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NTDB id 617 LCA RS06480 WP 011375001.1
NTDB id 586 KW2 RS10855 WP 011836048.1
NTDB id 404831 GEO24 RS00840 WP 003046182.1
NTDB id 584 DLJ51 RS00890 WP 019777327.1
NTDB id 394 FSA28 RS09405 WP 002291652.1
NTDB id 385 SMU RS09035 WP 0026263435.1
NTDB id 429 SGO RS09420 WP 012130942.1
NTDB id 500 SM12261 RS00945 WP 000249545.1
NTDB id 270 KZH43 RS09265 WP 000249564.1
NTDB id 229 SPD RS09895 WP 000249564.1
NTDB id 195 SPR RS09430 WP 000249564.1
NTDB id 160 SP RS10380 WP 000249564.1
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Protein	Sequence	Score
1	MVQEIAQEIIIRSAKKGAQDIYFYVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	79
2	MVQKKAQELIQKAIEMASDIYFIASGNLYKIYIRQQLGRTLTEEVNQEIGLALLTHFKFLAGMNTGERRRVQLGACW	78
3	MVQALAKSLIQKEAEQVQAQDIYIIPRADQYELFLRIGDERRLIDVYRGDRMAHLISHFKFVAGMTVGKEKRRSQLGSCD	78
4	MVEVQELGKELIRQAVEEQAQDIYLLPKPAVKIYLRFGKEKRLHITQCPPEQAAGLISHFKFLAGMNVGEKRRSQLGACD	80
5	MVQKLGKRIIAEAVQNKAAQDIYIIPKKESYELYMRIGNERRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCD	78
6	MVQKLGKRIIAEAVQNKAAQDIYIIPKKESYELYMRIGNERRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCD	78
7	MVQKIAQAIVRQAKECAQDIYFVPKDDCYELHMRIGDERRFITQYDFDQLAAVISHFKFLAGMNVGEKRRSQLGSCD	78
8	MVQEIAQEIIIRSAKKGAQDIYFVPKLDAYELHMRVGDERCKIGCYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
9	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
10	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
11	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
12	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
13	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78
14	MVQEIAQEIIIRSAKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKEFVAGMNVGEKRRSQLGSCD	78

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[illegible]

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NTDB id 617 LCA RS06480 WP 011375001.1
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NTDB id 617 LCA RS06480 WP 011375001.1	QGVVARLLDLGISELQLRACLTGTAYQSLVTKDDVVQAH...YELLTGSDYFSK.....KEGGCDV.....	296
NTDB id 586 KW2 RS10855 WP 011836048.1	KGVVQRLLELGLSDWELKNGLEAVVYQRLIAGKGVLDIAKSKFDTWSPKKWNEKTIENLYANGHLTAIEAEREKISINQAS	315
NTDB id 404831 GEO24 RS00840 WP 003046182.1	SGVYARLLELGVTRAELDNCLALIAQRLINGGALIDATQKNFEHYLPDRWNQQLDQLLAAGHLSPKQARLEKIVQ....	313
NTDB id 584 DLJ51 RS00890 WP 019777327.1	PGVYARILELGVSDDELNCLAGIAYQRLIGGGGLIDFAQDHFQNHQAECWNEKIDQLLAAGHLTEEEAAAAEKIKD....	315
NTDB id 394 FSA28 RS09405 WP 002291652.1	PGVYARMLELGTSSSEELQNALCGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAQAEIEIED....	313
NTDB id 385 SMU RS09035 WP 002263435.1	PGVYARMLELGTSSSEELQNALRGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAQAEIEIED....	313
NTDB id 429 SGO RS09420 WP 012130942.1	PGVYERLLELGVSEEEELKIVLQGCYQRLIGGGGVIDFASDNYQEHEPTVWNQQIDQLLAAGHIHPEQAEAEKIRNQQAK	316
NTDB id 500 SM12261 RS00945 WP 000249545.1	RGVYERLLELGVSEEEELAVVLQGCYQRLIGGGGIVDFANKDYQEHQSTSWNAQIDQLLDGHITSLQAETEKISYS...	313
NTDB id 270 KZH43 RS09265 WP 000249564.1	RGVYERLLELGVSEEEELAVVLQGCYQRLIGGGGIVDFASRDYQEHQAQKWNQEQIDQLLDGHITSLQAETEKISYS...	313
NTDB id 229 SPD RS09895 WP 000249564.1	RGVYERLLELGVSEEEELAVVLQGCYQRLIGGGGIVDFASRDYQEHQAQKWNQEQIDQLLDGHITSLQAETEKISYS...	313
NTDB id 195 SPR RS09430 WP 000249564.1	RGVYERLLELGVSEEEELAVVLQGCYQRLIGGGGIVDFASRDYQEHQAQKWNQEQIDQLLDGHITSLQAETEKISYS...	313
NTDB id 160 SP RS10380 WP 000249564.1	RGVYERLLELGVSEEEELAVVLQGCYQRLIGGGGIVDFASRDYQEHQAQKWNQEQIDQLLDGHITSLQAETEKISYS...	313
consensus	!!*!*!!!!*****! !**!!*!***** **** * * **** ***** ***** ** *	

logo

NTDB id 617 LCA RS06480 WP 011375001.1	KIDTTDGESEFE	296
NTDB id 586 KW2 RS10855 WP 011836048.1	KIDTTDGESEFE	326
NTDB id 404831 GEO24 RS00840 WP 003046182.1		313
NTDB id 584 DLJ51 RS00890 WP 019777327.1		315
NTDB id 394 FSA28 RS09405 WP 002291652.1		313
NTDB id 385 SMU RS09035 WP 002263435.1		313
NTDB id 429 SGO RS09420 WP 012130942.1	TSY.....	319
NTDB id 500 SM12261 RS00945 WP 000249545.1		313
NTDB id 270 KZH43 RS09265 WP 000249564.1		313
NTDB id 229 SPD RS09895 WP 000249564.1		313
NTDB id 195 SPR RS09430 WP 000249564.1		313
NTDB id 160 SP RS10380 WP 000249564.1		313
consensus		

- X non conserved
- X similar
- X ≥ 50% conserved