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# Protein and peptide identifications combining all three YS40 phage lysate MudPIT analyses.

Multiple loci are grouped together if each is identified by the same set of peptides. Loci are shown in order of decreasing sequence coverage. Each locus name is followed by the number of peptides, the number of spectrum copies present for this protein, the sequence coverage (what percentage of the residues are represented in observed peptides), length of the amino acid sequence, molecular weight, approximate pI, and descriptive name.

The peptide identifications are shown below the protein to which they belong. The information includes whether or not the peptide sequence is unique to this locus (indicated by an asterisk at the start of the line), the spectrum file name (the last number being the precursor ion charge state), the XCorr and DeltCN scores, the observed and calculated M+H+ masses, the rank by preliminary scoring, the preliminary score itself, the percentage of ions expected that were found, the number of times this peptide was identified, and the sequence of this peptide. The peptides are listed in the order in which they align to the full protein sequence.

| **Criteria sets:** | |
|---|---|
| Minimum +1 XCorr | 1.8 |
| Minimum +2 XCorr | 2.5 |
| Minimum +3 XCorr | 3.5 |
| Minimum DeltCN | 0.11 |
| Minimum charge state | 1 |
| Maximum charge state | 3 |
| Maximum Sp rank | 10 |
| Tryptic status requirement | Full |
| Multiple, ambiguous IDs allowed | FALSE |
| Minimum sequence length | 7 |
| Maximum sequence length | 100 |
| Purge duplicate peptides by protein | XCorr |
| Include only loci with unique peptide | FALSE |
| Remove subset proteins | TRUE |
| Exclude protein names matching | Contaminant |
| Minimum redundancy for low coverage loci | 10 |
| Minimum peptides per locus | 1 |

| Locus | Sequence Count | Spectrum Count | Sequence Coverage | Length | MolWt | pI | Validation Status | Descriptive Name | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Unique | FileName | XCorr | DeltCN | M+H+ | CalcM+H+ | TotalIntensity | SpRank | SpScore | IonProportion | Redundancy | Sequence |
| gi\|5000000066 | 13 | 86 | 69.50% | 246 | 27366 | 5.1 | U | Translation: 56362..57102 (reverse), 247 amino acids | | | |
| * | _304.2806.2807.1 | 3.2167 | 0.1846 | 1469.25 | 1469.721 | 8916.3 | 1 | 761 | 58.3 | 9 | K.TSQFAEIYLIGVK.T |
| * | _207.2752.2752.2 | 4.5773 | 0.4601 | 1469.52 | 1469.721 | 8519.9 | 1 | 1769.4 | 79.2 | 4 | K.TSQFAEIYLIGVK.T |
| * | _305.2994.2994.2 | 4.345 | 0.5222 | 1470.14 | 1469.721 | 7412 | 1 | 1730.7 | 79.2 | 19 | K.TSQFAEIYLIGVK.T |
| * | _303.4049.4049.2 | 4.087 | 0.3865 | 2514.57 | 2511.939 | 4720.3 | 1 | 698.7 | 54.5 | 8 | R.TVIGTPIPIFVPGFYDGSITMER.A |
| * | _204.2287.2287.2 | 2.7828 | 0.1577 | 1021.3 | 1021.245 | 5231.6 | 4 | 793.3 | 81.2 | 1 | R.ATILLQSFK.N |
| * | _303.3302.3302.2 | 5.4846 | 0.5244 | 2351.27 | 2352.667 | 8277.4 | 1 | 1715.6 | 60 | 7 | K.NGVNINPLLAYSSEIYMPEAR.G |
| * | _302.3550.3550.3 | 3.9243 | 0.4388 | 2352.84 | 2352.667 | 7999.6 | 1 | 964.7 | 33.8 | 2 | K.NGVNINPLLAYSSEIYMPEAR.G |
| * | _305.3418.3418.3 | 7.3459 | 0.5711 | 3346.37 | 3347.665 | 8361.9 | 1 | 1853.3 | 33.6 | 19 | K.RVELPSDVNGTPLPNDFLSSNTTFYYVSGR.E |
| * | _307.3394.3394.2 | 3.1239 | 0.3319 | 1367.03 | 1367.717 | 2961.8 | 1 | 558.7 | 81.8 | 1 | K.YIPGFLFVVALK.D |
| * | _307.3605.3606.1 | 2.342 | 0.1576 | 1367.36 | 1367.717 | 5718.6 | 1 | 886.8 | 72.7 | 2 | K.YIPGFLFVVALK.D |
| * | _304.2667.2667.2 | 3.8759 | 0.3975 | 1122.15 | 1122.371 | 5559.6 | 1 | 1346.8 | 94.4 | 5 | R.NAGLYLAMLR.D |
| * | _307.0359.0359.2 | 5.8981 | 0.4715 | 2414.99 | 2414.675 | 7528.2 | 1 | 1491.9 | 54.8 | 8 | R.DFSVSYSSENAIILENITALAR.P |
| * | _307.3369.3369.3 | 4.9819 | 0.4921 | 3525.79 | 3526.886 | 13348 | 1 | 1337.9 | 25 | 1 | R.PLYNSGWYQVLADTFNTGASFGYIYSDPHKL.- |
| gi\|55981452\|ref\| | 14 | 53 | 62.30% | 228 | 25667 | 6.4 | U | conserved putative protein [Thermus thermophilus HB8] | | | |
| * | _304.2346.2346.2 | 3.3981 | 0.4179 | 1133.03 | 1133.252 | 7553.8 | 1 | 1331.8 | 87.5 | 5 | K.SRDYAAFFR.I |
| * | _303.3564.3565.2 | 3.7592 | 0.4794 | 2837.75 | 2838.235 | 4854.3 | 1 | 690.9 | 45.8 | 2 | R.ILSEAHLPTAYVPGPQDAPIWEYLR.E |
| * | _302.3949.3949.3 | 3.7679 | 0.3519 | 2838.82 | 2838.235 | 5604.5 | 1 | 905.6 | 34.4 | 1 | R.ILSEAHLPTAYVPGPQDAPIWEYLR.E |
| * | _305.2782.2782.1 | 2.4867 | 0.3561 | 1336 | 1337.48 | 3949.8 | 1 | 261.4 | 66.7 | 1 | R.NVHETFTFWR.G |
| * | _305.2748.2750.2 | 2.9675 | 0.1102 | 1336.9 | 1337.48 | 6499.7 | 1 | 839.1 | 83.3 | 1 | R.NVHETFTFWR.G |
| * | _303.2962.2962.3 | 4.8814 | 0.44 | 2594.44 | 2595.782 | 6640.3 | 1 | 738.4 | 30.2 | 2 | R.GPYLVAGVGGEIADEGEPEEHEALR.Y |
| * | _307.2983.2983.3 | 5.6189 | 0.5178 | 3732.11 | 3732.057 | 5361.4 | 1 | 1069.6 | 28.8 | 19 | R.GPYLVAGVGGEIADEGEPEEHEALRYPAWVAEYR.L |
| * | _305.2888.2888.1 | 2.4189 | 0.2704 | 1433.51 | 1434.742 | 4261.6 | 2 | 302.6 | 60 | 2 | K.IFLFHTMPYHK.G |
| * | _306.2753.2754.2 | 4.3548 | 0.3667 | 1436.17 | 1434.742 | 9101.8 | 1 | 1669.5 | 85 | 8 | K.IFLFHTMPYHK.G |
| * | _304.2020.2022.2 | 4.6384 | 0.4868 | 1632.2 | 1632.817 | 7731.5 | 1 | 1425.6 | 71.4 | 1 | K.GLNEQGSHEVAHLIK.T |
| * | _306.2821.2821.1 | 2.9453 | 0.4164 | 1261.25 | 1262.538 | 5105.4 | 1 | 536.3 | 59.1 | 2 | K.THNPLLVLVAGK.G |
| * | _305.2887.2887.2 | 3.2378 | 0.4551 | 1262.28 | 1262.538 | 4636.1 | 1 | 817.3 | 77.3 | 4 | K.THNPLLVLVAGK.G |
| * | _305.4434.4434.3 | 5.7474 | 0.4744 | 2873.54 | 2874.238 | 8016.8 | 1 | 1645.4 | 38 | 4 | K.HEMLGASWVVVPGDLSEGEYSLLDLR.A |
| * | _305.4480.4480.2 | 3.8355 | 0.3986 | 2873.83 | 2874.238 | 4329.2 | 1 | 735.1 | 48 | 1 | K.HEMLGASWVVVPGDLSEGEYSLLDLR.A |
| gi\|55981644\|ref\| | 13 | 123 | 61.10% | 162 | 17557 | 10.1 | U | 30S ribosomal protein S5 [Thermus thermophilus HB8] | | | |
| * | _107.2472.2472.2 | 4.0715 | 0.3512 | 1033.38 | 1033.216 | 6547.8 | 1 | 1550.4 | 94.4 | 7 | R.FGALVVVGDR.Q |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _305.2506.2506.2 | 4.1588 | 0.4313 | 1710.3 | 1711.057 | 5847.6 | | 1 | 1045.3 | 62.5 | 2 | R.VGLGFGKAPEVPLAVQK.A |
| * | _305.3815.3815.2 | 4.2994 | 0.4363 | 2795.8 | 2796.171 | 8212.9 | | 1 | 985.1 | 43.8 | 2 | R.RNMVEVPLQNGTIPHEIEVEFGASK.I |
| * | _305.3966.3966.3 | 5.5878 | 0.5186 | 2798.14 | 2796.171 | 7961.5 | | 1 | 1773.2 | 39.6 | 5 | R.RNMVEVPLQNGTIPHEIEVEFGASK.I |
| * | _303.3230.3230.2 | 4.9952 | 0.4903 | 2637.56 | 2639.983 | 4839 | | 1 | 750.3 | 50 | 17 | R.NMVEVPLQNGTIPHEIEVEFGASK.I |
| * | _302.3789.3789.3 | 3.9345 | 0.247 | 2639.9 | 2639.983 | 4045.4 | | 1 | 515.9 | 31.5 | 2 | R.NMVEVPLQNGTIPHEIEVEFGASK.I |
| * | _303.2248.2250.3 | 4.2903 | 0.3179 | 1787.68 | 1788.187 | 8101.5 | | 1 | 1205.4 | 38.9 | 6 | K.IVLKPAAPGTGVIAGAVPR.A |
| * | _302.0106.0106.2 | 4.0888 | 0.4457 | 1788.41 | 1788.187 | 3126.4 | | 1 | 791.2 | 72.2 | 9 | K.IVLKPAAPGTGVIAGAVPR.A |
| * | _303.1818.1818.2 | 4.5092 | 0.5873 | 1333.96 | 1334.561 | 5250 | | 1 | 1530 | 85.7 | 3 | K.PAAPGTGVIAGAVPR.A |
| * | _302.3493.3493.2 | 5.1583 | 0.4915 | 1457.41 | 1457.751 | 6246.7 | | 1 | 1785.9 | 84.6 | 40 | R.AILELAGVTDILTK.E |
| * | _304.3167.3167.1 | 3.7747 | 0.4672 | 1457.42 | 1457.751 | 8905.7 | | 1 | 1143.3 | 65.4 | 26 | R.AILELAGVTDILTK.E |
| * | _207.2930.2930.2 | 2.719 | 0.2823 | 1458.27 | 1457.751 | 8135.1 | | 1 | 885.7 | 61.5 | 1 | R.AILELAGVTDILTK.E |
| * | _303.3376.3376.2 | 4.3048 | 0.4331 | 1577.02 | 1577.839 | 6466.8 | | 1 | 1419.3 | 76.9 | 3 | R.NPINIAYATMEALR.Q |
| gi\|5000000072 | 43 | 615 | 59.60% | 470 | 52303 | 6.1 | U | Translation: 61756..63168 (reverse), 471 amino acids | | | | |
| * | _203.2127.2127.2 | 4.3439 | 0.4513 | 1428.67 | 1429.573 | 9458.1 | | 1 | 1962 | 76.9 | 5 | K.ALNAAGQVAESLER.E |
| * | _302.2023.2023.1 | 3.2213 | 0.4815 | 1429.16 | 1429.573 | 3743.1 | | 1 | 230.7 | 53.8 | 2 | K.ALNAAGQVAESLER.E |
| * | _303.2046.2046.2 | 4.4839 | 0.45 | 1429.79 | 1429.573 | 7427.8 | | 1 | 1957.5 | 84.6 | 9 | K.ALNAAGQVAESLER.E |
| * | _303.4392.4392.3 | 7.6085 | 0.5034 | 3992.74 | 3994.442 | 7945.9 | | 1 | 1110.1 | 25.7 | 28 | K.ALNAAGQVAESLEREDLEPEVTQLNVLDTPLTDLLSK.N |
| * | _107.2971.2972.2 | 5.1243 | 0.5659 | 2584.68 | 2583.893 | 9210.4 | | 1 | 1068.7 | 45.5 | 8 | R.EDLEPEVTQLNVLDTPLTDLLSK.N |
| * | _302.0015.0015.1 | 2.8422 | 0.327 | 1451.29 | 1452.566 | 5590.2 | | 1 | 446.6 | 54.5 | 1 | K.AYEHEYNVVTAR.H |
| * | _302.0014.0014.2 | 3.839 | 0.4983 | 1451.98 | 1452.566 | 5959.5 | | 1 | 1288.1 | 81.8 | 6 | K.AYEHEYNVVTAR.H |
| * | _107.2284.2284.2 | 3.9082 | 0.4513 | 1452.61 | 1452.566 | 7621.1 | | 1 | 1562.7 | 81.8 | 15 | K.AYEHEYNVVTAR.H |
| * | _207.2326.2326.2 | 3.0532 | 0.1738 | 1407.56 | 1407.615 | 8927.2 | | 1 | 745.6 | 58.3 | 3 | K.IGYAAFREGGLPR.T |
| * | _103.1714.1714.2 | 3.3337 | 0.245 | 916.63 | 916.065 | 2939 | | 1 | 657.4 | 92.9 | 2 | R.TVEVNVVR.R |
| * | _103.1966.1966.2 | 3.4504 | 0.3737 | 1004.37 | 1004.172 | 5693.3 | | 1 | 981.8 | 87.5 | 10 | R.ITVTELATR.T |
| * | _302.2334.2334.1 | 2.7066 | 0.2471 | 1575.09 | 1576.805 | 6376.8 | | 1 | 368.9 | 50 | 1 | R.TTQNGVMQIDELVK.R |
| * | _303.2347.2347.2 | 3.8847 | 0.4721 | 1576.3 | 1576.805 | 5626.1 | | 1 | 839.2 | 65.4 | 9 | R.TTQNGVMQIDELVK.R |
| * | _305.1656.1656.2 | 3.2918 | 0.3646 | 1311.28 | 1311.443 | 3465.3 | | 2 | 438.1 | 66.7 | 1 | K.RGAPQNVLDAGGR.P |
| * | _305.4256.4258.2 | 3.2166 | 0.2985 | 2821.69 | 2822.153 | 7687.7 | | 1 | 380.5 | 34 | 7 | K.RGAPQNVLDAGGRPLSIDLLWEAESR.V |
| * | _306.3293.3294.3 | 5.3951 | 0.4501 | 2823.74 | 2822.153 | 5852.7 | | 1 | 1071.6 | 35 | 90 | K.RGAPQNVLDAGGRPLSIDLLWEAESR.V |
| * | _304.4061.4061.3 | 5.1296 | 0.5054 | 2664.8 | 2665.966 | 5653 | | 1 | 939.3 | 35.4 | 26 | R.GAPQNVLDAGGRPLSIDLLWEAESR.V |
| * | _305.3734.3735.2 | 3.658 | 0.4413 | 2665.71 | 2665.966 | 5904.3 | | 1 | 469.8 | 39.6 | 42 | R.GAPQNVLDAGGRPLSIDLLWEAESR.V |
| * | _305.4316.4316.2 | 3.6951 | 0.4026 | 1530.04 | 1529.733 | 9755.4 | | 1 | 1275.2 | 66.7 | 2 | R.PLSIDLLWEAESR.V |
| * | _303.3382.3382.3 | 5.2036 | 0.475 | 2157.28 | 2158.459 | 9170 | | 1 | 1286.1 | 39.5 | 4 | R.VVSTQAFANPTAVFISYVDK.L |
| * | _303.3580.3580.2 | 7.0644 | 0.5779 | 2158.14 | 2158.459 | 5234.3 | | 1 | 1151.5 | 63.2 | 31 | R.VVSTQAFANPTAVFISYVDK.L |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _305.2922.2922.2 | 4.5913 | 0.4471 | 1439.98 | 1440.642 | 6670.6 | 1 | 1469.3 | 86.4 | 78 | K.LNLQASFYQISR.V |
| * | _303.2759.2760.1 | 2.879 | 0.2999 | 1440.26 | 1440.642 | 4281.1 | 1 | 314.9 | 63.6 | 11 | K.LNLQASFYQISR.V |
| * | _305.2819.2819.2 | 3.8085 | 0.4022 | 1648.49 | 1647.875 | 4567.5 | 1 | 1092.2 | 73.3 | 2 | R.RAGLLGADAQSYIGVR.G |
| * | _302.0207.0211.1 | 3.5304 | 0.3951 | 1491.39 | 1491.687 | 2853.4 | 1 | 345.9 | 60.7 | 12 | R.AGLLGADAQSYIGVR.G |
| * | _107.2535.2535.2 | 5.4388 | 0.4831 | 1491.65 | 1491.687 | 7806.7 | 1 | 2111.6 | 78.6 | 4 | R.AGLLGADAQSYIGVR.G |
| * | _302.2687.2687.2 | 5.4583 | 0.4922 | 1493.53 | 1491.687 | 6472.6 | 1 | 1777.3 | 82.1 | 94 | R.AGLLGADAQSYIGVR.G |
| * | _305.3835.3835.3 | 4.092 | 0.3638 | 3335.63 | 3335.703 | 9605.7 | 1 | 918.7 | 26.7 | 2 | R.AGLLGADAQSYIGVRGEHSLYPSQFLGDFHK.F |
| * | _302.0200.0202.2 | 4.8604 | 0.4176 | 1863.36 | 1863.039 | 5119.5 | 1 | 932.5 | 70 | 11 | R.GEHSLYPSQFLGDFHK.F |
| * | _302.0203.0203.3 | 4.8567 | 0.4661 | 1863.6 | 1863.039 | 7562.8 | 1 | 1330.5 | 46.7 | 10 | R.GEHSLYPSQFLGDFHK.F |
| * | _103.1647.1647.1 | 2.4526 | 0.2985 | 1128.47 | 1129.214 | 9051.9 | 1 | 650.2 | 65 | 2 | K.AANFYGESAAK.Y |
| * | _103.1642.1642.2 | 2.9026 | 0.2804 | 1129.11 | 1129.214 | 5687.5 | 1 | 468.1 | 65 | 2 | K.AANFYGESAAK.Y |
| * | _304.2315.2315.2 | 3.9056 | 0.5038 | 1474.23 | 1474.607 | 5070 | 1 | 1597.7 | 87.5 | 12 | K.YIDVYIDSTEAGK.G |
| * | _103.2110.2110.2 | 3.9138 | 0.4107 | 1475.45 | 1474.607 | 5505.9 | 1 | 1363 | 83.3 | 3 | K.YIDVYIDSTEAGK.G |
| * | _303.2404.2404.1 | 2.493 | 0.2576 | 1475.5 | 1474.607 | 7818.7 | 1 | 1014.2 | 66.7 | 4 | K.YIDVYIDSTEAGK.G |
| * | _306.2767.2769.1 | 2.7693 | 0.3457 | 1188.34 | 1189.403 | 3741.7 | 1 | 523.5 | 66.7 | 1 | R.FQFHGLVNVK.W |
| * | _306.2771.2773.2 | 3.3894 | 0.3259 | 1189.07 | 1189.403 | 5096.5 | 1 | 1152 | 88.9 | 8 | R.FQFHGLVNVK.W |
| * | _302.2814.2815.3 | 5.5855 | 0.5239 | 2855.61 | 2855.047 | 5162.7 | 1 | 931 | 34 | 20 | K.VSTVNGDFTWIDDGHETVTTPSGVYR.W |
| * | _307.2691.2693.2 | 4.3149 | 0.4835 | 2855.67 | 2855.047 | 8708.7 | 1 | 683.1 | 36 | 11 | K.VSTVNGDFTWIDDGHETVTTPSGVYR.W |
| * | _305.2735.2738.1 | 3.63 | 0.3916 | 1553.32 | 1553.844 | 5609.4 | 1 | 635.8 | 58.3 | 7 | R.LPPALTHDYVIWK.V |
| * | _302.0150.0150.2 | 4.2732 | 0.5303 | 1554 | 1553.844 | 5699.7 | 1 | 1164.5 | 79.2 | 10 | R.LPPALTHDYVIWK.V |
| * | _307.3309.3309.2 | 2.8342 | 0.1392 | 2635.82 | 2634.05 | 9126.9 | 1 | 480.6 | 34.8 | 1 | K.VASVFSRAPEFNFLIVNVGQEPIV.- |
| * | _305.4474.4474.2 | 4.6123 | 0.4124 | 1886.15 | 1887.186 | 8469.9 | 1 | 1054.5 | 56.2 | 8 | R.APEFNFLIVNVGQEPIV.- |
| gi\|55980144\|ref\|Y | 3 | 12 | 57.50% | 73 | 8185 | 8.6 | U | cold shock protein [Thermus thermophilus HB8] | | | |
| * | _304.2728.2728.3 | 6.2545 | 0.5053 | 2603.59 | 2603.85 | 7371.2 | 1 | 1380 | 37.5 | 2 | K.GYGFIEREGDTDVFVHYTAINAK.G |
| * | _302.2506.2506.2 | 4.4898 | 0.3256 | 1763.12 | 1762.914 | 7779.5 | 1 | 2022.7 | 76.7 | 4 | R.TLNEGDIVTFDVEPGR.N |
| * | _302.2435.2435.2 | 3.956 | 0.4155 | 2063.78 | 2062.244 | 8277.3 | 1 | 899.1 | 50 | 6 | R.TLNEGDIVTFDVEPGRNGK.G |
| gi\|55980214\|ref\|Y | 5 | 61 | 52.50% | 101 | 11973 | 6.9 | U | 30S ribosomal protein S6 (TS9) [Thermus thermophilus HB8] | | | |
| * | _304.2774.2775.2 | 5.6053 | 0.4957 | 2457.93 | 2457.789 | 6556.8 | 1 | 1279.1 | 60 | 39 | R.RYEVNIVLNPNLDQSQLALEK.E |
| * | _107.2641.2643.2 | 5.0769 | 0.4414 | 2301.62 | 2301.602 | 5344 | 1 | 871.7 | 57.9 | 9 | R.YEVNIVLNPNLDQSQLALEK.E |
| * | _302.3355.3355.2 | 5.0788 | 0.5509 | 2173.06 | 2174.392 | 6708.2 | 1 | 1664.5 | 65.6 | 10 | K.DPQGYFLWYQVEMPEDR.V |
| * | _303.3254.3254.3 | 4.3517 | 0.496 | 2843.99 | 2843.143 | 5656.3 | 1 | 809.9 | 33 | 2 | K.DPQGYFLWYQVEMPEDRVNDLAR.E |
| * | _102.2450.2450.1 | 1.9232 | 0.2693 | 977.27 | 977.062 | 5641.7 | 1 | 438.1 | 62.5 | 1 | K.SQEPFLANA.- |
| gi\|55981647\|ref\|Y | 10 | 22 | 48.60% | 138 | 15837 | 10.3 | U | 30S ribosomal protein S8 [Thermus thermophilus HB8] | | | |
| * | _205.3152.3152.2 | 2.5388 | 0.3243 | 1378.1 | 1377.657 | 5504.2 | 1 | 720.7 | 68.2 | 1 | -.MLTDPIADMLTR.I |
| * | _103.1499.1499.2 | 3.4565 | 0.3759 | 1352.33 | 1352.487 | 6439.1 | 1 | 948.6 | 72.7 | 2 | R.VYKESTDVPASR.F |
| * | _107.2305.2308.1 | 2.2424 | 0.1481 | 934.6 | 935.111 | 4110.2 | 1 | 428 | 83.3 | 1 | R.FKEEILR.I |
| * | _107.2292.2292.1 | 2.1454 | 0.2078 | 1161.67 | 1162.331 | 3248.6 | 6 | 284.9 | 61.1 | 1 | R.VDVDGKPYLR.V |
| * | _107.2279.2279.2 | 2.8845 | 0.2918 | 1162.5 | 1162.331 | 5529.8 | 1 | 926.7 | 88.9 | 2 | R.VDVDGKPYLR.V |
| * | _306.2225.2225.2 | 2.6548 | 0.185 | 813.82 | 813.978 | 3951 | 1 | 483.9 | 91.7 | 1 | R.RISKPGR.R |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _107.2229.2229.2 | 2.9135 | 0.1935 | 821.11 | 821.01 | 3590.9 | | 7 | 660 | 100 | 1 | R.RVYVGVK.E |
| * | _306.2726.2726.2 | 3.5532 | 0.4426 | 1216.52 | 1216.467 | 7010.8 | | 1 | 1250.5 | 81.8 | 4 | R.RGLGIAILSTSK.G |
| * | _107.2547.2547.1 | 2.9529 | 0.1888 | 1059.64 | 1060.279 | 8493.9 | | 3 | 634.3 | 65 | 2 | R.GLGIAILSTSK.G |
| * | _205.2368.2368.2 | 4.344 | 0.3228 | 1060.34 | 1060.279 | 5505 | | 1 | 1196.6 | 85 | 7 | R.GLGIAILSTSK.G |
| gi\|5000000018 | 17 | 207 | 48.40% | 411 | 45738 | 5.1 | U | Translation: 17108..18343 (reverse), 412 amino acids | | | | |
| * | _302.0324.0326.2 | 4.3955 | 0.465 | 2626.32 | 2626.966 | 5450.5 | | 1 | 1001 | 50 | 14 | R.LVFGGSTATPVFDATPDLSNFELVK.V |
| * | _303.3030.3030.1 | 1.9155 | 0.2375 | 956.58 | 957.247 | 5914.8 | | 3 | 392.8 | 71.4 | 1 | R.VVPLLLFR.V |
| * | _303.2306.2306.2 | 4.9462 | 0.5564 | 1705.01 | 1704.89 | 8168.9 | | 1 | 1871 | 71.9 | 10 | K.WITVASACAGSGAPTVR.F |
| * | _302.3889.3889.2 | 5.5679 | 0.5195 | 1718.41 | 1718.86 | 5778.6 | | 1 | 1684.9 | 88.5 | 60 | R.FVDNDIYLDVDFSR.Y |
| * | _302.2995.2995.3 | 6.1622 | 0.5595 | 2775.05 | 2777.04 | 7651.6 | | 1 | 2174 | 41.3 | 34 | R.YITHDSVALQNDEHLFGMSNTLNR.G |
| * | _304.2623.2623.2 | 6.4143 | 0.5757 | 2776.03 | 2777.04 | 11030 | | 1 | 2166.2 | 52.2 | 13 | R.YITHDSVALQNDEHLFGMSNTLNR.G |
| * | _205.2816.2816.2 | 3.2273 | 0.4203 | 1135.04 | 1135.305 | 5928.2 | | 1 | 918.4 | 77.8 | 4 | R.GSFFYSVLSK.V |
| * | _302.0314.0314.3 | 3.6108 | 0.307 | 3119.95 | 3118.58 | 4377.4 | | 1 | 325.5 | 28 | 1 | K.YQIIPFYDTLPKPMNGNYTVFGRPER.L |
| * | _305.1958.1958.2 | 3.0931 | 0.2195 | 1638.46 | 1638.841 | 4770 | | 1 | 585.6 | 69.2 | 3 | K.PMNGNYTVFGRPER.L |
| * | _302.2275.2275.1 | 2.9742 | 0.366 | 1448.29 | 1449.647 | 7937 | | 1 | 575.5 | 53.8 | 5 | R.LVDFNNVVSGAVSK.V |
| * | _203.2383.2383.2 | 5.0651 | 0.4541 | 1449.36 | 1449.647 | 8032.5 | | 1 | 2015.5 | 84.6 | 2 | R.LVDFNNVVSGAVSK.V |
| * | _304.2292.2294.2 | 5.0162 | 0.496 | 1450.96 | 1449.647 | 6390.2 | | 1 | 1683 | 84.6 | 12 | R.LVDFNNVVSGAVSK.V |
| * | _302.1746.1746.2 | 2.8396 | 0.169 | 1117.88 | 1118.316 | 5153.7 | | 1 | 773.4 | 75 | 1 | K.VAALISDTTVK.T |
| * | _303.3074.3074.2 | 4.4852 | 0.5582 | 2395.2 | 2396.656 | 6177.2 | | 1 | 937.8 | 52.5 | 33 | K.AISVPVTFGDTFDYTTLEYQK.A |
| * | _302.3179.3179.3 | 4.7604 | 0.4944 | 2396.62 | 2396.656 | 6429.8 | | 1 | 771.7 | 35 | 4 | K.AISVPVTFGDTFDYTTLEYQK.A |
| * | _302.3174.3174.2 | 4.292 | 0.4885 | 3186.43 | 3187.446 | 7640.2 | | 1 | 689.4 | 35.7 | 9 | K.SYVTGPYGAIPVYDDNGNLIGWYSDAYSK.- |
| * | _206.2813.2813.3 | 3.7412 | 0.4752 | 3188.13 | 3187.446 | 5864.8 | | 1 | 1111.4 | 33 | 1 | K.SYVTGPYGAIPVYDDNGNLIGWYSDAYSK.- |
| gi\|5000000073 | 25 | 283 | 46.90% | 544 | 61500 | 4.7 | U | Translation: 63204..64838 (reverse), 545 amino acids | | | | |
| * | _304.1656.1656.2 | 2.761 | 0.181 | 923.74 | 924.172 | 3744.3 | | 5 | 328.9 | 78.6 | 1 | K.VPEIKPIK.G |
| * | _306.2719.2721.2 | 3.8187 | 0.368 | 1632.29 | 1631.999 | 6522.7 | | 1 | 666.9 | 65.4 | 2 | K.VPEIKPIKGEFFVK.R |
| * | _307.0388.0388.3 | 5.4101 | 0.3627 | 3340.97 | 3340.841 | 5307.4 | | 1 | 679.3 | 28.3 | 4 | K.NLELKPGDWVIFGVASTPSIDLVNDAILDVK.Y |
| * | _302.3118.3118.2 | 5.3946 | 0.6202 | 1721.04 | 1721.821 | 8117.2 | | 1 | 1780.9 | 75 | 9 | K.YTFGDSLEEFVNSGR.I |
| * | _303.3174.3174.2 | 4.7048 | 0.5783 | 2191.71 | 2191.489 | 7097.8 | | 1 | 1449.3 | 65.8 | 3 | K.HPDIDVPIGIPIAAEIYDNK.L |
| * | _304.1764.1764.2 | 3.0663 | 0.4956 | 1405.82 | 1405.51 | 8234.9 | | 1 | 863 | 68.2 | 1 | K.HLQSADDRFTSK.I |
| * | _306.2697.2698.2 | 3.671 | 0.3968 | 1594.66 | 1593.951 | 4634.2 | | 1 | 555.7 | 60 | 3 | K.IGLSIGAIPIGKPQTK.V |
| * | _302.0298.0298.2 | 5.0791 | 0.5471 | 2038.12 | 2038.348 | 4802.8 | | 1 | 945.8 | 67.6 | 5 | R.LYEVSITGQPINIDTFVK.V |
| * | _302.3306.3306.3 | 6.5767 | 0.5545 | 3333.92 | 3333.408 | 10389 | | 1 | 2590.4 | 34.5 | 8 | K.NPEEEKQEGVLEALEEEVQADASEDASEEK.Q |
| * | _302.3799.3799.3 | 4.9612 | 0.2512 | 3848.77 | 3850.021 | 9451 | | 2 | 600.2 | 21.2 | 3 | K.NPEEEKQEGVLEALEEEVQADASEDASEEKQEMK.Q |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _302.3513.3513.2 | 6.4044 | 0.5045 | 2604.28 | 2606.667 | 10247 | | 1 | 2288.2 | 56.5 | 20 | K.QEGVLEALEEEVQADASEDASEEK.Q |
| * | _303.3342.3342.3 | 4.624 | 0.4234 | 3124.31 | 3123.28 | 8399.9 | | 1 | 892.7 | 27.8 | 1 | K.QEGVLEALEEEVQADASEDASEEKQEMK.Q |
| * | _305.2428.2428.3 | 5.4692 | 0.3717 | 4390.03 | 4391.435 | 8557.3 | | 1 | 889.8 | 21.2 | 10 | K.QDEAQVLDLGDLQGEASEEPSEEDKEEGALEGQNEETQDK.V |
| * | _303.1875.1875.2 | 3.3126 | 0.2775 | 1538.11 | 1539.682 | 8361.2 | | 1 | 949.3 | 66.7 | 2 | K.VALVQEEVEEHEK.E |
| * | _304.2839.2839.2 | 4.8269 | 0.433 | 3035.26 | 3037.26 | 10362 | | 1 | 1122.1 | 41.7 | 48 | K.VALVQEEVEEHEKEDEETFNYILDK.L |
| * | _302.4154.4155.3 | 7.4161 | 0.4907 | 3039.04 | 3037.26 | 8968.4 | | 1 | 1787.9 | 36.5 | 101 | K.VALVQEEVEEHEKEDEETFNYILDK.L |
| * | _302.2292.2292.2 | 3.9726 | 0.3612 | 1515.91 | 1516.601 | 6936.7 | | 1 | 1557 | 86.4 | 2 | K.EDEETFNYILDK.L |
| * | _302.0154.0154.1 | 2.7878 | 0.2986 | 1121.28 | 1122.365 | 7237.4 | | 1 | 730.2 | 70 | 3 | K.LSGVLSMLSSK.A |
| * | _206.2685.2685.1 | 2.5731 | 0.3394 | 1121.51 | 1122.365 | 8349.4 | | 1 | 560.8 | 60 | 2 | K.LSGVLSMLSSK.A |
| * | _303.2607.2607.2 | 3.2837 | 0.1353 | 1122.08 | 1122.365 | 4749.4 | | 2 | 771.7 | 75 | 2 | K.LSGVLSMLSSK.A |
| * | _205.2644.2644.2 | 3.6163 | 0.2684 | 1122.32 | 1122.365 | 5515.2 | | 1 | 1129.7 | 85 | 4 | K.LSGVLSMLSSK.A |
| * | _203.2462.2462.2 | 5.8263 | 0.6376 | 1988.63 | 1990.128 | 7419.9 | | 1 | 2538.1 | 75 | 21 | K.APQEESEDAVVSSSLAELK.S |
| * | _304.2362.2362.2 | 5.6695 | 0.6003 | 1989.1 | 1990.128 | 6906.6 | | 1 | 2076.9 | 72.2 | 17 | K.APQEESEDAVVSSSLAELK.S |
| * | _304.2366.2366.3 | 4.3271 | 0.3308 | 1990.02 | 1990.128 | 7116.3 | | 1 | 1059.2 | 37.5 | 5 | K.APQEESEDAVVSSSLAELK.S |
| * | _203.2448.2450.3 | 4.6296 | 0.3545 | 1990.68 | 1990.128 | 7723.4 | | 1 | 1111.6 | 38.9 | 6 | K.APQEESEDAVVSSSLAELK.S |
| gi\|55981451\|ref\| | 6 | 66 | 45.10% | 144 | 16233 | 4.9 | U | bacterioferritin [Thermus thermophilus HB8] | | | | |
| * | _303.4004.4004.2 | 4.8429 | 0.5136 | 1510.32 | 1510.687 | 7403.3 | | 1 | 1927.7 | 86.4 | 52 | K.EFFLAEIQDELR.H |
| * | _303.3878.3878.1 | 2.3094 | 0.4004 | 1510.38 | 1510.687 | 2455.1 | | 1 | 152.7 | 59.1 | 2 | K.EFFLAEIQDELR.H |
| * | _303.1683.1683.2 | 3.5108 | 0.3025 | 929.72 | 930.051 | 6416.4 | | 1 | 1493.5 | 100 | 2 | R.HAQFLADK.I |
| * | _304.1734.1734.3 | 4.2857 | 0.2831 | 2145.05 | 2144.479 | 5479.5 | | 1 | 1200.8 | 40.5 | 3 | K.IAALGGKPTTQPAPVPEAATPR.A |
| * | _302.0016.0016.2 | 5.2198 | 0.5079 | 2145.61 | 2144.479 | 4365.4 | | 1 | 735.7 | 57.1 | 3 | K.IAALGGKPTTQPAPVPEAATPR.A |
| * | _302.3790.3791.2 | 5.8338 | 0.4992 | 2588.94 | 2586.728 | 10014 | | 1 | 2027.9 | 56.8 | 4 | K.QAEAYGDYGLANDLQEIISEETR.H |
| gi\|5000000068 | 18 | 93 | 41.50% | 648 | 71884 | 5.4 | U | Translation: 57775..59721 (reverse), 649 amino acids | | | | |
| * | _303.4218.4218.2 | 4.4828 | 0.5117 | 2261.31 | 2261.58 | 8354.8 | | 1 | 1061.1 | 47.7 | 4 | K.QINGVGTGIVALLGLAEGGETYK.P |
| * | _305.4328.4328.2 | 2.9215 | 0.3063 | 2677.48 | 2678.06 | 8967.5 | | 1 | 413.1 | 30 | 1 | K.QINGVGTGIVALLGLAEGGETYKPYR.L |
| * | _305.3198.3198.2 | 3.6749 | 0.5297 | 1314.14 | 1313.536 | 7660.4 | | 1 | 1985.3 | 90.9 | 8 | R.LTSFAEAVSIFK.G |
| * | _304.1806.1806.2 | 3.1281 | 0.2111 | 964.25 | 964.153 | 5109.5 | | 3 | 855.9 | 81.2 | 2 | K.GGPLLEHIK.A |
| * | _107.2447.2447.2 | 4.6414 | 0.3321 | 1318.62 | 1317.531 | 6624.1 | | 1 | 1941.9 | 84.6 | 12 | K.AAFIGGAGEVVAVR.I |
| * | _303.2710.2710.3 | 5.3592 | 0.4825 | 3611.94 | 3611.901 | 4902.5 | | 1 | 781.6 | 28.7 | 1 | R.IGNPTTASVSIPVAQNTSDTSPANLNFVSYEASTR.S |
| * | _305.2530.2530.2 | 3.019 | 0.3531 | 1198.09 | 1198.367 | 3996.3 | | 1 | 446.7 | 77.8 | 3 | K.RGSTLFFVDR.S |
| * | _305.4682.4682.3 | 5.3679 | 0.396 | 2195.92 | 2197.626 | 7458.2 | | 1 | 1391.1 | 36.9 | 7 | R.SIVNAALAAGPAFQTALINLLK.E |
| * | _305.4718.4719.2 | 5.0075 | 0.4509 | 2198.57 | 2197.626 | 5218.5 | | 1 | 954.7 | 57.1 | 16 | R.SIVNAALAAGPAFQTALINLLK.E |
| * | _304.2782.2782.3 | 6.4533 | 0.4733 | 2379.72 | 2379.678 | 8301.3 | | 1 | 2544.3 | 47.5 | 3 | K.DAYTINHLVDTTINPHILATR.I |
| * | _302.0159.0159.2 | 4.6082 | 0.4671 | 1977.89 | 1977.246 | 7090.4 | | 1 | 1221.3 | 61.8 | 2 | K.GIASTFLSHVQTMSQVNR.R |
| * | _302.0164.0166.2 | 5.1811 | 0.5539 | 2567.49 | 2568.846 | 6190 | | 1 | 982.1 | 54.3 | 12 | R.VGVFGLPAPSPNESVTASEYLYNR.N |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _303.4090.4090.2 | 3.142 | 0.2496 | 1611.22 | 1610.825 | 6711.2 | | 1 | 870.6 | 64.3 | 1 | R.NILNTISAMFGGTDR.A |
| * | _307.3339.3339.2 | 4.8839 | 0.5038 | 2577.16 | 2578.936 | 7157.6 | | 1 | 919.7 | 50 | 6 | R.IHHNPTTWLGPVTQGFQEFVLR.R |
| * | _307.3534.3534.3 | 7.5897 | 0.5934 | 2579.03 | 2578.936 | 8661.1 | | 1 | 3362.9 | 48.8 | 6 | R.IHHNPTTWLGPVTQGFQEFVLR.R |
| * | _303.2714.2714.2 | 4.294 | 0.519 | 1547.1 | 1547.751 | 7197.3 | | 1 | 1425 | 81.8 | 4 | R.RIDDFLQSYVYK.N |
| * | _206.2754.2754.2 | 4.6114 | 0.5099 | 1407.46 | 1407.65 | 7578.8 | | 1 | 1662.7 | 83.3 | 4 | K.VYTEALLSNLVGK.Q |
| * | _307.3194.3194.2 | 2.9825 | 0.2857 | 2028.2 | 2027.324 | 11255 | | 1 | 737.9 | 46.7 | 1 | K.TVYYVEFFYQPVTEIK.F |
| gi\|5000000166 | 11 | 45 | 40.00% | 497 | 56961 | 4.8 | U | Translation: 148736..150229 (direct), 498 amino acids | | | | |
| * | _303.2779.2779.2 | 4.9902 | 0.5258 | 2453.23 | 2454.66 | 8370 | | 1 | 969 | 50 | 4 | K.DYWQQIDRPINDEYVGGWAK.L |
| * | _303.3352.3352.3 | 5.7834 | 0.5578 | 3951.71 | 3954.336 | 5958.6 | | 1 | 1021.3 | 28.6 | 3 | R.IYNDSSYTDQTISPSSSYIGNLEPATKFEVLSGLVR.I |
| * | _305.0011.0011.3 | 6.2875 | 0.536 | 3780.94 | 3783.29 | 6812.6 | | 1 | 1055.8 | 29.7 | 4 | K.MLSFAPIINIYYPIGFDETSGLPNDAYTLFQNR.L |
| * | _302.2794.2794.2 | 3.8237 | 0.4952 | 1469.29 | 1469.634 | 8797.8 | | 1 | 2419.4 | 90.9 | 8 | R.LTEFETWLTNSK.F |
| * | _303.1676.1676.2 | 3.0971 | 0.3999 | 1152 | 1152.298 | 5677.1 | | 1 | 1026.7 | 87.5 | 2 | K.WVQHVPETR.N |
| * | _307.2821.2821.2 | 3.4108 | 0.4999 | 1937.11 | 1937.072 | 9172.7 | | 1 | 1109 | 56.7 | 3 | R.NVWDADYYQITFADSK.I |
| * | _205.2844.2844.2 | 2.7815 | 0.1529 | 1100.38 | 1100.303 | 3902.4 | | 1 | 592.5 | 81.2 | 2 | K.IPLPFDELR.L |
| * | _303.2322.2322.2 | 4.02 | 0.3899 | 1883.25 | 1884.098 | 8337.9 | | 1 | 1470 | 66.7 | 2 | R.VWDENYSVLGQYGKPK.D |
| * | _307.3126.3126.2 | 5.8973 | 0.5875 | 3042.34 | 3043.32 | 7035.4 | | 1 | 837.5 | 40.7 | 8 | K.DINEVINNDNIIYVLGQNFSGYAAGTAR.R |
| * | _304.4066.4066.3 | 5.2635 | 0.3697 | 3044.25 | 3043.32 | 11774 | | 1 | 2141.4 | 34.3 | 4 | K.DINEVINNDNIIYVLGQNFSGYAAGTAR.R |
| * | _307.0402.0402.2 | 5.0764 | 0.4752 | 2219.73 | 2218.514 | 9602.5 | | 1 | 1322.8 | 55.3 | 5 | R.RVLLEGYLGNYAGTLTYSIN.- |
| gi\|55980830\|ref\| | 11 | 55 | 38.30% | 256 | 29277 | 5.6 | U | 30S ribosomal protein S2 [Thermus thermophilus HB8] | | | | |
| * | _302.3358.3358.2 | 3.9305 | 0.4008 | 1494.72 | 1494.65 | 8959 | | 1 | 1380.7 | 75 | 7 | K.ELLEAGVHFGHER.K |
| * | _302.2972.2972.2 | 2.7293 | 0.2655 | 1167.12 | 1167.411 | 3809.9 | | 1 | 540.4 | 83.3 | 1 | R.WLGGMLTNFK.T |
| * | _305.4374.4374.3 | 6.2161 | 0.4654 | 2493.43 | 2493.822 | 6537.4 | | 1 | 2751.4 | 52.5 | 14 | R.VHRLEELEALFASPEIEERPK.K |
| * | _304.2900.2902.2 | 5.4002 | 0.4498 | 2494.17 | 2493.822 | 6974.6 | | 1 | 878.1 | 55 | 12 | R.VHRLEELEALFASPEIEERPK.K |
| * | _307.2898.2898.2 | 3.3544 | 0.4156 | 2621.2 | 2621.996 | 9809 | | 1 | 393.5 | 38.1 | 1 | R.VHRLEELEALFASPEIEERPKK.E |
| * | _307.2730.2730.3 | 5.6968 | 0.4551 | 2621.57 | 2621.996 | 8182.2 | | 1 | 1933.1 | 41.7 | 9 | R.VHRLEELEALFASPEIEERPKK.E |
| * | _303.2927.2927.3 | 4.7461 | 0.3208 | 2101.84 | 2101.361 | 4400.3 | | 1 | 1150.3 | 47.1 | 2 | R.LEELEALFASPEIEERPK.K |
| * | _303.2931.2934.2 | 5.3108 | 0.4278 | 2101.99 | 2101.361 | 6360.3 | | 1 | 1499.1 | 70.6 | 1 | R.LEELEALFASPEIEERPK.K |
| * | _302.0155.0155.2 | 4.0712 | 0.4256 | 1472.12 | 1471.74 | 3698.5 | | 1 | 873.5 | 83.3 | 3 | K.RLPDAIFVVDPTK.E |
| * | _304.4633.4633.3 | 4.07 | 0.2533 | 3387.52 | 3386.824 | 4207.5 | | 6 | 228.6 | 20 | 3 | R.KLFIPVIALADTDSDPDLVDYIIPGNDDAIR.S |
| * | _303.2454.2454.2 | 3.4493 | 0.2198 | 998.76 | 999.199 | 5973.2 | | 3 | 1276.2 | 87.5 | 2 | R.AVDLIIQAR.G |
| gi\|55981366\|ref\| | 7 | 18 | 37.70% | 106 | 11703 | 11.9 | U | 30S ribosomal protein S20 [Thermus thermophilus HB8] | | | | |
| * | _103.1522.1522.1 | 2.6228 | 0.1455 | 957.52 | 958.103 | 7501.7 | | 3 | 693.4 | 68.8 | 1 | K.AIQLAQEGK.A |
| * | _103.1515.1515.2 | 2.6447 | 0.1191 | 958.37 | 958.103 | 6135.9 | | 2 | 1136.2 | 81.2 | 1 | K.AIQLAQEGK.A |
| * | _106.2424.2424.2 | 5.1741 | 0.364 | 1600.4 | 1599.825 | 9142.4 | | 1 | 2492 | 82.1 | 7 | K.AIQLAQEGKAEEALK.I |
| * | _104.1318.1318.2 | 3.2524 | 0.1602 | 904.22 | 904.051 | 4980.2 | | 9 | 650.9 | 85.7 | 3 | R.KAESLIDK.A |
| * | _102.2354.2354.1 | 2.1593 | 0.1543 | 775.61 | 775.877 | 5090.7 | | 2 | 507.5 | 75 | 1 | K.AESLIDK.A |
| * | _102.2538.2538.1 | 3.3541 | 0.3775 | 1537.58 | 1538.784 | 8062.4 | | 1 | 684.2 | 50 | 2 | R.QLLEAAGAPLIGGGLSA.- |
| * | _102.2539.2541.2 | 5.1912 | 0.5804 | 1537.84 | 1538.784 | 6703.8 | | 1 | 1640.5 | 71.9 | 3 | R.QLLEAAGAPLIGGGLSA.- |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| gi\|55981634\|ref\| | 9 | 20 | 37.30% | 209 | 24324 | 10.5 | U | 30S ribosomal protein S4 [Thermus thermophilus HB8] | | | | |
| * | _304.1519.1519.2 | 3.372 | 0.3042 | 964.02 | 964.069 | 4551.6 | | 1 | 918.9 | 100 | 3 | R.RPSDYAVR.L |
| * | _104.1805.1805.1 | 1.8223 | 0.1284 | 837.63 | 837.951 | 3817.4 | | 2 | 290.3 | 83.3 | 1 | R.IYGISER.Q |
| * | _103.1873.1873.1 | 2.6196 | 0.287 | 937.37 | 938.025 | 4284.1 | | 1 | 303.6 | 71.4 | 7 | R.NLFEEASK.K |
| * | _303.3578.3578.2 | 3.1742 | 0.351 | 1434.06 | 1435.663 | 10015 | | 1 | 1393.3 | 65.4 | 1 | K.GVTGSVFLGLLESR.L |
| * | _103.1658.1659.2 | 2.6295 | 0.1499 | 880.67 | 879.004 | 7876.7 | | 4 | 1205 | 91.7 | 2 | R.LDNVVYR.L |
| * | _303.1816.1816.2 | 2.6559 | 0.2478 | 1005.62 | 1006.15 | 5785.3 | | 1 | 665.1 | 85.7 | 1 | R.RVDLPSYR.V |
| * | _204.2164.2164.2 | 2.7146 | 0.158 | 1284.57 | 1284.455 | 7927 | | 1 | 951.1 | 68.2 | 1 | R.VRPGDEIAVAEK.S |
| * | _305.3048.3048.2 | 3.9381 | 0.4821 | 1559.71 | 1559.864 | 7464.6 | | 1 | 1649.3 | 73.1 | 1 | R.KVGPWLSLDVEGMK.G |
| * | _207.2780.2780.2 | 3.1239 | 0.2719 | 1431.39 | 1431.69 | 5416.6 | | 1 | 869.8 | 70.8 | 3 | K.VGPWLSLDVEGMK.G |
| gi\|5000000078 | 41 | 117 | 33.90% | 1524 | 172123 | 8.6 | U | Translation: 75309..79883 (reverse), 1525 amino acids | | | | |
| * | _205.2976.2976.2 | 3.5537 | 0.2263 | 1119.37 | 1119.306 | 7666.3 | | 1 | 1518.7 | 93.8 | 2 | K.FALEQILER.E |
| * | _203.1854.1854.2 | 3.874 | 0.4324 | 1301.22 | 1301.398 | 5807.2 | | 1 | 1171.4 | 85 | 2 | K.SINYSQFANEK.G |
| * | _203.2019.2019.2 | 4.3076 | 0.4329 | 1524.33 | 1524.673 | 7391.3 | | 1 | 1737.3 | 80.8 | 6 | K.VPAGYIAYNVEDGR.V |
| * | _204.3111.3111.2 | 3.9204 | 0.3506 | 1373.6 | 1373.546 | 8205.6 | | 1 | 1609.7 | 79.2 | 4 | K.EDVAGLIEASLQK.N |
| * | _203.2078.2078.2 | 4.3005 | 0.4205 | 1289.47 | 1289.385 | 6779.3 | | 1 | 1553.2 | 86.4 | 2 | K.DLLQAVDSDANK.Y |
| * | _203.2342.2342.2 | 3.1343 | 0.4591 | 1745.71 | 1746.871 | 8481.1 | | 1 | 921.6 | 57.7 | 1 | K.NNLDYVYVYDPENK.Y |
| * | _207.2600.2600.2 | 3.7266 | 0.462 | 1388.41 | 1388.604 | 5993.6 | | 1 | 842.8 | 77.3 | 7 | K.YLTNLSTYLATK.D |
| * | _203.2722.2722.2 | 2.6223 | 0.2205 | 1212.27 | 1212.388 | 4916 | | 1 | 667.2 | 77.8 | 2 | K.EVFFSDNLLK.L |
| * | _203.2230.2230.2 | 3.8357 | 0.42 | 1495.29 | 1495.629 | 5653.6 | | 1 | 529.2 | 57.7 | 2 | R.SQGASNEALFTELK.R |
| * | _207.2900.2900.2 | 4.8137 | 0.3533 | 1582.59 | 1582.838 | 9620.3 | | 1 | 1667.9 | 69.2 | 4 | R.ALDNLLTEIIQNPK.L |
| * | _206.2725.2725.1 | 2.1881 | 0.241 | 844.52 | 845.073 | 3496.3 | | 2 | 457.4 | 71.4 | 2 | K.IFGLPIGK.Q |
| * | _206.2730.2730.2 | 2.5863 | 0.1424 | 845.3 | 845.073 | 2091.3 | | 6 | 490.8 | 92.9 | 1 | K.IFGLPIGK.Q |
| * | _304.4366.4366.2 | 5.0454 | 0.4304 | 1990.75 | 1992.279 | 9084.7 | | 1 | 1833.6 | 70 | 6 | K.FKEELDDLWSLLNIQK.D |
| * | _304.4357.4357.3 | 4.4413 | 0.273 | 1993.48 | 1992.279 | 8198.1 | | 1 | 1636.4 | 45 | 4 | K.FKEELDDLWSLLNIQK.D |
| * | _306.3274.3274.2 | 4.0948 | 0.3193 | 1516.87 | 1517.974 | 5773 | | 1 | 1215.2 | 81.8 | 2 | K.FPLMWMPLLLQK.F |
| * | _306.3273.3273.1 | 2.9086 | 0.2067 | 1517.36 | 1517.974 | 8147.8 | | 1 | 805.6 | 59.1 | 1 | K.FPLMWMPLLLQK.F |
| * | _206.2491.2491.2 | 2.7179 | 0.2605 | 1096.13 | 1096.271 | 3958.1 | | 1 | 724.9 | 83.3 | 1 | K.FGIIGYNSPK.L |
| * | _207.2700.2700.2 | 3.6449 | 0.3997 | 1501.28 | 1501.809 | 2686.7 | | 1 | 597.9 | 70.8 | 2 | K.ISLQPYQVQALLK.F |
| * | _306.2598.2598.2 | 3.5533 | 0.4249 | 1302.03 | 1302.577 | 5638.6 | | 1 | 1595.8 | 87.5 | 2 | K.VGMFIAHATGLGK.T |
| * | _307.3507.3507.2 | 4.6209 | 0.5915 | 2496.83 | 2497.856 | 8069.2 | | 1 | 1435.2 | 54.5 | 3 | K.TFTGLLAYALATNLGLHTVSYNR.D |
| * | _302.4273.4273.2 | 4.5654 | 0.5022 | 1539.72 | 1538.7 | 7763.4 | | 1 | 2240.7 | 87.5 | 6 | K.GWIDDAETLFGWK.V |
| * | _203.2254.2254.2 | 4.3275 | 0.4264 | 1715.63 | 1714.919 | 7371.3 | | 1 | 1746.6 | 71.4 | 4 | K.VGQEIFVIEGNPQQR.R |
| * | _303.3219.3219.2 | 3.6807 | 0.3796 | 1289.26 | 1288.492 | 7584.6 | | 1 | 1558.7 | 88.9 | 1 | K.WSQLLDLWAR.A |
| * | _306.2937.2937.2 | 4.12 | 0.4169 | 1688.4 | 1689.995 | 6482.6 | | 1 | 780.1 | 60.7 | 2 | K.YFLNLLSGPSIISHK.G |
| * | _305.4110.4110.2 | 4.2911 | 0.5019 | 2050.89 | 2052.37 | 7215.1 | | 1 | 1023.7 | 59.4 | 4 | K.DFSSAMEMLFYQGHLFK.R |
| * | _204.2187.2187.2 | 3.7628 | 0.4796 | 1414.79 | 1415.645 | 7345.3 | | 1 | 1470.5 | 79.2 | 2 | K.TPSGPIINEDMLK.T |
| * | _305.3531.3531.2 | 3.807 | 0.4298 | 2875.5 | 2876.146 | 10460 | | 1 | 983.9 | 39.6 | 3 | R.ALEYGFTSFDEEGPFIIVDEENKPK.N |
| * | _303.3282.3282.3 | 4.5929 | 0.4538 | 2878.02 | 2876.146 | 6243.4 | | 1 | 547.5 | 26 | 1 | R.ALEYGFTSFDEEGPFIIVDEENKPK.N |
| * | _206.2797.2797.2 | 3.5785 | 0.3729 | 1716.59 | 1716.929 | 5724.5 | | 1 | 1063.9 | 66.7 | 3 | R.SLVDTLSSVSPNILDR.F |
| * | _306.2658.2658.2 | 3.2889 | 0.357 | 1252.38 | 1252.461 | 6468.1 | | 1 | 807.2 | 72.2 | 4 | K.IRFPGYAWNK.K |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _203.1928.1928.2 | 3.1743 | 0.3147 | 1060.39 | 1060.195 | 6841.7 | | 1 | 1211.5 | 88.9 | 1 | R.TGVSGLLEQR.K |
| * | _304.2463.2463.2 | 4.2414 | 0.5347 | 1938.8 | 1938.15 | 4542.5 | | 1 | 1107.1 | 80 | 4 | K.HLYYPVIENTAQGEFR.I |
| * | _302.2763.2766.2 | 3.8105 | 0.315 | 2023.88 | 2022.222 | 9153.1 | | 2 | 509.7 | 44.1 | 3 | K.AAPFLNEDGTLNENFQIK.Q |
| * | _203.1926.1926.2 | 3.7019 | 0.3915 | 1444.96 | 1444.584 | 5941.9 | | 1 | 900.8 | 70.8 | 4 | K.ASYNAIATTEQFK.R |
| * | _305.2324.2324.2 | 3.8602 | 0.4677 | 1664.07 | 1662.927 | 5610.7 | | 1 | 881.7 | 67.9 | 1 | K.RVVEEALKPFATSSK.T |
| * | _205.2268.2268.2 | 3.0852 | 0.2251 | 1277.3 | 1277.547 | 6337.8 | | 1 | 1245.7 | 81.8 | 3 | K.ILITSPSTAFVK.S |
| * | _204.2682.2682.2 | 3.7664 | 0.3448 | 1242.14 | 1242.374 | 5788.9 | | 1 | 977.6 | 83.3 | 4 | K.SLDYVFDNIR.K |
| * | _305.1979.1979.2 | 2.7091 | 0.4497 | 1994.81 | 1994.258 | 7550.4 | | 1 | 440.3 | 44.1 | 1 | K.IIESHNANNKPSITVLSR.A |
| * | _307.3207.3209.2 | 5.9154 | 0.6136 | 2135.05 | 2136.517 | 7487.2 | | 1 | 1433.4 | 63.9 | 3 | K.IVVHGATFSYETILQMLGR.A |
| * | _304.4259.4259.2 | 3.6317 | 0.2531 | 1994.88 | 1996.398 | 4361.3 | | 1 | 508.5 | 47.4 | 2 | K.GKVDASIILPQSVASVLGLK.S |
| * | _205.2536.2536.2 | 3.6846 | 0.3841 | 1369.45 | 1369.645 | 6485.8 | | 1 | 895 | 70.8 | 5 | K.VVDALSNIITPVK.I |
| gi\|55981862\|ref\|Y | 17 | 54 | 33.00% | 928 | 98037 | 4.8 | U | S-layer protein precursor (P100 protein) [Thermus thermophilus | | | | |
| * | _306.0515.0515.3 | 3.7243 | 0.3169 | 3250.98 | 3252.606 | 12984 | | 1 | 1088.2 | 24.1 | 1 | R.SQVEANADAIQALNELAVLLNQDVLSLQDR.V |
| * | _305.4188.4190.2 | 3.0931 | 0.359 | 2740.46 | 2741.925 | 7532.8 | | 1 | 354.4 | 30 | 2 | R.YSISGSLSATYGTVVTDTGTNFDIDR.L |
| * | _302.2110.2110.2 | 2.869 | 0.3502 | 1501.67 | 1499.623 | 8058.8 | | 1 | 605.2 | 57.7 | 1 | K.GNVDGQAFSVVYSR.A |
| * | _303.2902.2902.3 | 4.1552 | 0.4219 | 1940.62 | 1940.247 | 4561.6 | | 1 | 1851.6 | 51.3 | 2 | K.FPLAPEVTVVAGVAGPDATK.D |
| * | _303.2876.2876.2 | 5.5183 | 0.5368 | 1941.4 | 1940.247 | 5933 | | 1 | 2376.2 | 78.9 | 2 | K.FPLAPEVTVVAGVAGPDATK.D |
| * | _306.3075.3077.3 | 4.7182 | 0.4388 | 2347.93 | 2349.695 | 9879.4 | | 1 | 2190.3 | 40.5 | 1 | R.TAVKPFSALNLALNYATNLGNR.S |
| * | _306.3081.3082.2 | 5.9022 | 0.5748 | 2349.52 | 2349.695 | 5749.2 | | 1 | 1405.8 | 61.9 | 5 | R.TAVKPFSALNLALNYATNLGNR.S |
| * | _304.3831.3833.2 | 5.0879 | 0.5501 | 1948.88 | 1950.205 | 7115.8 | | 1 | 1726.3 | 70.6 | 6 | K.PFSALNLALNYATNLGNR.S |
| * | _304.3866.3866.3 | 5.2916 | 0.3534 | 1949.67 | 1950.205 | 8588.1 | | 1 | 2874 | 52.9 | 5 | K.PFSALNLALNYATNLGNR.S |
| * | _306.0180.0180.3 | 6.1202 | 0.5698 | 3871.08 | 3872.195 | 5374.5 | | 1 | 910.5 | 27.9 | 2 | K.LSGLWVSSQTPGSPFADFFDNTLSDWAYYAQAEAK.L |
| * | _303.2550.2550.3 | 6.1242 | 0.5204 | 3949.67 | 3951.18 | 8373.8 | | 1 | 933.1 | 25 | 3 | K.LGPLSLSANYHAVDPQYADGQAGMSENEDTTYYGGEK.A |
| * | _304.3899.3899.2 | 4.0623 | 0.4853 | 1490.29 | 1489.755 | 7036.5 | | 1 | 1042 | 63.3 | 6 | R.GLGVSASVGFGPVTLK.G |
| * | _302.3651.3651.2 | 3.0966 | 0.3427 | 3074.55 | 3076.262 | 4653.1 | | 1 | 225.8 | 27.6 | 2 | K.GYAESEGDYNLAPGSVNDAWGVAATLGSFR.G |
| * | _305.4252.4254.2 | 4.7599 | 0.5425 | 2353.8 | 2352.649 | 10404 | | 1 | 951.8 | 45.5 | 12 | K.GGVQVSTDPLLFGLSLDGAVSYR.R |
| * | _305.2471.2471.2 | 3.5471 | 0.3994 | 2383.73 | 2384.567 | 6012.7 | | 1 | 269.3 | 41.7 | 2 | R.RTQYTNNPSNVTTYELYYR.A |
| * | _303.2180.2180.2 | 3.0615 | 0.4004 | 2229.75 | 2228.379 | 9177.2 | | 1 | 530.5 | 44.1 | 1 | R.TQYTNNPSNVTTYELYYR.A |
| * | _305.3463.3463.3 | 3.6767 | 0.3391 | 3570.67 | 3572.918 | 8404.5 | | 1 | 618.9 | 24.2 | 1 | K.LNFSVAYAHYEGDQLAGTGLPVVGSGNQAFNFAR.D |
| gi\|55981652\|ref\|Y | 8 | 19 | 32.40% | 105 | 12298 | 10.3 | U | 30S ribosomal protein S17 [Thermus thermophilus HB8] | | | | |
| * | _103.1817.1817.1 | 2.9417 | 0.3721 | 1016.53 | 1017.211 | 8722 | | 1 | 685.3 | 66.7 | 2 | K.VLTGVVVSDK.M |
| * | _203.1702.1702.1 | 2.6854 | 0.4111 | 1016.62 | 1017.211 | 10025 | | 1 | 825.1 | 66.7 | 2 | K.VLTGVVVSDK.M |
| * | _103.1822.1822.2 | 3.0856 | 0.3858 | 1016.97 | 1017.211 | 3866.7 | | 1 | 744.1 | 88.9 | 1 | K.VLTGVVVSDK.M |
| * | _203.1708.1708.2 | 2.8255 | 0.374 | 1017.41 | 1017.211 | 4548.1 | | 1 | 724.3 | 83.3 | 2 | K.VLTGVVVSDK.M |
| * | _103.1117.1117.2 | 2.7477 | 0.1276 | 1102.36 | 1102.189 | 6418.9 | | 1 | 1034.5 | 81.2 | 2 | K.YLAHDPEEK.Y |
| * | _106.2715.2715.1 | 2.6807 | 0.2722 | 1229.56 | 1230.404 | 4547.7 | | 1 | 414.4 | 60 | 2 | K.LGDVVEIIESR.P |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _106.2709.2709.2 | 3.9154 | 0.2987 | 1230.47 | 1230.404 | 7083.6 | | 1 | 1314.4 | 80 | 5 | K.LGDVVEIIESR.P |
| * | _206.2975.2977.2 | 3.8104 | 0.4492 | 1655.65 | 1655.932 | 9022.7 | | 1 | 1163.2 | 64.3 | 3 | K.LGDVVEIIESRPISK.R |
| gi\|5000000167 | 19 | 154 | 31.90% | 361 | 40658 | 6 | U | Translation: 150256..151341 (direct), 362 amino acids | | | | |
| * | _301.0144.0144.1 | 1.9917 | 0.1798 | 1032.53 | 1033.167 | 8037.7 | | 4 | 503.8 | 61.1 | 1 | K.SVVDVTVEGK.V |
| * | _302.1936.1936.2 | 3.0842 | 0.3474 | 1033.45 | 1033.167 | 3697.6 | | 1 | 795.6 | 88.9 | 2 | K.SVVDVTVEGK.V |
| * | _307.2969.2969.2 | 3.8176 | 0.4752 | 2449.28 | 2450.662 | 10273 | | 1 | 672.3 | 38.6 | 12 | K.SSGESGQTGSLKEEIREEVVVTK.S |
| * | _303.3252.3252.3 | 4.4911 | 0.4897 | 2450.36 | 2450.662 | 7232.6 | | 1 | 1021.4 | 35.2 | 17 | K.SSGESGQTGSLKEEIREEVVVTK.S |
| * | _302.3280.3280.1 | 2.5399 | 0.2162 | 1330.56 | 1331.509 | 4208.8 | | 1 | 411.7 | 65 | 4 | K.EEIREEVVVTK.S |
| * | _302.2756.2758.2 | 3.7631 | 0.3369 | 1330.96 | 1331.509 | 6211.7 | | 1 | 958.5 | 80 | 59 | K.EEIREEVVVTK.S |
| * | _302.2976.2976.2 | 6.7541 | 0.6181 | 2187.19 | 2188.309 | 5082.8 | | 1 | 1526 | 72.2 | 2 | K.HSVEEDDSNVPFLDDVIEK.L |
| * | _105.1726.1726.2 | 2.7218 | 0.1908 | 828.35 | 828.002 | 5310.6 | | 1 | 1227.7 | 92.9 | 4 | R.AALVNALR.V |
| * | _203.1915.1915.2 | 3.2666 | 0.3169 | 1139.22 | 1139.309 | 3754.8 | | 1 | 653 | 87.5 | 1 | R.VIEEFMQDK.L |
| * | _302.3270.3270.2 | 6.6594 | 0.6074 | 2126.44 | 2126.297 | 5730.8 | | 1 | 1976.2 | 73.7 | 11 | K.TNLSTAISDVDMALSEESNK.S |
| * | _205.3584.3585.2 | 2.8251 | 0.4969 | 2126.68 | 2126.297 | 6261.4 | | 1 | 555.2 | 50 | 2 | K.TNLSTAISDVDMALSEESNK.S |
| * | _205.3518.3520.3 | 3.5137 | 0.428 | 2126.68 | 2126.297 | 12208 | | 1 | 1360.5 | 35.5 | 1 | K.TNLSTAISDVDMALSEESNK.S |
| * | _303.3180.3180.3 | 5.6885 | 0.4704 | 2127.7 | 2126.297 | 6661.2 | | 1 | 1486.5 | 43.4 | 7 | K.TNLSTAISDVDMALSEESNK.S |
| * | _302.2119.2120.1 | 2.571 | 0.172 | 1433.27 | 1433.599 | 9487.5 | | 1 | 948.8 | 61.5 | 7 | K.ALEATSATVEALEK.E |
| * | _203.2054.2054.2 | 4.4136 | 0.5333 | 1433.69 | 1433.599 | 7782.6 | | 1 | 1813.1 | 80.8 | 4 | K.ALEATSATVEALEK.E |
| * | _302.2112.2114.2 | 4.3849 | 0.4926 | 1435.03 | 1433.599 | 7541.4 | | 1 | 1449.4 | 76.9 | 8 | K.ALEATSATVEALEK.E |
| * | _305.2892.2894.2 | 5.275 | 0.4172 | 2758.86 | 2760.065 | 10940 | | 1 | 1172.4 | 40 | 10 | K.ALEATSATVEALEKEDLESEVVPVTK.S |
| * | _307.2709.2709.3 | 4.5666 | 0.4239 | 2760.89 | 2760.065 | 5426.8 | | 1 | 1574.2 | 39 | 1 | K.ALEATSATVEALEKEDLESEVVPVTK.S |
| * | _301.0108.0108.1 | 2.2111 | 0.16 | 1345.86 | 1345.489 | 4946.6 | | 2 | 259.7 | 50 | 1 | K.EDLESEVVPVTK.S |
| gi\|55981400\|ref\|Y | 1 | 2 | 31.90% | 69 | 7748 | 6.1 | U | hypothetical protein TTHA1431 [Thermus thermophilus HB8] | | | | |
| * | _307.3133.3133.2 | 2.576 | 0.247 | 2259.24 | 2256.561 | 9118.2 | | 1 | 383.8 | 35.7 | 2 | K.KVELVGTSEEGLEAAIQAALAR.A |
| gi\|55979971\|ref\|Y | 7 | 30 | 31.80% | 422 | 45501 | 5.1 | U | enolase (2-phosphoglycerate dehydratase) [Thermus thermophi | | | | |
| * | _302.3873.3873.2 | 3.8099 | 0.2915 | 2228.48 | 2227.67 | 7041.4 | | 1 | 696.2 | 45.2 | 1 | R.YLGGVQGVTLPVPLMNVINGGK.H |
| * | _303.3981.3981.2 | 3.4622 | 0.3729 | 2256.21 | 2256.581 | 3452.6 | | 1 | 410.3 | 50 | 3 | R.VDFQEFMLVPAGAGSFAEALR.I |
| * | _302.1998.1998.2 | 4.0209 | 0.4764 | 1755.16 | 1755.838 | 6128.6 | | 1 | 1100.4 | 65.6 | 2 | K.GYSTNVGDEGGFAPDLR.S |
| * | _106.2841.2841.2 | 4.6707 | 0.562 | 2337.97 | 2339.564 | 6917 | | 1 | 811.7 | 47.6 | 5 | R.AGYTPGQEVSLALDPATSELYR.D |
| * | _106.2759.2759.2 | 4.5382 | 0.556 | 1701.84 | 1702.905 | 8358.2 | | 1 | 2317.7 | 78.6 | 5 | K.VQLVGDDLFVTNPER.L |
| * | _303.2868.2868.2 | 3.7238 | 0.5095 | 1643.97 | 1644.866 | 7692.7 | | 1 | 1083.6 | 67.9 | 1 | K.VNQIGTLSETLEAIR.L |
| * | _304.4335.4337.2 | 4.9603 | 0.4995 | 2236.91 | 2236.441 | 9959.7 | | 1 | 1485.1 | 52.4 | 13 | R.SGETEDSFIADLAVAVNAGQIK.T |
| gi\|55981650\|ref\|Y | 4 | 13 | 30.90% | 110 | 12057 | 10.1 | U | 50S ribosomal protein L24 [Thermus thermophilus HB8] | | | | |
| * | _107.2527.2527.2 | 4.5733 | 0.2943 | 1304.48 | 1304.572 | 6836.7 | | 1 | 1983.3 | 90.9 | 2 | K.YAVIVEGVNIVK.K |
| * | _103.1857.1857.2 | 2.8053 | 0.2199 | 1038.88 | 1039.176 | 6015.5 | | 1 | 1359.3 | 93.8 | 2 | K.YPQGGFIEK.E |
| * | _307.2297.2297.2 | 3.4591 | 0.2838 | 1512.23 | 1512.728 | 4994.9 | | 1 | 619.4 | 70.8 | 6 | K.VRPICPACGKPTR.V |
| * | _306.2285.2285.3 | 4.0254 | 0.3954 | 1512.91 | 1512.728 | 6736.1 | | 2 | 993.5 | 45.8 | 3 | K.VRPICPACGKPTR.V |
| gi\|55981665\|ref\|Y | 4 | 7 | 30.10% | 156 | 18016 | 10.4 | U | 30S ribosomal protein S7 [Thermus thermophilus HB8] | | | | |
| * | _304.4369.4369.2 | 3.4006 | 0.4923 | 2136.37 | 2134.48 | 8680.9 | | 1 | 778.7 | 47.2 | 1 | R.QLQPDLVYGDVLVTAFINK.I |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _305.1932.1932.2 | 4.1247 | 0.3728 | 1760.37 | 1761.009 | 5286 | | 1 | 970.2 | 70 | 1 | R.RVGGANYQVPMEVSPR.R |
| * | _204.1950.1950.2 | 3.5823 | 0.2916 | 1605.65 | 1604.821 | 4273.9 | | 1 | 474.7 | 57.1 | 2 | R.VGGANYQVPMEVSPR.R |
| * | _305.1839.1839.2 | 3.1514 | 0.3187 | 1468.26 | 1468.658 | 8452.6 | | 1 | 1216.1 | 77.3 | 3 | R.WLVQAANQRPER.R |
| gi\|5000000052 | 4 | 8 | 29.70% | 175 | 21205 | 5.5 | U | Translation: 43411..43938 (direct), 176 amino acids | | | | |
| * | _304.3354.3354.2 | 4.794 | 0.4328 | 1593.08 | 1593.819 | 6490.3 | | 1 | 1609.6 | 83.3 | 3 | K.IYFVNDFEGIFTK.E |
| * | _304.3143.3143.2 | 3.6547 | 0.4406 | 1787.74 | 1787.065 | 4312.2 | | 1 | 783.2 | 71.4 | 2 | R.VAYELSPTEYFVVLR.N |
| * | _206.2554.2554.1 | 2.0353 | 0.1489 | 840.62 | 840.053 | 5796.2 | | 4 | 554.9 | 75 | 1 | K.FLGVLYK.N |
| * | _304.4242.4242.2 | 3.1224 | 0.4145 | 1977.56 | 1978.311 | 6787 | | 1 | 617.3 | 53.1 | 2 | K.NNLPLSLVDYIMLETNK.R |
| gi\|55981433\|ref\| | 3 | 3 | 29.70% | 128 | 14383 | 10.4 | U | 30S ribosomal protein S9 [Thermus thermophilus HB8] | | | | |
| * | _303.2947.2947.2 | 2.5094 | 0.2926 | 1986.42 | 1987.179 | 9223.7 | | 1 | 428.8 | 40.6 | 1 | K.VTVNGQDFNEYFQGLVR.A |
| * | _103.1931.1931.2 | 3.2527 | 0.3815 | 1239.08 | 1239.373 | 5946.2 | | 1 | 1208.3 | 88.9 | 1 | R.ALVQYNPDYR.A |
| * | _306.2793.2793.2 | 2.6481 | 0.1546 | 1245.15 | 1244.566 | 3842.6 | | 1 | 622 | 80 | 1 | R.AKLKPLGFLTR.D |
| gi\|55981655\|ref\| | 8 | 26 | 29.30% | 239 | 26701 | 10.7 | U | 30S ribosomal protein S3 [Thermus thermophilus HB8] | | | | |
| * | _306.2706.2706.2 | 4.5335 | 0.4675 | 1973.41 | 1974.314 | 7295.2 | | 1 | 1307.5 | 57.9 | 7 | R.AADNVAVTVHVAKPGVVIGR.G |
| * | _306.2730.2730.3 | 4.164 | 0.4253 | 1973.54 | 1974.314 | 4942.8 | | 1 | 986.3 | 43.4 | 2 | R.AADNVAVTVHVAKPGVVIGR.G |
| * | _303.2392.2392.3 | 5.7614 | 0.4464 | 2373.87 | 2375.69 | 8952.4 | | 1 | 1840.5 | 41.7 | 3 | K.NVALNVQEVQNPNLSAPLVAQR.V |
| * | _303.2387.2387.2 | 5.7467 | 0.5351 | 2373.92 | 2375.69 | 6824.9 | | 1 | 1174.3 | 54.8 | 2 | K.NVALNVQEVQNPNLSAPLVAQR.V |
| * | _206.2570.2570.3 | 4.906 | 0.474 | 2375.3 | 2375.69 | 10462 | | 3 | 1052.8 | 31 | 1 | K.NVALNVQEVQNPNLSAPLVAQR.V |
| * | _106.2680.2680.2 | 5.8698 | 0.5225 | 2375.41 | 2375.69 | 7040.1 | | 1 | 1238.5 | 57.1 | 2 | K.NVALNVQEVQNPNLSAPLVAQR.V |
| * | _306.2819.2819.2 | 4.976 | 0.502 | 1620.26 | 1620.932 | 5927.6 | | 1 | 1704.8 | 82.1 | 8 | K.AYIFLGEVIGGQKPK.A |
| * | _306.2315.2315.2 | 3.3492 | 0.227 | 1550.28 | 1549.773 | 4111.6 | | 2 | 349.7 | 62.5 | 1 | K.ARPELPKAEERPR.R |
| gi\|55980200\|ref\| | 1 | 2 | 25.40% | 67 | 7730 | 4.5 | U | 2-oxoisovalerate dehydrogenase, E1 component beta subunit [T | | | | |
| * | _103.2222.2222.2 | 2.8136 | 0.1441 | 1922.82 | 1924.114 | 5266.5 | | 1 | 544.4 | 50 | 2 | R.ALGEAIFTEGETWEELK.E |
| gi\|55980212\|ref\| | 3 | 4 | 25.00% | 88 | 10231 | 11.5 | U | 30S ribosomal protein S18 [Thermus thermophilus HB8] | | | | |
| * | _306.2635.2635.2 | 3.2261 | 0.3658 | 1417.24 | 1417.695 | 4216.3 | | 1 | 528.9 | 72.7 | 1 | K.RFLSETGKILPR.R |
| * | _206.2819.2819.1 | 2.3405 | 0.3215 | 1130.46 | 1131.401 | 4643.5 | | 2 | 409.8 | 66.7 | 1 | R.ILGLLPFTEK.L |
| * | _207.2786.2788.2 | 3.078 | 0.1821 | 1131.48 | 1131.401 | 3781.7 | | 2 | 708.3 | 83.3 | 2 | R.ILGLLPFTEK.L |
| gi\|55980315\|ref\| | 3 | 10 | 24.80% | 149 | 16313 | 4.5 | U | peptidyl-prolyl cis-trans isomerase [Thermus thermophilus HB8] | | | | |
| * | _307.3153.3153.2 | 3.1728 | 0.4222 | 2545.56 | 2544.783 | 11217 | | 1 | 641.7 | 38.1 | 1 | R.YTLQVEGEVLDQGELSYLHGHR.N |
| * | _306.2565.2565.2 | 4.2934 | 0.3774 | 1696.07 | 1696.863 | 7240.4 | | 1 | 1679.2 | 75 | 6 | K.VREATPEELLHGHAH.- |
| * | _305.2536.2536.3 | 4.8363 | 0.3571 | 1696.33 | 1696.863 | 7016.9 | | 1 | 2786.1 | 60.7 | 3 | K.VREATPEELLHGHAH.- |
| gi\|55981573\|ref\| | 1 | 2 | 23.90% | 88 | 9652 | 5.3 | U | hypothetical protein TTHA1604 [Thermus thermophilus HB8] | | | | |
| * | _305.4319.4319.2 | 3.0205 | 0.258 | 2287.26 | 2288.652 | 6443.5 | | 2 | 375.7 | 35 | 2 | K.NEFILDFALLQPQGGALVVSR.I |
| gi\|55981651\|ref\| | 3 | 7 | 23.80% | 122 | 13303 | 9.8 | U | 50S ribosomal protein L14 [Thermus thermophilus HB8] | | | | |
| * | _107.2572.2572.1 | 2.9036 | 0.4019 | 1321.36 | 1322.544 | 9133.6 | | 1 | 742.7 | 58.3 | 3 | K.YATVGDVIVASVK.E |
| * | _107.2573.2573.2 | 3.787 | 0.4344 | 1324.66 | 1322.544 | 5277.8 | | 1 | 1161.9 | 83.3 | 1 | K.YATVGDVIVASVK.E |
| * | _103.2377.2377.2 | 4.7891 | 0.3297 | 1829.72 | 1830.007 | 7252.7 | | 1 | 1630.3 | 73.3 | 3 | R.FDDNAAVIINNQLEPR.G |
| gi\|5000000065 | 2 | 6 | 22.70% | 88 | 10331 | 8.7 | U | Translation: 56049..56315 (direct), 89 amino acids | | | | |
| * | _306.2702.2702.1 | 2.0702 | 0.1978 | 1062.26 | 1063.328 | 4062.7 | | 1 | 440 | 71.4 | 2 | K.LIHIYYIK.S |
| * | _203.2706.2706.2 | 3.7582 | 0.3058 | 1419.55 | 1419.581 | 8003.6 | | 1 | 1410.2 | 77.3 | 4 | K.DLCVQLDDISIK.S |
| gi\|5000000053 | 2 | 7 | 22.40% | 161 | 18882 | 4.6 | U | Translation: 43940..44425 (direct), 162 amino acids | | | | |
| * | _303.4264.4264.2 | 4.8947 | 0.5352 | 2036.12 | 2036.248 | 8213 | | 1 | 1161.5 | 62.5 | 6 | K.NFGFIEDNVLSVFQDYK.N |
| * | _305.4470.4470.2 | 2.8314 | 0.3155 | 2119.16 | 2118.346 | 10346 | | 1 | 578.5 | 41.7 | 1 | K.ASLVSNEQTETIEINLDLK.V |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| gi\|55981645\|ref\| | 4 | 7 | 21.40% | 112 | 12612 | 11 | U | 50S ribosomal protein L18 [Thermus thermophilus HB8] | | | | |
| * | _303.2263.2263.2 | 3.9024 | 0.4338 | 1345.19 | 1345.495 | 4298.2 | | 1 | 1065.7 | 90 | 1 | K.HIYAQIIDDEK.G |
| * | _303.2668.2670.1 | 1.9478 | 0.2463 | 1245.24 | 1246.49 | 8491.3 | | 2 | 445.3 | 50 | 1 | K.GVTLVSASSLALK.L |
| * | _303.2679.2679.2 | 3.2614 | 0.418 | 1245.83 | 1246.49 | 6360.8 | | 1 | 1318.1 | 79.2 | 3 | K.GVTLVSASSLALK.L |
| * | _107.2520.2520.2 | 4.3767 | 0.5314 | 1247.21 | 1246.49 | 7258.5 | | 1 | 1497.9 | 79.2 | 2 | K.GVTLVSASSLALK.L |
| gi\|55981107\|ref\| | 1 | 8 | 20.20% | 89 | 10554 | 10.5 | U | 30S ribosomal protein S15 [Thermus thermophilus HB8] | | | | |
| * | _305.3274.3274.2 | 4.5488 | 0.4615 | 1904.54 | 1905.158 | 10913 | | 1 | 1877.8 | 61.8 | 8 | R.FPGDTGSTEVQVALLTLR.I |
| gi\|5000000154 | 1 | 2 | 19.80% | 116 | 13449 | 4.7 | U | Translation: 137294..137644 (direct), 117 amino acids | | | | |
| * | _302.3559.3559.2 | 3.2205 | 0.417 | 2490.66 | 2490.778 | 10530 | | 1 | 352.8 | 31.8 | 2 | R.GAVNILNSDFPDGNLAVYNIINR.E |
| gi\|55981752\|ref\| | 1 | 4 | 19.80% | 101 | 11047 | 10.1 | U | 50S ribosomal protein L21 [Thermus thermophilus HB8] | | | | |
| * | _107.2847.2847.2 | 5.0531 | 0.4024 | 2021.7 | 2022.346 | 6668.7 | | 1 | 1121.9 | 60.5 | 4 | K.LDAEPGATVELPVLLLGGEK.T |
| gi\|5000000050 | 4 | 10 | 19.40% | 490 | 55567 | 6.4 | U | Translation: 41010..42482 (direct), 491 amino acids | | | | |
| * | _204.2131.2131.2 | 3.0901 | 0.4449 | 1492.75 | 1491.65 | 7687.7 | | 1 | 639.9 | 53.8 | 1 | K.ASSIEGFCPPLGQK.I |
| * | _303.3183.3183.3 | 6.4956 | 0.5174 | 3500.99 | 3501.701 | 6358.1 | | 1 | 1260.3 | 32 | 2 | R.GVGYASSADYSFLGSYLHGTYGLQNIDDENGTK.T |
| * | _305.2838.2839.2 | 5.5628 | 0.6077 | 2312.41 | 2312.585 | 8743.6 | | 1 | 1286.9 | 50 | 5 | K.TIFITTGGSTNSVHILSGNYTK.V |
| * | _305.3338.3338.3 | 5.0271 | 0.4434 | 2838.13 | 2837.322 | 7001.9 | | 1 | 1074.1 | 32 | 2 | K.NSISGYTTSPPDSKPPVMFPIIVTMR.G |
| gi\|55981657\|ref\| | 1 | 2 | 19.40% | 93 | 10581 | 10.1 | U | 30S ribosomal protein S19 [Thermus thermophilus HB8] | | | | |
| * | _304.2523.2524.2 | 5.6354 | 0.5723 | 1917.1 | 1917.23 | 4721.2 | | 1 | 1180.7 | 70.6 | 2 | R.STIVPEMVGHTIAVYNGK.Q |
| gi\|55981636\|ref\| | 2 | 46 | 18.30% | 126 | 14305 | 11.1 | U | 30S ribosomal protein S13 [Thermus thermophilus HB8] | | | | |
| * | _306.3027.3027.2 | 4.6033 | 0.5622 | 1568.44 | 1568.856 | 8337.7 | | 1 | 2675.5 | 84.6 | 43 | K.RVDVALTYIYGIGK.A |
| * | _304.2064.2064.2 | 3.2677 | 0.2773 | 1183.94 | 1184.365 | 4134.9 | | 1 | 880.7 | 93.8 | 3 | K.RLMDIGCYR.G |
| gi\|55981918\|ref\| | 5 | 16 | 18.10% | 415 | 45474 | 9.4 | U | hypothetical protein TTHA1949 [Thermus thermophilus HB8] | | | | |
| * | _303.3355.3355.2 | 4.3975 | 0.4215 | 1723.83 | 1722.04 | 6031.3 | | 1 | 1216.1 | 71.4 | 3 | R.IVWSPYVVFLNANAK.A |
| * | _306.2563.2563.2 | 3.7745 | 0.4289 | 1382.34 | 1382.565 | 6648.6 | | 1 | 1302.9 | 75 | 6 | R.RVGVDHWALSGGK.L |
| * | _303.4457.4457.2 | 4.5203 | 0.4359 | 2160.21 | 2159.534 | 9951.7 | | 1 | 1070.6 | 47.4 | 3 | R.VIATNYGNNVITVIDLLGLR.T |
| * | _305.4415.4415.3 | 4.3606 | 0.3198 | 2161.26 | 2159.534 | 11561 | | 1 | 2168.9 | 42.1 | 2 | R.VIATNYGNNVITVIDLLGLR.T |
| * | _304.4099.4099.2 | 3.5126 | 0.4528 | 2917.47 | 2916.22 | 6734.2 | | 1 | 413.6 | 30.8 | 2 | K.VIETGQTNGGGQVLNVWTNVFEELPRG.- |
| gi\|5000000067 | 2 | 10 | 18.10% | 216 | 23927 | 4.8 | U | Translation: 57104..57754 (reverse), 217 amino acids | | | | |
| * | _303.3195.3195.2 | 3.8674 | 0.5344 | 2782.11 | 2783.156 | 4341.1 | | 1 | 545.9 | 46 | 4 | R.PVWGIGEPTNPIVVPNNYSATISISR.M |
| * | _303.0216.0218.2 | 4.097 | 0.3128 | 1255.05 | 1255.457 | 9048.6 | | 3 | 1386 | 70.8 | 6 | R.GLIENLANALLGG.- |
| gi\|55981662\|ref\| | 1 | 4 | 18.10% | 105 | 11930 | 11.1 | U | 30S ribosomal protein S10 [Thermus thermophilus HB8] | | | | |
| * | _305.0526.0526.2 | 4.147 | 0.4206 | 2142.97 | 2144.529 | 6607.4 | | 1 | 797.8 | 52.8 | 4 | K.TIEQLMTLDLPTGVEIEIK.T |
| gi\|55981298\|ref\| | 8 | 17 | 17.30% | 446 | 50557 | 6.7 | U | glutamine synthetase [Thermus thermophilus HB8] | | | | |
| * | _306.3270.3270.2 | 4.3752 | 0.5514 | 2374.22 | 2374.744 | 6207.3 | | 1 | 1014.3 | 57.9 | 1 | K.KLGFDNLYAGPEPEFFLFLR.T |
| * | _305.4616.4616.2 | 3.7448 | 0.3433 | 2247.01 | 2246.57 | 5455.8 | | 1 | 836.9 | 58.3 | 3 | K.LGFDNLYAGPEPEFFLFLR.T |
| * | _306.2667.2667.1 | 2.9047 | 0.4166 | 1532.32 | 1532.829 | 3902.1 | | 1 | 391 | 57.7 | 2 | R.IALNHGLHATFLPK.P |
| * | _305.2623.2623.2 | 4.0642 | 0.5145 | 1533.03 | 1532.829 | 6527 | | 1 | 988.2 | 65.4 | 3 | R.IALNHGLHATFLPK.P |
| * | _305.2627.2627.3 | 4.1481 | 0.4643 | 1533.38 | 1532.829 | 4309.7 | | 1 | 982 | 53.8 | 2 | R.IALNHGLHATFLPK.P |
| * | _305.2283.2283.2 | 3.7883 | 0.385 | 2105.46 | 2105.318 | 5766.9 | | 1 | 435.3 | 50 | 3 | K.RLTPGYEAPTNIAWSASNR.S |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _305.1814.1814.2 | 2.9053 | 0.1108 | 1055.12 | 1055.266 | 6509.2 | | 7 | 818.9 | 75 | 1 | K.IRELPGTLR.E |
| * | _305.2674.2674.2 | 3.9208 | 0.5108 | 1742.98 | 1743.96 | 7273 | | 1 | 1352.1 | 75 | 2 | R.EALGEHVYTHFLQAK.Q |
| gi\|5000000077 | 1 | 13 | 16.50% | 121 | 14307 | 4.6 | U | Translation: 74931..75296 (reverse), 122 amino acids | | | | |
| * | _305.3867.3867.2 | 4.2579 | 0.4838 | 2275 | 2276.461 | 8477.2 | | 1 | 1494.2 | 57.9 | 13 | K.FAEYLSGLSALVEFEQNDDK.F |
| gi\|55981455\|ref\| | 1 | 1 | 16.30% | 129 | 14369 | 5.2 | U | hypothetical protein TTHA1486 [Thermus thermophilus HB8] | | | | |
| * | _305.3039.3039.3 | 4.0113 | 0.4479 | 2264.07 | 2262.574 | 5836.5 | | 1 | 789.2 | 36.2 | 1 | R.RGASLPPAPKPEEGGWETLLR.L |
| gi\|55981661\|ref\| | 2 | 12 | 16.00% | 206 | 22408 | 10.4 | U | 50S ribosomal protein L3 [Thermus thermophilus HB8] | | | | |
| * | _207.2638.2640.2 | 4.3493 | 0.5056 | 1777.06 | 1777.127 | 6359.5 | | 1 | 934.1 | 59.4 | 1 | R.AVPVTVILAGPCPVVQR.R |
| * | _106.2744.2744.2 | 4.7109 | 0.4869 | 1748.89 | 1748.976 | 6099 | | 1 | 1155.4 | 63.3 | 11 | K.DGYTAVQLGFLPQNPK.R |
| gi\|55981004\|ref\| | 2 | 11 | 15.90% | 88 | 10387 | 10.6 | U | 30S ribosomal protein S16 [Thermus thermophilus HB8] | | | | |
| * | _106.2641.2641.1 | 3.1771 | 0.4135 | 1564.7 | 1565.726 | 4010.6 | | 1 | 340.8 | 61.5 | 1 | R.YWLSVGAQPTDTAR.R |
| * | _105.1986.1986.2 | 4.2233 | 0.4436 | 1565.18 | 1565.726 | 6193.8 | | 1 | 1748.7 | 84.6 | 10 | R.YWLSVGAQPTDTAR.R |
| gi\|55981603\|ref\| | 5 | 11 | 15.00% | 622 | 70470 | 9 | U | peptide ABC transporter, peptide-binding protein [Thermus ther | | | | |
| * | _305.3863.3864.2 | 3.9329 | 0.504 | 2862.03 | 2863.195 | 4320.8 | | 1 | 663.4 | 45.7 | 3 | R.NFTLIFEPAYYYDTYGPINTYAPK.H |
| * | _305.2911.2911.3 | 4.8819 | 0.4029 | 2970.17 | 2970.332 | 7152.9 | | 1 | 453.1 | 26 | 4 | K.RWVPGNSIEMERNPNFPIKPEGGESK.Y |
| * | _306.3071.3071.2 | 5.8546 | 0.5474 | 2892.34 | 2894.348 | 9086.1 | | 1 | 1204.6 | 44 | 2 | K.AFFDGLQPVAHTWIAPVNPLFNPNVK.K |
| * | _306.3070.3070.3 | 5.5634 | 0.4425 | 2895.11 | 2894.348 | 7225.9 | | 1 | 907.5 | 31 | 1 | K.AFFDGLQPVAHTWIAPVNPLFNPNVK.K |
| * | _303.3051.3051.2 | 2.8738 | 0.3957 | 1892.38 | 1892.122 | 7504.2 | | 1 | 868.9 | 56.2 | 1 | K.INNAPSAVVFADEFIQR.A |
| gi\|55981643\|ref\| | 1 | 1 | 15.00% | 60 | 6785 | 10.2 | U | 50S ribosomal protein L30 [Thermus thermophilus HB8] | | | | |
| * | _103.1802.1802.2 | 2.8687 | 0.1857 | 1013.75 | 1014.167 | 3777.7 | | 1 | 837.7 | 87.5 | 1 | R.VLEDTPAIR.G |
| gi\|55981659\|ref\| | 1 | 1 | 14.60% | 96 | 10737 | 10.2 | U | 50S ribosomal protein L23 [Thermus thermophilus HB8] | | | | |
| * | _106.2872.2872.2 | 3.7306 | 0.4025 | 1519.5 | 1519.778 | 6781.9 | | 1 | 610.5 | 53.8 | 1 | K.TAYDVILAPVLSEK.A |
| gi\|55981318\|ref\| | 1 | 2 | 14.40% | 97 | 10452 | 10.2 | U | DNA-binding protein HU (DNA-binding protein II) [Thermus ther | | | | |
| * | _205.2946.2948.2 | 4.1378 | 0.4225 | 1429.79 | 1429.613 | 8245.2 | | 1 | 1926 | 80.8 | 2 | K.ADLVDQVAQATGLK.K |
| gi\|55980228\|ref\| | 2 | 5 | 13.70% | 322 | 35749 | 8.7 | U | phosphate ABC transporter, periplasmid phosphate-biniding pro | | | | |
| * | _306.0511.0511.2 | 4.5193 | 0.4909 | 2301.98 | 2303.707 | 3669.9 | | 1 | 725 | 60 | 3 | K.AGIQFIEIPVAYDALSILVNR.Q |
| * | _305.4623.4623.2 | 4.2981 | 0.4728 | 2468.95 | 2469.771 | 8921.4 | | 1 | 1542.1 | 56.8 | 2 | R.IVLFGAGTDSGTFDYFTEAIMGR.A |
| gi\|55980526\|ref\| | 2 | 4 | 13.70% | 204 | 23230 | 6.9 | U | superoxide dismutase [Mn] [Thermus thermophilus HB8] | | | | |
| * | _303.2271.2271.2 | 3.7387 | 0.4702 | 1536.59 | 1533.771 | 4475.5 | | 1 | 850.3 | 76.9 | 1 | R.HLAALPQDIQTAVR.N |
| * | _306.2727.2729.2 | 4.5671 | 0.4916 | 1610.51 | 1609.747 | 5924.1 | | 1 | 1031.4 | 73.1 | 3 | R.NNGGGHLNHSLFWR.L |
| gi\|55981840\|ref\| | 3 | 3 | 13.00% | 346 | 35975 | 4.5 | U | hypothetical protein TTHA1871 [Thermus thermophilus HB8] | | | | |
| * | _306.3175.3175.2 | 2.6706 | 0.277 | 1972.12 | 1973.326 | 6479.5 | | 1 | 565.3 | 52.8 | 1 | R.TLLSGGQPAAFVVSWVALR.H |
| * | _305.3072.3072.2 | 4.0586 | 0.4732 | 2694.19 | 2695.917 | 10679 | | 1 | 1919.1 | 50 | 1 | R.HYGTGSAGCLGQGPVSFQAVLYPDGR.V |
| * | _305.3063.3064.3 | 3.961 | 0.4189 | 2695.82 | 2695.917 | 7034.7 | | 1 | 860.8 | 30 | 1 | R.HYGTGSAGCLGQGPVSFQAVLYPDGR.V |
| gi\|55981635\|ref\| | 1 | 1 | 12.40% | 129 | 13713 | 10.4 | U | 30S ribosomal protein S11 [Thermus thermophilus HB8] | | | | |
| * | _304.2259.2259.2 | 3.6186 | 0.472 | 1589.29 | 1589.832 | 6903 | | 1 | 1467 | 73.3 | 1 | R.KGTPYAAQLAALDAAK.K |
| gi\|55980325\|ref\| | 3 | 5 | 11.90% | 429 | 48119 | 9.4 | U | ABC transporter, periplasmic substrate-binding protein [Thermus | | | | |
| * | _303.3696.3696.2 | 3.1572 | 0.4402 | 1878.06 | 1878.178 | 5124.1 | | 1 | 488.5 | 53.3 | 1 | K.LTSLPFFTDAGILYYR.K |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _306.2526.2526.3 | 3.7621 | 0.2111 | 1857.64 | 1858.151 | 7420.7 | | 1 | 1024.8 | 41.7 | 1 | R.LPTRPALYTDRDVLAR.N |
| * | _305.4520.4520.2 | 3.9514 | 0.5061 | 2191.18 | 2190.42 | 7447.8 | | 1 | 740.7 | 50 | 3 | R.YNQVSEAIWTEVHSVLTGR.K |
| gi\|5000000079 | 2 | 6 | 11.80% | 287 | 33357 | 5.2 | U | Translation: 79880..80743 (reverse), 288 amino acids | | | | |
| * | _302.2920.2920.2 | 5.3717 | 0.5479 | 2689.94 | 2690.79 | 5454 | | 1 | 953.3 | 50 | 2 | K.DQGLFYDPTIDIYDDEGNIDENK.V |
| * | _206.2753.2753.2 | 3.5632 | 0.3957 | 1212.32 | 1211.403 | 5739.3 | | 1 | 1025.4 | 80 | 4 | K.VGEFFGLNLSK.N |
| gi\|55981658\|ref\| | 1 | 2 | 11.60% | 276 | 30468 | 11.1 | U | 50S ribosomal protein L2 [Thermus thermophilus HB8] | | | | |
| * | _306.2851.2851.3 | 7.7284 | 0.5478 | 3328.08 | 3327.855 | 8088 | | 1 | 2411.1 | 36.3 | 2 | K.RYIIAPDGLQVGQQVVAGPDAPIQVGNALPLR.F |
| gi\|55981558\|ref\| | 1 | 1 | 11.20% | 206 | 23205 | 5.3 | U | 50S ribosomal protein L25 (TL5) [Thermus thermophilus HB8] | | | | |
| * | _306.3023.3023.2 | 3.7589 | 0.3168 | 2525.43 | 2523.938 | 5850.7 | | 1 | 331.6 | 38.6 | 1 | R.QASIHHVIVLELPDGQSLPTLVR.Q |
| gi\|5000000001 | 7 | 15 | 11.10% | 881 | 102237 | 8.5 | U | Translation: 1941..4586 (reverse), 882 amino acids | | | | |
| * | _307.3019.3019.3 | 5.1396 | 0.4871 | 2785.02 | 2784.291 | 4957.5 | | 1 | 1239.8 | 40.6 | 3 | K.VPPGYILLHKPTGMFFPPESSPGWK.G |
| * | _205.2846.2848.2 | 3.6166 | 0.3918 | 1528.48 | 1528.702 | 10979 | | 1 | 1715.3 | 75 | 1 | K.FLNSAQDLTDYLK.T |
| * | _204.1991.1991.2 | 4.0129 | 0.4345 | 1279.44 | 1279.433 | 6330.3 | | 1 | 1240.7 | 79.2 | 2 | K.SLSSGVSLSNLSK.Q |
| * | _304.2507.2507.3 | 3.6984 | 0.3016 | 1861.9 | 1860.12 | 10238 | | 1 | 1390 | 43.3 | 1 | R.KGNFISVPIHEEFVDK.G |
| * | _207.2772.2772.2 | 3.4054 | 0.1505 | 1350.49 | 1349.575 | 7505.8 | | 1 | 1058.2 | 75 | 4 | K.GQQNYFLPILR.V |
| * | _204.2488.2488.2 | 3.1348 | 0.435 | 1126.41 | 1125.269 | 5521.3 | | 1 | 725.1 | 77.8 | 2 | K.SGPVFDFTVR.E |
| * | _204.3010.3010.2 | 3.0315 | 0.2319 | 1217.24 | 1217.491 | 4271.7 | | 2 | 868.5 | 77.8 | 2 | K.EVIPIIYELK.A |
| gi\|55979996\|ref\| | 1 | 1 | 11.10% | 316 | 35882 | 5.6 | U | probable potassium channel, beta subunit (oxidoreductase) [The | | | | |
| * | _305.3138.3138.3 | 3.9007 | 0.2807 | 3603.15 | 3604.055 | 5252.7 | | 1 | 510.4 | 22.8 | 1 | R.LPGISSAITGATRPEQIRENLGAAGVDLPQEALEK.I |
| gi\|55980600\|ref\| | 1 | 1 | 10.60% | 188 | 19689 | 7.5 | U | heat shock protein HslV [Thermus thermophilus HB8] | | | | |
| * | _103.2537.2537.2 | 3.8837 | 0.4932 | 1978.38 | 1978.21 | 6442.5 | | 1 | 1041.3 | 57.9 | 1 | K.DGVTALAGDGQVTFGQTVLK.R |
| gi\|55980215\|ref\| | 2 | 3 | 10.50% | 229 | 24831 | 9.5 | U | 50S ribosomal protein L1 [Thermus thermophilus HB8] | | | | |
| * | _303.2880.2880.2 | 3.3947 | 0.3364 | 1347.29 | 1347.557 | 6149.1 | | 1 | 1129 | 75 | 2 | K.AGTVGFNIGEIIR.E |
| * | _304.1504.1504.2 | 3.1135 | 0.2789 | 1151.51 | 1151.308 | 8978.8 | | 1 | 1199.5 | 75 | 1 | R.ALEAHKPEGAK.G |
| gi\|5000000153 | 1 | 4 | 10.00% | 299 | 33193 | 7.3 | U | Translation: 136388..137287 (direct), 300 amino acids | | | | |
| * | _306.3325.3325.3 | 6.2743 | 0.439 | 3458.67 | 3459.973 | 10176 | | 1 | 1314.4 | 30.2 | 4 | K.EDNTPIVLRPQASNAPLFNPQSYLPFILFR.Y |
| gi\|5000000051 | 2 | 2 | 10.00% | 290 | 30341 | 5.1 | U | Translation: 42536..43408 (direct), 291 amino acids | | | | |
| * | _304.4110.4110.2 | 2.5908 | 0.3581 | 1838.21 | 1838.07 | 8209.3 | | 1 | 742.7 | 53.1 | 1 | R.SVIFNILGLDFGNADNK.W |
| * | _305.3874.3874.2 | 2.5453 | 0.3847 | 1520.12 | 1518.795 | 6401.8 | | 1 | 495.3 | 63.6 | 1 | K.VPFYNLTFLFEK.Y |
| gi\|55981660\|ref\| | 1 | 5 | 9.50% | 210 | 23235 | 10 | U | 50S ribosomal protein L4 [Thermus thermophilus HB8] | | | | |
| * | _106.2845.2847.2 | 5.3218 | 0.3665 | 2058.14 | 2059.281 | 6888.6 | | 1 | 1670.7 | 68.4 | 5 | K.EAGLDGSESVLLVTGNELVR.R |
| gi\|55981900\|ref\| | 2 | 4 | 9.50% | 210 | 22553 | 6.2 | U | quinol-cytochrome c reductase, Rieske iron-sulfur subunit [Ther | | | | |
| * | _307.2586.2586.3 | 3.5656 | 0.2983 | 2087.97 | 2087.479 | 5173.2 | | 1 | 1171.2 | 42.1 | 1 | R.HGAQVIAGPPPRPVPQLPVR.V |
| * | _307.2601.2602.2 | 3.6258 | 0.3069 | 2088.93 | 2087.479 | 9315.3 | | 2 | 589.3 | 44.7 | 3 | R.HGAQVIAGPPPRPVPQLPVR.V |
| gi\|55981632\|ref\| | 1 | 1 | 9.30% | 118 | 13715 | 11.4 | U | 50S ribosomal protein L17 [Thermus thermophilus HB8] | | | | |
| * | _306.2859.2859.2 | 3.8221 | 0.4757 | 1249.79 | 1250.486 | 9605.8 | | 1 | 2026.1 | 85 | 1 | R.GFVDHLIHLAK.R |
| gi\|55980715\|ref\| | 1 | 2 | 8.50% | 284 | 31512 | 8.8 | U | iron ABC transporter, substrate-binding protein [Thermus therm | | | | |
| * | _303.4429.4429.2 | 3.8328 | 0.4275 | 2688.73 | 2689.077 | 5828.5 | | 1 | 519.6 | 41.3 | 2 | R.VYYEIDPTPYTVGPESFIGVLISK.A |
| gi\|5000000144 | 1 | 1 | 8.20% | 316 | 36357 | 5.4 | U | Translation: 125598..126548 (reverse), 317 amino acids | | | | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _303.3818.3818.2 | 4.9664 | 0.5656 | 2962.19 | 2962.201 | 8814.3 | | 1 | 936.8 | 40 | 1 | R.SFGIEGFNASFGNNGLLYENLYNEYK.E |
| gi\|55981666\|ref\|Y | 2 | 4 | 8.10% | 135 | 14883 | 11 | U | | 30S ribosomal protein S12 [Thermus thermophilus HB8] | | | |
| * | _103.1585.1585.1 | 2.3084 | 0.2432 | 879.45 | 879.988 | 7378 | | 1 | 745.7 | 75 | 1 | R.GVYDAAGVK.D |
| * | _104.1622.1622.2 | 2.917 | 0.3799 | 1151.55 | 1151.264 | 6919.9 | | 1 | 830.8 | 70 | 3 | R.GVYDAAGVKDR.K |
| gi\|55981487\|ref\|Y | 1 | 3 | 8.00% | 237 | 26218 | 5.7 | U | | 2-haloalkanoic acid dehalogenase-related protein [Thermus ther | | | |
| * | _306.2965.2966.2 | 4.9891 | 0.3551 | 1948.18 | 1947.331 | 4679.5 | | 1 | 858.6 | 63.9 | 3 | R.IFALLGAPHDPGLIALTAR.R |
| gi\|55981642\|ref\|Y | 1 | 4 | 8.00% | 150 | 16281 | 11.2 | U | | 50S ribosomal protein L15 [Thermus thermophilus HB8] | | | |
| * | _106.2689.2689.2 | 3.6536 | 0.4138 | 1388.99 | 1389.591 | 6211.3 | | 1 | 1522.4 | 86.4 | 4 | R.FEGEVTPELLVR.A |
| gi\|55981067\|ref\|Y | 3 | 7 | 7.80% | 395 | 42201 | 4.7 | U | | membrane lipoprotein [Thermus thermophilus HB8] | | | |
| * | _305.3391.3391.3 | 3.878 | 0.4641 | 1755.16 | 1755.128 | 4302.6 | | 1 | 888.6 | 46.9 | 2 | R.TGVVGFIGGMDIPLIHK.F |
| * | _305.3382.3382.2 | 4.5781 | 0.4426 | 1755.64 | 1755.128 | 5639.3 | | 1 | 1228.3 | 68.8 | 4 | R.TGVVGFIGGMDIPLIHK.F |
| * | _103.2099.2101.2 | 3.8883 | 0.3919 | 1568.63 | 1568.77 | 6954.7 | | 1 | 822 | 65.4 | 1 | K.QAIINGEIQVPETR.- |
| gi\|55980256\|ref\|Y | 2 | 2 | 7.70% | 455 | 49058 | 7.2 | U | | 2-oxoglutarate dehydrogenase E3 component (dihydrolipoamide | | | |
| * | _304.3911.3913.2 | 3.3743 | 0.4138 | 2474.29 | 2474.862 | 4957.5 | | 4 | 168.4 | 31 | 1 | R.YILIATGSAPLIPPWAQVDYER.V |
| * | _306.2679.2679.2 | 2.6836 | 0.3882 | 1401.04 | 1400.621 | 4724.2 | | 1 | 479.1 | 62.5 | 1 | R.APHAHPSLSEILK.E |
| gi\|55980220\|ref\|Y | 2 | 5 | 7.60% | 406 | 44782 | 5.6 | U | | translation elongation factor EF-Tu.B [Thermus thermophilus HE | | | |
| gi\|55981663\|ref\|Y | 2 | 5 | 7.60% | 406 | 44782 | 5.6 | U | | elongation factor Tu (EF-Tu) [Thermus thermophilus HB8] | | | |
| YS40_lysate_Ti | _304.3679.3679.2 | 2.5075 | 0.2089 | 1723.84 | 1723.04 | 3750.7 | | 3 | 341.9 | 53.6 | 1 | K.PFLMPVEDVFTITGR.G |
| YS40_lysate_Ti | _205.2581.2581.2 | 3.3904 | 0.3544 | 1655.37 | 1655.892 | 6545.3 | | 1 | 773.5 | 56.7 | 4 | K.TLQEGIAGDNVGVLLR.G |
| gi\|5000000002 | 5 | 11 | 7.30% | 945 | 108509 | 5.2 | U | | Translation: 4573..7410 (reverse), 946 amino acids | | | |
| * | _305.3923.3923.2 | 4.0296 | 0.3676 | 2134.05 | 2134.362 | 4649.6 | | 1 | 476.5 | 59.4 | 4 | K.ERDWWNIIQGQLNTGFR.S |
| * | _305.3934.3934.3 | 5.0415 | 0.4252 | 2135.85 | 2134.362 | 10138 | | 1 | 2092.5 | 46.9 | 3 | K.ERDWWNIIQGQLNTGFR.S |
| * | _307.2826.2826.2 | 3.3807 | 0.3338 | 2557.06 | 2555.712 | 8126.9 | | 1 | 470.1 | 34.8 | 2 | K.SVGLDSVSEFIENNSQTDVEVSAK.D |
| * | _302.2168.2168.2 | 2.9834 | 0.4674 | 1775.25 | 1775.907 | 7785.4 | | 1 | 805.3 | 57.1 | 1 | K.YNSLVEDETIYATEK.D |
| * | _203.2544.2546.2 | 2.9095 | 0.3163 | 1624.01 | 1623.67 | 8652.6 | | 1 | 909.5 | 58.3 | 1 | K.NYDSFDYLDDVEK.L |
| gi\|5000000155 | 1 | 2 | 7.30% | 287 | 33770 | 5.3 | U | | Translation: 137634..138497 (direct), 288 amino acids | | | |
| * | _304.4331.4331.2 | 2.802 | 0.3055 | 2402.73 | 2400.731 | 7235.3 | | 2 | 263.5 | 32.5 | 2 | R.SYLLSLTSDAFYIEDPILPNK.E |
| gi\|55981453\|ref\|Y | 2 | 7 | 7.30% | 137 | 15743 | 6.2 | U | | small heat shock protein, HSP20 family [Thermus thermophilus | | | |
| * | _306.2810.2810.1 | 2.3374 | 0.3421 | 1140.43 | 1141.405 | 3834.6 | | 3 | 316.1 | 66.7 | 2 | R.HGVLHLLVPR.A |
| * | _306.2805.2805.2 | 4.0323 | 0.5055 | 1140.97 | 1141.405 | 7579.5 | | 1 | 1910.2 | 94.4 | 5 | R.HGVLHLLVPR.A |
| gi\|5000000076 | 8 | 14 | 7.20% | 1744 | 200633 | 4.7 | U | | Translation: 69684..74918 (reverse), 1745 amino acids | | | |
| * | _204.2996.2996.2 | 2.6178 | 0.4101 | 1779.18 | 1779.849 | 10862 | | 1 | 820.8 | 50 | 1 | K.EGSEALEEISEELESK.E |
| * | _304.4023.4023.2 | 2.5362 | 0.2794 | 1787.33 | 1787.923 | 8015 | | 1 | 376.9 | 46.2 | 1 | K.EWEIESYLDSFVNR.F |
| * | _203.2575.2575.2 | 3.846 | 0.3604 | 1436.34 | 1436.558 | 6842 | | 1 | 1399 | 81.8 | 2 | K.EVAFEDLENLEK.T |
| * | _204.2479.2479.2 | 3.5744 | 0.2506 | 1243.56 | 1243.486 | 4115.2 | | 1 | 913.5 | 90 | 4 | K.IIGTLQLEDLK.K |
| * | _203.2379.2379.2 | 3.8706 | 0.5372 | 1856.42 | 1855.95 | 7369.4 | | 1 | 1018.7 | 59.4 | 1 | K.AVDEAFETISEATSQEK.L |
| * | _204.1876.1878.2 | 3.8566 | 0.2895 | 1259.61 | 1259.445 | 7381.7 | | 1 | 1223.2 | 85 | 1 | K.LLNSSIEQLNK.A |
| * | _304.4323.4325.2 | 4.9773 | 0.5622 | 2341.39 | 2341.622 | 6698.6 | | 1 | 1608.7 | 65.8 | 3 | K.VSPYFVSIDNAYAYLVDFEK.A |
| * | _305.4540.4542.2 | 2.8658 | 0.1724 | 2667.1 | 2668.954 | 9847.1 | | 1 | 600.7 | 37 | 1 | K.IVAVYDLSEEDLSSLIEGLDFPDK.I |
| gi\|55980011\|ref\|Y | 1 | 1 | 7.10% | 98 | 10978 | 10.8 | U | | 50S ribosomal protein L28 [Thermus thermophilus HB8] | | | |
| * | _103.1834.1834.1 | 1.9585 | 0.1359 | 907.31 | 908.042 | 5122.3 | | 1 | 523.9 | 83.3 | 1 | K.VYELVER.A |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| gi\|55981241\|ref\|Y | 2 | 4 | 6.90% | 478 | 53160 | 5.4 | U | | V-type ATP synthase subunit B [Thermus thermophilus HB8] | | | |
| * | _304.2496.2496.3 | 3.8008 | 0.3486 | 2050.46 | 2050.409 | 6824.3 | | 1 | 1003.9 | 40.3 | 1 | R.RFNGIGKPIDGLPPITPEK.R |
| * | _306.2737.2737.2 | 3.9533 | 0.3525 | 1517.38 | 1517.858 | 5016.7 | | 1 | 856.3 | 73.1 | 3 | K.RLPITGLPLNPVAR.R |
| gi\|55981649\|ref\|Y | 2 | 4 | 6.60% | 182 | 21030 | 9.7 | U | | 50S ribosomal protein L5 [Thermus thermophilus HB8] | | | |
| * | _303.4125.4125.2 | 3.6246 | 0.4151 | 1276.02 | 1276.564 | 5104.3 | | 1 | 1032.5 | 80 | 2 | R.ALLELLGFPFR.K |
| * | _306.3101.3101.2 | 3.3128 | 0.2679 | 1404.08 | 1404.739 | 5624.4 | | 3 | 646 | 63.6 | 2 | R.ALLELLGFPFRK.- |
| gi\|55981297\|ref\|Y | 2 | 3 | 6.50% | 552 | 59970 | 8.7 | U | | 5'-nucleotidase precursor [Thermus thermophilus HB8] | | | |
| * | _304.4327.4327.2 | 3.5218 | 0.583 | 2480.42 | 2479.754 | 10477 | | 1 | 825.3 | 45 | 1 | K.NPLFLDAGDVFQGTLYFNQYR.G |
| * | _304.2852.2854.2 | 3.3025 | 0.3321 | 1535.43 | 1534.798 | 4402.5 | | 1 | 878.2 | 78.6 | 2 | K.GLFAPYAVVVVGGER.V |
| gi\|55981434\|ref\|Y | 1 | 1 | 6.40% | 140 | 15895 | 10.2 | U | | 50S ribosomal protein L13 [Thermus thermophilus HB8] | | | |
| * | _106.2668.2668.1 | 2.4221 | 0.3367 | 1030.56 | 1031.197 | 8035.5 | | 1 | 826.4 | 75 | 1 | R.WVLIDAEGK.T |
| gi\|55980240\|ref\|Y | 3 | 9 | 6.30% | 543 | 57889 | 5.2 | U | | 60 kDa chaperonin (Protein Cpn60) (GroEL protein) [Thermus th | | | |
| * | _305.2390.2390.3 | 3.9202 | 0.322 | 1330.4 | 1330.446 | 5658.2 | | 1 | 2016 | 72.5 | 3 | K.HRFEDALNATR.A |
| * | _304.2395.2395.2 | 3.6976 | 0.2493 | 1331.78 | 1330.446 | 4724.9 | | 1 | 931.8 | 85 | 4 | K.HRFEDALNATR.A |
| * | _303.4001.4001.2 | 4.3496 | 0.599 | 2402.92 | 2402.681 | 8419.4 | | 1 | 980.4 | 45.5 | 2 | R.YGFNAATGEFVDMVEAGIVDPAK.V |
| gi\|55981140\|ref\|Y | 1 | 1 | 6.30% | 254 | 28308 | 9 | U | | amino acid ABC transporter, periplasmic amino acid-binding pro | | | |
| * | _304.2751.2751.2 | 2.6311 | 0.3427 | 1905.86 | 1904.173 | 4976.8 | | 2 | 356.8 | 53.3 | 1 | R.KLENTLQVGELVFQER.V |
| gi\|5000000150 | 2 | 6 | 6.20% | 631 | 71505 | 5.3 | U | | Translation: 129964..131859 (direct), 632 amino acids | | | |
| * | _302.2795.2795.2 | 4.7795 | 0.5557 | 1945.35 | 1945.133 | 6281 | | 1 | 1494.1 | 75 | 4 | R.FSDLSSLNEENTSFLLK.L |
| * | _302.2918.2918.2 | 4.2742 | 0.516 | 2444.06 | 2445.688 | 7522.1 | | 1 | 867.7 | 45.2 | 2 | K.ENIPILYVNGTPQFSSDFSTSK.D |
| gi\|55981871\|ref\|Y | 2 | 3 | 6.20% | 520 | 59169 | 6.2 | U | | hypothetical protein TTHA1902 [Thermus thermophilus HB8] | | | |
| * | _302.3099.3099.2 | 4.3929 | 0.4563 | 2516.02 | 2517.714 | 8341.2 | | 1 | 990.5 | 47.6 | 2 | R.NPETTLQVWSADYGYPGEGLYR.E |
| * | _306.2559.2559.2 | 2.979 | 0.3703 | 1218.28 | 1218.36 | 3940.6 | | 1 | 620.2 | 88.9 | 1 | K.DPLSGLHHWR.V |
| gi\|5000000164 | 1 | 3 | 6.20% | 209 | 23532 | 4.9 | U | | Translation: 147677..148306 (direct), 210 amino acids | | | |
| * | _204.2563.2563.2 | 3.3674 | 0.418 | 1428.12 | 1428.627 | 6172.7 | | 1 | 1203 | 75 | 3 | K.FVFVGDSFTSPPK.I |
| gi\|5000000075 | 6 | 13 | 5.60% | 1525 | 176943 | 5 | U | | Translation: 65085..69662 (reverse), 1526 amino acids | | | |
| * | _306.2610.2610.2 | 2.8239 | 0.3209 | 1345.43 | 1345.587 | 5817.9 | | 1 | 482.4 | 65 | 3 | K.RVPEGFVLYHK.D |
| * | _205.2892.2892.2 | 3.8147 | 0.3167 | 2247.76 | 2248.454 | 4579.7 | | 1 | 672.8 | 58.3 | 2 | K.NGVIVNQPDSNWILEEYEK.Y |
| * | _207.2946.2946.2 | 2.6971 | 0.3743 | 1416.43 | 1416.571 | 9070.7 | | 1 | 783.4 | 57.7 | 1 | R.NVASDLADLLADAK.A |
| * | _304.4127.4127.2 | 4.2785 | 0.3237 | 1392.4 | 1390.666 | 8008.2 | | 1 | 1616.9 | 81.8 | 3 | K.FVVDIINTLLSR.Y |
| * | _306.3109.3109.2 | 5.5072 | 0.6053 | 2258 | 2259.61 | 7328.2 | | 1 | 1711.5 | 62.5 | 3 | R.IAAANLLTHLANPSTLAEYFK.I |
| * | _305.2540.2540.2 | 3.043 | 0.2851 | 1095.78 | 1095.289 | 5486.9 | | 1 | 556.4 | 81.2 | 1 | K.RFPAFLTSR.Y |
| gi\|55980750\|ref\|Y | 1 | 1 | 5.40% | 426 | 45694 | 6.3 | U | | dihydroorotase (PyrC) [Thermus thermophilus HB8] | | | |
| * | _306.2779.2779.3 | 4.5614 | 0.414 | 2483.5 | 2484.818 | 10443 | | 1 | 1736.1 | 37.5 | 1 | K.RAGLPVTAEATPHHLTLTEEALR.T |
| gi\|55981305\|ref\|Y | 1 | 2 | 5.00% | 501 | 56774 | 9.6 | U | | peptide ABC transporter oligopeptide-binding protein [Thermus t | | | |
| * | _306.2917.2917.3 | 5.7823 | 0.5152 | 2672.43 | 2673.047 | 5539 | | 1 | 1106.8 | 37.5 | 2 | K.NPFAPILAHLTHSSTAIQSPTAIQR.L |
| gi\|55981905\|ref\|Y | 1 | 1 | 5.00% | 398 | 44132 | 9.4 | U | | glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-ph | | | |
| * | _304.4566.4566.2 | 2.5671 | 0.315 | 2349.81 | 2348.706 | 8886.5 | | 1 | 328.1 | 34.2 | 1 | R.FGLPFNTSTPVLFYNLDVFR.A |
| gi\|5000000151 | 2 | 6 | 4.40% | 796 | 89275 | 4.8 | U | | Translation: 131870..134260 (direct), 797 amino acids | | | |
| * | _204.2860.2860.2 | 2.6266 | 0.3497 | 1426.08 | 1424.596 | 8359 | | 1 | 919.5 | 63.6 | 1 | K.SNDIAEVFIPYR.Y |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| * | _304.4005.4005.2 | 4.7868 | 0.4878 | 2542.65 | 2543.876 | 5574 | | 1 | 794.7 | 47.7 | 5 | K.VFSPISIDLSDPSNIQVYFSSVK.S |
| gi\|5000000069 | 1 | 2 | 4.20% | 236 | 27414 | 5.1 | U | Translation: 59782..60492 (reverse), 237 amino acids | | | | |
| * | _303.2439.2439.2 | 3.2387 | 0.2654 | 1203.1 | 1202.399 | 5844 | | 1 | 726.3 | 77.8 | 2 | K.RGIPDFVIER.Y |
| gi\|55981182\|ref\| | 1 | 2 | 3.90% | 562 | 60981 | 6.7 | U | acetolactate synthase, large subunit [Thermus thermophilus HB | | | | |
| * | _302.2927.2927.2 | 3.2125 | 0.315 | 2281.68 | 2279.61 | 10187 | | 1 | 1350.6 | 50 | 2 | R.ALIGTDAFQEADVTGVTMPITK.H |
| gi\|5000000141 | 3 | 3 | 3.80% | 1014 | 111507 | 9.2 | U | Translation: 120953..123997 (reverse), 1015 amino acids | | | | |
| * | _303.4328.4328.3 | 3.8008 | 0.351 | 2337.6 | 2337.592 | 7309.7 | | 1 | 1429 | 44.7 | 1 | R.NTQQLIETLQQLEYSVSSVR.R |
| * | _303.4340.4341.2 | 5.8502 | 0.5257 | 2337.61 | 2337.592 | 9742.4 | | 1 | 2210.4 | 65.8 | 1 | R.NTQQLIETLQQLEYSVSSVR.R |
| * | _303.2335.2335.2 | 2.6927 | 0.419 | 2091.32 | 2089.269 | 4339.3 | | 1 | 191.3 | 38.9 | 1 | R.VFPANQGFTTEEYLGTSAR.L |
| gi\|55981843\|ref\| | 2 | 4 | 3.80% | 954 | 100494 | 5.4 | U | hypothetical protein TTHA1874 [Thermus thermophilus HB8] | | | | |
| * | _103.2034.2034.2 | 3.4953 | 0.3685 | 1709.48 | 1709.894 | 3636 | | 1 | 382.2 | 56.7 | 1 | K.TLTNLEPGSYTVQASK.T |
| * | _107.2703.2703.2 | 4.9846 | 0.4416 | 2008.88 | 2009.351 | 4787.6 | | 1 | 968.7 | 60.5 | 3 | K.TTTVVLNLLPVPAASPTEGK.V |
| gi\|55981621\|ref\| | 1 | 1 | 3.80% | 398 | 43092 | 9.3 | U | maltose ABC transporter, periplasmic maltose-binding protein [T | | | | |
| * | _206.2695.2695.2 | 2.6197 | 0.2558 | 1514.32 | 1514.764 | 4941 | | 6 | 333.5 | 46.4 | 1 | K.VDFGIAPFPTPPGAK.N |
| gi\|5000000152 | 1 | 1 | 3.30% | 703 | 81102 | 5 | U | Translation: 134253..136364 (direct), 704 amino acids | | | | |
| * | _303.3537.3537.2 | 3.476 | 0.4235 | 2598.08 | 2599.813 | 7054.6 | | 1 | 537.3 | 38.6 | 1 | K.SYSGALETINNISLAEFYETYGR.E |
| gi\|55980058\|ref\| | 1 | 1 | 3.20% | 438 | 48632 | 7.5 | U | NADH-quinone oxidoreductase chain 1 [Thermus thermophilus | | | | |
| * | _305.2560.2560.2 | 3.0251 | 0.3917 | 1626.03 | 1624.898 | 4588.1 | | 1 | 379.2 | 57.7 | 1 | K.RPGVYELPMGTTFR.E |
| gi\|55981869\|ref\| | 2 | 3 | 3.20% | 281 | 31735 | 6.4 | U | NH(3)-dependent NAD(+) synthetase [Thermus thermophilus H | | | | |
| * | _306.2611.2611.1 | 2.1163 | 0.1507 | 1089.21 | 1090.316 | 4881.8 | | 1 | 319.2 | 62.5 | 1 | R.VHALFLPHR.E |
| * | _306.2609.2609.2 | 3.3711 | 0.2665 | 1090.68 | 1090.316 | 5109.4 | | 1 | 1249.7 | 93.8 | 2 | R.VHALFLPHR.E |
| gi\|5000000080 | 1 | 3 | 2.90% | 650 | 75157 | 5.1 | U | Translation: 80788..82740 (reverse), 651 amino acids | | | | |
| * | _304.4034.4034.2 | 4.1658 | 0.4803 | 2187.46 | 2187.466 | 5025.1 | | 1 | 984.8 | 61.1 | 3 | R.GNSYLDFCPSLPSVLIFTR.D |
| gi\|5000000057 | 1 | 2 | 2.90% | 616 | 69898 | 5 | U | Translation: 47564..49414 (direct), 617 amino acids | | | | |
| * | _303.3368.3371.2 | 4.6717 | 0.3464 | 1874.05 | 1875.216 | 5758.6 | | 1 | 786.2 | 55.9 | 2 | R.SLGTINSFTPLEAAVILK.F |
| gi\|55981242\|ref\| | 1 | 2 | 2.90% | 578 | 63632 | 5.2 | U | V-type ATP synthase subunit A [Thermus thermophilus HB8] | | | | |
| * | _104.1654.1654.2 | 2.8444 | 0.3217 | 1737.11 | 1738.185 | 8325.7 | | 1 | 829.2 | 50 | 2 | -.MIQGVIQKIAGPAVIAK.G |
| gi\|55981141\|ref\| | 1 | 1 | 2.80% | 819 | 91993 | 6.5 | U | alpha-glucan phosphorylase [Thermus thermophilus HB8] | | | | |
| * | _305.3747.3747.2 | 3.1221 | 0.4079 | 2486.36 | 2486.853 | 7683.8 | | 1 | 653.7 | 40.9 | 1 | R.ALGLAPAFFHMNEGHSAFLGLER.L |
| gi\|55980077\|ref\| | 1 | 1 | 2.80% | 651 | 71879 | 6.6 | U | transketolase [Thermus thermophilus HB8] | | | | |
| * | _302.3152.3152.2 | 3.1485 | 0.4175 | 1935.88 | 1934.153 | 6440 | | 1 | 741.2 | 50 | 1 | R.ISIDGPTDLAFTEDVLAR.Y |
| gi\|55980202\|ref\| | 1 | 1 | 2.80% | 464 | 49084 | 6.9 | U | pyruvate dehydrogenase complex, dihydrolipoamide dehydroge | | | | |
| * | _306.2682.2682.2 | 2.9741 | 0.3071 | 1454.49 | 1454.715 | 6750.5 | | 1 | 739.1 | 70.8 | 1 | K.ALLHAAETLHHLK.V |
| gi\|5000000149 | 1 | 6 | 2.60% | 662 | 75908 | 5.3 | U | Translation: 127979..129967 (direct), 663 amino acids | | | | |
| * | _304.4463.4463.2 | 4.861 | 0.5656 | 2031.14 | 2032.343 | 7491 | | 1 | 1542.6 | 68.8 | 6 | R.IAIPIFDLDEVYANYFK.I |
| gi\|55980044\|ref\| | 1 | 2 | 0.70% | 2202 | 243290 | 7.7 | U | ribonucleoside-diphosphate reductase [Thermus thermophilus H | | | | |
| * | _306.2701.2701.2 | 3.6353 | 0.3914 | 1756.34 | 1757.005 | 8103.3 | | 1 | 1170.2 | 64.3 | 2 | R.VFLSAHDIHPLDHVR.M |