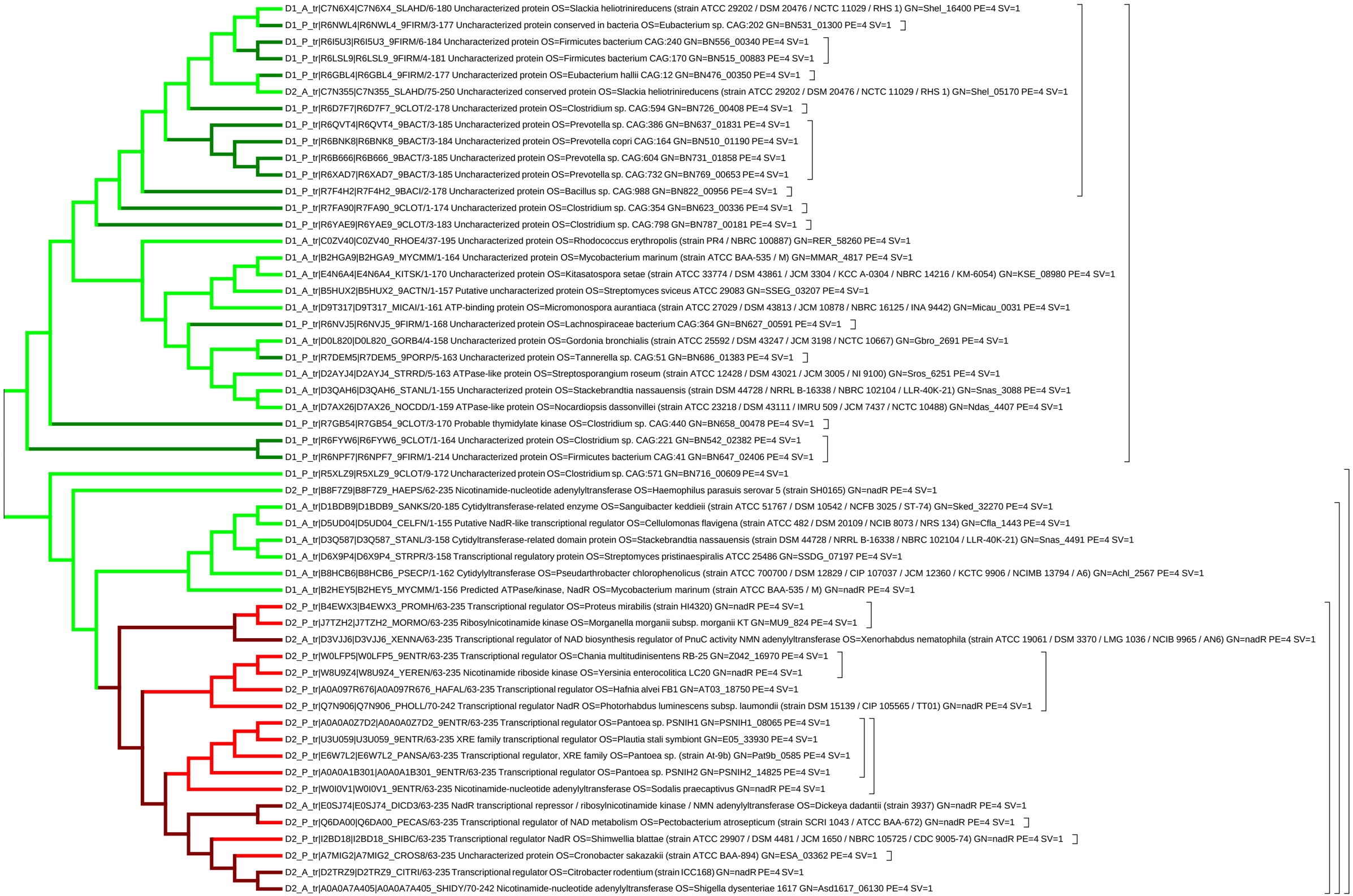
D1_A_tr|C7N6X4|C7N6X4_SLAHD/6-180 Uncharacterized protein OS=Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) GN=Shel_16400 PE=4 SV=1
D1_P_tr|R6NWL4|R6NWL4_9FIRM/3-177 Uncharacterized protein conserved in bacteria OS=Eubacterium sp. CAG:202 GN=BN531_01300 PE=4 SV=1
D1_P_tr|R6I5U3|R6I5U3_9FIRM/6-184 Uncharacterized protein OS=Firmicutes bacterium CAG:240 GN=BN556_00340 PE=4 SV=1
D1_P_tr|R6LSL9|R6LSL9_9FIRM/4-181 Uncharacterized protein OS=Firmicutes bacterium CAG:170 GN=BN515_00883 PE=4 SV=1
D1_P_tr|R6GBL4|R6GBL4_9FIRM/2-177 Uncharacterized protein OS=Eubacterium hallii CAG:12 GN=BN476_00350 PE=4 SV=1
D2_A_tr|C7N355|C7N355_SLAHD/75-250 Uncharacterized conserved protein OS=Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) GN=Shel_05170 PE=4 SV=1
D1_P_tr|R6D7F7|R6D7F7_9CLOT/2-178 Uncharacterized protein OS=Clostridium sp. CAG:594 GN=BN726_00408 PE=4 SV=1
D1_P_tr|R6QVT4|R6QVT4_9BACT/3-185 Uncharacterized protein OS=Prevotella sp. CAG:386 GN=BN637_01831 PE=4 SV=1
D1_P_tr|R6BNK8|R6BNK8_9BACT/3-184 Uncharacterized protein OS=Prevotella copri CAG:164 GN=BN510_01190 PE=4 SV=1
D1_P_tr|R6B666|R6B666_9BACT/3-185 Uncharacterized protein OS=Prevotella sp. CAG:604 GN=BN731_01858 PE=4 SV=1
D1_P_tr|R6XAD7|R6XAD7_9BACT/3-185 Uncharacterized protein OS=Prevotella sp. CAG:732 GN=BN769_00653 PE=4 SV=1
D1_P_tr|R7F4H2|R7F4H2_9BACI/2-178 Uncharacterized protein OS=Bacillus sp. CAG:988 GN=BN822_00956 PE=4 SV=1
D1_P_tr|R7FA90|R7FA90_9CLOT/1-174 Uncharacterized protein OS=Clostridium sp. CAG:354 GN=BN623_00336 PE=4 SV=1
D1_P_tr|R6YAE9|R6YAE9_9CLOT/3-183 Uncharacterized protein OS=Clostridium sp. CAG:798 GN=BN787_00181 PE=4 SV=1
D1_A_tr|C0ZV40|C0ZV40_RHOE4/37-195 Uncharacterized protein OS=Rhodococcus erythropolis (strain PR4 / NBRC 100887) GN=RER_58260 PE=4 SV=1
D1_A_tr|B2HGA9|B2HGA9_MYCMM/1-164 Uncharacterized protein OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=MMAR_4817 PE=4 SV=1
D1_A_tr|E4N6A4|E4N6A4_KITSK/1-170 Uncharacterized protein OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=KSE_08980 PE=4 SV=1
D1_A_tr|B5HUX2|B5HUX2_9ACTN/1-157 Putative uncharacterized protein OS=Streptomyces sviceus ATCC 29083 GN=SSEG_03207 PE=4 SV=1
D1_A_tr|D9T317|D9T317_MICAI/1-161 ATP-binding protein OS=Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442) GN=Micau_0031 PE=4 SV=1
D1_P_tr|R6NVJ5|R6NVJ5_9FIRM/1-168 Uncharacterized protein OS=Lachnospiraceae bacterium CAG:364 GN=BN627_00591 PE=4 SV=1
D1_A_tr|D0L820|D0L820_GORB4/4-158 Uncharacterized protein OS=Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) GN=Gbro_2691 PE=4 SV=1
D1_P_tr|R7DEM5|R7DEM5_9PORP/5-163 Uncharacterized protein OS=Tannerella sp. CAG:51 GN=BN686_01383 PE=4 SV=1
D1_A_tr|D2AYJ4|D2AYJ4_STRRD/5-163 ATPase-like protein OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_6251 PE=4 SV=1
D1_A_tr|D3QAH6|D3QAH6_STANL/1-155 Uncharacterized protein OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_3088 PE=4 SV=1
D1_A_tr|D7AX26|D7AX26_NOCDD/1-159 ATPase-like protein OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_4407 PE=4 SV=1
D1_P_tr|R7GB54|R7GB54_9CLOT/3-170 Probable thymidylate kinase OS=Clostridium sp. CAG:440 GN=BN658_00478 PE=4 SV=1
D1_P_tr|R6FYW6|R6FYW6_9CLOT/1-164 Uncharacterized protein OS=Clostridium sp. CAG:221 GN=BN542_02382 PE=4 SV=1
D1_P_tr|R6NPF7|R6NPF7_9FIRM/1-214 Uncharacterized protein OS=Firmicutes bacterium CAG:41 GN=BN647_02406 PE=4 SV=1
D1_P_tr|R5XLZ9|R5XLZ9_9CLOT/9-172 Uncharacterized protein OS=Clostridium sp. CAG:571 GN=BN716_00609 PE=4 SV=1
D2_P_tr|B8F7Z9|B8F7Z9_HAEPS/62-235 Nicotinamide-nucleotide adenylyltransferase OS=Haemophilus parasuis serovar 5 (strain SH0165) GN=nadR PE=4 SV=1
D1_A_tr|D1BDB9|D1BDB9_SANKS/20-185 Cytidyltransferase-related enzyme OS=Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74) GN=Sked_32270 PE=4 SV=1
D1_A_tr|D5UD04|D5UD04_CELFN/1-155 Putative NadR-like transcriptional regulator OS=Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134) GN=Cfla_1443 PE=4 SV=1
D1_A_tr|D3Q587|D3Q587_STANL/3-158 Cytidyltransferase-related domain protein OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_4491 PE=4 SV=1
D1_A_tr|D6X9P4|D6X9P4_STRPR/3-158 Transcriptional regulatory protein OS=Streptomyces pristinaespiralis ATCC 25486 GN=SSDG_07197 PE=4 SV=1
D1_A_tr|B8HCB6|B8HCB6_PSECP/1-162 Cytidylyltransferase OS=Pseudarthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / CIP 107037 / JCM 12360 / KCTC 9906 / NCIMB 13794 / A6) GN=Achl_2567 PE=4 SV=1
D1_A_tr|B2HEY5|B2HEY5_MYCMM/1-156 Predicted ATPase/kinase, NadR OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=nadR PE=4 SV=1
D2_P_tr|B4EWX3|B4EWX3_PROMH/63-235 Transcriptional regulator OS=Proteus mirabilis (strain HI4320) GN=nadR PE=4 SV=1
D2_P_tr|J7TZH2|J7TZH2_MORMO/63-235 Ribosylnicotinamide kinase OS=Morganella morganii subsp. morganii KT GN=MU9_824 PE=4 SV=1
D2_A_tr|D3VJJ6|D3VJJ6_XENNA/63-235 Transcriptional regulator of NAD biosynthesis regulator of PnuC activity NMN adenylyltransferase OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=nadR PE=4 SV=1
D2_P_tr|W0LFP5|W0LFP5_9ENTR/63-235 Transcriptional regulator OS=Chania multitudinisentens RB-25 GN=Z042_16970 PE=4 SV=1
D2_P_tr|W8U9Z4|W8U9Z4_YEREN/63-235 Nicotinamide riboside kinase OS=Yersinia enterocolitica LC20 GN=nadR PE=4 SV=1
D2_P_tr|A0A097R676|A0A097R676_HAFAL/63-235 Transcriptional regulator OS=Hafnia alvei FB1 GN=AT03_18750 PE=4 SV=1
D2_P_tr|Q7N906|Q7N906_PHOLL/70-242 Transcriptional regulator NadR OS=Photorhabdus luminescens subsp. laumondii (strain DSM 15139 / CIP 105565 / TT01) GN=nadR PE=4 SV=1
D2_P_tr|A0A0A0Z7D2|A0A0A0Z7D2_9ENTR/63-235 Transcriptional regulator OS=Pantoea sp. PSNIH1 GN=PSNIH1_08065 PE=4 SV=1
D2_P_tr|U3U059|U3U059_9ENTR/63-235 XRE family transcriptional regulator OS=Plautia stali symbiont GN=E05_33930 PE=4 SV=1
D2_P_tr|E6W7L2|E6W7L2_PANSA/63-235 Transcriptional regulator, XRE family OS=Pantoea sp. (strain At-9b) GN=Pat9b_0585 PE=4 SV=1
D2_P_tr|A0A0A1B301|A0A0A1B301_9ENTR/63-235 Transcriptional regulator OS=Pantoea sp. PSNIH2 GN=PSNIH2_14825 PE=4 SV=1
D2_P_tr|W0I0V1|W0I0V1_9ENTR/63-235 Nicotinamide-nucleotide adenylyltransferase OS=Sodalis praecaptivus GN=nadR PE=4 SV=1
D2_A_tr|E0SJ74|E0SJ74_DICD3/63-235 NadR transcriptional repressor / ribosylnicotinamide kinase / NMN adenylyltransferase OS=Dickeya dadantii (strain 3937) GN=nadR PE=4 SV=1
D2_P_tr|Q6DA00|Q6DA00_PECAS/63-235 Transcriptional regulator of NAD metabolism OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=nadR PE=4 SV=1
D2_P_tr|I2BD18|I2BD18_SHIBC/63-235 Transcriptional regulator NadR OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=nadR PE=4 SV=1
D2_P_tr|A7MIG2|A7MIG2_CROS8/63-235 Uncharacterized protein OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=ESA_03362 PE=4 SV=1
D2_A_tr|D2TRZ9|D2TRZ9_CITRI/63-235 Transcriptional regulator OS=Citrobacter rodentium (strain ICC168) GN=nadR PE=4 SV=1
D2_A_tr|A0A0A7A405|A0A0A7A405_SHIDY/70-242 Nicotinamide-nucleotide adenylyltransferase OS=Shigella dysenteriae 1617 GN=Asd1617_06130 PE=4 SV=1