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NTDB id 1159 ABDM36 RS04765 WP 001166105.1
NTDB id 1150 A1552VC RS08580 WP 001166105.1
NTDB id 1395 DSB67 RS04445 WP 010649155.1
NTDB id 1362 HI 1008 AAC22669.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
NTDB id 595 KW2 RS08725 WP 021037687.1
NTDB id 521 SMSK321 RS04960 WP 000443804.1
NTDB id 493 SM12261 RS04300 WP 000387351.1
NTDB id 263 KZH43 RS04195 WP 000387330.1
NTDB id 222 SPD RS04535 WP 000387330.1
NTDB id 188 SPR RS04295 WP 000387330.1
NTDB id 153 SP RS04730 WP 000387344.1
NTDB id 1069 ABD1 RS03060 WP 043960841.1
NTDB id 1041 HON27 RS14740 WP 005124713.1
NTDB id 105 BSU 25590 NP 390437.1
NTDB id 36 MW RS08230 WP 001793467.1
NTDB id 20 SA RS08005 WP 001802022.1
NTDB id 1014 ACIAD RS13855 WP 004924483.1
NTDB id 1066879 ACH6FP RS00050 WP 002853093.1
NTDB id 1242 Cj0011c YP 002343483.1
NTDB id 1127 NGFG RS10560 WP 003703428.1
NTDB id 1126 NGFG RS09375 WP 003703428.1
NTDB id 1125 NGFG RS07215 WP 003703428.1
NTDB id 1108 NGFG RS06525 WP 003703428.1
consensus

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[illegible]

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NTDB id 1159 ABDM36 RS04765 WP 001166105.1
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NTDB id 1108 NGFG RS06525 WP 003703428.1
consensus

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EQDLITVDVKGAVKSPGIYMLVYSRYVDAYKAGGLTEQADSKSLNLASKVYKDELYFYPTKKEEASORTCOSTO	MQIKTK.IVTLFLSLCLPT.....LPLLANAETAPAAQ.....	33
EQDLITVDVKGAVKSPGIYDLVSGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEESASQHTGSGAP..	MQIKTK.IVTLFLSLCLPT.....LPLLANAETAPAAQ.....	33
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	MKWMLTLCLLT.....LAPMSWAE.TKTKAD.....	25
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	MKTTL...FTSVVLGAL.....VSSSFAEEKATXQTAQSVVTT.....	36
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	MKKL.SRYTFSLLFG.L.....FSATTFAEEKVTTSTEHTPVVM.....	37
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	NKNEIMVDLKGAIVAKPNVYQISSDE.RLVDLIRQAGGFTDQADQKSINLSAKLKDEEVYVVPKVGESSSSSESTDSPTG..	142
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	146
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	146
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	146
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	146
EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	EQDLITVDVKGAVKSPGIYDLVPGS.RVNDAVQKAGGLTEQADSKSLNLAQKVVSDEALVYVPTKGEAASQQAGPGTA..	146
.....MQYSMRFWKNKYFVLIIMLCGLV.....ISPSVCAQSFDQNFQEWKVKQMYDQ.....	MQYSMRFWKNKYFVLIIMLCGLV.....ISPSVCAQSFDQNFQEWKVKQMYDQ.....	48
SNETIVIDIKGAVQHPGVYEMRTGD.RVSAITKAGGTSEQADEAQVNLAEITQDGTVVYIPKKGEETAV.....Q	MQYSMRFWKNKYFVLIIMLCGLV.....ISPSVCAQSFDQNFQEWKVKQMYDQ.....	48
NKGPVYVDVKGAVKHPNVYKMTSKD.RVVDLLDKAQ.LLEDADVQINLSEKLTQDKMIFIPH.....K.GQKNVEP	SNETIVIDIKGAVQHPGVYEMRTGD.RVSAITKAGGTSEQADEAQVNLAEITQDGTVVYIPKKGEETAV.....Q	127
NKGPVYVDVKGAVKHPNVYKMTSKD.RVVDLLDKAQ.LLDDADVSRINLSEKLTQDKMIFIPH.....K.GQKNVEP	NKGPVYVDVKGAVKHPNVYKMTSKD.RVVDLLDKAQ.LLEDADVQINLSEKLTQDKMIFIPH.....K.GQKNVEP	149
.....MSIR.HFF...T...FFWAT....LL..TLFSMQIVFAQGFDRQYDAWKTTQKAHDT	MSIR.HFF...T...FFWAT....LL..TLFSMQIVFAQGFDRQYDAWKTTQKAHDT	44
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MKKLLFLE..F.....	9
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MKKLLFLE..F.....	9
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	43
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	43
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	43
.....MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	MSRGGA...TPYRFLLR.HIV...ARCG.LLFAT....LKGKTMKKMFVLF CML.....	43

NTDB	id	1159	ABDM36	RS04765	WP	001166105.1	VEEGIVIT	VNINTASAEELATLLKGIGLKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	94
NTDB	id	1150	A1552VC	RS08580	WP	001166105.1	VEEGIVIT	VNINTASAEELATLLKGIGLKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	94
NTDB	id	1395	DSB67	RS04445	WP	010649155.1	KYEGIEIT	VNNSATAQEIATLLIGIGEKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	86
NTDB	id	1362	HI	1008	AAC22669.1		QAEA.....QVAPAVVSDK	LNINTATASEIQKSLTGIGAKKAAIVDYREANGPFTTHIDDLTNVKGIGEA	103
NTDB	id	1382	A4U84	RS07375	WP	062924234.1	QQ.V.....AATQKVNANV	VNINTATASEIQDKLVGIGAKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	103
NTDB	id	595	KW2	RS08725	WP	021037687.1	S.....S.VSNQISTTSGPK	VNINKADLTTELKQLTGIGQKKAQIDIDFRMKNNGDFKSIDELGKVS	208
NTDB	id	521	SMSK321	RS04960	WP	000443804.1	SSTSCKDKK	LNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGAK	206
NTDB	id	493	SM12261	RS04300	WP	000387351.1	SSTSCKKK	VNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGAK	206
NTDB	id	263	KZH43	RS04195	WP	000387330.1	SSISKEKK	VNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGGK	206
NTDB	id	222	SPD	RS04535	WP	000387330.1	SSISKEKK	VNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGGK	206
NTDB	id	188	SPR	RS04295	WP	000387330.1	SSISKEKK	VNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGGK	206
NTDB	id	153	SP	RS04730	WP	000387344.1	SSTSCKKK	VNINKASLEELKQVKGIGGKRAQIDIDHREANGKFKSVDELKKVSGIGGK	206
NTDB	id	1069	ABD1	RS03060	WP	043960841.1	IHLNQANVNEFQQ	IKLGIGEKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	127
NTDB	id	1041	HN027	RS14740	WP	005124713.1	IHLNQANVNEFQQ	IKLGIGEKKAAQIVDYREANGPFTTHIDDLTNVKGIGEA	127
NTDB	id	105	BSU	25590	NP	390437.1	QGGG.....GSV.....QSDGGKGAL	VNINTATLEELQGISGVGPSKAEIAYREANGPFTTHIDDLTNVKGIGEA	195
NTDB	id	36	MW	RS08230	WP	001793467.1	QIGVNSV.....HV.....KNGNTNNTK	VNINTASVSELMSVPGVGQAKANAIVDYREANGPFTTHIDDLTNVKGIGEA	219
NTDB	id	20	SA	RS08005	WP	001802022.1	QIEVNSV.....HV.....KNGNTNNTK	VNINTASVSELMSVPGVGQAKANAIVDYREANGPFTTHIDDLTNVKGIGEA	219
NTDB	id	1014	ACIAD	RS13855	WP	004924483.1	RLNSSASHHSLSKP...TQQSGTGVK	VNINSATAKELQQHLHGVEKKALAEYRQYQKFAFVDDLQKVKGIGPK	119
NTDB	id	1066879	ACH6FP	RS00050	WP	002853093.1	ALTAFLFGA	VNINTATLTKELKSLNGIGEAKAKAILEYRKEANFTSIDDLQKVKGIGDK	69
NTDB	id	1242	Cj0011c	YP	002343483.1		ALTAFLFGA	VNINTATLTKELKSLNGIGEAKAKAILEYRKEANFTSIDDLQKVKGIGDK	69
NTDB	id	1127	NGFG	RS10560	WP	003703428.1	FSCAFSLAA	VNINAASQQLEALPGIGPAKAKAIAEYRAQNGAFKSVDDLQKVKGIGPAV	104
NTDB	id	1126	NGFG	RS09375	WP	003703428.1	FSCAFSLAA	VNINAASQQLEALPGIGPAKAKAIAEYRAQNGAFKSVDDLQKVKGIGPAV	104
NTDB	id	1125	NGFG	RS07215	WP	003703428.1	FSCAFSLAA	VNINAASQQLEALPGIGPAKAKAIAEYRAQNGAFKSVDDLQKVKGIGPAV	104
NTDB	id	1108	NGFG	RS06525	WP	003703428.1	FSCAFSLAA	VNINAASQQLEALPGIGPAKAKAIAEYRAQNGAFKSVDDLQKVKGIGPAV	104
consensus							***! !*! *	***! !*! *	***! !*! *

NTDB	id	1159	ABDM36	RS04765	WP	001166105.1	RNNAARILL.....	103
NTDB	id	1150	A1552VC	RS08580	WP	001166105.1	RNNAARILL.....	103
NTDB	id	1395	DSB67	RS04445	WP	010649155.1	RKNEDRILL.....	95
NTDB	id	1362	HI	1008	AAC22669.1	EKNRDRIF.....	112	
NTDB	id	1382	A4U84	RS07375	WP	062924234.1	EKNRDCIVIE.....	113
NTDB	id	595	KW2	RS08725	WP	021037687.1	EKLKDEISID.....	218
NTDB	id	521	SMSK321	RS04960	WP	000443804.1	EKLKDYVTVD.....	216
NTDB	id	493	SM12261	RS04300	WP	000387351.1	EKLKDYVTVD.....	216
NTDB	id	263	KZH43	RS04195	WP	000387330.1	EKLKDYVTVD.....	216
NTDB	id	222	SPD	RS04535	WP	000387330.1	EKLKDYVTVD.....	216
NTDB	id	188	SPR	RS04295	WP	000387330.1	EKLKDYVTVD.....	216
NTDB	id	153	SP	RS04730	WP	000387344.1	EKLKDYVTVD.....	216
NTDB	id	1069	ABD1	RS03060	WP	043960841.1	EKNKSRLAL.....	136
NTDB	id	1041	HON27	RS14740	WP	005124713.1	EKNKSRLAL.....	136
NTDB	id	105	BSU	25590	NP	390437.1	EKTSSITVK.....	205
NTDB	id	36	MW	RS08230	WP	001793467.1	DCLKSYFTI.....	228
NTDB	id	20	SA	RS08005	WP	001802022.1	DCLKSYFTI.....	228
NTDB	id	1014	ACIAD	RS13855	WP	004924483.1	EKNRDLAI.....	128
NTDB	id	1066879	ACH6FP	RS00050	WP	002853093.1	EKITNDITIE.....	79
NTDB	id	1242	Cj0011c	YP	002343483.1	EKITNDITIE.....	79	
NTDB	id	1127	NGFG	RS10560	WP	003703428.1	AKLKDQASVGAPAPKGPAKPVLPAVKK	131
NTDB	id	1126	NGFG	RS09375	WP	003703428.1	AKLKDQASVGAPAPKGPAKPVLPAVKK	131
NTDB	id	1125	NGFG	RS07215	WP	003703428.1	AKLKDQASVGAPAPKGPAKPVLPAVKK	131
NTDB	id	1108	NGFG	RS06525	WP	003703428.1	AKLKDQASVGAPAPKGPAKPVLPAVKK	131
consensus							* * * * *	

 non conserved
 similar
 $\geq 50\%$ conserved