

logo

NTDB id 1028 TT RS08215 WP 011173991.1	MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNLDLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	RLTPEKRLRPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEYPSPGK	158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPALE..GDLRLVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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[illegible]

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consensus

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Sequence	Position
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NPPDPKVALMPEATARRVYVVPVRLQGNLSLVAMKDPNRNVFALDDDLKLITG.....KETLPVAMAEKDIIRLIERYFGE	472
YPRHRVLMGVLTTEEQMVEFHCVPFVFRGDKVFFAVSDPTQMPQIQKTVSAAG.....TAVELVIVEDDQLAGLLDWVGSR	140
YDYANLCQQGLGLRELITRYDALPIAKQGNLILLAVSDPTLLQAEEEFRFATG.....LQVELALADHRAALQAAIRRLYGR	141
YEYASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQAEDDFRFATG.....LQVELVLADFRELSTAIRRLYGR	141
YEYASLCQQLGLRLDLITRHNALPLNRSTSTLLAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAAIRRLYGR	141
IDVGTIPVNLVNEKLIKRRHAMVPLFSRGNTLYLATDDPSKQASIKETIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
VDKESQPRDLVSEKLIHQHRAALPLWFRGNKLFVAISDPTNHQAVTDIQFSTG.....LNTAILVEDDKLGDAIEKFFDS	147
YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNTEADAIKRFNSK.....LLVEPVIVEHHKLEKVLGGHFAE	149
FDPALFLDKDIDEKLIQKYRIMPLVHRGHVLYVATSNPTNLEAMDAIKRFNSK.....LKVEPIIVEHDKLERLLSEHFE	149



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consensus
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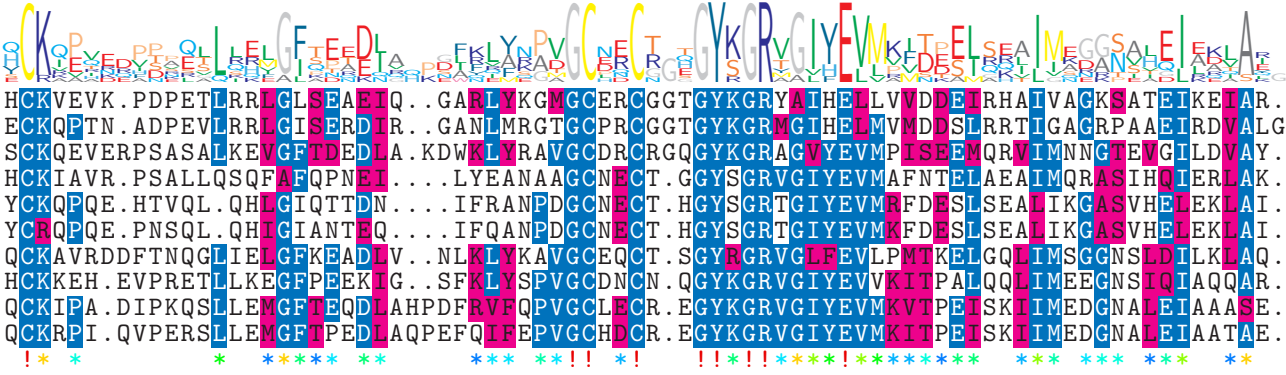
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consensus



782
779
449
458
458
458
467
462
462
462

logo

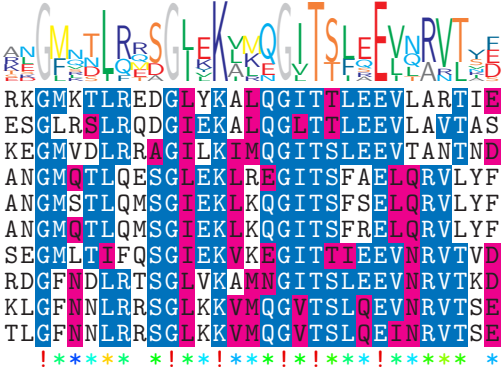
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consensus



858
856
527
531
530
530
543
537
539
539

logo

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consensus



889
887
558
562
561
561
574
568
570
570

[X] non conserved
[X] similar
[X] ≥ 50% conserved