



Motif Scan Results

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user: GUEST width: 600
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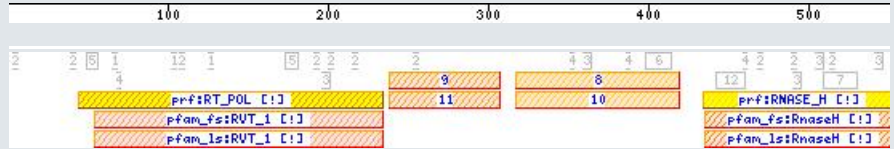
- Tools
- Hub
- Results**
- Stored results
- Private area
- Misc
- Deprecated

Query Protein temporarily stored [here](#).
 Database of motifs HAMAP profiles [hamap], PROSITE patterns [pat], More profiles [pre], Pfam HMMs (local models) [pfam_fs], Pfam HMMs (global models) [pfam_ls], PROSITE patterns (frequent match producers) [freq_pat], PROSITE profiles [prf].

- searching HAMAP profiles
- searching PROSITE patterns
- searching PROSITE patterns (frequent match producers)
- searching More profiles
- searching PROSITE profiles
- searching Pfam HMMs (local models)
- searching Pfam HMMs (global models)
- postprocessing

Summary

Original output [hamap](#), [pat](#), [freq_pat](#), [pre](#), [prf](#), [pfam_fs](#), [pfam_ls](#).



Matches map (features from query are above the ruler, matches of the motif scan are below the ruler)

Legends: 1, freq_pat:CAMP_PHOSPHO_SITE [?]; 2, freq_pat:CK2_PHOSPHO_SITE [?]; 3, freq_pat:MYRISTYL [?]; 4, freq_pat:PKC_PHOSPHO_SITE [?]; 5, freq_pat:TYR_PHOSPHO_SITE [?]; 6, prf:TRP_RICH [?]; 7, pfam_fs:G-alpha [?]; 8, pfam_fs:RVT_connect [!]; 9, pfam_fs:RVT_thumb [!]; 10, pfam_ls:RVT_connect [!]; 11, pfam_ls:RVT_thumb [!]; 12, pfam_ls:RtxA [?].

FT	MYHIT	65	68	freq_pat:CAMP_PHOSPHO_SITE [?]
FT	MYHIT	102	105	freq_pat:CAMP_PHOSPHO_SITE [?]
FT	MYHIT	125	128	freq_pat:CAMP_PHOSPHO_SITE [?]
FT	MYHIT	3	6	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	39	42	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	107	110	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	191	194	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	200	203	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	215	218	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	253	256	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	468	471	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	489	492	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	513	516	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	196	201	freq_pat:MYRISTYL [?]
FT	MYHIT	359	364	freq_pat:MYRISTYL [?]
FT	MYHIT	490	495	freq_pat:MYRISTYL [?]
FT	MYHIT	504	509	freq_pat:MYRISTYL [?]
FT	MYHIT	541	546	freq_pat:MYRISTYL [?]
FT	MYHIT	68	70	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	351	353	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	386	388	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	459	461	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	49	56	freq_pat:TYR_PHOSPHO_SITE [?]
FT	MYHIT	173	181	freq_pat:TYR_PHOSPHO_SITE [?]
FT	MYHIT	434	557	prf:RNASE_H [!]
FT	MYHIT	44	234	prf:RT_POL [!]
FT	MYHIT	398	414	prf:TRP_RICH [?]
FT	MYHIT	509	530	pfam_fs:G-alpha [?]
FT	MYHIT	54	234	pfam_fs:RVT_1 [!]
FT	MYHIT	317	419	pfam_fs:RVT_connect [!]
FT	MYHIT	238	307	pfam_fs:RVT_thumb [!]
FT	MYHIT	435	557	pfam_fs:RnaseH [!]
FT	MYHIT	54	234	pfam_ls:RVT_1 [!]
FT	MYHIT	317	419	pfam_ls:RVT_connect [!]
FT	MYHIT	238	307	pfam_ls:RVT_thumb [!]
FT	MYHIT	435	557	pfam_ls:RnaseH [!]
FT	MYHIT	442	460	pfam_ls:RtxA [?]

List of matches

Detail of matches

match detail	match score	motif information
1 KK T RRXS :: KKDS	Status: ? pos.: 65-68	freq_pat: CAMP_PHOSPHO_SITE CAMP- and cGMP-dependent protein
1 KK T RRXS	Status: ?	

RKYT

pos.: 125-128

site.

[[entry](#)]Legends: 1, phosphorylation.

[^ image ^](#)

<pre> 1 T E SXXD : : SPIE </pre>	<p>Status: ? pos.: 3-6</p>	
<pre> 1 T E SXXD : : TEME </pre>	<p>Status: ? pos.: 39-42</p>	
<pre> 1 T E SXXD : : TVLD </pre>	<p>Status: ? pos.: 107-110</p>	
<pre> 1 T E SXXD : : SDLE </pre>	<p>Status: ? pos.: 191-194</p>	
<pre> 1 T E SXXD : : TKIE </pre>	<p>Status: ? pos.: 200-203</p>	<p>freq_pat:CK2_ PHOSPHO_SITE Casein kinase II phosphorylation site. [entry]Legends: 1, phosphorylation.</p>
<pre> 1 T E SXXD : : TTPD </pre>	<p>Status: ? pos.: 215-218</p>	
<pre> 1 T E SXXD : : TVND </pre>	<p>Status: ? pos.: 253-256</p>	
<pre> 1 T E SXXD : : TLTD </pre>	<p>Status: ? pos.: 468-471</p>	
<pre> 1 T E SXXD : : SGLE </pre>	<p>Status: ? pos.: 489-492</p>	
<pre> 1 T E SXXD : : SESE </pre>	<p>Status: ? pos.: 513-516</p>	

[^ image ^](#)

<pre> 1 Y W V T S R R R O N M L K I H V T S Q N M L I G C GAXXSA I: :: GQHRTK </pre>	<p>Status: ? pos.: 196-201</p>	
<pre> 1 Y W V T S R R R O N M L K I H V T S Q N M L I G C GAXXSA I: :: GAHTND </pre>	<p>Status: ? pos.: 359-364</p>	
<pre> 1 Y W V T S R R R O N M L K I H V T S Q N M L I G C GAXXSA I: :: </pre>	<p>Status: ? pos.: 490-495</p>	<p>freq_pat:MYRISTYL N-myristoylation site. [entry]Legends: 1, myristyl.</p>

V T S Q N M L I G C
 N M L K I H N G C F E A D T C
 G A X X S A
 I : : :
 G I I Q A Q

Status: ?
 pos.: 504-509

Y W V T S R Q N M L K I H N G C F E A D T C
 V T S Q N M L I G C
 G A X X S A
 I : : :
 G I G G N E

Status: ?
 pos.: 541-546

[^ image ^](#)

T K
 S X R
 : : :
 S T K

Status: ?
 pos.: 68-70

T K
 S X R
 : : :
 T G K

Status: ?
 pos.: 351-353

freq_pat: PKC_
 PHOSPHO_SITE
 Protein kinase C
 phosphorylation site.
[\[entry \]](#) Legends: 1,
 phosphorylation.

T K
 S X R
 : : :
 T P K

Status: ?
 pos.: 386-388

T K
 S X R
 : : :
 T N R

Status: ?
 pos.: 459-461

[^ image ^](#)

K E
 R X X D X X Y
 : : :
 K I G P E N P Y

Status: ?
 pos.: 49-56

freq_pat: TYR_
 PHOSPHO_SITE
 Tyrosine kinase
 phosphorylation site.
[\[entry \]](#) Legends: 1,
 phosphorylation.

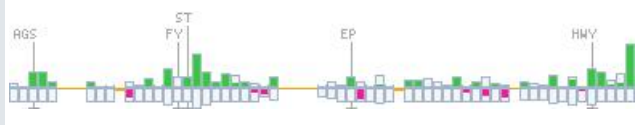
K E
 R X X D X X Y
 : : :
 K Q N P D I V I Y

Status: ?
 pos.: 173-181

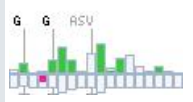
[^ image ^](#)



IVGAETFYVDGAAAnretk1gkaguwTNRG-----RQKVVTLTDTTNQKTELQAI



YLALQ---DSG-LEVNIVTDSQYALGII----QAQPQQSEELVNQIIIEQLIkKEKVVYLAWVPAH

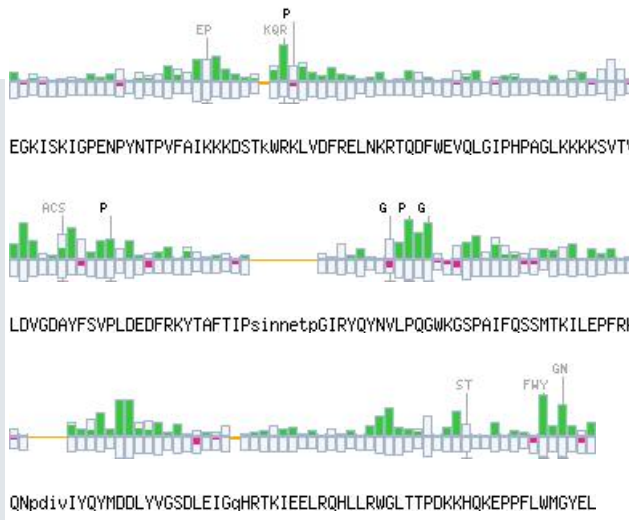


KGIGGNEQVOKLVSAGIR

Status: !
 pos.: 434-557
 raw-score = 905
 N-score = 20.069
 E-value = 1.8e-13

prf: RNASE_H
 RNase H domain
 profile.
[\[entry \]](#)
[\[graphics \]](#)

[^ image ^](#)



Status: !
 pos.: 44-234
 raw-score = 2347
 N-score = 50.161
 E-value = 1.5e-43

prf:RT_POL
 Reverse transcriptase (RT) catalytic domain profile.
[\[entry \]](#)
[\[graphics \]](#)

[^ image ^](#)



Status: ?
 pos.: 398-414
 raw-score = 37
 N-score = 7.251
 E-value = 1.2

prf:TRP_RICH
 Tryptophan-rich region profile.
[\[entry \]](#)
[\[graphics \]](#)

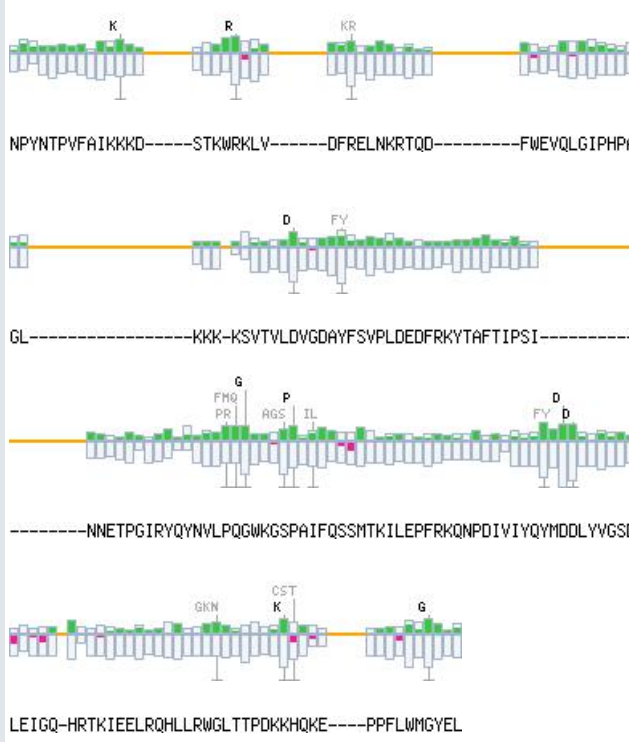
[^ image ^](#)



Status: ?
 pos.: 509-530
 raw-score = 2.1
 N-score = 8.563
 E-value = 0.058

pfam_fs:G-alpha
 G-protein alpha subunit
[\[entry \]](#)

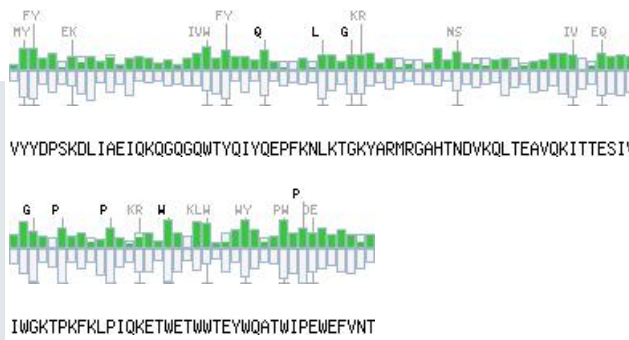
[^ image ^](#)



Status: !
 pos.: 54-234
 raw-score = 213.8
 N-score = 69.285
 E-value = 1.1e-62

pfam_fs:RVT_1
 Reverse transcriptase (RNA-dependent DNA polymerase)
[\[entry \]](#)

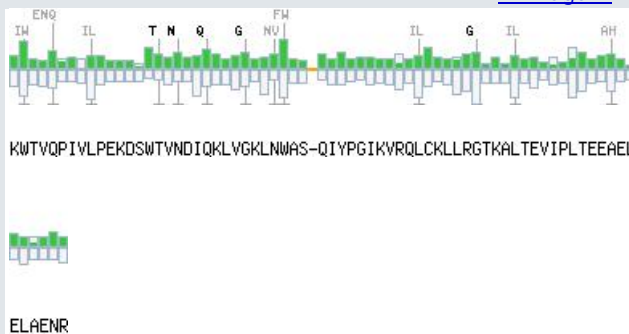
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Status: !
 pos.: 317-419
 raw-score = 252.1
 N-score = 86.326
 E-value = 1e-79

pfam_fs: RVT_connect
 Reverse transcriptase
 connection domain
[\[entry \]](#)

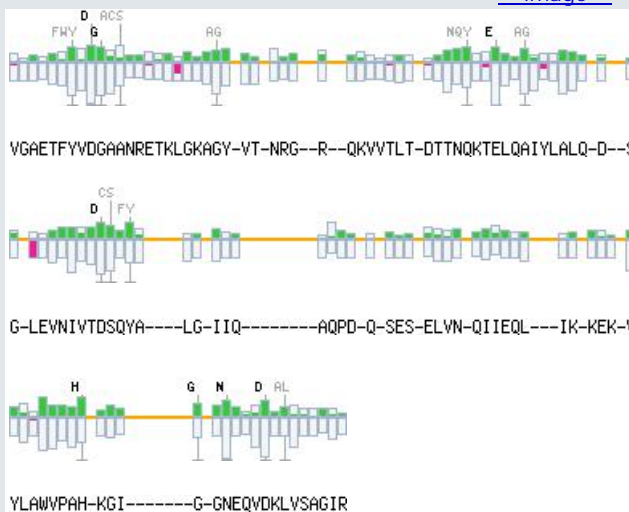
[^ image ^](#)



Status: !
 pos.: 238-307
 raw-score = 172.0
 N-score = 57.586
 E-value = 5.5e-51

pfam_fs: RVT_thumb
 Reverse transcriptase
 thumb domain
[\[entry \]](#)

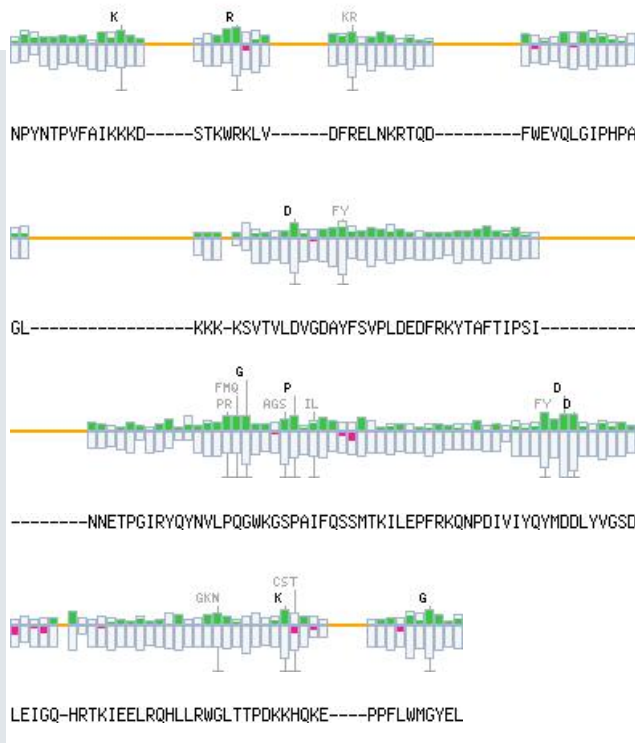
[^ image ^](#)



Status: !
 pos.: 435-557
 raw-score = 184.3
 N-score = 62.946
 E-value = 2.4e-56

pfam_fs: RnaseH
 RNase H
[\[entry \]](#)

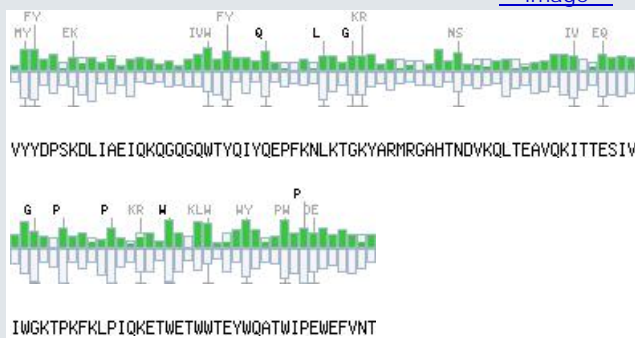
[^ image ^](#)



Status: !
 pos.: 54-234
 raw-score = 215.5
 N-score = 69.835
 E-value = 3.1e-63

pfam_Is: RVT_1
 Reverse transcriptase
 (RNA-dependent DNA
 polymerase)
[\[entry \]](#)

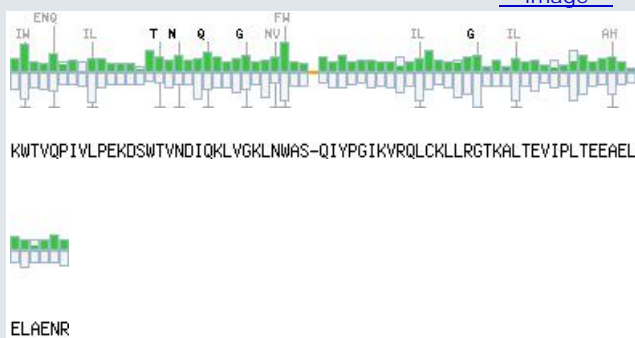
[^ image ^](#)



Status: !
 pos.: 317-419
 raw-score = 254.1
 N-score = 81.457
 E-value = 7.4e-75

pfam_Is: RVT_connect
 Reverse transcriptase
 connection domain
[\[entry \]](#)

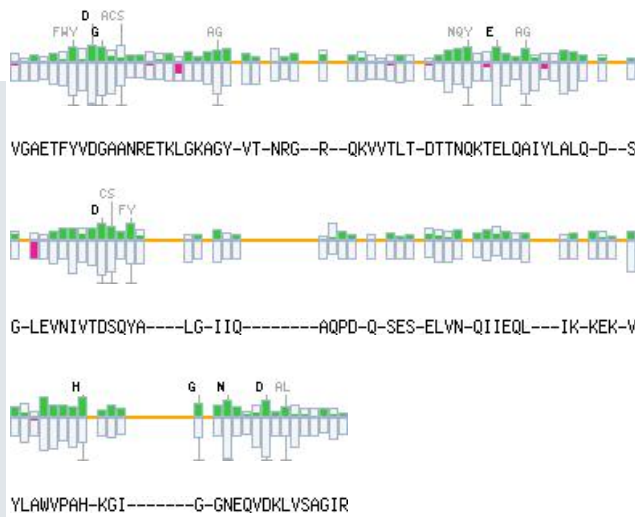
[^ image ^](#)



Status: !
 pos.: 238-307
 raw-score = 174.0
 N-score = 57.326
 E-value = 1e-50

pfam_Is: RVT_thumb
 Reverse transcriptase
 thumb domain
[\[entry \]](#)

[^ image ^](#)



Status: !
 pos.: 435-557
 raw-score = 186.0
 N-score = 60.946
 E-value = 2.4e-54

pfam_Is: RnaseH
 RNase H
[\[entry \]](#)

[^ image ^](#)



Status: ?
 pos.: 442-460
 raw-score = 5.4
 N-score = 7.602
 E-value = 0.53

pfam_Is: RtxA
 RtxA repeat
[\[entry \]](#)

[^ image ^](#)

Sigrist CJ, Cerutti L, de Castro E, Langendijk-Genevaux PS, Bulliard V, Bairoch A, Hulo N. PROSITE, a protein domain database for functional characterization and annotation. Nucleic Acids Res. 2010; 38(Database issue):D161-6. [\[RIS\]](#)