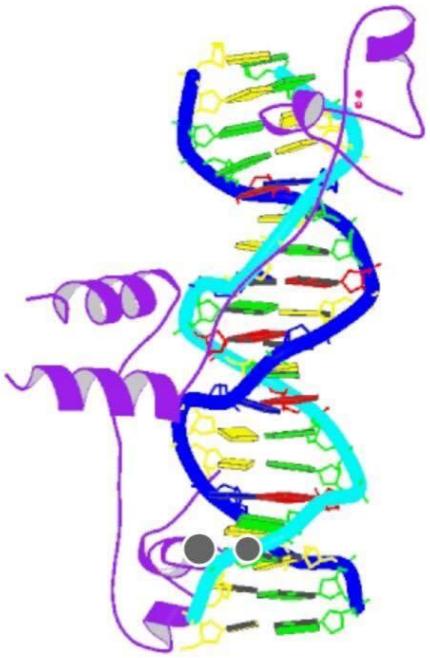
Δομική Βιοχημεία & Στοιχεία Βιοπληροφορικής

Θ. Χολή

Λιόγκα Μελπομένη (8331)
Πεπανιάν Άννα (8633)
Σκορδά Αικατερίνη (8376)

Πρωτεΐνη: 1D66



FASTA SEQUENCE

MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESR
LERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPL
TLRQHRISATSSSEESSNKGQRQLTVSIDSAAHHDNSTIPLDFMPRDALHGFDWSEEDDM
SDGLPFLKTDPNNNGFFGDGSLLCILRSIGFKPENYTNSNVNRLPTMITDRYTLASRSTT
SRLLQSYLNNFHPYCPIVHSPTLMMLYNNQIEIASKDQWQILFNCILAIGAWCIEGESTD
IDVFYYQNAKSHLTSKVFESGSIILVTALHLLSRYTQWRQKTNTSYNFHSFSIRMAISLG
LNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLSQNTISFPSSVDDVQRTT
TGPTIYHGIIETARLLQVFTKIYELDKTVTAEKSPICAKKCLMICNEIEEVSRQAPKFLQ
MDISTTALTNLLKEHPWLSFTRFELKWKQLSLIIYVLRDFFTNFTQKKSQLEQDQNDHQS
YEVKRCSIMLSDAAQRTVMSVSSYMDNHNVTPYFAWNCSYYLFNAVLVPIKTLLSNSKSN
AENNETAQLLQQINTVLMLLKKLATFKIQTCEKYIQVLEEVCAPFLLSQCAIPLPHISYN
NSNGSAIKNIVGSATIAQYPTLPEENVNNISVKYVSPGSVGPSPVPLKSGASFSDLVKLL
SNRPPSRNSPVTIPRSTPSHRSVTPFLGQQQQLQSLVPLTPSALFGGANFNQSGNIADSS
LSFTFTNSSNGPNLITTQTNSQALSQPIASSNVHDNFMNNEITASKIDDGNNSKPLSPGW
TDQTAYNAFGITTGMFNTTTMDDVYNYLFDDEDTPPNPKKE

ProtParam

User-provided sequence:

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        10         20         30         40         50         60
MKLLSSIEQA CDICRLKKLK CSKEKPKCAK CLKNNWECRY SPKTKRSPLT RAHLTEVESR

        70         80         90        100        110        120
LERLEQLFLL IFPREDLDMI LKMDSLQDIK ALLTGLFVQD NVNKDAVTDR LASVETDMPL

       130        140        150        160        170        180
TLRQHRISAT SSSEESSNKG QRQLTVSIDS AAHHDNSTIP LDFMPRDALH GFDWSEEDDM

       190        200        210        220        230        240
SDGLPFLKTD PNNNGFFGDG SLLCILRSIG FKPENYTNSN VNRLPTMITD RYTLASRSTT

       250        260        270        280        290        300
SRLLQSYLNN FHPYCPIVHS PTLMMLYNNQ IEIASKDQWQ ILFNCILAIG AWCIEGESTD

       310        320        330        340        350        360
IDVFYYQNAK SHLTSKVFES GSIILVTALH LLSRYTQWRQ KTNTSYNFHS FSIRMAISLG

       370        380        390        400        410        420
LNRDLPSSFS DSSILEQRRR IWWSVYSWEI QLSLLYGRSI QLSQNTISFP SSVDDVQRTT

       430        440        450        460        470        480
TGPTIYHGII ETARLLQVFT KIYELDKTVT AEKSPICAKK CLMICNEIEE VSRQAPKFLQ

       490        500        510        520        530        540
MDISTTALTN LLKEHPWLSF TRFELKWKQL SLIIYVLRDF FTNFTQKKSQ LEQDQNDHQS

       550        560        570        580        590        600
YEVKRCSIML SDAAQRTVMS VSSYMDNHNV TPYFAWNCSY YLFNAVLVPI KTLLSNSKSN

       610        620        630        640        650        660
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AENNETAQLL QQINTVLMLL KKLATFKIQT CEKYIQVLEE VCAPFLLSQC AIPLPHISYN

       670        680        690        700        710        720
NSNGSAIKNI VGSATIAQYP TLPEENVNNI SVKYVSPGSV GPSPVPLKSG ASFSDLVKLL

       730        740        750        760        770        780
SNRPPSRNSP VTIPRSTPSH RSVTPFLGQQ QQLQSLVPLT PSALFGGANF NQSGNIADSS

       790        800        810        820        830        840
LSFTFTNSSN GPNLITTQTN SQALSQPIAS SNVHDNFMNN EITASKIDDG NNSKPLSPGW

       850        860        870        880
TDQTAYNAFG ITTGMFNTTT MDDVYNYLFD DEDTPPNPKK E
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References and documentation are available.

Number of amino acids: 881

Molecular weight: 99402.8

Theoretical pI: 6.79

Amino acid composition:

Ala (A)	43	4.9%
Arg (R)	36	4.1%
Asn (N)	62	7.0%
Asp (D)	45	5.1%
Cys (C)	18	2.0%
Gln (Q)	46	5.2%
Glu (E)	40	4.5%
Gly (G)	29	3.3%
His (H)	17	1.9%
Ile (I)	56	6.4%
Leu (L)	95	10.8%
Lys (K)	47	5.3%
Met (M)	19	2.2%
Phe (F)	38	4.3%
Pro (P)	46	5.2%
Ser (S)	100	11.4%
Thr (T)	66	7.5%
Trp (W)	12	1.4%
Tyr (Y)	27	3.1%
Val (V)	39	4.4%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 85
Total number of positively charged residues (Arg + Lys): 83

Atomic composition:

Carbon	C	4406
Hydrogen	H	6926
Nitrogen	N	1190

Oxygen O 1353
Sulfur S 37

Formula: $C_{4406}H_{6926}N_{1190}O_{1353}S_{37}$
Total number of atoms: 13912

Extinction coefficients:

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

Ext. coefficient 107355
Abs 0.1% (=1 g/l) 1.080, assuming all pairs of Cys residues form cystines

Ext. coefficient 106230
Abs 0.1% (=1 g/l) 1.069, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 46.47
This classifies the protein as unstable.

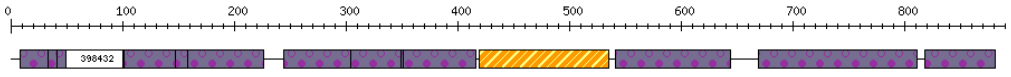
Aliphatic index: 84.56

Grand average of hydropathicity (GRAVY): -0.330

database: multiple alignments
Program: ncbi-blastp
Matrix: BLOSUM62
Expect: 0.01
Filter: seg

Graphical results and forms to other applications

The following is the graphical representation of the HSP found by BLAST.
Please note that HSPs are sorted from highest to lowest scores, so that lower scoring HSPs may be hidden.



Align subsequence with ProDom domains, using Multalin

Domain ID	BEGIN	END	
PD142134	419	534	Υποβολή
PDA044Z4	541	643	Υποβολή
PDC3J281	669	810	Υποβολή
PDB087H7	158	225	Υποβολή
PDA0B366	818	880	Υποβολή
PDC683Q8	244	303	Υποβολή
PDA98416	351	415	Υποβολή
PD398432	49	99	Υποβολή
PDB9K6A9	304	348	Υποβολή
PDB0G2D8	352	399	Υποβολή
PDA2S4D4	101	146	Υποβολή
PDC1H611	41	83	Υποβολή
PDA2T7D8	33	68	Υποβολή
PDD6J756	84	158	Υποβολή
PDA000V1	305	362	Υποβολή
PDA1P8G1	8	48	Υποβολή
PD024698	326	394	Υποβολή
PDC7F6U6	352	403	Υποβολή
PDC596Z5	350	410	Υποβολή
PDB0D1A0	352	415	Υποβολή

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END	
PD398432	49	99	Υποβολή
PDA1P8G1	8	48	Υποβολή

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END	
PD398432	49	99	Υποβολή
PDA1P8G1	8	48	Υποβολή

HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

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blastp 2.2.26 [Sep-21-2011]   Reference: Altschul, Stephen F., Thomas L.
Madden, Alejandro A. Schaffer,  Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997),  _quot;Gapped BLAST and PSI-BLAST: a new generation
of protein database search programs_quot;,  Nucleic Acids Res. 25:3389-3402.
Query: unkwown   (881 letters)  Database: prodom2010.1 multiple alignments
         45,292,438 sequences; 2,147,483,647 total letters    ProDom domains
producing High-scoring Segment Pairs:    Position  ProDom domain
Score E value        8-48  #PDA1P8G1
119 5e-05      33-68  #PDA2T7D8
129 3e-06      41-83  #PDC1H611
175 2e-12      49-99  #PD398432
256 2e-23     84-158  #PDD6J756
122 3e-05    101-146  #PDA2S4D4
182 2e-13    158-225  #PDB087H7
373 4e-39    244-303  #PDC683Q8
333 8e-34    304-348  #PDB9K6A9
237 7e-21    305-362  #PDA000V1
120 4e-05    326-394  #PD024698
118 7e-05    350-410  #PDC596Z5
110 0.001    351-415  #PDA98416
332 1e-33    352-399  #PDB0G2D8
191 1e-14    352-403  #PDC7F6U6
114 0.0002    352-415  #PDB0D1A0
109 0.001    419-534  #PD142134
617 2e-72    541-643  #PDA044Z4
545 1e-62    669-810  #PDC3J281
498 1e-55    818-880  #PDA0B366
339 1e-34   >PD142134 (Closest domain: GAL4_YEAST 419-534) Number of domains
in family: 19 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-
BINDING NUCLEUS SUBNAME: REGULATION ZINC FULL=PUTATIVE UNCHARACTERIZED
FULL=PISO0_001283   Length = 116 Score = 617  (242.3 bits), Expect = 2e-72
Identities = 116/116 (100%), Positives = 116/116 (100%)
 Query:    419
TTTGPTIYHGIIETARLLQVFTKIYELDKTVTAEKSPICAKKCLMICNEIEEVSRQAPKF 478
TTTGPTIYHGIIETARLLQVFTKIYELDKTVTAEKSPICAKKCLMICNEIEEVSRQAPKF  Sbjct:
419 TTTGPTIYHGIIETARLLQVFTKIYELDKTVTAEKSPICAKKCLMICNEIEEVSRQAPKF 478
Query:    479
LQMDISTTALTNLLKEHPWLSFTRFELKWKQLSLIIYVLRDFFTNFTQKKSQLEQD 534
LQMDISTTALTNLLKEHPWLSFTRFELKWKQLSLIIYVLRDFFTNFTQKKSQLEQD  Sbjct:
479 LQMDISTTALTNLLKEHPWLSFTRFELKWKQLSLIIYVLRDFFTNFTQKKSQLEQD 534
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>**PDA044Z4** (Closest domain: GAL4_YEAST 541-643) Number of domains in family: 72 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING ZINC NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FACTOR Length = 103
Score = 545 (214.5 bits), Expect = 1e-62 Identities = 103/103 (100%), Positives = 103/103 (100%)

Query: 541
YEVKRCSIMLSDAAQRTVMSVSSYMDNHNVTPYFAWNCSYYLFNAVLVPIKTLLSNSKSN 600
YEVKRCSIMLSDAAQRTVMSVSSYMDNHNVTPYFAWNCSYYLFNAVLVPIKTLLSNSKSN Sbjct: 541 YEVKRCSIMLSDAAQRTVMSVSSYMDNHNVTPYFAWNCSYYLFNAVLVPIKTLLSNSKSN 600
Query: 601 AENNETAQLLQQINTVLMLLKKLATFKIQTCEKYIQVLEEVCA 643
AENNETAQLLQQINTVLMLLKKLATFKIQTCEKYIQVLEEVCA Sbjct: 601 AENNETAQLLQQINTVLMLLKKLATFKIQTCEKYIQVLEEVCA 643

>**PDC3J281** (Closest domain: GAL4_YEAST 669-810) Number of domains in family: 7 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-BINDING NUCLEUS SUBNAME: REGULATION ZINC METABOLISM GAL4 FULL=REGULATORY Length = 142
Score = 498 (196.4 bits), Expect = 1e-55 Identities = 114/142 (80%), Positives = 114/142 (80%)

Query: 669
NIVGSATIAQYPTLPEENVNNIXXXXXXXXXXXXXXXXLKSGASFSDLVKLLSNRPPSRN 728
NIVGSATIAQYPTLPEENVNNI LKSGASFSDLVKLLSNRPPSRN Sbjct: 669 NIVGSATIAQYPTLPEENVNNISVKYVSPGSVGPSPVPLKSGASFSDLVKLLSNRPPSRN 728
Query: 729
SPVTIPRSTPSHRSVTPFLGQQQQLQSLVPLTPSALFGGANFNQSGNIADXXXXXXXXXX 788
SPVTIPRSTPSHRSVTPFLGQQQQLQSLVPLTPSALFGGANFNQSGNIAD Sbjct: 729 SPVTIPRSTPSHRSVTPFLGQQQQLQSLVPLTPSALFGGANFNQSGNIADSSLSFTFTNS 788
Query: 789 XXGPNLITTQTNSQALSQPIAS 810
GPNLITTQTNSQALSQPIAS Sbjct: 789 SNGPNLITTQTNSQALSQPIAS 810

>**PDB087H7** (Closest domain: G2WNT8_YEASK 158-225) Number of domains in family: 27 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING DNA-BINDING ZINC NUCLEUS REGULATION FULL=PUTATIVE UNCHARACTERIZED FULL=C6
Length = 68 Score = 373 (148.3 bits), Expect = 4e-39 Identities = 68/68 (100%), Positives = 68/68 (100%)

Query: 158
TIPLDFMPRDALHGFDWSEEDDMSDGLPFLKTDPNNNGFFGDGSLLCILRSIGFKPENYT 217
TIPLDFMPRDALHGFDWSEEDDMSDGLPFLKTDPNNNGFFGDGSLLCILRSIGFKPENYT Sbjct: 158 TIPLDFMPRDALHGFDWSEEDDMSDGLPFLKTDPNNNGFFGDGSLLCILRSIGFKPENYT 217
Query: 218 NSNVNRLP 225
NSNVNRLP Sbjct: 218 NSNVNRLP 225

>**PDA0B366** (Closest domain: GAL4_YEAST 818-880) Number of domains in family: 13 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-BINDING NUCLEUS SUBNAME: REGULATION ZINC FULL=PUTATIVE UNCHARACTERIZED METABOLISM Length = 63 Score = 339 (135.2 bits), Expect = 1e-34 Identities = 63/63 (100%), Positives = 63/63 (100%)

Query: 818
MNNEITASKIDDGNNSKPLSPGWTDQTAYNAFGITTGMFNTTTMDDVYNYLFDDEDTPPN 877
MNNEITASKIDDGNNSKPLSPGWTDQTAYNAFGITTGMFNTTTMDDVYNYLFDDEDTPPN Sbjct: 818 MNNEITASKIDDGNNSKPLSPGWTDQTAYNAFGITTGMFNTTTMDDVYNYLFDDEDTPPN 877
Query: 878 PKK 880
PKK Sbjct: 878 PKK 880

>**PDC683Q8** (Closest domain: GAL4_YEAST 244-303) Number of domains in family: 73 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING ZINC NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FACTOR Length = 60
Score = 333 (132.9 bits), Expect = 8e-34 Identities = 60/60 (100%), Positives = 60/60 (100%)

Query: 244
LQSYLNNFHPYCPIVHSPTLMMLYNNQIEIASKDQWQILFNCILAIGAWCIEGESTDIDV 303
LQSYLNNFHPYCPIVHSPTLMMLYNNQIEIASKDQWQILFNCILAIGAWCIEGESTDIDV Sbjct: 244 LQSYLNNFHPYCPIVHSPTLMMLYNNQIEIASKDQWQILFNCILAIGAWCIEGESTDIDV 303

>**PDA98416** (Closest domain: GAL4_YEAST 351-415) Number of domains in family: 283 Commentary (automatic): TRANSCRIPTION SUBNAME: ZINC METAL-BINDING NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FACTOR Length = 65 Score = 332 (132.5 bits), Expect = 1e-33 Identities = 65/65 (100%), Positives = 65/65 (100%)

Query: 351
FSIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLSQNTISFP 410

FSIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLSQNTISFP Sbjct: 351 FSIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLSQNTISFP 410
Query: 411 SSVDD 415 SSVDD Sbjct: 411 SSVDD 415

>**PD398432** (Closest domain: GAL4_YEAST 49-99) Number of domains in family: 21 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING DNA-BINDING ZINC NUCLEUS REGULATION FULL=PUTATIVE UNCHARACTERIZED METABOLISM Length = 51 Score = 256 (103.2 bits), Expect = 2e-23 Identities = 51/51 (100%), Positives = 51/51 (100%)

Query: 49 LTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQ 99
LTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQ Sbjct: 49 LTRAHLTEVESRLERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQ 99

>**PDB9K6A9** (Closest domain: GAL4_YEAST 304-348) Number of domains in family: 67 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING ZINC NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FACTOR Length = 45 Score = 237 (95.9 bits), Expect = 7e-21 Identities = 45/45 (100%), Positives = 45/45 (100%), Gaps = 6/45 (13%)

Query: 304 FYYQNAKSHLTSKVFESGSIILVTALHLLSRYTQWRQKTNTSYNF 348
FYYQNAKSHLTSKVFESGSIILVTALHLLSRYTQWRQKTNTSYNF Sbjct: 304 FYYQNAKSHLTSKVFESGSIILVTALHLLSRYTQWRQKTNTSYNF 348

>**PDB0G2D8** (Closest domain: D3XDC8_SACKU 352-399) Number of domains in family: 3 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING DNA-BINDING REGULATION ZINC NUCLEUS FULL=GAL4P FULL=ZYRO0E08272P FULL=PREDICTED Length = 48 Score = 191 (78.2 bits), Expect = 1e-14 Identities = 34/48 (70%), Positives = 43/48 (89%), Gaps = 4/48 (8%)

Query: 352 SIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRS 399
S+RMA+SLGLN++L SF+D +ILEQRRRIWWS+Y+WE L+LLYGRS Sbjct: 352 SMRMALSLGLNKNLHPSFNDKNILEQRRRIWWSLYTWEFHLALLYGRS 399

>**PDA2S4D4** (Closest domain: G2WNT8_YEASK 101-146) Number of domains in family: 4 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-BINDING NUCLEUS SUBNAME: REGULATION ZINC METABOLISM GAL4 FULL=REGULATORY Length = 46 Score = 182 (74.7 bits), Expect = 2e-13 Identities = 39/46 (84%), Positives = 39/46 (84%), Gaps = 1/46 (2%)

Query: 101 NVNKDAVTDRLASVETDMPLTLRQHRISATXXXXXXXNKGQRQLTV 146
NVNKDAVTDRLASVETDMPLTLRQHRISAT NKGQRQLTV Sbjct: 101 NVNKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTV 146

>**PDC1H611** (Closest domain: D3XDC8_SACKU 41-83) Number of domains in family: 14 Commentary (automatic): SUBNAME: TRANSCRIPTION METAL-BINDING ZINC FULL=PUTATIVE NUCLEUS UNCHARACTERIZED DNA-BINDING REGULATION SPECIFIC Length = 43 Score = 175 (72.0 bits), Expect = 2e-12 Identities = 35/43 (81%), Positives = 38/43 (88%), Gaps = 1/43 (2%)

Query: 41 SPKTKRSPLTRAHLTEVESRLERLEQLFLLIFPREDLDMILKM 83
SPK RSPLTRAHLTEVESRLE+LE LFLL+FPRE+LD IL M Sbjct: 41 SPKAMRSPLTRAHLTEVESRLEKLEDLFLLMFPRENLDSILNM 83

>**PDA2T7D8** (Closest domain: G8YMR4_MILFA 14-74) Number of domains in family: 214 Commentary (automatic): TRANSCRIPTION SUBNAME: ZINC METAL-BINDING NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FULL=C6 Length = 61 Score = 129 (54.3 bits), Expect = 3e-06 Identities = 22/36 (61%), Positives = 29/36 (80%), Gaps = 7/36 (19%)

Query: 33 KNNWECRYSPKTKRSPLTRAHLTEVESRLERLEQLF 68
++NW+C YSP+T RSPLTR HLT+VE R+ LE+L Sbjct: 38 EHNWKCVYSPRTIRSPLTRTHLTKVEGRVSSLERLL 73

>**PDD6J756** (Closest domain: D3XDC8_SACKU 84-158) Number of domains in family: 1 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-BINDING SUBNAME: REGULATION ZINC FULL=GAL4P NUCLEUS Length = 75 Score = 122 (51.6 bits), Expect = 3e-05 Identities = 29/75 (38%), Positives = 42/75 (56%), Gaps = 4/75 (5%)

Query: 84
DSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHRISATXXXXXXXNKGQRQ 143
DSL ++K +L L++QD + DA D L +E M R+H +AT + Q Q Sbjct: 84 DSLDEVKVMLKQLYMQDYGDTDAAMDSLTPMENGMSEGPRKHMKTATSSPKVDEDGSQSQ 143
Query: 144 LTVSIDSAAHHDNST 158 L+VS+DS A D+ST
Sbjct: 144 LSVSLDSVAQLDDST 158

>**PDA000V1** (Closest domain: B0XYW3_ASPFC 62-120) Number of domains in family: 44 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING NUCLEUS ZINC

DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED REFERENCE Length = 59 Score = 120 (50.8 bits), Expect = 4e-05 Identities = 31/59 (52%), Positives = 42/59 (71%), Gaps = 1/59 (1%)

Query: 305 YYQNAKSHLTS-
KVFESGSIILVTALHLLSRYTQWRQKTNTSYNFHSFSIRMAISLGLN 362
+YQ A+SHL VFE+G++ L+ AL LLS Y Q R K NT +NF ++RMA+SLGL+ Sbjct:
62 FYQEARSHLQQVSVFETGNLTLILALLLLSNYAQKRNKPNTGWNFLGLAVRMAMSLGLH 120

>**PDA1P8G1** (Closest domain: GAL4_YEAST 8-48) Number of domains in family: 1072 Commentary (automatic): TRANSCRIPTION SUBNAME: ZINC METAL-BINDING NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FULL=C6 Length = 41 Score = 119 (50.4 bits), Expect = 5e-05 Identities = 23/41 (56%), Positives = 23/41 (56%), Gaps = 1/41 (2%)

Query: 8 EQACDIXXXXXXXXXXXXXXXXXLKNNWECRYSPKTKRSP 48
EQACDI LKNNWECRYSPKTKRSP Sbjct: 8
EQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSP 48

>**PD024698** (Closest domain: B0XMF9_ASPFC 315-384) Number of domains in family: 362 Commentary (automatic): TRANSCRIPTION SUBNAME: ZINC METAL-BINDING NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED FACTOR Length = 70 Score = 118 (50.1 bits), Expect = 7e-05 Identities = 24/69 (34%), Positives = 37/69 (53%), Gaps = 4/69 (5%)

Query: 326
VTALHLLSRYTQWRQKTNTSYNFHSFSIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSV 385
V A LL YT + +Y ++ +I MAI G++R D+ +E R R+WWS Sbjct:
316 VQAFLLLGVYTLPIDTSGLAYTYYGLAINMAIQNGMHRRFAGDGLDARTIEVRNRLWWSA 375
Query: 386 YSWEIQLSL 394 YS E ++S+ Sbjct: 376
YSLEKRISI 384

>**PDC7F6U6** (Closest domain: G0WFT2_NAUDC 360-420) Number of domains in family: 9 Commentary (automatic): TRANSCRIPTION METAL-BINDING DNA-BINDING SUBNAME: REGULATION ZINC NUCLEUS FULL=PUTATIVE UNCHARACTERIZED ACTIVATOR Length = 61 Score = 114 (48.5 bits), Expect = 0.0002 Identities = 28/60 (46%), Positives = 40/60 (66%), Gaps = 8/60 (13%)

Query: 352 SIRMAISLGLNRDLPSS--------
FSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLS 403 SI+MAIS+GL
++LP S S+I+EQRRRIWW + + + QLS+L+ R Q+S Sbjct: 361
SIKMAISIGLFKELPEKSIPSSSSSSSSNIVEQRRRIWWCLSNHDFQLSILFDRPSQIS 420

>**PDC596Z5** (Closest domain: B6QLK2_PENMQ 356-457) Number of domains in family: 11 Commentary (automatic): TRANSCRIPTION SUBNAME: ZINC METAL-BINDING DNA-BINDING REGULATION NUCLEUS FACTOR FULL=C6 SPECIFIC Length = 102 Score = 110 (47.0 bits), Expect = 0.001 Identities = 22/61 (36%), Positives = 36/61 (59%), Gaps = 1/61 (1%)

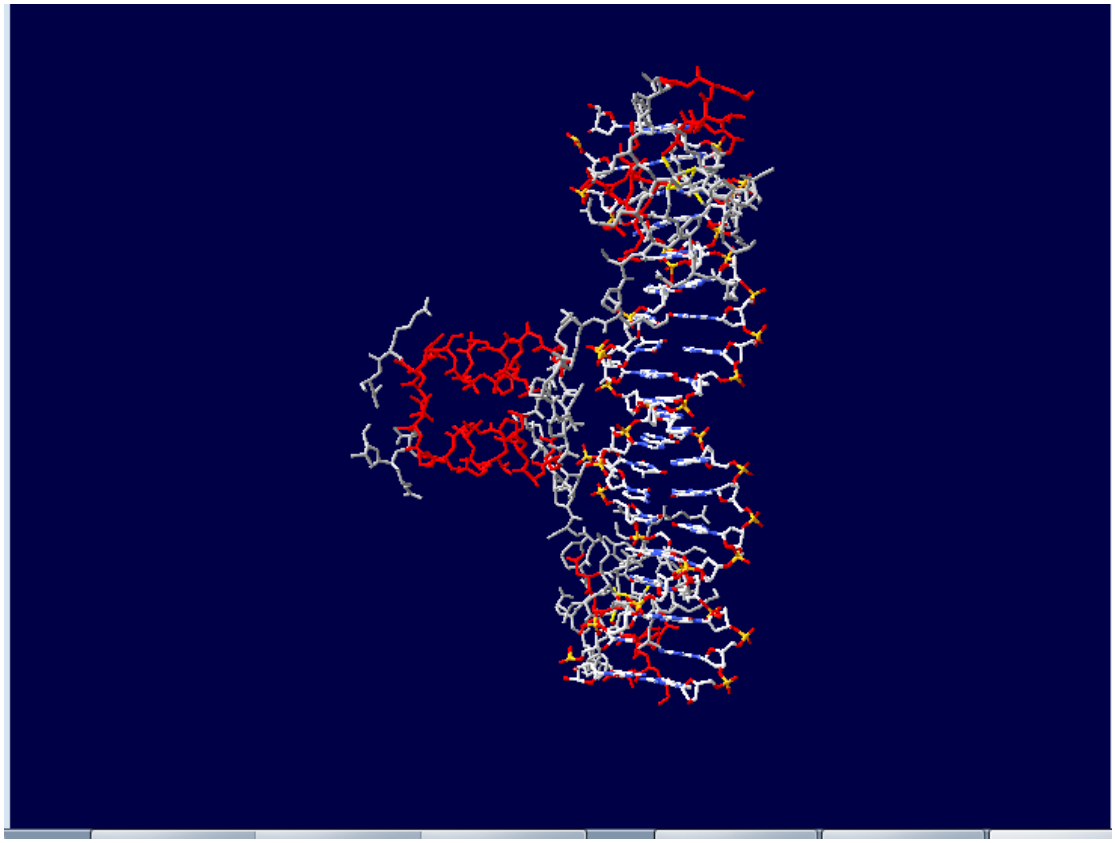
Query: 350
SFSIRMAISLGLNRDLPSSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRSIQLSQNTISF 409
+ ++R LGL+ P SD E R+R+WW+VY+ EI+++L GR + L+ + I Sbjct:
362 AMAVRTGTILGLHWHPPGKVSDQQA-EFRKRLWWTVYALEIKMTLELGRPLALTMSQIPC 420
Query: 410 P 410 P Sbjct: 421 P 421

>**PDB0D1A0** (Closest domain: C5P202_COCP7 305-372) Number of domains in family: 57 Commentary (automatic): TRANSCRIPTION SUBNAME: METAL-BINDING ZINC NUCLEUS DNA-BINDING REGULATION FULL=PUTATIVE UNCHARACTERIZED REFERENCE Length = 68 Score = 109 (46.6 bits), Expect = 0.001 Identities = 25/67 (37%), Positives = 43/67 (64%), Gaps = 6/67 (8%)

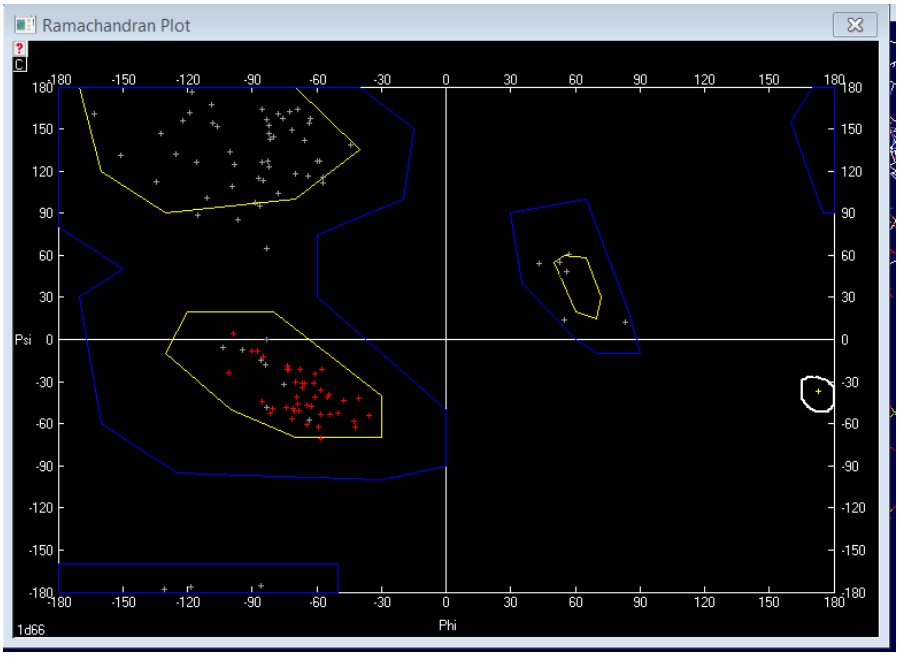
Query: 352 SIRMAISLGLNRDLP-SSFSDSSILEQRRRIWWSVYSWEIQLSLLYGRS--
IQLSQNTIS 408 ++R A +LGL+RD+P ++ D+ E RRRIWW +++ +I
S+ GR+ I S + + Sbjct: 305 AVRNAQALGLDRDVPGKNYIDT---
ELRRRIWWELFNCDIFQSMCLGRAPLISTSPSKVP 361 Query: 409 FPSSVDD 415
FP+ +D Sbjct: 362 FPAHCND 368

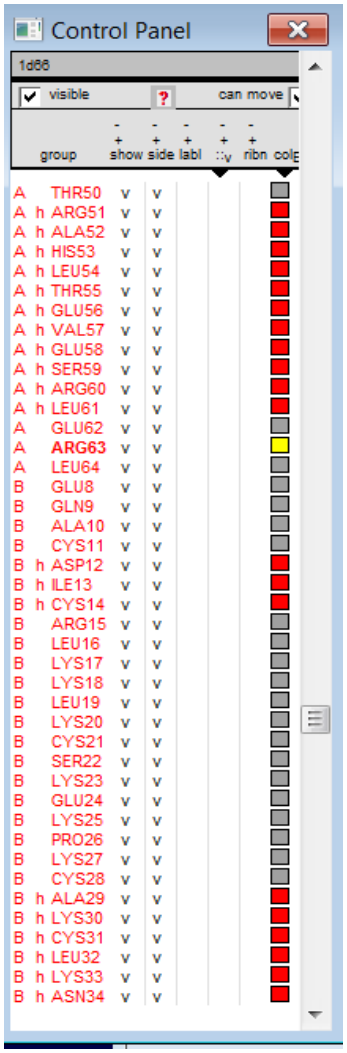
1D66

Render by 3D, Colored by Secondary Structure



Ramachandran Plot





Το διάγραμμα Ramachandram Plot περιγράφει τις δυνατές διαμορφώσεις που μπορεί να λάβει μια πολυπεπτιδική αλυσίδα κατά την αναδίπλωσή της. Οι διαμορφώσεις αυτές εκφράζονται μέσω των γωνιών φ και ψ, οι επιτρεπτές τιμές των οποίων φαίνονται στο διάγραμμα ως συνάρτηση της γωνίας ψ ως προς φ. Θεωρητικά, οι γωνίες μπορούν να έχουν οποιαδήποτε τιμή μεταξύ των -180 και +180 μοιρών, ωστόσο μερικές απορρίπτονται εξαιτίας της στερεοχημικής παρεμπόδισης που προκύπτει ανάμεσα στα κατάλοιπα της αλυσίδας. Συγκεκριμένα, επιτρεπτές θεωρούνται οι δομές όπου απουσιάζουν πλήρως οι στερεοειδικές παρεμβολές, ενώ λιγότερο επιτρεπτές οι δομές όπου παρατηρείται μικρή ευκαμψία των δεσμών.

Σημειώνεται, πως η δευτεροταγής δομή μιας πρωτεΐνης μπορεί να περιγραφεί πλήρως από τις γωνίες φ και ψ, και το διάγραμμα καθενός αμινοξέως φανερώνει τη διαμόρφωση στην οποία σταθεροποιείται ευνοϊκότερα, λαμβάνοντας υπόψιν το φορτίο και το μέγεθός του. Χαρακτηριστικά, πάνω αριστερά φαίνονται οι διαμορφώσεις με β-πτυχωτές επιφάνειες, ενώ κάτω δεξιά η α-έλικα. Τέλος, αναφέρεται πως η γλυκίνη, είναι το μόνο αμινοξύ το οποίο είναι επιτρεπτό και εκτός των ορίων, καθώς η μικρή και εύκαμπτη πλευρική αλυσίδα δεν εισάγει στερεοχημική ή άλλου είδους παρεμπόδιση.

Όσον αφορά την πρωτεΐνη 1D66, φαίνεται από το διάγραμμα πως ένα κατάλοιπο αργινίνης, το ARG63 χρωματισμένο με κίτρινο χρώμα, είναι εκτός των επιτρεπτών ορίων (δεξιά περίπου στη μέση).