

A

AtHSP90.2

Predicted NLSs in query sequence	
HSPATHALIANATARATGADAEETFAFQAIEINQLLSLIINTFYSNKEIF	50
LRELISNSSDVRSLSTLTYCVSRLLDADGSDVGLGALDKIRFESLT	100
DKSKLDGQPELFIHZIPKNTWLTZIDSGGTAKADLVNMLDZARSOT	150
KEFHAAAGADSVHIGQGVGFYSALVADKVVVTKHNDQYVHESQ	200
AGGSFTVTRDTSGETLGRGTHVLYLKEDELVEERRKLDVKKHSFEI	250
SYPISLIEZKTZEKISDDEEEKKEDEKGVVEEDKEEKEKKKKIK	300
EVSHEDLVNKKQPIHPRKEEENKEEYAFYKSLSDNHEHLAVKHFSV	350
EQGLFEKAILFVKRAPPDLFDTKKPNKILVYRVFIDNDCEDZIPE	400
LGFVKGVDSDLPNLSRHTLQQNKILKVRKRNKLVKCLLFFEAEN	450
EDYVNFYFAFNSKLNKLGIDHESQWRTILAEILLRHSKSGDELSTLIDVY	500
TRPKEGQDIFVITGESKAVENSPFLERLKKKGEVLVYWDADYEZIG	550
QLKEFGKILVSATKGLKDETEDEKKKELKKEKFGGLCKIVDILGD	600
KVEKIVSDRVVSDPCLVTGEYGHANMERIKAKQALRDSHAGVHSSK	650
KTHEINPENSINDELKRADAKNDKSVKDLVLLFPETALLSGFSLDEP	700
NFTGSRHRLKGLSDDDDAVEADAPPLLEDDADGSEKIEIVD	747

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Predicted NLSs in query sequence	
MHSPHAAETETFAFQAIEINQLLSLIINTFYSNKEIFRELISNADSLD	50
KIRFESLTKSKLDGQPELFIHZIPKNTWLTZIDSGGTAKADLVNML	100
GTZARSOTKEFHAAAGADSVHIGQGVGFYSALVADKVVVTKHNDQ	150
EQYVHESQAGGSFTVTRDTSGETLGRGTHVLYLKEDELVEERRKLD	200
IKKHSFEISYPSLIEZKTZEKISDDEEEKKEDEKGVVEEDKEEKE	250
EKKKKIKVEVSHEDLVNKKQPIHPRKEEENKEEYAFYKSLNDWEEH	300
LAVKHFSVEQGLFEKAILFVKRAPPDLFDTRKPNKILVYRVFIDN	350
CEELIPEYLSFVKGVDSDLPNLSRHTLQQNKILKVRKRNKLVKCL	400
FFEAENKEDYVNFYFAFNSKLNKLGIDHESQWRTILAEILLRHSKSG	450
DELSTLIDVYTRPKEGQDIFVITGESKAVENSPFLERLKKKGEVLV	500
YWDADYEZIGQLKEFGKILVSATKGLKDETEDEKKKELKKEKFGGL	550
CKIVDILGDKVEKIVSDRVVSDPCLVTGEYGHANMERIKAKQALRDS	600
HAGVHSSKKTHEINPENSINDELKRADAKNDKSVKDLVLLFPETALL	650
SGFSLDDPNTGSRHRIHRLKGLSDDDDAVEADAPPLLEAADDGSEK	700
EIVD	704

Predicted monopartite NLS		
Pos.	Sequence	Score
402	GFVKGVDSDLPNLSRHTLQQNKILKVI	6.3

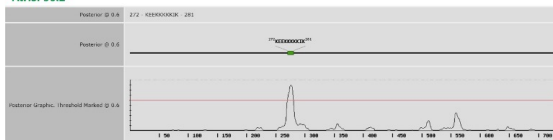
Predicted monopartite NLS		
Pos.	Sequence	Score
361	FVKGVDSDLPNLSRHTLQQNKILKVI	6.1

Predicted bipartite NLS		
Pos.	Sequence	Score
402	GFVKGVDSDLPNLSRHTLQQNKILKVI	6.3

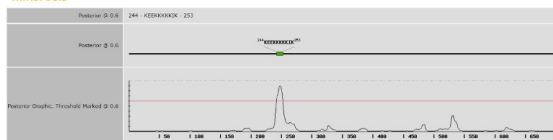
Predicted bipartite NLS		
Pos.	Sequence	Score
361	FVKGVDSDLPNLSRHTLQQNKILKVI	6.1

B

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C

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The NucPRed score for your sequence is 0.46 (see <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1111111/> below)

1	MADAEETFAFQAIEINQLLSLIINTFYSNKEIFRELISNADSLD	50
51	LTYCVSRLLDADGSDVGLGALDKIRFESLT	100
101	DKSKLDGQPELFIHZIPKNTWLTZIDSGGTAKADLVNMLDZARSOT	150
151	KEFHAAAGADSVHIGQGVGFYSALVADKVVVTKHNDQYVHESQ	200
201	AGGSFTVTRDTSGETLGRGTHVLYLKEDELVEERRKLDVKKHSFEI	250
251	SYPISLIEZKTZEKISDDEEEKKEDEKGVVEEDKEEKEKKKKIK	300
301	EVSHEDLVNKKQPIHPRKEEENKEEYAFYKSLSDNHEHLAVKHFSV	350
351	EQGLFEKAILFVKRAPPDLFDTKKPNKILVYRVFIDNDCEDZIPE	400
401	LGFVKGVDSDLPNLSRHTLQQNKILKVRKRNKLVKCLLFFEAEN	450
451	EDYVNFYFAFNSKLNKLGIDHESQWRTILAEILLRHSKSGDELSTLIDVY	500
501	TRPKEGQDIFVITGESKAVENSPFLERLKKKGEVLVYWDADYEZIG	550
551	QLKEFGKILVSATKGLKDETEDEKKKELKKEKFGGLCKIVDILGD	600
601	KVEKIVSDRVVSDPCLVTGEYGHANMERIKAKQALRDSHAGVHSSK	650
651	KTHEINPENSINDELKRADAKNDKSVKDLVLLFPETALLSGFSLDEP	700
701	NFTGSRHRLKGLSDDDDAVEADAPPLLEDDADGSEKIEIVD	750

MiHSP90.3

The NucPRed score for your sequence is 0.51 (see <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1111111/> below)

1	MADAEETFAFQAIEINQLLSLIINTFYSNKEIFRELISNADSLD	50
51	LTYCVSRLLDADGSDVGLGALDKIRFESLT	100
101	DKSKLDGQPELFIHZIPKNTWLTZIDSGGTAKADLVNMLDZARSOT	150
151	KEFHAAAGADSVHIGQGVGFYSALVADKVVVTKHNDQYVHESQ	200
201	AGGSFTVTRDTSGETLGRGTHVLYLKEDELVEERRKLDVKKHSFEI	250
251	SYPISLIEZKTZEKISDDEEEKKEDEKGVVEEDKEEKEKKKKIK	300
301	EVSHEDLVNKKQPIHPRKEEENKEEYAFYKSLSDNHEHLAVKHFSV	350
351	EQGLFEKAILFVKRAPPDLFDTKKPNKILVYRVFIDNDCEDZIPE	400
401	LGFVKGVDSDLPNLSRHTLQQNKILKVRKRNKLVKCLLFFEAEN	450
451	EDYVNFYFAFNSKLNKLGIDHESQWRTILAEILLRHSKSGDELSTLIDVY	500
501	TRPKEGQDIFVITGESKAVENSPFLERLKKKGEVLVYWDADYEZIG	550
551	QLKEFGKILVSATKGLKDETEDEKKKELKKEKFGGLCKIVDILGD	600
601	KVEKIVSDRVVSDPCLVTGEYGHANMERIKAKQALRDSHAGVHSSK	650
651	KTHEINPENSINDELKRADAKNDKSVKDLVLLFPETALLSGFSLDEP	700
701	NFTGSRHRLKGLSDDDDAVEADAPPLLEAADDGSEKIEIVD	750

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

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