SUPLEMENTARY MATERIALS:

Table S1.
Summary of X-ray data and model parameters of RutD protein

Summary of Crystallographic Information	
A. Data Collection and Phasing	
Beamline	21 ID-F ANL
Wavelength (Å)	0.9787
Space group	$P4_12_12$
Resolution range (Å)	50.00-2.10 (2.10-2.14)
Unit cell parameters	
Length (Å)	a = 79.6 b = 79.6 c = 161.8
Angles (^{o})	$\alpha = \beta = \gamma = 90$
Wilson plot B (Å^2)	25.1
R_{merge}	0.357*
I/σ(I)	11.6 (2.9)
Completeness (%)	98.0 (95.0)
Redundancy	10.2 (8.4)
No. of observations	315760
No of unique reflections	19039 (898)
Figure of merit for SAD phasing (after DM)	0.808
B. Refinement	
R_{work}/R_{free} (%)	16.9/22.6
No. of protein atoms (B-factor, Å^2)	4060 (37.6)
No. of solvent atoms (B-factor, Å^2)	313 (41.7)
No. of ligand atoms (B-factor, Å^2)	33 (42.3)
R.m.s. deviations	
Bond lengths (Å)	0.013
Bond angles (^{o})	1.5
Ramachandran plot	
Most favored (%)	98.86
Allowed (%)	1.14
Disallowed (%)	0

* High value of R_{merge} is caused by multiple crystal lattices (Supplementary figure S3). When corrections for radiation decay and anisotropic diffraction are applied [40,41] the traditional crystallographic parameters are not the best to describe the quality of the diffraction data. Despite the very high R_{merge} the R, R_{free}, and geometrical parameters obtained after structure refinement are significantly better than for other structures deposited to PDB during the last two years.

Fig.S1. Multiple sequence alignment of protein sequences belonging to the RutD family, obtained by CLANS clustering. 100% conserved putative active site residues are highlighted: H87 and H237 in magenta, R128 in blue, and D209 in red (following the RutD sequence numbering). The residue C-terminal to H87 is also highlighted: A in teal, and S in grey. The RutD sequence is underscored.

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                                         10        20        30        40        50        60        70        80        90       100       110
                                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
gi|316935663|ref|YP_004110645_  -----------------MPIVQLSDVALRYEIIGTGEPVLLVAGLGGSAGYWAPNVEAFAAR-HQVVLHDHRGTG--GSTRSEMEYSVELLADDLLRLMDHLKIEKAHLV
D2MBB2_RHOPA_22-255             --------------------------------------VLLVAGLGGSAGYWAPNVEAFAAR-HQVVLHDHRGTG--GSTRSEMEYSVELLADDLLRLMDHLKIEKAHLV
gi|300715742|ref|YP_003740545_  -----------------MPSIMTNGILTHYEIQGTGPAIVFVSGLGGTAAYWQPQIAAFAKD-FTVLTYDQRGSG--TTEHPAGPYSIETLVDDLFCLLSELKLERPILI
gi|260429719|ref|ZP_05783695_1  --------------MTSLTVETGDGAVLKVRRQGRGAPVVLVSGLGGTAGFWDP-VIARLQDRFEFITFDQRGIAGSTR--GSAPVNIAQLARDVLTICDALELTRAAFL
D0DBU3_9RHOB_25-257             --------------------------------------VVLVSGLGGTAGFWDP-VIARLQDRFEFITFDQRGIAGSTR--GSAPVNIAQLARDVLTICDALELTRAAFL
gi|114762401|ref|ZP_01441859_1  --------------MTELVVTTPDGAKLKARRHGQGQPLVLVSGLGGTAGFWDP-AIALLGSEFELITFDQRGIAGSSR--GSAPVDIAQLAADVLTVCDAMGVESADFL
Q0FUQ8_9RHOB_25-257             --------------------------------------LVLVSGLGGTAGFWDP-AIALLGSEFELITFDQRGIAGSSR--GSAPVDIAQLAADVLTVCDAMGVESADFL
gi|90418551|ref|ZP_01226463_1|  --------------MTDFSVSAGDGAVLKASREGAGAPLVLISGLGGTAGFWAP-VVAGLRDRFEILTFDQRGIGASTR--GTAETDIAQLADDVQAVLDAAGIEAATIV
Q1YL57_MOBAS_25-257             --------------------------------------LVLISGLGGTAGFWAP-VVAGLRDRFEILTFDQRGIGASTR--GTAETDIAQLADDVQAVLDAAGIEAATIV
gi|33600731|ref|NP_888291_1|_p  ---------MIRQRMTDFTVILPDGARLAARETGAGEAVLLVSGLGGTGAFWTP-VAAGLQGR-RCVMFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
Q7WLJ9_BORBR_30-260             --------------------------------------VLLVSGLGGTGAFWTP-VAAGLQGR-RCVMFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
gi|33596897|ref|NP_884540_1|_p  ---------MIRQRMTDLTVILPDGARLAARETGAGEAVLLVSGLGGTGAFWTP-VAAGLQGR-RCVVFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
gi|33592963|ref|NP_880607_1|_p  ---------MIRQRMTDFTVILPDGARLAARETGAGEAVLLVSGLGGTGAFWTP-VAAGLQGR-RCVVFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
Q7VX84_BORPE_30-260             --------------------------------------VLLVSGLGGTGAFWTP-VAAGLQGR-RCVVFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
Q7W851_BORPA_30-260             --------------------------------------VLLVSGLGGTGAFWTP-VAAGLQGR-RCVVFDQRGVAGSTR--GDAAVDIARLAADAWAVLDARGIERAHLV
gi|119383793|ref|YP_914849_1|_  ----------------MPVHVADDGCRIHCQLDGNGPPCLLIPGLGGEAGFWQG-VASTLENDYRLIRIDHRGAGASDR--PTGGYSIPRIMRDVLGVLDDLHIPRAHVV
A1B0V9_PARDP_23-255             --------------------------------------CLLIPGLGGEAGFWQG-VASTLENDYRLIRIDHRGAGASDR--PTGGYSIPRIMRDVLGVLDDLHIPRAHVV
gi|298291572|ref|YP_003693511_  ----------------MPLMTASDGCRVHYEVRGQGEPVVLIPGLGGDGRFWEP-VADRLEGQFRLLLVDHRGAGRSDR--PDSPYTIEAIAGDVLAIVDAEGCSRAHLV
B3I7K9_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLQQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B3WNJ4_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLQQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C8U5H1_ECO10_16-250             --------------------------------------VVLISGLGGSGSYWLQQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B6I985_ECOSE_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C6EHJ8_ECOBD_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C4ZQD7_ECOBW_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
RUTD_ECOLI_16-250               --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B7M8Z4_ECO8A_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C9QZ67_ECOD1_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C5W2W8_ECOBB_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C6UFC0_ECOBR_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B3IQ15_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B3XEU2_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B1X9D0_ECODH_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B2N536_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C8TNB9_ECO26_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
C8UMM5_ECO1A_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B7LFB9_ECO55_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
Q3Z3A4_SHISS_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
B3HD65_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIEHYAVV
A7ZYW4_ECOHS_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQVLVAAGIEHYAVV
B1IV88_ECOLC_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQVLVAAGIEHYAVV
B2NNW4_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B2P113_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B3BZK7_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B3BI46_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B3AZR6_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B3AK70_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B3A4A8_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B2PKQ2_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B5YU51_ECO5E_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
C3TF07_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
C6UPN1_ECO5T_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
B7A0I9_ECO57_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
RUTD_ECO57_16-250               --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
D3QPK2_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIEHYAVV
A7ZKB4_ECO24_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSITQMAAELHQALVAAGIERYAVV
D2AC40_SHIF2_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
Q83LK8_SHIFL_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
Q0T625_SHIF8_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B3WZB6_SHIDY_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
A1A9R4_ECOK1_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLVQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B7MIF6_ECO45_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLVQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
C1HFA9_9ESCH_25-259             --------------------------------------VVLISGLGGSGSYWLPQLAVLVQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
Q1RDK8_ECOUT_25-259             --------------------------------------VVLISGLGGSGSYWLPQLAVLVQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B7UNZ2_ECO27_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLDQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
D2NGI6_ECOS5_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLDQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B7NLB7_ECO7I_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B3HT09_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
Q0TJ58_ECOL5_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
D3H122_ECO44_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVICYDQRGTGNNPDTLEED-YSIAQMAAELHQALVAAGIERYAVV
C2DK76_ECOLX_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLDQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
Q8FJ43_ECOL6_25-259             --------------------------------------VVLISGLGGSGSYWLPQLAVLDQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B7MTF2_ECO81_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLDQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVI
B1LIZ6_ECOSM_16-250             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIERYAVV
B7N3G5_ECOLU_25-259             --------------------------------------VVLISGLGGSGSYWLPQLAVLEQE-YQVVCYDQRGTGNNPDTLAED-YSIAQMAAELHQALVAAGIKRYAVV
gi|146311179|ref|YP_001176253_  -----------------------MKISLSPPPFADAPVVVLIAGLGGSGSYWLPQLAALEQE-YQVVCYDQRGTGNNAGELPHG-YTLGNMADELYQALLNAGIPRFTVI
A4W922_ENT38_16-250             --------------------------------------VVLIAGLGGSGSYWLPQLAALEQE-YQVVCYDQRGTGNNAGELPHG-YTLGNMADELYQALLNAGIPRFTVI
gi|296102971|ref|YP_003613117_  -----------------------MKLSVSPPPFDGAPVVVLIAGLGGGGSYWLPQLAALEQE-YQVVCYDQRGTGNNPDTLPEE-YTLAQMAGELAQALTAVGITRYCVV
gi|295096275|emb|CBK85365_1|_p  -----------------------MKLSISPPPFAGAPVVVLIAGLGGSGSYWLPQLAVLGQE-YQVVCYDQRGTGNNPDTLPED-YTLAHMADELALALAEAGIARYCVV
gi|238894074|ref|YP_002918808_  -----------------------MRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEEQ-YQLVSYDHNGTGENAGPLPAD-YSLATMAGELFSALQAAGIARFALV
C4X6I3_KLEPN_16-250             --------------------------------------VVLSAGLGGGGGYWLAQRAALEEQ-YQLVSYDHNGTGENAGPLPAD-YSLATMAGELFSALQAAGIARFALV
A6T799_KLEP7_16-250             --------------------------------------VVLSAGLGGGGGYWLAQRAALEEQ-YQLVSYDHNGTGENAGPLPAG-YSLATMAGELFSALQAAGIARFALV
gi|288936197|ref|YP_003440256_  ----------------------MMRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEAQ-YQLVSYDHNGTGENAGPLPAD-YSMATMAQELLSALQAAGITRFALV
gi|206580846|ref|YP_002239344_  -----------------------MRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEAQ-YQLVSYDHNGTGENAGPLPAD-YSMATMAQELLSALQAAGITRFALV
B5XXN3_KLEP3_16-250             --------------------------------------VVLSAGLGGGGGYWLAQRAALEAQ-YQLVSYDHNGTGENAGPLPAD-YSMATMAQELLSALQAAGITRFALV
gi|290510748|ref|ZP_06550118_1  -----------------------MRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEAQ-YQLVSYDHNGTGENAGPLPAD-YSMATMAQELLSALQAAGITRFALV
D3RKL3_KLEVA_17-251             --------------------------------------VVLSAGLGGGGGYWLAQRAALEAQ-YQLVSYDHNGTGENAGPLPAD-YSMATMAQELLSALQAAGITRFALV
gi|152969591|ref|YP_001334700_  -----------------------MRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEEQ-YQLVSYDHNGTGENAGPLPAG-YSLATMAGELFSALQAAGIARFALV
gi|156934532|ref|YP_001438448_  ----------------------MMKLRVSEAPFPGAPVMVMIAGLGGLGGYWLAQQSALSRD-YQVVVYDQRGTGDNADTLPEG-YTLADMAQELHRALLIHGVHRYAVL
A7MFY0_ENTS8_17-251             --------------------------------------MVMIAGLGGLGGYWLAQQSALSRD-YQVVVYDQRGTGDNADTLPEG-YTLADMAQELHRALLIHGVHRYAVL
gi|260597382|ref|YP_003209953_  -----------------------MKLRISDAPFPGAPVMVMISGLGGLGGYWLAQQNALSQA-YQVVVYDQRGTGDNADTLPEG-YTLTDMAQELHRALALHGVQRYAVL
C9Y0S4_CROTZ_16-250             --------------------------------------MVMISGLGGLGGYWLAQQNALSQA-YQVVVYDQRGTGDNADTLPEG-YTLTDMAQELHRALALHGVQRYAVL
gi|317047621|ref|YP_004115269_  -----------------------MHLEIQGLQTEDAPTLVLSSGLGGVTGFWQPQLAALGQH-YRVVTYDQRGTGRSADTLPEG-YSMAMMAAELAAALTEHGIEHFDLI
C8QEM5_9ENTR_16-250             --------------------------------------LVLSSGLGGVTGFWQPQLAALGQH-YRVVTYDQRGTGRSADTLPEG-YSMAMMAAELAAALTEHGIEHFDLI
gi|304397134|ref|ZP_07379013_1  -----------------------MQLDFLGLQNPEAPTLVLSSGLGGVAGFWQPQLAALTAR-YRVVLYDQRGTGRSAESLPEG-YSMAMMAAELAEALAQHGILRFSLI
gi|300716142|ref|YP_003740945_  -----------------------MHIELSGSTDPQARTLVLSAGLGGLANFWLPQLNALREH-YRVVVYDQRGTGRSPDMLPAG-YSMGDMAAELAHELAALGIESYDVI
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gi|123442221|ref|YP_001006202_  -----------------------MYFEITGQNSPAAKTVVLSAGLGGSGRFWQPQLSALGQH-FRVITYDQYGTGRSAGVIPSG-YTLADMADELADLLASQHIERYHFV
A1JMX1_YERE8_16-250             --------------------------------------VVLSAGLGGSGRFWQPQLSALGQH-FRVITYDQYGTGRSAGVIPSG-YTLADMADELADLLASQHIERYHFV
gi|270261263|ref|ZP_06189536_1  -----------------------MYFEILGKDTPLAPTVVLSAGLGGAGSFWQPQIEALSEH-FRVVVYDHQGTARSQGEVPAG-YSMADMADEVAQLLRSIGVEHCYFV
D1RPC7_SEROD_16-250             --------------------------------------VVLSAGLGGAGSFWQPQIEALSEH-FRVVVYDHQGTARSQGEVPAG-YSMADMADEVAQLLRSIGVEHCYFV
gi|157370062|ref|YP_001478051_  -----------------------MYFEILGKDTPLAPTLVLSAGLGGAGSFWQPQINALGEH-FRVVVYDHFGTARSKGSVPDG-YSMADMADEVAQLLRSLNVDCCYFV
A8GCT3_SERP5_16-250             --------------------------------------LVLSAGLGGAGSFWQPQINALGEH-FRVVVYDHFGTARSKGSVPDG-YSMADMADEVAQLLRSLNVDCCYFV
gi|291619589|ref|YP_003522331_  -----------------------MYYKVLGQQNADAETVVLSSGLGGSGGFWQPQLAMLSAH-FRVVVYDQYGTGASQGSVPAG-YRMEDMADELAGLLNALNISRCHLV
D4GEU7_PANAN_16-250             --------------------------------------VVLSSGLGGSGGFWQPQLAMLSAH-FRVVVYDQYGTGASQGSVPAG-YRMEDMADELAGLLNALNISRCHLV
gi|322833714|ref|YP_004213741_  -----------------------MYYKVLGKKNADAETVVLSSGLGGSGGFWQPQLTMLAEH-FRVVVYDQHGTGVSQGTVPAG-YRMEDMADELAGMLNGLDISRCHLV
gi|146283917|ref|YP_001174070_  -----------------------MHYELHGRMEPDAPTLVLSSGLGGAAAFWLPQLPALTQD-YRVLVYDQLGTNKSPANLPAG-YSIESMAVELLELLDTLGIRRCHFI
A4VQH7_PSEU5_16-250             --------------------------------------LVLSSGLGGAAAFWLPQLPALTQD-YRVLVYDQLGTNKSPANLPAG-YSIESMAVELLELLDTLGIRRCHFI
gi|302189116|ref|ZP_07265789_1  -----------------------MFHEFHACQHADAPTLVLSSGLGGSGRYWADDLAVLTRD-YRVLVYDHAGSGRSPAVLPAD-YSIRHMAIELLALLDSLDIQRCHFM
gi|66044249|ref|YP_234090_1|_A  -----------------------MFHEFHACQHADAPTLVLSSGLGGSGRYWADDLTLLTRD-YHVLVYDHAGTGRSPAVLPAD-YSIRHMAIELLALLDSLDIQRCHFM
Q4ZXS0_PSEU2_16-250             --------------------------------------LVLSSGLGGSGRYWADDLTLLTRD-YHVLVYDHAGTGRSPAVLPAD-YSIRHMAIELLALLDSLDIQRCHFM
gi|71735511|ref|YP_273315_1|_a  -----------------------MFHEIHRCQHADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLGIQRCHFM
Q48MQ7_PSE14_16-248             --------------------------------------LVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLGIQRCHFM
gi|289626193|ref|ZP_06459147_1  -----------------------MFHEIHRCQHADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLDIQRCHFM
gi|257482056|ref|ZP_05636097_1  -----------------------MFHEIHRCQHADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLDIQRCHFM
gi|289648344|ref|ZP_06479687_1  -----------------------MFHEIHRCQHADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLDIQRCHFM
gi|320325736|gb|EFW81797_1|_al  -----------------------MFHEIHRCQHADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPADLPAD-YSIRHMAMELLTLLDSLDIQRCHFM
gi|28868369|ref|NP_790988_1|_a  -----------------------MFHEIHRCQLADAPLLVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPAALPSD-YSIRHMAVELLALLDSLGIQRCHFM
Q887X6_PSESM_16-250             --------------------------------------LVLSSGLGGSSRYWADDLAALTRD-HDVLVYDHAGTGRSPAALPSD-YSIRHMAVELLALLDSLGIQRCHFM
gi|213967180|ref|ZP_03395329_1  -----------------------MFHEIHRCQLADAPLLVLSSGLGGSSRYWADDLAVLTRD-HDVLVYDHAGTGRSPAALPSD-YSIRHMAVELLALLDSLGIQRCHFM
gi|196155582|ref|YP_002125071_  MPSEMQAG----GTSMKSEMRGKTHYEIHGLTSPDAPTVVFSSGLGGAAKFWQPQLADFTQH-YRVITYDQLGTNKSEADLCSE-YSILHMADELDVLLKKLEVQQCHFV
B4RRW2_ALTMD_35-269             --------------------------------------VVFSSGLGGAAKFWQPQLADFTQH-YRVITYDQLGTNKSEADLCSE-YSILHMADELDVLLKKLEVQQCHFV
gi|239994720|ref|ZP_04715244_1  MHSDVQASYAHISGEMNGEMRNKLHYEIHGLTSPDAPTIVFSSGLGGAAKFWQPQLGDFAQD-YRVITYDQRGTNKSVGDLPAN-YSISNMTYELAALLRKLEVQACHFV
gi|262376021|ref|ZP_06069252_1  ----------------------MSLFIH-HAAQADAPYVVLSSGLGGHASFWNPQIRVLQQH-FHVVTYDQEGCHSDSELLPTP-YSIDHMAGQILDLLINDGIREFHFI
D0SV49_ACILW_16-255             --------------------------------------VVLSSGLGGHASFWNPQIRVLQQH-FHVVTYDQEGCHSDSELLPTP-YSIDHMAGQILDLLINDGIREFHFI
gi|293611018|ref|ZP_06693317_1  ----------------------MKYYIYPCSSQKDAPYLIFSSGLGGHASFWNPQLESLSTH-FNIVTYDQEGCHQDSALLPAH-YHICDMANQVLHLLEHLQIHEFHMI
gi|262368332|ref|ZP_06061661_1  ----------------------MNVQIFPSHIE-DADYVVLSSGLGGHAQFWQPQIQDLQTK-FHVLTYDQEGCHENSTLLKPD-YCIRDLGQQLLLILKQQHIQRFHFI
D0S9G1_ACIJO_16-250             --------------------------------------VVLSSGLGGHAQFWQPQIQDLQTK-FHVLTYDQEGCHENSTLLKPD-YCIRDLGQQLLLILKQQHIQRFHFI
gi|50083320|ref|YP_044830_1|_a  -----------------------MNYQLFKHSDENASYVVFSSGLGGHGSFWQAQLDVFRQY-FHVLIYDQEGCHASSELLADG-YSFEHLALQVKQLLQQLNIVRFHFI
Q6FFZ9_ACIAD_16-255             --------------------------------------VVFSSGLGGHGSFWQAQLDVFRQY-FHVLIYDQEGCHASSELLADG-YSFEHLALQVKQLLQQLNIVRFHFI
gi|255319344|ref|ZP_05360561_1  -----------------------MTVEIYPCKNHSVQTVVLSSGLGGHANFWQPQIEALREY-FQVICYDHEGIGSQSPELPEN-YSIQHLAEQLAKILKQHQQQNCHFI
C6RN00_ACIRA_16-250             --------------------------------------VVLSSGLGGHANFWQPQIEALREY-FQVICYDHEGIGSQSPELPEN-YSIQHLAEQLAKILKQHQQQNCHFI
D0T3M4_ACIRA_16-250             --------------------------------------VVLSSGLGGHANFWQPQIEALREY-FQVICYDHEGIGSQSPELPEN-YSIQHLAEQLAKILKQHQQQNCHFI
gi|316935661|ref|YP_004110643_  ---------------MNASDSAVLVAEIVGRPESDAPTIVLSAGLGGAAAFWLPQIEALAQQ-YRVVLYDHRGTGRNPATLPDG-YSIGDMADEVIALLQAQQIERCHFM
D2MBB4_RHOPA_24-258             --------------------------------------IVLSAGLGGAAAFWLPQIEALAQQ-YRVVLYDHRGTGRNPATLPDG-YSIGDMADEVIALLQAQQIERCHFM
gi|159185242|ref|NP_355444_2|_  -----------------------MHFEVHGRTDAEAPTILLSSGLGGSSAYWLPQIEALSDH-FRIVTYDHRGTGRTGGEVPTE-GGISAMADDVLEIVSALNLEKFHFM
Q7CWX3_AGRT5_16-250             --------------------------------------ILLSSGLGGSSAYWLPQIEALSDH-FRIVTYDHRGTGRTGGEVPTE-GGISAMADDVLEIVSALNLEKFHFM
gi|222080882|ref|YP_002540245_  -----------------------MHFEVHGLDRPDAKTIILSSGLGGSGSYWAPQIEALATD-FRIVTYDHRGTGRTGGDVPDT-GGISAMADDVLEIAARLQLDRFDFM
B9JLT6_AGRRK_16-250             --------------------------------------IILSSGLGGSGSYWAPQIEALATD-FRIVTYDHRGTGRTGGDVPDT-GGISAMADDVLEIAARLQLDRFDFM
gi|239817801|ref|YP_002946711_  ---------------------MPLHYEVHGPADGEA--VLLSSGLGGSAAFWQPQLGALLEAGHRVIAYDQRGTGRSPAALDAG-YAIADMARDVVQILDATATPRCHLV
C5CN82_VARPS_16-250             --------------------------------------VLLSSGLGGSAAFWQPQLGALLEAGHRVIAYDQRGTGRSPAALDAG-YAIADMARDVVQILDATATPRCHLV
gi|167647941|ref|YP_001685604_  ---------------MQSGTVDGLYHEVHGGPASDRQTVILSAGLGGSGTFWAPQMQALMSR-FRVVLYDHRGTGRSARTLTDP-HTVAAMGDDIVKLMDALGLERAHVV
B0SW62_CAUSK_24-258             --------------------------------------VILSAGLGGSGTFWAPQMQALMSR-FRVVLYDHRGTGRSARTLTDP-HTVAAMGDDIVKLMDALGLERAHVV
gi|295689471|ref|YP_003593164_  ---------------MTTGTVDGICYEVHGWPVAGREVVLLSSGLGGSAAFWAPQMKALTER-WPVVTYDHRGTGRSVRALPPGPYSVDDMAQDMVKVMDALGLTKAHVV
D0XXH0_9CAUL_24-258             --------------------------------------VLLSSGLGGSAAFWAPQMKALTER-WPVVTYDHRGTGRSVRALPPGPYSVDDMAQDMVKVMDALGLTKAHVV
gi|16127029|ref|NP_421593_1|_a  ------------MRRMTIGTVDGLHYELHGGPIAGREVVLLSSGLGGSGAFWAPQMQALTQR-WPVVTYDHRGTGRSVRELPPR-YTLAHMADDMVKVMDALGLAKAHVV
B8H1Q3_CAUCN_27-261             --------------------------------------VLLSSGLGGSGAFWAPQMQALTQR-WPVVTYDHRGTGRSVRELPPR-YTLAHMADDMVKVMDALGLAKAHVV
Q9A4N3_CAUCR_27-261             --------------------------------------VLLSSGLGGSGAFWAPQMQALTQR-WPVVTYDHRGTGRSVRELPPR-YTLAHMADDMVKVMDALGLAKAHVV
gi|170747999|ref|YP_001754259_  --------------------MGPLHHAVAGP--AGGRPVLLSPGLGGAAGYFAPQMAALTAR-FRVVTYDHRGTGRSPGRLAPD-HDVPAMARDARAVLDAAGIERADVV
B1M5I5_METRJ_17-251             --------------------------------------VLLSPGLGGAAGYFAPQMAALTAR-FRVVTYDHRGTGRSPGRLAPD-HDVPAMARDARAVLDAAGIERADVV
gi|218530013|ref|YP_002420829_  -------------------MAAPVHHEVHGP--AGGRTVLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPSPLEPG-HDIAAMARDVLALLDHLGIGTADIV
B7KWT4_METC4_18-252             --------------------------------------VLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPSPLEPG-HDIAAMARDVLALLDHLGIGTADIV
gi|163851162|ref|YP_001639205_  -------------------MAAPVHHEVHGP--AGGRTVLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDLLDIGTADIV
A9W3H8_METEP_18-252             --------------------------------------VLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDLLDIGTADIV
gi|240138315|ref|YP_002962787_  -------------------MAAPVHHEVHGP--EGGRKVLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDHLDIGTADIV
C5B0U6_METEA_18-252             --------------------------------------VLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDHLDIGTADIV
gi|254560857|ref|YP_003067952_  -------------------MAAPVHHEVHGP--AGGRTVLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDHLGIGTADIV
C7CM33_METED_18-252             --------------------------------------VLLSPGLGGSAHYFAPQVPVLAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLDLLDHLGIGTADIV
gi|188580343|ref|YP_001923788_  -------------------MAAPVHHALHGP--EGARTVLLSPGLGGSAHYFAPQVPALAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLALLDHLGIGTTDIV
B1ZB18_METPB_18-252             --------------------------------------VLLSPGLGGSAHYFAPQVPALAER-FRVVTYDHRGTGRSPGPLEPG-HDIAAMARDVLALLDHLGIGTTDIV
gi|158424120|ref|YP_001525412_  -----------------MPYAHGGDADLYYEIHGAGTPILLSAGMGGGAGFWRPQIEALAAR-HQVILYDHAGTGRSGRDIGPR--SITEMARDMARVLDAAGVEDAHVA
A8IAD8_AZOC5_22-255             --------------------------------------ILLSAGMGGGAGFWRPQIEALAAR-HQVILYDHAGTGRSGRDIGPR--SITEMARDMARVLDAAGVEDAHVA

                                        120       130       140       150       160       170       180       190       200       210       220
                                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
gi|316935663|ref|YP_004110645_  GHSTGGAMGIVLGAKAP---ERIASLVLYATWAELDAQMESCLSLRRRILRGMGEAEYHRATPLFLYPPYYMRDHKADLEREVAAAIAATPSRSIMDARAAGIMAFDGLR
D2MBB2_RHOPA_22-255             GHSTGGAMGIVLGAKAP---ERIASLVLYATWAELDAQMESCLSLRRRILRGMGEAEYHRATPLFLYPPYYMRDHKADLEREVAAAIAATPSRSIMDARAAGIMAFDGLR
gi|300715742|ref|YP_003740545_  GHSTGGAIGQILAARHP---DLLAGMVMYASWAKSDRHFNWCFRMRRALLVGSTVEEYVHGSALFLYPPDHVRANAEVLSPALLASAAKFPQREVVLSRIDAIMAHDAIA
gi|260429719|ref|ZP_05783695_1  GHSTGGCIVQTIAATAP---ERVERLALSAAWLKPGNYLTALFEFRLGLLHRD-PRAYAESAALLSYAPGWLESHWDKYERATANPPADPGTQAIVAERIRVLLDFDGSD
D0DBU3_9RHOB_25-257             GHSTGGCIVQTIAATAP---ERVERLALSAAWLKPGNYLTALFEFRLGLLHRD-PRAYAESAALLSYAPGWLESHWDKYERATANPPADPGTQAIVAERIRVLLDFDGSD
gi|114762401|ref|ZP_01441859_1  GHSTGGCIVQTIAVTAA---ERVRNLVLSAAWLRPGNYLKALFEFRLRLLATD-PAAYAESAALLSYAPEWLEANWTKYERATATPPTDPAKQAIVAERIRALLAYDGSD
Q0FUQ8_9RHOB_25-257             GHSTGGCIVQTIAVTAA---ERVRNLVLSAAWLRPGNYLKALFEFRLRLLATD-PAAYAESAALLSYAPEWLEANWTKYERATATPPTDPAKQAIVAERIRALLAYDGSD
gi|90418551|ref|ZP_01226463_1|  GHSTGGCIAQSLAARAP---ERVTGLGLSATWLRPSRYMTALFRTRLDLLRLD-PVAYTATATLISYAPEWLEANWSAYERAVAKAPTSDTARQIVAERIEALLAFDGSA
Q1YL57_MOBAS_25-257             GHSTGGCIAQSLAARAP---ERVTGLGLSATWLRPSRYMTALFRTRLDLLRLD-PVAYTATATLISYAPEWLEANWSAYERAVAKAPTSDTARQIVAERIEALLAFDGSA
gi|33600731|ref|NP_888291_1|_p  GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLEAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
Q7WLJ9_BORBR_30-260             GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLEAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
gi|33596897|ref|NP_884540_1|_p  GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLAAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
gi|33592963|ref|NP_880607_1|_p  GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLAAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
Q7VX84_BORPE_30-260             GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLAAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
Q7W851_BORPA_30-260             GHSTGGCIVQEMALSAP---ARAASLVLGGTWGGRNAYMQSLFAMRAALLAAS-PALYEQAGAYLSYPAAWLLAHPEAVPAAAAPWPAQR--VAVVRERIAALLAYDRLD
gi|119383793|ref|YP_914849_1|_  GHSTGGMIAQTLAVEAP---ERVAGLVLSGTWERVDTRFTRLFQARLALLEQAGPIAYHKLTQALGHDAGWIEANRAALDAELEQAEARLQPIAVQAARIRMLMEHDVFD
A1B0V9_PARDP_23-255             GHSTGGMIAQTLAVEAP---ERVAGLVLSGTWERVDTRFTRLFQARLALLEQAGPIAYHKLTQALGHDAGWIEANRAALDAELEQAEARLQPIAVQAARIRMLMEHDVFD
gi|298291572|ref|YP_003693511_  GHSTGGTVVQTLAPDAP---ARIGSVVVSGSWPSPDARFRTLFRARLALLEAGRADIYQAFTHVLGYDADWIAAHEEELEAATGRANETLAPLAVTAARIRMLLAYDRAA
B3I7K9_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3WNJ4_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C8U5H1_ECO10_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B6I985_ECOSE_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C6EHJ8_ECOBD_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C4ZQD7_ECOBW_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
RUTD_ECOLI_16-250               GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7M8Z4_ECO8A_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARVPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C9QZ67_ECOD1_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C5W2W8_ECOBB_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C6UFC0_ECOBR_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3IQ15_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3XEU2_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B1X9D0_ECODH_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B2N536_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C8TNB9_ECO26_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C8UMM5_ECO1A_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7LFB9_ECO55_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
Q3Z3A4_SHISS_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3HD65_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
A7ZYW4_ECOHS_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B1IV88_ECOLC_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B2NNW4_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B2P113_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3BZK7_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3BI46_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3AZR6_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3AK70_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
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B3A4A8_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B2PKQ2_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B5YU51_ECO5E_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C3TF07_ECOLX_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C6UPN1_ECO5T_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7A0I9_ECO57_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
RUTD_ECO57_16-250               GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
D3QPK2_ECOLX_16-250             GHALGALVGMQLALDHP---ASVTVLVCVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
A7ZKB4_ECO24_16-250             GHALGALVGMQLALDYP---ASVTVLISVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
D2AC40_SHIF2_16-250             GHALGALVGMQLALDYP---ASVTMLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
Q83LK8_SHIFL_16-250             GHALGALVGMQLALDYP---ASVTMLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
Q0T625_SHIF8_16-250             GHALGALVGMQLALDYP---ASVTMLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3WZB6_SHIDY_16-250             GHALGALVGMQLALDYP---ASVTMLVSVNGWLRINAHTRRCFQVRERLLYSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
A1A9R4_ECOK1_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7MIF6_ECO45_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
C1HFA9_9ESCH_25-259             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
Q1RDK8_ECOUT_25-259             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7UNZ2_ECO27_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEALPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
D2NGI6_ECOS5_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINTHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B7NLB7_ECO7I_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVAAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
B3HT09_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSR
Q0TJ58_ECOL5_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSR
D3H122_ECO44_16-250             GHALGALVGMQLALDYP---ASLTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSR
C2DK76_ECOLX_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEGALALAHFQGKNNLLRRLNALKRADFSR
Q8FJ43_ECOL6_25-259             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEGALALAHFQGKNNLLRRLNALKRADFSR
B7MTF2_ECO81_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSR
B1LIZ6_ECOSM_16-250             GHALGALVGMQLALDYP---ASVTVLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSR
B7N3G5_ECOLU_25-259             GHALGALVGMQLALDYP---ASVTMLVSVNGWLRINAHTRRCFQVREQLLHSGGAQAWVEAQPLFLYPADWMAARAPRLEAEDALALAHFQGKNNLLRRLNALKRADFSH
gi|146311179|ref|YP_001176253_  GHALGALVGLQLAIAHP---DAVRALVCVNGWLSLNAHTRRCFQIRERLLHAGGAQAWVEAQPLFLYPADWMAARAPRMEAEEALALAHFQGTNNLQRRLLALKQADFRA
A4W922_ENT38_16-250             GHALGALVGLQLAIAHP---DAVRALVCVNGWLSLNAHTRRCFQIRERLLHAGGAQAWVEAQPLFLYPADWMAARAPRMEAEEALALAHFQGTNNLQRRLLALKQADFRA
gi|296102971|ref|YP_003613117_  GHALGALIGLQLALDTP---DALKALVCVNGWLTLNAHTRRCFQIRERLLHAGGAQAWVEAQPLFLYPADWMAARAPRLEAEEALALAHFQGKNNLLRRLNALKKADFSR
gi|295096275|emb|CBK85365_1|_p  GHALGALVGLRLAIDKP---DALTALVCVNGWLTLNAHTRRCFDVRERLLHAGGAQAWVEAQPLFLYPADWMAARAPRLEAEEALALAHFQGKANLLRRLHALKQADFSR
gi|238894074|ref|YP_002918808_  GHALGALIGLQLALDRP---EAVSALALVNGWLSLSPHTRRCFQVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
C4X6I3_KLEPN_16-250             GHALGALIGLQLALDRP---EAVSALALVNGWLSLSPHTRRCFQVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
A6T799_KLEP7_16-250             GHALGALIGLQLALDRP---EAVSALALVNGWLSLSPHTRRCFQVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
gi|288936197|ref|YP_003440256_  GHALGALIGLQLALDRP---EAVSALVLVNGWLTLSPHTRRCFLVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
gi|206580846|ref|YP_002239344_  GHALGALIGLQLALDRP---EAVSALVLVNGWLTLSPHTRRCFLVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
B5XXN3_KLEP3_16-250             GHALGALIGLQLALDRP---EAVSALVLVNGWLTLSPHTRRCFLVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
gi|290510748|ref|ZP_06550118_1  GHALGALIGLQLALDRP---EAVSALVLVNGWLTLSPHTRRCFLVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
D3RKL3_KLEVA_17-251             GHALGALIGLQLALDRP---EAVSALVLVNGWLTLSPHTRRCFLVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
gi|152969591|ref|YP_001334700_  GHALGALIGLQLALDRP---EAVSALALVNGWLSLSPHTRRCFQVRERLLHAGGAQAWVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSR
gi|156934532|ref|YP_001438448_  GHALGGLVGLELALAFP---EAVSALVIVNGWLSLSAWTRRCFEARERLLLDSGPAAYIAAQPLFLYPPSWAQENQPRLEAEEALHNAHFQGTENLLRRLWALKNADYRE
A7MFY0_ENTS8_17-251             GHALGGLVGLELALAFP---EAVSALVIVNGWLSLSAWTRRCFEARERLLLDSGPAAYIAAQPLFLYPPSWAQENQPRLEAEEALHNAHFQGTENLLRRLWALKNADYRE
gi|260597382|ref|YP_003209953_  GHALGGLVGLELALAYP---RAVSALVIINGWLSLGTWTRRCFDARERLLLDSGPAVYVAAQPLFLYPPQWAQENQPRLEAEEALQNAHFQGTENLLRRLWALKTADYRE
C9Y0S4_CROTZ_16-250             GHALGGLVGLELALAYP---RAVSALVIINGWLSLGTWTRRCFDARERLLLDSGPAVYVAAQPLFLYPPQWAQENQPRLEAEEALQNAHFQGTENLLRRLWALKTADYRE
gi|317047621|ref|YP_004115269_  GHALGGLIGLQLALDYP---QRVGRVVVINGWLSLNAHTRRCFQVRQDLLLNVGVEAFVRAQPLFLYPAEWMARNQTRLEQEDTHHVQHFQGMENLLRRLHALQSADFRP
C8QEM5_9ENTR_16-250             GHALGGLIGLQLALDYP---QRVGRVVVINGWLSLNAHTRRCFQVRQDLLLNVGVEAFVRAQPLFLYPAEWMARNQTRLEQEDTHHVQHFQGMENLLRRLHALQSADFRP
gi|304397134|ref|ZP_07379013_1  GHALGGLVGMQLALDYP---DRIERIVVINGWLTLHPHTRRCFQVRQDLLLNVGVEAFVRAQPLFLYPAEWMAEHQTRLEQEDSHHITHFQGMENLMRRLHALMSADFSA
gi|300716142|ref|YP_003740945_  GHALGGMVAMQLAVDFP---QRVGRLVIVNGWLRLNAHTRRCFTVRQELLLNVGVESYVRAQPLFLYPADWLADNQARIEAEDALHAAHFQGTENLLRRLNALMACDFTE
gi|123442221|ref|YP_001006202_  GHALGGMIGLQLALSHP---QCVERLVAINSWPVLDSQTRRCFHVRQDLLLNSGVAAYVRAQPLFLYPADWLSRNTLLLEQEEVQQIAHFQGMENLLRRLNALMNADFRS
A1JMX1_YERE8_16-250             GHALGGMIGLQLALSHP---QCVERLVAINSWPVLDSQTRRCFHVRQDLLLNSGVAAYVRAQPLFLYPADWLSRNTLLLEQEEVQQIAHFQGMENLLRRLNALMNADFRS
gi|270261263|ref|ZP_06189536_1  GHALGGMIGLQLALAHP---QLVAKLVVVNGWPTLDSQTRRCFKVRQDLLLNSGVEAYVRAQPLFLFPADWLSRHEALLDEELTHQVAHFQGTENLLRRLGALMNADFRP
D1RPC7_SEROD_16-250             GHALGGMIGLQLALAHP---QLVAKLVVVNGWPTLDSQTRRCFKVRQDLLLNSGVEAYVRAQPLFLFPADWLSRHEALLDEELTHQVAHFQGTENLLRRLGALMNADFRP
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gi|322833714|ref|YP_004213741_  GHALGGIIGLHLALRYP---ALLQSLVVINGWTKLDSQTRRCFEVRQNLLLNSGVDAYVQAQPLFLYPGDWLSEHDALLQEERQHQVAHFQGMENLLHRLQALMNSDLTA
gi|146283917|ref|YP_001174070_  GHALGGLVGLQIALLRP---QLLQSLVPINAWSSPNPHSARCFAVRLKLLHDSGPAAYVQAQSLFLYPADWIAANSERLARDDAHALAHFPPTMNLVRRIEALLAFDIEA
A4VQH7_PSEU5_16-250             GHALGGLVGLQIALLRP---QLLQSLVPINAWSSPNPHSARCFAVRLKLLHDSGPAAYVQAQSLFLYPADWIAANSERLARDDAHALAHFPPTMNLVRRIEALLAFDIEA
gi|302189116|ref|ZP_07265789_1  GHALGGLVGLELALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPEAYVQAQALFLYPADWIAANGPRLADDEAHALAHFPDTDNLLRRIHALETFDVEA
gi|66044249|ref|YP_234090_1|_A  GHALGGLVGLELALLRP---ELLHSQVLINAWSSPNPHSARCFSVRKKLLLNSGPEAYVQAQALFLYPADWIAANGPRLADDEAHALAHFPDTDNLLRRIHALETFDVSA
Q4ZXS0_PSEU2_16-250             GHALGGLVGLELALLRP---ELLHSQVLINAWSSPNPHSARCFSVRKKLLLNSGPEAYVQAQALFLYPADWIAANGPRLADDEAHALAHFPDTDNLLRRIHALETFDVSA
gi|71735511|ref|YP_273315_1|_a  GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPGTDNLLRRIHALQTFDVEA
Q48MQ7_PSE14_16-248             GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPGTDNLLRRIHALQTFDVEA
gi|289626193|ref|ZP_06459147_1  GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPDTDNLLRRIHALQTFDVEA
gi|257482056|ref|ZP_05636097_1  GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPDTDNLLRRIHALQTFDVEA
gi|289648344|ref|ZP_06479687_1  GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPYTDNLLRRIHALQTFDVEA
gi|320325736|gb|EFW81797_1|_al  GHALGGLVGLEIALLRP---ELLQSQVLINAWSSPNPHSARCFSVRKKLLLNSGPDAYVQAQALFLYPADWIAANGARLADDEAHALAHFPDTDNLLRRIHALQTFDVEA
gi|28868369|ref|NP_790988_1|_a  GHALGGLIGLELALLRP---QLLQSQVLINVWSSPNPHSARCFSVRKQLLLNSGPQAYVQAQALFLYPADWIAANSARLADDEAHALAHFPDTENLLRRIHALETFNIEA
Q887X6_PSESM_16-250             GHALGGLIGLELALLRP---QLLQSQVLINVWSSPNPHSARCFSVRKQLLLNSGPQAYVQAQALFLYPADWIAANSARLADDEAHALAHFPDTENLLRRIHALETFNIEA
gi|213967180|ref|ZP_03395329_1  GHALGGLIGLELALLRP---QLLQSQVLINAWSSPNPHSARCFSVRKQLLLNSGPQAYVQAQALFLYPADWIAANSARLADDEAHALAHFPDTENLLRRIHALETFNIEA
gi|196155582|ref|YP_002125071_  GHALGGLVGLQLALTQP---DLLKSMVLVNAWSSPNPHTLRCFDIRKALLAADRKDMYLQLQALLLFPPDWIAQNAEHLEEEEAQLLNHFPNVNNLLARIGALSTFDIDD
B4RRW2_ALTMD_35-269             GHALGGLVGLQLALTQP---DLLKSMVLVNAWSSPNPHTLRCFDIRKALLAADRKDMYLQLQALLLFPPDWIAQNAEHLEEEEAQLLNHFPNVNNLLARIGALSTFDIDD
gi|239994720|ref|ZP_04715244_1  GHALGGLVGLELALSKP---KLLQSLVLVNAWSSPNPHTLRCFNIRKALLAAGRKDMYLQLQALLLFPPDWIAANAAHLAEEEAHLLNHFPNEENLLARIGALSTFNIDK
gi|262376021|ref|ZP_06069252_1  GHALGGHIGMQLATYQAERKFKLLSLTMLNAWGELDAHTQKCFEARTSLLLNSKAEAYVRAQALFLYPPQWISTHIDQLTEAENKQLLDFPPIKNVLARLQAVQTFKLNT
D0SV49_ACILW_16-255             GHALGGHIGMQLATYQAERKFKLLSLTMLNAWGELDAHTQKCFEARTSLLLNSKAEAYVRAQALFLYPPQWISTHIDQLTEAENKQLLDFPPIKNVLARLQAVQTFKLNT
gi|293611018|ref|ZP_06693317_1  GHALGGIIGMELAKQLKSSSITMLSLTLINAWDELDAHTQKCFDARIALLASAGAEAYVRAQALFLYPPAWISQNHSHIKSTEDIQLQGFPPKTNVFARLKALMRFQLQA
gi|262368332|ref|ZP_06061661_1  GHALGGFIGAELAYLCQSTEYQMLSITILNGWDTLDVHTYKCFETRINLLTFAGTEAYVKAQALFLYPPAWISTNIECIQKQEQFQIQNFPPHENVLRRLSALMNFQLSE
D0S9G1_ACIJO_16-250             GHALGGFIGAELAYLCQSTEYQMLSITILNGWDTLDVHTYKCFETRINLLTFAGTEAYVKAQALFLYPPAWISTNIECIQKQEQFQIQNFPPHENVLRRLSALMNFQLSE
gi|50083320|ref|YP_044830_1|_a  GHALGGFIGIELAHRYASETCQLLSLTLINAWQQLDPHTLRCFTTRIALLQHAGTAAYLHAQALFLYPPLWISEHTALLEQQEAKMQSDFPPHANVLKRLNALMQYQVNT
Q6FFZ9_ACIAD_16-255             GHALGGFIGIELAHRYASETCQLLSLTLINAWQQLDPHTLRCFTTRIALLQHAGTAAYLHAQALFLYPPLWISEHTALLEQQEAKMQSDFPPHANVLKRLNALMQYQVNT
gi|255319344|ref|ZP_05360561_1  GHALGGFIGIELVRLYPELVN---RLVLINAWDRLDSHTEKCFSTRIALLRYAGIEAYIRAQALFLYPPAWISAHSLQLNEQENKMIGIFAPLENVFKRLHALQNYQPFE
C6RN00_ACIRA_16-250             GHALGGFIGIELVRLYPELVN---RLVLINAWDRLDSHTEKCFSTRIALLRYAGIEAYIRAQALFLYPPAWISAHSLQLNEQENKMIGIFAPLENVFKRLHALQNYQPFE
D0T3M4_ACIRA_16-250             GHALGGFIGIELVRLYPELVN---RLVLINAWDRLDSHTEKCFSTRIALLRYAGIEAYIRAQALFLYPPAWISAHSLQLNEQENKMIGIFAPLENVFKRLHALQNYQPFE
gi|316935661|ref|YP_004110643_  GHALGGLVGLELALRAP---QMLDRLVLVNAWAAPNPHTKRCFDVRRDLLRGVGVEAYVRAQPIFLYPPAWMVANAARVAEEEAHGVRHFQGADNIERRIAALLAFDVAA
D2MBB4_RHOPA_24-258             GHALGGLVGLELALRAP---QMLDRLVLVNAWAAPNPHTKRCFDVRRDLLRGVGVEAYVRAQPIFLYPPAWMVANAARVAEEEAHGVRHFQGADNIERRIAALLAFDVAA
gi|159185242|ref|NP_355444_2|_  GHALGGLIGLDIALRQP---RLIDRLVLINAWSKADPHSGRCFDVRIELLEKSGVDAFVKAQPLFLYPAAWMSEHQERLARDDAHGVAHFQGKTNVLRRIAALRAFDIDA
Q7CWX3_AGRT5_16-250             GHALGGLIGLDIALRQP---RLIDRLVLINAWSKADPHSGRCFDVRIELLEKSGVDAFVKAQPLFLYPAAWMSEHQERLARDDAHGVAHFQGKTNVLRRIAALRAFDIDA
gi|222080882|ref|YP_002540245_  GHALGGLIGLDIALRRP---ELIGKLILINAWSKADPHSGRCFDIRIELLERSGVEAFVKAQPLFLYPAVWMSENAERMAADERHGVAHFQGKANVLKRIAALRAFDIDD
B9JLT6_AGRRK_16-250             GHALGGLIGLDIALRRP---ELIGKLILINAWSKADPHSGRCFDIRIELLERSGVEAFVKAQPLFLYPAVWMSENAERMAADERHGVAHFQGKANVLKRIAALRAFDIDD
gi|239817801|ref|YP_002946711_  GHALGGLVGLQLALDEP---ARVASLVLVNAWSKPNAHSARCFDARLALLDACGPRAYVEAQPIFLYPAAWCAEHAQRVADEVDHAFAHFPGEANMRARIGALRAFDIDA
C5CN82_VARPS_16-250             GHALGGLVGLQLALDEP---ARVASLVLVNAWSKPNAHSARCFDARLALLDACGPRAYVEAQPIFLYPAAWCAEHAQRVADEVDHAFAHFPGEANMRARIGALRAFDIDA
gi|167647941|ref|YP_001685604_  GHAAGGNAGLALALNHP---DRLDKLVVVNGWSRPDPHIKRCFDTRLALLNDTGIAAYVHAQPLFLYPADWLSANNARLEAEEVHHINGFPSPDVMRTRIQALLEFDIDE
B0SW62_CAUSK_24-258             GHAAGGNAGLALALNHP---DRLDKLVVVNGWSRPDPHIKRCFDTRLALLNDTGIAAYVHAQPLFLYPADWLSANNARLEAEEVHHINGFPSPDVMRTRIQALLEFDIDE
gi|295689471|ref|YP_003593164_  GHAAGGNAGLALALNHP---DRLGKLVVVNGWSRPDPHIQRCFDTRIHLLNDTGIKAYVHAQPIFLYPADWISRNHARLMAEEAHHVAGFPPREVMLARINALLAFDIDA
D0XXH0_9CAUL_24-258             GHAAGGNAGLALALNHP---DRLGKLVVVNGWSRPDPHIQRCFDTRIHLLNDTGIKAYVHAQPIFLYPADWISRNHARLMAEEAHHVAGFPPREVMLARINALLAFDIDA
gi|16127029|ref|NP_421593_1|_a  GHAAGGNAGLQLALDHP---DRLAKLVVVNGWSRPDPHIRRCFDTRLHLLNDTGPEAYVHAQPIFLYPADWISRNHTRLMAEEAHHVAAFPPREVMLARINALLAFDIDA
B8H1Q3_CAUCN_27-261             GHAAGGNAGLQLALDHP---DRLAKLVVVNGWSRPDPHIRRCFDTRLHLLNDTGPEAYVHAQPIFLYPADWISRNHTRLMAEEAHHVAAFPPREVMLARINALLAFDIDA
Q9A4N3_CAUCR_27-261             GHAAGGNAGLQLALDHP---DRLAKLVVVNGWSRPDPHIRRCFDTRLHLLNDTGPEAYVHAQPIFLYPADWISRNHTRLMAEEAHHVAAFPPREVMLARINALLAFDIDA
gi|170747999|ref|YP_001754259_  GHALGGLIALQMALDAP---DRVGRVVVINGWDALDPATRRCFAARRAILAGGGPEAFVRAQAIFLYPAAWLSAQAERVEADEAQALAHFPGAETVLTRIAALEGFAIAD
B1M5I5_METRJ_17-251             GHALGGLIALQMALDAP---DRVGRVVVINGWDALDPATRRCFAARRAILAGGGPEAFVRAQAIFLYPAAWLSAQAERVEADEAQALAHFPGAETVLTRIAALEGFAIAD
gi|218530013|ref|YP_002420829_  GHALGGLIALQLALTHP---ERVGRIVVINGWAAMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVAADEAQALAHFPGTRTALARITALETFDATA
B7KWT4_METC4_18-252             GHALGGLIALQLALTHP---ERVGRIVVINGWAAMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVAADEAQALAHFPGTRTALARITALETFDATA
gi|163851162|ref|YP_001639205_  GHALGGLIALQLALTHP---ERVGRIVVINGWAVMDLATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVADDEAQALAHFPGEETVLARIAALETFDATG
A9W3H8_METEP_18-252             GHALGGLIALQLALTHP---ERVGRIVVINGWAVMDLATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVADDEAQALAHFPGEETVLARIAALETFDATG
gi|240138315|ref|YP_002962787_  GHALGGLIALQLALTHP---ERVGRIVVINGWAAMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARLADDEAQALAHFAGTRTVLTRIAALETFDATA
C5B0U6_METEA_18-252             GHALGGLIALQLALTHP---ERVGRIVVINGWAAMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARLADDEAQALAHFAGTRTVLTRIAALETFDATA
gi|254560857|ref|YP_003067952_  GHALGGLIALQLALTHP---ERVGRIVVINGWAVMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVANDEAQALAHFPGEETVLARISALEAFDGTA
C7CM33_METED_18-252             GHALGGLIALQLALTHP---ERVGRIVVINGWAVMDPATRRCFAARKALLRHAGPEAFVRAQAIFLYPAPWLSENAARVANDEAQALAHFPGEETVLARISALEAFDGTA
gi|188580343|ref|YP_001923788_  GHALGGLIALHLALTHP---ERVERIVVINGWAVMDPATRRCFSARKALLTQAGPEAFVRAQAIFLYPAPWLSENAARVADDEAQALAHFPGAKTVLARIAALEAFDATA
B1ZB18_METPB_18-252             GHALGGLIALHLALTHP---ERVERIVVINGWAVMDPATRRCFSARKALLTQAGPEAFVRAQAIFLYPAPWLSENAARVADDEAQALAHFPGAKTVLARIAALEAFDATA
gi|158424120|ref|YP_001525412_  GHAIGGIIGMELALAAP---ERVRSLTIVNGWARADGFLRRCFEVRKRILLASGPEAYVRAQPLFLYPPRWIAENIAVLEEEEAQMVAHFPGTQTMLNRIETFLAFDGRE
A8IAD8_AZOC5_22-255             GHAIGGIIGMELALAAP---ERVRSLTIVNGWARADGFLRRCFEVRKRILLASGPEAYVRAQPLFLYPPRWIAENIAVLEEEEAQMVAHFPGTQTMLNRIETFLAFDGRE
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                                        230       240       250       260       270       280       290       300
                                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
gi|316935663|ref|YP_004110645_  YLDKIRC--PTMVLVAQDDILTPPYSSELIAARIAGAELIQVPRGGHAFSRVEPVAFNNLTLDFLAAHPIGTYAHV-------------
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gi|260429719|ref|ZP_05783695_1  QIGAVTA--ETTIIGAQDDMIVPAFLQEELARHLPGAALRMLPDGGHFYPASRTDAFVAIVTDWLDAPLTSERTER-------------
D0DBU3_9RHOB_25-257             QIGAVTA--ETTIIGAQDDMIVPAFLQEELARHLPGAALRMLPDGGHFYPASRTDAFVAI-----------------------------
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Q0FUQ8_9RHOB_25-257             QIGRVAA--RTLVLGARDDMIVPAFLQEDLAAELAGAELRLLPDGGHFYPGSRTETFAPL-----------------------------
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Q1YL57_MOBAS_25-257             SVPQLTM--PAMIIGAADDMIVPAFLQRDLATALPAAPLTLLPEGGHFFPASRTDAFVAA-----------------------------
gi|33600731|ref|NP_888291_1|_p  DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAALLDWLGHHSL-------------------
Q7WLJ9_BORBR_30-260             DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAAL----------------------------
gi|33596897|ref|NP_884540_1|_p  DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAALLDWFGHHSL-------------------
gi|33592963|ref|NP_880607_1|_p  DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAALLDWFGHHSL-------------------
Q7VX84_BORPE_30-260             DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAAL----------------------------
Q7W851_BORPA_30-260             DLPGLDA--PALVLGARDDQIVPFALQQQLARVLPGAQLRPLEHGGHFFPIVRGADYVAAL----------------------------
gi|119383793|ref|YP_914849_1|_  RLGRITA--PTLVIGGSDDALIPFASSERLAAAIPGARLASLP-GGHFFPRAYPAPYAALLAGFLKEIDI-------------------
A1B0V9_PARDP_23-255             RLGRITA--PTLVIGGSDDALIPFASSERLAAAIPGARLASLP-GGHFFPRAYPAPYAAL-----------------------------
gi|298291572|ref|YP_003693511_  DLGRIEA--PALVVGGRDDAMIPFEQSERIARSIPGAKLVELD-GGHFYPRTSADLFARHVGEFLCGKPL-------------------
B3I7K9_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B3WNJ4_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C8U5H1_ECO10_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B6I985_ECOSE_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C6EHJ8_ECOBD_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C4ZQD7_ECOBW_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
RUTD_ECOLI_16-250               HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B7M8Z4_ECO8A_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C9QZ67_ECOD1_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C5W2W8_ECOBB_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C6UFC0_ECOBR_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B3IQ15_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B3XEU2_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B1X9D0_ECODH_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B2N536_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C8TNB9_ECO26_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
C8UMM5_ECO1A_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B7LFB9_ECO55_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
Q3Z3A4_SHISS_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3HD65_ECOLX_16-250             HADRICC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
A7ZYW4_ECOHS_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B1IV88_ECOLC_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B2NNW4_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B2P113_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3BZK7_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3BI46_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3AZR6_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3AK70_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3A4A8_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B2PKQ2_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B5YU51_ECO5E_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
C3TF07_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
C6UPN1_ECO5T_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7A0I9_ECO57_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
RUTD_ECO57_16-250               HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
D3QPK2_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
A7ZKB4_ECO24_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
D2AC40_SHIF2_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
Q83LK8_SHIFL_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
Q0T625_SHIF8_16-250             HADRIRR--PVQIICASDDLLVPTACSSELHAALPDSQKMVMPYGGHACNVTDPETFNAL-----------------------------
B3WZB6_SHIDY_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
A1A9R4_ECOK1_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7MIF6_ECO45_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
C1HFA9_9ESCH_25-259             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
Q1RDK8_ECOUT_25-259             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7UNZ2_ECO27_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
D2NGI6_ECOS5_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7NLB7_ECO7I_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B3HT09_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
Q0TJ58_ECOL5_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
D3H122_ECO44_16-250             HTDRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
C2DK76_ECOLX_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
Q8FJ43_ECOL6_25-259             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7MTF2_ECO81_16-250             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTAPETFNAL-----------------------------
B1LIZ6_ECOSM_16-250             HADRIRC--PVQIICASDDLLVPTACSSELHAALPDSQKMVMRYGGHACNVTDPETFNAL-----------------------------
B7N3G5_ECOLU_25-259             HADRIRC--PVQIICASDDLLVPSACSSELHAALPDSQKMVMRYGGHACNVTHPETFNAL-----------------------------
gi|146311179|ref|YP_001176253_  QAKHVHC--PVQIICSTDDLLVPSVCSTELHAALPGSHKTVMRQGGHACNVTDPDTFNALLLNGLASLMHNPEPVFKESQ---------
A4W922_ENT38_16-250             QAKHVHC--PVQIICSTDDLLVPSVCSTELHAALPGSHKTVMRQGGHACNVTDPDTFNAL-----------------------------
gi|296102971|ref|YP_003613117_  HAARMAC--PVHLICSADDLLVPSVCSSELQAALPHSHSVVMRQGGHACNVTEPETFNTLLLNGLASLLHSHEPAL-------------
gi|295096275|emb|CBK85365_1|_p  HAARVRC--PVQIICSTDDLLVPSVCSAELHAALPHARKTVMRQGGHACNVTVPDIFNTLLLNGLASLLHSPEPAL-------------
gi|238894074|ref|YP_002918808_  RASAIAC--PTLIISAADDLLVPASCSRVLQTAIPGSQLVEMPWGGHACNVTDADTFNTILRDGLSAMLPVARETR-------------
C4X6I3_KLEPN_16-250             RASAIAC--PTLIISAADDLLVPASCSRVLQTAIPGSQLVEMPWGGHACNVTDADTFNTI-----------------------------
A6T799_KLEP7_16-250             RASAIAC--PTLIISAADDLLVPASCSRVLQTAIPGSQLVEMPWGGHACNVTDADTFNTI-----------------------------
gi|288936197|ref|YP_003440256_  RAAAIAC--PTLIVSAADDLLVPASCSRVLQAAIPGSQRVEMPWGGHACNVTDADTFNTILCDGLAAMLPVAREI--------------
gi|206580846|ref|YP_002239344_  RAAAIAC--PTLIVSAADDLLVPASCSRVLQAAIPGSQRVEMPWGGHACNVTDADTFNTILCDGLAAMLPVAREIR-------------
B5XXN3_KLEP3_16-250             RAAAIAC--PTLIVSAADDLLVPASCSRVLQAAIPGSQRVEMPWGGHACNVTDADTFNTI-----------------------------
gi|290510748|ref|ZP_06550118_1  RAAAIAC--PTLIVSAADDLLVPASCSRVLQTAIPGSQRVEMPWGGHACNVTDADTFNTILRDGLAAMLPVAREIR-------------
D3RKL3_KLEVA_17-251             RAAAIAC--PTLIVSAADDLLVPASCSRVLQAAIPGSQRVEMPWGGHACNVTDADTFNTI-----------------------------
gi|152969591|ref|YP_001334700_  RASAIAC--PTLIISAADDLLVPASCSRVLQTAIPGSQLVEMPWGGHACNVTDADTFNTILRDGLSAMLPVARETR-------------
gi|156934532|ref|YP_001438448_  RAARVIT--PVQIICARDDMLVPWTCSQALHEALPHSRLDVMDFGGHACNVTAPQPFHSLLYAGLASLAPAPHKETV------------
A7MFY0_ENTS8_17-251             RAARVIT--PVQIICARDDMLVPWTCSQALHEALPHSRLDVMDFGGHACNVTAPQPFHSL-----------------------------
gi|260597382|ref|YP_003209953_  RAARVTT--PVQLICARDDVLVPWTCSQALHEALPHSRLDVMTSGGHACNVTAPQRFNSLLYAGLAALTPAPHKETV------------
C9Y0S4_CROTZ_16-250             RAARVTT--PVQLICARDDVLVPWTCSQALHEALPHSRLDVMTSGGHACNVTAPQRFNSL-----------------------------
gi|317047621|ref|YP_004115269_  DAGKITQ--PVLAIYSQDDLLVPWSCSPELAAALPNASLIEMAWGGHAMSVTDAENFNALLLQWLSRSHAPQEASDEYA----------
C8QEM5_9ENTR_16-250             DAGKITQ--PVLAIYSQDDLLVPWSCSPELAAALPNASLIEMAWGGHAMSVTDAENFNAL-----------------------------
gi|304397134|ref|ZP_07379013_1  RAAAIPQ--PVLVIASQDDLLVPWSCSTELAATLPNATEQMMAWGGHAMSVTDPEKFNALLLQWLDQTDDVQPLQRVAG----------
gi|300716142|ref|YP_003740945_  LAGQIAQ--PVLLICSQDDLLVPWTCSQTLLEALPNATLEKMAWGGHAMSVTDSSTFNPLLLNWLSDTPASSPAELELIWQKP------
gi|123442221|ref|YP_001006202_  VLPHITT--PTLALCATDDLLVPYPCSQALAELLPDGEWAQMSYGGHAMSVTNSEQFNGILLSYLLMDTGIAKCELALNQSNTSAIHL-
A1JMX1_YERE8_16-250             VLPHITT--PTLALCATDDLLVPYPCSQALAELLPDGEWAQMSYGGHAMSVTNSEQFNGI-----------------------------
gi|270261263|ref|ZP_06189536_1  YLADIST--PTLALCSRDDLLVPYHCSHQLAESLPFGELAQMAYGGHAMSVTDADNFNRILLGWLLKTHGQSSACNPADAQLEPTGLKH
D1RPC7_SEROD_16-250             YLADIST--PTLALCSRDDLLVPYHCSHQLAESLPFGELAQMAYGGHAMSVTDADNFNRI-----------------------------
gi|157370062|ref|YP_001478051_  HLADITT--PTLALCSRDDLLVPYHCSHQLAASLPNGELAEMAYGGHAMSVTDTEHFNRILLGWLLKTQNAQTRLQP------------
A8GCT3_SERP5_16-250             HLADITT--PTLALCSRDDLLVPYHCSHQLAASLPNGELAEMAYGGHAMSVTDTEHFNRI-----------------------------
gi|291619589|ref|YP_003522331_  SLKGVIA--PTLALSAKDDLLVPWSCSADLASRLPHGEHLQMGYGGHAMSVTDPDTFNPILLDWLQRQASHPSGTPSDFIPVEMP----
D4GEU7_PANAN_16-250             SLKGVIA--PTLALSAKDDLLVPWSCSADLASRLPHGEHLQMGYGGHAMSVTDPDTFNPI-----------------------------
gi|322833714|ref|YP_004213741_  SLGQVIT--PTLAFSCKDDLLVPWSRSVDLASRLPNGEHTQMLYGGHAMSVTDPETFNPILLDWLLRHSSQASATPSGHLPTETSWPKH
gi|146283917|ref|YP_001174070_  ELPRITT--PTLLIANRDDMLVPWQRSQHLADNMPNAQLALLNYGGHASSVSDSEPFNQILLDHLAEQCGQVAAA--------------
A4VQH7_PSEU5_16-250             ELPRITT--PTLLIANRDDMLVPWQRSQHLADNMPNAQLALLNYGGHASSVSDSEPFNQI-----------------------------
gi|302189116|ref|ZP_07265789_1  DLSRIHT--PTLLIANRDDMLVPWQQSRHLANALPNATLVLLDYGGHASNITDPLPFQRALLAFLSIHP--------------------
gi|66044249|ref|YP_234090_1|_A  ELSRIHT--PTLLIANRDDMLVPWQQSRHLANALPNATLVLLEYGGHASNITDPLPFQRALRAFLSTQP--------------------
Q4ZXS0_PSEU2_16-250             ELSRIHT--PTLLIANRDDMLVPWQQSRHLANALPNATLVLLEYGGHASNITDPLPFQRA-----------------------------
gi|71735511|ref|YP_273315_1|_a  SLARIQT--PTLLIANRDDMLVPWQQSQHLAEALPNARLVLLEYGGHASNITDPLPFQRTLLDFLNAQT--------------------
Q48MQ7_PSE14_16-248             SLARIQT--PTLLIANRDDMLVPWQQSQHLAEALPNARLVLLEYGGHASNITDPLPFQ-------------------------------
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gi|289626193|ref|ZP_06459147_1  SLARIQT--PTLLIANRDDMLVPWQQSQHLAEALPNARLVLLEYGGHASNITDPLPFQRTLLDFLNAQT--------------------
gi|257482056|ref|ZP_05636097_1  SLARIQT--PTLLIANRDDMLVPWQQSQHLAETLPNARLVLLEYGGHASNITDPLPFQRTLLDFLNAQT--------------------
gi|289648344|ref|ZP_06479687_1  SLARIQT--PTLLIANRDDMLVPWQQSQHLAEALPNARLVLLEYGGHASNITDPLPFQRTLLDFLNAQT--------------------
gi|320325736|gb|EFW81797_1|_al  SLTRIQT--PTLLIANRDDMLVPWQQSQHLAEALPNARLVLLEYGGHASNITDPVPFQRALLDFLNAQT--------------------
gi|28868369|ref|NP_790988_1|_a  QLARIQT--PTLLIANRDDMLVPWQQSRHLAKVLPNARLVLLEYGGHASSISDPLPFQRALLDFLSAQT--------------------
Q887X6_PSESM_16-250             QLARIQT--PTLLIANRDDMLVPWQQSRHLAKVLPNARLVLLEYGGHASSISDPLPFQRA-----------------------------
gi|213967180|ref|ZP_03395329_1  QLARIQT--PTLLIANRDDMLVPWQQSRHLAEVLPNARLVLLEYGGHASSISDPLPFQRALLDFLSAQT--------------------
gi|196155582|ref|YP_002125071_  KLKGITT--PTFALANKDDTLVPWQRSQMLVDRMPNAELSVMEYGGHASSITVPDAFNKLVLEYLQRVA--------------------
B4RRW2_ALTMD_35-269             KLKGITT--PTFALANKDDTLVPWQRSQMLVDRMPNAELSVMEYGGHASSITVPDAFNKL-----------------------------
gi|239994720|ref|ZP_04715244_1  RLHAITT--PTLALANKDDTLVPWQRSQMLAEAMPNAELSVMEYGGHASSITNPIAFNELLRGYLGQVT--------------------
gi|262376021|ref|ZP_06069252_1  EHQQALKDIPIHLLANQNDFLVPYQRSQQLQQCLPHSQLSLLATGAHASTVTETDQVNQLILSFLISP---------------------
D0SV49_ACILW_16-255             EHQQALKDIPIHLLANQNDFLVPYQRSQQLQQCLPHSQLSLLATGAHASTVTETDQVNQL-----------------------------
gi|293611018|ref|ZP_06693317_1  EHLQALQDTAIHIVANQDDFLVPAHKSQDIFTKLGHGQLCILPSGAHASTVTESQQLNQTFIQFFHSIKALS-----------------
gi|262368332|ref|ZP_06061661_1  EIRAALQNIPMHLIANQDDFLVPYQRSQNLKQLFPHAQLTLLKQGAHAATVTETVLMNKEMLGFLTVQESSV-----------------
D0S9G1_ACIJO_16-250             EIRAALQNIPMHLIANQDDFLVPYQRSQNLKQLFPHAQLTLLKQGAHAATVTETV----------------------------------
gi|50083320|ref|YP_044830_1|_a  ARIDTLKQLPVCLIANQDDMLVPYVQSLNLWKKLPDAQLKLLPYGGHASTVTEARQVNQLMLDFLKTSAPT------------------
Q6FFZ9_ACIAD_16-255             ARIDTLKQLPVCLIANQDDMLVPYVQSLNLWKKLPDAQLKLLPYGGHASTVTEARQVNQL-----------------------------
gi|255319344|ref|ZP_05360561_1  VARQIQN--PTLVLTNQDDFLVPWKRGLALAKLIKNAELELMPNGGHASTITQAQSVNEILIKFLTKTTD-------------------
C6RN00_ACIRA_16-250             VARQIQN--PTLVLTNQDDFLVPWKRGLALAKLIKNAELELMPNGGHASTITQAQSVNEI-----------------------------
D0T3M4_ACIRA_16-250             VARQIQN--PTLVLTNQDDFLVPWKRGLALAKLIKNAELELMPNGGHASTITQAQSVNEI-----------------------------
gi|316935661|ref|YP_004110643_  RLDEIRH--STLVLASKDDTLVPWTCSQHLAAGLPSAEFVLMPEGGHGVTVTEADAFNRAVLDFLAPAA--------------------
D2MBB4_RHOPA_24-258             RLDEIRH--STLVLASKDDTLVPWTCSQHLAAGLPSAEFVLMPEGGHGVTVTEADAFNRA-----------------------------
gi|159185242|ref|NP_355444_2|_  RLGEIGN--PVLVVATKDDLLVPYTRSLRLAEGLPQSELCLLDFGAHAVNITEPDLFNTRLLQFLLPADQT------------------
Q7CWX3_AGRT5_16-250             RLGEIGN--PVLVVATKDDLLVPYTRSLRLAEGLPQSELCLLDFGAHAVNITEPDLFNTR-----------------------------
gi|222080882|ref|YP_002540245_  RLSEIRT--PTLVVGTRDDLLVPYTRSVRLAEGLSAAELALSDFGAHAVNVVEPEEFNNKVLRFLRARSEVR-----------------
B9JLT6_AGRRK_16-250             RLSEIRT--PTLVVGTRDDLLVPYTRSVRLAEGLSAAELALSDFGAHAVNVVEPEEFNNK-----------------------------
gi|239817801|ref|YP_002946711_  RLGAITA--PTLVAAAMDDALVPWTCSQRLADGLKDVTLHFLPHGGHAHSVTEAAVFNRSLLDFLARVSAPGVPA--------------
C5CN82_VARPS_16-250             RLGAITA--PTLVAAAMDDALVPWTCSQRLADGLKDVTLHFLPHGGHAHSVTEAAVFNR------------------------------
gi|167647941|ref|YP_001685604_  DLETIRC--PVLVSASADDMLVPLSCSRRLAERLPNATLDIAPWGGHGFTVTAPEAFNAAVLNFLSGEAA-------------------
B0SW62_CAUSK_24-258             DLETIRC--PVLVSASADDMLVPLSCSRRLAERLPNATLDIAPWGGHGFTVTAPEAFNAA-----------------------------
gi|295689471|ref|YP_003593164_  RLEEIPH--RVLVSASADDMLVPMSCSQRLAARLPNADFQQVAWGGHGFTVTDPETFNEGLIKFLEGA---------------------
D0XXH0_9CAUL_24-258             RLEEIPH--RVLVSASADDMLVPMSCSQRLAARLPNADFQQVAWGGHGFTVTDPETFNE------------------------------
gi|16127029|ref|NP_421593_1|_a  RLEDITH--RVLISASADDMLVPMSCSQRLAGRLPNADFQQVAWGGHGFTVTDPETFNEALVSFLEGA---------------------
B8H1Q3_CAUCN_27-261             RLEDITH--RVLISASADDMLVPMSCSQRLAGRLPNADFQQVAWGGHGFTVTDPETFNEA-----------------------------
Q9A4N3_CAUCR_27-261             RLEDITH--RVLISASADDMLVPMSCSQRLAGRLPNADFQQVAWGGHGFTVTDPETFNEA-----------------------------
gi|170747999|ref|YP_001754259_  RLGAIGH--ETLVMAARDDVLVPYTRSERLAAALPNARLALAPEGGHAHSVTRPEAFNRALLDFLDRD---------------------
B1M5I5_METRJ_17-251             RLGAIGH--ETLVMAARDDVLVPYTRSERLAAALPNARLALAPEGGHAHSVTRPEAFNRA-----------------------------
gi|218530013|ref|YP_002420829_  ALGRIPH--ETLLMAARDDVLVPFTASDVLAAGLPNARLDLAPEGGHAHSVTRPEAFNRTLLDFLASP---------------------
B7KWT4_METC4_18-252             ALGRIPH--ETLLMAARDDVLVPFTASDVLAAGLPNARLDLAPEGGHAHSVTRPEAFNRT-----------------------------
gi|163851162|ref|YP_001639205_  ALPRIPH--ETLLMAARDDVLVPYTASDILAAGLPNARLDLAPEGGHAHSVTRPEAFNRTLLDFLASP---------------------
A9W3H8_METEP_18-252             ALPRIPH--ETLLMAARDDVLVPYTASDILAAGLPNARLDLAPEGGHAHSVTRPEAFNRT-----------------------------
gi|240138315|ref|YP_002962787_  ALGRIPH--ETLLMAARDDVLVPFTASDILAAGLPNARLDLAPEGGHAHSATRPEAFNRTLLDFLTSP---------------------
C5B0U6_METEA_18-252             ALGRIPH--ETLLMAARDDVLVPFTASDILAAGLPNARLDLAPEGGHAHSATRPEAFNRT-----------------------------
gi|254560857|ref|YP_003067952_  ALARIPH--ETLLMAARDDVLVPFTASDILAAGLPNARLDLAPEGGHAHSVTRSASFNRTLLDFLASP---------------------
C7CM33_METED_18-252             ALARIPH--ETLLMAARDDVLVPFTASDILAAGLPNARLDLAPEGGHAHSVTRSASFNRT-----------------------------
gi|188580343|ref|YP_001923788_  ALARIPH--ETLLMAARDDVLVPFTASDALAAGLPNARLDLAPEGGHAHSVTRPDAFNRTLLDFLASP---------------------
B1ZB18_METPB_18-252             ALARIPH--ETLLMAARDDVLVPFTASDALAAGLPNARLDLAPEGGHAHSVTRPDAFNRT-----------------------------
gi|158424120|ref|YP_001525412_  RLADIRV--PTLLAAAKDDALVPSYLSTLLAEGIPDARIAEVDWGAHAFSAVTPDVFNEMLLGFCGEIDQ-------------------
A8IAD8_AZOC5_22-255             RLADIRV--PTLLAAAKDDALVPSYLSTLLAEGIPDARIAEVDWGAHAFSAVTPDVFNEM-----------------------------
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Fig S2. Two-dimensional projection of the CLANS clustering results obtained for the α/βhydrolase_6 sequences. Proteins are indicated by dots, and clusters are circled and labeled according to their membership in different families. Lines indicate sequence similarity as reported by BLAST and are colored in shades of grey according to the BLAST P-value. The diagram shows 14000 sequences remaining after initial clustering and is zoomed in on the RutD and PcaD clusters.

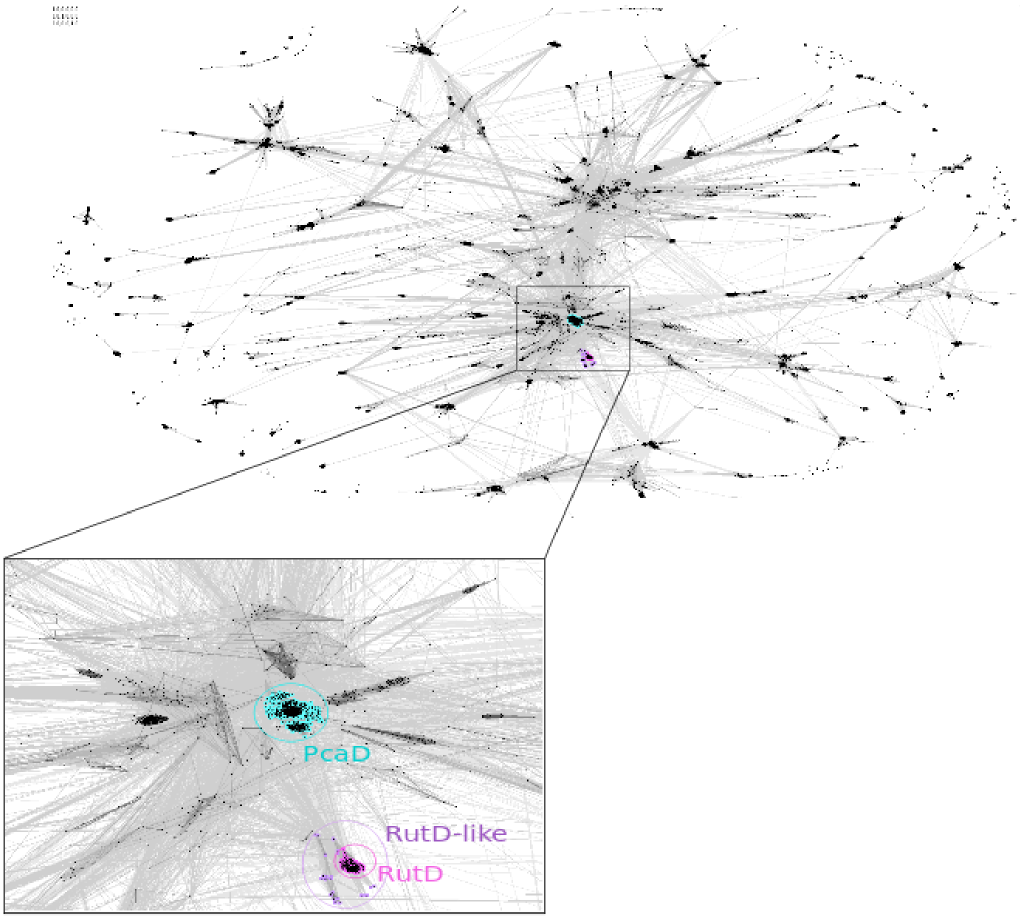

Fig.S3. Diffraction image of RutD crystal. Image shows presence of multiple crystal lattices.