ScanProsite Results Viewer

Ouput format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [help].

show profile 'low score' hits

Hits for all PROSITE (release 20.103) motifs on sequences gi-340617012-ref-YP_004735465-1--13-288, gi-340618576-ref-YP_004737029-1--1-

found: 5 hits in 5 sequences

GI-537742208-EMB-CDF79851-1--1-278 (278 aa)

```
MKKISIFIFLIYNVAFSQLPEISDGKEWVLVENLSDEFEGNNLDTSKWQSEPVGNDWNWDGRPPGL
FKSENVTLKDGKLNVTVGKLEQPVNSKGKTFIYQGGIVRSLFPGKVGCYFEAKMKANQTVMSSTFW
LMTKYDCEKKQELDIQECVGRITDKTEDWAKEWDQIFHSNAIHRTTTCNPESKRVQKQIRPNTKNH
EAFYVYGAWWKSPTEILFYLDGKYAYTLNPTIEWDMPAFIQMAIETYDWNPVPEDGGLVVHGTWEQ
RTTQYEWVRTWEIE
```

gi-340619340-ref-YP_004737793-1--71-353 (283 aa)

```
DDKKWIKVEGVSDEFNDSELDLTKWSPTPEFIWNGQDRGWYGGSRSLFEADNVSVGNGFLRIEGEK
FDSPKYSPKDNTDTPPQRRYGGAYVYGKTLAEPGYYIEARMRASKTAMSAAFWLKTETKPCGENLN
DGENLEIDIQECVGVFTGELGDEWTKDDWAVNANWDRIFHYNTHRHNSPCNNIGDRQTKGGKANFD
KKNSDEFHIYAAYWHADGSKIDFYIDGELEKSITPVIPFKGALRLIMSSNFYDWIEETSAEDMGFN
RPLEDRYTQFDWVRVWQLE
```

gi-340619604-ref-YP_004738057-1--15-274 (260 aa)

```
AAYGQTPPPPEGFRWVKNESFSDEFDGEVLDTTKWYARSPYWVNGRPPATFRAGSVSVKEGKLQIK
NSVLDGDKKYNIAGGAVASVAKDALYGYYEARMKASSISMSSTFWMKNKPDTKECPFEVQELDIVE
VVGQQKTGWDFRTNLKSNTHIFYTDCDGEKTVKSAGGTEAKIDPPADEAYHVYGCWWVDANTIKIY
LDGEYQFTMNPSTHFRDTPFNKPMYMHMVTETYNWETPPTPEELADDTKNTTYYDWVRSYTL
```

gi-340618576-ref-YP_004737029-1--1-224 (224 aa)

```
MKKVLLFLIFLVSANLSAQLPSPTNGKKWEKVEQLSDEFNGNSIDTNKWYDYHPFWEGRAPSNFKK
GNAFVSDGFLNLRSTLRKEPSSVQDPFKDIWVDAAAAVSKTKAQPGYYYEARFKASSLSMTSSFWF
RVGQFSEIDVIEHIGNPSKENRQDDLPYQYHVNTHYYGKHAGLQPLGTEYKMPGRGRDNFYTYGFW
WKSPNELLFYFNGKQVMRIVPRVPLD
```

gi-340619592-ref-YP_004738045-1--38-305 (268 aa)

```
PKPPMGKRWVLNPDFSDEFNGTELDTTKWLDHHPTWIGRAPGLFMSSQVSVGDGFLKMEGKKLEKD
TIVHAYGKDITFNIAGAAVVSKKATKFGYYECRVKAAATTMSTTFWFSSSNNFKGPKDCDRYGLEW
DIHESIGREGDFNGSYFASGMHSNAHFWYTDCNGKKYDHRAPQVKFEDAKLTSEDFNVYGGWWRDE
STASYYYNNRPPKHQKFYDKVKKKPFDQPMYMRLVNETYPFPWIELPNAEELSDPSKNTVYYDWVR
AYRL
```

Legend:

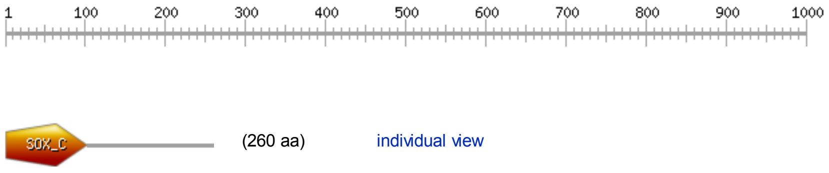
⊓	♦	—	♦
disulfide bridge	active site	other 'ranges'	other sites

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to http://prosite.expasy.org/mydomains/.

hits by profiles: [2 hits (by 2 distinct profiles) on 2 sequences]

Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.

ruler:



gi-340619604-ref-YP_004738057-1--15-274 (gi-340619604- ref-YP_004738 057-1--15-274)

(260 aa) individual view

PS51516 **SOX_C** *Sox C-terminal domain profile* :

1 - 101: **score** = 6.715 [warning: hit with a low confidence level (-1)]

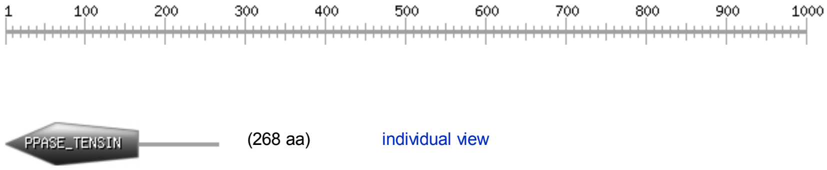
```
--------------------------------AAYGQTPPPPEGFRWVKNESFSDefDGE
VLDTTKWYARSPYWVNGRPPATFRAGSVSVKEGKLQiknsvldGDKKYNIAGGAVASVAK
DALYGYYEARMKA
```

Predicted feature:

DOMAIN	1	101	Sox C-terminal	[condition: none]

ruler:

gi-340619592-ref-YP_004738045-1--38-305 (gi-340619592- ref-YP_004738 045-1--38-305)



(268 aa) individual view

PS51181 **PPASE_TENSIN** *Phosphatase tensin-type domain profile* :

1 - 166: **score =** 4.729 [warning: hit with a low confidence level (-1)]

```
------------------------------------------------PKPpmGKRWVL-
-NPDFSDE--FNGTELDtTKWLDHHPTwigraPGLFMSSQVSVGDGFLKMegkklekdti
vhaygkditfNIAGAAVVSKKATKfgyyeCRvkaaATTMSTTFWFSSSNnFKGPKDCDRY
GlewdiheSIGREGDF--NGSYFASGMHSNAHFWYTDCNG
```

Predicted feature:

DOMAIN	1	166	Phosphatase tensin-type	[condition: none]

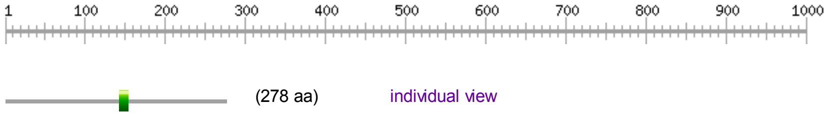
Absent feature:

ACT_SITE	88		Phosphocysteine intermediate (Potential)	[condition not true: C]

hits by patterns: [3 hits (by 2 distinct patterns) on 3 sequences]

ruler:

GI-537742208-EMB-CDF79851-1--1-278



(278 aa) individual view

PS01034 **GLYCOSYL_HYDROL_F16** *Glycosyl hydrolases family 16 active sites* :

144 - 155: [confidence level: (-1)] `ELDIqEcvGRiT`

Predicted features:

ACT_SITE	144	Nucleophile (By similarity)	[condition: none]
ACT_SITE	149	Proton donor (By similarity)	[condition: none]

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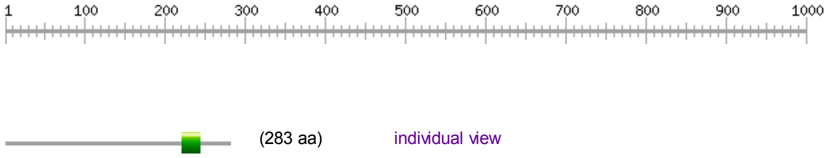
ruler:

gi-340619340-ref-YP_004737793-1--71-353 (gi-340619340- ref-YP_004737 793-1--71-353)



(283 aa) individual view

PS00260 **GLUCAGON** *Glucagon / GIP / secretin / VIP family signature* :

222 - 244: [confidence level: (-1)] `YIDGELeKSItpvipfkgALRLI`

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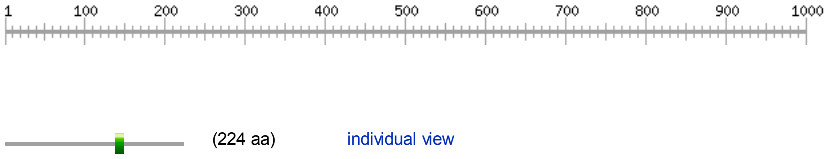
ruler:

gi-340618576-ref-YP_004737029-1--1-224 (gi-340618576- ref-YP_004737 029-1--1-224)



(224 aa) individual view

PS01034 **GLYCOSYL_HYDROL_F16** *Glycosyl hydrolases family 16 active sites* :

139 - 150: [confidence level: (-1)] `EIDViEhiGNpS`

Predicted features:

ACT_SITE	139	Nucleophile (By similarity)	[condition: none]
ACT_SITE	144	Proton donor (By similarity)	[condition: none]

horizontal scaling: 0.6

do not show text labels: ☐

do not show sites in hits: ☐
do not show ranges in hits: ☐
redisplay
