

logo

		MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNLDLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
NTDB id 1293	VP RS12240 WP 005479695.1		0
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 300889	CSC44 RS20275 WP 023100230.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		RLTPEKRLAALLAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEVPSPGK	
NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDLRLVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
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NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
NTDB id 1028	TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
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[illegible]

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Sequence	Position
DPPDPGAPILLPEDLCRRYGVFPHRLEGNRLVLLMKDPRNLLA	1-20
DDVRLALTKRKGLNVEVAPAVATEAAITKLI	21-30
ERFYCK	31-35
NPDPKVALMPEATARRYVVPVRLQGNLSLVAMKDPNRVFA	36-45
DDLKLITG	46-50
YPRHRVLMGVLTIEEQMVEFHCPVFRRGDKVFFAVSDPTQMPQIQKT	51-60
VSAG	61-65
YDYANI	66-70
CQQGLGRELITRYDALPIAKQGNLLLLAVSDPTLLQAE	71-80
EEFRFATG	81-85
YEYAS	86-90
CQQGLGRELITRHNALPLHRTPTSTLLAVADPTNQQA	91-100
EDDFRFATG	101-105
YEYAS	106-110
CQTLGLRDLITRHNALPLNRSTSTLLAVADPTNQQA	111-120
EDDFRFATG	121-125
IDVGTIPVNLVNEKLIKRRHAMVPLFSRGNTNLYLATDDPSKQAS	126-135
KEIQFHTG	136-140
LDRDSLPKDLISEKLVQRHRVVPVLRWRRGNKLFVGS	141-150
SDPANHQAINDVQFSTG	151-160
YDTSQIPKDLVDQKLILKRRILPLIQRGQILYVATSNPSNTEA	161-170
DAIRFNSK	171-175
FDPAFLFKDKIDLEKLIKQRYIMPLVHRGHVLYVATSNPTNTEAM	176-185
DAIRFNSK	186-190
LKVEPTIVEHDKLERLLSEHFE	191-200

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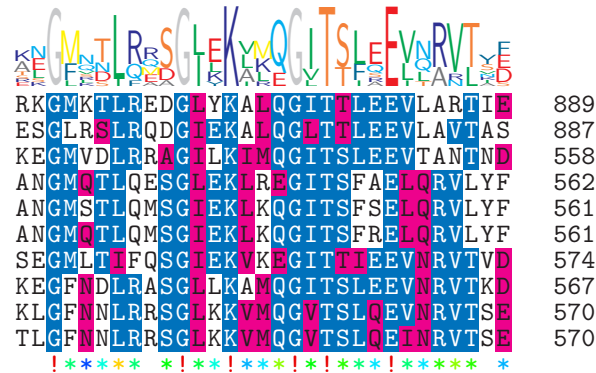
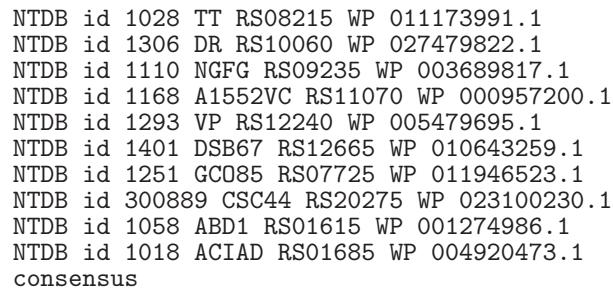
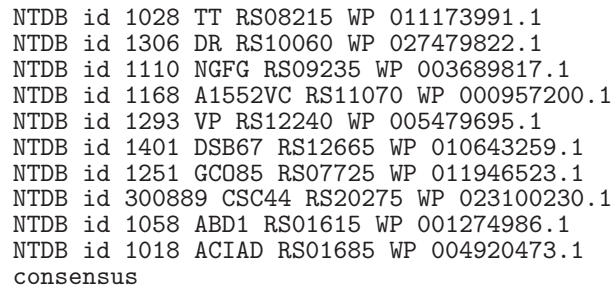
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```



-  non conserved
-  similar
-  > 50% conserved