Subcellular Localization Signals of bHLH-PAS Proteins: their Significance, Current State of Knowledge and Future Perspectives

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Supplementary Materials Table 1

Predictors used for NLS prediction:

cNLS Mapper	a
NLStradamus	b
NucPred	c
PSORT II	d
SeqNLS	e
ELM	f

Predictors used for NES prediction:

ELM	f
NES Finder	g
NetNES	h
LocNES	i

hAhR

```
>sp|P35869|AHR_HUMAN Aryl hydrocarbon receptor OS=Homo sapiens OX=9606
GN=AHR PE=1 SV=2
MNSSSANITYASRKRRKPVQKTVKPIPAEGIKSNPSKRHRDRLNTELDRLASLLPFPQDV
INKLDKLSVLRLSVSYLRAKSFFDVALKSSPTERNGGQDNCRAANFREGLNLQEGEFLLQ
ALNGFVLVVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQRQLHWALNP
SQCTESGQGIEEATGLPQTVVCYNPDQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQ
GKLKYLHGQKKKGKDGSILPPQLALFAIATPLQPPSILEIRTKNFIFRTKHKLDFTPIGC
DAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLTKNNRW
TWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLRKRNTKLPFMFTTGEAVLYEATNPF
PAIMDPLPLRTKNGTSGKDSATTSTLSKDSLNPSSLLAAMMQQDESIYLYPASSTSSTAP
FENNFFNESMNECRNWQDNTAPMGNDTILKHEQIDQPQDVNSFAGGHPGLFQDSKNSDLY
SIMKNLGIDFEDIRHMQNEKFFRNDFSGEVDFRDIDLTDEILTYVQDSLSKSPFIPSDYQ
QQQSLALNSSCMVQEHLHLEQQQQHHQKQVVVEPQQQLCQKMKHMQVNGMFENWNSNQFV
PFNCPQQDPQQYNVFTDLHGISQEFPYKSEMDSMPYTQNFISCNQPVLPQHSKCTELDYP
MGSFEPSPYPTTSSLEDFVTCLQLPENQKHGLNPQSAIITPQTCYAGAVSMYQCQPEPQH
THVGQMQYNPVLPGQQAFLNKFQNGVLNETYPAELNNINNTQTTTHLQPLHHPSEARPFP
DLTSSGFL
```

cNLS Mapper Results cut-off score 2.0

Predicted NLSs in query sequence

```
MNSSSANITYASRKRRKPVQKTVKPIPAEGIKSNPSKRHRDRLNTELDRL    50
ASLLPFPQDVINKLDKLSVLRLSVSYLRAKSFFDVALKSSPTERNGGQDN   100
CRAANFREGLNLQEGEFLLQALNGFVLVVTTDALVFYASSTIQDYLGFQQ   150
SDVIHQSVYELIHTEDRAEFQRQLHWALNPSQCTESGQGIEEATGLPQTV   200
VCYNPDQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLHGQK   250
KKGKDGSILPPQLALFAIATPLQPPSILEIRTKNFIFRTKHKLDFTPIGC   300
DAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIV   350
FRLLTKNNRWTWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLRKRNT   400
KLPFMFTTGEAVLYEATNPFPAIMDPLPLRTKNGTSGKDSATTSTLSKDS   450
LNPSSLLAAMMQQDESIYLPASSTSSTAPFENNFFNESMNECRNWQDNT   500
APMGNDTILKHEQIDQPQDVNSFAGGHPGLFQDSKNSDLYSIMKNLGIDF   550
EDIRHMQNEKFFRNDFSGEVDFRDIDLTDEILTYVQDSLSKSPFIPSDYQ   600
QQQSLALNSSCMVQEHLHLEQQQQHHQKQVVVEPQQQLCQKMKHMQVNGM   650
FENWNSNQFVPFNCPQQDPQQYNVFTDLHGISQEFPYKSEMDSMPYTQNF   700
ISCNQPVLPQHSKCTELDYPMGSFEPSPYPTTSSLEDFVTCLQLPENQKH   750
GLNPQSAIITPQTCYAGAVSMYQCQPEPQHTHVGQMQYNPVLPGQQAFLN   800
KFQNGVLNETYPAELNNINNTQTTTHLQPLHHPSEARPFPDLTSSGFL     848
```

Predicted monopartite NLS

Pos.	Sequence	Score
10	YASRKRRKPV	9
11	ASRKRRKPVQ	11

Predicted bipartite NLS

Pos.	Sequence	Score
13	RKRRKPVQKTVKPIPAEGIKSNPSKRH	4.4
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRD	5.4
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDR	2.4
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDR	3.4
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDR	2
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDRL	3.7
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDR	3.2
13	RKRRKPVQKTVKPIPAEGIKSNPSKRHRDRLNTELD	2.3
34	NPSKRHRDRLNTELDRLASLLPFPQDVINK	2.9
34	NPSKRHRDRLNTELDRLASLLPFPQDVIN	4.9
37	KRHRDRLNTELDRLASLLPFPQDVINKLD	2.5
38	RHRDRLNTELDRLASLLPFPQDVINKLDKLS	2.3
63	KLDKLSVLRLSVSYLRAKSFFDVALKSSPTE	2
78	RAKSFFDVALKSSPTERNGGQDNCRAANF	3
218	RCFICRLRCLLDNSSGFLAMNFQGKLKYLHG	2
218	RCFICRLRCLLDNSSGFLAMNFQGKLKYLHGQK	2.2
239	FQGKLKYLHGQKKKGKDGSILPPQLALFAI	2.2
241	GKLKYLHGQKKKGKDGSILPPQLALFAIATP	2.1
248	GQKKKGKDGSILPPQLALFAIATPLQPPSI	2.3
250	KKKGKDGSILPPQLALFAIATPLQPPSILEI	3.1
279	EIRTKNFIFRTKHKLDFTPIGCDAKGRIVLGY	2.2
368	RLLYKNGRPDYIIVTQRPLTDEEGTEHLRKR	3.7
368	RLLYKNGRPDYIIVTQRPLTDEEGTEHLRKRNT	3.5
393	EHLRKRNTKLPFMFTTGEAVLYEATNPFPAI	3.4
396	RKRNTKLPFMFTTGEAVLYEATNPFPAIMDPLP	3
640	QKMKHMQVNGMFENWNSNQFVPFNCPQQD	2.7

643	KHMQVNGMFENWNSNQFVPFNCPQQDP	2.5
684	EFPYKSEMDSMPYTQNFISCNQPVLPQHSKCT	2.1
746	ENQKHGLNPQSAIITPQTCYAGAVSMYQCQP	2.9

NLStradamus

Cut-off 0.3 4 state static

12 - SRKRRKPVQKTVKPIPAEGIKSNPSKRHRDR - 42

247 - HGQKKKGK – 254

NucPred

The NucPred score for your sequence is 0.94 (see score help below)

```
   1   MNSSSANITYASRKRRKPVQKTVKPIPAEGIKSNPSKRHRDRLNTELDRL    50
  51   ASLLPFPQDVINKLDKLSVLRLSVSYLRAKSFFDVALKSSPTERNGGQDN   100
 101   CRAANFREGLNLQEGEFLLQALNGFVLVVTTDALVFYASSTIQDYLGFQQ   150
 151   SDVIHQSVYELIHTEDRAEFQRQLHWALNPSQCTESGQGIEEATGLPQTV   200
 201   VCYNPDQIPPENSPLMERCFICRLRCLLDNSSGFLAMNFQGKLKYLHGQK   250
 251   KKGKDGSILPPQLALFAIATPLQPPSILEIRTKNFIFRTKHKLDFTPIGC   300
 301   DAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIV   350
 351   FRLLTKNNRWTWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLRKRNT   400
 401   KLPFMFTTGEAVLYEATNPFPAIMDPLPLRTKNGTSGKDSATTSTLSKDS   450
 451   LNPSSLLAAMMQQDESIYLYPASSTSSTAPFENNFFNESMNECRNWQDNT   500
 501   APMGNDTILKHEQIDQPQDVNSFAGGHPGLFQDSKNSDLYSIMKNLGIDF   550
 551   EDIRHMQNEKFFRNDFSGEVDFRDIDLTDEILTYVQDSLSKSPFIPSDYQ   600
 601   QQQSLALNSSCMVQEHLHLEQQQQHHQKQVVVEPQQQLCQKMKHMQVNGM   650
 651   FENWNSNQFVPFNCPQQDPQQYNVFTDLHGISQEFPYKSEMDSMPYTQNF   700
 701   ISCNQPVLPQHSKCTELDYPMGSFEPSPYPTTSSLEDFVTCLQLPENQKH   750
 751   GLNPQSAIITPQTCYAGAVSMYQCQPEPQHTHVGQMQYNPVLPGQQAFLN   800
 801   KFQNGVLNETYPAELNNINNTQTTTHLQPLHHPSEARPFPDLTSSGFL     848
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

NUCDISC: discrimination of nuclear localization signals
```
      pat4: RKRR (5) at   13
      pat4: KRRK (5) at   14
      pat4: RRKP (4) at   15
      pat4: KRHR (3) at   37
      pat7: PSKRHRD (4) at   35
      bipartite: none
      content of basic residues:   8.8%
      NLS Score:  0.94
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
AhR: MNSSSANITYASRKRRKPVQKTVKPIPAEGIKSNPSKRHRDRLNTELDRLASLLPFPQDV

Definition of different colors in predictions

score range	color
0.1-0.3	■ (dark blue)
0.3-0.5	■ (blue)
0.5-0.7	■ (cyan)
0.7-0.8	■ (green)
0.8-0.86	■ (yellow)
0.86-0.89	■ (orange)
>0.89	■ (red)

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
AhR	ASRKRRKPVQKTVK	11	24	0.887
AhR	PAEGIKSNPSKRHRDRL	27	43	0.886

ELM

Motif Probability Cutoff:100

TRG_NLS_MonoCore_2   2.345e-04

SRKRRK   12-17

RKRRKP   13-18

Monopartite variant of the classical basically charged NLS. Strong core version.

TRG_NLS_MonoExtC_3   7.252e-04

SRKRRK   12-17

RKRRKP   13-18

QKKKGK   249-254

Monopartite variant of the classical basically charged NLS. C-extended version.

TRG_NLS_MonoExtN_4   1.276e-03

RKRRKP   13-18

Monopartite variant of the classical basically charged NLS. N-extended version.

TRG_NES_CRM1_1   7.626e-04

DLYSIMKNLGIDFED   538-552

NES Finder

Position	NES	Type
47	LDRLASLLPF	2-3-1
60	VINKLDKLSV	3-2-1
63	KLDKLSVLRL	2-2-1
259	LPPQLALFAI	3-2-1
420	FPAIMDPLPL	3-2-1
539	LYSIMKNLGI	3-2-1
735	LEDFVTCLQL	3-2-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES1759629158_0	46-60	RLNTELDRLASLLPF	0.394
>LocNES1759629158_0	59-73	PFPQDVINKLDKLSV	0.746
>LocNES1759629158_0	62-76	QDVINKLDKLSVLRL	0.658
>LocNES1759629158_0	64-78	VINKLDKLSVLRLSV	0.444
>LocNES1759629158_0	67-81	KLDKLSVLRLSVSYL	0.452
>LocNES1759629158_0	77-91	SVSYLRAKSFFDVAL	0.026
>LocNES1759629158_0	102-116	QDNCRAANFREGLNL	0.043
>LocNES1759629158_0	117-131	QEGEFLLQALNGFVL	0.053
>LocNES1759629158_0	118-132	EGEFLLQALNGFVLV	0.081
>LocNES1759629158_0	119-133	GEFLLQALNGFVLVV	0.055
>LocNES1759629158_0	126-140	LNGFVLVVTTDALVF	0.043
>LocNES1759629158_0	138-152	LVFYASSTIQDYLGF	0.015
>LocNES1759629158_0	236-250	SGFLAMNFQGKLKYL	0.045
>LocNES1759629158_0	258-272	KDGSILPPQLALFAI	0.138
>LocNES1759629158_0	277-291	QPPSILEIRTKNFIF	0.013
>LocNES1759629158_0	285-299	RTKNFIFRTKHKLDF	0.017
>LocNES1759629158_0	298-312	DFTPIGCDAKGRIVL	0.027
>LocNES1759629158_0	330-344	HAADMLYCAESHIRM	0.013

>LocNES1759629158_0	331-345	AADMLYCAESHIRMI	0.022
>LocNES1759629158_0	413-427	GEAVLYEATNPFPAI	0.021
>LocNES1759629158_0	417-431	LYEATNPFPAIMDPL	0.118
>LocNES1759629158_0	419-433	EATNPFPAIMDPLPL	0.083
>LocNES1759629158_0	538-552	SKNSDLYSIMKNLGI	0.070
>LocNES1759629158_0	543-557	LYSIMKNLGIDFEDI	0.043
>LocNES1759629158_0	562-576	NEKFFRNDFSGEVDF	0.005
>LocNES1759629158_0	567-581	RNDFSGEVDFRDIDL	0.020
>LocNES1759629158_0	575-589	DFRDIDLTDEILTYV	0.029
>LocNES1759629158_0	637-651	EPQQQLCQKMKHMQV	0.026
>LocNES1759629158_0	732-746	PYPTTSSLEDFVTCL	0.174
>LocNES1759629158_0	734-748	PTTSSLEDFVTCLQL	0.128

NetNES 1.1 Server prediction results

>Sequence - NetNES 1.1 prediction

NetNES 1.1: Predicted NES signals in Sequence
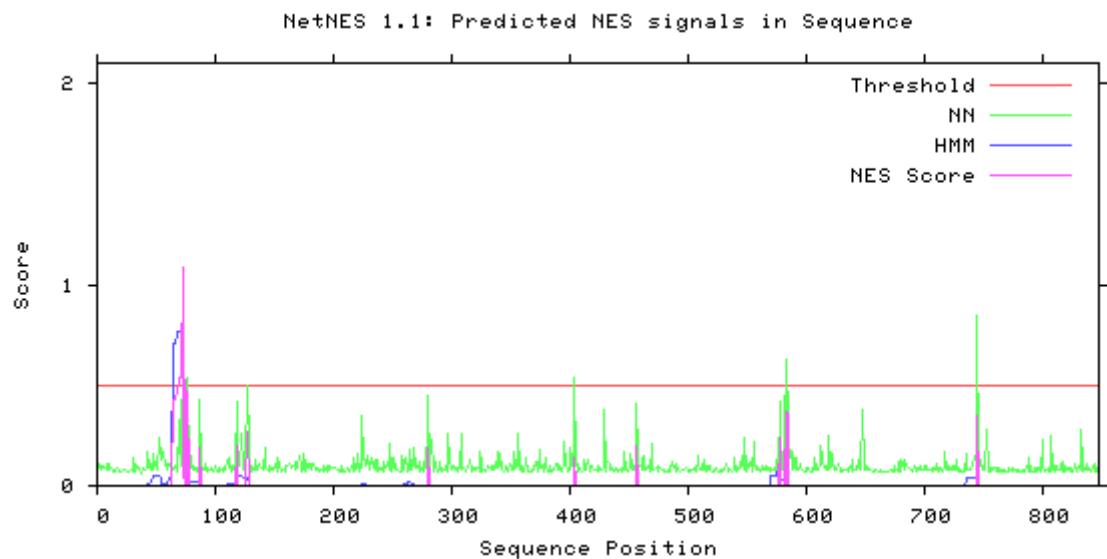
hHIF1α

>sp|Q16665|HIF1A_HUMAN Hypoxia-inducible factor 1-alpha OS=Homo sapiens
OX=9606 GN=HIF1A PE=1 SV=1
MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM

```
RLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYM
GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNTQRSFFLRMKCTLTSRGR
TMNIKSATWKVLHCTGHIHVYDTNSNQPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK
TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQV
TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSGIIQHDLIFSLQQTECV
LKPVESSDMKMTQLFTKVESEDTSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET
DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP
NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDSDMVNEFKLELVEKLF
AEDTEAKNPFSTQDTDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT
VFQQTQIQEPTANATTTTATTDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR
DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR
KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC
RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN
```

cNLS Mapper Result cut-off score 2.0

Predicted NLSs in query sequence

```
MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNV  50
SSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFV  100
MVLTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTH  150
RNGLVKKGKEQNTQRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHV  200
YDTNSNQPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDM  250
KFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQV  300
TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSGIIQHDL  350
IFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKLKKEPDALTLL  400
APAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM  450
SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDQTPS  500
PSDGSTRQSSPEPNSPSEYCFYVDSDMVNEFKLELVEKLFAEDTEAKNPF  550
STQDTDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT  600
VFQQTQIQEPTANATTTTATTDELKTVTKDRMEDIKILIASPSPTHIHKE  650
TTSATSSPYRDTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTT  700
VPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQPDDHAATTSL  750
SWKRVKGCKSSEQNGMEQKTIILIPSDLACRLLGQSMDESGLPQLTSYDC  800
EVNAPIQGSRNLLQGEELLRALDQVN                          826
```

Predicted monopartite NLS

Pos.	Sequence	Score
716	AQRKRKMEHD	8

Predicted bipartite NLS

Pos.	Sequence	Score
8	NDKKKISSERRKEKSRDAARSRRSKESEV	2.6
23	RDAARSRRSKESEVFYELAHQLPLPHNVSSHLDK	2.4
68	RVRKLLDAGDLDIEDDMKAQMNCFYLKALD	2.6
68	RVRKLLDAGDLDIEDDMKAQMNCFYLKALD	2.9
189	WKVLHCTGHIHVYDTNSNQPQCGYKKPP	2.6
211	GYKKPPMTCLVLICEPIPHPSNIEIPLDSKT	2.1

```
245   RHSLDMKFSYCDERITELMGYEPEELLGRSIYEY   2.8
285   DHLTKTHHDMFTKGQVTTGQYRMLAKRGGY       2.3
303   GQYRMLAKRGGYVWVETQATVIYNTKNSQP       2.4
306   RMLAKRGGYVWVETQATVIYNTKNSQPQCIV      2.3
365   ESSDMKMTQLFTKVESEDTSSLFDKLKKEPDA     2.7
647   IHKETTSATSSPYRDTQSRTASPNRAGKG        2.4
697   QRTTVPEEELNPKILALQNAQRKRKME          2.6
697   QRTTVPEEELNPKILALQNAQRKRKMEHD        2.7
717   QRKRKMEHDGSLFQAVGIGTLLQQPDDHA        3.2
```

NLStradamus

cutoff 0.1 4 state HMM

3 - GAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELA - 41

155 - VKKGKE - 160

709 - KILALQNAQRKRKME – 723

NucPred

The NucPred score for your sequence is 0.94 (see score help below)

```
  1   MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNV    50
 51   SSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFV   100
101   MVLTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTH   150
151   RNGLVKKGKEQNTQRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHV   200
201   YDTNSNQPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDM   250
251   KFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQV   300
301   TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSGIIQHDL   350
351   IFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKLKKEPDALTLL   400
401   APAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM   450
451   SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDQTPS   500
501   PSDGSTRQSSPEPNSPSEYCFYVDSDMVNEFKLELVEKLFAEDTEAKNPF   550
551   STQDTDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT   600
601   VFQQTQIQEPTANATTTTATTDELKTVTKDRMEDIKILIASPSPTHIHKE   650
651   TTSATSSPYRDTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTT   700
701   VPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQPDDHAATTSL   750
751   SWKRVKGCKSSEQNGMEQKTIILIPSDLACRLLGQSMDESGLPQLTSYDC   800
801   EVNAPIQGSRNLLQGEELLRALDQVN                          826
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

NUCDISC: discrimination of nuclear localization signals

```
      pat4: RKRK (5) at   718
      pat7: none
      bipartite: RRKEKSRDAARSRRSKE at    17
      content of basic residues:  10.3%
      NLS Score:  0.33
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Hif1a: MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Hif1a	KKKISSERRKEKSRDAARSRRSKE	10	33	0.964
Hif1a	SVM	58	60	0.696
Hif1a	SEVFYE	34	39	0.568

ELM

TRG_NLS_MonoCore_2   2.345e-04

QRKRKM   717-722

Monopartite variant of the classical basically charged NLS. Strong core version.

TRG_NLS_MonoExtC_3   7.252e-04

QRKRKME   717-723

Monopartite variant of the classical basically charged NLS. C-extended version.

TRG_NES_CRM1_1   7.626e-04

DDMKAQMNCFYLKALD   82-97 ;

DMKAQMNCFYLKALD   83-97

Some proteins re-exported from the nucleus contain a Leucine-rich nuclear export signal (NES) binding to the CRM1 exportin protein.

NES Finder

Position   NES   Type

============================

  37   FYELAHQLPL   2-3-1

  60   MRLTISYLRV   3-2-1

  84   MKAQMNCFYL   3-2-1

 559   LEMLAPYIPM   2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES223789098_0	36-50	KESEVFYELAHQLPL	0.072
>LocNES223789098_0	52-66	HNVSSHLDKASVMRL	0.122
>LocNES223789098_0	54-68	VSSHLDKASVMRLTI	0.026
>LocNES223789098_0	57-71	HLDKASVMRLTISYL	0.090
>LocNES223789098_0	59-73	DKASVMRLTISYLRV	0.110
>LocNES223789098_0	70-84	YLRVRKLLDAGDLDI	0.103
>LocNES223789098_0	83-97	DIEDDMKAQMNCFYL	0.046
>LocNES223789098_0	91-105	QMNCFYLKALDGFVM	0.022
>LocNES223789098_0	92-106	MNCFYLKALDGFVMV	0.012
>LocNES223789098_0	93-107	NCFYLKALDGFVMVL	0.011
>LocNES223789098_0	112-126	DMIYISDNVNKYMGL	0.035
>LocNES223789098_0	117-131	SDNVNKYMGLTQFEL	0.027
>LocNES223789098_0	125-139	GLTQFELTGHSVFDF	0.009
>LocNES223789098_0	190-204	SATWKVLHCTGHIHV	0.011
>LocNES223789098_0	335-349	QPQCIVCVNYVVSGI	0.019
>LocNES223789098_0	342-356	VNYVVSGIIQHDLIF	0.066
>LocNES223789098_0	354-368	LIFSLQQTECVLKPV	0.012
>LocNES223789098_0	403-417	LLAPAAGDTIISLDF	0.028
>LocNES223789098_0	443-457	PNEKLQNINLAMSPL	0.284
>LocNES223789098_0	466-480	LRSSADPALNQEVAL	0.114
>LocNES223789098_0	523-537	YCFYVDSDMVNEFKL	0.065
>LocNES223789098_0	558-572	DTDLDLEMLAPYIPM	0.190
>LocNES223789098_0	627-641	ELKTVTKDRMEDIKI	0.365

NetNES 1.1 Server - prediction results

>sp_Q16665_HIF1A_HUMAN - NetNES 1.1 prediction

NetNES 1.1: Predicted NES signals in sp Q16665 HIF1A HUMAN

#
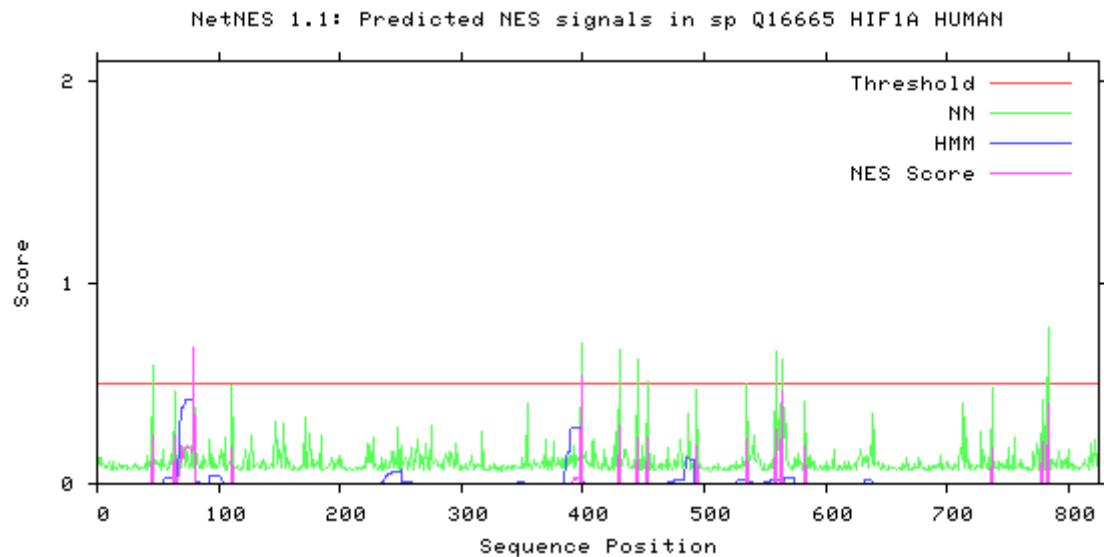
hHIF2α

>sp|Q99814|EPAS1_HUMAN Endothelial PAS domain-containing protein 1 OS=Homo
sapiens OX=9606 GN=EPAS1 PE=1 SV=3
MTADKEKKRSSSERRKEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLA
ISFLRTHKLLSSVCSENESEAEADQQMDNLYLKALEGFIAVVTQDGDMIFLSENISKFMG
LTQVELTGHSIFDFTHPCDHEEIRENLSLKNGSGFGKKSKDMSTERDFFMRMKCTVTNRG

```
RTVNLKSATWKVLHCTGQVKVYNNCPPHNSLCGYKEPLLSCLIIMCEPIQHPSHMDIPLD
SKTFLSRHSMDMKFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKG
QVVSGQYRMLAKHGGYVWLETQGTVIYNPRNLQPQCIMCVNYVLSEIEKNDVVFSMDQTE
SLFKPHLMAMNSIFDSSGKGAVSEKSNFLFTKLKEEPEELAQLAPTPGDAIISLDFGNQN
FEESSAYGKAILPPSQPWATELRSHSTQSEAGSLPAFTVPQAAAPGSTTPSATSSSSSCS
TPNSPEDYYTSLDNDLKIEVIEKLFAMDTEAKDQCSTQTDFNELDLETLAPYIPMDGEDF
QLSPICPEERLLAENPQSTPQHCFSAMTNIFQPLAPVAPHSPFLLDKFQQQLESKKTEPE
HRPMSSIFFDAGSKASLPPCCGQASTPLSSMGGRSNTQWPPDPPLHFGPTKWAVGDQRTE
FLGAAPLGPPVSPPHVSTFKTRSAKGFGARGPDVLSPAMVALSNKLKLKRQLEYEEQAFQ
DLSGGDPPGGSTSHLMWKRMKNLRGGSCPLMPDKPLSANVPNDKFTQNPMRGLGHPLRHL
PLPQPPSAISPGENSKSRFPPQCYATQYQDYSLSSAHKVSGMASRLLGPSFESYLLPELT
RYDCEVNVPVLGSSTLLQGGDLLRALDQAT
```

cNLS Mapper Result cut-off score 2.0

Predicted NLSs in query sequence	
MTADKEKKRSSSERRKEKSRDAARCRRSKETEVFYELAHELPLPHSVSSH	50
LDKASIMRLAISFLRTHKLLSSVCSENESEAEADQQMDNLYLKALEGFIA	100
VVTQDGDMIFLSENISKFMGLTQVELTGHSIFDFTHPCDHEEIRENLSLK	150
NGSGFGKKSKDMSTERDFFMRMKCTVTNRGRTVNLKSATWKVLHCTGQVK	200
VYNNCPPHNSLCGYKEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSM	250
DMKFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKG	300
QVVSGQYRMLAKHGGYVWLETQGTVIYNPRNLQPQCIMCVNYVLSEIEKN	350
DVVFSMDQTESLFKPHLMAMNSIFDSSGKGAVSEKSNFLFTKLKEEPEEL	400
AQLAPTPGDAIISLDFGNQNFEESSAYGKAILPPSQPWATELRSHSTQSE	450
AGSLPAFTVPQAAAPGSTTPSATSSSSSCSTPNSPEDYYTSLDNDLKIEV	500
IEKLFAMDTEAKDQCSTQTDFNELDLETLAPYIPMDGEDFQLSPICPEER	550
LLAENPQSTPQHCFSAMTNIFQPLAPVAPHSPFLLDKFQQQLESKKTEPE	600
HRPMSSIFFDAGSKASLPPCCGQASTPLSSMGGRSNTQWPPDPPLHFGPT	650
KWAVGDQRTEFLGAAPLGPPVSPPHVSTFKTRSAKGFGARGPDVLSPAMV	700
ALSNKLKLKRQLEYEEQAFQDLSGGDPPGGSTSHLMWKRMKNLRGGSCPL	750
MPDKPLSANVPNDKFTQNPMRGLGHPLRHLPLPQPPSAISPGENSKSRFP	800
PQCYATQYQDYSLSSAHKVSGMASRLLGPSFESYLLPELTRYDCEVNVPV	850
LGSSTLLQGGDLLRALDQAT	870

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
3	ADKEKKRSSSERRKEKSRDAARCRRSKETE	2
5	KEKKRSSSERRKEKSRDAARCRRSKETEV	2.5
6	EKKRSSSERRKEKSRDAARCRRSKETEV	2.1
20	RDAARCRRSKETEVFYELAHELPLPHSVSSH	2
20	RDAARCRRSKETEVFYELAHELPLPHSVSSHLDK	2.6
24	RCRRSKETEVFYELAHELPLPHSVSSHLDKASI	2
65	RTHKLLSSVCSENESEAEADQQMDNLYLKA	3.8
144	RENLSLKNGSGFGKKSKDMSTERDFFMRMKCT	2.2

```
144   RENLSLKNGSGFGKKSKDMSTERDFFMRMKCTVT   2.9
179   RGRTVNLKSATWKVLHCTGQVKVYNNCPPHNSLC   2.2
197   GQVKVYNNCPPHNSLCGYKEPLLSCLIIMCE      2.5
247   RHSMDMKFTYCDDRITELIGYHPEELLGRSAYE    2.3
360   ESLFKPHLMAMNSIFDSSGKGAVSEKSNFLFT      2
610   DAGSKASLPPCCGQASTPLSSMGGRSNTQWPP     2.4
682   RSAKGFGARGPDVLSPAMVALSNKLKLKR        4.1
704   NKLKLKRQLEYEEQAFQDLSGGDPPGGST        2.6
705   KLKLKRQLEYEEQAFQDLSGGDPPGGSTSH       4.2
705   KLKLKRQLEYEEQAFQDLSGGDPPGGSTSHL      5.4
737   WKRMKNLRGGSCPLMPDKPLSANVPNDKFT       3.2
752   PDKPLSANVPNDKFTQNPMRGLGHPLRHLP       2.5
793   ENSKSRFPPQCYATQYQDYSLSSAHKVSGM        4
817   HKVSGMASRLLGPSFESYLLPELTRYDCE        3.2
```

NLStradamus

0.1 cut-off 4 state HMM static

3 - ADKEKKRSSSERRKEKSRDAARCRRSKETEV - 33

156 - GKKSK - 160

680 - KTRSAKGFGARGPDVLSPAMVALSNKLKLKR - 710

738 - KRMK - 741

NucPred

The NucPred score for your sequence is 0.86 (see score help below)

```
  1   MTADKEKKRSSSERRKEKSRDAARCRRSKETEVFYELAHELPLPHSVSSH    50
 51   LDKASIMRLAISFLRTHKLLSSVCSENESEAEADQQMDNLYLKALEGFIA   100
101   VVTQDGDMIFLSENISKFMGLTQVELTGHSIFDFTHPCDHEEIRENLSLK   150
151   NGSGFGKKSKDMSTERDFFMRMKCTVTNRGRTVNLKSATWKVLHCTGQVK   200
201   VYNNCPPHNSLCGYKEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHSM   250
251   DMKFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKG   300
301   QVVSGQYRMLAKHGGYVWLETQGTVIYNPRNLQPQCIMCVNYVLSEIEKN   350
351   DVVFSMDQTESLFKPHLMAMNSIFDSSGKGAVSEKSNFLFTKLKEEPEEL   400
401   AQLAPTPGDAIISLDFGNQNFEESSAYGKAILPPSQPWATELRSHSTQSE   450
451   AGSLPAFTVPQAAAPGSTTPSATSSSSSCSTPNSPEDYYTSLDNDLKIEV   500
501   IEKLFAMDTEAKDQCSTQTDFNELDLETLAPYIPMDGEDFQLSPICPEER   550
551   LLAENPQSTPQHCFSAMTNIFQPLAPVAPHSPFLLDKFQQQLESKKTEPE   600
601   HRPMSSIFFDAGSKASLPPCCGQASTPLSSMGGRSNTQWPPDPPLHFGPT   650
651   KWAVGDQRTEFLGAAPLGPPVSPPHVSTFKTRSAKGFGARGPDVLSPAMV   700
701   ALSNKLKLKRQLEYEEQAFQDLSGGDPPGGSTSHLMWKRMKNLRGGSCPL   750
751   MPDKPLSANVPNDKFTQNPMRGLGHPLRHLPLPQPPSAISPGENSKSRFP   800
801   PQCYATQYQDYSLSSAHKVSGMASRLLGPSFESYLLPELTRYDCEVNVPV   850
851   LGSSTLLQGGDLLRALDQAT                                870
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

NUCDISC: discrimination of nuclear localization signals
      pat4: none
      pat7: none
      bipartite: RRKEKSRDAARCRRSKE at   14
      content of basic residues: 9.8%
      NLS Score: 0.02

Seq NLS

Prediction result (The predicted NLS(s) are underlined)
Hif2a: MTADKEK**KRSSSE****RRKEKSRDAARCRRSKE**TEV**FYELAHE**LPLPHSVSSHLDKASIMRLA

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Hif2a	KRSSSERRKEKSRDAARCRRSKE	8	30	0.916
Hif2a	FYELAHE	34	40	0.844

ELM

Motif Probability Cutoff:100   No NLS and NES positive result

NES Finder

Position   NES   Type

==============================

  34   FYELAHELPL   2-3-1

  92   LKALEGFIAV   2-3-1

  498   IEVIEKLFAM   2-3-1

  526   LETLAPYIPM   2-3-1

 699   MVALSNKLKL   2-3-1

  773   LGHPLRHLPL   3-2-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES1396965342_0	33-47	KETEVFYELAHELPL	0.135
>LocNES1396965342_0	49-63	HSVSSHLDKASIMRL	0.190
>LocNES1396965342_0	51-65	VSSHLDKASIMRLAI	0.078

>LocNES1396965342_0	53-67	SHLDKASIMRLAISF	0.084
>LocNES1396965342_0	54-68	HLDKASIMRLAISFL	0.171
>LocNES1396965342_0	63-77	LAISFLRTHKLLSSV	0.047
>LocNES1396965342_0	82-96	ESEAEADQQMDNLYL	0.158
>LocNES1396965342_0	91-105	MDNLYLKALEGFIAV	0.020
>LocNES1396965342_0	92-106	DNLYLKALEGFIAVV	0.011
>LocNES1396965342_0	108-122	QDGDMIFLSENISKF	0.043
>LocNES1396965342_0	111-125	DMIFLSENISKFMGL	0.059
>LocNES1396965342_0	116-130	SENISKFMGLTQVEL	0.105
>LocNES1396965342_0	124-138	GLTQVELTGHSIFDF	0.014
>LocNES1396965342_0	191-205	SATWKVLHCTGQVKV	0.011
>LocNES1396965342_0	337-351	QPQCIMCVNYVLSEI	0.045
>LocNES1396965342_0	449-463	HSTQSEAGSLPAFTV	0.032
>LocNES1396965342_0	497-511	DNDLKIEVIEKLFAM	0.234
>LocNES1396965342_0	516-530	KDQCSTQTDFNELDL	0.203
>LocNES1396965342_0	525-539	FNELDLETLAPYIPM	0.038
>LocNES1396965342_0	564-578	PQHCFSAMTNIFQPL	0.124
>LocNES1396965342_0	567-581	CFSAMTNIFQPLAPV	0.008
>LocNES1396965342_0	698-712	VLSPAMVALSNKLKL	0.354
>LocNES1396965342_0	770-784	TQNPMRGLGHPLRHL	0.056
>LocNES1396965342_0	772-786	NPMRGLGHPLRHLPL	0.166

NetNES 1.1 Server - prediction results

>Sequence - NetNES 1.1 prediction
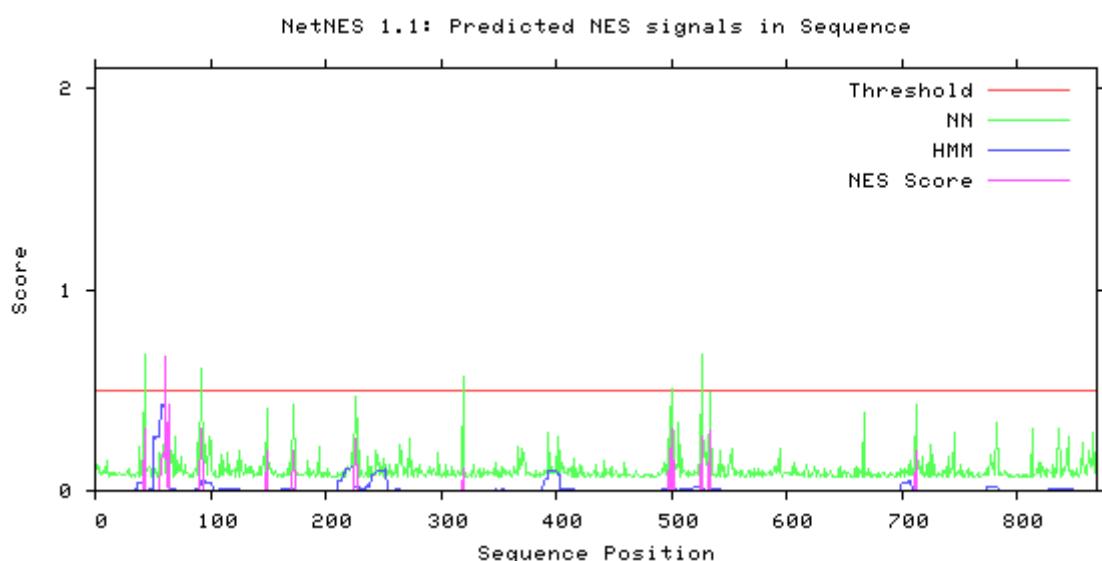
hHIF3α

```
>sp|Q9Y2N7|HIF3A_HUMAN Hypoxia-inducible factor 3-alpha OS=Homo sapiens
OX=9606 GN=HIF3A PE=1 SV=2
MALGLQRARSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLT
ISYLRMHRLCAAGEWNQVGAGGEPLDACYLKALEGFVMVLTAEGDMAYLSENVSKHLGLS
QLELIGHSIFDFIHPCDQEELQDALTPQQTLSRRKVEAPTERCFSLRMKSTLTSRGRTLN
LKAATWKVLNCSGHMRAYKPPAQTSPAGSPDSEPPLQCLVLICEAIPHPGSLEPPLGRGA
FLSRHSLDMKFTYCDDRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAV
TGQYRFLARSGGYLWTQTQATVVSGGRGPQSESIVCVHFLISQVEETGVVLSLEQTEQHS
RRPIQRGAPSQKDTPNPGDSLDTPGPRILAFLHPPSLSEAALAADPRRFCSPDLRRLLGP
ILDGASVAATPSTPLATRHPQSPLSADLPDELPVGTENVHRLFTSGKDTEAVETDLDIAQ
DADALDLEMLAPYISMDDDFQLNASEQLPRAYHRPLGAVPRPRARSFHGLSPPALEPSLL
PRWGSDPRLSCSSPSRGDPSASSPMAGARKRTLAQSSEDEDEGVELLGVRPPKRSPSPEH
ENFLLFPLSLSFLLTGGPAPGSLQDPSTPLLNLNEPLGLGPSLLSPYSDEDTTQPGGPFQ
PRAGSAQAD
```

cNLS Mapper Result cut-off 2.0

Predicted NLSs in query sequence
MALGLQRARSTTELRKEKS**RDAARSRRSQETEVLYQLAHTLPFARGVSAH** 50
LDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYLKALEGFVMVL 100
TAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPQQT 150
LS**RRKVEAPTERCFSLRMKSTLTSRGRTLNLK**AATWKVLNCS**GHMRAYKP** 200
PAQTSPAGSPDSEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMK 250
FTYCDDRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAV 300
TGQYRFLARSGGYLWTQTQATVVSGGRGPQSESIVCVHFLISQVEETGVV 350
LSLEQTEQHS**RRPIQRGAPSQKDTPNPGDSLDTPGPRILAFL**HPPSLSEA 400
ALAA**DPRRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQSPLSADLPD** 450
ELPVGTENVHRLFTSGKDTEAVETDLDIAQDADALDLEMLAPYISMDDDF 500
QLNASEQLPRAYHRPLGAVP**RPRARSFHGLSPPALEPSLLPRWGSDPRLS** 550
CSSPSRGDPSASSPMAGARKRTLAQSSEDEDEGVELLGVRPPKRSPSPEH 600
ENFLLFPLSLSFLLTGGPAPGSLQDPSTPLLNLNEPLGLGPSLLSPYSDE 650
DTTQPGGPFQPRAGSAQAD 669

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
20	RDAARSRRSQETEVLYQLAHTLPFARGVSAHLDK	2.3
153	RRKVEAPTERCFSLRMKSTLTSRGRTLNLK	2.6
193	GHMRAYKPPAQTSPAGSPDSEPPLQCLVLI	2
196	RAYKPPAQTSPAGSPDSEPPLQCLVLICE	2.7
196	RAYKPPAQTSPAGSPDSEPPLQCLVLICEAI	3.3
361	RRPIQRGAPSQKDTPNPGDSLDTPGPRILAFL	2.3
405	DPRRFCSPDLRRLLGPILDGASVAATPSTP	2
407	RRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQS	3.3

438	RHPQSPLSADLPDELPVGTENVHRLFTS	3.6
521	RPRARSFHGLSPPALEPSLLPRWGSDPRLSCS	2
542	RWGSDPRLSCSSPSRGDPSASSPMAGARKRTLA	3.7
569	RKRTLAQSSEDEDEGVELLGVRPPKRSP	2.3
567	GARKRTLAQSSEDEDEGVELLGVRPP	2.5
567	GARKRTLAQSSEDEDEGVELLGVRPPKRS	3.5
567	GARKRTLAQSSEDEDEGVELLGVRPPKRSP	5.2
567	GARKRTLAQSSEDEDEGVELLGVRPPKRSPS	6.8
569	RKRTLAQSSEDEDEGVELLGVRPPKRSPSP	5.9
590	RPPKRSPSPEHENFLLFPLSLSFLLTGGP	2
590	RPPKRSPSPEHENFLLFPLSLSFLLTGGPAP	3

NLStradamus

Pre-loaded models cutoff 0.1   4 state HMM static

7 - RARSTTELRKEKSRDAARSRRSQE - 30

512 - YHRPLGAVPRPRARSFHGLSPP - 533

563 - SPMAGARKRTLAQSSEDEDEGVELLGVRPPKRSPS - 597

NucPred

The NucPred score for your sequence is 0.90 (see score help below)

```
   1   MALGLQRARSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAH    50
  51   LDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYLKALEGFVMVL   100
 101   TAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPQQT   150
 151   LSRRKVEAPTERCFSLRMKSTLTSRGRTLNLKAATWKVLNCSGHMRAYKP   200
 201   PAQTSPAGSPDSEPPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMK   250
 251   FTYCDDRIAEVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAV   300
 301   TGQYRFLARSGGYLWTQTQATVVSGGRGPQSESIVCVHFLISQVEETGVV   350
 351   LSLEQTEQHSRRPIQRGAPSQKDTPNPGDSLDTPGPRILAFLHPPSLSEA   400
 401   ALAADPRRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQSPLSADLPD   450
 451   ELPVGTENVHRLFTSGKDTEAVETDLDIAQDADALDLEMLAPYISMDDDF   500
 501   QLNASEQLPRAYHRPLGAVPRPRARSFHGLSPPALEPSLLPRWGSDPRLS   550
 551   CSSPSRGDPSASSPMAGARKRTLAQSSEDEDEGVELLGVRPPKRSPSPEH   600
 601   ENFLLFPLSLSFLLTGGPAPGSLQDPSTPLLNLNEPLGLGPSLLSPYSDE   650
 651   DTTQPGGPFQPRAGSAQAD                                 669
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

```
     pat4: none
     pat7: none
     bipartite: none
     content of basic residues:    9.6%
     NLS Score: -0.47
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Hif3a: MALGLQRARSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLT

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Hif3a	RSRRSQETEVLY	24	35	0.805

ELM

Motif Probability Cutoff: 100, 50   No positive NLS/NES result

NES Finder

Position   NES   Type

============================

  34   LYQLAHTLPF   2-3-1

  57   MRLTISYLRM   3-2-1

  487   LEMLAPYISM   2-3-1

  603   FLLFPLSLSF   2-3-1

  630   LLNLNEPLGL   2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES1659617645_0	33-47	QETEVLYQLAHTLPF	0.091
>LocNES1659617645_0	49-63	RGVSAHLDKASIMRL	0.069
>LocNES1659617645_0	51-65	VSAHLDKASIMRLTI	0.095
>LocNES1659617645_0	54-68	HLDKASIMRLTISYL	0.224
>LocNES1659617645_0	56-70	DKASIMRLTISYLRM	0.265
>LocNES1659617645_0	88-102	PLDACYLKALEGFVM	0.043
>LocNES1659617645_0	89-103	LDACYLKALEGFVMV	0.011

>LocNES1659617645_0	90-104	DACYLKALEGFVMVL	0.016
>LocNES1659617645_0	99-113	GFVMVLTAEGDMAYL	0.075
>LocNES1659617645_0	109-123	DMAYLSENVSKHLGL	0.237
>LocNES1659617645_0	114-128	SENVSKHLGLSQLEL	0.256
>LocNES1659617645_0	122-136	GLSQLELIGHSIFDF	0.019
>LocNES1659617645_0	156-170	SRRKVEAPTERCFSL	0.016
>LocNES1659617645_0	334-348	QSESIVCVHFLISQV	0.022
>LocNES1659617645_0	343-357	FLISQVEETGVVLSL	0.032
>LocNES1659617645_0	444-458	PQSPLSADLPDELPV	0.089
>LocNES1659617645_0	468-482	TSGKDTEAVETDLDI	0.014
>LocNES1659617645_0	477-491	ETDLDIAQDADALDL	0.387
>LocNES1659617645_0	486-500	ADALDLEMLAPYISM	0.108
>LocNES1659617645_0	600-614	PSPEHENFLLFPLSL	0.265
>LocNES1659617645_0	602-616	PEHENFLLFPLSLSF	0.539
>LocNES1659617645_0	603-617	EHENFLLFPLSLSFL	0.500
>LocNES1659617645_0	604-618	HENFLLFPLSLSFLL	0.320
>LocNES1659617645_0	629-643	DPSTPLLNLNEPLGL	0.547

NetNES 1.1 Server - prediction results

>Sequence - NetNES 1.1 prediction

NetNES 1.1: Predicted NES signals in Sequence
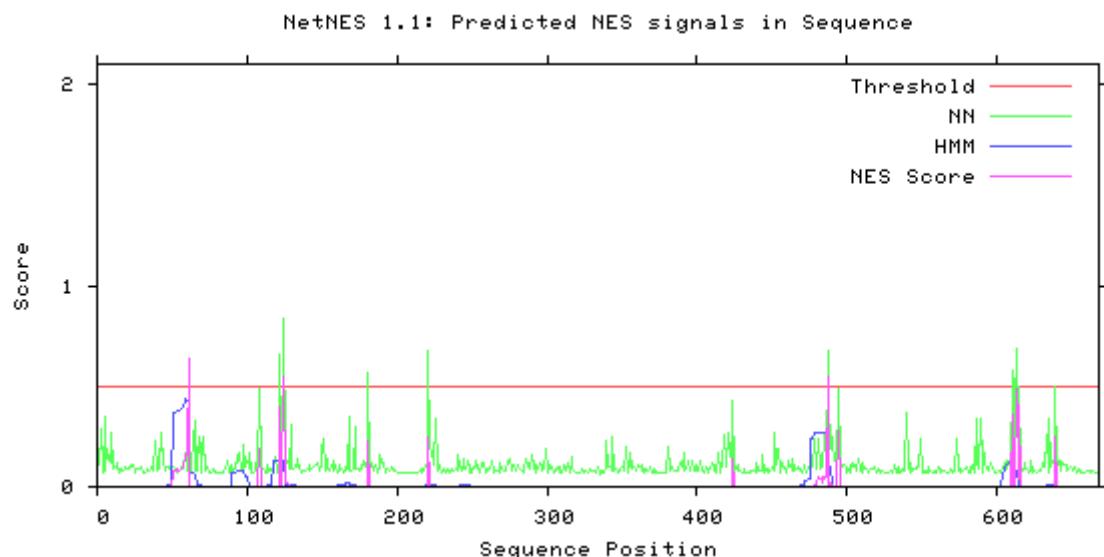
hSIM1

>sp|P81133|SIM1_HUMAN Single-minded homolog 1 OS=Homo sapiens OX=9606
GN=SIM1 PE=2 SV=2
MKEKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGL
GEAWGHSSRTSPLDNVGRELGSHLLQTLDGFIFVVAPDGKIMYISETASVHLGLSQVELT

```
GNSIYEYIHPADHDEMTAVLTAHQPYHSHFVQEYEIERSFFLRMKCVLAKRNAGLTCGGY
KVIHCSGYLKIRQYSLDMSPFDGCYQNVGLVAVGHSLPPSAVTEIKLHSNMFMFRASLDM
KLIFLDSRVAELTGYEPQDLIEKTLYHHVHGCDTFHLRCAHHLLLVKGQVTTKYYRFLAK
HGGWVWVQSYATIVHNSRSSRPHCIVSVNYVLTDTEYKGLQLSLDQISASKPAFSYTSSS
TPTMTDNRKGAKSRLSSSKSKSRTSPYPQYSGFHTERSESDHDSQWGGSPLTDTASPQLL
DPADRPGSQHDASCAYRQFSDRSSLCYGFALDHSRLVEERHFHTQACEGGRCEAGRYFLG
TPQAGREPWWGSRAALPLTKASPESREAYENSMPHIASVHRIHGRGHWDEDSVVSSPDPG
SASESGDRYRTEQYQSSPHEPSKIETLIRATQQMIKEEENRLQLRKAPSDQLASINGAGK
KHSLCFANYQQPPPTGEVCHGSALANTSPCDHIQQREGKMLSPHENDYDNSPTALSRISS
PNSDRISKSSLILAKDYLHSDISPHQTAGDHPTVSPNCFGSHRQYFDKHAYTLTGYALEH
LYDSETIRNYSLGCNGSHFDVTSHLRMQPDPAQGHKGTSVIITNGS
```

cNLS Mapper Result cut-off 2.0

Predicted NLSs in query sequence

```
MKEKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYL  50
KMRVVFPEGLGEAWGHSSRTSPLDNVGRELGSHLLQTLDGFIFVVAPDGK  100
IMYISETASVHLGLSQVELTGNSIYEYIHPADHDEMTAVLTAHQPYHSHF  150
VQEYEIERSFFLRMKCVLAKRNAGLTCGGYKVIHCSGYLKIRQYSLDMSP  200
FDGCYQNVGLVAVGHSLPPSAVTEIKLHSNMFMFRASLDMKLIFLDSRVA  250
ELTGYEPQDLIEKTLYHHVHGCDTFHLRCAHHLLLVKGQVTTKYYRFLAK  300
HGGWVWVQSYATIVHNSRSSRPHCIVSVNYVLTDTEYKGLQLSLDQISAS  350
KPAFSYTSSSTPTMTDNRKGAKSRLSSSKSKSRTSPYPQYSGFHTERSES  400
DHDSQWGGSPLTDTASPQLLDPADRPGSQHDASCAYRQFSDRSSLCYGFA  450
LDHSRLVEERHFHTQACEGGRCEAGRYFLGTPQAGREPWWGSRAALPLTK  500
ASPESREAYENSMPHIASVHRIHGRGHWDEDSVVSSPDPGSASESGDRYR  550
TEQYQSSPHEPSKIETLIRATQQMIKEEENRLQLRKAPSDQLASINGAGK  600
KHSLCFANYQQPPPTGEVCHGSALANTSPCDHIQQREGKMLSPHENDYDN  650
SPTALSRISSPNSDRISKSSLILAKDYLHSDISPHQTAGDHPTVSPNCFG  700
SHRQYFDKHAYTLTGYALEHLYDSETIRNYSLGCNGSHFDVTSHLRMQPD  750
PAQGHKGTSVIITNGS  766
```

Predicted monopartite NLS

Pos.	Sequence	Score

Predicted bipartite NLS

Pos.	Sequence	Score
2	KEKSKNAARTRREKENSEFYELAKLLPLP	2
4	KSKNAARTRREKENSEFYELAKLLPLPSAI	3
6	KNAARTRREKENSEFYELAKLLPLPSAITS	2.3
10	RTRREKENSEFYELAKLLPLPSAITSQLDKASI	2
74	DNVGRELGSHLLQTLDGFIFVVAPDGKIMYIS	2.3
158	RSFFLRMKCVLAKRNAGLTCGGYKVIHCSGYLKI	2.4
163	RMKCVLAKRNAGLTCGGYKVIHCSGYLKIRQYS	3.3
163	RMKCVLAKRNAGLTCGGYKVIHCSGYLKIRQY	2.4
163	RMKCVLAKRNAGLTCGGYKVIHCSGYLKIRQYSLD	3.4
187	GYLKIRQYSLDMSPFDGCYQNVGLVAVGH	2.3

```
223    TEIKLHSNMFMFRASLDMKLIFLDSRVAELT          2.2
235    RASLDMKLIFLDSRVAELTGYEPQDLIEKTLYH        2.8
293    KYYRFLAKHGGWVWVQSYATIVHNSRSS             2.4
347    ISASKPAFSYTSSSTPTMTDNRKGAKSRLSSS         2.7
486    REPWWGSRAALPLTKASPESREAYENSMPHIASV       2
493    RAALPLTKASPESREAYENSMPHIASVHRIHGRG       2.2
581    RLQLRKAPSDQLASINGAGKKHSLCFANYQQPP        3
597    GAGKKHSLCFANYQQPPPTGEVCHGSALANT          2
600    KKHSLCFANYQQPPPTGEVCHGSALANTS            3.6
636    REGKMLSPHENDYDNSPTALSRISSPNSDRI          2.2
703    RQYFDKHAYTLTGYALEHLYDSETIRNYSLGC         2.6
```

NLStradamus

cutoff 0.1; Pre-loaded models 4 state HMM static

2 - KEKSKNAARTRREKENSEFYELA - 24

365 - TDNRKGAKSRLSSSKSKSRTSP - 386

PSORTII

NUCDISC: discrimination of nuclear localization signals
```
     pat4: none
     pat7: none
     bipartite: none
     content of basic residues:  10.3%
     NLS Score: -0.47
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Sim1: MKEKSKNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGL
The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction

No NLS positive result

ELM

Motif Probability Cutoff: 100 and 50 No positive NLS/NES result

NES Finder

Position   NES   Type

============================

20   FYELAKLLPL   2-3-1

231   MFMFRASLDM   2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES1522303438_0	19-33	KENSEFYELAKLLPL	0.254
>LocNES1522303438_0	35-49	SAITSQLDKASIIRL	0.253
>LocNES1522303438_0	42-56	DKASIIRLTTSYLKM	0.368
>LocNES1522303438_0	46-60	IIRLTTSYLKMRVVF	0.011
>LocNES1522303438_0	83-97	ELGSHLLQTLDGFIF	0.062
>LocNES1522303438_0	84-98	LGSHLLQTLDGFIFV	0.066
>LocNES1522303438_0	85-99	GSHLLQTLDGFIFVV	0.042
>LocNES1522303438_0	102-116	DGKIMYISETASVHL	0.130
>LocNES1522303438_0	104-118	KIMYISETASVHLGL	0.200
>LocNES1522303438_0	107-121	YISETASVHLGLSQV	0.030
>LocNES1522303438_0	109-123	SETASVHLGLSQVEL	0.088
>LocNES1522303438_0	217-231	VGHSLPPSAVTEIKL	0.042
>LocNES1522303438_0	223-237	PSAVTEIKLHSNMFM	0.087
>LocNES1522303438_0	230-244	KLHSNMFMFRASLDM	0.042
>LocNES1522303438_0	232-246	HSNMFMFRASLDMKL	0.029
>LocNES1522303438_0	233-247	SNMFMFRASLDMKLI	0.011
>LocNES1522303438_0	234-248	NMFMFRASLDMKLIF	0.034
>LocNES1522303438_0	235-249	MFMFRASLDMKLIFL	0.113
>LocNES1522303438_0	242-256	LDMKLIFLDSRVAEL	0.046
>LocNES1522303438_0	275-289	GCDTFHLRCAHHLLL	0.098
>LocNES1522303438_0	276-290	CDTFHLRCAHHLLLV	0.023
>LocNES1522303438_0	737-751	GCNGSHFDVTSHLRM	0.029

NetNES 1.1 Server - prediction results

>Sequence - NetNES 1.1 prediction

NetNES 1.1: Predicted NES signals in Sequence
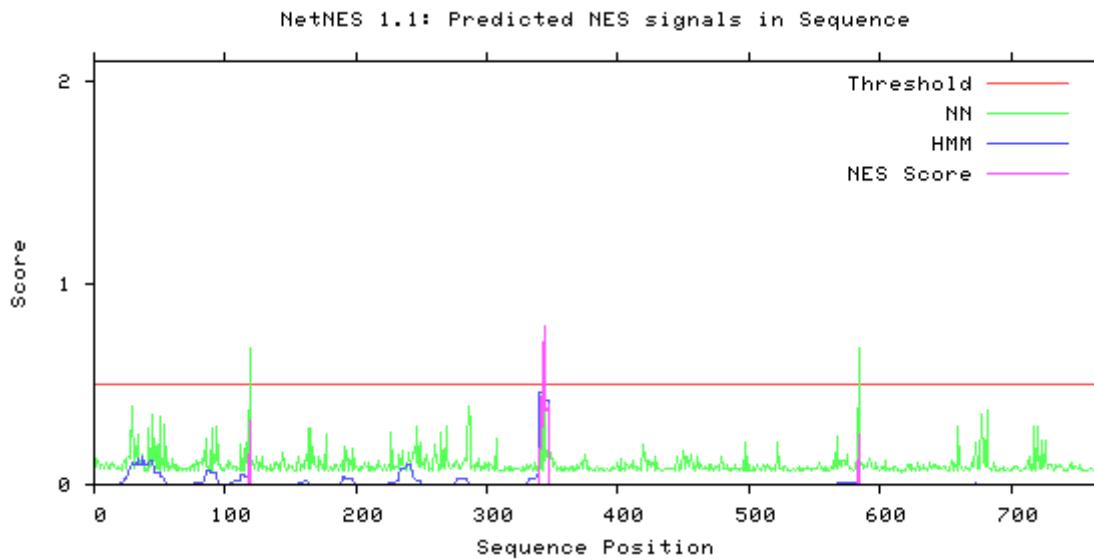
hSIM2

```
>sp|Q14190|SIM2_HUMAN Single-minded homolog 2 OS=Homo sapiens OX=9606
GN=SIM2 PE=1 SV=2
MKEKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEGL
GDAWGQPSRAGPLDGVAKELGSHLLQTLDGFVFVVASDGKIMYISETASVHLGLSQVELT
GNSIYEYIHPSDHDEMTAVLTAHQPLHHHLLQEYEIERSFFLRMKCVLAKRNAGLTCSGY
KVIHCSGYLKIRQYMLDMSLYDSCYQIVGLVAVGQSLPPSAITEIKLYSNMFMFRASLDL
KLIFLDSRVTEVTGYEPQDLIEKTLYHHVHGCDVFHLRYAHHLLLVKGQVTTKYYRLLSK
RGGWVWVQSYATVVHNSRSSRPHCIVSVNYVLTEIEYKELQLSLEQVSTAKSQDSWRTAL
STSQETRKLVKPKNTKMKTKLRTNPYPPQQYSSFQMDKLECGQLGNWRASPPASAAAPPE
LQPHSESSDLLYTPSYSLPFSYHYGHFPLDSHVFSSKKPMLPAKFGQPQGSPCEVARFFL
STLPASGECQWHYANPLVPSSSSPAKNPPEPPANTARHSLVPSYEAPAAAVRRFGEDTAP
PSFPSCGHYREEPALGPAKAARQAARDGARLALARAAPECCAPPTPEAPGAPAQLPFVLL
NYHRVLARRGPLGGAAPAASGLACAPGGPEAATGALRLRHPSPAATSPPGAPLPHYLGAS
VIITNGR
```

cNLS Mapper Result cut-off score 2.0

Predicted NLSs in query sequence

```
MKEKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYL  50
KMRAVFPEGLGDAWGQPSRAGPLDGVAKELGSHLLQTLDGFVFVVASDGK  100
IMYISETASVHLGLSQVELTGNSIYEYIHPSDHDEMTAVLTAHQPLHHHL  150
LQEYEIERSFFLRMKCVLAKRNAGLTCSGYKVIHCSGYLKIRQYMLDMSL  200
YDSCYQIVGLVAVGQSLPPSAITEIKLYSNMFMFRASLDLKLIFLDSRVT  250
EVTGYEPQDLIEKTLYHHVHGCDVFHLRYAHHLLLVKGQVTTKYYRLLSK  300
RGGWVWVQSYATVVHNSRSSRPHCIVSVNYVLTEIEYKELQLSLEQVSTA  350
KSQDSWRTALSTSQETRKLVKPKNTKMKTKLRTNPYPPQQYSSFQMDKLE  400
CGQLGNWRASPPASAAAPPELQPHSESSDLLYTPSYSLPFSYHYGHFPLD  450
SHVFSSKKPMLPAKFGQPQGSPCEVARFFLSTLPASGECQWHYANPLVPS  500
SSSPAKNPPEPPANTARHSLVPSYEAPAAAVRRFGEDTAPPSFPSCGHYR  550
```

```
EEPALGPAKAARQAARDGARLALARAAPECCAPPTPEAPGAPAQLPFVLL  600
NYHRVLARRGPLGGAAPAASGLACAPGGPEAATGALRLRHPSPAATSPPG  650
APLPHYLGASVIITNGR                                   667
```

Predicted monopartite NLS

Pos.	Sequence	Score

Predicted bipartite NLS

Pos.	Sequence	Score
2	KEKSKNAAKTRREKENGEFYELAKLLPLP	2
4	KSKNAAKTRREKENGEFYELAKLLPLPSAI	2.9
6	KNAAKTRREKENGEFYELAKLLPLPSAITS	3.7
74	DGVAKELGSHLLQTLDGFVFVVASDGKIMYIS	3.5
158	RSFFLRMKCVLAKRNAGLTCSGYKVIHCSGYLKI	2.4
163	RMKCVLAKRNAGLTCSGYKVIHCSGYLKIRQY	3.5
163	RMKCVLAKRNAGLTCSGYKVIHCSGYLKIRQYM	2.7
163	RMKCVLAKRNAGLTCSGYKVIHCSGYLKIRQYMLD	3.2
187	GYLKIRQYMLDMSLYDSCYQIVGLVAVGQ	2.1
235	RASLDLKLIFLDSRVTEVTGYEPQDLIEKTLYH	2.8
273	DVFHLRYAHHLLLVKGQVTTKYYRLLSKRGGW	2.2
293	KYYRLLSKRGGWVWVQSYATVVHNSRSS	2.2
296	RLLSKRGGWVWVQSYATVVHNSRSSRPHCI	2.3
296	RLLSKRGGWVWVQSYATVVHNSRSSRPHCIVS	2.7
351	KSQDSWRTALSTSQETRKLVKPKNTKMK	6.1
365	ETRKLVKPKNTKMKTKLRTNPYPPQQYSSF	2.4
373	KNTKMKTKLRTNPYPPQQYSSFQMDKLECG	2.8
375	TKMKTKLRTNPYPPQQYSSFQMDKLECGQL	2.6
454	FSSKKPMLPAKFGQPQGSPCEVARFFLSTLP	2.6
454	FSSKKPMLPAKFGQPQGSPCEVARFFLSTLP	2.4
556	GPAKAARQAARDGARLALARAAPECCAPPTP	2.4
637	RLRHPSPAATSPPGAPLPHYLGASVIITN	2.9

NLStradamus

Prediction cutoff 0.1; Pre-loaded models 4 state HMM static

```
2 - KEKSKNAAKTRREKENGEFYELAK - 25
```

```
363 - SQETRKLVKPKNTKMKTKLRTNPY - 386
```

```
556 - GPAKAARQAARDGARLA - 572
```

NucPred

The NucPred score for your sequence is 0.47 (see score help below)

```
  1  MKEKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYL    50
 51  KMRAVFPEGLGDAWGQPSRAGPLDGVAKELGSHLLQTLDGFVFVVASDGK   100
```

```
101   IMYISETASVHLGLSQVELTGNSIYEYIHPSDHDEMTAVLTAHQPLHHHL   150
151   LQEYEIERSFFLRMKCVLAKRNAGLTCSGYKVIHCSGYLKIRQYMLDMSL   200
201   YDSCYQIVGLVAVGQSLPPSAITEIKLYSNMFMFRASLDLKLIFLDSRVT   250
251   EVTGYEPQDLIEKTLYHHVHGCDVFHLRYAHHLLLVKGQVTTKYYRLLSK   300
301   RGGWVWVQSYATVVHNSRSSRPHCIVSVNYVLTEIEYKELQLSLEQVSTA   350
351   KSQDSWRTALSTSQETRKLVKPKNTKMKTKLRTNPYPPQQYSSFQMDKLE   400
401   CGQLGNWRASPPASAAAPPELQPHSESSDLLYTPSYSLPFSYHYGHFPLD   450
451   SHVFSSKKPMLPAKFGQPQGSPCEVARFFLSTLPASGECQWHYANPLVPS   500
501   SSSPAKNPPEPPANTARHSLVPSYEAPAAAVRRFGEDTAPPSFPSCGHYR   550
551   EEPALGPAKAARQAARDGARLALARAAPECCAPPTPEAPGAPAQLPFVLL   600
601   NYHRVLARRGPLGGAAPAASGLACAPGGPEAATGALRLRHPSPAATSPPG   650
651   APLPHYLGASVIITNGR                                   667
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive

PSORTII

NUCDISC: discrimination of nuclear localization signals

```
      pat4: none
      pat7: none
      bipartite: none
      content of basic residues:  10.3%
      NLS Score: -0.47
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)

Sim2: MKEK**SKNAAKTRREKENGEF**YELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEGL

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Sim2	SKNAAKTRREKENGEF	5	20	0.598

ELM

Motif Probability Cutoff: 100 and 50 No positive NLS/NES result

NES Finder

```
Position    NES      Type

=============================

  8     MANSINGLEM   3-2-1

 65     FYELAKLLPL   2-3-1

 276    MFMFRASLDL   2-3-1
```

LocNES

Protein Name	Position	Sequence	Score
>LocNES112173684_0	19-33	KENGEFYELAKLLPL	0.228
>LocNES112173684_0	35-49	SAITSQLDKASIIRL	0.352
>LocNES112173684_0	42-56	DKASIIRLTTSYLKM	0.338
>LocNES112173684_0	83-97	ELGSHLLQTLDGFVF	0.029
>LocNES112173684_0	84-98	LGSHLLQTLDGFVFV	0.055
>LocNES112173684_0	85-99	GSHLLQTLDGFVFVV	0.032
>LocNES112173684_0	102-116	DGKIMYISETASVHL	0.130
>LocNES112173684_0	104-118	KIMYISETASVHLGL	0.200
>LocNES112173684_0	107-121	YISETASVHLGLSQV	0.030
>LocNES112173684_0	109-123	SETASVHLGLSQVEL	0.088
>LocNES112173684_0	190-204	SGYLKIRQYMLDMSL	0.105
>LocNES112173684_0	217-231	VGQSLPPSAITEIKL	0.048
>LocNES112173684_0	223-237	PSAITEIKLYSNMFM	0.044
>LocNES112173684_0	230-244	KLYSNMFMFRASLDL	0.081
>LocNES112173684_0	232-246	YSNMFMFRASLDLKL	0.124
>LocNES112173684_0	233-247	SNMFMFRASLDLKLI	0.039
>LocNES112173684_0	234-248	NMFMFRASLDLKLIF	0.136
>LocNES112173684_0	235-249	MFMFRASLDLKLIFL	0.080
>LocNES112173684_0	242-256	LDLKLIFLDSRVTEV	0.018
>LocNES112173684_0	275-289	GCDVFHLRYAHHLLL	0.083
>LocNES112173684_0	276-290	CDVFHLRYAHHLLLV	0.026
>LocNES112173684_0	325-339	RPHCIVSVNYVLTEI	0.026
>LocNES112173684_0	590-604	PEAPGAPAQLPFVLL	0.054
>LocNES112173684_0	653-667	PGAPLPHYLGASVII	0.085

NetNES 1.1 Server - prediction results

```
>Sequence - NetNES 1.1 prediction
```

NetNES 1.1: Predicted NES signals in Sequence
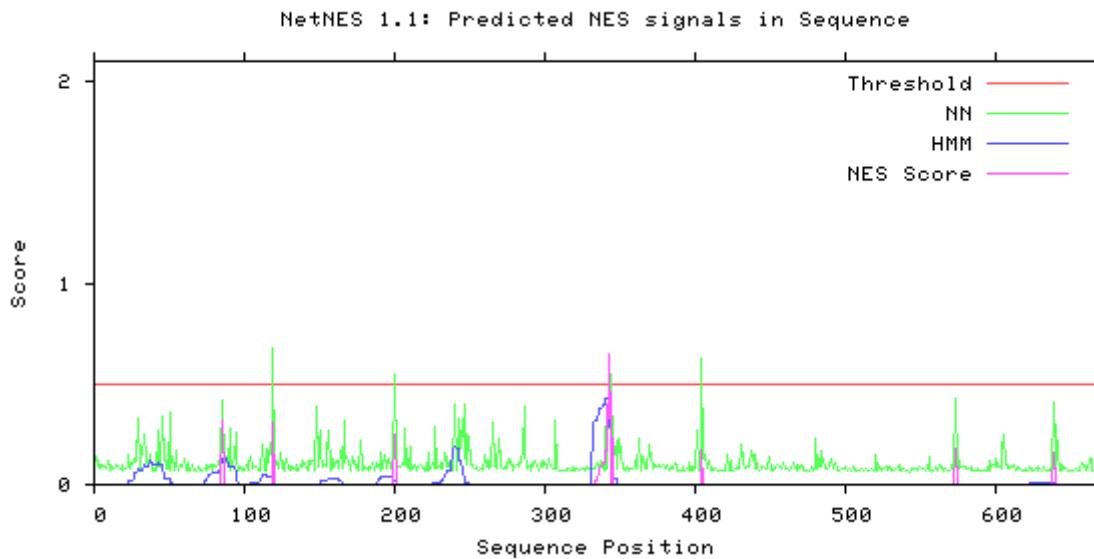
hClock

```
>sp|O15516|CLOCK_HUMAN Circadian locomoter output cycles protein kaput
OS=Homo sapiens OX=9606 GN=CLOCK PE=1 SV=1
MLFTVSCSKMSSIVDRDDSSIFDGLVEEDDKDKAKRVSRNKSEKKRRDQFNVLIKELGSM
LPGNARKMDKSTVLQKSIDFLRKHKEITAQSDASEIRQDWKPTFLSNEEFTQLMLEALDG
FFLAIMTDGSIIYVSESVTSLLEHLPSDLVDQSIFNFIPEGEHSEVYKILSTHLLESDSL
TPEYLKSKNQLEFCCHMLRGTIDPKEPSTYEYVKFIGNFKSLNSVSSSAHNGFEGTIQRT
HRPSYEDRVCFVATVRLATPQFIKEMCTVEEPNEEFTSRHSLEWKFLFLDHRAPPIIGYL
PFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQWIWLQTHYYITYH
QWNSRPEFIVCTHTVVSYAEVRAERRRELGIEESLPETAADKSQDSGSDNRINTVSLKEA
LERFDHSPTPSASSRSSRKSSHTAVSDPSSTPTKIPTDTSTPPRQHLPAHEKMVQRRSSF
SSQSINSQSVGSSLTQPVMSQATNLPIPQGMSQFQFSAQLGAMQHLKDQLEQRTRMIEAN
IHRQQEELRKIQEQLQMVHGQGLQMFLQQSNPGLNFGSVQLSSGNSSNIQQLAPINMQGQ
VVPTNQIQSGMNTGHIGTTQHMIQQQTLQSTSTQSQQNVLSGHSQQTSLPSQTQSTLTAP
LYNTMVISQPAAGSMVQIPSSMPQNSTQSAAVTTFTQDRQIRFSQGQQLVTKLVTAPVAC
GAVMVPSTMLMGQVVTAYPTFATQQQQSQTLSVTQQQQQQSSQEQQLTSVQQPSQAQLTQ
PPQQFLQTSRLLHGNPSTQLILSAAFPLQQSTFPQSHHQQHQSQQQQQLSRHRTDSLPDP
SKVQPQ
```

cNLS Mapper Result score 2.0

Predicted NLSs in query sequence	
MLFTVSCSKMSSIVDRDDSSIFDGLVEEDDKDKAK**RVSRNKSEKKRRDQF**	50
NVLIKELGSMLPGNARKMDKSTVLQKSIDFLRKHKEITAQSDASEIRQDW	100
KPTFLSNEEFTQLMLEALDGFFLAIMTDGSIIYVSESVTSLLEHLPSDLV	150
DQSIFNFIPEGEHSEVYKILSTHLLESDSLTPEYLKSKNQLEFCCHMLRG	200
TIDPKEPSTYEYVKFIGNFKSLNSVSSSAHNGFEGTIQ**RTHRPSYEDRVC**	250
FVATVRLATPQFIKEMCTVEEPNEEFTSRHSLEWKFLFLDHRAPPIIGYL	300
PFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQWIW	350
LQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAERRRELGIEESLPETAA	400
DKSQDSGSDN**RINTVSLKEALERFDHSPTPSASSRSSRKSSHTAVSDPSS**	450
TPTKIPTDTSTPPRQHLPAHEKMVQRRSSFSSQSINSQSVGSSLTQPVMS	500
QATNLPIPQGMSQFQFSAQLGAMQH**LKDQLEQRTRMIEANIHRQQEELRK**	550

```
IQEQLQMVHGQGLQMFLQQSNPGLNFGSVQLSSGNSSNIQQLAPINMQGQ  600
VVPTNQIQSGMNTGHIGTTQHMIQQQTLQSTSTQSQQNVLSGHSQQTSLP  650
SQTQSTLTAPLYNTMVISQPAAGSMVQIPSSMPQNSTQSAAVTTFTQDRQ  700
IRFSQGQQLVTKLVTAPVACGAVMVPSTMLMGQVVTAYPTFATQQQQSQT  750
LSVTQQQQQQSSQEQQLTSVQQPSQAQLTQPPQQFLQTSRLLHGNPSTQL  800
ILSAAFPLQQSTFPQSHHQQHQSQQQQQLSRHRTDSLPDPSKVQPQ       846
```

Predicted monopartite NLS		
Pos.	**Sequence**	**Score**

Predicted bipartite NLS		
Pos.	**Sequence**	**Score**
36	RVSRNKSEKKRRDQFNVLIKELGSMLPGNARKMDKS	3.7
39	RNKSEKKRRDQFNVLIKELGSMLPGNARKMDKS	2.8
39	RNKSEKKRRDQFNVLIKELGSMLPGNARKMDKST	7.3
39	RNKSEKKRRDQFNVLIKELGSMLPGNARKMDKST	3.2
239	RTHRPSYEDRVCFVATVRLATPQFIKEMCT	2.9
248	RVCFVATVRLATPQFIKEMCTVEEPNEEFTSRHSLE	2.1
256	RLATPQFIKEMCTVEEPNEEFTSRHSLEWKFLFLD	3.4
256	RLATPQFIKEMCTVEEPNEEFTSRHSLEWKFLFLD	2.4
411	RINTVSLKEALERFDHSPTPSASSRSSRKSSHT	3.5
411	RINTVSLKEALERFDHSPTPSASSRSSRKSSHTA	2.5
435	RSSRKSSHTAVSDPSSTPTKIPTDTSTPPR	2.4
451	TPTKIPTDTSTPPRQHLPAHEKMVQRRS	3.7
451	TPTKIPTDTSTPPRQHLPAHEKMVQRRSSFS	3.9
526	LKDQLEQRTRMIEANIHRQQEELRKIQE	3.1

NLStradamus cutoff 0.1

Posterior @ 0.1	27 - EEDDKDKAKRVSRNKSEKKRRDQFNVLIKELGSMLPGNARKMDKSTVLQKSIDFLRKHK - 85

NucPred

The NucPred score for your sequence is 0.94 (see score help below)

```
  1   MLFTVSCSKMSSIVDRDDSSIFDGLVEEDDKDKAKRVSRNKSEKKRRDQF   50
 51   NVLIKELGSMLPGNARKMDKSTVLQKSIDFLRKHKEITAQSDASEIRQDW  100
101   KPTFLSNEEFTQLMLEALDGFFLAIMTDGSIIYVSESVTSLLEHLPSDLV  150
151   DQSIFNFIPEGEHSEVYKILSTHLLESDSLTPEYLKSKNQLEFCCHMLRG  200
201   TIDPKEPSTYEYVKFIGNFKSLNSVSSSAHNGFEGTIQRTHRPSYEDRVC  250
251   FVATVRLATPQFIKEMCTVEEPNEEFTSRHSLEWKFLFLDHRAPPIIGYL  300
301   PFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGKGKSCYYRFLTKGQQWIW  350
351   LQTHYYITYHQWNSRPEFIVCTHTVVSYAEVRAERRRELGIEESLPETAA  400
```

```
401   DKSQDSGSDNRINTVSLKEALERFDHSPTPSASSRSSRKSSHTAVSDPSS   450
451   TPTKIPTDTSTPPRQHLPAHEKMVQRRSSFSSQSINSQSVGSSLTQPVMS   500
501   QATNLPIPQGMSQFQFSAQLGAMQHLKDQLEQRTRMIEANIHRQQEELRK   550
551   IQEQLQMVHGQGLQMFLQQSNPGLNFGSVQLSSGNSSNIQQLAPINMQGQ   600
601   VVPTNQIQSGMNTGHIGTTQHMIQQQTLQSTSTQSQQNVLSGHSQQTSLP   650
651   SQTQSTLTAPLYNTMVISQPAAGSMVQIPSSMPQNSTQSAAVTTFTQDRQ   700
701   IRFSQGQQLVTKLVTAPVACGAVMVPSTMLMGQVVTAYPTFATQQQQSQT   750
751   LSVTQQQQQQSSQEQQLTSVQQPSQAQLTQPPQQFLQTSRLLHGNPSTQL   800
801   ILSAAFPLQQSTFPQSHHQQHQSQQQQQLSRHRTDSLPDPSKVQPQ       846
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

PSORTII

NUCDISC: discrimination of nuclear localization signals

```
      pat4: KKRR (5) at    44
      pat4: RKHK (3) at    82
      pat7: none
      bipartite: none
      content of basic residues:    8.5%
      NLS Score:  0.03
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Clock: MLFTVSCSKMSSIVDRDDSSIFDGLVEEDDKDKAKRVSRNKSEKKRRDQFNVLIKELGSM

Definition of different colors in predictions

score range	color
0.1-0.3	
0.3-0.5	
0.5-0.7	
0.7-0.8	
0.8-0.86	
0.86-0.89	
>0.89	

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Clock	KKRR	44	47	0.862
Clock	SCSKMSSIVDR	6	16	0.522

ELM cutoff 100

No positive NLS result

TRG_NES_CRM1_1   7.626e-04

546-561

547-561

NES Finder

```
Position    NES      Type
=============================
 507    IPQGMSQFQF   3-2-1
 548    LRKIQEQLQM   2-3-1
 588    NIQQLAPINM   2-2-1
```

LocNES

Protein Name	Position	Sequence	Score
>LocNES1255047839_0	50-64	RRDQFNVLIKELGSM	0.139
>LocNES1255047839_0	111-125	NEEFTQLMLEALDGF	0.373
>LocNES1255047839_0	113-127	EFTQLMLEALDGFFL	0.290
>LocNES1255047839_0	115-129	TQLMLEALDGFFLAI	0.612
>LocNES1255047839_0	131-145	TDGSIIYVSESVTSL	0.015
>LocNES1255047839_0	247-261	PSYEDRVCFVATVRL	0.059
>LocNES1255047839_0	259-273	VRLATPQFIKEMCTV	0.038
>LocNES1255047839_0	292-306	FLDHRAPPIIGYLPF	0.030
>LocNES1255047839_0	414-428	NRINTVSLKEALERF	0.119
>LocNES1255047839_0	497-511	SLTQPVMSQATNLPI	0.062
>LocNES1255047839_0	506-520	ATNLPIPQGMSQFQF	0.056
>LocNES1255047839_0	547-561	RQQEELRKIQEQLQM	0.122
>LocNES1255047839_0	548-562	QQEELRKIQEQLQMV	0.103
>LocNES1255047839_0	571-585	LQQSNPGLNFGSVQL	0.050
>LocNES1255047839_0	587-601	SGNSSNIQQLAPINM	0.073
>LocNES1255047839_0	657-671	TQSTLTAPLYNTMVI	0.047
>LocNES1255047839_0	721-735	PVACGAVMVPSTMLM	0.029
>LocNES1255047839_0	798-812	GNPSTQLILSAAFPL	0.136

NetNES 1.1 Server - prediction results

```
>Sequence - NetNES 1.1 prediction
```

NetNES 1.1: Predicted NES signals in Sequence
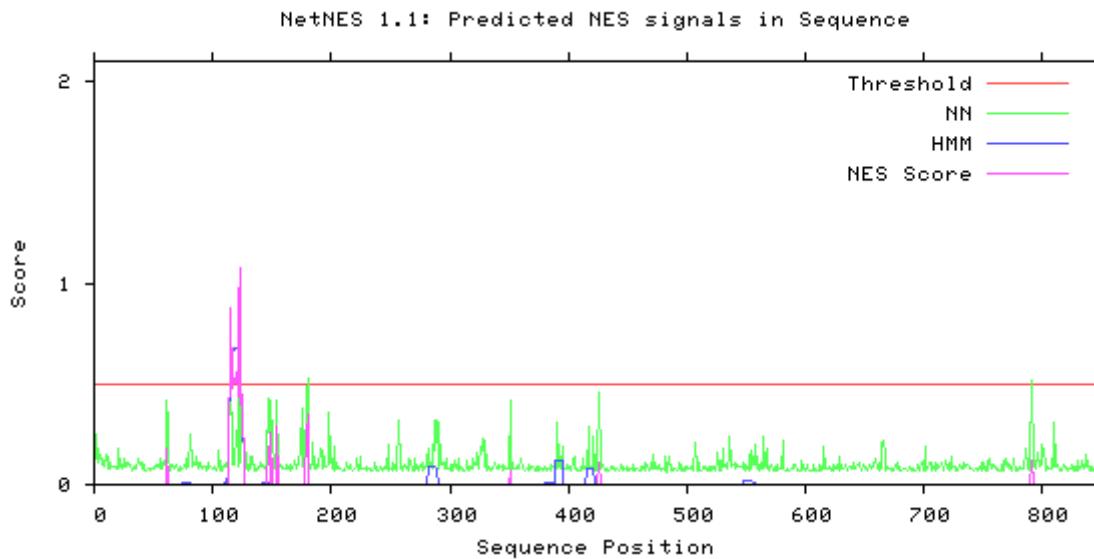
hNPAS1

>sp|Q99742|NPAS1_HUMAN Neuronal PAS domain-containing protein 1 OS=Homo
sapiens OX=9606 GN=NPAS1 PE=2 SV=2
MAAPYPGSGGGSEVKCVGGRGASVPWDFLPGLMVKAPSGPCLQAQRKEKSRNAARSRRGK
ENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPPAGLA
PGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGS
SVFDYIHPGDHSEVLEQLGLRTPTPGPPTPPSVSSSSSSSSSLADTPEIEASLTKVPPSS
LVQERSFFVRMKSTLTKRGLHVKASGYKVIHVTGRLRAHALGLVALGHTLPPAPLAELPL
HGHMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRIRQSHVDLLDK
GQVMTGYYRWLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQTPLDAFQL
PASVACEEASSPGPEPTEPEPPTEGKQAAPAENEAPQTQGKRIKVEPGPRETKGSEDSGD
EDPSSHPATPRPEFTSVIRAGVLKQDPVRPWGLAPPGDPPPTLLHAGFLPPVVRGLCTPG
TIRYGPAELGLVYPHLQRLGPGPALPEAFYPPLGLPYPGPAGTRLPRKGD

cNLS Mapper Result cut-off 2.0

Predicted NLSs in query sequence
MAAPYPGSGGGSEVKCVGGRGASVPWDFLPGLMVKAPSGPCLQAQRKEKS 50
RNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRF 100
AALGAPPWGLRAAGPPAGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFV 150
FALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYIHPGDHSEVLEQLGL 200
RTPTPGPPTPPSVSSSSSSSSSLADTPEIEASLTKVPPSSLVQERSFFVR 250
MKSTLTKRGLHVKASGYKVIHVTGRLRAHALGLVALGHTLPPAPLAELPL 300
HGHMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRI 350
RQSHVDLLDKGQVMTGYYRWLQRAGGFVWLQSVATVAGSGKSPGEHHVLW 400
VSHVLSQAEGGQTPLDAFQLPASVACEEASSPGPEPTEPEPPTEGKQAAP 450
AENEAPQTQGKRIKVEPGPRETKGSEDSGDEDPSSHPATPRPEFTSVIRA 500
GVLKQDPVRPWGLAPPGDPPPTLLHAGFLPPVVRGLCTPGTIRYGPAELG 550
LVYPHLQRLGPGPALPEAFYPPLGLPYPGPAGTRLPRKGD 590

Predicted monopartite NLS		
Pos.	**Sequence**	**Score**

Predicted bipartite NLS		
Pos.	**Sequence**	**Score**
33	MVKAPSGPCLQAQRKEKSRNAARSRRGKE	3.1
45	QRKEKSRNAARSRRGKENLEFFELAKLLP	2.5
46	RKEKSRNAARSRRGKENLEFFELAKLLPLP	2.4
46	RKEKSRNAARSRRGKENLEFFELAKLLPLP	2.4
51	RNAARSRRGKENLEFFELAKLLPLPGAISSQLDK	2.3
55	RSRRGKENLEFFELAKLLPLPGAISSQLDKASI	2.9
89	RLSVTYLRLRRFAALGAPPWGLRAAGPPAGLAPG	2.2
96	RLRRFAALGAPPWGLRAAGPPAGLAPGRRGP	2
230	EASLTKVPPSSLVQERSFFVRMKSTLTKRGLH	3.3
245	RSFFVRMKSTLTKRGLHVKASGYKVIHVTGRLRA	2.7
250	RMKSTLTKRGLHVKASGYKVIHVTGRLRAHALGL	3
458	TQGKRIKVEPGPRETKGSEDSGDEDPSSHP	2.2

NLStradamus

Posterior cutoff 0.1

33 - MVKAPSGPCLQAQRKEKSRNAARSRRGKENLEFFELAKLLPLPG - 76

96 - RLRRFAALGAPPWGLRAAGPPAGLAPGRRGPAA - 128

258 - RG - 259

456 - PQTQGKRIKVEPGPRETKGS - 475

579 - GPAGTRLPRKGD - 590

NucPred

The NucPred score for your sequence is 0.22 (see score help below)

```
  1  MAAPYPGSGGGSEVKCVGGRGASVPWDFLPGLMVKAPSGPCLQAQRKEKS   50
 51  RNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRF  100
101  AALGAPPWGLRAAGPPAGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFV  150
151  FALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYIHPGDHSEVLEQLGL  200
201  RTPTPGPPTPPSVSSSSSSSSSLADTPEIEASLTKVPPSSLVQERSFFVR  250
251  MKSTLTKRGLHVKASGYKVIHVTGRLRAHALGLVALGHTLPPAPLAELPL  300
301  HGHMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRI  350
351  RQSHVDLLDKGQVMTGYYRWLQRAGGFVWLQSVATVAGSGKSPGEHHVLW  400
401  VSHVLSQAEGGQTPLDAFQLPASVACEEASSPGPEPTEPEPPTEGKQAAP  450
451  AENEAPQTQGKRIKVEPGPRETKGSEDSGDEDPSSHPATPRPEFTSVIRA  500
501  GVLKQDPVRPWGLAPPGDPPPTLLHAGFLPPVVRGLCTPGTIRYGPAELG  550
551  LVYPHLQRLGPGPALPEAFYPPLGLPYPGPAGTRLPRKGD            590
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive

PSORTII

NUCDISC: discrimination of nuclear localization signals

```
        pat4: none
        pat7: none
        bipartite: none
        content of basic residues:    9.7%
        NLS Score: -0.47
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Npas1: MAAPYPGSGGGSEVKCVGGRGASVPWDFLPGLMVKAPSGP**CLQAQRKEK**SR**NAARSRRGK**

Definition of different colors in predictions

score range	color
0.1-0.3	
0.3-0.5	
0.5-0.7	
0.7-0.8	
0.8-0.86	
0.86-0.89	
>0.89	

The predicted NLS(s) (score cutoff = 0.3)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Npas1	CLQAQRKEK	41	49	0.447
Npas1	NAARSRRGK	52	60	0.351

ELM score 100

TRG_NLS_MonoExtC_3   7.252e-04

GKRIKVE   460-466

Monopartite variant of the classical basically charged NLS. C-extended version.

No positive NES result

NES Finder

Position   NES   Type

=============================

  65   FFELAKLLPL   2-3-1

  88   VRLSVTYLRL   3-2-1

 300   LHGHMIVFRL   3-2-1

 304   MIVFRLSLGL   2-3-1

 306   VFRLSLGLTI   2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES859122758_0	24-38	RGASVPWDFLPGLMV	0.049
>LocNES859122758_0	64-78	KENLEFFELAKLLPL	0.245
>LocNES859122758_0	80-94	GAISSQLDKASIVRL	0.123
>LocNES859122758_0	82-96	ISSQLDKASIVRLSV	0.095
>LocNES859122758_0	85-99	QLDKASIVRLSVTYL	0.215
>LocNES859122758_0	87-101	DKASIVRLSVTYLRL	0.295
>LocNES859122758_0	90-104	SIVRLSVTYLRLRRF	0.143
>LocNES859122758_0	141-155	HLGGHILQSLDGFVF	0.026
>LocNES859122758_0	143-157	GGHILQSLDGFVFAL	0.035
>LocNES859122758_0	158-172	NQEGKFLYISETVSI	0.024
>LocNES859122758_0	160-174	EGKFLYISETVSIYL	0.012
>LocNES859122758_0	162-176	KFLYISETVSIYLGL	0.037
>LocNES859122758_0	165-179	YISETVSIYLGLSQV	0.005
>LocNES859122758_0	167-181	SETVSIYLGLSQVEM	0.024
>LocNES859122758_0	226-240	SLADTPEIEASLTKV	0.011
>LocNES859122758_0	273-287	VIHVTGRLRAHALGL	0.780
>LocNES859122758_0	276-290	VTGRLRAHALGLVAL	0.235
>LocNES859122758_0	290-304	LGHTLPPAPLAELPL	0.200
>LocNES859122758_0	296-310	PAPLAELPLHGHMIV	0.144
>LocNES859122758_0	299-313	LAELPLHGHMIVFRL	0.083
>LocNES859122758_0	301-315	ELPLHGHMIVFRLSL	0.190
>LocNES859122758_0	303-317	PLHGHMIVFRLSLGL	0.093
>LocNES859122758_0	305-319	HGHMIVFRLSLGLTI	0.139
>LocNES859122758_0	306-320	GHMIVFRLSLGLTIL	0.211
>LocNES859122758_0	410-424	SQAEGGQTPLDAFQL	0.029

>LocNES859122758_0	526-540	TLLHAGFLPPVVRGL	0.074
>LocNES859122758_0	549-563	GPAELGLVYPHLQRL	0.057
>LocNES859122758_0	565-579	PGPALPEAFYPPLGL	0.038

NetNES 1.1 Server - prediction results

```
>Sequence - NetNES 1.1 prediction
```


NetNES 1.1: Predicted NES signals in Sequence
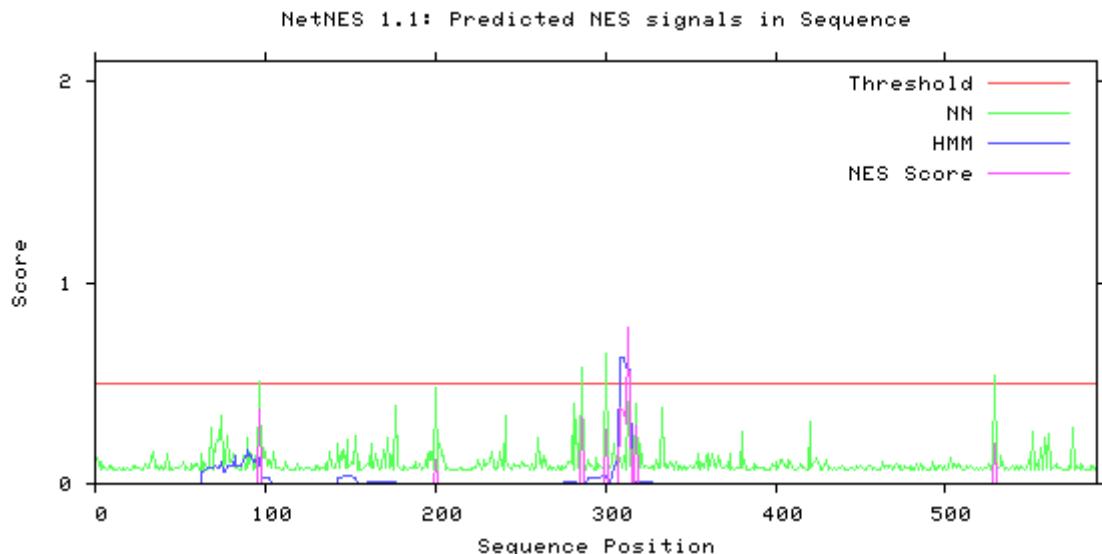
hNPAS2

```
>sp|Q99743|NPAS2_HUMAN Neuronal PAS domain-containing protein 2 OS=Homo
sapiens OX=9606 GN=NPAS2 PE=1 SV=3
MDEDEKDRAKRASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLEKVIGFLQKHN
EVSAQTEICDIQQDWKPSFLSNEEFTQLMLEALDGFIIAVTTDGSIIYVSDSITPLLGHL
PSDVMDQNLLNFLPEQEHSEVYKILSSHMLVTDSPSPEYLKSDSDLEFYCHLLRGSLNPK
EFPTYEYIKFVGNFRSYNNVPSPSCNGFDNTLSRPCRVPLGKEVCFIATVRLATPQFLKE
MCIVDEPLEEFTSRHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCH
QHLMQFGKGKSCCYRFLTKGQQWIWLQTHYYITYHQWNSKPEFIVCTHSVVSYADVRVER
RQELALEDPPSEALHSSALKDKGSSLEPRQHFNTLDVGASGLNTSHSPSASSRSSHKSSH
TAMSEPTSTPTKLMAEASTPALPRSATLPQELPVPGLSQAATMPAPLPSPSSCDLTQQLL
PQTVLQSTPAPMAQFSAQFSMFQTIKDQLEQRTRILQANIRWQQEELHKIQEQLCLVQDS
NVQMFLQQPAVSLSFSSTQRPEAQQQLQQRSAAVTQPQLGAGPQLPGQISSAQVTSQHLL
RESSVISTQGPKPMRSSQLMQSSGRSGSSLVSPFSSATAALPPSLNLTTPASTSQDASQC
QPSPDFSHDRQLRLLLSQPIQPMMPGSCDARQPSEVSRTGRQVKYAQSQTVFQNPDAHPA
NSSSAPMPVLLMGQAVLHPSFPASQPSPLQPAQARQQPPQHYLQVQAPTSLHSEQQDSLL
LSTYSQQPGTLGYPQPPPAQPQPLRPPRRVSSLSESSGLQQPPR
```

cNLS Mapper Result cut-off score 2.0

Predicted NLSs in query sequence

```
MDEDEKDRAKRASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLE  50
KVIGFLQKHNEVSAQTEICDIQQDWKPSFLSNEEFTQLMLEALDGFIIAV 100
TTDGSIIYVSDSITPLLGHLPSDVMDQNLLNFLPEQEHSEVYKILSSHML 150
VTDSPSPEYLKSDSDLEFYCHLLRGSLNPKEFPTYEYIKFVGNFRSYNNV 200
PSPSCNGFDNTLSRPCRVPLGKEVCFIATVRLATPQFLKEMCIVDEPLEE 250
FTSRHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCH 300
QHLMQFGKGKSCCYRFLTKGQQWIWLQTHYYITYHQWNSKPEFIVCTHSV 350
VSYADVRVERRQELALEDPPSEALHSSALKDKGSSLEPRQHFNTLDVGAS 400
GLNTSHSPSASSRSSHKSSHTAMSEPTSTPTKLMAEASTPALPRSATLPQ 450
ELPVPGLSQAATMPAPLPSPSSCDLTQQLLPQTVLQSTPAPMAQFSAQFS 500
MFQTIKDQLEQRTRILQANIRWQQEELHKIQEQLCLVQDSNVQMFLQQPA 550
VSLSFSSTQRPEAQQQLQQRSAAVTQPQLGAGPQLPGQISSAQVTSQHLL 600
RESSVISTQGPKPMRSSQLMQSSGRSGSSLVSPFSSATAALPPSLNLTTP 650
ASTSQDASQCQPSPDFSHDRQLRLLLSQPIQPMMPGSCDARQPSEVSRTG 700
RQVKYAQSQTVFQNPDAHPANSSSAPMPVLLMGQAVLHPSFPASQPSPLQ 750
PAQARQQPPQHYLQVQAPTSLHSEQQDSLLLSTYSQQPGTLGYPQPPPAQ 800
PQPLRPPRRVSSLSESSGLQQPPR                           824
```

Predicted monopartite NLS

Pos.	Sequence	Score

Predicted bipartite NLS

Pos.	Sequence	Score
11	RASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDK	2.2
11	RASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKT	3.6
14	RNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKT	2.7
14	RNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTT	7.3
14	RNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTT	3.2
192	GNFRSYNNVPSPSCNGFDNTLSRPCRVPLGK	2
214	RPCRVPLGKEVCFIATVRLATPQFLKEMCI	3.4
227	IATVRLATPQFLKEMCIVDEPLEEFTSRHSLE	2
231	RLATPQFLKEMCIVDEPLEEFTSRHSLEWKFLFLD	3.7
231	RLATPQFLKEMCIVDEPLEEFTSRHSLEWKFLFLD	2.6
379	LKDKGSSLEPRQHFNTLDVGASGLNTSHS	2.1
502	FQTIKDQLEQRTRILQANIRWQQEELHKIQE	2.2
669	DRQLRLLLSQPIQPMMPGSCDARQPSEVSRT	2
698	RTGRQVKYAQSQTVFQNPDAHPANSSSAPMPVL	2.5

NLStradamus

4 - DEKDRAKRASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKT - 46

803 - PLRPPRRVSSLSES - 816

821 - QPPR - 824

NucPred

The NucPred score for your sequence is 0.89 (see score help below)

```
    1  MDEDEKDRAKRASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLE     50
   51  KVIGFLQKHNEVSAQTEICDIQQDWKPSFLSNEEFTQLMLEALDGFIIAV    100
  101  TTDGSIIYVSDSITPLLGHLPSDVMDQNLLNFLPEQEHSEVYKILSSHML    150
  151  VTDSPSPEYLKSDSDLEFYCHLLRGSLNPKEFPTYEYIKFVGNFRSYNNV    200
  201  PSPSCNGFDNTLSRPCRVPLGKEVCFIATVRLATPQFLKEMCIVDEPLEE    250
  251  FTSRHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDLELLARCH    300
  301  QHLMQFGKGKSCCYRFLTKGQQWIWLQTHYYITYHQWNSKPEFIVCTHSV    350
  351  VSYADVRVERRQELALEDPPSEALHSSALKDKGSSLEPRQHFNTLDVGAS    400
  401  GLNTSHSPSASSRSSHKSSHTAMSEPTSTPTKLMAEASTPALPRSATLPQ    450
  451  ELPVPGLSQAATMPAPLPSPSSCDLTQQLLPQTVLQSTPAPMAQFSAQFS    500
  501  MFQTIKDQLEQRTRILQANIRWQQEELHKIQEQLCLVQDSNVQMFLQQPA    550
  551  VSLSFSSTQRPEAQQQLQQRSAAVTQPQLGAGPQLPGQISSAQVTSQHLL    600
  601  RESSVISTQGPKPMRSSQLMQSSGRSGSSLVSPFSSATAALPPSLNLTTP    650
  651  ASTSQDASQCQPSPDFSHDRQLRLLLSQPIQPMMPGSCDARQPSEVSRTG    700
  701  RQVKYAQSQTVFQNPDAHPANSSSAPMPVLLMGQAVLHPSFPASQPSPLQ    750
  751  PAQARQQPPQHYLQVQAPTSLHSEQQDSLLLSTYSQQPGTLGYPQPPPAQ    800
  801  PQPLRPPRRVSSLSESSGLQQPPR                              824
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

NUCDISC: discrimination of nuclear localization signals

```
     pat4: KKRR (5) at   19
     pat7: none
     bipartite: none
     content of basic residues:   8.4%
     NLS Score: -0.16
```

SeqNLS cut-off 0,5

Prediction result (The predicted NLS(s) are underlined)

Npas2: MDEDEKDRAKRASRNKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLEKVIGFLQKHN

Definition of different colors in predictions

score range	color
0.1-0.3	
0.3-0.5	
0.5-0.7	
0.7-0.8	
0.8-0.86	
0.86-0.89	
>0.89	

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Npas2	KKRR	19	22	0.873

ELM cut-off 100 and 50

No NLS positive result

TRG_NES_CRM1_1   7.626e-04   525-539; 526-539

## NES Finder

```
Position        NES         Type
==============================
  492        MAQFSAQFSM     2-3-1
  527        LHKIQEQLCL     2-3-1
```

LocNES

Protein Name	Position	Sequence	Score
>LocNES271820630_0	25-39	RRDQFNVLIKELSSM	0.348
>LocNES271820630_0	45-59	RKMDKTTVLEKVIGF	0.027
>LocNES271820630_0	46-60	KMDKTTVLEKVIGFL	0.133
>LocNES271820630_0	86-100	NEEFTQLMLEALDGF	0.373
>LocNES271820630_0	88-102	EFTQLMLEALDGFII	0.398
>LocNES271820630_0	90-104	TQLMLEALDGFIIAV	0.172
>LocNES271820630_0	106-120	TDGSIIYVSDSITPL	0.010
>LocNES271820630_0	141-155	EHSEVYKILSSHMLV	0.018
>LocNES271820630_0	222-236	VPLGKEVCFIATVRL	0.054
>LocNES271820630_0	233-247	TVRLATPQFLKEMCI	0.010
>LocNES271820630_0	234-248	VRLATPQFLKEMCIV	0.019
>LocNES271820630_0	241-255	FLKEMCIVDEPLEEF	0.006
>LocNES271820630_0	267-281	FLDHRAPPIIGYLPF	0.034
>LocNES271820630_0	485-499	PQTVLQSTPAPMAQF	0.044
>LocNES271820630_0	491-505	STPAPMAQFSAQFSM	0.033
>LocNES271820630_0	492-506	TPAPMAQFSAQFSMF	0.029
>LocNES271820630_0	526-540	WQQEELHKIQEQLCL	0.150
>LocNES271820630_0	527-541	QQEELHKIQEQLCLV	0.030
>LocNES271820630_0	545-559	NVQMFLQQPAVSLSF	0.187
>LocNES271820630_0	637-651	PFSSATAALPPSLNL	0.055
>LocNES271820630_0	722-736	HPANSSSAPMPVLLM	0.022

NetNES 1.1 Server - prediction results

NetNES 1.1: Predicted NES signals in Sequence
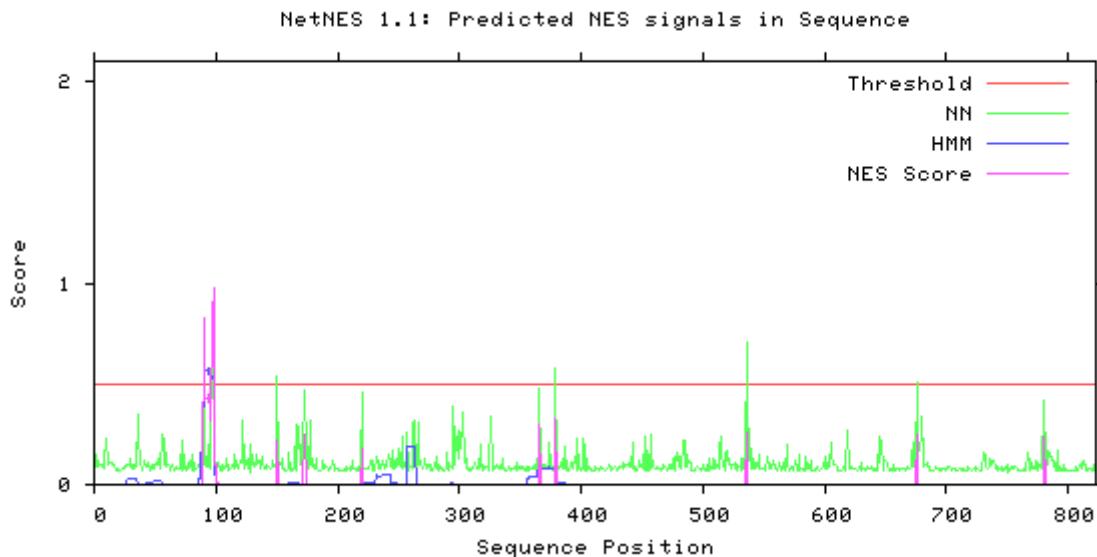
hNPAS3

>sp|Q8IXF0|NPAS3_HUMAN Neuronal PAS domain-containing protein 3 OS=Homo
sapiens OX=9606 GN=NPAS3 PE=2 SV=1
MAPTKPSFQQDPSRRERITAQHPLPNQSECRKIYRYDGIYCESTYQNLQALRKEKSRDAA
RSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEG
PPPNTSVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGFVFALNQEGKFLYISETVSI
YLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMKLPPGRGLLSQGTAEDGASSASSSSQSE
TPEPVESTSPSLLTTDNTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSLSH
GRTVPSQIMGLVVVAHALPPPTINEVRIDCHMFVTRVNMDLNIIYCENRISDYMDLTPVD
IVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVTKYYRWMQKNGGYIWIQSSATIAINAKN
ANEKNIIWVNYLLSNPEYKDTPMDIAQLPHLPEKTSESSETSDSESDSKDTSGITEDNEN
SKSDEKGNQSENSEDPEPDRKKSGNACDNDMNCNDDGHSSSNPDSRDSDDSFEHSDFENP
KAGEDGFGALGAMQIKVERYVESESDLRLQNCESLTSDSAKDSDSAGEAGAQASSKHQKR
KKRRKRQKGGSASRRRLSSASSPGGLDAGLVEPPRLLSSPNSASVLKIKTEISEPINFDN
DSSIWNYPPNREISRNESPYSMTKPPSSEHFPSPQGGGGGGGGGGGLHVAIPDSVLTPPG
ADGAAARKTQFGASATAALAPVASDPLSPPLSASPRDKHPGNGGGGGGGGGGGAGGGGPSA
SNSLLYTGDLEALQRLQAGNVVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAM
QSNLLPNAHAVNFVDVNSPGFGLDPKTPMEMLYHHVHRLNMSGPFGGAVSAASLTQMPAG
NVFTTAEGLFSTLPFPVYSNGIHAAQTLERKED

cNLS Mapper Result 2.0

Predicted NLSs in query sequence

MAPTKPSFQQDPSRRERITAQHPLPNQSECRKIYRYDGIYCESTYQNLQA 50
LRKEKSRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISY 100
LKMRDFANQGDPPWNLRMEGPPPNTSVKVIGAQRRRSPSALAIEVFEAHL 150

```
GSHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVELTGSSVFDYVHP  200
GDHVEMAEQLGMKLPPGRGLLSQGTAEDGASSASSSSQSETPEPVESTSP  250
SLLTTDNTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSLSH  300
GRTVPSQIMGLVVVAHALPPPTINEVRIDCHMFVTRVNMDLNIIYCENRI  350
SDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVTKYYRWMQ  400
KNGGYIWIQSSATIAINAKNANEKNIIWVNYLLSNPEYKDTPMDIAQLPH  450
LPEKTSESSETSDSESDSKDTSGITEDNENSKSDEKGNQSENSEDPEPDR  500
KKSGNACDNDMNCNDDGHSSNPDSRDSDDSFEHSDFENPKAGEDGFGAL  550
GAMQIKVERYVESESDLRLQNCESLTSDSAKDSDSAGEAGAQASSKHQKR  600
KKRRKRQKGGSASRRRLSSASSPGGLDAGLVEPPRLLSSPNSASVLKIKT  650
EISEPINFDNDSSIWNYPPNREISRNESPYSMTKPPSSEHFPSPQGGGGG  700
GGGGGGLHVAIPDSVLTPPGADGAAARKTQFGASATAALAPVASDPLSPP  750
LSASPRDKHPGNGGGGGGGGGGGAGGGGPSASNSLLYTGDLEALQRLQAGN  800
VVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQSNLLPNAHA  850
VNFVDVNSPGFGLDPKTPMEMLYHHVHRLNMSGPFGGAVSAASLTQMPAG  900
NVFTTAEGLFSTLPFPVYSNGIHAAQTLERKED                   933
```

Predicted monopartite NLS

Pos.	Sequence	Score
596	KHQKRKKRR	2.5
596	KHQKRKKRRK	4
597	HQKRKKRRKR	10
599	KRKKRRKRQ	8
598	QKRKKRRKRQ	6
599	KRKKRRKRQK	10
600	RKKRRKRQKGG	9

Predicted bipartite NLS

Pos.	Sequence	Score
3	PTKPSFQQDPSRRERITAQHPLPNQSECRK	2.1
29	ECRKIYRYDGIYCESTYQNLQALRKEKSRD	3.4
51	LRKEKSRDAARSRRGKENFEFYELAKLLP	2.6
57	RDAARSRRGKENFEFYELAKLLPLPAAITSQLDK	2.2
61	RSRRGKENFEFYELAKLLPLPAAITSQLDKASI	2.3
95	RLTISYLKMRDFANQGDPPWNLRMEGPPPNTSV	2
130	IGAQRRRSPSALAIEVFEAHLGSHILQSLDG	3
261	RSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRL	2.6
266	RMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSLS	2.2
266	RMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSL	2.7
360	DIVGKRCYHFIHAEDVEGIRHSHLDLLNKG	2.5
374	DVEGIRHSHLDLLNKGQCVTKYYRWMQKNGGYI	2
392	VTKYYRWMQKNGGYIWIQSSATIAINAKN	2
497	EPDRKKSGNACDNDMNCNDDGHSSNPDSRDS	2
578	DSAKDSDSAGEAGAQASSKHQKRKKRRKRQK	3.9
596	KHQKRKKRRKRQKGGSASRRRLSSASSPGG	2.1
600	RKKRRKRQKGGSASRRRLSSASSPGGLDAGLVE	2.6
606	RQKGGSASRRRLSSASSPGGLDAGLVEPPRLLSSP	4.2
606	RQKGGSASRRRLSSASSPGGLDAGLVEPPRLLSS	5.1
614	RRRLSSASSPGGLDAGLVEPPRLLSSP	2.3
614	RRRLSSASSPGGLDAGLVEPPRLLSSP	3.3
614	RRRLSSASSPGGLDAGLVEPPRLLSSPNS	2.7
645	VLKIKTEISEPINFDNDSSIWNYPPNREIS	3.2
649	KTEISEPINFDNDSSIWNYPPNREISR	2.7

| 682 | MTKPPSSEHFPSPQGGGGGGGGGGGGLHVAI | 2 |
| 727 | RKTQFGASATAALAPVASDPLSPPLSASP635 | 3.6 |

NLSstradamus cut-off 0,1

Viterbi Path	596 - KHQKRKKRRKRQKGGSASRRR - 616
Posterior @ 0.1	44 - TYQNLQALRKEKSRDAARSRRGKENFEFYELAKLL - 78
	133 - QRRR - 136
	273 - KR - 274
	582 - DSDSAGEAGAQASSKHQKRKKRRKRQKGGSASRRRLSSASSPGGLDAGLVEPPR - 635
	754 - SPRDKHPGNGGGGGGGGGGA - 773

NucPred

The NucPred score for your sequence is 0.96 (see score help below)

```
  1   MAPTKPSFQQDPSRRERITAQHPLPNQSECRKIYRYDGIYCESTYQNLQA    50
 51   LRKEKSRDAARSRRGKENFEFYELAKLLPLPAAITSQLDKASIIRLTISY   100
101   LKMRDFANQGDPPWNLRMEGPPPNTSVKVIGAQRRRSPSALAIEVFEAHL   150
151   GSHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVELTGSSVFDYVHP   200
201   GDHVEMAEQLGMKLPPGRGLLSQGTAEDGASSASSSSQSETPEVESTSP   250
251   SLLTTDNTLERSFFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRVSLSH   300
301   GRTVPSQIMGLVVVAHALPPPTINEVRIDCHMFVTRVNMDLNIIYCENRI   350
351   SDYMDLTPVDIVGKRCYHFIHAEDVEGIRHSHLDLLNKGQCVTKYYRWMQ   400
401   KNGGYIWIQSSATIAINAKNANEKNIIWVNYLLSNPEYKDTPMDIAQLPH   450
451   LPEKTSESSETSDSESDSKDTSGITEDNENSKSDEKGNQSENSEDPEPDR   500
501   KKSGNACDNDMNCNDDGHSSSNPDSRDSDDSFEHSDFENPKAGEDGFGAL   550
551   GAMQIKVERYVESESDLRLQNCESLTSDSAKDSDSAGEAGAQASSKHQKR   600
601   KKRRKRQKGGSASRRRLSSASSPGGLDAGLVEPPRLLSSPNSASVLKIKT   650
651   EISEPINFDNDSSIWNYPPNREISRNESPYSMTKPPSSEHFPSPQGGGGG   700
701   GGGGGGLHVAIPDSVLTPPGADGAAARKTQFGASATAALAPVASDPLSPP   750
751   LSASPRDKHPGNGGGGGGGGGGAGGGGPSASNSLLYTGDLEALQRLQAGN   800
801   VVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQSNLLPNAHA   850
851   VNFVDVNSPGFGLDPKTPMEMLYHHVHRLNMSGPFGGAVSAASLTQMPAG   900
901   NVFTTAEGLFSTLPFPVYSNGIHAAQTLERKED                   933
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORTII

<u>NUCDISC: discrimination of nuclear localization signals</u>
```
      pat4: KRKK (5) at   599
      pat4: RKKR (5) at   600
      pat4: KKRR (5) at   601
      pat4: KRRK (5) at   602
      pat4: RRKR (5) at   603
      pat7: PSRRERI (4) at    12
      pat7: PEPDRKK (3) at   496
      pat7: PDRKKSG (5) at   498
      bipartite: RKKRRKRQKGGSASRRR at   600
      bipartite: KKRRKRQKGGSASRRRL at   601
      bipartite: KRRKRQKGGSASRRRLS at   602
      content of basic residues:  10.3%
      NLS Score:  3.61
```

SeqNLS

Prediction result (The predicted NLS(s) are underlined)
Npas3: **MAPTKPSFQQDPSRR**ERITAQHPLPNQSECRKIYRYDGIYCESTYQNLQALRKEKSRDAA

Definition of different colors in predictions

score range	color
0.1-0.3	■
0.3-0.5	■
0.5-0.7	■
0.7-0.8	■
0.8-0.86	■
0.86-0.89	■
>0.89	■

The predicted NLS(s) (score cutoff = 0.5)

Protein ID	Predicted NLS	Start	Stop	The highest score of matches within the prediction
Npas3	MAPTKPSFQQDPSRRERI	1	18	0.908

ELM cut-off 100

TRG_NLS_MonoCore_2   2.345e-04

QKRKKR   598-603

KRKKRR   599-604

RKKRRK   600-605

KKRRKR   601-606

Monopartite variant of the classical basically charged NLS. Strong core version.

TRG_NLS_MonoExtC_3   7.252e-04

QKRKKR   598-603

KRKKRR   599-604

RKKRRK   600-604

KKRRKR   601-605

RRKRQK   603-608

Monopartite variant of the classical basically charged NLS. C-extended version.

TRG_NLS_MonoExtN_4   1.276e-03

KHQKRKKR   596-603

KRKKRRKR   599-606

RKKRRKR   600-606

KKRRKRQK   601-608

KRRKRQKG   602-609

RRKRQKG   603-609

RKRQKG   604-609

Monopartite variant of the classical basically charged NLS. N-extended version.

No NES positive results

NES Finder

Position   NES   Type

==============================

  71   FYELAKLLPL   2-3-1

  94   IRLTISYLKM   3-2-1

  285   VIHITGRLRL   2-3-1

  334   VTRVNMDLNI   2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES264943790_0	70-84	KENFEFYELAKLLPL	0.101
>LocNES264943790_0	86-100	AAITSQLDKASIIRL	0.297
>LocNES264943790_0	88-102	ITSQLDKASIIRLTI	0.507
>LocNES264943790_0	91-105	QLDKASIIRLTISYL	0.318
>LocNES264943790_0	93-107	DKASIIRLTISYLKM	0.409
>LocNES264943790_0	153-167	HLGSHILQSLDGFVF	0.057
>LocNES264943790_0	155-169	GSHILQSLDGFVFAL	0.030
>LocNES264943790_0	170-184	NQEGKFLYISETVSI	0.027
>LocNES264943790_0	172-186	EGKFLYISETVSIYL	0.097
>LocNES264943790_0	174-188	KFLYISETVSIYLGL	0.323
>LocNES264943790_0	177-191	YISETVSIYLGLSQV	0.052
>LocNES264943790_0	179-193	SETVSIYLGLSQVEL	0.127
>LocNES264943790_0	202-216	VHPGDHVEMAEQLGM	0.122
>LocNES264943790_0	255-269	SLLTTDNTLERSFFI	0.022
>LocNES264943790_0	284-298	SSGYKVIHITGRLRL	0.266
>LocNES264943790_0	288-302	KVIHITGRLRLRVSL	0.112
>LocNES264943790_0	303-317	SHGRTVPSQIMGLVV	0.020
>LocNES264943790_0	304-318	HGRTVPSQIMGLVVV	0.012
>LocNES264943790_0	318-332	VAHALPPPTINEVRI	0.012
>LocNES264943790_0	329-343	EVRIDCHMFVTRVNM	0.014
>LocNES264943790_0	331-345	RIDCHMFVTRVNMDL	0.014
>LocNES264943790_0	333-347	DCHMFVTRVNMDLNI	0.084
>LocNES264943790_0	334-348	CHMFVTRVNMDLNII	0.043
>LocNES264943790_0	351-365	ENRISDYMDLTPVDI	0.014
>LocNES264943790_0	545-559	KAGEDGFGALGAMQI	0.039
>LocNES264943790_0	547-561	GEDGFGALGAMQIKV	0.030
>LocNES264943790_0	648-662	SVLKIKTEISEPINF	0.059
>LocNES264943790_0	793-807	DLEALQRLQAGNVVL	0.233
>LocNES264943790_0	828-842	YTTGTIRYAPAEVTL	0.013
>LocNES264943790_0	843-857	AMQSNLLPNAHAVNF	0.022
>LocNES264943790_0	846-860	SNLLPNAHAVNFVDV	0.006
>LocNES264943790_0	869-883	PKTPMEMLYHHVHRL	0.038
>LocNES264943790_0	871-885	TPMEMLYHHVHRLNM	0.079
>LocNES264943790_0	903-917	AGNVFTTAEGLFSTL	0.187
>LocNES264943790_0	905-919	NVFTTAEGLFSTLPF	0.136
>LocNES264943790_0	907-921	FTTAEGLFSTLPFPV	0.020

NetNES 1.1 Server - prediction results

>Sequence - NetNES 1.1 prediction
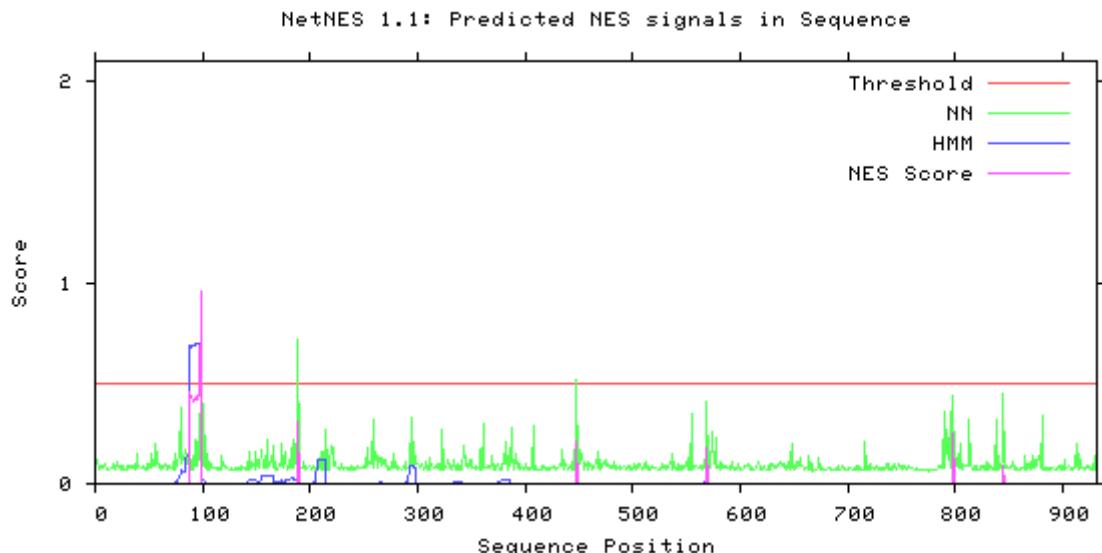
hNPAS4

```
>sp|Q8IUM7|NPAS4_HUMAN Neuronal PAS domain-containing protein 4 OS=Homo
sapiens OX=9606 GN=NPAS4 PE=1 SV=1
MYRSTKGASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYTRKGVFFAGGT
PLAGPTGLLSAQELEDIVAALPGFLLVFTAEGKLLYLSESVSEHLGHSMVDLVAQGDSIY
DIIDPADHLTVRQQLTLPSALDTDRLFRCRFNTSKSLRRQSAGNKLVLIRGRFHAHPPGA
YWAGNPVFTAFCAPLEPRPRPGPGPGPGPASLFLAMFQSRHAKDLALLDISESVLIYLGF
ERSELLCKSWYGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLYS
EGPEGPITANNYPISDMEAWSLRQQLNSEDTQAAYVLGTPTMLPSFPENILSQEECSSTN
PLFTAALGAPRSTSFPSAPELSVVSASEELPRPSKELDFSYLTFPSGPEPSLQAELSKDL
VCTPPYTPHQPGGCAFLFSLHEPFQTHLPTPSSTLQEQLTPSTATFSDQLTPSSATFPDP
LTSPLQGQLTETSVRSYEDQLTPCTSTFPDQLLPSTATFPEPLGSPAHEQLTPPSTAFQA
HLDSPSQTFPEQLSPNPTKTYFAQEGCSFLYEKLPPSPSSPGNGDCTLLALAQLRGPLSV
DVPLVPEGLLTPEASPVKQSFFHYSEKEQNEIDRLIQQISQLAQGMDRPFSAEAGTGGLE
PLGGLEPLDSNLSLSGAGPPVLSLDLKPWKCQELDFLADPDNMFLEETPVEDIFMDLSTP
DPSEEWGSGDPEAEGPGGAPSPCNNLSPEDHSFLEDLATYETAFETGVSAFPYDGFTDEL
HQLQSQVQDSFHEDGSGGEPTF
```

cNLS Mapper Result score cut-off 2.0

Predicted NLSs in query sequence
MYRSTKGAS**KARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYT** 50
RKGVFFAGGTPLAGPTGLLSAQELEDIVAALPGFLLVFTAEGKLLYLSES 100
VSEHLGHSMVDLVAQGDSIYDIIDPADHLTVRQQLTLPSALDTDRLFRCR 150
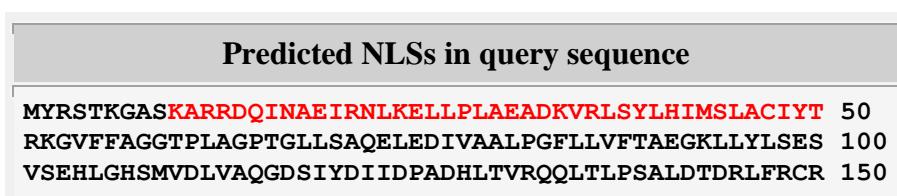
```
FNTSKSLRRQSAGNKLVLIRGRFHAHPPGAYWAGNPVFTAFCAPLEPRPR  200
PGPGPGPGPASLFLAMFQSRHAKDLALLDISESVLIYLGFERSELLCKSW  250
YGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLYS  300
EGPEGPITANNYPISDMEAWSLRQQLNSEDTQAAYVLGTPTMLPSFPENI  350
LSQEECSSTNPLFTAALGAPRSTSFPSAPELSVVSASEELPRPSKELDFS  400
YLTFPSGPEPSLQAELSKDLVCTPPYTPHQPGGCAFLFSLHEPFQTHLPT  450
PSSTLQEQLTPSTATFSDQLTPSSATFPDPLTSPLQGQLTETSVRSYEDQ  500
LTPCTSTFPDQLLPSTATFPEPLGSPAHEQLTPPSTAFQAHLDSPSQTFP  550
EQLSPNPTKTYFAQEGCSFLYEKLPPSPSSPGNGDCTLLALAQLRGPLSV  600
DVPLVPEGLLTPEASPVKQSFFHYSEKEQNEIDRLIQQISQLAQGMDRPF  650
SAEAGTGGLEPLGGLEPLDSNLSLSGAGPPVLSLDLKPWKCQELDFLADP  700
DNMFLEETPVEDIFMDLSTPDPSEEWGSGDPEAEGPGGAPSPCNNLSPED  750
HSFLEDLATYETAFETGVSAFPYDGFTDELHQLQSQVQDSFHEDGSGGEP  800
TF                                                  802
```

Predicted monopartite NLS		
Pos.	**Sequence**	**Score**

Predicted bipartite NLS		
Pos.	**Sequence**	**Score**
10	KARRDQINAEIRNLKELLPLAEADKVRLSY	2.5
19	EIRNLKELLPLAEADKVRLSYLHIMSLACIYT	2.3
158	RRQSAGNKLVLIRGRFHAHPPGAYWAGNPVFTAF	2.1
220	RHAKDLALLDISESVLIYLGFERSELLCKSW	3.2
283	RLQAKTGGWAWIYCLLYSEGPEGPITANNYPI	2.3
593	QLRGPLSVDVPLVPEGLLTPEASPVKQSF	3

NLSStradamus cut-off 0,1 4HMM static

8 - ASKARRDQI - 16

158 - RRQSAGNKLVLIRGRFHAHPP - 178

193 - APLEPRPRPGPGPGPGPAS - 211

NucPred

The NucPred score for your sequence is 0.51 (see score help below)

```
  1  MYRSTKGASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYT   50
 51  RKGVFFAGGTPLAGPTGLLSAQELEDIVAALPGFLLVFTAEGKLLYLSES  100
101  VSEHLGHSMVDLVAQGDSIYDIIDPADHLTVRQQLTLPSALDTDRLFRCR  150
151  FNTSKSLRRQSAGNKLVLIRGRFHAHPPGAYWAGNPVFTAFCAPLEPRPR  200
201  PGPGPGPGPASLFLAMFQSRHAKDLALLDISESVLIYLGFERSELLCKSW  250
251  YGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLYS  300
```

```
301   EGPEGPITANNYPISDMEAWSLRQQLNSEDTQAAYVLGTPTMLPSFPENI   350
351   LSQEECSSTNPLFTAALGAPRSTSFPSAPELSVVSASEELPRPSKELDFS   400
401   YLTFPSGPEPSLQAELSKDLVCTPPYTPHQPGGCAFLFSLHEPFQTHLPT   450
451   PSSTLQEQLTPSTATFSDQLTPSSATFPDPLTSPLQGQLTETSVRSYEDQ   500
501   LTPCTSTFPDQLLPSTATFPEPLGSPAHEQLTPPSTAFQAHLDSPSQTFP   550
551   EQLSPNPTKTYFAQEGCSFLYEKLPPSPSSPGNGDCTLLALAQLRGPLSV   600
601   DVPLVPEGLLTPEASPVKQSFFHYSEKEQNEIDRLIQQISQLAQGMDRPF   650
651   SAEAGTGGLEPLGGLEPLDSNLSLSGAGPPVLSLDLKPWKCQELDFLADP   700
701   DNMFLEETPVEDIFMDLSTPDPSEEWGSGDPEAEGPGGAPSPCNNLSPED   750
751   HSFLEDLATYETAFETGVSAFPYDGFTDELHQLQSQVQDSFHEDGSGGEP   800
801   TF                                                 802
```

Positively and negatively influencing subsequences are coloured according to the following scale:

(non-nuclear) negative ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| positive (nuclear)

PSORT II

No NLS positive result

SeqNLS cut-0ff 0,5

No predicted NLS

Prediction result (The predicted NLS(s) are underlined)
Npas4: MYRSTKGASKARRDQINAEIRNLKELLPLAEADKVRLSYLHIMSLACIYTRKGVFFAGGT

Definition of different colors in predictions

score range	color
0.1-0.3	
0.3-0.5	
0.5-0.7	
0.7-0.8	
0.8-0.86	
0.86-0.89	
>0.89	

ELM cut-off 50

No NLS positive result

TRG_NES_CRM1_1   QLRGPLSVDVPLVPE   593-607   7.626e-04

NESFinder

Position	NES	Type

===============================

20	IRNLKELLPL	2-3-1
591	LAQLRGPLSV	2-3-1
665	LEPLDSNLSL	2-3-1

LocNES

Protein Name	Position	Sequence	Score
>LocNES576996605_0	19-33	QINAEIRNLKELLPL	0.104
>LocNES576996605_0	27-41	LKELLPLAEADKVRL	0.059
>LocNES576996605_0	32-46	PLAEADKVRLSYLHI	0.664
>LocNES576996605_0	35-49	EADKVRLSYLHIMSL	0.198
>LocNES576996605_0	71-85	GLLSAQELEDIVAAL	0.145
>LocNES576996605_0	74-88	SAQELEDIVAALPGF	0.112
>LocNES576996605_0	76-90	QELEDIVAALPGFLL	0.081
>LocNES576996605_0	77-91	ELEDIVAALPGFLLV	0.060
>LocNES576996605_0	78-92	LEDIVAALPGFLLVF	0.130
>LocNES576996605_0	87-101	GFLLVFTAEGKLLYL	0.019
>LocNES576996605_0	121-135	DSIYDIIDPADHLTV	0.151
>LocNES576996605_0	220-234	MFQSRHAKDLALLDI	0.531
>LocNES576996605_0	226-240	AKDLALLDISESVLI	0.118
>LocNES576996605_0	230-244	ALLDISESVLIYLGF	0.343
>LocNES576996605_0	336-350	QAAYVLGTPTMLPSF	0.040
>LocNES576996605_0	373-387	APRSTSFPSAPELSV	0.028
>LocNES576996605_0	394-408	LPRPSKELDFSYLTF	0.143
>LocNES576996605_0	590-604	CTLLALAQLRGPLSV	0.124
>LocNES576996605_0	594-608	ALAQLRGPLSVDVPL	0.030
>LocNES576996605_0	632-646	EQNEIDRLIQQISQL	0.068
>LocNES576996605_0	664-678	EPLGGLEPLDSNLSL	0.602
>LocNES576996605_0	674-688	SNLSLSGAGPPVLSL	0.142
>LocNES576996605_0	676-690	LSLSGAGPPVLSLDL	0.070
>LocNES576996605_0	705-719	DNMFLEETPVEDIFM	0.094

NetNES 1.1 Server - prediction results

>Sequence - NetNES 1.1 prediction

NetNES 1.1: Predicted NES signals in Sequence