

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAALLDQGYLGNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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 190710 A6L46 RS10655 WP 002221967.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

logo

NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIYVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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 190710 A6L46 RS10655 WP 002221967.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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 190710 A6L46 RS10655 WP 002221967.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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[illegible]

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DQLREALIQVQAREGKVKPLGEVITELGFASPDHVSATLQKQNVCGGRIEDTLVQSGKLSPEMLARSLLAAQLGYEFLDPIQ 397
 EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEALQKQRRCGGRIEDTLVQSGKLRPEALAQAVATQLGYPVDPEE 397
MLTNLVAILRQAE LISATQEQAVVTQVSASGTSVPEALLLSIFHAQELTEQLSHIFGLPETDLSR 66
MHSNLSTILRQKGLLTFSGEESLIEQVKASGISMPEALLSSGFFTSSELAETHSSIFGLSQPELSQ 66
MLTNLSTVLRQAGILTFSGEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSVFGLSCTSLNQ 66
MSVGLLRILVQNQVVTVEQAHHYY.NESQAGKEVLPMLFSDGVITSPKSLAALIARVFSYSILDLRH 65
MSVGLLRILVQNQVVTVEQAHHYY.NESQAGKEVLPMLFSDGVITSPKSLAALIARVFSYSILDLRH 65
MALATEEYRLQIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFVGPMLDINC 74
MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKFKFKQDIVPYLIDNFSISPLTIAEITISLEFGEPLDLGLV 74
MSALHTSPKFTGFRRRLVEEKHVSAAATMTALDAAKRAKQDITWAYLIEEVHISPSLSLAETISAEFAEYPFDLDV 74
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consensus
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Sequence	Position
NPPDPKVALMIP	1
EDATARRVV	2
VRVLRQ	3
NSLV	4
VMKDP	5
NFAL	6
DDL	7
DLK	8
LITG	9
.....	10
KE	11
LP	12
AV	13
MAEKD	14
IIR	15
LIER	16
YFGE	17
472	
DPDPGAPLL	18
PE	19
DL	20
LCRRYG	21
VFP	22
PHR	23
LEGN	24
RLV	25
LMKDP	26
NRIL	27
AL	28
DDV	29
RL	30
LALK	31
RK	32
GLN	33
YEV	34
AP	35
AV	36
ATEA	37
ITK	38
LIER	39
YFGK	40
477	
YDYANLC	41
QQLGL	42
RELIT	43
RYDAL	44
PIAK	45
QGNL	46
LL	47
LAV	48
SDPT	49
LL	50
QA	51
EE	52
FR	53
FATG	54
.....	55
LQ	56
VEL	57
AL	58
AD	59
HRA	60
LQA	61
AI	62
RR	63
LY	64
GR	65
141	
YEYASLC	66
QQLGL	67
RELIT	68
RHNAL	69
PLH	70
RT	71
PSTL	72
LL	73
AV	74
ADPT	75
NQ	76
QA	77
ED	78
DF	79
FATG	80
.....	81
LQ	82
VEL	83
LA	84
DF	85
REL	86
STA	87
IR	88
RR	89
LY	90
GR	91
141	
YEYASLC	92
QQLGL	93
RELIT	94
RHNAL	95
PLN	96
RT	97
STSL	98
LL	99
AV	100
ADPT	101
NQ	102
QA	103
ED	104
DF	105
FATG	106
.....	107
LQ	108
VEL	109
LA	110
DF	111
REL	112
STA	113
IR	114
RR	115
LY	116
GR	117
141	
YPRHRV	118
LMGT	119
LT	120
EE	121
QMV	122
FHC	123
VP	124
VFR	125
RGDK	126
V	127
FA	128
VS	129
DPT	130
Q	131
MP	132
Q	133
IQ	134
KT	135
VS	136
AA	137
AG	138
.....	139
E	140
V	141
E	142
V	143
E	144
D	145
D	146
Q	147
LA	148
GL	149
LD	150
W	151
GS	152
140	
YPRHRV	153
LMGT	154
LT	155
EE	156
QMV	157

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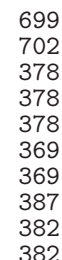
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NTDB id 1306 DR RS10060 WP 027479822.1
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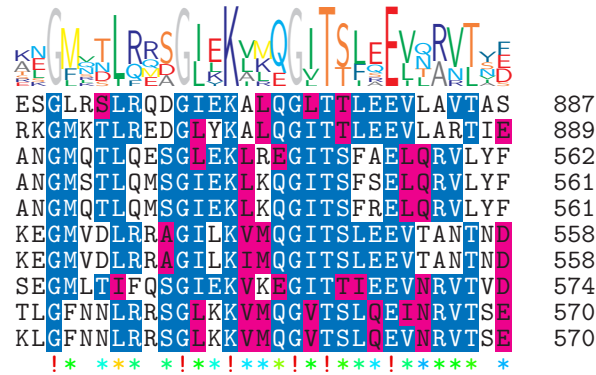
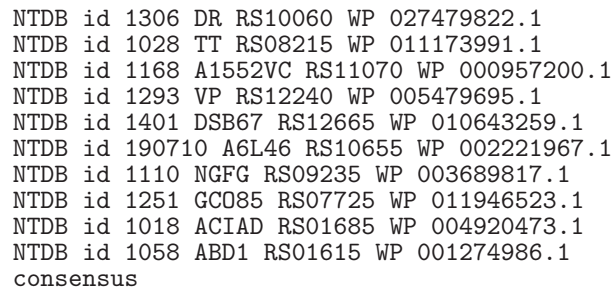
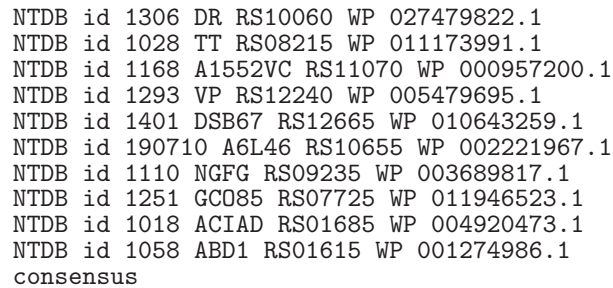
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consensus

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-  non conserved
-  similar
-  > 50% conserved