ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	969
Number of 16mers from the input sequence	954
Threshold setting (Default value is 0.5)	0.51

TABULAR RESULT

Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.
Higher score of the peptide means the higher probability to be as epitope.
All the peptides shown here are above the threshold value chosen.

Rank	Sequence	Start position	Score	
1	TGAIMAVPGHDQRDWD	437	0.96	
1	TESPTAGPGGVPRADD	2	0.96	
2	QGYIQAYAYTDARGSY	694	0.93	
2	LGHVSSREPYRRLVNQ	679	0.93	
2	NEEVTADGRSDRGNFP	252	0.93	
3	AGRGRARIEFKLRDWL	506	0.92	
4	DGEVEVFQEFGKIGKS	728	0.91	
4	GARCLDGGRDWAKLTA	205	0.91	
5	GEAIAAYRRAIAAKSD	381	0.90	
5	GRLGFGHDSRRSFSTT	150	0.90	
6	AKLIEYTNHLTKKHRD	842	0.89	

6	ENEAYWMGPRPAEHGP	631	0.89	
6	DVPDYSPVLFDPDDAD	556	0.89	
6	PFPIVYDSDGRPHALD	531	0.89	
6	GGRDWAKLTAGERADV	211	0.89	
6	IFLQIYNAWFDTTANK	176	0.89	
7	AGSSWYELRYTDPHNS	609	0.88	
7	LWTYGGGTPGEAIAAY	372	0.88	
7	ARLERTWQENWARLGT	33	0.88	
8	AYLVDETVEYPVQVNG	903	0.87	
8	DEICDAYGADTLRVYE	751	0.87	
8	EQVIERGDRFVYPGPD	713	0.87	
8	GNISESAYTGDGILVN	468	0.87	
8	TGTHPRTRTEANVVNF	130	0.87	
9	LGDGLKPYSRDTNVMP	591	0.86	
9	DDADSEPSPPLAKATE	568	0.86	
9	PVGSLAPPDGAAVPDD	54	0.86	
9	PAEQYAVQTGTHPRTR	122	0.86	
10	APHIAEELWLRLGNTT	875	0.85	
10	LFSARAASDDGFEVDI	317	0.85	
11	YEMSMGPLEASRPWAT	765	0.84	
11	TEWVHVDLDLGDGLKP	582	0.84	
12	EHTGETRVADGVELDI	800	0.83	
12	GPRPAEHGPDDPGGVD	638	0.83	
12	QRDWDFARAFGLPIVE	448	0.83	
12	PVPIFIADYVLAGYGT	422	0.83	
13	PGGVPRADDADSDVPR	9	0.82	
13	GVSEDFAALRNNTATA	827	0.82	
13	LGTFNVPNPVGSLAPP	46	0.82	
14	ATDVYARYFRMVGRNV	95	0.81	
14	GKSLKNSVSPDEICDA	741	0.81	
14	PGGVDLYVGGAEHAVL	649	0.81	
14	ALPVELPDVPDYSPVL	549	0.81	
15	GLHVGHPLGYIATDVY	84	0.80	
15	SRRSFSTTDVDFYRWT	158	0.80	

15	GFDAFGLPAEQYAVQT	115	0.80	
16	VVVAADTDEETLKAAV	924	0.79	
16	GVELDIDTLRALHRTI	810	0.79	
16	FVQDMFPYPSGEGLHV	72	0.79	
16	LRQWMMRITAYADRLL	273	0.79	
16	RSDRGNFPVFRKRLRQ	260	0.79	
16	GRNVLHALGFDAFGLP	107	0.79	
17	YSRFWHKVLYDLGHVS	668	0.78	
18	GAAVPDDKLFVQDMFP	63	0.77	
18	VDRLESAGRGRARIEF	500	0.77	
18	WPAGVNPLWTYGGGTP	365	0.77	
18	ADVIDEYRLVYRADSL	224	0.77	
19	TKDVVGAYRFLQRVWR	780	0.76	
19	MQRNWIGRSTGAVALF	303	0.76	
19	VYRADSLVNWCPGLGT	233	0.76	
20	LRYTDPHNSERFCAKE	616	0.75	
21	DRFVYPGPDGEVEVFQ	720	0.74	
21	PSPPLAKATEWVHVDL	574	0.74	
22	PYPSGEGLHVGHPLGY	78	0.73	
22	GRSTGAVALFSARAAS	309	0.73	
23	YRRAIAAKSDLERQES	387	0.72	
24	LVDELVAASWPAGVNP	356	0.71	
24	AWFDTTANKARPISEL	183	0.71	
25	EETLKAAVLTDEKVQA	932	0.70	
25	TTSLAHGPFPKADAAY	889	0.70	
25	AYTGDGILVNSDYLNG	474	0.70	
25	IVEVIAGGNISESAYT	461	0.70	
25	RAFGLPIVEVIAGGNI	455	0.70	
25	VFTTRPDTLFGATYLV	334	0.70	
25	ADSDVPRYRYTAELAA	18	0.70	
26	VLTDEKVQAFLAGATP	939	0.69	
26	FPKADAAYLVDETVEY	897	0.69	
26	DAVPRAAVEPLVQMLA	857	0.69	
27	QMLAPLAPHIAEELWL	869	0.68	

27	DGFEVDIEVFTTRPDT	326	0.68	
28	AGATPRKVIVVAGRLV	950	0.67	
28	SREKTGVFLGSYAINP	402	0.67	
29	PEQVKTMQRNWIGRST	297	0.66	
29	AYADRLLDDLDVLDWP	282	0.66	
30	NHLTKKHRDAVPRAAV	849	0.65	
30	YTDARGSYVPAEQVIE	702	0.65	
31	LWLRLGNTTSLAHGPF	882	0.64	
31	VFLGSYAINPANGEPV	408	0.64	
31	WQENWARLGTFNVPNP	39	0.64	
31	WCPGLGTVLANEEVTA	242	0.64	
32	QRVWRLVVDEHTGETR	791	0.63	
32	DLDVLDWPEQVKTMQR	290	0.63	
33	AKSDLERQESREKTGV	393	0.62	
34	TLFGATYLVLAPEHDL	341	0.60	
35	INPANGEPVPIFIADY	415	0.57	

OVERLAP DISPLAY

VTESPTAGPGGVPRADDADSDVPRYRYTAELAARLERTWQENWARLGTFNVPNPVGSLAPPDGAAVPDDKLFVQDMFPYPSGE
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VDFYRWTQWIFLQIYNAWFDTTANKARPISELVAEFESGARCLDGGRDWAKLTAGERADVIDEYRLVYRADSLVNWCPGLGTV
LANEEVTADGRSDRGNFPVFRKRLRQWMMRITAYADRLLDDLDVLDWPEQVKTMQRNWIGRSTGAVALFSARAASDDGFEVDI
EVFTTRPDTLFGATYLVLAPEHDLVDELVAASWPAGVNPLWTYGGGTPGEAIAAYRRAIAAKSDLERQESREKTGVFLGSYAI
NPANGEPVPIFIADYVLAGYGTGAIMAVPGHDQRDWDFARAFGLPIVEVIAGGNISESAYTGDGILVNSDYLNGMSVPAAKRA
IVDRLESAGRGRARIEFKLRDWLFARQRYWGEPFPIVYDSDGRPHALDEAALPVELPDVPDYSPVLFDPDDADSEPSPPLAKA
TEWVHVDLDLGDGLKPYSRDTNVMPQWAGSSWYELRYTDPHNSERFCAKENEAYWMGPRPAEHGPDDPGGVDLYVGGAEHAVL
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TGAIMAVPGHDQRDWD----------

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TESPTAGPGGVPRADD--

QGYIQAYAYTDARGSY--

LGHVSSREPYRRLVNQ--

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NEEVTADGRSDRGNFP--


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IFLQIYNAWFDTTANK--

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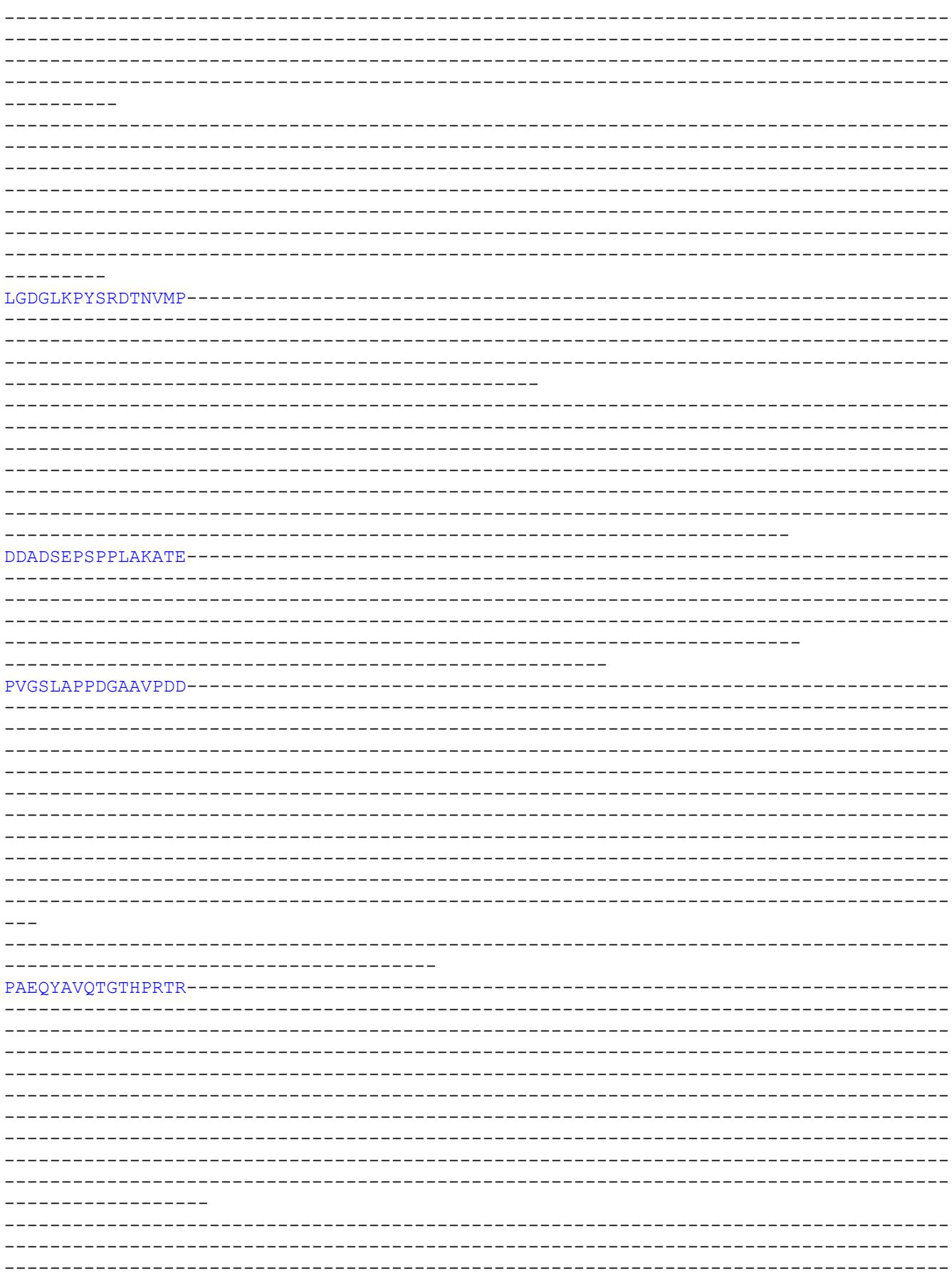
LWTYGGGTPGEAIAAY--

ARLERTWQENWARLGT--



APHIAEELWLRLGNTT----------

LFSARAASDDGFEVDI----------

YEMSMGPLEASRPWAT----------

TEWVHVDLDLGDGLKP----------

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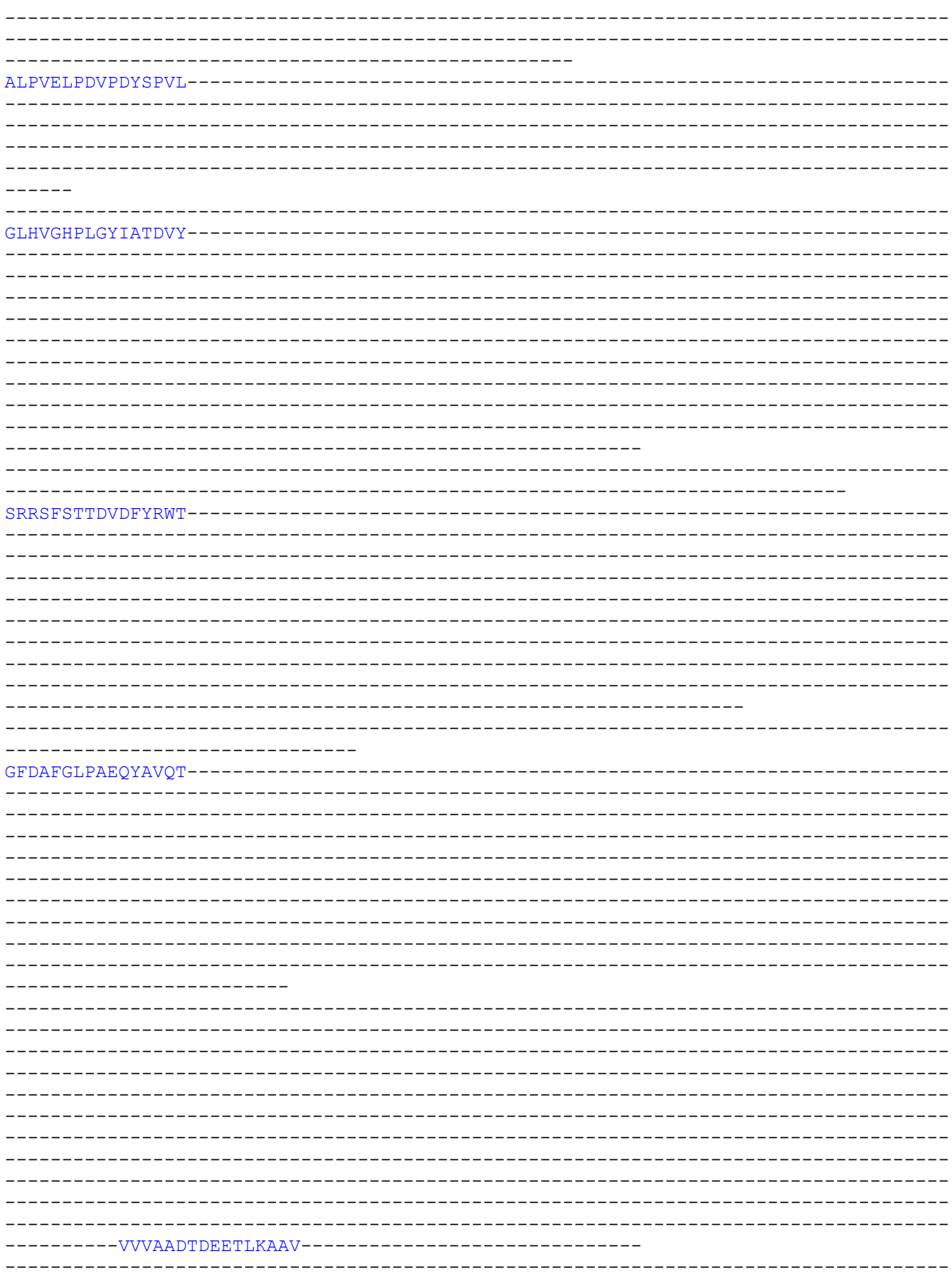

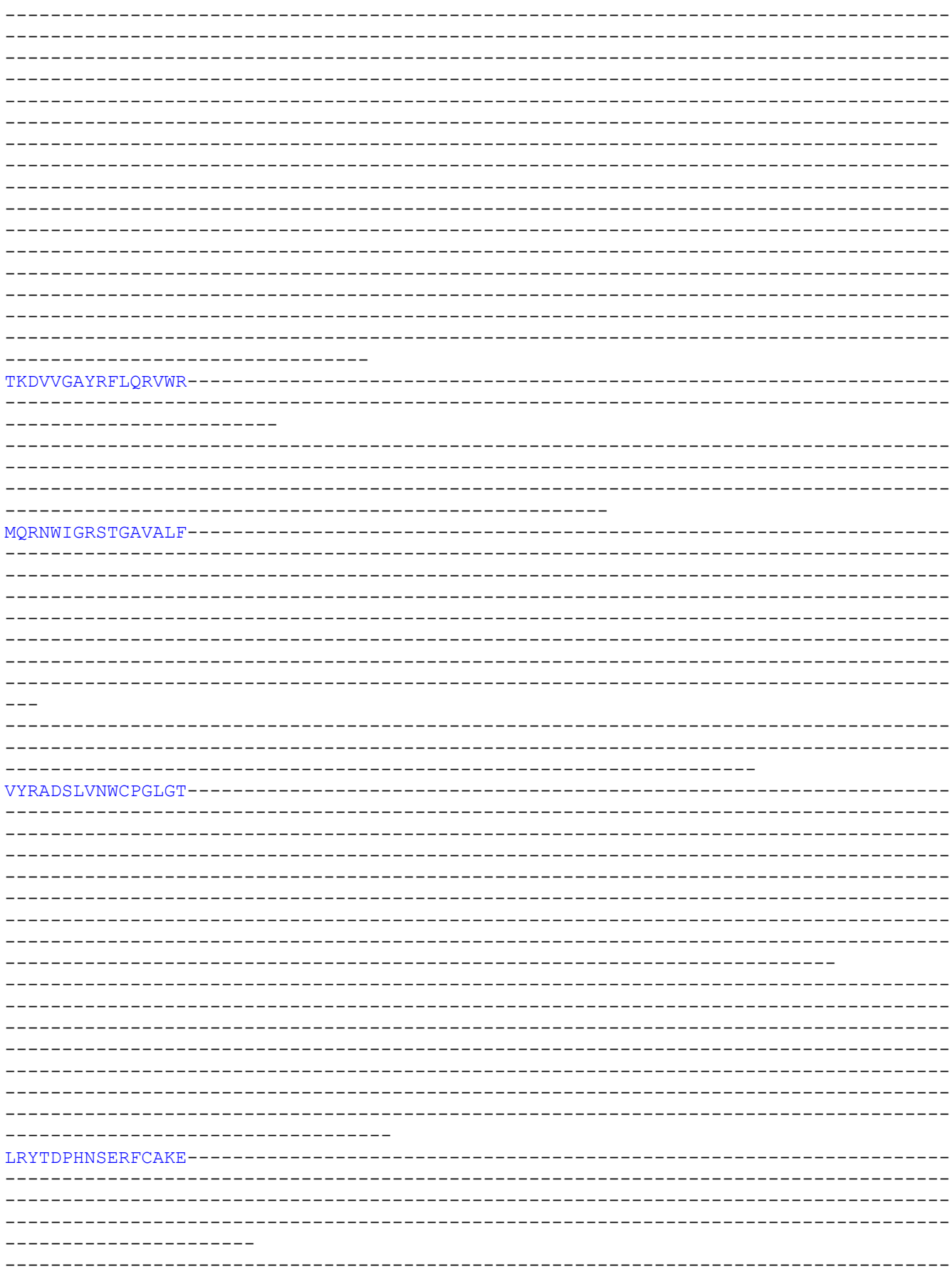

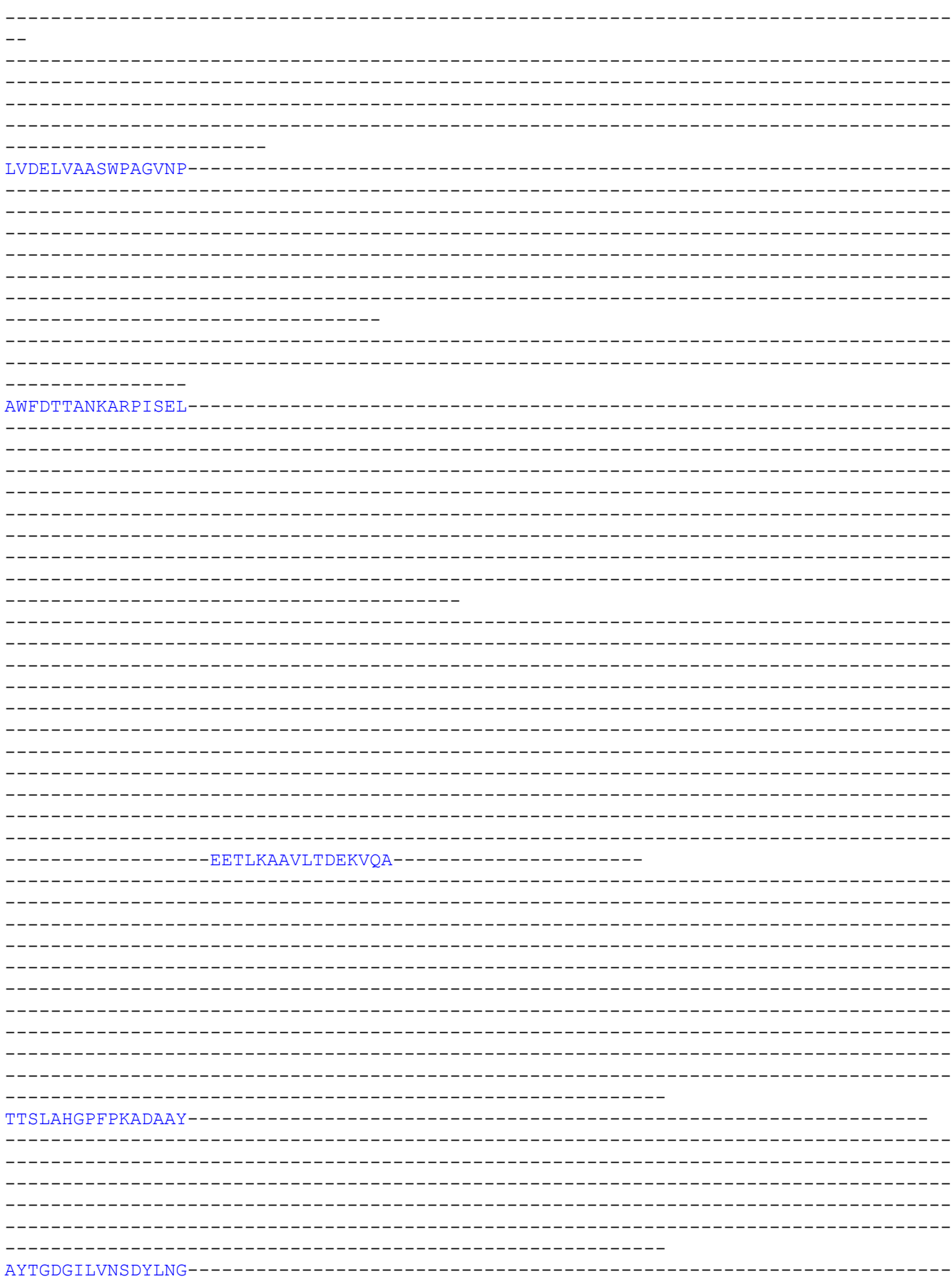

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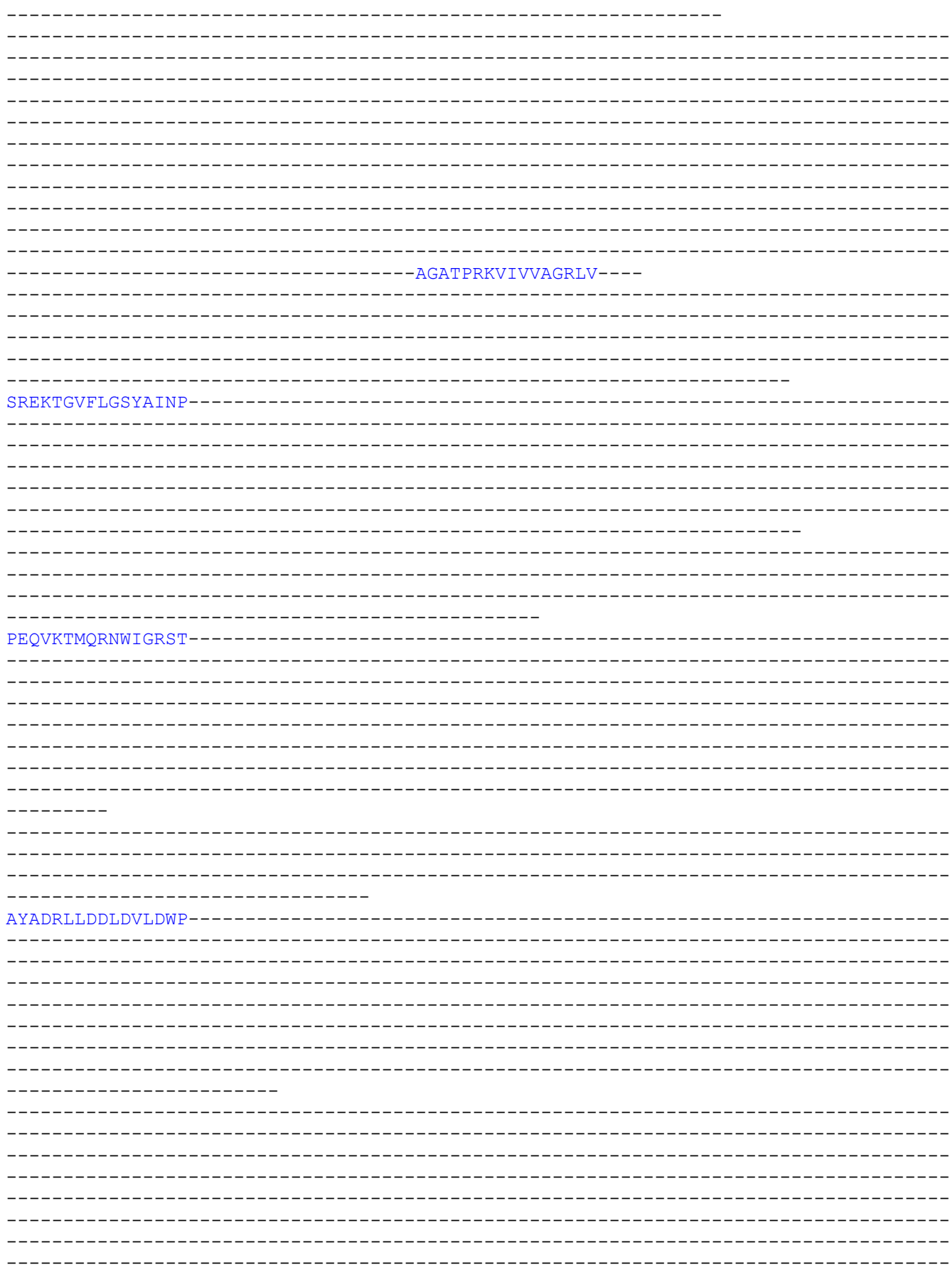

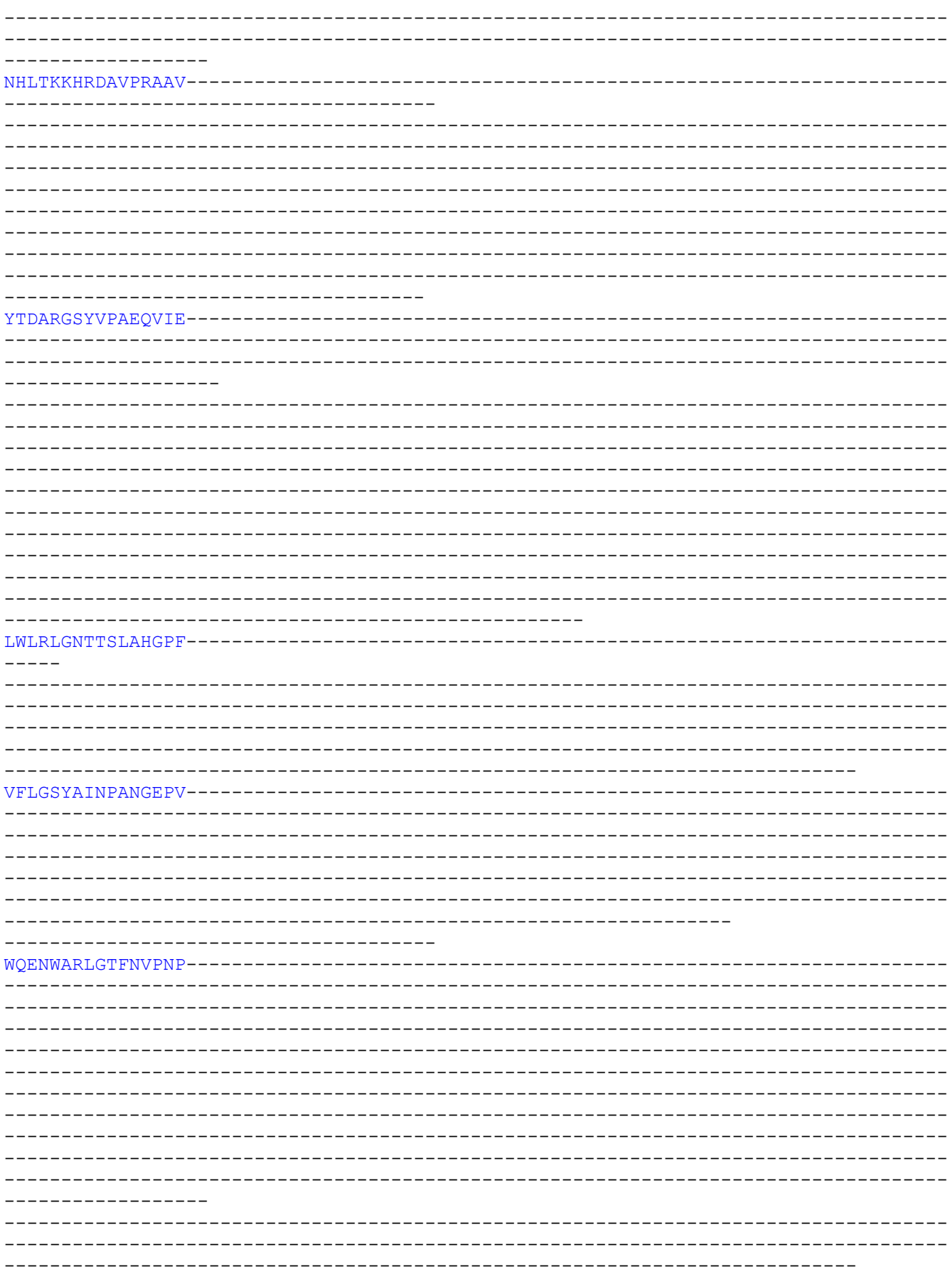

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